Supplementary Tables

Supplementary Table 1 Differentially expressed lncRNAs in 3 hepatoma cell lines

Expression level	ID	LncRNAs-probe name	Chromosome	LncRNA -start	LncRNA -end	Strand	LncRNA_source	Fold change
Up	NR_027992.1	pl115790	chr15	20961259	20961480	-	Other_database	3.467231077
	BX647894	pl115715	chr2	122348461	122355452	-	NCBI	2.984218861
	AK094334	pl115506	chr3	15021445	15023109	+	NCBI	7.167243077
	gnl|ncrnascan|RNS2056	pl115470	chr22	48236295	48236457	-	ncRNASCAN	3.092574542
	AK021665	pl114899	chr3	171942518	171944095	+	NCBI	5.387402761
	HMlincRNA325	pl114815	chr14	60649741	60650565	+	array-star	3.490202655
	NR_027783.1	pl114479	chrX	23803803	23804327	+	Other_database	4.239416154
	uc002ued	pl114404	chr2	169628463	169642936	-	UCSC	2.501752261
	NR_024380	pl114290	chr10	42827313	42863493	-	NCBI	11.20414003
	AK129996	pl114178	chr1	56995797	56997409	-	NCBI	3.834113009
	ENST00000417409	pl113937	chr1	190449509	190463427	+	Ensembl	3.37523063
	HMlincRNA1014	pl113780	chr4	152243990	152244383	+	array-star	2.754496186
	ENST00000440744	pl113433	chr7	135710509	135769416	+	Ensembl	43.88523421
		pl113290	chr3	88108419	88178191	-	Agilent	2.889167766
	uc001bfh	pl113075	chr1	22147942	22149041	+	UCSC	2.779130974
	AK130290	pl113056	chr20	3461004	3464537	+	NCBI	5.121712165
		pl112918	chr11	38083599	38261799	-	Agilent	6.30562943
	HMlincRNA565	pl112638	chr8	141669167	142011332	+	array-star	2.638528998
	NR_028045.1	pl112513	chr12	10741077	10742144	-	Other_database	5.824997828
	AK024373	pl112373	chr19	438420	2083745	-	NCBI	2.863118048
	AK130406	pl112125	chr3	15461392	15504863	-	NCBI	3.715732996

gnl|UG|Hs#S15910783	pl112017	chr10	18831567	18832076	+	Other_database	5.117809923
	pl111837	chr13	104132524	104237799	-	Agilent	3.421187769
gnl|UG|Hs#S3539368	pl111818	chr21	33676982	33677208	+	Other_database	2.19228363
	pl111777	chr10	17765994	17773319	+	Agilent	2.852506895
ENST00000556016	pl111611	chr14	85669193	85705818	-	Ensembl	2.559476208
gnl|UG|Hs#S29439920	pl111092	chr5	12844948	12845161	+	Other_database	9.019291678
NR_027245	pl110699	chr18	61747242	61816260	-	NCBI	2.578337402
AK129947	pl110494	chr14	31180268	31183566	+	NCBI	4.033407989
	pl110114	chr11	38083599	38261799	-	Agilent	3.064220247
ENST00000435237	pl109867	chr2	21444047	22193831	+	Ensembl	2.47384515
HMlincRNA216	pl109623	chr12	69616287	69618022	+	array-star	2.782007548
	pl109587	chr11	38083599	38261799	-	Agilent	2.892693923
uc001gch	pl109571	chr1	162751900	162756362	+	UCSC	36.78393951
AL050355	pl109416	chr3	125165500	125187695	+	NCBI	24.76226595
uc001emi	pl109349	chr1	145004780	145005285	+	UCSC	5.270280392
AK300325	pl109311	chr15	94774766	94901835	+	array-star	2.506991105
	pl109302	chr8	103953859	103990104	+	Agilent	8.390181195
gnl|UG|Hs#S29653495	pl109175	chr21	10474636	10474772	-	Other_database	8.548445966
	pl109159	chr16	22410637	22418757	-	Agilent	2.625715946
AK097339	pl109072	chr22	38339056	38340905	+	NCBI	2.965745331
NR_033678.1	pl109006	chr19	48711344	48713550	-	Other_database	4.651972525
gnl|UG|Hs#S1645670	pl108996	chr6	16738181	16738445	-	Other_database	4.079224617
uc002snu	pl108978	chr2	78245158	78517815	-	UCSC	3.025147946
uc002snu	pl108833	chr2	78245158	78517815	-	UCSC	2.492364248
HMlincRNA1447	pl108587	chr12	57008566	57030137	+	array-star	2.443451777
gnl|ncrnascan|RNS1314	pl108302	chr19	436805	436994	-	ncRNASCAN	2.685643501

gnl|UG|Hs#S48816529	pl107951	chr5	95267227	95267333	+	Other_database	3.487005268
	pl107850	chr9	4869500	4896050	+	Agilent	3.520860475
NR_024042	pl107503	chr11	76391209	76432833	-	NCBI	2.882403501
BC036877	pl107263	chr1	14925212	15441219	-	NCBI	19.44527512
	pl107022	chr7	116032764	116048889	-	Agilent	3.068799279
NR_037877.1	pl106978	chr4	22328977	22329512	-	Other_database	17.65338471
HMlincRNA1147	pl106749	chr1	31849969	31850331	+	array-star	3.039911656
AK025015	pl106713	chr8	99202060	99204410	-	NCBI	127.4264668
AK025161	pl106574	chr6	16429674	16431507	-	NCBI	7.993040265
AK021554	pl106297	chr12	116598576	116600425	-	NCBI	5.19459967
AL133101	pl106110	chr6	118781941	118784634	-	NCBI	3.459876559
BC064139	pl106072	chr1	85618179	85619886	-	NCBI	11.91117606
uc001dbm	pl105897	chr1	64645310	64647177	+	UCSC	18.73761816
uc003fhx	pl105808	chr3	171757417	171905078	+	UCSC	3.166305953
	pl105702	chr11	38083599	38261799	-	Agilent	10.8992838
uc003ksb	pl105371	chr5	118332006	118373361	-	UCSC	2.145679346
NR_034060.1	pl105250	chr19	21125607	21126783	+	Other_database	14.40107672
uc001xbf	pl105112	chr14	55154714	55201855	+	UCSC	2.36601853
	pl105104	chr1	118374652	118400852	-	Agilent	2.565984447
uc003gai	pl105086	chr4	492988	516627	+	UCSC	5.313769382
ENST00000513051	pl105080	chr5	12574969	12759760	+	Ensembl	14.32791659
BQ329856	pl104753	chr8	59355920	59560809	+	array-star	4.747171586
AK023517	pl104632	chr1	243646129	243648345	+	NCBI	2.716537671
uc004atm	pl104520	chr9	96198893	96213846	-	UCSC	3.419181396
NR_037859.2	pl104368	chrX	15363713	15364381	-	Other_database	7.37420425
ENST00000430140	pl103456	chrX	107137827	107179210	-	Ensembl	5.953896082

HMlincRNA1349	pl103171	chr12	19556999	19672289	+	array-star	2.496546289
uc002snu	pl102762	chr2	78245158	78517815	-	UCSC	3.670026827
BE064019	pl102619	chr10	72059475	72391429	+	array-star	2.317304179
NR_024380	pl102601	chr10	42827313	42863493	-	NCBI	5.097657941
AK130682	pl102522	chr22	37967920	37977411	+	NCBI	8.912594768
gnl|ncrnascan|RNS1808	pl101461	chr20	17615208	17615395	-	ncRNASCAN	3.306319287
AK130888	pl101098	chr4	52731302	52735289	+	NCBI	3.12254736
ENST00000499475	pl101051	chr19	48758932	48761452	+	Ensembl	8.311185798
uc003ezg	pl101015	chr3	151985828	152020238	+	UCSC	5.701974769
uc003fhx	pl100926	chr3	171757417	171905078	+	UCSC	9.870489271
ENST00000438810	pl100296	chr22	48081990	48086596	+	Ensembl	5.043366085
BC040326	pl100169	chr12	90102735	90105445	+	NCBI	2.729296917
uc001ssy	pl100136	chr12	66232298	66251296	+	UCSC	6.924258014
gnl|UG|Hs#S48817022	pl099742	chr2	173958088	173958307	+	Other_database	3.335361623
AK129547	pl099270	chr6	16394151	16396501	-	NCBI	6.630765888
uc002cvu	pl099189	chr16	3710742	3715456	+	UCSC	3.999522763
AK027270	pl098844	chr2	136686257	136687847	-	NCBI	2.143652981
	pl098426	chr4	15657202	15695627	-	Agilent	5.136144459
exon2407	pl098205	chr20	31164464	31164598	+	array-star	5.056014005
AK129947	pl097910	chr14	31180268	31183566	+	NCBI	4.322812664
AK096504	pl097762	chr8	8640866	8643120	-	NCBI	2.993782539
ENST00000518181	pl097439	chr8	35861834	35952564	-	Ensembl	2.169836422
uc002lkh	pl097311	chr18	66382490	66422236	+	UCSC	12.33586954
	pl097222	chr11	38083599	38261799	-	Agilent	5.975156637
uc002vlk	pl095981	chr2	220253217	220268355	+	UCSC	3.918471694
uc003ppy	pl095778	chr6	99910340	99958106	-	UCSC	3.353885702

uc001uoi	pl095573	chr13	22615113	22850657	+	UCSC	3.032813806
	pl094862	chr22	18404600	18411525	-	Agilent	3.612130081
AK001092	pl094303	chr1	57031107	57036506	-	NCBI	3.630913721
gnl|UG|Hs#S32193504	pl093899	chr5	83236416	83236934	-	Other_database	62.75720692
NR_045562.1	pl093750	chr2	189458667	189460202	+	Other_database	12.20529076
ENST00000502335	pl093664	chr18	36787591	36920602	-	Ensembl	2.75915197
ENST00000542763	pl093637	chr12	132341965	132348596	+	Ensembl	3.108508454
	pl093276	chr1	89749037	89787237	-	Agilent	37.77951923
ENST00000557544	pl093195	chr14	62147759	62162541	-	Ensembl	7.367295969
HMlincRNA1014	pl092932	chr4	152243990	152244383	+	array-star	2.50115334
uc001tvl	pl092630	chr12	114188832	114211488	-	UCSC	9.859238132
gnl|UG|Hs#S16509641	pl092514	chr6	53510481	53510842	-	Other_database	4.035070864
ENST00000445461	pl092290	chr21	17566788	17979542	+	Ensembl	4.436915992
AK125562	pl092220	chr9	104338475	104340640	+	NCBI	5.643953393
DN914976	pl092179	chrX	6894606	6895134	+	array-star	7.66527442
AK130335	pl091931	chr7	73023591	73025832	-	NCBI	2.709860015
ENST00000445461	pl091756	chr21	17566788	17979542	+	Ensembl	4.734158825
uc002snu	pl091153	chr2	78245158	78517815	-	UCSC	5.130997908
gnl|ncrnascan|RNS1506	pl091093	chr20	4954276	4954468	-	ncRNASCAN	2.644869245
uc001omv	pl091036	chr11	67653966	67658816	+	UCSC	3.634483886
uc002vje	pl091015	chr2	219765535	219795358	-	UCSC	2.82561826
HMlincRNA622	pl090991	chr3	186164014	186164368	+	array-star	2.602352907
NR_023353	pl090936	chr3	45017740	45054158	+	NCBI	6.466875974
HMlincRNA565	pl090557	chr8	141669167	142011332	+	array-star	3.936929726
uc010jvv	pl090211	chr6	35378763	35391925	+	UCSC	3.095245118
gnl|UG|Hs#S681551	pl090173	chr2	55886659	55886909	+	Other_database	3.963514223

AX747026	pl090162	chr1	235427538	235430537	-	Other_database	2.73752842
	pl089372	chr11	38083599	38261799	-	Agilent	21.20720931
uc002snu	pl089354	chr2	78245158	78517815	-	UCSC	7.768666565
AK126190	pl089142	chr8	17073714	17076761	+	NCBI	8.277509596
	pl088960	chr11	38083599	38261799	-	Agilent	3.171367767
gnl|UG|Hs#S4403094	pl088312	chr3	194197528	194197661	-	Other_database	2.523879521
AF086110	pl088179	chr2	160570686	160571432	+	NCBI	5.113574692
DN918054	pl088099	chr1	66890612	67423817	+	array-star	3.551701387
	pl087776	chr6	64248003	64248516	+	Agilent	5.691802596
NR_026737.1	pl087760	chr6	10687199	10687397	-	Other_database	15.21988389
ENST00000513051	pl087743	chr5	12574969	12759760	+	Ensembl	2.753916944
NR_024597.1	pl087359	chr11	86056626	86056985	+	Other_database	4.142944653
DR731346	pl087261	chr18	44190740	44236937	+	array-star	58.58411659
gnl|UG|Hs#S29653495	pl087140	chr9	45950338	45950774	+	Other_database	8.936255014
AK092571	pl086824	chr12	28732271	28734444	+	NCBI	10.48734941
BX649024	pl086556	chr2	114519999	114524481	+	NCBI	3.374623677
NR_027716.1	pl085809	chr12	14930574	14930936	+	Other_database	2.594112253
uc003fhx	pl085803	chr3	171757417	171905078	+	UCSC	4.207076144
HMlincRNA880	pl085304	chr11	57060753	57061272	+	array-star	9.023639258
ENST00000498993	pl085247	chr19	9732193	9745538	+	Ensembl	5.779015108
AF085919	pl085104	chr12	133441390	133441902	-	NCBI	9.983363334
uc003hlm	pl085058	chr4	79808285	79860582	-	UCSC	2.889562053
ENST00000501726	pl084582	chr15	57592563	57599959	+	Ensembl	2.47622697
	pl084566	chr5	10160975	10213797	-	Agilent	2.693225428
uc003fhx	pl084511	chr3	171757417	171905078	+	UCSC	4.125501662
	pl084413	chr3	42056396	42105521	+	Agilent	2.751777989

AM392777	pl084237	chr2	200990424	201342751	+	array-star	3.167387125
ENST00000426575	pl083890	chr1	175873898	175889649	-	Ensembl	4.422227779
NR_034138.1	pl083603	chr4	66535679	66536391	+	Other_database	32.10062166
uc002wif	pl083584	chr20	3190134	3204506	+	UCSC	3.198327514
AF116701	pl083549	chr9	138716694	138798984	+	NCBI	3.314517311
ENST00000556923	pl083477	chr14	48236803	48259146	-	Ensembl	3.438565739
AW135489	pl082587	chr2	192787269	192895368	+	array-star	31.30873551
	pl082240	chr18	36928543	37115790	+	Agilent	3.647230133
AK128416	pl082079	chr8	12306532	12312147	+	NCBI	4.844841352
ENST00000424926	pl081933	chr13	85937736	86118705	+	Ensembl	3.126519382
AK096239	pl081866	chr12	50691303	50699144	+	NCBI	2.467910169
uc010grs	pl081585	chr22	19538881	19554330	-	UCSC	2.512650784
	pl081047	chr3	42056396	42105521	+	Agilent	3.715928541
gnl|UG|Hs#S952583	pl080815	chrUn_gl000223	92169	92604	+	Other_database	4.212884916
HMlincRNA787	pl080446	chr18	56529831	56653197	+	array-star	3.01810521
HMlincRNA565	pl080415	chr8	141669167	142011332	+	array-star	8.22340607
uc003ppy	pl080196	chr6	99910340	99958106	-	UCSC	4.671748227
uc002oyx	pl080110	chr19	44732356	44807605	-	UCSC	7.760876731
ENST00000437979	pl079515	chr2	38685779	38690256	-	Ensembl	3.053991778
BC094870	pl078957	chr7	156811521	156813191	+	NCBI	9.915280764
AK125443	pl078643	chr1	113669608	113674881	+	NCBI	2.441542667
ENST00000522265	pl078332	chr8	64326191	64382757	-	Ensembl	5.674401187
uc009zhq	pl077839	chr12	11000963	11002075	-	UCSC	15.70350992
uc010hdm	pl077584	chr3	10327437	10334601	+	UCSC	3.110743387
uc001uxo	pl077361	chr13	41371126	41382169	-	UCSC	10.45865296
uc002snu	pl077105	chr2	78245158	78517815	-	UCSC	3.16519784

	pl076974	chr11	38083599	38261799	-	Agilent	11.34576708
ENST00000499171	pl076954	chr19	19945686	20008579	-	Ensembl	3.369331644
NR_034138.1	pl076850	chr4	66535679	66536391	+	Other_database	29.70235828
AY927591	pl076495	chr7	155494809	155495975	-	NCBI	2.610357233
uc001rgr	pl076435	chr12	25386768	25403863	-	UCSC	4.851856626
uc003wfy	pl076314	chr7	149244251	149321818	-	UCSC	2.713977083
NR_023358	pl076250	chrX	20154183	20154531	-	NCBI	3.250429567
uc001rgr	pl076150	chr12	25386768	25403863	-	UCSC	3.217461028
BX648454	pl076148	chr12	132241768	132244346	+	NCBI	2.4555841
AK022789	pl075592	chr8	80951666	80954017	-	NCBI	2.970073584
AK098142	pl075520	chr11	106555150	106557515	-	NCBI	55.65269242
AL117552	pl075437	chr7	65838365	65917175	-	NCBI	2.783034254
	pl075097	chr10	124021160	124029935	+	Agilent	4.041975895
uc003gid	pl075039	chr4	4543930	4712662	+	UCSC	2.402607836
	pl074656	chr8	138331518	138433693	-	Agilent	2.822640242
	pl073862	chr15	77786745	77868170	+	Agilent	3.504897119
uc002gsn	pl073751	chr17	18079871	18088067	-	UCSC	85.90349119
uc001ulk	pl073505	chr12	133518709	133532592	-	UCSC	2.672927979
uc010fgg	pl073450	chr2	85581935	85614348	+	UCSC	2.441108352
uc003fhx	pl072717	chr3	171757417	171905078	+	UCSC	4.607679435
AF070579	pl072680	chr3	179058109	179059674	+	NCBI	2.566124048
gnl|UG|Hs#S1691475	pl071102	chr22	36781206	36781460	+	Other_database	6.85344466
ENST00000441820	pl070304	chr21	17909601	17979569	+	Ensembl	2.604278207
ENST00000444750	pl070173	chr1	212341549	212363601	+	Ensembl	6.657896871
AK024925	pl069468	chr1	144989308	144991365	+	NCBI	3.625835389
uc001vks	pl068702	chr13	78493823	79158296	+	UCSC	2.387346049

uc004atm	pl068674	chr9	96198893	96213846	-	UCSC	2.250031806
HMlincRNA544	pl067649	chr8	121072018	121244326	+	array-star	4.437223883
HMlincRNA565	pl067041	chr8	141669167	142011332	+	array-star	2.102726358
uc002snu	pl067033	chr2	78245158	78517815	-	UCSC	2.478630373
uc003fhx	pl066475	chr3	171757417	171905078	+	UCSC	4.198704159
ENST00000513051	pl066269	chr5	12574969	12759760	+	Ensembl	4.170243767
ENST00000397645	pl064425	chr3	193675161	193721448	-	Ensembl	5.420323614
BI089392	pl063549	chr12	85736249	86096782	+	array-star	3.68097967
NR_027346	pl063530	chr12	116971239	116974317	+	NCBI	15.34583426
NR_003698	pl063478	chr2	96676298	96688884	+	NCBI	3.919730994
AK024588	pl063339	chr6	119498376	119499616	-	NCBI	3515.394012
uc003fxp	pl062924	chr3	196805333	197024986	-	UCSC	4.945146921
AL137436	pl062900	chr15	42188136	42189031	-	NCBI	4.875811434
AF086278	pl062401	chr2	144695639	144696173	-	NCBI	13.75592954
BC047512	pl062369	chr20	10268654	10271295	+	NCBI	4.827213274
gnl|UG|Hs#S4295867	pl062186	chr9	45950144	45950879	-	Other_database	6.705628537
AF147346	pl061518	chr6	157408664	157408937	+	NCBI	2.859513292
uc001pen	pl061348	chr11	93800139	93862566	-	UCSC	10.15884336
uc003fhx	pl061285	chr3	171757417	171905078	+	UCSC	2.511151328
NR_027791.1	pl061116	chr21	17981807	17982094	+	Other_database	13.79729391
AK129547	pl060672	chr6	16394151	16396501	-	NCBI	5.367756876
gnl|UG|Hs#S120668	pl059982	chr7	149972776	149973074	-	Other_database	5.41570053
uc003fhx	pl059977	chr3	171757417	171905078	+	UCSC	2.906782158
uc004cyt	pl059793	chrX	18908413	18913090	+	UCSC	3.156547043
gnl|UG|Hs#S48809995	pl058930	chr3	171873592	171873787	+	Other_database	3.120821546
AF085930	pl058906	chr14	90346918	90347521	-	NCBI	3.808731945

AK091159	pl058607	chr14	103110367	103113470	+	NCBI	2.281908225
ENST00000529088	pl058600	chr11	97093644	97130987	-	Ensembl	2.588646588
AK021674	pl058551	chr1	61718873	61720825	+	NCBI	4.117902133
AW104394	pl058454	chr1	192943284	192943684	+	array-star	8.686245097
AK098256	pl057996	chr5	76435073	76444348	+	NCBI	5.440822771
	pl057761	chr4	8357101	8357609	-	Agilent	5.263600581
	pl057456	chr11	38083599	38261799	-	Agilent	10.85233984
uc003fhx	pl057362	chr3	171757417	171905078	+	UCSC	9.990526431
	pl056924	chr12	79939394	79966869	-	Agilent	2.297995082
ENST00000446720	pl056557	chr5	135802366	135855987	+	Ensembl	174.0946235
uc003fhx	pl056548	chr3	171757417	171905078	+	UCSC	3.549999314
ENST00000414603	pl056054	chr3	6532490	6599646	+	Ensembl	5.211966465
AK024373	pl056015	chr19	438420	2083745	-	NCBI	2.226979791
	pl055365	chr3	182651981	182660175	-	Agilent	4.333099538
BQ638647	pl055351	chr13	45258810	45289952	+	array-star	2.25695439
AK092571	pl054994	chr12	28732271	28734444	+	NCBI	5.219939985
uc010jvv	pl054693	chr6	35378763	35391925	+	UCSC	5.467271697
AF086137	pl054510	chr2	220233340	220233999	-	NCBI	6.446752428
	pl054446	chr11	38083599	38261799	-	Agilent	10.26534195
uc003fhx	pl054268	chr3	171757417	171905078	+	UCSC	8.881223029
HMlincRNA1339	pl054245	chr12	5454390	5454785	+	array-star	22.06562993
BC018659	pl053937	chr2	75751193	75769832	+	NCBI	2.754743241
AK024898	pl053836	chr9	19453374	19455169	+	NCBI	3.285054449
uc003gai	pl053534	chr4	492988	516627	+	UCSC	2.743710998
uc009yuu	pl053476	chr11	77300435	77320693	+	UCSC	2.450914475
uc003fhx	pl053293	chr3	171757417	171905078	+	UCSC	2.726243819

uc002oyx	pl053140	chr19	44732356	44807605	-	UCSC	3.855585465
uc001aue	pl053131	chr1	12640550	12656106	-	UCSC	3.006330034
uc001bpk	pl052445	chr1	28314993	28415131	-	UCSC	3.433212344
AL161979	pl052396	chr16	50700121	50705489	+	NCBI	5.837508129
	pl052371	chr2	184032455	184084780	+	Agilent	2.538121786
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HMlincRNA122	pl052287	chr1	160968449	161008784	+	array-star	3.112633855
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	pl051512	chr11	38083599	38261799	-	Agilent	4.333784901
uc003kun	pl050381	chr5	127276134	127418766	-	UCSC	2.58100003
BC032033	pl050236	chr12	105500701	105501411	-	NCBI	2.349907223
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uc010iay	pl049705	chr4	53226	68380	+	UCSC	26.55222809
ENST00000429315	pl049241	chr3	47205987	47285546	+	Ensembl	6.498233973
AB075504	pl048731	chr3	66445023	66447872	+	NCBI	2.718431093
	pl048679	chr11	38083599	38261799	-	Agilent	6.070138039
uc003ppy	pl047883	chr6	99910340	99958106	-	UCSC	7.475861267
NR_003512.2	pl047049	chr11	2152478	2154453	-	Other_database	2041.011252
ENST00000497379	pl046335	chr3	164431889	164549268	-	Ensembl	2.169842487
uc001tvl	pl046311	chr12	114188832	114211488	-	UCSC	15.77017752
	pl046046	chr5	12642289	12668043	+	Agilent	6.998925268
uc003ciu	pl045885	chr3	39093506	39138149	+	UCSC	2.276663452
NR_026964	pl045870	chr9	139216997	139221779	-	NCBI	4.619329828
BX648062	pl045798	chr1	93847978	93851185	+	NCBI	15.82830251
NR_038971.1	pl045494	chr14	21668238	21670092	-	Other_database	4.161936767
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uc003fbw	pl045000	chr3	158263008	158288855	-	UCSC	4.263638544
BQ024591	pl044976	chr4	84172466	84173279	+	array-star	3.441475332
uc003ndl	pl044055	chr6	21898950	22214732	+	UCSC	2.18998548
AK127629	pl043847	chr4	152178226	152180345	-	NCBI	2.186861522
	pl043840	chr15	25324097	25327840	+	Agilent	6.009473315
BC031321	pl043625	chr1	81771844	82200257	+	NCBI	3.00126655
gnl|UG|Hs#S3570804	pl043485	chr2	108155491	108156021	+	Other_database	10.27111565
uc003ppy	pl043383	chr6	99910340	99958106	-	UCSC	3.148470011
uc003biq	pl043117	chr22	49808175	50051190	-	UCSC	2.464447586
BC043642	pl042900	chr2	37502053	37505367	+	NCBI	2.624519509
gnl|UG|Hs#S2913136	pl042859	chr12	98989737	98990195	-	Other_database	7.813562447
uc001igy	pl042746	chr10	3360886	3791666	+	UCSC	3.041561811
uc010bhe	pl042739	chr15	65385337	65395022	-	UCSC	2.248852208
NR_038302.1	pl042572	chr3	183172987	183173801	-	Other_database	7.483361204
AK024197	pl042520	chr6	139237377	139239161	-	NCBI	2.547555597
AF086424	pl042252	chr7	39622403	39622929	+	NCBI	4.977872336
uc004cja	pl041796	chr9	139648839	139650253	-	UCSC	3.457571043
AW340752	pl041495	chr8	8978686	8978930	+	array-star	4.873107081
	pl041443	chr6	64248003	64248516	+	Agilent	11.33560335
NR_024380	pl041200	chr10	42827313	42863493	-	NCBI	5.616862846
NR_033652.1	pl040960	chr8	72964774	72966745	+	Other_database	4.806977785
AW340752	pl040717	chr8	8978686	8978930	+	array-star	3.901458649
NR_003561.2	pl040628	chr7	102815460	102815858	-	Other_database	9.313204181
gnl|UG|Hs#S2943948	pl040361	chr2	120188867	120189157	+	Other_database	2.660702964
HMlincRNA1230	pl040359	chr12	112600193	112685348	+	array-star	2.505516866
ENST00000556923	pl039207	chr14	48236803	48259146	-	Ensembl	3.775913298

AI914372	pl039189	chr2	114600904	114639517	+	array-star	3.368094994
CR994053	pl039155	chr5	68216807	68864027	+	array-star	2.164800076
uc001gch	pl039019	chr1	162751900	162756362	+	UCSC	28.76274769
HMlincRNA565	pl038905	chr8	141669167	142011332	+	array-star	2.379085331
AK057576	pl038829	chr12	133442440	133444544	-	NCBI	6.460137885
AK090398	pl038787	chr9	35038621	35044323	-	NCBI	5.775295229
AK129572	pl038713	chr16	67239077	67240752	-	NCBI	3.604745903
HMlincRNA880	pl038650	chr11	57060753	57061272	+	array-star	5.112693767
uc003fxp	pl038262	chr3	196805333	197024986	-	UCSC	2.984287736
uc003fhx	pl037208	chr3	171757417	171905078	+	UCSC	4.148118481
AK095209	pl037044	chr8	102845861	102848029	-	NCBI	3.030959584
gnl|UG|Hs#S857758	pl036224	chr7	134474948	134475311	+	Other_database	3.646629337
NR_024380	pl035959	chr10	42827313	42863493	-	NCBI	5.499007574
HMlincRNA1230	pl035626	chr12	112600193	112685348	+	array-star	2.583340926
AK091873	pl035542	chr2	75078642	75080823	+	NCBI	2.810791975
AL710266	pl034915	chr2	63978507	63978572	+	array-star	3.569027785
DA100307	pl034870	chr11	88123120	88123615	+	array-star	3.198725148
	pl034798	chr19	48146663	48181363	+	Agilent	4.039297089
NR_026989	pl034698	chr1	87595447	87634884	+	NCBI	7.753680903
uc002oyx	pl034078	chr19	44732356	44807605	-	UCSC	3.424283872
uc003fhx	pl033739	chr3	171757417	171905078	+	UCSC	3.338125343
gnl|UG|Hs#S2931883	pl033110	chr7	152095155	152095560	-	Other_database	3.129600477
	pl032879	chr2	39745754	39826679	-	Agilent	2.348738573
NR_034165.1	pl032441	chr14	69708447	69710737	+	Other_database	3.408685343
uc002oyx	pl032197	chr19	44732356	44807605	-	UCSC	2.590485303
AK026032	pl032154	chr6	155210129	155211898	+	NCBI	4.783629907

NR_026737.1	pl031994	chr6	10687199	10687397	-	Other_database	14.71382572
HMlincRNA216	pl031805	chr12	69616287	69618022	+	array-star	2.650131936
HMlincRNA333	pl031698	chr14	69840096	69840444	+	array-star	3.239998693
NR_003290	pl031654	chr12	132568857	132610742	+	NCBI	7.933882488
gnl|UG|Hs#S216330	pl031578	chr3	182655946	182656174	+	Other_database	3.858474574
ENST00000555350	pl031040	chr14	28103331	28105875	+	Ensembl	3.866973014
uc002snu	pl030168	chr2	78245158	78517815	-	UCSC	10.953622
	pl030144	chr2	32065896	32092592	-	Agilent	4.827009713
ENST00000420000	pl028880	chr3	3292371	3668980	-	Ensembl	3.079665974
gnl|UG|Hs#S11150666	pl028839	chr11	74738527	74738879	+	Other_database	3.636748811
uc001ica	pl028777	chr1	247108853	247242069	-	UCSC	3.634441908
AK055655	pl028336	chr3	44708903	44710855	+	NCBI	2.762625656
uc001mss	pl028123	chr11	30851924	30946955	-	UCSC	7.039329894
DB284010	pl028094	chr1	59522314	59554121	+	array-star	4.525842348
	pl027908	chr5	52531518	52727218	-	Agilent	2.282098721
	pl027835	chr18	35246652	35296677	-	Agilent	3.095781319
uc001mpt	pl027803	chr11	20044387	20044678	+	UCSC	2.714399746
	pl027783	chr1	118374652	118400852	-	Agilent	5.134448118
ENST00000430593	pl027588	chr15	37090798	37110707	-	Ensembl	2.499653875
gnl|UG|Hs#S3176614	pl027494	chr18	47807392	47807540	-	Other_database	3.063963899
uc001mfk	pl027164	chr11	7597997	7674984	+	UCSC	5.44684406
AK097147	pl027074	chr1	27044463	27047361	+	NCBI	7.027003188
ENST00000445461	pl027059	chr21	17566788	17979542	+	Ensembl	2.536257268
uc003fhx	pl027017	chr3	171757417	171905078	+	UCSC	4.152380296
uc010dzr	pl026724	chr19	14800869	14827050	+	UCSC	3.272262906
uc003fxp	pl026437	chr3	196805333	197024986	-	UCSC	5.008925297

AK021937	pl026224	chr12	19459711	19461995	+	NCBI	8.527762064
BQ638647	pl025882	chr13	45258810	45289952	+	array-star	2.441507173
NR_036641.1	pl025724	chr4	157682832	157684358	-	Other_database	30.368575
BC040657	pl025260	chr2	176851296	176853066	+	NCBI	2.49067092
AK093022	pl024690	chr8	82608602	82610929	-	NCBI	3.544697781
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	pl023716	chr1	118374652	118400852	-	Agilent	2.823016706
AK092985	pl023668	chr12	26097789	26099944	-	NCBI	3.606874613
AK098019	pl023548	chr9	80519264	80521584	-	NCBI	3.221513173
BP357146	pl023356	chr8	116823925	116824026	+	array-star	3.036112097
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	pl022980	chr13	104132524	104237799	-	Agilent	4.125731103
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	pl022455	chr18	37236475	37243812	+	Agilent	2.493335121
uc002myf	pl022404	chr19	14247990	14282073	+	UCSC	3.629152811
AK021572	pl022037	chr2	37547592	37549138	-	NCBI	2.282704706
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AJ604570	pl021889	chr8	122653494	122653761	-	NCBI	6.556287683
	pl021540	chr3	19004860	19168654	+	Agilent	2.302063689
AL137363	pl021459	chr2	152342790	152354727	+	NCBI	8.852829115
uc001ufc	pl020848	chr12	123942650	123956909	+	UCSC	2.688344679
AK027272	pl020722	chr2	23994526	23996417	-	NCBI	2.939025596
uc009web	pl020620	chr1	100810593	100963763	+	UCSC	2.189673075
uc001rvm	pl020333	chr12	50305735	50320118	+	UCSC	6.347245258
BC041996	pl020036	chr6	133108782	133109360	-	NCBI	2.691638989
uc002ofp	pl018944	chr19	37672481	37674920	-	UCSC	5.350719846

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gnl|ncrnascan|RNS1247	pl018420	chr7	129240125	129240296	+	ncRNASCAN	4.656572231
NR_033678.1	pl018361	chr19	48711344	48713550	-	Other_database	5.177889904
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AK057724	pl017928	chr15	86277125	86279269	-	NCBI	2.849145661
AK123736	pl017799	chr3	124509965	124511951	-	NCBI	2.640033678
uc002ued	pl017721	chr2	169628463	169642936	-	UCSC	26.26676539
ASO3483	pl017684	chr1	117568103	117602112	-	NCBI	4.636679268
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ENST00000502335	pl016764	chr18	36787591	36920602	-	Ensembl	2.584734734
uc003fhx	pl016691	chr3	171757417	171905078	+	UCSC	8.252694651
uc003fxp	pl016528	chr3	196805333	197024986	-	UCSC	7.466223835
DA492035	pl016453	chr2	144966196	145277686	+	array-star	2.609299302
BC028116	pl016432	chr3	186542096	186543048	-	NCBI	5.085306887
uc003fux	pl016373	chr3	195426821	195438745	+	UCSC	10.99871761
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R65829	pl015937	chr1	192943284	192943684	+	array-star	10.77600613
	pl015411	chr11	38083599	38261799	-	Agilent	5.335338196
BF511070	pl015206	chr8	60513962	60526324	+	array-star	2.569947486
uc003kun	pl014791	chr5	127276134	127418766	-	UCSC	4.075246436
AK123636	pl014671	chr16	4656110	4659189	-	NCBI	2.133219962
	pl014634	chr11	38083599	38261799	-	Agilent	4.497996608
BC114921	pl014393	chr2	114661662	114662835	+	NCBI	2.380957063

AB007954	pl013902	chr1	61590157	61597315	+	NCBI	2.432719617
AL109667	pl013764	chr15	81186190	81189808	-	NCBI	3.840598279
NR_026588	pl013713	chr1	245133630	245251148	+	NCBI	2.17028451
uc001gdq	pl013537	chr1	166029415	166039595	-	UCSC	2.269562628
uc002snu	pl013211	chr2	78245158	78517815	-	UCSC	6.49335763
ENST00000500478	pl012751	chr16	25078258	25080246	+	Ensembl	3.222190692
NR_033678.1	pl012266	chr19	48713541	48715232	-	Other_database	4.627233364
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NR_024391.1	pl011361	chr18	36786888	36788753	-	Other_database	3.481942984
ENST00000445461	pl011314	chr21	17566788	17979542	+	Ensembl	2.380235132
gnl|UG|Hs#S390293	pl011302	chr16	22345455	22345759	-	Other_database	2.973802494
uc002ruu	pl011283	chr2	45903872	46072896	+	UCSC	3.143596634
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AL833114	pl010819	chr12	65675436	65680495	+	NCBI	3.365828053
NR_038894.1	pl010667	chr21	37513694	37514244	-	Other_database	5.677171781
	pl010425	chr6	22181638	22194615	-	Agilent	2.877986257
NR_038302.1	pl010228	chr3	183172987	183173801	+	Other_database	4.812333029
uc002woo	pl009564	chr20	13765681	13797874	+	UCSC	2.304161956
NR_027464.1	pl009466	chr22	21335281	21335649	+	Other_database	4.372752726
uc002snu	pl009130	chr2	78245158	78517815	-	UCSC	4.256755479
ENST00000520306	pl009115	chr8	90629158	90633104	-	Ensembl	4.527828453
ENST00000435697	pl008309	chr21	17791752	17860215	+	Ensembl	9.703289435
BG216273	pl008167	chr3	176097788	176097921	+	array-star	5.615966072
uc010aov	pl008069	chr14	57757672	57762434	+	UCSC	3.674546817

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	pl007711	chr1	67454362	67462537	-	Agilent	4.772035115
uc009xlm	pl007683	chr10	31610063	31803636	+	UCSC	5.779737575
ENST00000492054	pl007540	chr7	149737610	149773744	+	Ensembl	18.14291377
ENST00000522554	pl007195	chr4	185505247	185546184	-	Ensembl	2.756771518
AK124563	pl006995	chr3	195000423	195004640	-	NCBI	3.105744274
BX647176	pl006991	chr10	34911773	34916902	-	NCBI	4.027821495
	pl006972	chr3	194190336	194206820	-	Agilent	2.835798858
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uc002oyx	pl006098	chr19	44732356	44807605	-	UCSC	10.39656901
ENST00000431071	pl005668	chr7	119344610	119547429	-	Ensembl	2.163265222
uc002snu	pl005666	chr2	78245158	78517815	-	UCSC	5.926398623
ENST00000445461	pl005578	chr21	17566788	17979542	+	Ensembl	5.384428197
	pl005002	chr17	49425	59094	-	Agilent	7.054463203
uc003xpf	pl004978	chr8	42390081	42396646	-	UCSC	4.222317624
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	pl004560	chr6	5047814	5048418	+	Agilent	37.81073342
HMlincRNA583	pl004355	chr22	43193596	43253188	+	array-star	2.547290875
uc002ndy	pl003805	chr19	16466058	16582762	-	UCSC	2.13281227
BQ638647	pl003789	chr13	45258810	45289952	+	array-star	2.756757611
NR_037918.1	pl003758	chr12	11083258	11083676	+	Other_database	6.034783881
ENST00000441820	pl003123	chr21	17909601	17979569	+	Ensembl	9.339135467
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NR_026717.1	pl002953	chr6	31939646	31940288	+	Other_database	2.843331718

	HMlincRNA1482	pl002850	chr16	67116169	67579168	+	array-star	3.972304201
	NR_033257.1	pl002820	chrX	52239019	52239371	+	Other_database	1120.857812
	NR_039993.1	pl002623	chr5	87732090	87732491	+	Other_database	46.56603745
	HMlincRNA714	pl002236	chr2	108792457	108793750	+	array-star	2.568627081
	ENST00000424953	pl001939	chr1	74100899	74175264	+	Ensembl	2.464170215
	uc001xxv	pl001754	chr14	90303364	90421089	-	UCSC	3.520577619
	ENST00000557544	pl001600	chr14	62147759	62162541	-	Ensembl	13.86028234
	uc003fhx	pl001486	chr3	171757417	171905078	+	UCSC	4.014054158
	ENST00000455460	pl001367	chr17	67957848	67979614	+	Ensembl	3.033868669
	ENST00000445461	pl001344	chr21	17566788	17979542	+	Ensembl	3.794776036
	gnl|ncrnascan|RNS1863	pl000921	chr20	31898873	31899065	-	ncRNASCAN	2.855591729
	uc001syj	pl000794	chr12	77157853	77216311	+	UCSC	2.674955914
	uc004cjw	pl000552	chr9	139831623	139832440	-	UCSC	4.971252835
	ENST00000435697	pl000241	chr21	17791752	17860215	+	Ensembl	3.186968758
Down	ENST00000447194	pl116123	chr2	195595319	195626159	+	Ensembl	0.274535621
	AK096739	pl116110	chr8	103905961	103908782	-	NCBI	0.207850359
	exon2029	pl115979	chr18	71353458	71353810	+	array-star	0.2071833
	DA201452	pl115957	chr6	139609950	139645074	+	array-star	0.129122829
	gnl|UG|Hs#S4090933	pl115920	chr17	43047205	43047737	+	Other_database	0.45818189
	BC038988	pl115860	chr19	15366992	15443306	+	array-star	0.145235396
	gnl|UG|Hs#S1155958	pl115785	chr3	193695414	193695892	+	Other_database	0.256155461
		pl115661	chr20	49262518	49308093	+	Agilent	0.2539691
	BM677952	pl115541	chr16	83970749	83971024	+	array-star	0.306788431
	ENST00000424506	pl115490	chr6	94873638	94904376	+	Ensembl	0.057159757
	ENST00000437088	pl115385	chr7	12693804	12694610	+	Ensembl	0.054279465
	AK130649	pl115081	chr7	38417296	38418405	+	NCBI	0.132926694

ENST00000497872	pl115073	chr14	106170301	106170939	-	UCSC	0.173262434
BI089392	pl115007	chr12	85736249	86096782	+	array-star	0.234022989
BC042827	pl114514	chr2	198115584	198167243	-	NCBI	0.368390889
HMlincRNA167	pl114512	chr6	123135447	123154467	+	array-star	0.226453804
	pl114484	chr6	53428854	53481760	-	Agilent	0.030964707
HMlincRNA1210	pl114332	chr4	87857561	87869721	+	array-star	0.382192227
ENST00000452852	pl114301	chr13	74120525	74222390	-	Ensembl	0.216606638
AK057465	pl114136	chr18	45027542	45029477	+	NCBI	0.129538176
ENST00000513211	pl113787	chr4	31999019	32157028	+	Ensembl	0.040410228
gnl|UG|Hs#S11124369	pl113783	chr7	145926996	145927263	-	Other_database	0.135580025
AK127450	pl113763	chr10	43946230	43950100	+	NCBI	0.36991241
HMlincRNA282	pl113616	chr17	79319546	79320211	+	array-star	0.313480108
NR_037710.1	pl113588	chr2	62052619	62053734	-	Other_database	0.325247098
NR_003087	pl113526	chr21	15646119	15673692	+	NCBI	0.284276213
gnl|ncrnascan|RNS1293	pl113366	chr22	48729475	48729665	+	ncRNASCAN	0.263080874
NR_003950	pl113300	chr22	23732791	23744799	-	NCBI	0.306321081
BX647721	pl113154	chr10	95334362	95338173	+	NCBI	0.418102603
uc001clo	pl112771	chr1	44509602	44570647	+	UCSC	0.155710513
uc002xln	pl112630	chr20	42839725	42854666	+	UCSC	0.281514929
ENST00000474444	pl112624	chr3	149919961	149942977	-	Ensembl	0.145652643
BC037794	pl112521	chr5	50962471	50964737	-	NCBI	0.025830152
ENST00000536131	pl112256	chr12	24857499	24927147	+	Ensembl	0.117129372
BU164084	pl112242	chr16	65266958	65466747	+	array-star	0.09907714
	pl112233	chr11	102257165	102265615	-	Agilent	0.32144746
AK123611	pl112152	chr9	131668613	131672083	-	NCBI	0.397359914
uc002bwo	pl112048	chr15	101433944	101459488	-	UCSC	0.230123998

ENST00000527283	pl111911	chr11	24257023	24283751	-	Ensembl	0.174664335
NR_045014.1	pl111898	chr12	16701822	16704261	-	Other_database	0.037488839
gnl|UG|Hs#S11148112	pl111665	chr3	133612253	133612764	+	Other_database	0.085435282
NR_024425.1	pl111537	chr9	130890808	130892913	+	Other_database	0.221893008
ENST00000525097	pl111513	chr11	29357425	29615842	-	Ensembl	0.112967129
ENST00000509470	pl111354	chr12	119825796	120032306	-	UCSC	0.460804442
uc001qoi	pl111279	chr12	6561396	6575601	+	UCSC	0.093139972
AK128605	pl111215	chr11	126280572	126284531	+	NCBI	0.238249044
ENST00000455068	pl111156	chr2	237642025	237661449	+	Ensembl	0.047218023
	pl111116					Homologous	0.261191779
ENST00000522265	pl111078	chr8	64326191	64382757	-	Ensembl	0.069804707
ENST00000503177	pl111049	chr19	52188616	52196709	-	Ensembl	0.315328637
AK124277	pl111035	chr20	56130114	56134053	-	NCBI	0.050785578
ENST00000446401	pl110800	chr2	114588765	114600933	-	Ensembl	0.323115132
	pl110690	chr4	128758375	128769050	-	Agilent	0.073405443
BC073826	pl110587	chr6	1384027	1385301	-	NCBI	0.174479946
AK127567	pl110296	chr17	74573675	74577063	-	NCBI	0.247718421
HMlincRNA783	pl110182	chr18	10737660	10748498	+	array-star	0.214101942
HMlincRNA1147	pl110159	chr1	31849969	31850331	+	array-star	0.187554559
ENST00000445615	pl110098	chr7	47009300	47023027	+	Ensembl	0.17810543
	pl110037	chr17	21233207	21252532	+	array-star	0.248888062
HMlincRNA106	pl109923	chr1	184634908	184635276	+	array-star	0.317255007
	pl109786	chr18	35246652	35296677	-	Agilent	0.169960754
BC039384	pl109785	chr2	152194343	152235885	-	NCBI	0.326385
uc.378+	pl109756	chr14	80327476	80327727	+	NCBI	0.294420353
ENST00000507514	pl109740	chr5	75987264	76012040	-	Ensembl	0.268238753

gnl|UG|Hs#S919818	pl109634	chr2	29996169	29996543	+	Other_database	0.078839949
ENST00000507808	pl109553	chr4	58471860	58524966	-	Ensembl	0.177032293
DB495516	pl109408	chr8	104369498	104370036	+	array-star	0.287633963
W95626	pl109305	chrX	51140217	51140982	+	array-star	0.151371555
ENST00000432146	pl109274	chr1	95975726	96088290	+	Ensembl	0.081612363
uc009xox	pl109070	chr10	54056608	54073888	-	UCSC	0.261677506
	pl108940	chr3	162937703	162996391	-	Agilent	0.139352632
	pl108878	chr4	71997061	72013886	+	array-star	0.281122264
DB172247	pl108877	chr5	44832601	44833148	+	array-star	0.336708608
	pl108704	chr11	68954749	69025524	-	Agilent	0.143959106
BF743269	pl108687	chr16	74821436	74821578	+	array-star	0.324097797
	pl108657					Homologous	0.096858441
uc001yfx	pl108465	chr14	98399398	98444447	-	UCSC	0.195789489
ENST00000509416	pl108282	chr4	28437071	28601897	+	Ensembl	0.198762674
	pl108236	chr18	10080425	10093725	+	array-star	0.099848243
exon2258	pl108234	chr2	165516311	165517010	+	array-star	0.048310947
uc003vkf	pl108228	chr7	121946185	121950131	+	UCSC	0.289185988
NR_034180.1	pl108072	chr1	155402971	155404053	+	Other_database	0.271349787
ENST00000519844	pl107987	chr8	101393488	101426687	-	Ensembl	0.451799594
AK223466	pl107934	chr7	139478198	139720092	+	array-star	0.117276586
AK024373	pl107918	chr19	438420	2083745	-	NCBI	0.39765264
uc003apt	pl107630	chr22	37099962	37117494	+	UCSC	0.296685863
uc001glv	pl107554	chr1	178482211	178517734	+	UCSC	0.287024179
gnl|ncrnascan|RNS2025	pl107468	chr20	60036466	60036633	+	ncRNASCAN	0.319425356
uc001gdd	pl107352	chr1	165446078	165551392	-	UCSC	0.402526181
gnl|UG|Hs#S1335333	pl107341	chr2	176810728	176811168	+	Other_database	0.152987842

NR_024107	pl107304	chr8	39308564	39380470	-	NCBI	0.162591629
ENST00000549551	pl106782	chr12	90313469	90383066	+	Ensembl	0.170159276
uc001qdq	pl106582	chr11	126210852	126225482	-	UCSC	0.254151762
ENST00000505511	pl106416	chr4	92809037	92825486	+	Ensembl	0.060192825
HMlincRNA783	pl106245	chr18	10737660	10748498	+	array-star	0.210879835
ENST00000517368	pl106139	chr8	86851934	86920842	+	Ensembl	0.105293433
	pl106096	chr2	32237771	32245946	-	Agilent	0.382425927
	pl105812	chr6	139809107	140148457	+	Agilent	0.384738012
HMlincRNA784	pl105729	chr18	10857083	10979616	+	array-star	0.253542704
gnl|UG|Hs#S4002992	pl105706	chr9	35576538	35577077	+	Other_database	0.15715239
gnl|ncrnascan|RNS1536	pl105600	chr20	37470936	37471017	-	ncRNASCAN	0.237633753
ENST00000435237	pl105533	chr2	21444047	22193831	+	Ensembl	0.098386965
ENST00000443154	pl105509	chr12	133609245	133613808	-	Ensembl	0.432162116
HMlincRNA880	pl105416	chr11	57060753	57061272	+	array-star	0.188238008
ENST00000453459	pl105349	chr7	112262433	112348135	+	Ensembl	0.312767703
ENST00000468964	pl105325	chr10	135083957	135084929	-	Ensembl	0.314455359
DC295389	pl105093	chr4	26165175	26364251	+	array-star	0.070761501
ENST00000522173	pl104966	chr4	97231883	97740015	+	Ensembl	0.237269605
CB047659	pl104948	chr6	14168333	14168655	+	array-star	0.355730836
AK024129	pl104925	chr10	126775661	126779173	-	NCBI	0.275501318
gnl|UG|Hs#S29621384	pl104858	chr6	138164002	138164544	+	Other_database	0.276691174
NR_001447	pl104374	chr16	56651372	56652730	+	NCBI	0.318823273
HMlincRNA827	pl104260	chr10	109565231	109565844	+	array-star	0.147459276
ENST00000500627	pl104235	chr17	79885705	79888628	+	Ensembl	0.370256704
uc010hqr	pl104203	chr3	116428815	116435278	+	UCSC	0.092948405
gnl|UG|Hs#S32157747	pl103994	chr19	13783105	13783527	-	Other_database	0.064839166

uc003qlt	pl103918	chr6	147163036	147525750	-	UCSC	0.156707727
HMlincRNA1269	pl103904	chr7	139954781	139955675	+	array-star	0.105751168
ENST00000432697	pl103853	chr13	62578226	62603681	-	Ensembl	0.146711103
NR_015454	pl103780	chr17	79888069	79888292	+	NCBI	0.347204779
ENST00000549742	pl103626	chr14	29061429	29082829	-	Ensembl	0.302521857
NR_033917.1	pl103619	chr20	4176173	4176600	+	Other_database	0.264171169
DA856530	pl103588	chr10	33247772	33370514	+	array-star	0.3380374
Z34283	pl103572	chr11	1212760	1212885	+	NCBI	0.176814308
uc001kwr	pl103490	chr10	104958489	105036751	-	UCSC	0.194532658
uc001acg	pl103372	chr1	910583	912021	-	UCSC	0.070317241
gnl|UG|Hs#S6103306	pl103345	chr6	48025769	48026215	+	Other_database	0.281679297
	pl103129	chr12	48153483	48166083	-	Agilent	0.134732514
	pl102983	chr14	42861350	43287750	+	Agilent	0.198752265
DB024730	pl102915	chr5	142869419	142910915	+	array-star	0.389920642
NR_024344	pl102901	chr11	133766329	133771635	-	NCBI	0.033995749
HMlincRNA75	pl102889	chr2	122660225	122978498	+	array-star	0.306881491
HMlincRNA1153	pl102783	chr1	27535137	27535184	+	array-star	0.218113626
gnl|UG|Hs#S1251306	pl102652	chr18	29267672	29267932	-	Other_database	0.326453173
	pl102465	chr1	91997737	92078987	-	Agilent	0.426497909
	pl102436	chr8	16325260	16353389	+	Agilent	0.053819344
HMlincRNA1377	pl102403	chr15	31727659	31727855	+	array-star	0.055168535
DB151746	pl102386	chr10	119210079	119210532	+	array-star	0.164314895
uc001xsf	pl102337	chr14	76452095	76548783	+	UCSC	0.393574574
ENST00000547559	pl102292	chr12	55403530	55408031	+	Ensembl	0.391782999
BF979550	pl102267	chr2	208265953	208266331	+	array-star	0.060556603
ENST00000538905	pl102244	chr12	24520869	24715316	-	Ensembl	0.269413804

gnl|UG|Hs#S16772959	pl101958	chr15	48001635	48002080	-	Other_database	0.159250181
ENST00000433101	pl101951	chr21	24849960	24863043	+	Ensembl	0.063031073
uc001xjj	pl101867	chr14	67920796	67982202	-	UCSC	0.176941305
	pl101816	chr8	128301923	128335401	-	Agilent	0.116364181
gnl|UG|Hs#S11131546	pl101697	chr1	81227459	81227964	+	Other_database	0.140788495
ENST00000439406	pl101608	chr6	30734602	30760027	+	Ensembl	0.047874223
NR_024564	pl101320	chr20	19222945	19265240	-	NCBI	0.046767943
ENST00000533459	pl101146	chr11	103546722	103765999	-	Ensembl	0.364205589
L10717	pl101080	chr5	156607921	156682175	+	NCBI	0.122624127
CR748637	pl101045	chr3	142871098	143101003	+	array-star	0.02403174
uc002nvo	pl100413	chr19	35085571	35166604	-	UCSC	0.045506372
HMlincRNA1613	pl100343	chrX	118619272	118629135	+	array-star	0.118328728
BC043241	pl100299	chr16	63090692	63163558	-	NCBI	0.179245146
ENST00000508521	pl100219	chr5	88238904	88371148	+	Ensembl	0.173394584
gnl|UG|Hs#S1662514	pl099787	chr6	72082955	72083479	+	Other_database	0.334218035
ENST00000471176	pl099716	chr3	149694542	149697115	+	Ensembl	0.075364823
gnl|ncrnascan|RNS1303	pl099676	chr7	75676778	75676859	-	ncRNASCAN	0.258812081
CR748637	pl099672	chr3	142871098	143101003	+	array-star	0.046892568
AL710266	pl099473	chr2	63978507	63978572	+	array-star	0.418468496
AW135489	pl099375	chr2	192787269	192895368	+	array-star	0.26736874
BC043233	pl099315	chr10	75007124	75036742	+	NCBI	0.127314667
HMlincRNA282	pl099255	chr17	79319546	79320211	+	array-star	0.301698434
HMlincRNA827	pl099192	chr10	109565231	109565844	+	array-star	0.018955473
ENST00000479349	pl099067	chr3	141382041	141404009	+	Ensembl	0.277383471
gnl|UG|Hs#S1701995	pl098995	chr3	67798470	67798927	-	Other_database	0.151205105
BC042074	pl098974	chr5	16373470	16441211	-	NCBI	0.163013665

ENST00000524167	pl098961	chr8	35719641	35788228	+	Ensembl	0.119366549
ENST00000421331	pl098773	chr1	78347033	78355224	-	Ensembl	0.304838662
BQ707656	pl098635	chr1	172885606	172886064	+	array-star	0.116057691
NR_040662.1	pl098511	chr6	31431148	31433586	+	Other_database	0.279454046
HMlincRNA1664	pl098424	chrX	52976959	52993397	+	array-star	0.266764116
HMlincRNA1339	pl098319	chr12	5454390	5454785	+	array-star	0.046295249
HMlincRNA1140	pl098272	chr1	35178360	35325336	+	array-star	0.362951044
	pl098130	chr2	2842093	2864943	-	Agilent	0.113735424
uc003ypj	pl098016	chr8	122966846	123139423	-	UCSC	0.19886415
	pl097906	chr2	62814221	62825121	+	Agilent	0.092155056
gnl|UG|Hs#S1295831	pl097882	chr12	125774651	125774940	-	Other_database	0.067056038
gnl|UG|Hs#S1934440	pl097815	chr11	1212832	1212866	+	Other_database	0.260760049
ENST00000463297	pl097763	chr3	153599315	153658625	+	Ensembl	0.047987522
AK026607	pl097687	chr11	44580598	44972434	+	array-star	0.284938099
BM786152	pl097648	chr2	224720507	224744958	+	array-star	0.103353484
gnl|UG|Hs#S2134487	pl097358	chr11	117143342	117143733	+	Other_database	0.258347115
NR_026991	pl097355	chr3	129035113	129043412	+	NCBI	0.40004485
gnl|UG|Hs#S2300571	pl097324	chr10	11270146	11270682	-	Other_database	0.138830667
BC031321	pl097212	chr1	81771844	82200257	+	NCBI	0.049760608
ENST00000452500	pl096975	chr21	23305635	23348000	-	Ensembl	0.152925723
HMlincRNA109	pl096971	chr1	177362814	177714046	+	array-star	0.284818921
NR_033967.1	pl096857	chr1	43424720	43425248	+	Other_database	0.390181264
gnl|UG|Hs#S1492440	pl096629	chrX	53412714	53412937	+	Other_database	0.253398766
BF743269	pl096595	chr16	74821436	74821578	+	array-star	0.090570898
uc001vso	pl096586	chr13	113556508	113612477	+	UCSC	0.294961995
ENST00000435981	pl096514	chr7	114719012	114766368	+	Ensembl	0.205549915

uc002joy	pl096479	chr17	73642645	73644053	+	UCSC	0.25385598
ENST00000445615	pl096374	chr7	47009300	47023027	+	Ensembl	0.175260654
NR_027303.1	pl096343	chr2	12880452	12882860	+	Other_database	0.105737356
HMlincRNA1059	pl096148	chr1	94615402	94740624	+	array-star	0.035970254
uc001jeo	pl096134	chr10	47746919	47770843	+	UCSC	0.167287126
BC004503	pl096133	chr11	64253242	64621138	+	array-star	0.335994756
	pl096033	chr4	90602655	90613743	-	Agilent	0.034112949
	pl095895	chr1	205410835	205411291	-	Agilent	0.065617759
NR_002939	pl095871	chr16	29302540	29385597	+	NCBI	0.145915219
uc009vyn	pl095790	chr1	47333618	47366147	-	UCSC	0.394758578
ENST00000397645	pl095757	chr3	193675161	193721448	-	Ensembl	0.203435487
HMlincRNA188	pl095719	chr21	46799592	46799875	+	array-star	0.123187968
	pl095514	chr16	85205424	85218749	-	Agilent	0.309647074
BE048618	pl095419	chr12	28286181	28603351	+	array-star	0.131428213
HMlincRNA1660	pl095407	chrX	55172330	55187587	+	array-star	0.455152088
ENST00000518181	pl095349	chr8	35861834	35952564	-	Ensembl	0.366130282
HMlincRNA1468	pl095328	chr4	145495175	145506200	+	array-star	0.301376983
ENST00000449333	pl095286	chr6	10434549	10452480	+	Ensembl	0.148738678
NR_027781.1	pl095227	chr16	56678622	56678853	+	Other_database	0.257330729
uc001ayl	pl095074	chr1	16722175	16763919	-	UCSC	0.169008146
uc001wby	pl094970	chr14	22309748	22356675	+	UCSC	0.139186847
uc002aro	pl094839	chr15	69222863	69317192	+	UCSC	0.245217405
	pl094788	chr18	73856462	73868712	+	Agilent	0.059327451
uc010kkv	pl094618	chr6	169819100	169825251	-	UCSC	0.019755644
exon4127	pl094506	chr8	37192351	37192711	+	array-star	0.174360194
ENST00000522129	pl094413	chr8	9232408	9293715	-	Ensembl	0.322879834

NR_037173.1	pl094407	chr6_mann_hap4	4270391	4271473	+	Other_database	0.319327922
gnl|UG|Hs#S775136	pl094344	chr7	20414052	20414266	+	Other_database	0.24809654
uc003kkb	pl094311	chr5	91686129	91742352	+	UCSC	0.223188024
uc002fkc	pl094298	chr16	87527792	87549236	+	UCSC	0.213365942
	pl094176	chr7	109181989	109272589	-	Agilent	0.156511855
HMlincRNA1183	pl094067	chr2	27929629	27938599	+	array-star	0.224932474
uc001jzu	pl093925	chr10	79998011	80434727	+	UCSC	0.051434856
	pl093907	chr4	108746776	108807351	-	Agilent	0.218654087
ENST00000439207	pl093764	chr6	167655379	167659404	+	Ensembl	0.165432522
	pl093579	chr13	110652899	110676049	-	Agilent	0.041615669
	pl093530	chr13	54812799	54928899	-	Agilent	0.350342635
AK023559	pl093483	chr10	50726990	50729600	-	NCBI	0.3116417
ENST00000505289	pl093470	chr4	134015015	134070268	-	Ensembl	0.13807085
ENST00000425050	pl093450	chr10	109631334	109829052	-	Ensembl	0.073493216
	pl093410	chr1	181309852	181429627	-	Agilent	0.223548492
ENST00000435411	pl093077	chr2	181988564	182264286	+	Ensembl	0.046468762
HMlincRNA216	pl092692	chr12	69616287	69618022	+	array-star	0.040650823
BC021142	pl092646	chr16	11032744	11033901	-	NCBI	0.42488779
HMlincRNA48	pl092628	chr2	222686212	222825543	+	array-star	0.441553935
NR_003923	pl092544	chr13	51568647	51640293	-	NCBI	0.127844987
ENST00000446671	pl092478	chr17	14918122	14955593	+	Ensembl	0.285586409
	pl092477	chr2	40946996	41235296	-	Agilent	0.288496053
HMlincRNA368	pl092416	chr6	28912574	28922841	+	array-star	0.14065751
DB495516	pl092328	chr8	104369498	104370036	+	array-star	0.444572876
ENST00000433433	pl092291	chr2	105481955	105488910	-	Ensembl	0.379891076
AL512720	pl092287	chr4	15484288	15485765	+	NCBI	0.239722052

ENST00000419614	pl092229	chr1	189744595	189784048	+	Ensembl	0.162386888
HMlincRNA866	pl092136	chr2	173254424	173255061	+	array-star	0.09250004
HMlincRNA1311	pl092025	chr3	13573823	13679512	+	array-star	0.093987043
ENST00000422117	pl092016	chr15	25729978	25823938	-	Ensembl	0.150615906
ENST00000510065	pl091972	chr5	12914180	13032998	-	Ensembl	0.069098452
uc003ykm	pl091798	chr8	102961418	103129048	-	UCSC	0.039542112
BC017884	pl091723	chr1	39687789	39688637	+	NCBI	0.413581163
uc001xsf	pl091719	chr14	76452095	76548783	+	UCSC	0.200085316
AK299815	pl091673	chr4	113739264	114304891	+	array-star	0.248406243
	pl091356	chr2	19532269	19547044	-	Agilent	0.431029574
ENST00000551040	pl091284	chr14	29734031	29847862	-	Ensembl	0.047708587
HMlincRNA783	pl091218	chr18	10737660	10748498	+	array-star	0.249266267
uc001mti	pl091111	chr11	31838113	31908587	+	UCSC	0.29480866
ENST00000553346	pl091023	chr14	86481030	86529304	-	Ensembl	0.166703486
AK126294	pl090956	chr11	129730351	129731580	-	NCBI	0.403796441
gnl|ncrnascan|RNS1765	pl090900	chr14	100036721	100036912	+	ncRNASCAN	0.359815233
ENST00000556016	pl090633	chr14	85669193	85705818	-	Ensembl	0.162631222
ENST00000510238	pl090489	chr16	52586008	52640847	-	Ensembl	0.093611788
ENST00000455977	pl090356	chr13	62798230	62824080	+	Ensembl	0.092440071
HMlincRNA1660	pl090346	chrX	55172330	55187587	+	array-star	0.203224681
AF090100	pl090291	chr2	69698050	69699647	+	NCBI	0.142863694
ENST00000440744	pl090225	chr7	135710509	135769416	+	Ensembl	0.133120212
ENST00000481773	pl089865	chr3	113933160	113954241	+	Ensembl	0.321416161
uc003tfz	pl089856	chr7	38288843	38356709	-	UCSC	0.025668115
AA292843	pl089828	chr5	106300100	106300653	+	array-star	0.216575064
ENST00000473636	pl089553	chr3	106830713	106959488	-	Ensembl	0.256221258

ES313504	pl089480	chr5	172896684	172911589	+	array-star	0.326587857
ENST00000542627	pl089184	chr12	133033746	133036610	+	Ensembl	0.202098422
uc003hho	pl088612	chr4	74988990	75047508	+	UCSC	0.236520186
	pl088450	chr2	224569543	224588684	-	Agilent	0.175440859
CR626211	pl088442	chr20	23161580	23162378	+	NCBI	0.289404175
ENST00000518181	pl088397	chr8	35861834	35952564	-	Ensembl	0.275988826
NR_038209.1	pl088364	chr8	96356511	96356673	+	Other_database	0.250674023
ENST00000507599	pl088298	chr5	5038799	5057986	+	Ensembl	0.443535719
	pl088165	chr4	38197205	38433455	-	Agilent	0.04992656
ENST00000522896	pl087998	chr8	111346972	111361836	-	Ensembl	0.128453711
ENST00000513718	pl087938	chr4	160587655	160698936	-	Ensembl	0.131304078
ENST00000507365	pl087931	chr4	138466885	138524584	+	Ensembl	0.081881135
NR_028501.1	pl087920	chr2	233250460	233251754	-	Other_database	0.252103177
HMlincRNA1147	pl087848	chr1	31849969	31850331	+	array-star	0.219117488
ENST00000521055	pl087818	chr8	16461764	16522388	+	Ensembl	0.183797948
gnl|UG|Hs#S11129957	pl087674	chr2	30996810	30997268	+	Other_database	0.145257487
HMlincRNA836	pl087673	chr10	7513448	7514006	+	array-star	0.140670329
uc001daw	pl087593	chr1	63635822	63782901	-	UCSC	0.268737069
	pl087510	chr8	128301923	128335401	-	Agilent	0.264242221
ASO1803	pl087381	chr17	4383674	4389747	-	NCBI	0.17803474
uc002tpv	pl087353	chr2	129999745	130031421	-	UCSC	0.306715442
gnl|UG|Hs#S4719665	pl087273	chr16	53165856	53166463	+	Other_database	0.295819433
NR_003601	pl087027	chr10	47658233	47701446	+	NCBI	0.345538107
NR_024524	pl086772	chr10	38464598	38503272	+	NCBI	0.229288649
ENST00000523502	pl086668	chr8	131607545	131667958	-	Ensembl	0.153220989
AK299815	pl086126	chr4	113739264	114304891	+	array-star	0.074088982

HMlincRNA1420	pl086077	chr10	123716296	123716609	+	array-star	0.340119471
AK093009	pl086030	chr20	36129478	36132377	-	NCBI	0.412427364
uc010hpe	pl085968	chr3	99357453	99422736	+	UCSC	0.270526248
	pl085904	chr3	104348945	104626311	-	Agilent	0.255957618
ENST00000450290	pl085520	chr2	80926513	81097315	-	Ensembl	0.11305233
	pl085319	chrX	139795484	139814909	+	Agilent	0.183405478
uc003ikz	pl084995	chr4	148488757	148515739	+	UCSC	0.343616736
uc009xjd	pl084943	chr10	13048110	13141713	-	UCSC	0.015659494
	pl084900	chr5	61931044	61948469	-	Agilent	0.068250202
	pl084867	chr2	238357611	238370161	-	Agilent	0.39245033
gnl|UG|Hs#S11145666	pl084813	chr2	112293955	112294612	+	Other_database	0.126544569
ASO3530	pl084674	chr5	44388833	44414090	+	NCBI	0.203378694
uc002vso	pl084458	chr2	232888986	233201686	+	UCSC	0.008768873
ENST00000455554	pl084452	chr6	77232168	77303340	+	Ensembl	0.073344344
	pl084445	chr3	129602510	129611708	-	Agilent	0.044284661
NR_026816	pl084427	chr6	31141511	31145676	-	NCBI	0.126962569
	pl084385	chr3	37886971	37901921	-	Agilent	0.454021888
uc003jge	pl084165	chr5	20611948	20937800	+	UCSC	0.073902996
BC055423	pl084052	chr10	2342513	2357268	-	NCBI	0.060412557
ENST00000550019	pl083881	chr12	47747537	47763718	+	Ensembl	0.094644229
uc001uiy	pl083837	chr12	131832014	131852100	+	UCSC	0.365139094
ENST00000521014	pl083772	chr8	130902711	130914004	+	Ensembl	0.396121784
	pl083737	chr5	8437875	8473025	-	Agilent	0.12776846
AA307003	pl083717	chr4	104177315	104374815	+	array-star	0.092937655
DN918054	pl083504	chr1	66890612	67423817	+	array-star	0.184997189
	pl083461	chr6	155216183	155236483	-	Agilent	0.196390536

uc003fbw	pl083432	chr3	158263008	158288855	-	UCSC	0.376632795
uc010azs	pl083409	chr15	30864573	30900548	+	UCSC	0.247905197
DQ438906	pl083365	chr9	3937093	4035998	-	NCBI	0.189157452
NR_036482.1	pl082966	chr7	29726895	29727859	+	Other_database	0.062739124
ENST00000531136	pl082859	chr11	13076162	13156386	-	Ensembl	0.258510069
	pl082332	chr8	90737074	90737855	+	Agilent	0.362195204
	pl082155	chr1	186969952	187183302	-	Agilent	0.230103684
HMlincRNA730	pl082097	chr2	44396015	44471522	+	array-star	0.346591933
BC031056	pl082046	chr18	52895458	53303130	+	array-star	0.426574867
uc002iqz	pl082023	chr17	48585811	48608862	+	UCSC	0.223261743
	pl081967	chr6	28075525	28083457	+	Agilent	0.33468357
uc001jeo	pl081932	chr10	47746919	47770843	+	UCSC	0.111555034
NR_024239.1	pl081546	chr11	104877810	104878061	-	Other_database	0.071785726
HMlincRNA1482	pl081461	chr16	67116169	67579168	+	array-star	0.394590475
ENST00000417751	pl081377	chr2	13850656	14541087	-	Ensembl	0.083162036
uc001qed	pl081232	chr11	126419180	126873355	-	UCSC	0.38712136
BC004968	pl081094	chr16	728518	729737	-	NCBI	0.248100903
NR_033963.1	pl080856	chr7	564491	564869	+	Other_database	0.301321573
uc001rfu	pl080606	chr12	23117505	23327057	+	UCSC	0.129344547
AF070529	pl080532	chr19	8478276	8503901	-	NCBI	0.277939388
ENST00000554862	pl080514	chr14	97925153	98047938	+	Ensembl	0.078410233
gnl|UG|Hs#S1741773	pl080104	chr12	59306819	59307111	+	Other_database	0.174192017
uc002voq	pl080093	chr2	228092485	228189880	-	UCSC	0.360033869
ENST00000417751	pl080043	chr2	13850656	14541087	-	Ensembl	0.14384893
gnl|UG|Hs#S19974232	pl079922	chr4	128801368	128801953	-	Other_database	0.383805227
	pl079761	chr20	49035543	49051793	-	Agilent	0.102880458

AK124383	pl079740	chr13	40768645	40794639	-	NCBI	0.185068164
ENST00000546414	pl079699	chr12	116248164	116323942	-	Ensembl	0.138653872
ENST00000513419	pl079632	chr5	1939886	1959015	+	Ensembl	0.170619166
DA222960	pl079554	chr8	94873924	94874305	+	array-star	0.213171546
	pl079413	chr8	96692149	96730174	-	Agilent	0.122728404
HMlincRNA622	pl079243	chr3	186164014	186164368	+	array-star	0.141418668
ENST00000549532	pl079083	chr12	94885322	94890218	-	Ensembl	0.307946111
uc001als	pl078935	chr1	5936013	6052531	-	UCSC	0.221132504
	pl078872					Homologous	0.01936858
	pl078723	chr4	10167202	10405252	+	Agilent	0.067014565
ENST00000510005	pl078595	chr4	189376747	189523062	+	Ensembl	0.198462442
uc003laj	pl078585	chr5	134368969	134680370	+	UCSC	0.139906134
ENST00000520513	pl078476	chr8	94225531	94304914	-	Ensembl	0.2051359
uc001deb	pl078216	chr1	68297985	68668670	+	UCSC	0.392430435
LIT3319	pl078199	chr12	97858798	97958795	+	NCBI	0.158077963
uc002bms	pl078056	chr15	89128801	89147834	-	UCSC	0.062924848
uc003ypj	pl077831	chr8	122966846	123139423	-	UCSC	0.129009985
	pl077767	chr12	112757053	112819896	+	Agilent	0.107674226
AK123095	pl077650	chr2	112945940	112948212	+	NCBI	0.400796761
HMlincRNA470	pl077621	chr3	56719314	56719729	+	array-star	0.410369774
ENST00000514304	pl077599	chr4	95596396	95623721	+	Ensembl	0.280752365
BC146594	pl077547	chr7	534709	537708	-	Other_database	0.209691731
AK123834	pl077377	chr1	89003195	89150887	-	NCBI	0.036920768
	pl077091	chr5	52531518	52727218	-	Agilent	0.289152214
BQ707656	pl076854	chr1	172885606	172886064	+	array-star	0.258802787
ENST00000513133	pl076617	chr5	147618133	147622157	+	Ensembl	0.231826638

NR_027082	pl076385	chr10	10826401	10836877	-	NCBI	0.14885304
ENST00000448597	pl076240	chrX	39164210	39186616	-	Ensembl	0.071531975
ENST00000422374	pl076167	chr1	56046710	56200675	+	Ensembl	0.030177013
HMlincRNA1249	pl076165	chr7	93719942	94020845	+	array-star	0.110309383
ENST00000433315	pl076070	chr7	42869271	42884037	-	Ensembl	0.072043345
ENST00000522896	pl076022	chr8	111346972	111361836	-	Ensembl	0.133637672
BC065212	pl075954	chr2	160800328	160801653	-	NCBI	0.155616703
BU078958	pl075804	chr2	37859864	37860072	+	array-star	0.095710689
HMlincRNA1318	pl075789	chr3	72596626	72597031	+	array-star	0.26547151
ENST00000527492	pl075614	chr11	29616465	29652211	+	Ensembl	0.106139576
uc002wxa	pl075606	chr20	30458513	30532764	+	UCSC	0.253225603
	pl075349	chr5	139536903	139548370	+	Agilent	0.239552097
ENST00000513573	pl075009	chr5	20305674	20331565	+	Ensembl	0.065923025
AK024373	pl075008	chr19	438420	2083745	-	NCBI	0.327003788
ENST00000428156	pl074795	chr2	171496884	171551884	-	Ensembl	0.299929926
ENST00000506305	pl074792	chr5	4033826	4041877	-	Ensembl	0.315876152
	pl074513	chr15	39591539	39713152	-	Agilent	0.055100616
ENST00000505347	pl074466	chr4	19173958	19458617	-	Ensembl	0.138970994
NR_024564	pl074430	chr20	19222945	19265240	-	NCBI	0.143690943
uc001jeo	pl074315	chr10	47746919	47770843	+	UCSC	0.169348925
	pl074294	chr16	72557245	72661585	-	Agilent	0.12980112
ENST00000500767	pl074238	chr17	65871895	65881544	-	Ensembl	0.312272117
AK025054	pl074214	chr2	197897137	198095300	-	NCBI	0.064916908
CB111670	pl074105	chr22	35615035	35615518	+	array-star	0.13496418
gnl|ncrnascan|RNS2076	pl074081	chr14	91035348	91035537	-	ncRNASCAN	0.254144168
AK094780	pl074027	chr3	15935568	16270147	+	array-star	0.252465934

uc010agq	pl073969	chr13	113777112	113801800	+	UCSC	0.045772539
ENST00000557070	pl073966	chr14	87819414	88039366	-	Ensembl	0.345642259
gnl|ncrnascan|RNS1012	pl073917	chr13	64583331	64583395	-	ncRNASCAN	0.139396137
AA307003	pl073875	chr4	104177315	104374815	+	array-star	0.111053588
uc003sng	pl073699	chr7	4834284	4923335	-	UCSC	0.16403201
NR_027115	pl073602	chr6	961241	1101567	-	NCBI	0.116771184
AK024910	pl073532	chr2	199613214	199616031	-	NCBI	0.244571987
AL832516	pl073519	chr12	132514308	132534942	-	NCBI	0.241199988
ENST00000441660	pl073338	chr20	59654196	59655235	+	Ensembl	0.206604714
ENST00000507299	pl073220	chr4	125070532	125173199	-	Ensembl	0.042347385
uc001qeg	pl073191	chr11	126936896	126971201	+	UCSC	0.109052915
gnl|UG|Hs#S711718	pl072993	chr6	109069391	109069766	-	Other_database	0.168143036
ENST00000507299	pl072925	chr4	125070532	125173199	-	Ensembl	0.090430162
ENST00000422117	pl072895	chr15	25729978	25823938	-	Ensembl	0.156511221
ENST00000498938	pl072796	chr15	69854059	69863779	+	Ensembl	0.315936274
	pl072743	chr10	97639610	97667003	-	Agilent	0.377690007
uc010afo	pl072701	chr13	96635777	96705637	-	UCSC	0.278041597
uc001arm	pl072695	chr1	10535002	10638484	+	UCSC	0.352972288
ENST00000422558	pl072626	chr2	34608855	34860407	+	Ensembl	0.048794536
HMlincRNA1141	pl072512	chr1	33430675	33431256	+	array-star	0.17289888
HMlincRNA1513	pl072496	chr11	133782189	133782774	+	array-star	0.450610426
CR608805	pl072449	chr9	128519872	128520523	+	NCBI	0.267067075
HMlincRNA1432	pl072183	chr8	38758828	38826184	+	array-star	0.270765583
uc001xbf	pl072108	chr14	55154714	55201855	+	UCSC	0.043321966
uc003kov	pl072038	chr5	109624933	109765804	-	UCSC	0.181919426
NR_026794	pl071917	chr10	26932036	26942382	+	NCBI	0.200253402

ENST00000426491	pl071720	chr20	10055085	10200154	-	Ensembl	0.300424596
	pl071668	chr5	95303844	95350319	-	Agilent	0.180364353
uc001lww	pl071647	chr11	2909009	2924970	-	UCSC	0.305658453
BC036877	pl071536	chr1	14925212	15441219	-	NCBI	0.063886914
AK128043	pl071481	chr1	52042850	52254068	+	array-star	0.351479499
	pl071238	chr11	126219244	126219612	+	Agilent	0.413978653
BC036877	pl071185	chr1	14925212	15441219	-	NCBI	0.035253372
BC037164	pl071158	chr20	61088967	61091152	-	NCBI	0.392311979
BF746429	pl071117	chr1	39183439	39183984	+	array-star	0.25898583
uc003ymx	pl071017	chr8	109619079	109799770	-	UCSC	0.033457169
ENST00000412835	pl070972	chr2	175412102	175530417	+	Ensembl	0.261721146
DA492035	pl070774	chr2	144966196	145277686	+	array-star	0.136231968
BC042074	pl070709	chr5	16373470	16441211	-	NCBI	0.156890644
ENST00000527528	pl070683	chr11	96461317	96584822	+	Ensembl	0.012874621
ENST00000452501	pl070624	chrX	41134992	41136031	+	Ensembl	0.145047234
NR_024249	pl070227	chr11	67559239	67572807	-	NCBI	0.381482998
uc010dtl	pl070076	chr19	3538647	3540042	-	UCSC	0.302205997
uc001vpc	pl070071	chr13	102250502	102371131	+	UCSC	0.017779857
HMlincRNA1333	pl070063	chr12	9008171	9029370	+	array-star	0.149732994
HMlincRNA141	pl070006	chr6	148659743	148660138	+	array-star	0.386917387
uc003qmh	pl069981	chr6	149275399	149285820	-	UCSC	0.296846044
ENST00000507844	pl069941	chr4	134792401	134931845	-	Ensembl	0.330969193
uc004crw	pl069926	chrX	7065292	7171377	+	UCSC	0.266003127
ENST00000431401	pl069837	chr6	10474733	10478735	-	Ensembl	0.124517708
ENST00000536744	pl069787	chr12	22852875	23041867	+	Ensembl	0.160607674
uc001gle	pl069783	chr1	176945189	177001985	-	UCSC	0.098494896

uc003ehc	pl069685	chr3	123697522	123710984	-	UCSC	0.240774601
	pl069595	chr4	80995226	81008001	+	Agilent	0.376931432
AK126270	pl069565	chr16	19429029	19431584	+	NCBI	0.286902563
gnl|ncrnascan|RNS1587	pl069409	chr19	16974633	16974781	+	ncRNASCAN	0.227830287
NR_028032.1	pl069372	chr6	29942892	29943294	+	Other_database	0.312213908
uc001jeo	pl069328	chr10	47746919	47770843	+	UCSC	0.276990454
BC036877	pl069264	chr1	14925212	15441219	-	NCBI	0.268215779
uc002zsv	pl069005	chr22	20970517	21011201	-	UCSC	0.258988147
HMlincRNA798	pl068994	chr18	44497556	44624853	+	array-star	0.170400672
HMlincRNA124	pl068332	chr1	227058968	227083797	+	array-star	0.262146852
NR_023359.1	pl068323	chr18	20837191	20839544	+	Other_database	0.350983874
uc002cwe	pl068303	chr16	4390251	4457685	-	UCSC	0.123570438
uc002vyi	pl068252	chr2	239419330	239463695	-	UCSC	0.304712816
HMlincRNA881	pl068152	chr11	45489988	45490384	+	array-star	0.187090164
ENST00000544515	pl068098	chr12	119287159	119346735	-	Ensembl	0.135681992
uc003dqi	pl068083	chr3	84687556	84918726	-	UCSC	0.121643809
AK130231	pl067987	chr3	24535577	24541502	+	NCBI	0.299785005
AK025388	pl067659	chr12	62253242	62628921	-	NCBI	0.274486025
NR_002215	pl067415	chr21	30699450	31003071	-	NCBI	0.193178848
	pl067391					Homologous	0.233325785
ENST00000536744	pl067257	chr12	22852875	23041867	+	Ensembl	0.081533636
NR_038254.1	pl067241	chr15	31062550	31065212	+	Other_database	0.135961678
	pl066804					Homologous	0.412303444
BC042947	pl066540	chr17	26218970	26221778	-	NCBI	0.285774281
uc002sed	pl066377	chr2	68350067	68384678	-	UCSC	0.202374537
HMlincRNA216	pl066318	chr12	69616287	69618022	+	array-star	0.098554645

AK093681	pl066076	chr9	5520912	5522711	-	NCBI	0.182118758
gnl|UG|Hs#S1785675	pl065990	chr7	33637609	33637855	+	Other_database	0.075220107
ENST00000451962	pl065969	chr7	112594701	112635689	-	Ensembl	0.085316104
ENST00000357045	pl065951	chr2	178467817	178483300	+	Ensembl	0.23258657
uc001ibs	pl065921	chr1	246939314	246955685	+	UCSC	0.352259841
HMlincRNA1482	pl065912	chr16	67116169	67579168	+	array-star	0.379076584
NR_023359.1	pl065880	chr18	20839535	20840434	+	Other_database	0.248010316
ENST00000508178	pl065419	chr3	109056665	109101875	+	Ensembl	0.141582815
uc010aym	pl065319	chr15	25366624	25420017	+	UCSC	0.107236247
	pl065270	chr1	108867152	108884252	+	Agilent	0.017545866
uc003png	pl065237	chr6	90311323	90348474	-	UCSC	0.091347287
uc001hox	pl065225	chr1	225428495	225585747	+	UCSC	0.200490106
ENST00000511515	pl065193	chr18	68047378	68243317	-	Ensembl	0.324217231
ENST00000450290	pl065041	chr2	80926513	81097315	-	Ensembl	0.157512886
	pl064931	chr3	162445031	162502906	+	Agilent	0.123083728
ENST00000450980	pl064849	chr10	38536850	38622083	+	Ensembl	0.091905489
uc001vii	pl064348	chr13	64560503	64650144	-	UCSC	0.063273072
HMlincRNA881	pl064286	chr11	45489988	45490384	+	array-star	0.289748355
ENST00000457178	pl064255	chr2	241166977	241195452	-	Ensembl	0.26787311
AF129755	pl064236	chr9	125157089	125157981	+	array-star	0.204413203
uc004crw	pl064191	chrX	7065292	7171377	+	UCSC	0.112712468
BQ638647	pl064188	chr13	45258810	45289952	+	array-star	0.361797302
ENST00000455247	pl063881	chr1	46921495	46948147	+	Ensembl	0.166983877
uc001kab	pl063873	chr10	80777213	80828536	-	UCSC	0.340910634
uc002btf	pl063791	chr15	94443929	94517161	+	UCSC	0.135353022
	pl063743	chr4	3572927	3634877	+	Agilent	0.337645519

uc004ajp	pl063615	chr9	77567884	77612298	+	UCSC	0.321837222
	pl063594	chr19	35281385	35321960	-	Agilent	0.419708168
ENST00000447206	pl063564	chr20	1784662	1798252	-	Ensembl	0.196069128
NR_040029.1	pl063545	chr19	29887314	29887858	-	Other_database	0.195156616
gnl|UG|Hs#S11153167	pl063538	chr10	101993817	101994181	+	Other_database	0.276902843
	pl063535	chr8	2360442	2383576	-	Agilent	0.253090587
CR749568	pl063532	chr10	105401917	105408105	-	NCBI	0.338482392
uc002gqr	pl063331	chr17	16826228	16838153	-	UCSC	0.236983533
ENST00000425176	pl063227	chr2	16535524	16613970	+	Ensembl	0.030025656
BC042675	pl063036	chr1	38674706	38678125	-	NCBI	0.329606896
NR_033440.1	pl062694	chr5	102201527	102201988	+	Other_database	0.405278964
HMlincRNA259	pl062494	chr17	33306242	33306872	+	array-star	0.213289939
ENST00000424820	pl062446	chr1	143347958	143365041	+	Ensembl	0.056431769
	pl062426	chr4	22361802	22371827	+	array-star	0.404943902
AX747026	pl062356	chr1	235690658	235693657	-	Other_database	0.252050855
ENST00000522173	pl062234	chr4	97231883	97740015	+	Ensembl	0.371395801
NR_003923	pl062202	chr13	51568647	51640293	-	NCBI	0.391008875
uc002jgm	pl062099	chr17	66097695	66122029	+	UCSC	0.321910193
ENST00000449333	pl061958	chr6	10434549	10452480	+	Ensembl	0.029783134
NR_045553.1	pl061650	chr1	155165379	155165601	-	Other_database	0.168446574
uc003wqb	pl061626	chr8	2554055	2585957	-	UCSC	0.31404197
gnl|UG|Hs#S29628089	pl061479	chr1	204463987	204464522	+	Other_database	0.283012139
uc010auv	pl061471	chr14	94770584	94789688	-	UCSC	0.403418931
uc001jlq	pl061316	chr10	63172652	63213208	-	UCSC	0.120197688
ENST00000425050	pl061286	chr10	109631334	109829052	-	Ensembl	0.215932645
DB020275	pl061222	chr12	125760196	125760639	+	array-star	0.072504867

uc009yfv	pl061202	chr11	10352116	10432385	+	UCSC	0.112502257
DA169732	pl061074	chr12	124727702	124728224	+	array-star	0.151126086
HIV1671	pl060969	chr11	27717858	27899195	-	NCBI	0.271289301
AF086561	pl060937	chr11	108018338	108018961	+	NCBI	0.410584699
	pl060823	chr12	105724564	105765318	-	Agilent	0.350232023
uc010jgq	pl060617	chr5	147443534	147475468	+	UCSC	0.057513843
NR_029455.1	pl060588	chr16	4845716	4845859	+	Other_database	0.034720339
ENST00000457178	pl060507	chr2	241166977	241195452	-	Ensembl	0.175020968
ENST00000427918	pl060470	chr13	80446721	80492079	+	Ensembl	0.024422639
BC004503	pl060334	chr11	64253242	64621138	+	array-star	0.054725463
HMlincRNA448	pl060299	chr5	57447268	57555573	+	array-star	0.10487017
NR_027255	pl060264	chr17	79139306	79156964	+	NCBI	0.257739525
uc003qgq	pl059606	chr6	136175173	136546762	-	UCSC	0.256642072
BG195202	pl059381	chr8	122381351	122396934	+	array-star	0.314488638
ENST00000518536	pl059361	chr8	59004001	59018853	-	Ensembl	0.089877491
DN995775	pl059220	chr7	7994792	7995376	+	array-star	0.092264218
HMlincRNA878	pl059147	chr2	188194853	188195100	+	array-star	0.285965462
	pl059098					Homologous	0.075644571
BC022402	pl059072	chr8	74964574	75012085	+	NCBI	0.101146959
BE254843	pl059044	chr7	38076646	38077303	+	array-star	0.290759439
uc.155+	pl058804	chr5	76934363	76934570	+	NCBI	0.070468153
ENST00000557070	pl058714	chr14	87819414	88039366	-	Ensembl	0.087073541
ENST00000511073	pl058534	chr11	28923828	29085368	+	Ensembl	0.076236818
NR_024377	pl058432	chr20	34146506	34195484	-	NCBI	0.041847225
HMlincRNA37	pl058271	chr2	208560105	208560502	+	array-star	0.398509936
uc010mzg	pl058241	chr9	134062675	134109091	+	UCSC	0.41474785

ENST00000430692	pl058128	chr2	126468546	126523419	+	Ensembl	0.404354837
BX092772	pl058108	chr1	229294744	229295273	+	array-star	0.33596884
ENST00000531136	pl057897	chr11	13076162	13156386	-	Ensembl	0.199391772
BX648590	pl057833	chrX	28520041	28523402	-	NCBI	0.18889622
uc001kpb	pl057654	chr10	100143323	100171634	-	UCSC	0.336637397
uc002uib	pl057379	chr2	174062442	174146581	-	UCSC	0.018536859
AK056769	pl057151	chr17	1311760	1475838	-	NCBI	0.250681035
ENST00000529088	pl057150	chr11	97093644	97130987	-	Ensembl	0.368487017
AK130268	pl057012	chr1	8086797	8182763	+	NCBI	0.148021147
gnl|UG|Hs#S11129466	pl056953	chr1	109073814	109074235	-	Other_database	0.22963753
ENST00000527492	pl056891	chr11	29616465	29652211	+	Ensembl	0.255202104
NR_024344	pl056880	chr11	133766329	133771635	-	NCBI	0.076522473
uc010ige	pl056867	chr4	46736846	46911252	-	UCSC	0.183297412
HMlincRNA1153	pl056847	chr1	27535137	27535184	+	array-star	0.186154458
ENST00000445072	pl056780	chr1	188874819	189006393	+	Ensembl	0.098742357
uc001ytr	pl056764	chr15	21899846	21902842	-	Other_database	0.281504305
AK096981	pl056669	chr11	120039684	120042387	+	NCBI	0.137069076
BM678241	pl056630	chr17	68774744	69000634	+	array-star	0.05111295
ENST00000519568	pl056519	chr8	10587088	10628902	+	Ensembl	0.072764285
ENST00000435411	pl056362	chr2	181988564	182264286	+	Ensembl	0.112166454
NR_003245.1	pl056273	chr20	61726844	61733671	-	LNCRNA-DB	0.239641559
BC043241	pl056224	chr16	63090692	63163558	-	NCBI	0.090315604
ENST00000455406	pl056182	chr1	71547007	71703406	+	Ensembl	0.21726372
ENST00000398664	pl056162	chr16	32264040	32267240	+	Ensembl	0.131368201
uc003qlt	pl056067	chr6	147163036	147525750	-	UCSC	0.087047636
ENST00000537498	pl056033	chr16	89112580	89119373	-	Ensembl	0.342153629

uc001amm	pl055996	chr1	6297870	6299490	+	UCSC	0.403869988
AK055900	pl055942	chr18	13239541	13242075	+	NCBI	0.350617506
BC033713	pl055742	chr3	123329583	123330850	-	NCBI	0.381605013
ENST00000522807	pl055721	chr8	79338338	79470728	-	Ensembl	0.202457163
NR_027300.2	pl055663	chr19	10184593	10184814	+	Other_database	0.270571397
	pl055196	chrX	45555906	45580831	-	Agilent	0.100562006
	pl054959	chr2	131622680	131659080	-	Agilent	0.08109548
	pl054896	chr6	378525	386550	-	Agilent	0.049807788
ENST00000509470	pl054872	chr12	119825796	120032306	-	UCSC	0.286454978
ENST00000435411	pl054664	chr2	181988564	182264286	+	Ensembl	0.095302756
HMlincRNA48	pl054661	chr2	222686212	222825543	+	array-star	0.194422296
BC033352	pl054643	chr6	164092635	164181405	+	NCBI	0.277193557
AK128292	pl054532	chr11	129944692	129947507	+	NCBI	0.406399945
uc010aym	pl054506	chr15	25366624	25420017	+	UCSC	0.282982398
DB125499	pl054356	chr18	20500724	20513726	+	array-star	0.189540658
ENST00000505347	pl054293	chr4	19173958	19458617	-	Ensembl	0.181613009
uc003oke	pl054223	chr6	35172922	35178950	-	UCSC	0.186242107
HMlincRNA975	pl054177	chr4	122589037	122589523	+	array-star	0.353089385
AK126802	pl054134	chr5	6686437	6707824	-	NCBI	0.07127354
AK097109	pl054083	chr15	83652802	83654866	-	NCBI	0.402085455
uc001twt	pl053897	chr12	118539409	118541749	-	UCSC	0.307520097
HMlincRNA783	pl053810	chr18	10737660	10748498	+	array-star	0.374238734
AF495723	pl053717	chr3	46934286	46936550	+	NCBI	0.156330482
NR_034152.1	pl053650	chr20	31196112	31196695	+	Other_database	0.158127817
uc001dsd	pl053590	chr1	99469831	99614408	+	UCSC	0.165924953
	pl053387	chr18	39101339	39212100	-	Agilent	0.204214391

ENST00000522460	pl053307	chr8	34085957	34204249	+	Ensembl	0.148050519
	pl053232	chr4	3297502	3310352	+	array-star	0.106695035
uc003ppy	pl053124	chr6	99910340	99958106	-	UCSC	0.334467945
CU693173	pl053119	chr5	153311396	153433272	+	array-star	0.271183094
BI771000	pl053068	chr12	32101722	32101790	+	array-star	0.208588509
	pl052977	chr2	129195780	129215280	-	Agilent	0.09159287
NR_003189.2	pl052883	chr20	44038572	44039250	+	Other_database	0.200655406
ENST00000431158	pl052802	chr20	62667016	62670354	+	Ensembl	0.157547664
ENST00000441069	pl052438	chr10	102874956	102901023	-	Ensembl	0.277847225
uc001vks	pl052387	chr13	78493823	79158296	+	UCSC	0.060534031
uc002ylj	pl052335	chr21	26212863	26430052	+	UCSC	0.056815417
AK055697	pl052284	chr6	96996505	97142303	-	NCBI	0.115263008
BC036122	pl052169	chr1	90098630	90230061	+	array-star	0.390720041
ENST00000422117	pl051985	chr15	25729978	25823938	-	Ensembl	0.29648229
uc002uab	pl051816	chr2	159514848	159591514	-	UCSC	0.199204741
ENST00000522776	pl051814	chr8	83426803	83589388	-	Ensembl	0.079768675
	pl051810	chr8	124456094	124469294	+	Agilent	0.404364521
DB151746	pl051799	chr10	119210079	119210532	+	array-star	0.325438987
HMlincRNA188	pl051721	chr21	46799592	46799875	+	array-star	0.088129624
HMlincRNA926	pl051675	chr20	35973087	36011190	+	array-star	0.254736793
BC045646	pl051471	chr2	13047428	13049982	-	NCBI	0.056711693
AF073328	pl051418	chr13	44350357	44350758	+	NCBI	0.120471113
AX765694	pl050996	chr2	206057922	206166352	-	NCBI	0.125340781
ENST00000409758	pl050986	chr21	26541745	26706139	-	Ensembl	0.318550531
BC033875	pl050896	chr20	43375282	43375841	+	NCBI	0.088195504
ENST00000445035	pl050878	chr17	14741279	14803871	+	Ensembl	0.356020329

gnl|UG|Hs#S1453017	pl050798	chr3	45019388	45019582	-	Other_database	0.251997289
ENST00000527819	pl050749	chr11	30065605	30105890	-	Ensembl	0.053906591
ENST00000525097	pl050670	chr11	29357425	29615842	-	Ensembl	0.080086725
HMlincRNA752	pl050568	chr5	139740229	139880985	+	array-star	0.068425091
ENST00000514863	pl050382	chr4	14166079	14244437	+	Ensembl	0.255974817
AK130578	pl050375	chr16	89232790	89235555	+	NCBI	0.160838243
AB209630	pl050273	chr9	71863611	71870118	-	NCBI	0.193246619
uc001mmh	pl050158	chr11	16285994	16760190	-	UCSC	0.432290454
uc001awg	pl050151	chr1	15707196	15726776	+	UCSC	0.116293471
	pl050064	chr20	23985300	24015300	+	array-star	0.190673657
BG182718	pl050017	chr11	98014749	98014947	+	array-star	0.086294441
HMlincRNA1147	pl049989	chr1	31849969	31850331	+	array-star	0.200576305
	pl049928	chr5	54162493	54208143	-	Agilent	0.456562181
HMlincRNA975	pl049503	chr4	122589037	122589523	+	array-star	0.366476272
DN918054	pl049454	chr1	66890612	67423817	+	array-star	0.044193954
NR_028439.1	pl049444	chr17	73632675	73635674	+	Other_database	0.206176592
uc001pwp	pl049370	chr11	119252519	119397374	+	UCSC	0.183724275
AA292843	pl049358	chr5	106300100	106300653	+	array-star	0.024018583
CR613812	pl049158	chr9	503056	504746	-	NCBI	0.325837314
uc003uhk	pl049102	chr7	81205702	81320722	-	UCSC	0.157218174
uc010bad	pl048903	chr15	32322725	32404564	+	UCSC	0.135726004
HMlincRNA965	pl048800	chr3	168819873	169381208	+	array-star	0.301825788
exon3200	pl048665	chr5	149993807	149993875	+	array-star	0.250660171
DN918054	pl048518	chr1	66890612	67423817	+	array-star	0.151764229
	pl048364	chr2	129403638	129408192	-	Agilent	0.322043125
HMlincRNA784	pl048066	chr18	10857083	10979616	+	array-star	0.26958177

ENST00000435237	pl048059	chr2	21444047	22193831	+	Ensembl	0.133662678
ENST00000415869	pl048006	chr3	193920805	193967942	-	Ensembl	0.137128465
ENST00000432481	pl047571	chr2	229347977	229476111	-	Ensembl	0.411329898
ENST00000509964	pl047534	chr4	17173380	17187682	-	Ensembl	0.159926374
	pl047439	chr5	79293744	79313769	-	Agilent	0.369109665
CN413842	pl047364	chr10	58860945	58868511	+	array-star	0.184416438
HMlincRNA752	pl047302	chr5	139740229	139880985	+	array-star	0.173237433
	pl047152	chr8	128301923	128335401	-	Agilent	0.163415444
AK124532	pl047126	chr8	53063379	53068443	-	NCBI	0.082137012
	pl047074	chr10	65236069	65272880	-	Agilent	0.341515015
AK092436	pl046972	chr17	29295903	29297911	-	NCBI	0.057462871
uc010mrt	pl046917	chr9	98242671	98268881	-	UCSC	0.065535356
BC033654	pl046881	chr19	34991859	34992074	+	NCBI	0.373886948
ENST00000430468	pl046867	chr22	27539439	27555840	+	Ensembl	0.082712167
BC020465	pl046856	chr2	182414361	182521833	+	NCBI	0.416315821
ENST00000449903	pl046763	chr7	157294016	157296271	+	Ensembl	0.169331473
HMlincRNA188	pl046642	chr21	46799592	46799875	+	array-star	0.128643721
uc003qlt	pl046578	chr6	147163036	147525750	-	UCSC	0.100628768
AW135489	pl046471	chr2	192787269	192895368	+	array-star	0.31672474
ENST00000479592	pl046067	chr7	149731	153490	+	Ensembl	0.266478674
ENST00000422763	pl045955	chr10	54211074	54230293	-	Ensembl	0.167849735
ENST00000537498	pl045942	chr16	89112580	89119373	-	Ensembl	0.237420768
ENST00000436350	pl045927	chr1	65458602	65468123	-	Ensembl	0.158735359
AK025378	pl045697	chr19	39692192	39692522	+	NCBI	0.111338472
ENST00000544164	pl045481	chr3	104241218	104331339	+	Ensembl	0.049308035
gnl|UG|Hs#S21643699	pl045376	chrX	119204641	119204736	+	Other_database	0.262849352

exon2400	pl045364	chr20	31164464	31164598	+	array-star	0.275186398
ENST00000415342	pl045345	chr2	69927324	69940979	-	Ensembl	0.081796257
ENST00000452690	pl045285	chrX	40122170	40146973	+	Ensembl	0.066958979
ENST00000432665	pl045077	chr2	11539295	11542387	+	Ensembl	0.181961218
uc003ixc	pl044759	chr4	185973049	186028402	+	UCSC	0.132222333
uc002xml	pl044751	chr20	43289218	43367608	-	UCSC	0.197872937
	pl044567	chr8	76121095	76189420	-	Agilent	0.149990358
uc002ljy	pl044435	chr18	61880319	61927288	-	UCSC	0.207657011
ENST00000525111	pl044428	chr17	35289409	35293921	-	Ensembl	0.198164932
ENST00000434983	pl044268	chr1	191190289	191197597	+	Ensembl	0.091313159
ENST00000522265	pl044259	chr8	64326191	64382757	-	Ensembl	0.172824007
ENST00000413094	pl044097	chr7	68652820	68654305	-	Ensembl	0.307939814
NR_027064	pl044051	chr19	5558179	5568005	-	NCBI	0.256507174
uc009vji	pl043814	chr1	578101	581100	-	Other_database	0.34968208
NR_031766.2	pl043719	chr12	117476728	117477015	-	Other_database	0.244272103
ENST00000550506	pl043636	chr12	82347498	82386912	+	Ensembl	0.075095548
NR_002817	pl043600	chr9	67270214	67289492	-	NCBI	0.128237771
ENST00000541769	pl043478	chr12	127112718	127174868	-	Ensembl	0.158187422
NR_026816	pl043397	chr6	31141511	31145676	-	NCBI	0.173289362
uc004bcy	pl043310	chr9	109378338	109442079	+	UCSC	0.330609959
HMlincRNA975	pl043297	chr4	122589037	122589523	+	array-star	0.407755998
HMlincRNA93	pl043224	chr1	203128624	203317403	+	array-star	0.138112995
gnl|UG|Hs#S979456	pl043143	chr3	133101814	133102279	+	Other_database	0.139362123
uc001llc	pl043135	chr10	134020995	134062612	-	UCSC	0.418348163
ENST00000429389	pl043027	chr1	2730997	2731563	-	Ensembl	0.113342864
NR_038453.1	pl043014	chr10	72976981	72977392	-	Other_database	0.271125205

ENST00000448643	pl042971	chr1	166356964	166421869	-	Ensembl	0.213907701
HMlincRNA167	pl042876	chr6	123135447	123154467	+	array-star	0.302932401
NR_045553.1	pl042847	chr1	155174851	155175107	-	Other_database	0.200122492
ENST00000505347	pl042662	chr4	19173958	19458617	-	Ensembl	0.277116449
ENST00000437601	pl042589	chr1	234861148	234867390	+	Ensembl	0.305323815
	pl042566					Homologous	0.361957928
	pl042503	chrX	36772104	36806404	+	array-star	0.129946488
uc003laj	pl042455	chr5	134368969	134680370	+	UCSC	0.213511763
ENST00000425050	pl042452	chr10	109631334	109829052	-	Ensembl	0.072008512
ENST00000426491	pl042388	chr20	10055085	10200154	-	Ensembl	0.285014944
NR_026796	pl042387	chr14	56247853	56263392	-	NCBI	0.329939012
BC052960	pl042309	chr19	16653433	16655618	+	NCBI	0.410641455
gnl|UG|Hs#S15910530	pl042127	chr3	169377261	169377794	-	Other_database	0.429465056
NR_003245.1	pl042101	chr20	61726844	61733671	-	LNCRNA-DB	0.201078491
uc010ggb	pl041970	chr20	37434347	37459230	+	UCSC	0.094675899
ENST00000450290	pl041937	chr2	80926513	81097315	-	Ensembl	0.163590445
	pl041833	chr4	90636702	90646690	-	Agilent	0.198449852
NR_027064	pl041754	chr19	5558179	5568005	-	NCBI	0.205367091
	pl041707	chr13	27624125	27640099	-	Agilent	0.263704037
ENST00000551921	pl041700	chr12	87120982	87232905	-	Ensembl	0.168925575
	pl041608	chr14	42861350	43287750	+	Agilent	0.361065321
AW340752	pl041286	chr8	8978686	8978930	+	array-star	0.277455176
BC009643	pl041213	chr5	65509778	65510490	+	NCBI	0.250032932
ENST00000420000	pl041197	chr3	3292371	3668980	-	Ensembl	0.091238553
AK001551	pl041171	chr12	106097980	106137840	+	NCBI	0.407382065
CF593671	pl041159	chr16	48705761	48706178	+	array-star	0.340121678

uc001tyk	pl041122	chr12	120928822	120933728	-	UCSC	0.315891816
	pl040986	chr2	54242671	54312471	-	Agilent	0.11311547
ENST00000494340	pl040976	chr3	82035303	82251605	+	Ensembl	0.184433235
AK125472	pl040975	chr13	113257141	113260731	-	NCBI	0.237992545
ENST00000527770	pl040837	chr11	15574401	15612644	+	Ensembl	0.058255182
AK126088	pl040803	chr15	75761708	75767662	+	NCBI	0.094668787
uc002cmj	pl040734	chr16	1756220	1797276	+	UCSC	0.033030852
AK098015	pl040503	chr20	44033584	44035723	-	NCBI	0.174361543
uc004bls	pl040410	chr9	124646914	124725998	-	UCSC	0.054620722
HMlincRNA1497	pl040398	chr16	87857093	87857622	+	array-star	0.179885383
AK130172	pl040272	chr1	2495246	2497050	-	NCBI	0.106073477
HMlincRNA798	pl039976	chr18	44497556	44624853	+	array-star	0.289829166
DC295389	pl039631	chr4	26165175	26364251	+	array-star	0.152173747
ENST00000447916	pl039579	chr1	102665295	102855186	-	Ensembl	0.180039365
NR_027082	pl039446	chr10	10826401	10836877	-	NCBI	0.089605582
HMlincRNA1448	pl039242	chr4	185410647	185410993	+	array-star	0.438856367
ENST00000514474	pl039188	chr5	5057844	5067442	+	Ensembl	0.16970082
uc001alp	pl039172	chr1	5621768	5728315	-	UCSC	0.210910495
NR_026941	pl039153	chr10	119806331	119859641	+	NCBI	0.265991036
uc001wds	pl039140	chr14	22849082	22951948	-	UCSC	0.215971983
	pl039021	chrX	38863681	38944131	-	Agilent	0.411414126
ENST00000419463	pl038998	chr7	17414491	17506288	+	Ensembl	0.225012004
NR_039987.1	pl038946	chr7	63484794	63487382	-	Other_database	0.122483963
uc001jeo	pl038679	chr10	47746919	47770843	+	UCSC	0.116713375
HMlincRNA1472	pl038588	chr19	13976416	13976837	+	array-star	0.429025219
	pl038570	chr22	25873025	25887500	-	Agilent	0.150192512

uc002zrw	pl038375	chr22	20291560	20299716	+	UCSC	0.243641182
uc010jxu	pl038316	chr6	42237236	42419865	-	UCSC	0.103973981
uc003hzi	pl038241	chr4	110268630	110335566	-	UCSC	0.405392739
ENST00000524011	pl038110	chr8	49464575	49469001	-	Ensembl	0.116390805
	pl038048	chr18	43652652	43662027	-	Agilent	0.145336956
uc003ndl	pl038014	chr6	21898950	22214732	+	UCSC	0.054792447
AF495723	pl037942	chr3	46934286	46936550	+	NCBI	0.256425149
	pl037886	chr3	165198855	165244262	-	Agilent	0.044305692
AK123685	pl037711	chr14	45232359	45252032	-	NCBI	0.069868423
AK096940	pl037507	chr10	134228534	134231356	+	NCBI	0.477693186
uc010gwq	pl037439	chr22	33712070	33968248	-	UCSC	0.161364628
NR_038978.1	pl037279	chrX	102942880	102944408	+	Other_database	0.315264219
	pl037002	chr4	90602655	90613743	+	Agilent	0.15271105
uc003png	pl036763	chr6	90311323	90348474	-	UCSC	0.151418361
HMlincRNA699	pl036473	chr19	15687343	15694207	+	array-star	0.325909473
NR_036484.1	pl036256	chr7	121945342	121946316	+	Other_database	0.018873269
	pl036184					Homologous	0.04986718
gnl|UG|Hs#S1280128	pl036094	chr11	118756598	118757057	-	Other_database	0.200454177
NR_028439.1	pl035845	chr17	73635665	73636408	+	Other_database	0.05669018
ENST00000424084	pl035830	chr1	25370198	25439610	-	Ensembl	0.149294392
ENST00000415182	pl035808	chr21	25801095	25920256	+	Ensembl	0.167716005
uc001jtm	pl035603	chr10	74884659	74885290	-	UCSC	0.33886441
ENST00000444868	pl035313	chr21	18126838	18188007	-	Ensembl	0.331251677
CF541047	pl035216	chrX	106920110	106920484	+	array-star	0.258754994
ENST00000519185	pl034992	chr8	19103860	19106750	+	Ensembl	0.131683953
gnl|UG|Hs#S964976	pl034986	chr7	20371911	20372127	+	Other_database	0.237323993

ENST00000525097	pl034954	chr11	29357425	29615842	-	Ensembl	0.328698765
uc002hrd	pl034899	chr17	37186158	37209458	+	UCSC	0.030685788
HMlincRNA714	pl034819	chr2	108792457	108793750	+	array-star	0.1194197
AX747026	pl034779	chr1	235484348	235487347	-	Other_database	0.388209171
uc002vso	pl034657	chr2	232888986	233201686	+	UCSC	0.346047879
AK095144	pl034638	chr11	506462	514689	+	NCBI	0.297313085
NR_027242.1	pl034359	chr16	1114081	1116526	-	Other_database	0.291925742
uc002kwv	pl034227	chr18	29122109	29136874	-	UCSC	0.187543039
HMlincRNA783	pl034154	chr18	10737660	10748498	+	array-star	0.287495323
HMlincRNA784	pl034131	chr18	10857083	10979616	+	array-star	0.155581967
AK095422	pl034130	chr9	120985963	120988842	+	NCBI	0.147147152
uc004asr	pl034125	chr9	95571813	95650973	+	UCSC	0.177996247
uc001glv	pl034087	chr1	178482211	178517734	+	UCSC	0.358847077
BC036877	pl034021	chr1	14925212	15441219	-	NCBI	0.27249852
AK024235	pl033863	chr4	153696473	153699355	-	NCBI	0.24337001
AA456070	pl033807	chr15	99971296	99971642	+	array-star	0.148234873
ENST00000549896	pl033692	chr12	97417799	97444907	+	Ensembl	0.046779932
HMlincRNA460	pl033414	chr10	75386244	75386818	+	array-star	0.387323627
gnl|UG|Hs#S4859458	pl033273	chr5	138157628	138157842	+	Other_database	0.24589768
CR604114	pl033073	chr8	27727432	27728899	-	NCBI	0.047012548
NR_027012.1	pl033063	chr8	47766386	47767407	+	Other_database	0.344206432
	pl032883	chr3	99226030	99245957	+	Agilent	0.224275494
BE048618	pl032870	chr12	28286181	28603351	+	array-star	0.135745439
AK024373	pl032811	chr19	438420	2083745	-	NCBI	0.295449491
HMlincRNA1145	pl032608	chr1	32374259	32403955	+	array-star	0.131405801
NR_003187.2	pl032579	chr7	74203383	74203720	+	Other_database	0.24633639

ENST00000435466	pl032552	chr7	110072296	110174811	-	Ensembl	0.182188706
BM977434	pl032509	chr10	116568848	116569274	+	array-star	0.257086866
ENST00000422558	pl032415	chr2	34608855	34860407	+	Ensembl	0.07364687
uc001ihl	pl032354	chr10	4868401	5067607	+	UCSC	0.274683418
BU659324	pl032349	chr12	93397533	93771506	+	array-star	0.242222374
DB071720	pl032346	chr8	140126435	140140196	+	array-star	0.039528831
NR_033914.1	pl032177	chr16	1928286	1928711	-	Other_database	0.131067869
AK026607	pl032144	chr11	44580598	44972434	+	array-star	0.437114419
ENST00000515304	pl032109	chr5	148443049	148443737	+	Ensembl	0.245161804
HMlincRNA565	pl032041	chr8	141669167	142011332	+	array-star	0.020895554
uc002jpz	pl032035	chr17	73894723	73905899	-	UCSC	0.166902749
ENST00000430060	pl032016	chr21	23119305	23169735	+	Ensembl	0.126796197
AK094730	pl032006	chr12	117293949	117295968	-	NCBI	0.168927806
exon2407	pl031991	chr20	31164464	31164598	+	array-star	0.217393923
DN918054	pl031914	chr1	66890612	67423817	+	array-star	0.322366057
BE088726	pl031783	chr11	10747894	10748353	+	array-star	0.33107965
HMlincRNA965	pl031733	chr3	168819873	169381208	+	array-star	0.333052424
ENST00000445035	pl031725	chr17	14741279	14803871	+	Ensembl	0.156284203
AK310207	pl031699	chr3	183853163	184402546	+	array-star	0.137392929
DN995775	pl031434	chr7	7994792	7995376	+	array-star	0.039537872
AK055794	pl031400	chr6	168643617	168663258	+	NCBI	0.408413903
ENST00000498241	pl031363	chr3	157734160	157806786	+	Ensembl	0.116478308
	pl031333	chr9	36456325	36463750	+	Agilent	0.160291558
AA630432	pl031222	chr3	5795170	5795620	+	array-star	0.316472631
HMlincRNA1208	pl030829	chr4	82745704	82965396	+	array-star	0.06192027
uc002bwo	pl030658	chr15	101433944	101459488	-	UCSC	0.401166177

ENST00000432142	pl030521	chr2	19203707	19505815	-	Ensembl	0.42634974
	pl030516	chr20	36135611	36143561	-	Agilent	0.276035271
ENST00000444745	pl030502	chr7	67485240	67497677	+	Ensembl	0.033612626
ENST00000442182	pl030491	chr1	117838142	117863958	+	Ensembl	0.432745683
ENST00000523317	pl030295	chr8	135224108	135332690	-	Ensembl	0.227279082
ENST00000454965	pl030215	chr2	146051845	146089415	-	Ensembl	0.019499685
	pl030166	chr7	759174	766024	-	Agilent	0.285108374
	pl030006	chr5	1173255	1175321	+	Agilent	0.311610717
CR596092	pl029957	chr1	23940282	23945957	-	NCBI	0.242274504
HIV1163	pl029906	chr17	41382053	41382545	+	Other_database	0.186588243
uc002zrw	pl029867	chr22	20291560	20299716	+	UCSC	0.213954596
ENST00000436187	pl029859	chr2	8710461	8717085	-	Ensembl	0.20428783
uc001mmh	pl029693	chr11	16285994	16760190	-	UCSC	0.206543911
ENST00000456848	pl029681	chr13	36271864	36273393	+	Ensembl	0.026278726
AK123380	pl029649	chr11	8828480	8831406	-	NCBI	0.249950608
	pl029648	chr2	113961404	113966929	-	Agilent	0.389651406
ENST00000504537	pl029577	chr4	60416860	60496042	-	Ensembl	0.255555708
	pl029564	chr14	104345747	104366672	-	Agilent	0.141919035
	pl029474	chr7	18274475	18527150	+	Agilent	0.266698269
	pl029451	chr9	132251514	132265917	+	Agilent	0.303930995
uc002gnc	pl029420	chr17	11465073	11467378	+	UCSC	0.003103342
uc003ysp	pl029351	chr8	130228710	130253496	-	UCSC	0.104085491
uc001cjy	pl029149	chr1	44165357	44173012	-	UCSC	0.374620301
CR746141	pl029103	chr2	191708543	191709304	+	array-star	0.258636282
BC004503	pl028941	chr11	64253242	64621138	+	array-star	0.151428985
	pl028896	chr2	157003729	157110279	+	Agilent	0.289412758

HMlincRNA783	pl028866	chr18	10737660	10748498	+	array-star	0.231295801
	pl028833	chr3	136738660	136787685	-	Agilent	0.251104576
ENST00000556070	pl028800	chr2	113993113	114023294	+	Ensembl	0.207770911
	pl028780	chr12	76316708	76327283	+	Agilent	0.094708419
uc010jgq	pl028642	chr5	147443534	147475468	+	UCSC	0.060551413
BF746429	pl028495	chr1	39183439	39183984	+	array-star	0.317950344
HMlincRNA188	pl028380	chr21	46799592	46799875	+	array-star	0.078995059
BC040662	pl028325	chr10	68868454	68872073	+	NCBI	0.255294541
ENST00000499504	pl028231	chr11	86666754	86712001	+	Ensembl	0.137707868
gnl|UG|Hs#S3538626	pl028145	chr6	140589940	140590162	-	Other_database	0.103258572
HMlincRNA125	pl028018	chr1	226314861	226315111	+	array-star	0.165737801
uc003laj	pl027978	chr5	134368969	134680370	+	UCSC	0.164786201
ENST00000430635	pl027766	chr21	36096105	36109478	-	Ensembl	0.168294132
ENST00000515860	pl027737	chr4	139346677	139358023	+	Ensembl	0.103503213
HMlincRNA1104	pl027708	chr9	14087859	14398982	+	array-star	0.146125353
AW135489	pl027620	chr2	192787269	192895368	+	array-star	0.188895576
NR_024279	pl027500	chr1	16160709	16174642	-	NCBI	0.346523128
	pl027153	chr7	18274475	18527150	+	Agilent	0.094564954
uc009xbd	pl027109	chr1	204423796	204459474	-	UCSC	0.341135915
uc001jeo	pl027083	chr10	47746919	47770843	+	UCSC	0.273723999
uc002seq	pl026962	chr2	68756772	68857856	+	UCSC	0.246820131
ENST00000445967	pl026761	chr13	86634948	86745025	+	Ensembl	0.25194204
uc002wca	pl026713	chr2	242615156	242626227	-	UCSC	0.314975523
AK023763	pl026685	chr15	82044851	82048420	-	NCBI	0.421847652
DQ655919	pl026597	chrX	123094061	123164898	-	NCBI	0.235718985
uc010jgq	pl026594	chr5	147443534	147475468	+	UCSC	0.107374846

NR_026687	pl026566	chr9	27245683	27282791	-	NCBI	0.242206323
HMlincRNA742	pl026516	chr10	32086016	32086562	+	array-star	0.323748188
BC036859	pl026321	chr6	5892677	5986353	+	array-star	0.152787425
	pl026285	chr1	1100287	1108062	-	Agilent	0.218168339
	pl026145	chr14	96505728	96560235	-	Agilent	0.137559367
ENST00000445967	pl025960	chr13	86634948	86745025	+	Ensembl	0.209738608
	pl025926	chr2	64481986	64487773	+	Agilent	0.36988649
ENST00000508977	pl025907	chr4	172523834	172559914	-	Ensembl	0.068610468
gnl|UG|Hs#S1542105	pl025795	chr8	27758325	27758643	+	Other_database	0.232208843
	pl025774	chr2	131622680	131659080	-	Agilent	0.123185977
uc003sme	pl025540	chr7	2477397	2487484	+	UCSC	0.140431456
	pl025482	chr3	36919496	36994321	-	Agilent	0.098097894
ENST00000442026	pl025411	chr2	33931975	34286114	+	Ensembl	0.230808992
uc001mmh	pl025396	chr11	16285994	16760190	-	UCSC	0.103977553
uc002jis	pl025249	chr17	69093915	69198318	-	UCSC	0.301582431
NR_036491.1	pl025120	chr8	101145588	101145946	-	Other_database	0.304702652
uc002syn	pl025117	chr2	98703594	98928495	+	UCSC	0.08940606
gnl|UG|Hs#S29626772	pl024942	chr18	24981320	24981867	-	Other_database	0.158171879
gnl|ncrnascan|RNS1802	pl024803	chr7	1585494	1585681	+	ncRNASCAN	0.313677998
uc003hho	pl024747	chr4	74988990	75047508	+	UCSC	0.287683919
ENST00000525097	pl024619	chr11	29357425	29615842	-	Ensembl	0.077743159
ENST00000416069	pl024555	chr6	56979709	57037194	-	Ensembl	0.346640619
	pl024485	chr8	142243843	142266943	-	Agilent	0.30400679
HMlincRNA787	pl024459	chr18	56529831	56653197	+	array-star	0.070108849
	pl024126	chr21	15789329	15846029	+	array-star	0.044764149
HMlincRNA1147	pl024051	chr1	31849969	31850331	+	array-star	0.174697904

HMlincRNA361	pl023992	chr10	3852682	3853082	+	array-star	0.053528203
ENST00000421825	pl023844	chr7	119808399	119826118	+	Ensembl	0.218911912
ENST00000425050	pl023752	chr10	109631334	109829052	-	Ensembl	0.419455869
ENST00000357045	pl023744	chr2	178467817	178483300	+	Ensembl	0.329494795
uc.464-	pl023652	chrX	24916157	24916927	-	NCBI	0.136973165
AW665767	pl023574	chr8	104369498	104370036	+	array-star	0.083548673
NR_037844.1	pl023546	chr1	2487208	2488135	-	Other_database	0.041451927
HMlincRNA1482	pl023215	chr16	67116169	67579168	+	array-star	0.349816347
HMlincRNA1014	pl023181	chr4	152243990	152244383	+	array-star	0.165072945
DQ374660	pl022740	chr9	79379419	79399073	+	NCBI	0.046350101
gnl|UG|Hs#S845087	pl022739	chr4	143078444	143078689	+	Other_database	0.1362459
	pl022737	chr14	101825047	101840347	-	Agilent	0.284186435
HMlincRNA1575	pl022588	chr3	134334206	134670498	+	array-star	0.405261981
	pl022533	chrX	115860921	116031623	-	Agilent	0.142442067
HMlincRNA1153	pl022278	chr1	27535137	27535184	+	array-star	0.155145878
HMlincRNA1387	pl022086	chr15	86687043	86791045	+	array-star	0.421402992
ENST00000454441	pl022085	chr7	153097005	153109319	-	Ensembl	0.106080739
ENST00000443123	pl022039	chr2	107871147	107982329	-	Ensembl	0.221038369
BU659324	pl021982	chr12	93397533	93771506	+	array-star	0.325298399
CX166999	pl021884	chr1	38893048	38911529	+	array-star	0.129308503
W95626	pl021871	chrX	51140217	51140982	+	array-star	0.134526694
	pl021858	chr13	54812799	54928899	-	Agilent	0.205962941
gnl|ncrnascan|RNS2149	pl021705	chr19	710728	710867	+	ncRNASCAN	0.395957377
	pl021681	chr8	128976068	129037346	-	Agilent	0.071619981
BI481255	pl021389	chr6	118705640	118706006	+	array-star	0.244836792
NR_033122.1	pl021243	chr11	119060172	119060932	+	Other_database	0.23597877

uc003uhk	pl021220	chr7	81205702	81320722	-	UCSC	0.219306887
BC046120	pl021195	chr1	42312861	42501596	+	array-star	0.088963421
uc001gro	pl020980	chr1	185527513	185597620	-	UCSC	0.080991386
BC036235	pl020739	chr8	58173784	58179168	+	NCBI	0.168655573
BX648971	pl020668	chr4	166605790	166683930	+	NCBI	0.098896997
HMlincRNA784	pl020568	chr18	10857083	10979616	+	array-star	0.340700649
ENST00000420000	pl020452	chr3	3292371	3668980	-	Ensembl	0.177334315
uc009web	pl020440	chr1	100810593	100963763	+	UCSC	0.294788495
uc002jyi	pl020438	chr17	78326338	78388918	-	UCSC	0.157816949
uc010ixa	pl020293	chr5	66300498	66400403	+	UCSC	0.275522184
BG200518	pl020232	chr4	106269335	106269684	+	array-star	0.338309408
uc001wfa	pl020224	chr14	22975411	22975687	+	UCSC	0.437230311
ENST00000519040	pl020119	chr5	149855094	149865531	-	Ensembl	0.264013171
AK026607	pl020063	chr11	44580598	44972434	+	array-star	0.1998054
ENST00000424257	pl019839	chr2	105197279	105198348	-	Ensembl	0.019262801
HMlincRNA752	pl019776	chr5	139740229	139880985	+	array-star	0.181022374
BQ329856	pl019690	chr8	59355920	59560809	+	array-star	0.12685514
ENST00000523363	pl019681	chr9	26746951	26786872	+	Ensembl	0.165231418
AK054933	pl019665	chr17	79374889	79376779	+	NCBI	0.156737627
uc001mfk	pl019640	chr11	7597997	7674984	+	UCSC	0.206481176
ENST00000494340	pl019629	chr3	82035303	82251605	+	Ensembl	0.161153469
uc009wso	pl019582	chr1	157646278	157670647	-	UCSC	0.256869468
	pl019544	chr2	235075047	235108708	+	Agilent	0.165882811
uc002sir	pl019366	chr2	73276214	73298418	-	UCSC	0.060677097
	pl019286	chr10	49927719	49938069	-	Agilent	0.134288009
	pl019222	chr8	6554042	6564617	-	Agilent	0.42898606

uc001wds	pl019178	chr14	22849082	22951948	-	UCSC	0.090820197
ENST00000505347	pl019161	chr4	19173958	19458617	-	Ensembl	0.09612896
uc002syn	pl019136	chr2	98703594	98928495	+	UCSC	0.149463963
AL137463	pl019075	chr1	7549174	7550066	-	NCBI	0.282760169
uc001kab	pl018980	chr10	80777213	80828536	-	UCSC	0.347002962
AK123834	pl018790	chr1	89003195	89150887	-	NCBI	0.222732704
HMlincRNA590	pl018722	chr12	38862405	38887736	+	array-star	0.134435099
uc001mmh	pl018694	chr11	16285994	16760190	-	UCSC	0.21482306
	pl018691					Homologous	0.165816258
ENST00000507857	pl018653	chr4	63994029	64009599	+	Ensembl	0.174668003
uc010did	pl018286	chr17	79609348	79615778	+	UCSC	0.173030577
uc003jdi	pl018187	chr5	5132199	5134697	-	UCSC	0.087134032
ENST00000507514	pl018048	chr5	75987264	76012040	-	Ensembl	0.144562493
ENST00000532380	pl017929	chr11	22467234	22513565	-	Ensembl	0.360552122
NR_015454	pl017682	chr17	79887791	79887988	+	NCBI	0.375228014
uc001lkg	pl017656	chr10	129979399	130115990	+	UCSC	0.300961129
uc010bzh	pl017629	chr16	29831786	29848279	+	UCSC	0.171588964
ENST00000556070	pl017442	chr2	113993113	114023294	+	Ensembl	0.249281943
	pl017350	chr2	39745754	39826679	-	Agilent	0.203946408
BC114220	pl016992	chrX	39922207	40036336	+	array-star	0.258858991
HMlincRNA23	pl016975	chr2	191558680	191558969	+	array-star	0.311412273
AF086453	pl016931	chr17	26865333	26865917	+	NCBI	0.04698777
gnl|ncrnascan|RNS2042	pl016887	chr6	7262374	7262509	-	ncRNASCAN	0.425733895
ENST00000549515	pl016872	chr14	29859552	29905618	+	Ensembl	0.042335869
BC025662	pl016665	chr8	53320198	53322442	-	NCBI	0.279865125
NR_033967.1	pl016516	chr1	43424720	43425248	+	Other_database	0.162291981

ENST00000549278	pl016470	chr12	89441964	89703330	-	Ensembl	0.177199291
ENST00000522460	pl016242	chr8	34085957	34204249	+	Ensembl	0.249320488
ASO2077	pl016207	chr15	83316520	83361571	+	NCBI	0.193528126
uc001ihl	pl016170	chr10	4868401	5067607	+	UCSC	0.172711819
gnl|UG|Hs#S4360038	pl016165	chr4	144341424	144341928	-	Other_database	0.241110988
AK056769	pl015998	chr17	1311760	1475838	-	NCBI	0.394938336
ENST00000506429	pl015830	chr5	37953504	37967066	+	Ensembl	0.159188877
DB239440	pl015748	chr8	87229854	87333375	+	array-star	0.077968634
BC146594	pl015652	chr7	540689	543688	-	Other_database	0.26759462
NR_024279	pl015535	chr1	16160709	16174642	-	NCBI	0.314733973
BG206269	pl015445	chr1	143527886	143528309	+	array-star	0.211268984
uc001jeo	pl015401	chr10	47746919	47770843	+	UCSC	0.176600553
BC031261	pl015397	chr3	101818087	102196518	+	array-star	0.331792125
ENST00000509470	pl015169	chr12	119825796	120032306	-	UCSC	0.322309127
uc009xxw	pl015109	chr10	112659588	112678694	-	UCSC	0.166842281
CR608907	pl015017	chr2	237038320	237040416	+	NCBI	0.433234732
HMlincRNA75	pl014826	chr2	122660225	122978498	+	array-star	0.281182297
AK127359	pl014821	chr11	124627611	124631114	-	NCBI	0.283669406
AK024373	pl014809	chr19	438420	2083745	-	NCBI	0.357543197
ENST00000450750	pl014773	chr22	43796337	43805687	+	Ensembl	0.059946005
uc002qyw	pl014752	chr2	8063754	8116977	-	UCSC	0.033397176
AK055146	pl014748	chr2	99482967	99485101	-	NCBI	0.109123953
ENST00000546770	pl014625	chr12	74300720	74313117	+	Ensembl	0.123362166
BC036877	pl014604	chr1	14925212	15441219	-	NCBI	0.352113681
NR_028102.1	pl014566	chr2	39963200	39964199	-	Other_database	0.241466177
gnl|UG|Hs#S1071835	pl014514	chr5	147224791	147225249	+	Other_database	0.175870313

HMlincRNA1019	pl014513	chr1	156669400	156669701	+	array-star	0.140505244
ENST00000413328	pl014496	chrX	140013903	140079613	+	Ensembl	0.156476553
ENST00000533459	pl014471	chr11	103546722	103765999	-	Ensembl	0.336450599
NR_027471.1	pl014450	chr9	89623366	89625125	-	Other_database	0.169108748
ENST00000436266	pl014436	chr7	46341718	46383219	+	Ensembl	0.074324083
	pl014431	chr11	128420640	128439759	-	Agilent	0.207813712
	pl014310	chr2	3039393	3050593	-	Agilent	0.454353233
	pl014029	chr4	90602675	90606883	+	Agilent	0.233025918
ENST00000521139	pl013914	chr8	20207767	20230280	+	Ensembl	0.091259289
	pl013894	chr9	132265766	132275963	-	Agilent	0.367538047
ENST00000502287	pl013660	chr5	107035658	107052542	-	Ensembl	0.003653469
ENST00000422558	pl013555	chr2	34608855	34860407	+	Ensembl	0.129072175
AK223466	pl013398	chr7	139478198	139720092	+	array-star	0.439200049
NR_015350	pl013338	chr1	175126122	175161929	-	NCBI	0.123423324
	pl013322	chr4	90602675	90606883	-	Agilent	0.084564989
uc003aum	pl013270	chr22	38349717	38384341	+	UCSC	0.219432514
ENST00000428166	pl013268	chr10	91406046	91410579	-	Ensembl	0.185458096
	pl013213	chr3	161007906	161020056	+	Agilent	0.319091316
	pl013134	chr4	7132149	7143349	-	Agilent	0.405576162
ENST00000457707	pl013093	chr20	8000549	8008603	+	Ensembl	0.190956909
BC021141	pl013088	chr6	35188146	35189134	-	NCBI	0.380919615
	pl013027					Homologous	0.040677972
ENST00000420146	pl012991	chr7	122709303	122743643	-	Ensembl	0.309946222
ENST00000435106	pl012727	chr10	10477912	10504248	-	Ensembl	0.161763142
AK026607	pl012558	chr11	44580598	44972434	+	array-star	0.126606669
ENST00000429816	pl012474	chr2	181436439	181557181	-	Ensembl	0.210307225

uc009yax	pl012466	chr10	132896568	133058707	-	UCSC	0.181460467
BC082981	pl012449	chr20	43379635	43380954	+	NCBI	0.223332581
BC146594	pl012341	chr7	540689	543688	-	Other_database	0.287615825
ENST00000431706	pl012339	chrX	118386774	118391646	-	Ensembl	0.212658529
ENST00000467313	pl012312	chr3	181670162	181691133	+	Ensembl	0.162093513
	pl012007	chr13	65807549	66089674	+	Agilent	0.120581159
HIV1671	pl011987	chr11	27717858	27899195	-	NCBI	0.183151115
exon974	pl011867	chr12	32643729	32644063	+	array-star	0.382617002
uc001gle	pl011769	chr1	176945189	177001985	-	UCSC	0.183080403
ENST00000422374	pl011715	chr1	56046710	56200675	+	Ensembl	0.003370426
ENST00000442026	pl011582	chr2	33931975	34286114	+	Ensembl	0.13351764
uc003boy	pl011556	chr3	577913	887698	+	UCSC	0.360186156
	pl011509	chr21	47869772	47878247	+	Agilent	0.341713468
uc003vud	pl011358	chr7	138279029	138348316	-	UCSC	0.28709041
uc001jzu	pl011241	chr10	79998011	80434727	+	UCSC	0.202556521
	pl011136	chr6	11118364	11146189	+	Agilent	0.406807033
	pl011097	chr15	36695283	36727633	-	Agilent	0.031916734
uc003ymx	pl011058	chr8	109619079	109799770	-	UCSC	0.101270167
ENST00000498832	pl011043	chr3	73857752	73952017	+	Ensembl	0.126503354
uc001oox	pl010838	chr11	69061621	69089801	+	UCSC	0.279101091
HMlincRNA975	pl010650	chr4	122589037	122589523	+	array-star	0.414590312
HMlincRNA1147	pl010643	chr1	31849969	31850331	+	array-star	0.094956071
BX113181	pl010536	chr4	82524027	82965397	+	array-star	0.268203543
	pl010339	chr10	47000944	47006919	-	Agilent	0.244996445
ENST00000448643	pl010319	chr1	166356964	166421869	-	Ensembl	0.072521225
HMlincRNA965	pl010023	chr3	168819873	169381208	+	array-star	0.11886504

	pl010014					Homologous	0.104523626
ENST00000445615	pl009911	chr7	47009300	47023027	+	Ensembl	0.075669113
	pl009798	chr8	96692149	96730174	-	Agilent	0.04664995
ENST00000458615	pl009522	chr7	54398390	54417542	+	Ensembl	0.164847793
NR_024453	pl009498	chr16	432240	442960	+	NCBI	0.352067759
DC295389	pl009414	chr4	26165175	26364251	+	array-star	0.167758666
AF131813	pl009375	chr17	42980418	42982187	-	NCBI	0.225643146
	pl009364	chr3	58574932	58613271	-	Agilent	0.106781236
ENST00000502335	pl009272	chr18	36787591	36920602	-	Ensembl	0.218665298
NR_033917.1	pl009241	chr20	4176173	4176600	+	Other_database	0.269204086
NR_024489	pl008929	chr1	2281855	2284100	-	NCBI	0.342416699
AK130417	pl008897	chr2	74139024	74140297	+	NCBI	0.289367424
ENST00000509669	pl008544	chr5	117260703	117542666	+	Ensembl	0.207570903
	pl008427	chr15	47631314	47841473	+	Agilent	0.15600893
	pl008418	chr8	29628964	29629828	-	Agilent	0.143697667
BX383054	pl008350	chr11	3366642	3367189	+	array-star	0.242504159
	pl008304	chr18	39101339	39212100	-	Agilent	0.088162942
uc010lrs	pl008245	chr8	9577883	9588545	+	UCSC	0.348569347
HMlincRNA985	pl008172	chr4	133882115	133882572	+	array-star	0.071222746
ENST00000437601	pl007986	chr1	234861148	234867390	+	Ensembl	0.408474513
ENST00000502901	pl007919	chr8	137059264	137178365	+	Ensembl	0.17739653
ENST00000534653	pl007686	chr11	7244164	7252094	+	Ensembl	0.134215388
HMlincRNA1559	pl007605	chr15	59870269	59870659	+	array-star	0.200247654
ENST00000509015	pl007590	chr4	4323689	4335909	+	Ensembl	0.130125096
ENST00000418403	pl007479	chr6	71104590	71109120	+	Ensembl	0.344017705
	pl007423	chr14	48681275	48724375	-	Agilent	0.408612

AK091933.1	pl007321	chr7	27186781	27193904	+	LNCRNA-DB	0.131959821
BC030521	pl007029	chr5	71515352	71689054	+	array-star	0.205197874
ENST00000425974	pl006921	chr2	13106910	13147138	-	Ensembl	0.099348417
HMlincRNA1183	pl006878	chr2	27929629	27938599	+	array-star	0.075861175
uc002yyf	pl006780	chr21	40984971	41031839	+	UCSC	0.311675802
ENST00000438566	pl006745	chr2	105199610	105201812	+	Ensembl	0.086458122
uc.300+	pl006660	chr10	102547117	102547325	+	NCBI	0.256930889
HMlincRNA125	pl006504	chr1	226314861	226315111	+	array-star	0.363700406
AK172736	pl006480	chr10	62267256	62493082	-	NCBI	0.0963466
DA707535	pl006380	chr13	38628269	38857641	+	array-star	0.440160004
uc001lww	pl006223	chr11	2909009	2924970	-	UCSC	0.384639243
NR_024074	pl006184	chr15	23255241	23262743	+	NCBI	0.250857024
NR_026663.1	pl006104	chr9	3900833	3901248	+	Other_database	0.173375246
AK024180	pl006089	chr11	5568209	5692665	-	NCBI	0.154940341
HMlincRNA1140	pl005979	chr1	35178360	35325336	+	array-star	0.175638804
ENST00000544556	pl005708	chr7	34656519	34797884	-	Ensembl	0.225539035
HMlincRNA1450	pl005681	chr4	183802988	183803484	+	array-star	0.450486981
ENST00000536666	pl005635	chr12	20167714	20251802	+	Ensembl	0.178886973
NR_026960	pl005600	chr21	44869903	44873769	+	NCBI	0.314715779
gnl|UG|Hs#S2863492	pl005264	chrX	79376411	79376684	-	Other_database	0.129886863
ENST00000432146	pl005178	chr1	95975726	96088290	+	Ensembl	0.082681566
ENST00000512692	pl004899	chr4	141204880	141294514	-	Ensembl	0.381551944
uc002yec	pl004898	chr20	61640734	61716423	+	UCSC	0.203069013
uc009zdg	pl004778	chr11	134216283	134248235	+	UCSC	0.151305339
AJ227874	pl004774	chr11	126219412	126219885	+	NCBI	0.407760533
BF746429	pl004712	chr1	39183439	39183984	+	array-star	0.175753831

ENST00000446024	pl004570	chr7	36069221	36095041	+	Ensembl	0.293477464
ENST00000523151	pl004547	chr8	130363937	130587262	-	Ensembl	0.129718632
AK123269	pl004512	chr2	95717397	95719735	+	NCBI	0.068525058
NR_027064	pl004322	chr19	5558179	5568005	-	NCBI	0.107643225
BC044219	pl004294	chrX	13684193	13688357	+	NCBI	0.149632628
	pl004265	chr2	72150317	72161342	-	Agilent	0.39344608
DN995775	pl004259	chr7	7994792	7995376	+	array-star	0.339138943
uc009vji	pl004257	chr1	548201	551200	-	Other_database	0.077664032
NR_003087	pl004256	chr21	15646119	15673692	+	NCBI	0.003812036
AW028738	pl004129	chr11	10747894	10748353	+	array-star	0.199440019
ENST00000446458	pl004094	chr6	140407819	140414802	+	Ensembl	0.170655829
BC013821	pl003926	chr5	479246	480997	+	NCBI	0.098573359
AK026879	pl003914	chr1	113770397	113772501	+	NCBI	0.15644722
ENST00000510065	pl003877	chr5	12914180	13032998	-	Ensembl	0.227436236
uc001jeo	pl003808	chr10	47746919	47770843	+	UCSC	0.271564841
HMlincRNA121	pl003766	chr1	161109088	161109613	+	array-star	0.291366235
ENST00000548344	pl003483	chr12	98506792	98686223	-	Ensembl	0.094545118
HMlincRNA1141	pl003348	chr1	33430675	33431256	+	array-star	0.173247118
gnl|ncrnascan|RNS3262	pl003301	chr12	54812671	54812683	-	Other_database	0.323046849
ENST00000525111	pl003065	chr17	35289409	35293921	-	Ensembl	0.11243995
ENST00000509015	pl003057	chr4	4323689	4335909	+	Ensembl	0.355464564
BC024972	pl002974	chr13	96131699	96186165	-	NCBI	0.133919533
ENST00000522896	pl002796	chr8	111346972	111361836	-	Ensembl	0.05639435
gnl|UG|Hs#S29637520	pl002756	chr3	159471836	159472377	-	Other_database	0.175498984
HMlincRNA1476	pl002724	chr16	51158194	51158622	+	array-star	0.045054392
HIV2736	pl002694	chr18	55721940	55833070	+	NCBI	0.193987151

AX747026	pl002582	chr1	235430528	235433527	-	Other_database	0.081169674
ENST00000420477	pl002470	chr20	46983957	46995507	+	Ensembl	0.087899222
ENST00000439146	pl002005	chr1	101789393	101842869	+	Ensembl	0.198605959
gnl|UG|Hs#S11152693	pl001961	chr11	15450113	15450305	-	Other_database	0.095532939
HMlincRNA1162	pl001945	chr1	17308744	17311743	-	Other_database	0.118879715
ENST00000497379	pl001669	chr3	164431889	164549268	-	Ensembl	0.187881617
BC070168	pl001663	chr12	71518868	71835678	+	array-star	0.319336211
AK026861	pl001617	chr3	62953692	62955011	-	NCBI	0.231184506
AK024373	pl001555	chr19	438420	2083745	-	NCBI	0.070052347
uc009whb	pl001539	chr1	116935056	116961203	-	UCSC	0.285285408
ENST00000462937	pl001532	chr3	151491267	151501697	+	Ensembl	0.188220747
uc003vzg	pl001520	chr16	66896844	66897095	+	Other_database	0.181691735
gnl|ncrnascan|RNS1131	pl001414	chr20	60733065	60733247	-	ncRNASCAN	0.35104642
AK310207	pl001352	chr3	183853163	184402546	+	array-star	0.051079597
ENST00000500394	pl001224	chr4	14911585	15003669	-	Ensembl	0.12349523
ENST00000457848	pl001177	chr10	33867859	33888968	-	Ensembl	0.237885396
ENST00000519929	pl001033	chr5	163875428	163894408	-	Ensembl	0.234275858
uc010jos	pl000897	chr6	10747994	10852986	+	UCSC	0.24180644
	pl000744	chr16	90043749	90053849	-	Agilent	0.174075173
uc002fkc	pl000726	chr16	87527792	87549236	+	UCSC	0.3444115
uc002ycj	pl000542	chr20	60807015	60811355	+	UCSC	0.31161887
ENST00000523151	pl000515	chr8	130363937	130587262	-	Ensembl	0.208835647
BM977434	pl000482	chr10	116568848	116569274	+	array-star	0.137546147
BX537518	pl000427	chr8	65291789	65296452	+	NCBI	0.177716737
uc010hpe	pl000144	chr3	99357453	99422736	+	UCSC	0.165438223

Supplementary Table 2-1 Information of aberrantly expressed lncRNAs by GO annotation

LncRNAs-probe name	ID	Go_id	Go_term	Namespace
pl070063	HMlincRNA1333	GO:0004867	serine-type endopeptidase inhibitor activity	Function
pl070063	HMlincRNA1333	GO:0005615	extracellular space	Component
pl070063	HMlincRNA1333	GO:0010466	negative regulation of peptidase activity	Process
pl070063	HMlincRNA1333	GO:0030414	peptidase inhibitor activity	Function
pl070063	HMlincRNA1333	GO:0052548	regulation of endopeptidase activity	Process
pl060937	AF086561	GO:0001889	liver development	Process
pl060937	AF086561	GO:0003985	acetyl-CoA C-acetyltransferase activity	Function
pl060937	AF086561	GO:0005739	mitochondrion	Component
pl060937	AF086561	GO:0005743	mitochondrial inner membrane	Component
pl060937	AF086561	GO:0005759	mitochondrial matrix	Component
pl060937	AF086561	GO:0007420	brain development	Process
pl060937	AF086561	GO:0009083	branched chain family amino acid catabolic process	Process
pl060937	AF086561	GO:0009725	response to hormone stimulus	Process
pl060937	AF086561	GO:0014070	response to organic cyclic compound	Process
pl060937	AF086561	GO:0019899	enzyme binding	Function
pl060937	AF086561	GO:0034641	cellular nitrogen compound metabolic process	Process
pl060937	AF086561	GO:0042594	response to starvation	Process
pl060937	AF086561	GO:0042803	protein homodimerization activity	Function
pl060937	AF086561	GO:0044255	cellular lipid metabolic process	Process
pl060937	AF086561	GO:0044281	small molecule metabolic process	Process
pl060937	AF086561	GO:0046872	metal ion binding	Function
pl060937	AF086561	GO:0046950	cellular ketone body metabolic process	Process
pl060937	AF086561	GO:0046951	ketone body biosynthetic process	Process

pl060937	AF086561	GO:0046952	ketone body catabolic process	Process
pl060937	AF086561	GO:0050662	coenzyme binding	Function
pl060937	AF086561	GO:0051260	protein homooligomerization	Process
pl060937	AF086561	GO:0060612	adipose tissue development	Process
pl060937	AF086561	GO:0072229	metanephric proximal convoluted tubule development	Process
pl105325	ENST00000468964	GO:0000902	cell morphogenesis	Process
pl105325	ENST00000468964	GO:0001525	angiogenesis	Process
pl105325	ENST00000468964	GO:0002102	podosome	Component
pl105325	ENST00000468964	GO:0002523	leukocyte migration involved in inflammatory response	Process
pl105325	ENST00000468964	GO:0002675	positive regulation of acute inflammatory response	Process
pl105325	ENST00000468964	GO:0004222	metalloendopeptidase activity	Function
pl105325	ENST00000468964	GO:0005509	calcium ion binding	Function
pl105325	ENST00000468964	GO:0005515	protein binding	Function
pl105325	ENST00000468964	GO:0005737	cytoplasm	Component
pl105325	ENST00000468964	GO:0005886	plasma membrane	Component
pl105325	ENST00000468964	GO:0005887	integral to plasma membrane	Component
pl105325	ENST00000468964	GO:0006508	proteolysis	Process
pl105325	ENST00000468964	GO:0006954	inflammatory response	Process
pl105325	ENST00000468964	GO:0008237	metallopeptidase activity	Function
pl105325	ENST00000468964	GO:0008270	zinc ion binding	Function
pl105325	ENST00000468964	GO:0009986	cell surface	Component
pl105325	ENST00000468964	GO:0010954	positive regulation of protein processing	Process
pl105325	ENST00000468964	GO:0022407	regulation of cell-cell adhesion	Process
pl105325	ENST00000468964	GO:0032010	phagolysosome	Component

pl105325	ENST00000468964	GO:0032127	dense core granule membrane	Component
pl105325	ENST00000468964	GO:0033089	positive regulation of T cell differentiation in thymus	Process
pl105325	ENST00000468964	GO:0035419	activation of MAPK activity involved in innate immune response	Process
pl105325	ENST00000468964	GO:0042581	specific granule	Component
pl105325	ENST00000468964	GO:0043524	negative regulation of neuron apoptotic process	Process
pl105325	ENST00000468964	GO:0043621	protein self-association	Function
pl105325	ENST00000468964	GO:0045780	positive regulation of bone resorption	Process
pl105325	ENST00000468964	GO:0045785	positive regulation of cell adhesion	Process
pl105325	ENST00000468964	GO:0048247	lymphocyte chemotaxis	Process
pl105325	ENST00000468964	GO:0050714	positive regulation of protein secretion	Process
pl105325	ENST00000468964	GO:0050839	cell adhesion molecule binding	Function
pl105325	ENST00000468964	GO:0051044	positive regulation of membrane protein ectodomain proteolysis	Process
pl105325	ENST00000468964	GO:0051092	positive regulation of NF-kappaB transcription factor activity	Process
pl105325	ENST00000468964	GO:0051897	positive regulation of protein kinase B signaling cascade	Process
pl105325	ENST00000468964	GO:0070245	positive regulation of thymocyte apoptotic process	Process
pl105325	ENST00000468964	GO:0070820	tertiary granule	Component
pl105325	ENST00000468964	GO:0071065	alpha9-beta1 integrin-vascular cell adhesion molecule-1 complex	Component
pl105325	ENST00000468964	GO:0071133	alpha9-beta1 integrin-ADAM8 complex	Component
pl105325	ENST00000468964	GO:0071456	cellular response to hypoxia	Process
pl105325	ENST00000468964	GO:2000309	positive regulation of tumor necrosis factor (ligand) superfamily member 11 production	Process

pl105325	ENST00000468964	GO:2000391	positive regulation of neutrophil extravasation	Process
pl105325	ENST00000468964	GO:2000415	positive regulation of fibronectin-dependent thymocyte migration	Process
pl105325	ENST00000468964	GO:2000418	positive regulation of eosinophil migration	Process
pl115081	AK130649	GO:0005515	protein binding	Function
pl115081	AK130649	GO:0006897	endocytosis	Process
pl115081	AK130649	GO:0007268	synaptic transmission	Process
pl115081	AK130649	GO:0007612	learning	Process
pl115081	AK130649	GO:0008021	synaptic vesicle	Component
pl115081	AK130649	GO:0008022	protein C-terminus binding	Function
pl115081	AK130649	GO:0015629	actin cytoskeleton	Component
pl115081	AK130649	GO:0030054	cell junction	Component
pl115081	AK130649	GO:0030672	synaptic vesicle membrane	Component
pl115081	AK130649	GO:0043547	positive regulation of GTPase activity	Process
pl115081	AK130649	GO:0043679	axon terminus	Component
pl115081	AK130649	GO:0045807	positive regulation of endocytosis	Process
pl115081	AK130649	GO:0046982	protein heterodimerization activity	Function
pl115081	AK130649	GO:0048488	synaptic vesicle endocytosis	Process
pl049503	HMlincRNA975	GO:0004859	phospholipase inhibitor activity	Function
pl043297	HMlincRNA975	GO:0004859	phospholipase inhibitor activity	Function
pl049503	HMlincRNA975	GO:0005509	calcium ion binding	Function
pl043297	HMlincRNA975	GO:0005509	calcium ion binding	Function
pl049503	HMlincRNA975	GO:0005543	phospholipid binding	Function
pl043297	HMlincRNA975	GO:0005543	phospholipid binding	Function
pl049503	HMlincRNA975	GO:0005544	calcium-dependent phospholipid binding	Function
pl043297	HMlincRNA975	GO:0005544	calcium-dependent phospholipid binding	Function

pl049503	HMlincRNA975	GO:0005622	intracellular	Component
pl043297	HMlincRNA975	GO:0005622	intracellular	Component
pl049503	HMlincRNA975	GO:0005737	cytoplasm	Component
pl043297	HMlincRNA975	GO:0005737	cytoplasm	Component
pl049503	HMlincRNA975	GO:0006916	anti-apoptosis	Process
pl043297	HMlincRNA975	GO:0006916	anti-apoptosis	Process
pl049503	HMlincRNA975	GO:0007165	signal transduction	Process
pl043297	HMlincRNA975	GO:0007165	signal transduction	Process
pl049503	HMlincRNA975	GO:0007596	blood coagulation	Process
pl043297	HMlincRNA975	GO:0007596	blood coagulation	Process
pl049503	HMlincRNA975	GO:0009897	external side of plasma membrane	Component
pl043297	HMlincRNA975	GO:0009897	external side of plasma membrane	Component
pl049503	HMlincRNA975	GO:0010033	response to organic substance	Process
pl043297	HMlincRNA975	GO:0010033	response to organic substance	Process
pl049503	HMlincRNA975	GO:0014704	intercalated disc	Component
pl043297	HMlincRNA975	GO:0014704	intercalated disc	Component
pl049503	HMlincRNA975	GO:0030971	receptor tyrosine kinase binding	Function
pl043297	HMlincRNA975	GO:0030971	receptor tyrosine kinase binding	Function
pl049503	HMlincRNA975	GO:0042383	sarcolemma	Component
pl043297	HMlincRNA975	GO:0042383	sarcolemma	Component
pl049503	HMlincRNA975	GO:0042995	cell projection	Component
pl043297	HMlincRNA975	GO:0042995	cell projection	Component
pl049503	HMlincRNA975	GO:0043065	positive regulation of apoptotic process	Process
pl043297	HMlincRNA975	GO:0043065	positive regulation of apoptotic process	Process
pl049503	HMlincRNA975	GO:0043499	eukaryotic cell surface binding	Function
pl043297	HMlincRNA975	GO:0043499	eukaryotic cell surface binding	Function

pl049503	HMlincRNA975	GO:0050819	negative regulation of coagulation	Process
pl043297	HMlincRNA975	GO:0050819	negative regulation of coagulation	Process
pl049503	HMlincRNA975	GO:0051260	protein homooligomerization	Process
pl043297	HMlincRNA975	GO:0051260	protein homooligomerization	Process
pl049503	HMlincRNA975	GO:0072563	endothelial microparticle	Component
pl043297	HMlincRNA975	GO:0072563	endothelial microparticle	Component
pl081932	uc001jeo	GO:0005509	calcium ion binding	Function
pl074315	uc001jeo	GO:0005509	calcium ion binding	Function
pl038679	uc001jeo	GO:0005509	calcium ion binding	Function
pl081932	uc001jeo	GO:0005544	calcium-dependent phospholipid binding	Function
pl074315	uc001jeo	GO:0005544	calcium-dependent phospholipid binding	Function
pl038679	uc001jeo	GO:0005544	calcium-dependent phospholipid binding	Function
pl026962	uc002seq	GO:0000012	single strand break repair	Process
pl026962	uc002seq	GO:0000166	nucleotide binding	Function
pl026962	uc002seq	GO:0003906	DNA-(apurinic or apyrimidinic site) lyase activity	Function
pl026962	uc002seq	GO:0004520	endodeoxyribonuclease activity	Function
pl026962	uc002seq	GO:0005515	protein binding	Function
pl026962	uc002seq	GO:0005634	nucleus	Component
pl026962	uc002seq	GO:0005829	cytosol	Component
pl026962	uc002seq	GO:0006302	double-strand break repair	Process
pl026962	uc002seq	GO:0006974	response to DNA damage stimulus	Process
pl026962	uc002seq	GO:0008408	3'-5' exonuclease activity	Function
pl026962	uc002seq	GO:0046872	metal ion binding	Function
pl054532	AK128292	GO:0001967	suckling behavior	Process
pl054532	AK128292	GO:0003677	DNA binding	Function
pl054532	AK128292	GO:0004867	serine-type endopeptidase inhibitor activity	Function

pl054532	AK128292	GO:0005515	protein binding	Function
pl054532	AK128292	GO:0005634	nucleus	Component
pl054532	AK128292	GO:0005886	plasma membrane	Component
pl054532	AK128292	GO:0006878	cellular copper ion homeostasis	Process
pl054532	AK128292	GO:0007176	regulation of epidermal growth factor-activated receptor activity	Process
pl054532	AK128292	GO:0007186	G-protein coupled receptor signaling pathway	Process
pl054532	AK128292	GO:0007617	mating behavior	Process
pl054532	AK128292	GO:0007626	locomotory behavior	Process
pl054532	AK128292	GO:0008201	heparin binding	Function
pl054532	AK128292	GO:0009790	embryo development	Process
pl054532	AK128292	GO:0016021	integral to membrane	Component
pl054532	AK128292	GO:0030900	forebrain development	Process
pl054532	AK128292	GO:0030901	midbrain development	Process
pl054532	AK128292	GO:0042802	identical protein binding	Function
pl054532	AK128292	GO:0046914	transition metal ion binding	Function
pl054532	AK128292	GO:0050885	neuromuscular process controlling balance	Process
pl002582	AX747026	GO:0003674	molecular_function	Function
pl002582	AX747026	GO:0003677	DNA binding	Function
pl002582	AX747026	GO:0005515	protein binding	Function
pl002582	AX747026	GO:0005575	cellular_component	Component
pl002582	AX747026	GO:0005634	nucleus	Component
pl002582	AX747026	GO:0005737	cytoplasm	Component
pl002582	AX747026	GO:0006351	transcription, DNA-dependent	Process
pl002582	AX747026	GO:0006355	regulation of transcription, DNA-dependent	Process
pl002582	AX747026	GO:0008150	biological_process	Process

pl015109	uc009xxw	GO:0005515	protein binding	Function
pl015109	uc009xxw	GO:0005737	cytoplasm	Component
pl015109	uc009xxw	GO:0005929	cilium	Component
pl015109	uc009xxw	GO:0034464	BBSome	Component
pl015109	uc009xxw	GO:0042384	cilium assembly	Process
pl016992	BC114220	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl016992	BC114220	GO:0000415	negative regulation of histone H3-K36 methylation	Process
pl016992	BC114220	GO:0003714	transcription corepressor activity	Function
pl016992	BC114220	GO:0004842	ubiquitin-protein ligase activity	Function
pl016992	BC114220	GO:0005515	protein binding	Function
pl016992	BC114220	GO:0005634	nucleus	Component
pl016992	BC114220	GO:0006351	transcription, DNA-dependent	Process
pl016992	BC114220	GO:0007507	heart development	Process
pl016992	BC114220	GO:0008134	transcription factor binding	Function
pl016992	BC114220	GO:0030502	negative regulation of bone mineralization	Process
pl016992	BC114220	GO:0031072	heat shock protein binding	Function
pl016992	BC114220	GO:0031519	PcG protein complex	Component
pl016992	BC114220	GO:0035518	histone H2A monoubiquitination	Process
pl016992	BC114220	GO:0042476	odontogenesis	Process
pl016992	BC114220	GO:0042826	histone deacetylase binding	Function
pl016992	BC114220	GO:0044212	transcription regulatory region DNA binding	Function
pl016992	BC114220	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl016992	BC114220	GO:0051572	negative regulation of histone H3-K4 methylation	Process
pl016992	BC114220	GO:0060021	palate development	Process
pl016992	BC114220	GO:0065001	specification of axis polarity	Process

pl016992	BC114220	GO:0070171	negative regulation of tooth mineralization	Process
pl004898	uc002yec	GO:0003677	DNA binding	Function
pl004898	uc002yec	GO:0005634	nucleus	Component
pl004898	uc002yec	GO:0006351	transcription, DNA-dependent	Process
pl004898	uc002yec	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl004898	uc002yec	GO:0046671	negative regulation of retinal cell programmed cell death	Process
pl004898	uc002yec	GO:0048050	post-embryonic eye morphogenesis	Process
pl074238	ENST00000500767	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl074238	ENST00000500767	GO:0005515	protein binding	Function
pl074238	ENST00000500767	GO:0005634	nucleus	Component
pl074238	ENST00000500767	GO:0005730	nucleolus	Component
pl074238	ENST00000500767	GO:0005737	cytoplasm	Component
pl074238	ENST00000500767	GO:0006338	chromatin remodeling	Process
pl074238	ENST00000500767	GO:0006351	transcription, DNA-dependent	Process
pl074238	ENST00000500767	GO:0006355	regulation of transcription, DNA-dependent	Process
pl074238	ENST00000500767	GO:0007420	brain development	Process
pl074238	ENST00000500767	GO:0008094	DNA-dependent ATPase activity	Function
pl074238	ENST00000500767	GO:0008134	transcription factor binding	Function
pl074238	ENST00000500767	GO:0008270	zinc ion binding	Function
pl074238	ENST00000500767	GO:0016589	NURF complex	Component
pl074238	ENST00000500767	GO:0043565	sequence-specific DNA binding	Function
pl074238	ENST00000500767	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl115860	BC038988	GO:0000114	regulation of transcription involved in G1 phase of	Process

			mitotic cell cycle	
pl115860	BC038988	GO:0000790	nuclear chromatin	Component
pl115860	BC038988	GO:0000794	condensed nuclear chromosome	Component
pl115860	BC038988	GO:0001833	inner cell mass cell proliferation	Process
pl115860	BC038988	GO:0003677	DNA binding	Function
pl115860	BC038988	GO:0005515	protein binding	Function
pl115860	BC038988	GO:0005634	nucleus	Component
pl115860	BC038988	GO:0005730	nucleolus	Component
pl115860	BC038988	GO:0005737	cytoplasm	Component
pl115860	BC038988	GO:0006468	protein phosphorylation	Process
pl115860	BC038988	GO:0007059	chromosome segregation	Process
pl115860	BC038988	GO:0010971	positive regulation of G2/M transition of mitotic cell cycle	Process
pl115860	BC038988	GO:0032968	positive regulation of transcription elongation from RNA polymerase II promoter	Process
pl115860	BC038988	GO:0043388	positive regulation of DNA binding	Process
pl115860	BC038988	GO:0043983	histone H4-K12 acetylation	Process
pl115860	BC038988	GO:0044154	histone H3-K14 acetylation	Process
pl115860	BC038988	GO:0044419	interspecies interaction between organisms	Process
pl050158	uc001mmh	GO:0003674	molecular_function	Function
pl018694	uc001mmh	GO:0003674	molecular_function	Function
pl050158	uc001mmh	GO:0005575	cellular_component	Component
pl018694	uc001mmh	GO:0005575	cellular_component	Component
pl050158	uc001mmh	GO:0008150	biological_process	Process
pl018694	uc001mmh	GO:0008150	biological_process	Process
pl002953	NR_026717.1	GO:0004866	endopeptidase inhibitor activity	Function

pl002953	NR_026717.1	GO:0005576	extracellular region	Component
pl002953	NR_026717.1	GO:0005615	extracellular space	Component
pl002953	NR_026717.1	GO:0005886	plasma membrane	Component
pl002953	NR_026717.1	GO:0006954	inflammatory response	Process
pl002953	NR_026717.1	GO:0006956	complement activation	Process
pl002953	NR_026717.1	GO:0006958	complement activation, classical pathway	Process
pl002953	NR_026717.1	GO:0030449	regulation of complement activation	Process
pl002953	NR_026717.1	GO:0045087	innate immune response	Process
pl070257	uc010jpk	GO:0003779	actin binding	Function
pl070257	uc010jpk	GO:0005886	plasma membrane	Component
pl070257	uc010jpk	GO:0007010	cytoskeleton organization	Process
pl070257	uc010jpk	GO:0007163	establishment or maintenance of cell polarity	Process
pl070257	uc010jpk	GO:0007165	signal transduction	Process
pl070257	uc010jpk	GO:0007190	activation of adenylate cyclase activity	Process
pl070257	uc010jpk	GO:0007411	axon guidance	Process
pl101051	ENST00000499475	GO:0005515	protein binding	Function
pl101051	ENST00000499475	GO:0005634	nucleus	Component
pl101051	ENST00000499475	GO:0005737	cytoplasm	Component
pl101051	ENST00000499475	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	Process
pl101051	ENST00000499475	GO:0008656	cysteine-type endopeptidase activator activity involved in apoptotic process	Function
pl101051	ENST00000499475	GO:0032089	NACHT domain binding	Function
pl101051	ENST00000499475	GO:0042803	protein homodimerization activity	Function
pl101051	ENST00000499475	GO:0042981	regulation of apoptotic process	Process
pl101051	ENST00000499475	GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB	Process

			cascade	
pl101051	ENST00000499475	GO:0043280	positive regulation of cysteine-type endopeptidase activity involved in apoptotic process	Process
pl101051	ENST00000499475	GO:0050718	positive regulation of interleukin-1 beta secretion	Process
pl038829	AK057576	GO:0000166	nucleotide binding	Function
pl038829	AK057576	GO:0000209	protein polyubiquitination	Process
pl038829	AK057576	GO:0004842	ubiquitin-protein ligase activity	Function
pl038829	AK057576	GO:0005515	protein binding	Function
pl038829	AK057576	GO:0005634	nucleus	Component
pl038829	AK057576	GO:0007067	mitosis	Process
pl038829	AK057576	GO:0007093	mitotic cell cycle checkpoint	Process
pl038829	AK057576	GO:0008270	zinc ion binding	Function
pl038829	AK057576	GO:0016605	PML body	Component
pl038829	AK057576	GO:0019941	modification-dependent protein catabolic process	Process
pl038829	AK057576	GO:0051301	cell division	Process
pl112125	AK130406	GO:0001507	acetylcholine catabolic process in synaptic cleft	Process
pl112125	AK130406	GO:0005515	protein binding	Function
pl112125	AK130406	GO:0005581	collagen	Component
pl112125	AK130406	GO:0005605	basal lamina	Component
pl112125	AK130406	GO:0005615	extracellular space	Component
pl112125	AK130406	GO:0008105	asymmetric protein localization	Process
pl112125	AK130406	GO:0008201	heparin binding	Function
pl112125	AK130406	GO:0030054	cell junction	Component
pl112125	AK130406	GO:0043083	synaptic cleft	Component
pl014513	HMlincRNA1019	GO:0001972	retinoic acid binding	Function
pl014513	HMlincRNA1019	GO:0005215	transporter activity	Function

pl014513	HMlincRNA1019	GO:0005501	retinoid binding	Function
pl014513	HMlincRNA1019	GO:0005634	nucleus	Component
pl014513	HMlincRNA1019	GO:0005730	nucleolus	Component
pl014513	HMlincRNA1019	GO:0005737	cytoplasm	Component
pl014513	HMlincRNA1019	GO:0006355	regulation of transcription, DNA-dependent	Process
pl014513	HMlincRNA1019	GO:0007165	signal transduction	Process
pl014513	HMlincRNA1019	GO:0008544	epidermis development	Process
pl014513	HMlincRNA1019	GO:0016918	retinal binding	Function
pl014513	HMlincRNA1019	GO:0019841	retinol binding	Function
pl014513	HMlincRNA1019	GO:0035115	embryonic forelimb morphogenesis	Process
pl014513	HMlincRNA1019	GO:0042573	retinoic acid metabolic process	Process
pl104925	AK024129	GO:0005515	protein binding	Function
pl104925	AK024129	GO:0005634	nucleus	Component
pl104925	AK024129	GO:0006351	transcription, DNA-dependent	Process
pl104925	AK024129	GO:0008285	negative regulation of cell proliferation	Process
pl104925	AK024129	GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	Function
pl104925	AK024129	GO:0017053	transcriptional repressor complex	Component
pl104925	AK024129	GO:0019079	viral genome replication	Process
pl104925	AK024129	GO:0030054	cell junction	Component
pl104925	AK024129	GO:0045202	synapse	Component
pl104925	AK024129	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl104925	AK024129	GO:0050872	white fat cell differentiation	Process
pl104925	AK024129	GO:0051287	NAD binding	Function
pl098844	AK027270	GO:0003676	nucleic acid binding	Function
pl098844	AK027270	GO:0004046	aminoacylase activity	Function

pl098844	AK027270	GO:0004815	aspartate-tRNA ligase activity	Function
pl098844	AK027270	GO:0005515	protein binding	Function
pl098844	AK027270	GO:0005524	ATP binding	Function
pl098844	AK027270	GO:0005625	soluble fraction	Component
pl098844	AK027270	GO:0005737	cytoplasm	Component
pl098844	AK027270	GO:0005829	cytosol	Component
pl098844	AK027270	GO:0006412	translation	Process
pl098844	AK027270	GO:0006418	tRNA aminoacylation for protein translation	Process
pl098844	AK027270	GO:0006422	aspartyl-tRNA aminoacylation	Process
pl098844	AK027270	GO:0006461	protein complex assembly	Process
pl098844	AK027270	GO:0010467	gene expression	Process
pl004774	AJ227874	GO:0000184	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	Process
pl004774	AJ227874	GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	Process
pl004774	AJ227874	GO:0000290	deadenylation-dependent decapping of nuclear-transcribed mRNA	Process
pl004774	AJ227874	GO:0005515	protein binding	Function
pl004774	AJ227874	GO:0005634	nucleus	Component
pl004774	AJ227874	GO:0005730	nucleolus	Component
pl004774	AJ227874	GO:0005739	mitochondrion	Component
pl004774	AJ227874	GO:0005829	cytosol	Component
pl004774	AJ227874	GO:0010467	gene expression	Process
pl004774	AJ227874	GO:0016070	RNA metabolic process	Process
pl004774	AJ227874	GO:0016071	mRNA metabolic process	Process
pl004774	AJ227874	GO:0016787	hydrolase activity	Function

pl004774	AJ227874	GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	Process
pl055365		GO:0000151	ubiquitin ligase complex	Component
pl031578	gnl|UG|Hs	GO:0000151	ubiquitin ligase complex	Component
pl055365		GO:0005515	protein binding	Function
pl031578	gnl|UG|Hs	GO:0005515	protein binding	Function
pl055365		GO:0008150	biological_process	Process
pl031578	gnl|UG|Hs	GO:0008150	biological_process	Process
pl009498	NR_024453	GO:0000166	nucleotide binding	Function
pl009498	NR_024453	GO:0005102	receptor binding	Function
pl009498	NR_024453	GO:0005777	peroxisome	Component
pl009498	NR_024453	GO:0006636	unsaturated fatty acid biosynthetic process	Process
pl009498	NR_024453	GO:0008670	2,4-dienoyl-CoA reductase (NADPH) activity	Function
pl009498	NR_024453	GO:0016491	oxidoreductase activity	Function
pl038375	uc002zrw	GO:0005634	nucleus	Component
pl053131	uc001aue	GO:0000166	nucleotide binding	Function
pl053131	uc001aue	GO:0007601	visual perception	Process
pl053131	uc001aue	GO:0009055	electron carrier activity	Function
pl053131	uc001aue	GO:0016021	integral to membrane	Component
pl053131	uc001aue	GO:0016491	oxidoreductase activity	Function
pl053131	uc001aue	GO:0042572	retinol metabolic process	Process
pl053131	uc001aue	GO:0052650	NADP-retinol dehydrogenase activity	Function
pl065225	uc001hox	GO:0003777	microtubule motor activity	Function
pl065225	uc001hox	GO:0005524	ATP binding	Function
pl065225	uc001hox	GO:0005737	cytoplasm	Component
pl065225	uc001hox	GO:0005874	microtubule	Component

pl065225	uc001hox	GO:0007018	microtubule-based movement	Process
pl065225	uc001hox	GO:0030286	dynein complex	Component
pl065225	uc001hox	GO:0035085	cilium axoneme	Component
pl106096		GO:0005515	protein binding	Function
pl106096		GO:0005634	nucleus	Component
pl106096		GO:0005730	nucleolus	Component
pl106096		GO:0005794	Golgi apparatus	Component
pl106096		GO:0005802	trans-Golgi network	Component
pl106096		GO:0006351	transcription, DNA-dependent	Process
pl106096		GO:0006355	regulation of transcription, DNA-dependent	Process
pl106096		GO:0016197	endosomal transport	Process
pl106096		GO:0035097	histone methyltransferase complex	Component
pl106096		GO:0042802	identical protein binding	Function
pl106096		GO:0042803	protein homodimerization activity	Function
pl106096		GO:0048188	Set1C/COMPASS complex	Component
pl106096		GO:0051568	histone H3-K4 methylation	Process
pl038713	AK129572	GO:0000080	G1 phase of mitotic cell cycle	Process
pl038713	AK129572	GO:0000083	regulation of transcription involved in G1/S phase of mitotic cell cycle	Process
pl038713	AK129572	GO:0000278	mitotic cell cycle	Process
pl038713	AK129572	GO:0002064	epithelial cell development	Process
pl038713	AK129572	GO:0003677	DNA binding	Function
pl038713	AK129572	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl038713	AK129572	GO:0005515	protein binding	Function
pl038713	AK129572	GO:0005654	nucleoplasm	Component

pl038713	AK129572	GO:0005667	transcription factor complex	Component
pl038713	AK129572	GO:0006351	transcription, DNA-dependent	Process
pl038713	AK129572	GO:0006355	regulation of transcription, DNA-dependent	Process
pl038713	AK129572	GO:0006884	cell volume homeostasis	Process
pl038713	AK129572	GO:0008015	blood circulation	Process
pl038713	AK129572	GO:0008134	transcription factor binding	Function
pl038713	AK129572	GO:0008361	regulation of cell size	Process
pl038713	AK129572	GO:0009887	organ morphogenesis	Process
pl038713	AK129572	GO:0019904	protein domain specific binding	Function
pl038713	AK129572	GO:0042127	regulation of cell proliferation	Process
pl038713	AK129572	GO:0042384	cilium assembly	Process
pl076250	NR_023358	GO:0003743	translation initiation factor activity	Function
pl076250	NR_023358	GO:0005737	cytoplasm	Component
pl076250	NR_023358	GO:0005829	cytosol	Component
pl076250	NR_023358	GO:0006412	translation	Process
pl076250	NR_023358	GO:0006413	translational initiation	Process
pl076250	NR_023358	GO:0008135	translation factor activity, nucleic acid binding	Function
pl076250	NR_023358	GO:0010467	gene expression	Process
pl076250	NR_023358	GO:0044267	cellular protein metabolic process	Process
pl082023	uc002iqz	GO:0005634	nucleus	Component
pl082023	uc002iqz	GO:0008289	lipid binding	Function
pl082023	uc002iqz	GO:0030136	clathrin-coated vesicle	Component
pl082023	uc002iqz	GO:0048471	perinuclear region of cytoplasm	Component
pl093483	AK023559	GO:0000303	response to superoxide	Process
pl093483	AK023559	GO:0003677	DNA binding	Function
pl093483	AK023559	GO:0003678	DNA helicase activity	Function

pl093483	AK023559	GO:0003682	chromatin binding	Function
pl093483	AK023559	GO:0005515	protein binding	Function
pl093483	AK023559	GO:0005524	ATP binding	Function
pl093483	AK023559	GO:0005625	soluble fraction	Component
pl093483	AK023559	GO:0005634	nucleus	Component
pl093483	AK023559	GO:0005654	nucleoplasm	Component
pl093483	AK023559	GO:0005730	nucleolus	Component
pl093483	AK023559	GO:0006281	DNA repair	Process
pl093483	AK023559	GO:0006283	transcription-coupled nucleotide-excision repair	Process
pl093483	AK023559	GO:0006284	base-excision repair	Process
pl093483	AK023559	GO:0006289	nucleotide-excision repair	Process
pl093483	AK023559	GO:0006290	pyrimidine dimer repair	Process
pl093483	AK023559	GO:0006366	transcription from RNA polymerase II promoter	Process
pl093483	AK023559	GO:0006979	response to oxidative stress	Process
pl093483	AK023559	GO:0007256	activation of JNKK activity	Process
pl093483	AK023559	GO:0007257	activation of JUN kinase activity	Process
pl093483	AK023559	GO:0008022	protein C-terminus binding	Function
pl093483	AK023559	GO:0008023	transcription elongation factor complex	Component
pl093483	AK023559	GO:0008094	DNA-dependent ATPase activity	Function
pl093483	AK023559	GO:0008630	DNA damage response, signal transduction resulting in induction of apoptosis	Process
pl093483	AK023559	GO:0009411	response to UV	Process
pl093483	AK023559	GO:0009636	response to toxin	Process
pl093483	AK023559	GO:0010165	response to X-ray	Process
pl093483	AK023559	GO:0010224	response to UV-B	Process
pl093483	AK023559	GO:0010332	response to gamma radiation	Process

pl093483	AK023559	GO:0032403	protein complex binding	Function
pl093483	AK023559	GO:0032784	regulation of transcription elongation, DNA-dependent	Process
pl093483	AK023559	GO:0032786	positive regulation of transcription elongation, DNA-dependent	Process
pl093483	AK023559	GO:0045494	photoreceptor cell maintenance	Process
pl093483	AK023559	GO:0047485	protein N-terminus binding	Function
pl032441	NR_034165.1	GO:0003676	nucleic acid binding	Function
pl032441	NR_034165.1	GO:0005622	intracellular	Component
pl032441	NR_034165.1	GO:0008408	3'-5' exonuclease activity	Function
pl087848	HMlincRNA1147	GO:0005324	long-chain fatty acid transporter activity	Function
pl087848	HMlincRNA1147	GO:0005829	cytosol	Component
pl087848	HMlincRNA1147	GO:0006631	fatty acid metabolic process	Process
pl087848	HMlincRNA1147	GO:0006656	phosphatidylcholine biosynthetic process	Process
pl087848	HMlincRNA1147	GO:0008092	cytoskeletal protein binding	Function
pl087848	HMlincRNA1147	GO:0008285	negative regulation of cell proliferation	Process
pl087848	HMlincRNA1147	GO:0008289	lipid binding	Function
pl087848	HMlincRNA1147	GO:0016528	sarcoplasm	Component
pl087848	HMlincRNA1147	GO:0032868	response to insulin stimulus	Process
pl087848	HMlincRNA1147	GO:0042493	response to drug	Process
pl087848	HMlincRNA1147	GO:0050543	icosatetraenoic acid binding	Function
pl087848	HMlincRNA1147	GO:0070542	response to fatty acid	Process
pl053119	CU693173	GO:0005575	cellular_component	Component
pl053119	CU693173	GO:0008150	biological_process	Process
pl053119	CU693173	GO:0017076	purine nucleotide binding	Function
pl098426		GO:0003676	nucleic acid binding	Function

pl098773	ENST00000421331	GO:0016021	integral to membrane	Component
pl036256	NR_036484.1	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl036256	NR_036484.1	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	Function
pl036256	NR_036484.1	GO:0001764	neuron migration	Process
pl036256	NR_036484.1	GO:0005634	nucleus	Component
pl036256	NR_036484.1	GO:0006351	transcription, DNA-dependent	Process
pl036256	NR_036484.1	GO:0007411	axon guidance	Process
pl036256	NR_036484.1	GO:0008270	zinc ion binding	Function
pl036256	NR_036484.1	GO:0008285	negative regulation of cell proliferation	Process
pl036256	NR_036484.1	GO:0021772	olfactory bulb development	Process
pl036256	NR_036484.1	GO:0021797	forebrain anterior/posterior pattern specification	Process
pl036256	NR_036484.1	GO:0045666	positive regulation of neuron differentiation	Process
pl036256	NR_036484.1	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl100926	uc003fhx	GO:0005783	endoplasmic reticulum	Component
pl061285	uc003fhx	GO:0005783	endoplasmic reticulum	Component
pl054268	uc003fhx	GO:0005783	endoplasmic reticulum	Component
pl100926	uc003fhx	GO:0016021	integral to membrane	Component
pl061285	uc003fhx	GO:0016021	integral to membrane	Component
pl054268	uc003fhx	GO:0016021	integral to membrane	Component
pl100926	uc003fhx	GO:0045600	positive regulation of fat cell differentiation	Process
pl061285	uc003fhx	GO:0045600	positive regulation of fat cell differentiation	Process
pl054268	uc003fhx	GO:0045600	positive regulation of fat cell differentiation	Process
pl105104		GO:0032526	response to retinoic acid	Process
pl023548	AK098019	GO:0001501	skeletal system development	Process

pl023548	AK098019	GO:0001508	regulation of action potential	Process
pl023548	AK098019	GO:0001664	G-protein coupled receptor binding	Function
pl023548	AK098019	GO:0003924	GTPase activity	Function
pl023548	AK098019	GO:0004871	signal transducer activity	Function
pl023548	AK098019	GO:0005096	GTPase activator activity	Function
pl023548	AK098019	GO:0005515	protein binding	Function
pl023548	AK098019	GO:0005525	GTP binding	Function
pl023548	AK098019	GO:0005624	membrane fraction	Component
pl023548	AK098019	GO:0005737	cytoplasm	Component
pl023548	AK098019	GO:0005834	heterotrimeric G-protein complex	Component
pl023548	AK098019	GO:0005886	plasma membrane	Component
pl023548	AK098019	GO:0006184	GTP catabolic process	Process
pl023548	AK098019	GO:0006469	negative regulation of protein kinase activity	Process
pl023548	AK098019	GO:0006471	protein ADP-ribosylation	Process
pl023548	AK098019	GO:0007189	adenylate cyclase-activating G-protein coupled receptor signaling pathway	Process
pl023548	AK098019	GO:0007202	activation of phospholipase C activity	Process
pl023548	AK098019	GO:0007215	glutamate receptor signaling pathway	Process
pl023548	AK098019	GO:0007507	heart development	Process
pl023548	AK098019	GO:0007596	blood coagulation	Process
pl023548	AK098019	GO:0007610	behavior	Process
pl023548	AK098019	GO:0009791	post-embryonic development	Process
pl023548	AK098019	GO:0016322	neuron remodeling	Process
pl023548	AK098019	GO:0021884	forebrain neuron development	Process
pl023548	AK098019	GO:0030168	platelet activation	Process
pl023548	AK098019	GO:0031234	extrinsic to internal side of plasma membrane	Component

pl023548	AK098019	GO:0031683	G-protein beta/gamma-subunit complex binding	Function
pl023548	AK098019	GO:0035412	regulation of catenin import into nucleus	Process
pl023548	AK098019	GO:0042733	embryonic digit morphogenesis	Process
pl023548	AK098019	GO:0043547	positive regulation of GTPase activity	Process
pl023548	AK098019	GO:0045634	regulation of melanocyte differentiation	Process
pl023548	AK098019	GO:0046872	metal ion binding	Function
pl023548	AK098019	GO:0048066	developmental pigmentation	Process
pl023548	AK098019	GO:0050821	protein stabilization	Process
pl023548	AK098019	GO:0060158	phospholipase C-activating dopamine receptor signaling pathway	Process
pl045870	NR_026964	GO:0000139	Golgi membrane	Component
pl045870	NR_026964	GO:0001965	G-protein alpha-subunit binding	Function
pl045870	NR_026964	GO:0005092	GDP-dissociation inhibitor activity	Function
pl045870	NR_026964	GO:0005634	nucleus	Component
pl045870	NR_026964	GO:0005730	nucleolus	Component
pl045870	NR_026964	GO:0005789	endoplasmic reticulum membrane	Component
pl045870	NR_026964	GO:0005794	Golgi apparatus	Component
pl045870	NR_026964	GO:0005829	cytosol	Component
pl045870	NR_026964	GO:0005886	plasma membrane	Component
pl045870	NR_026964	GO:0007165	signal transduction	Process
pl045870	NR_026964	GO:0007399	nervous system development	Process
pl045870	NR_026964	GO:0008277	regulation of G-protein coupled receptor protein signaling pathway	Process
pl045870	NR_026964	GO:0030154	cell differentiation	Process
pl093750	NR_045562.1	GO:0004871	signal transducer activity	Function
pl093750	NR_045562.1	GO:0005737	cytoplasm	Component

pl093750	NR_045562.1	GO:0006869	lipid transport	Process
pl093750	NR_045562.1	GO:0006911	phagocytosis, engulfment	Process
pl093750	NR_045562.1	GO:0006915	apoptotic process	Process
pl093750	NR_045562.1	GO:0007165	signal transduction	Process
pl098511	NR_040662.1	GO:0006952	defense response	Process
pl027153		GO:0000118	histone deacetylase complex	Component
pl027153		GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl027153		GO:0003714	transcription corepressor activity	Function
pl027153		GO:0004407	histone deacetylase activity	Function
pl027153		GO:0005080	protein kinase C binding	Function
pl027153		GO:0005515	protein binding	Function
pl027153		GO:0005634	nucleus	Component
pl027153		GO:0005667	transcription factor complex	Component
pl027153		GO:0005737	cytoplasm	Component
pl027153		GO:0006351	transcription, DNA-dependent	Process
pl027153		GO:0006954	inflammatory response	Process
pl027153		GO:0007219	Notch signaling pathway	Process
pl027153		GO:0007507	heart development	Process
pl027153		GO:0008134	transcription factor binding	Function
pl027153		GO:0016575	histone deacetylation	Process
pl027153		GO:0030183	B cell differentiation	Process
pl027153		GO:0032041	NAD-dependent histone deacetylase activity (H3-K14 specific)	Function
pl027153		GO:0032869	cellular response to insulin stimulus	Process
pl027153		GO:0033558	protein deacetylase activity	Function

pl027153		GO:0034983	peptidyl-lysine deacetylation	Process
pl027153		GO:0035097	histone methyltransferase complex	Component
pl027153		GO:0042113	B cell activation	Process
pl027153		GO:0042826	histone deacetylase binding	Function
pl027153		GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl027153		GO:0046969	NAD-dependent histone deacetylase activity (H3-K9 specific)	Function
pl027153		GO:0046970	NAD-dependent histone deacetylase activity (H4-K16 specific)	Function
pl027153		GO:0048742	regulation of skeletal muscle fiber development	Process
pl027153		GO:0051153	regulation of striated muscle cell differentiation	Process
pl027153		GO:0070491	repressing transcription factor binding	Function
pl027153		GO:0070932	histone H3 deacetylation	Process
pl027153		GO:0070933	histone H4 deacetylation	Process
pl027153		GO:0090050	positive regulation of cell migration involved in sprouting angiogenesis	Process
pl068994	HMlincRNA798	GO:0016787	hydrolase activity	Function
pl068994	HMlincRNA798	GO:0046872	metal ion binding	Function
pl068994	HMlincRNA798	GO:0005524	ATP binding	Function
pl068994	HMlincRNA798	GO:0005737	cytoplasm	Component
pl068994	HMlincRNA798	GO:0005874	microtubule	Component
pl068994	HMlincRNA798	GO:0008568	microtubule-severing ATPase activity	Function
pl071185	BC036877	GO:0001533	cornified envelope	Component
pl071185	BC036877	GO:0005634	nucleus	Component
pl071185	BC036877	GO:0005730	nucleolus	Component
pl071185	BC036877	GO:0005737	cytoplasm	Component

pl071185	BC036877	GO:0030057	desmosome	Component
pl071185	BC036877	GO:0031424	keratinization	Process
pl071185	BC036877	GO:0031965	nuclear membrane	Component
pl071185	BC036877	GO:0043231	intracellular membrane-bounded organelle	Component
pl012449	BC082981	GO:0005244	voltage-gated ion channel activity	Function
pl012449	BC082981	GO:0005267	potassium channel activity	Function
pl012449	BC082981	GO:0016021	integral to membrane	Component
pl050236	BC032033	GO:0016197	endosomal transport	Process
pl050236	BC032033	GO:0071203	WASH complex	Component
pl025260	BC040657	GO:0007596	blood coagulation	Process
pl025260	BC040657	GO:0016021	integral to membrane	Component
pl025260	BC040657	GO:0035115	embryonic forelimb morphogenesis	Process
pl025260	BC040657	GO:0042733	embryonic digit morphogenesis	Process
pl025260	BC040657	GO:0060173	limb development	Process
pl065237	uc003png	GO:0005739	mitochondrion	Component
pl000897	uc010jos	GO:0001750	photoreceptor outer segment	Component
pl000897	uc010jos	GO:0001917	photoreceptor inner segment	Component
pl000897	uc010jos	GO:0003713	transcription coactivator activity	Function
pl000897	uc010jos	GO:0004672	protein kinase activity	Function
pl000897	uc010jos	GO:0004674	protein serine/threonine kinase activity	Function
pl000897	uc010jos	GO:0004693	cyclin-dependent protein kinase activity	Function
pl000897	uc010jos	GO:0005515	protein binding	Function
pl000897	uc010jos	GO:0005524	ATP binding	Function
pl000897	uc010jos	GO:0005634	nucleus	Component
pl000897	uc010jos	GO:0005813	centrosome	Component
pl000897	uc010jos	GO:0006351	transcription, DNA-dependent	Process

pl000897	uc010jos	GO:0006355	regulation of transcription, DNA-dependent	Process
pl000897	uc010jos	GO:0006468	protein phosphorylation	Process
pl000897	uc010jos	GO:0007275	multicellular organismal development	Process
pl000897	uc010jos	GO:0007283	spermatogenesis	Process
pl000897	uc010jos	GO:0030154	cell differentiation	Process
pl000897	uc010jos	GO:0030496	midbody	Component
pl000897	uc010jos	GO:0045494	photoreceptor cell maintenance	Process
pl000897	uc010jos	GO:0046777	protein autophosphorylation	Process
pl000897	uc010jos	GO:0072686	mitotic spindle	Component
pl048800	HMlincRNA965	GO:0000118	histone deacetylase complex	Component
pl048800	HMlincRNA965	GO:0001701	in utero embryonic development	Process
pl048800	HMlincRNA965	GO:0001780	neutrophil homeostasis	Process
pl048800	HMlincRNA965	GO:0003677	DNA binding	Function
pl048800	HMlincRNA965	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl048800	HMlincRNA965	GO:0005515	protein binding	Function
pl048800	HMlincRNA965	GO:0005634	nucleus	Component
pl048800	HMlincRNA965	GO:0006351	transcription, DNA-dependent	Process
pl048800	HMlincRNA965	GO:0006355	regulation of transcription, DNA-dependent	Process
pl048800	HMlincRNA965	GO:0006915	apoptotic process	Process
pl048800	HMlincRNA965	GO:0006954	inflammatory response	Process
pl048800	HMlincRNA965	GO:0008270	zinc ion binding	Function
pl048800	HMlincRNA965	GO:0009605	response to external stimulus	Process
pl048800	HMlincRNA965	GO:0009617	response to bacterium	Process
pl048800	HMlincRNA965	GO:0009791	post-embryonic development	Process
pl048800	HMlincRNA965	GO:0016607	nuclear speck	Component

pl048800	HMlincRNA965	GO:0030154	cell differentiation	Process
pl048800	HMlincRNA965	GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	Process
pl048800	HMlincRNA965	GO:0030900	forebrain development	Process
pl048800	HMlincRNA965	GO:0035115	embryonic forelimb morphogenesis	Process
pl048800	HMlincRNA965	GO:0035116	embryonic hindlimb morphogenesis	Process
pl048800	HMlincRNA965	GO:0042127	regulation of cell proliferation	Process
pl048800	HMlincRNA965	GO:0042803	protein homodimerization activity	Function
pl048800	HMlincRNA965	GO:0043069	negative regulation of programmed cell death	Process
pl048800	HMlincRNA965	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl048800	HMlincRNA965	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl048800	HMlincRNA965	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl048800	HMlincRNA965	GO:0046329	negative regulation of JNK cascade	Process
pl048800	HMlincRNA965	GO:0051726	regulation of cell cycle	Process
pl048800	HMlincRNA965	GO:0060039	pericardium development	Process
pl048800	HMlincRNA965	GO:0071425	hemopoietic stem cell proliferation	Process
pl111818	gnl|UG|Hs	GO:0005783	endoplasmic reticulum	Component
pl111818	gnl|UG|Hs	GO:0005886	plasma membrane	Component
pl111818	gnl|UG|Hs	GO:0016021	integral to membrane	Component
pl111818	gnl|UG|Hs	GO:0030819	positive regulation of cAMP biosynthetic process	Process
pl111818	gnl|UG|Hs	GO:0031780	corticotropin hormone receptor binding	Function
pl111818	gnl|UG|Hs	GO:0031781	type 3 melanocortin receptor binding	Function
pl111818	gnl|UG|Hs	GO:0031782	type 4 melanocortin receptor binding	Function
pl111818	gnl|UG|Hs	GO:0031783	type 5 melanocortin receptor binding	Function
pl111818	gnl|UG|Hs	GO:0034394	protein localization at cell surface	Process

pl111818	gnl|UG|Hs	GO:0048471	perinuclear region of cytoplasm	Component
pl111818	gnl|UG|Hs	GO:0050873	brown fat cell differentiation	Process
pl111818	gnl|UG|Hs	GO:0070996	type 1 melanocortin receptor binding	Function
pl095227	NR_027781.1	GO:0005507	copper ion binding	Function
pl095227	NR_027781.1	GO:0005634	nucleus	Component
pl095227	NR_027781.1	GO:0005737	cytoplasm	Component
pl095227	NR_027781.1	GO:0005764	lysosome	Component
pl095227	NR_027781.1	GO:0005829	cytosol	Component
pl095227	NR_027781.1	GO:0006875	cellular metal ion homeostasis	Process
pl095227	NR_027781.1	GO:0006882	cellular zinc ion homeostasis	Process
pl095227	NR_027781.1	GO:0007263	nitric oxide mediated signal transduction	Process
pl095227	NR_027781.1	GO:0008270	zinc ion binding	Function
pl095227	NR_027781.1	GO:0045926	negative regulation of growth	Process
pl095227	NR_027781.1	GO:0046870	cadmium ion binding	Function
pl095227	NR_027781.1	GO:0048471	perinuclear region of cytoplasm	Component
pl095227	NR_027781.1	GO:0071247	cellular response to chromate	Process
pl095227	NR_027781.1	GO:0071276	cellular response to cadmium ion	Process
pl095227	NR_027781.1	GO:0071294	cellular response to zinc ion	Process
pl024747	uc003hho	GO:0000105	histidine biosynthetic process	Process
pl088612	uc003hho	GO:0000105	histidine biosynthetic process	Process
pl024747	uc003hho	GO:0000166	nucleotide binding	Function
pl088612	uc003hho	GO:0000166	nucleotide binding	Function
pl024747	uc003hho	GO:0004477	methenyltetrahydrofolate cyclohydrolase activity	Function
pl088612	uc003hho	GO:0004477	methenyltetrahydrofolate cyclohydrolase activity	Function
pl024747	uc003hho	GO:0004487	methylenetetrahydrofolate dehydrogenase (NAD+) activity	Function

pl088612	uc003hho	GO:0004487	methylenetetrahydrofolate dehydrogenase (NAD+) activity	Function
pl024747	uc003hho	GO:0004488	methylenetetrahydrofolate dehydrogenase (NADP+) activity	Function
pl088612	uc003hho	GO:0004488	methylenetetrahydrofolate dehydrogenase (NADP+) activity	Function
pl024747	uc003hho	GO:0005743	mitochondrial inner membrane	Component
pl088612	uc003hho	GO:0005743	mitochondrial inner membrane	Component
pl024747	uc003hho	GO:0006164	purine nucleotide biosynthetic process	Process
pl088612	uc003hho	GO:0006164	purine nucleotide biosynthetic process	Process
pl024747	uc003hho	GO:0009086	methionine biosynthetic process	Process
pl088612	uc003hho	GO:0009086	methionine biosynthetic process	Process
pl024747	uc003hho	GO:0009396	folic acid-containing compound biosynthetic process	Process
pl088612	uc003hho	GO:0009396	folic acid-containing compound biosynthetic process	Process
pl024747	uc003hho	GO:0035999	tetrahydrofolate interconversion	Process
pl088612	uc003hho	GO:0035999	tetrahydrofolate interconversion	Process
pl032579	NR_003187.2	GO:0001878	response to yeast	Process
pl032579	NR_003187.2	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	Process
pl032579	NR_003187.2	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	Process
pl032579	NR_003187.2	GO:0002679	respiratory burst involved in defense response	Process
pl032579	NR_003187.2	GO:0003924	GTPase activity	Function
pl032579	NR_003187.2	GO:0005515	protein binding	Function
pl032579	NR_003187.2	GO:0005525	GTP binding	Function
pl032579	NR_003187.2	GO:0005625	soluble fraction	Component

pl032579	NR_003187.2	GO:0005829	cytosol	Component
pl032579	NR_003187.2	GO:0006184	GTP catabolic process	Process
pl032579	NR_003187.2	GO:0006612	protein targeting to membrane	Process
pl032579	NR_003187.2	GO:0006691	leukotriene metabolic process	Process
pl032579	NR_003187.2	GO:0006801	superoxide metabolic process	Process
pl032579	NR_003187.2	GO:0006954	inflammatory response	Process
pl032579	NR_003187.2	GO:0006968	cellular defense response	Process
pl032579	NR_003187.2	GO:0007154	cell communication	Process
pl032579	NR_003187.2	GO:0008283	cell proliferation	Process
pl032579	NR_003187.2	GO:0009055	electron carrier activity	Function
pl032579	NR_003187.2	GO:0016175	superoxide-generating NADPH oxidase activity	Function
pl032579	NR_003187.2	GO:0017124	SH3 domain binding	Function
pl032579	NR_003187.2	GO:0032010	phagolysosome	Component
pl032579	NR_003187.2	GO:0035091	phosphatidylinositol binding	Function
pl032579	NR_003187.2	GO:0042554	superoxide anion generation	Process
pl032579	NR_003187.2	GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	Process
pl032579	NR_003187.2	GO:0043020	NADPH oxidase complex	Component
pl032579	NR_003187.2	GO:0045087	innate immune response	Process
pl032579	NR_003187.2	GO:0045730	respiratory burst	Process
pl032579	NR_003187.2	GO:0045986	negative regulation of smooth muscle contraction	Process
pl032579	NR_003187.2	GO:0050665	hydrogen peroxide biosynthetic process	Process
pl032579	NR_003187.2	GO:0070946	neutrophil mediated killing of gram-positive bacterium	Process
pl032579	NR_003187.2	GO:0070947	neutrophil mediated killing of fungus	Process
pl002694	HIV2736	GO:0004842	ubiquitin-protein ligase activity	Function

pl002694	HIV2736	GO:0005515	protein binding	Function
pl002694	HIV2736	GO:0005622	intracellular	Component
pl002694	HIV2736	GO:0005634	nucleus	Component
pl002694	HIV2736	GO:0005737	cytoplasm	Component
pl002694	HIV2736	GO:0006814	sodium ion transport	Process
pl002694	HIV2736	GO:0006883	cellular sodium ion homeostasis	Process
pl002694	HIV2736	GO:0007588	excretion	Process
pl002694	HIV2736	GO:0010038	response to metal ion	Process
pl002694	HIV2736	GO:0010766	negative regulation of sodium ion transport	Process
pl002694	HIV2736	GO:0016567	protein ubiquitination	Process
pl002694	HIV2736	GO:0017080	sodium channel regulator activity	Function
pl002694	HIV2736	GO:0019871	sodium channel inhibitor activity	Function
pl002694	HIV2736	GO:0030104	water homeostasis	Process
pl002694	HIV2736	GO:0042176	regulation of protein catabolic process	Process
pl002694	HIV2736	GO:0042787	protein ubiquitination involved in ubiquitin-dependent protein catabolic process	Process
pl002694	HIV2736	GO:0044419	interspecies interaction between organisms	Process
pl002694	HIV2736	GO:0045807	positive regulation of endocytosis	Process
pl009498	NR_024453	GO:0004550	nucleoside diphosphate kinase activity	Function
pl009498	NR_024453	GO:0005524	ATP binding	Function
pl009498	NR_024453	GO:0005739	mitochondrion	Component
pl009498	NR_024453	GO:0005743	mitochondrial inner membrane	Component
pl009498	NR_024453	GO:0005758	mitochondrial intermembrane space	Component
pl009498	NR_024453	GO:0006165	nucleoside diphosphate phosphorylation	Process
pl009498	NR_024453	GO:0006183	GTP biosynthetic process	Process
pl009498	NR_024453	GO:0006228	UTP biosynthetic process	Process

pl009498	NR_024453	GO:0006241	CTP biosynthetic process	Process
pl009498	NR_024453	GO:0009116	nucleoside metabolic process	Process
pl009498	NR_024453	GO:0015949	nucleobase-containing small molecule interconversion	Process
pl009498	NR_024453	GO:0044281	small molecule metabolic process	Process
pl009498	NR_024453	GO:0046872	metal ion binding	Function
pl009498	NR_024453	GO:0055086	nucleobase-containing small molecule metabolic process	Process
pl060937	AF086561	GO:0000083	regulation of transcription involved in G1/S phase of mitotic cell cycle	Process
pl060937	AF086561	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl060937	AF086561	GO:0003713	transcription coactivator activity	Function
pl060937	AF086561	GO:0003714	transcription corepressor activity	Function
pl060937	AF086561	GO:0005515	protein binding	Function
pl060937	AF086561	GO:0005634	nucleus	Component
pl060937	AF086561	GO:0006351	transcription, DNA-dependent	Process
pl060937	AF086561	GO:0008022	protein C-terminus binding	Function
pl060937	AF086561	GO:0010468	regulation of gene expression	Process
pl060937	AF086561	GO:0015030	Cajal body	Component
pl060937	AF086561	GO:0044428	nuclear part	Component
pl060937	AF086561	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl060937	AF086561	GO:0047485	protein N-terminus binding	Function
pl018286	uc010did	GO:0005515	protein binding	Function
pl018286	uc010did	GO:0005634	nucleus	Component
pl018286	uc010did	GO:0005783	endoplasmic reticulum	Component

pl018286	uc010did	GO:0005829	cytosol	Component
pl018286	uc010did	GO:0006944	cellular membrane fusion	Process
pl018286	uc010did	GO:0007030	Golgi organization	Process
pl018286	uc010did	GO:0008270	zinc ion binding	Function
pl018286	uc010did	GO:0030433	ER-associated protein catabolic process	Process
pl018286	uc010did	GO:0042175	nuclear outer membrane-endoplasmic reticulum membrane network	Component
pl035603	uc001jtm	GO:0005739	mitochondrion	Component
pl035603	uc001jtm	GO:0016787	hydrolase activity	Function
pl035603	uc001jtm	GO:0046872	metal ion binding	Function
pl032349	BU659324	GO:0005622	intracellular	Component
pl032349	BU659324	GO:0005737	cytoplasm	Component
pl032349	BU659324	GO:0008486	diphosphoinositol-polyphosphate diphosphatase activity	Function
pl032349	BU659324	GO:0009187	cyclic nucleotide metabolic process	Process
pl032349	BU659324	GO:0019722	calcium-mediated signaling	Process
pl032349	BU659324	GO:0019935	cyclic-nucleotide-mediated signaling	Process
pl032349	BU659324	GO:0035556	intracellular signal transduction	Process
pl032349	BU659324	GO:0046831	regulation of RNA export from nucleus	Process
pl032349	BU659324	GO:0046872	metal ion binding	Function
pl032349	BU659324	GO:0046907	intracellular transport	Process
pl032349	BU659324	GO:0052840	inositol diphosphate tetrakisphosphate diphosphatase activity	Function
pl032349	BU659324	GO:0052843	inositol-1-diphosphate-2,3,4,5,6-pentakisphosphate diphosphatase activity	Function
pl032349	BU659324	GO:0052844	inositol-3-diphosphate-1,2,4,5,6-pentakisphosphate	Function

			diphosphatase activity	
pl032349	BU659324	GO:0052845	inositol-5-diphosphate-1,2,3,4,6-pentakisphosphate diphosphatase activity	Function
pl032349	BU659324	GO:0052846	inositol-1,5-bisdiphosphate-2,3,4,6-tetrakisphosphate 1-diphosphatase activity	Function
pl032349	BU659324	GO:0052847	inositol-1,5-bisdiphosphate-2,3,4,6-tetrakisphosphate 5-diphosphatase activity	Function
pl032349	BU659324	GO:0052848	inositol-3,5-bisdiphosphate-2,3,4,6-tetrakisphosphate 5-diphosphatase activity	Function
pl071481	AK128043	GO:0005543	phospholipid binding	Function
pl071481	AK128043	GO:0006869	lipid transport	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0005515	protein binding	Function
pl021705	gnl|ncrnascan|RNS2149	GO:0005886	plasma membrane	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0005887	integral to plasma membrane	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0006928	cellular component movement	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0007010	cytoskeleton organization	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0007194	negative regulation of adenylate cyclase activity	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0008360	regulation of cell shape	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0016023	cytoplasmic membrane-bounded vesicle	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0016323	basolateral plasma membrane	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0016327	apicolateral plasma membrane	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0030424	axon	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0031527	filopodium membrane	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0031750	D3 dopamine receptor binding	Function
pl021705	gnl|ncrnascan|RNS2149	GO:0043197	dendritic spine	Component
pl021705	gnl|ncrnascan|RNS2149	GO:0051491	positive regulation of filopodium assembly	Process

pl021705	gnl|ncrnascan|RNS2149	GO:0060074	synapse maturation	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0060160	negative regulation of dopamine receptor signaling pathway	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0060999	positive regulation of dendritic spine development	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0071257	cellular response to electrical stimulus	Process
pl021705	gnl|ncrnascan|RNS2149	GO:0072661	protein targeting to plasma membrane	Process
pl062694	NR_033440.1	GO:0001666	response to hypoxia	Process
pl062694	NR_033440.1	GO:0004504	peptidylglycine monooxygenase activity	Function
pl062694	NR_033440.1	GO:0004598	peptidylamidoglycolate lyase activity	Function
pl062694	NR_033440.1	GO:0005507	copper ion binding	Function
pl062694	NR_033440.1	GO:0005515	protein binding	Function
pl062694	NR_033440.1	GO:0005576	extracellular region	Component
pl062694	NR_033440.1	GO:0005624	membrane fraction	Component
pl062694	NR_033440.1	GO:0006464	cellular protein modification process	Process
pl062694	NR_033440.1	GO:0006518	peptide metabolic process	Process
pl062694	NR_033440.1	GO:0007417	central nervous system development	Process
pl062694	NR_033440.1	GO:0007507	heart development	Process
pl062694	NR_033440.1	GO:0009268	response to pH	Process
pl062694	NR_033440.1	GO:0016021	integral to membrane	Component
pl062694	NR_033440.1	GO:0030141	secretory granule	Component
pl062694	NR_033440.1	GO:0031418	L-ascorbic acid binding	Function
pl062694	NR_033440.1	GO:0032355	response to estradiol stimulus	Process
pl062694	NR_033440.1	GO:0042493	response to drug	Process
pl062694	NR_033440.1	GO:0043204	perikaryon	Component
pl062694	NR_033440.1	GO:0046688	response to copper ion	Process
pl062694	NR_033440.1	GO:0051384	response to glucocorticoid stimulus	Process

pl062694	NR_033440.1	GO:0060173	limb development	Process
pl015109	uc009xxw	GO:0003723	RNA binding	Function
pl015109	uc009xxw	GO:0005515	protein binding	Function
pl015109	uc009xxw	GO:0005634	nucleus	Component
pl015109	uc009xxw	GO:0005730	nucleolus	Component
pl015109	uc009xxw	GO:0005737	cytoplasm	Component
pl015109	uc009xxw	GO:0005829	cytosol	Component
pl015109	uc009xxw	GO:0006915	apoptotic process	Process
pl015109	uc009xxw	GO:0007569	cell aging	Process
pl015109	uc009xxw	GO:0043508	negative regulation of JUN kinase activity	Process
pl015109	uc009xxw	GO:0045786	negative regulation of cell cycle	Process
pl015109	uc009xxw	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl059793	uc004cyt	GO:0004553	hydrolase activity, hydrolyzing O-glycosyl compounds	Function
pl059793	uc004cyt	GO:0004689	phosphorylase kinase activity	Function
pl059793	uc004cyt	GO:0005516	calmodulin binding	Function
pl059793	uc004cyt	GO:0005829	cytosol	Component
pl059793	uc004cyt	GO:0005886	plasma membrane	Component
pl059793	uc004cyt	GO:0005964	phosphorylase kinase complex	Component
pl059793	uc004cyt	GO:0005975	carbohydrate metabolic process	Process
pl059793	uc004cyt	GO:0005980	glycogen catabolic process	Process
pl059793	uc004cyt	GO:0006006	glucose metabolic process	Process
pl059793	uc004cyt	GO:0006091	generation of precursor metabolites and energy	Process
pl059793	uc004cyt	GO:0006464	cellular protein modification process	Process
pl059793	uc004cyt	GO:0044281	small molecule metabolic process	Process
pl068994	HMlincRNA798	GO:0003677	DNA binding	Function

pl068994	HMlincRNA798	GO:0003713	transcription coactivator activity	Function
pl068994	HMlincRNA798	GO:0005515	protein binding	Function
pl068994	HMlincRNA798	GO:0005634	nucleus	Component
pl068994	HMlincRNA798	GO:0006351	transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0008270	zinc ion binding	Function
pl068994	HMlincRNA798	GO:0016605	PML body	Component
pl068994	HMlincRNA798	GO:0016607	nuclear speck	Component
pl068994	HMlincRNA798	GO:0016925	protein sumoylation	Process
pl068994	HMlincRNA798	GO:0019789	SUMO ligase activity	Function
pl068994	HMlincRNA798	GO:0030521	androgen receptor signaling pathway	Process
pl068994	HMlincRNA798	GO:0031625	ubiquitin protein ligase binding	Function
pl068994	HMlincRNA798	GO:0045667	regulation of osteoblast differentiation	Process
pl068994	HMlincRNA798	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl068994	HMlincRNA798	GO:0050681	androgen receptor binding	Function
pl068994	HMlincRNA798	GO:0060766	negative regulation of androgen receptor signaling pathway	Process
pl053810	HMlincRNA783	GO:0005216	ion channel activity	Function
pl053810	HMlincRNA783	GO:0006812	cation transport	Process
pl053810	HMlincRNA783	GO:0016021	integral to membrane	Component
pl090173	gnl|UG|Hs	GO:0000175	3'-5'-exoribonuclease activity	Function
pl090173	gnl|UG|Hs	GO:0000958	mitochondrial mRNA catabolic process	Process
pl090173	gnl|UG|Hs	GO:0000962	positive regulation of mitochondrial RNA catabolic process	Process
pl090173	gnl|UG|Hs	GO:0000964	mitochondrial RNA 5'-end processing	Process

pl090173	gnl|UG|Hs	GO:0000965	mitochondrial RNA 3'-end processing	Process
pl090173	gnl|UG|Hs	GO:0004654	polyribonucleotide nucleotidyltransferase activity	Function
pl090173	gnl|UG|Hs	GO:0005515	protein binding	Function
pl090173	gnl|UG|Hs	GO:0005737	cytoplasm	Component
pl090173	gnl|UG|Hs	GO:0005739	mitochondrion	Component
pl090173	gnl|UG|Hs	GO:0005758	mitochondrial intermembrane space	Component
pl090173	gnl|UG|Hs	GO:0005886	plasma membrane	Component
pl090173	gnl|UG|Hs	GO:0006378	mRNA polyadenylation	Process
pl090173	gnl|UG|Hs	GO:0006401	RNA catabolic process	Process
pl090173	gnl|UG|Hs	GO:0006402	mRNA catabolic process	Process
pl090173	gnl|UG|Hs	GO:0008266	poly(U) RNA binding	Function
pl090173	gnl|UG|Hs	GO:0034046	poly(G) RNA binding	Function
pl090173	gnl|UG|Hs	GO:0034599	cellular response to oxidative stress	Process
pl090173	gnl|UG|Hs	GO:0035198	miRNA binding	Function
pl090173	gnl|UG|Hs	GO:0035458	cellular response to interferon-beta	Process
pl090173	gnl|UG|Hs	GO:0035927	RNA import into mitochondrion	Process
pl090173	gnl|UG|Hs	GO:0035928	rRNA import into mitochondrion	Process
pl090173	gnl|UG|Hs	GO:0043457	regulation of cellular respiration	Process
pl090173	gnl|UG|Hs	GO:0043631	RNA polyadenylation	Process
pl090173	gnl|UG|Hs	GO:0045025	mitochondrial degradosome	Component
pl090173	gnl|UG|Hs	GO:0045926	negative regulation of growth	Process
pl090173	gnl|UG|Hs	GO:0051260	protein homooligomerization	Process
pl090173	gnl|UG|Hs	GO:0061014	positive regulation of mRNA catabolic process	Process
pl090173	gnl|UG|Hs	GO:0070207	protein homotrimerization	Process
pl090173	gnl|UG|Hs	GO:0070584	mitochondrion morphogenesis	Process
pl090173	gnl|UG|Hs	GO:0071042	nuclear polyadenylation-dependent mRNA catabolic	Process

			process	
pl090173	gnl|UG|Hs	GO:0071850	mitotic cell cycle arrest	Process
pl090173	gnl|UG|Hs	GO:2000627	positive regulation of miRNA catabolic process	Process
pl090173	gnl|UG|Hs	GO:2000772	regulation of cellular senescence	Process
pl011302	gnl|UG|Hs	GO:0003899	DNA-directed RNA polymerase activity	Function
pl011302	gnl|UG|Hs	GO:0005634	nucleus	Component
pl011302	gnl|UG|Hs	GO:0005654	nucleoplasm	Component
pl011302	gnl|UG|Hs	GO:0005730	nucleolus	Component
pl011302	gnl|UG|Hs	GO:0006383	transcription from RNA polymerase III promoter	Process
pl011302	gnl|UG|Hs	GO:0006385	transcription elongation from RNA polymerase III promoter	Process
pl011302	gnl|UG|Hs	GO:0006386	termination of RNA polymerase III transcription	Process
pl011302	gnl|UG|Hs	GO:0009615	response to virus	Process
pl011302	gnl|UG|Hs	GO:0010467	gene expression	Process
pl011302	gnl|UG|Hs	GO:0045087	innate immune response	Process
pl094303	AK001092	GO:0001568	blood vessel development	Process
pl094303	AK001092	GO:0001702	gastrulation with mouth forming second	Process
pl094303	AK001092	GO:0001933	negative regulation of protein phosphorylation	Process
pl094303	AK001092	GO:0004721	phosphoprotein phosphatase activity	Function
pl094303	AK001092	GO:0005178	integrin binding	Function
pl094303	AK001092	GO:0005515	protein binding	Function
pl094303	AK001092	GO:0005789	endoplasmic reticulum membrane	Component
pl094303	AK001092	GO:0005794	Golgi apparatus	Component
pl094303	AK001092	GO:0005886	plasma membrane	Component
pl094303	AK001092	GO:0005912	adherens junction	Component
pl094303	AK001092	GO:0006629	lipid metabolic process	Process

pl094303	AK001092	GO:0006644	phospholipid metabolic process	Process
pl094303	AK001092	GO:0006665	sphingolipid metabolic process	Process
pl094303	AK001092	GO:0008195	phosphatidate phosphatase activity	Function
pl094303	AK001092	GO:0008354	germ cell migration	Process
pl094303	AK001092	GO:0016020	membrane	Component
pl094303	AK001092	GO:0016021	integral to membrane	Component
pl094303	AK001092	GO:0030111	regulation of Wnt receptor signaling pathway	Process
pl094303	AK001092	GO:0030148	sphingolipid biosynthetic process	Process
pl094303	AK001092	GO:0034109	homotypic cell-cell adhesion	Process
pl094303	AK001092	GO:0042577	lipid phosphatase activity	Function
pl094303	AK001092	GO:0044281	small molecule metabolic process	Process
pl094303	AK001092	GO:0044328	canonical Wnt receptor signaling pathway involved in positive regulation of endothelial cell migration	Process
pl094303	AK001092	GO:0044329	canonical Wnt receptor signaling pathway involved in positive regulation of cell-cell adhesion	Process
pl094303	AK001092	GO:0044330	canonical Wnt receptor signaling pathway involved in positive regulation of wound healing	Process
pl094303	AK001092	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	Process
pl094303	AK001092	GO:0050821	protein stabilization	Process
pl094303	AK001092	GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	Process
pl090211	uc010jvv	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl090211	uc010jvv	GO:0003677	DNA binding	Function
pl090211	uc010jvv	GO:0003700	sequence-specific DNA binding transcription factor	Function

			activity	
pl090211	uc010jvv	GO:0003707	steroid hormone receptor activity	Function
pl090211	uc010jvv	GO:0004879	ligand-activated sequence-specific DNA binding RNA polymerase II transcription factor activity	Function
pl090211	uc010jvv	GO:0005504	fatty acid binding	Function
pl090211	uc010jvv	GO:0005634	nucleus	Component
pl090211	uc010jvv	GO:0005654	nucleoplasm	Component
pl090211	uc010jvv	GO:0006006	glucose metabolic process	Process
pl090211	uc010jvv	GO:0006091	generation of precursor metabolites and energy	Process
pl090211	uc010jvv	GO:0006355	regulation of transcription, DNA-dependent	Process
pl090211	uc010jvv	GO:0006357	regulation of transcription from RNA polymerase II promoter	Process
pl090211	uc010jvv	GO:0006367	transcription initiation from RNA polymerase II promoter	Process
pl090211	uc010jvv	GO:0006629	lipid metabolic process	Process
pl090211	uc010jvv	GO:0006635	fatty acid beta-oxidation	Process
pl090211	uc010jvv	GO:0006915	apoptotic process	Process
pl090211	uc010jvv	GO:0007566	embryo implantation	Process
pl090211	uc010jvv	GO:0008144	drug binding	Function
pl090211	uc010jvv	GO:0008203	cholesterol metabolic process	Process
pl090211	uc010jvv	GO:0008270	zinc ion binding	Function
pl090211	uc010jvv	GO:0008283	cell proliferation	Process
pl090211	uc010jvv	GO:0008284	positive regulation of cell proliferation	Process
pl090211	uc010jvv	GO:0008289	lipid binding	Function
pl090211	uc010jvv	GO:0008366	axon ensheathment	Process
pl090211	uc010jvv	GO:0009062	fatty acid catabolic process	Process

pl090211	uc010jvv	GO:0010467	gene expression	Process
pl090211	uc010jvv	GO:0014068	positive regulation of phosphatidylinositol 3-kinase cascade	Process
pl090211	uc010jvv	GO:0015758	glucose transport	Process
pl090211	uc010jvv	GO:0015908	fatty acid transport	Process
pl090211	uc010jvv	GO:0030154	cell differentiation	Process
pl090211	uc010jvv	GO:0030522	intracellular receptor mediated signaling pathway	Process
pl090211	uc010jvv	GO:0031589	cell-substrate adhesion	Process
pl090211	uc010jvv	GO:0042060	wound healing	Process
pl090211	uc010jvv	GO:0042640	anagen	Process
pl090211	uc010jvv	GO:0043401	steroid hormone mediated signaling pathway	Process
pl090211	uc010jvv	GO:0043565	sequence-specific DNA binding	Function
pl090211	uc010jvv	GO:0043616	keratinocyte proliferation	Process
pl090211	uc010jvv	GO:0045600	positive regulation of fat cell differentiation	Process
pl090211	uc010jvv	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl090211	uc010jvv	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl090211	uc010jvv	GO:0046697	decidualization	Process
pl090211	uc010jvv	GO:0050680	negative regulation of epithelial cell proliferation	Process
pl090211	uc010jvv	GO:0051546	keratinocyte migration	Process
pl090211	uc010jvv	GO:0060612	adipose tissue development	Process
pl090211	uc010jvv	GO:0070539	linoleic acid binding	Function
pl041970	uc010ggb	GO:0005515	protein binding	Function
pl041970	uc010ggb	GO:0005634	nucleus	Component
pl041970	uc010ggb	GO:0005886	plasma membrane	Component
pl041970	uc010ggb	GO:0007165	signal transduction	Process
pl041970	uc010ggb	GO:0019903	protein phosphatase binding	Function

pl041970	uc010ggb	GO:0051489	regulation of filopodium assembly	Process
pl105093	DC295389	GO:0000150	recombinase activity	Function
pl039631	DC295389	GO:0000150	recombinase activity	Function
pl105093	DC295389	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	Function
pl039631	DC295389	GO:0000978	RNA polymerase II core promoter proximal region sequence-specific DNA binding	Function
pl105093	DC295389	GO:0001077	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	Function
pl039631	DC295389	GO:0001077	RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription	Function
pl105093	DC295389	GO:0001103	RNA polymerase II repressing transcription factor binding	Function
pl039631	DC295389	GO:0001103	RNA polymerase II repressing transcription factor binding	Function
pl105093	DC295389	GO:0002193	MAML1-RBP-Jkappa- ICN1 complex	Component
pl039631	DC295389	GO:0002193	MAML1-RBP-Jkappa- ICN1 complex	Component
pl105093	DC295389	GO:0003677	DNA binding	Function
pl039631	DC295389	GO:0003677	DNA binding	Function
pl105093	DC295389	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl039631	DC295389	GO:0003700	sequence-specific DNA binding transcription factor	Function

			activity	
pl105093	DC295389	GO:0005515	protein binding	Function
pl039631	DC295389	GO:0005515	protein binding	Function
pl105093	DC295389	GO:0005634	nucleus	Component
pl039631	DC295389	GO:0005634	nucleus	Component
pl105093	DC295389	GO:0005654	nucleoplasm	Component
pl039631	DC295389	GO:0005654	nucleoplasm	Component
pl105093	DC295389	GO:0005730	nucleolus	Component
pl039631	DC295389	GO:0005730	nucleolus	Component
pl105093	DC295389	GO:0005737	cytoplasm	Component
pl039631	DC295389	GO:0005737	cytoplasm	Component
pl105093	DC295389	GO:0006310	DNA recombination	Process
pl039631	DC295389	GO:0006310	DNA recombination	Process
pl105093	DC295389	GO:0006355	regulation of transcription, DNA-dependent	Process
pl039631	DC295389	GO:0006355	regulation of transcription, DNA-dependent	Process
pl105093	DC295389	GO:0006367	transcription initiation from RNA polymerase II promoter	Process
pl039631	DC295389	GO:0006367	transcription initiation from RNA polymerase II promoter	Process
pl105093	DC295389	GO:0007219	Notch signaling pathway	Process
pl039631	DC295389	GO:0007219	Notch signaling pathway	Process
pl105093	DC295389	GO:0007221	positive regulation of transcription of Notch receptor target	Process
pl039631	DC295389	GO:0007221	positive regulation of transcription of Notch receptor target	Process
pl105093	DC295389	GO:0010467	gene expression	Process

pl039631	DC295389	GO:0010467	gene expression	Process
pl105093	DC295389	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl039631	DC295389	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl096479	uc002joy	GO:0003676	nucleic acid binding	Function
pl096479	uc002joy	GO:0003678	DNA helicase activity	Function
pl096479	uc002joy	GO:0005524	ATP binding	Function
pl096479	uc002joy	GO:0005634	nucleus	Component
pl096479	uc002joy	GO:0005654	nucleoplasm	Component
pl096479	uc002joy	GO:0005730	nucleolus	Component
pl096479	uc002joy	GO:0005737	cytoplasm	Component
pl096479	uc002joy	GO:0006259	DNA metabolic process	Process
pl096479	uc002joy	GO:0006281	DNA repair	Process
pl096479	uc002joy	GO:0006310	DNA recombination	Process
pl096479	uc002joy	GO:0008026	ATP-dependent helicase activity	Function
pl096479	uc002joy	GO:0016591	DNA-directed RNA polymerase II, holoenzyme	Component
pl096479	uc002joy	GO:0031965	nuclear membrane	Component
pl096479	uc002joy	GO:0032508	DNA duplex unwinding	Process
pl105897	uc001dbm	GO:0004714	transmembrane receptor protein tyrosine kinase activity	Function
pl105897	uc001dbm	GO:0005524	ATP binding	Function
pl105897	uc001dbm	GO:0005737	cytoplasm	Component
pl105897	uc001dbm	GO:0005886	plasma membrane	Component
pl105897	uc001dbm	GO:0005887	integral to plasma membrane	Component
pl105897	uc001dbm	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	Process
pl105897	uc001dbm	GO:0017147	Wnt-protein binding	Function

pl101461	gnl|ncrnascan|RNS1808	GO:0004872	receptor activity	Function
pl101461	gnl|ncrnascan|RNS1808	GO:0005783	endoplasmic reticulum	Component
pl101461	gnl|ncrnascan|RNS1808	GO:0005840	ribosome	Component
pl101461	gnl|ncrnascan|RNS1808	GO:0006412	translation	Process
pl101461	gnl|ncrnascan|RNS1808	GO:0007165	signal transduction	Process
pl101461	gnl|ncrnascan|RNS1808	GO:0015031	protein transport	Process
pl101461	gnl|ncrnascan|RNS1808	GO:0030176	integral to endoplasmic reticulum membrane	Component
pl097910	AK129947	GO:0001666	response to hypoxia	Process
pl097910	AK129947	GO:0005789	endoplasmic reticulum membrane	Component
pl097910	AK129947	GO:0005798	Golgi-associated vesicle	Component
pl097910	AK129947	GO:0005801	cis-Golgi network	Component
pl097910	AK129947	GO:0005886	plasma membrane	Component
pl097910	AK129947	GO:0006890	retrograde vesicle-mediated transport, Golgi to ER	Process
pl097910	AK129947	GO:0006892	post-Golgi vesicle-mediated transport	Process
pl097910	AK129947	GO:0006904	vesicle docking involved in exocytosis	Process
pl097910	AK129947	GO:0009636	response to toxin	Process
pl097910	AK129947	GO:0015031	protein transport	Process
pl097910	AK129947	GO:0017119	Golgi transport complex	Component
pl097910	AK129947	GO:0019905	syntaxin binding	Function
pl097910	AK129947	GO:0032580	Golgi cisterna membrane	Component
pl097910	AK129947	GO:0047485	protein N-terminus binding	Function
pl097910	AK129947	GO:0060628	regulation of ER to Golgi vesicle-mediated transport	Process
pl101958	gnl|UG|Hs	GO:0004872	receptor activity	Function
pl101958	gnl|UG|Hs	GO:0005794	Golgi apparatus	Component
pl101958	gnl|UG|Hs	GO:0005886	plasma membrane	Component
pl101958	gnl|UG|Hs	GO:0007411	axon guidance	Process

pl101958	gnl|UG|Hs	GO:0016021	integral to membrane	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0000805	X chromosome	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0000806	Y chromosome	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0001741	XY body	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0003682	chromatin binding	Function
pl069409	gnl|ncrnascan|RNS1587	GO:0003714	transcription corepressor activity	Function
pl069409	gnl|ncrnascan|RNS1587	GO:0005515	protein binding	Function
pl069409	gnl|ncrnascan|RNS1587	GO:0005634	nucleus	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0005654	nucleoplasm	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0005737	cytoplasm	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0006351	transcription, DNA-dependent	Process
pl069409	gnl|ncrnascan|RNS1587	GO:0007519	skeletal muscle tissue development	Process
pl069409	gnl|ncrnascan|RNS1587	GO:0030849	autosome	Component
pl069409	gnl|ncrnascan|RNS1587	GO:0044255	cellular lipid metabolic process	Process
pl069409	gnl|ncrnascan|RNS1587	GO:0044281	small molecule metabolic process	Process
pl069409	gnl|ncrnascan|RNS1587	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl069409	gnl|ncrnascan|RNS1587	GO:0048738	cardiac muscle tissue development	Process
pl002953	NR_026717.1	GO:0003723	RNA binding	Function
pl002953	NR_026717.1	GO:0004004	ATP-dependent RNA helicase activity	Function
pl002953	NR_026717.1	GO:0005524	ATP binding	Function
pl002953	NR_026717.1	GO:0005634	nucleus	Component
pl002953	NR_026717.1	GO:0055087	Ski complex	Component
pl103129		GO:0005765	lysosomal membrane	Component
pl103129		GO:0006810	transport	Process
pl103129		GO:0010008	endosome membrane	Component
pl103129		GO:0016021	integral to membrane	Component

pl041833	GO:0000287	magnesium ion binding	Function
pl041833	GO:0001774	microglial cell activation	Process
pl041833	GO:0001921	positive regulation of receptor recycling	Process
pl041833	GO:0001956	positive regulation of neurotransmitter secretion	Process
pl041833	GO:0005504	fatty acid binding	Function
pl041833	GO:0005507	copper ion binding	Function
pl041833	GO:0005509	calcium ion binding	Function
pl041833	GO:0005515	protein binding	Function
pl041833	GO:0005576	extracellular region	Component
pl041833	GO:0005634	nucleus	Component
pl041833	GO:0005737	cytoplasm	Component
pl041833	GO:0005739	mitochondrion	Component
pl041833	GO:0005829	cytosol	Component
pl041833	GO:0005886	plasma membrane	Component
pl041833	GO:0005938	cell cortex	Component
pl041833	GO:0006631	fatty acid metabolic process	Process
pl041833	GO:0006638	neutral lipid metabolic process	Process
pl041833	GO:0006644	phospholipid metabolic process	Process
pl041833	GO:0006916	anti-apoptosis	Process
pl041833	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	Process
pl041833	GO:0007006	mitochondrial membrane organization	Process
pl041833	GO:0008198	ferrous iron binding	Function
pl041833	GO:0008270	zinc ion binding	Function
pl041833	GO:0008344	adult locomotory behavior	Process
pl041833	GO:0010040	response to iron(II) ion	Process

pl041833	GO:0010517	regulation of phospholipase activity	Process
pl041833	GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	Process
pl041833	GO:0014048	regulation of glutamate secretion	Process
pl041833	GO:0014059	regulation of dopamine secretion	Process
pl041833	GO:0015629	actin cytoskeleton	Component
pl041833	GO:0016234	inclusion body	Component
pl041833	GO:0016491	oxidoreductase activity	Function
pl041833	GO:0019717	synaptosome	Component
pl041833	GO:0019894	kinesin binding	Function
pl041833	GO:0030054	cell junction	Component
pl041833	GO:0030424	axon	Component
pl041833	GO:0030426	growth cone	Component
pl041833	GO:0030544	Hsp70 protein binding	Function
pl041833	GO:0031092	platelet alpha granule membrane	Component
pl041833	GO:0031115	negative regulation of microtubule polymerization	Process
pl041833	GO:0031623	receptor internalization	Process
pl041833	GO:0031648	protein destabilization	Process
pl041833	GO:0032026	response to magnesium ion	Process
pl041833	GO:0032410	negative regulation of transporter activity	Process
pl041833	GO:0032496	response to lipopolysaccharide	Process
pl041833	GO:0032769	negative regulation of monooxygenase activity	Process
pl041833	GO:0033138	positive regulation of peptidyl-serine phosphorylation	Process
pl041833	GO:0034341	response to interferon-gamma	Process
pl041833	GO:0034599	cellular response to oxidative stress	Process

pl041833	GO:0035067	negative regulation of histone acetylation	Process
pl041833	GO:0040012	regulation of locomotion	Process
pl041833	GO:0042393	histone binding	Function
pl041833	GO:0042416	dopamine biosynthetic process	Process
pl041833	GO:0042493	response to drug	Process
pl041833	GO:0042775	mitochondrial ATP synthesis coupled electron transport	Process
pl041833	GO:0042802	identical protein binding	Function
pl041833	GO:0043014	alpha-tubulin binding	Function
pl041833	GO:0043027	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	Function
pl041833	GO:0043030	regulation of macrophage activation	Process
pl041833	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	Process
pl041833	GO:0043205	fibril	Component
pl041833	GO:0043206	fibril organization	Process
pl041833	GO:0043524	negative regulation of neuron apoptotic process	Process
pl041833	GO:0045202	synapse	Component
pl041833	GO:0045502	dynein binding	Function
pl041833	GO:0045807	positive regulation of endocytosis	Process
pl041833	GO:0045920	negative regulation of exocytosis	Process
pl041833	GO:0048156	tau protein binding	Function
pl041833	GO:0048169	regulation of long-term neuronal synaptic plasticity	Process
pl041833	GO:0048471	perinuclear region of cytoplasm	Component
pl041833	GO:0048488	synaptic vesicle endocytosis	Process
pl041833	GO:0050812	regulation of acyl-CoA biosynthetic process	Process

pl041833		GO:0051219	phosphoprotein binding	Function
pl041833		GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	Process
pl041833		GO:0051583	dopamine uptake involved in synaptic transmission	Process
pl041833		GO:0051585	negative regulation of dopamine uptake involved in synaptic transmission	Process
pl041833		GO:0051612	negative regulation of serotonin uptake	Process
pl041833		GO:0051622	negative regulation of norepinephrine uptake	Process
pl041833		GO:0055074	calcium ion homeostasis	Process
pl041833		GO:0055114	oxidation-reduction process	Process
pl041833		GO:0060079	regulation of excitatory postsynaptic membrane potential	Process
pl041833		GO:0060291	long-term synaptic potentiation	Process
pl041833		GO:0060732	positive regulation of inositol phosphate biosynthetic process	Process
pl041833		GO:0060961	phospholipase D inhibitor activity	Function
pl041833		GO:0070495	negative regulation of thrombin receptor signaling pathway	Process
pl041833		GO:0070555	response to interleukin-1	Process
pl041833		GO:0071280	cellular response to copper ion	Process
pl041833		GO:0071872	cellular response to epinephrine stimulus	Process
pl041833		GO:0071902	positive regulation of protein serine/threonine kinase activity	Process
pl062900	AL137436	GO:0003779	actin binding	Function
pl062900	AL137436	GO:0005543	phospholipid binding	Function
pl062900	AL137436	GO:0005829	cytosol	Component

pl062900	AL137436	GO:0007411	axon guidance	Process
pl062900	AL137436	GO:0008022	protein C-terminus binding	Function
pl062900	AL137436	GO:0008091	spectrin	Component
pl062900	AL137436	GO:0016020	membrane	Component
pl062900	AL137436	GO:0030036	actin cytoskeleton organization	Process
pl062900	AL137436	GO:0030507	spectrin binding	Function
pl062900	AL137436	GO:0045179	apical cortex	Component
pl062900	AL137436	GO:0046982	protein heterodimerization activity	Function
pl062900	AL137436	GO:0051015	actin filament binding	Function
pl062900	AL137436	GO:0051693	actin filament capping	Process
pl002953	NR_026717.1	GO:0004674	protein serine/threonine kinase activity	Function
pl002953	NR_026717.1	GO:0005524	ATP binding	Function
pl002953	NR_026717.1	GO:0005634	nucleus	Component
pl002953	NR_026717.1	GO:0006468	protein phosphorylation	Process
pl002953	NR_026717.1	GO:0016301	kinase activity	Function
pl064191	uc004crw	GO:0000299	integral to membrane of membrane fraction	Component
pl069926	uc004crw	GO:0000299	integral to membrane of membrane fraction	Component
pl064191	uc004crw	GO:0004773	steryl-sulfatase activity	Function
pl069926	uc004crw	GO:0004773	steryl-sulfatase activity	Function
pl064191	uc004crw	GO:0005624	membrane fraction	Component
pl069926	uc004crw	GO:0005624	membrane fraction	Component
pl064191	uc004crw	GO:0005635	nuclear envelope	Component
pl069926	uc004crw	GO:0005635	nuclear envelope	Component
pl064191	uc004crw	GO:0005764	lysosome	Component
pl069926	uc004crw	GO:0005764	lysosome	Component
pl064191	uc004crw	GO:0005768	endosome	Component

pl069926	uc004crw	GO:0005768	endosome	Component
pl064191	uc004crw	GO:0005783	endoplasmic reticulum	Component
pl069926	uc004crw	GO:0005783	endoplasmic reticulum	Component
pl064191	uc004crw	GO:0005789	endoplasmic reticulum membrane	Component
pl069926	uc004crw	GO:0005789	endoplasmic reticulum membrane	Component
pl064191	uc004crw	GO:0005792	microsome	Component
pl069926	uc004crw	GO:0005792	microsome	Component
pl064191	uc004crw	GO:0005794	Golgi apparatus	Component
pl069926	uc004crw	GO:0005794	Golgi apparatus	Component
pl064191	uc004crw	GO:0005886	plasma membrane	Component
pl069926	uc004crw	GO:0005886	plasma membrane	Component
pl064191	uc004crw	GO:0006665	sphingolipid metabolic process	Process
pl069926	uc004crw	GO:0006665	sphingolipid metabolic process	Process
pl064191	uc004crw	GO:0006687	glycosphingolipid metabolic process	Process
pl069926	uc004crw	GO:0006687	glycosphingolipid metabolic process	Process
pl064191	uc004crw	GO:0006706	steroid catabolic process	Process
pl069926	uc004crw	GO:0006706	steroid catabolic process	Process
pl064191	uc004crw	GO:0007565	female pregnancy	Process
pl069926	uc004crw	GO:0007565	female pregnancy	Process
pl064191	uc004crw	GO:0007611	learning or memory	Process
pl069926	uc004crw	GO:0007611	learning or memory	Process
pl064191	uc004crw	GO:0008284	positive regulation of cell proliferation	Process
pl069926	uc004crw	GO:0008284	positive regulation of cell proliferation	Process
pl064191	uc004crw	GO:0008484	sulfuric ester hydrolase activity	Function
pl069926	uc004crw	GO:0008484	sulfuric ester hydrolase activity	Function
pl064191	uc004crw	GO:0008544	epidermis development	Process

pl069926	uc004crw	GO:0008544	epidermis development	Process
pl064191	uc004crw	GO:0009268	response to pH	Process
pl069926	uc004crw	GO:0009268	response to pH	Process
pl064191	uc004crw	GO:0014070	response to organic cyclic compound	Process
pl069926	uc004crw	GO:0014070	response to organic cyclic compound	Process
pl064191	uc004crw	GO:0016021	integral to membrane	Component
pl069926	uc004crw	GO:0016021	integral to membrane	Component
pl064191	uc004crw	GO:0043434	response to peptide hormone stimulus	Process
pl069926	uc004crw	GO:0043434	response to peptide hormone stimulus	Process
pl064191	uc004crw	GO:0043588	skin development	Process
pl069926	uc004crw	GO:0043588	skin development	Process
pl064191	uc004crw	GO:0043627	response to estrogen stimulus	Process
pl069926	uc004crw	GO:0043627	response to estrogen stimulus	Process
pl064191	uc004crw	GO:0044281	small molecule metabolic process	Process
pl069926	uc004crw	GO:0044281	small molecule metabolic process	Process
pl064191	uc004crw	GO:0046872	metal ion binding	Function
pl069926	uc004crw	GO:0046872	metal ion binding	Function
pl081094	BC004968	GO:0000151	ubiquitin ligase complex	Component
pl081094	BC004968	GO:0000209	protein polyubiquitination	Process
pl081094	BC004968	GO:0004842	ubiquitin-protein ligase activity	Function
pl081094	BC004968	GO:0005515	protein binding	Function
pl081094	BC004968	GO:0005737	cytoplasm	Component
pl081094	BC004968	GO:0005829	cytosol	Component
pl081094	BC004968	GO:0006281	DNA repair	Process
pl081094	BC004968	GO:0006511	ubiquitin-dependent protein catabolic process	Process
pl081094	BC004968	GO:0006515	misfolded or incompletely synthesized protein	Process

			catabolic process	
pl081094	BC004968	GO:0016567	protein ubiquitination	Process
pl081094	BC004968	GO:0019899	enzyme binding	Function
pl081094	BC004968	GO:0019900	kinase binding	Function
pl081094	BC004968	GO:0030544	Hsp70 protein binding	Function
pl081094	BC004968	GO:0030579	ubiquitin-dependent SMAD protein catabolic process	Process
pl081094	BC004968	GO:0030674	protein binding, bridging	Function
pl081094	BC004968	GO:0030911	TPR domain binding	Function
pl081094	BC004968	GO:0031371	ubiquitin conjugating enzyme complex	Component
pl081094	BC004968	GO:0031398	positive regulation of protein ubiquitination	Process
pl081094	BC004968	GO:0031625	ubiquitin protein ligase binding	Function
pl081094	BC004968	GO:0031943	regulation of glucocorticoid metabolic process	Process
pl081094	BC004968	GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	Process
pl081094	BC004968	GO:0034450	ubiquitin-ubiquitin ligase activity	Function
pl081094	BC004968	GO:0042405	nuclear inclusion body	Component
pl081094	BC004968	GO:0042803	protein homodimerization activity	Function
pl081094	BC004968	GO:0043161	proteasomal ubiquitin-dependent protein catabolic process	Process
pl081094	BC004968	GO:0046332	SMAD binding	Function
pl081094	BC004968	GO:0051604	protein maturation	Process
pl081094	BC004968	GO:0051787	misfolded protein binding	Function
pl081094	BC004968	GO:0051865	protein autoubiquitination	Process
pl081094	BC004968	GO:0051879	Hsp90 protein binding	Function
pl081094	BC004968	GO:0070534	protein K63-linked ubiquitination	Process

pl081094	BC004968	GO:0071218	cellular response to misfolded protein	Process
pl081094	BC004968	GO:0090035	positive regulation of chaperone-mediated protein complex assembly	Process
pl106072	BC064139	GO:0005100	Rho GTPase activator activity	Function
pl106072	BC064139	GO:0005829	cytosol	Component
pl106072	BC064139	GO:0007264	small GTPase mediated signal transduction	Process
pl106072	BC064139	GO:0032862	activation of Rho GTPase activity	Process
pl106072	BC064139	GO:0051056	regulation of small GTPase mediated signal transduction	Process
pl107934	AK223466	GO:0001516	prostaglandin biosynthetic process	Process
pl107934	AK223466	GO:0004497	monooxygenase activity	Function
pl107934	AK223466	GO:0004796	thromboxane-A synthase activity	Function
pl107934	AK223466	GO:0005788	endoplasmic reticulum lumen	Component
pl107934	AK223466	GO:0005789	endoplasmic reticulum membrane	Component
pl107934	AK223466	GO:0006690	icosanoid metabolic process	Process
pl107934	AK223466	GO:0006692	prostanoid metabolic process	Process
pl107934	AK223466	GO:0006805	xenobiotic metabolic process	Process
pl107934	AK223466	GO:0009055	electron carrier activity	Function
pl107934	AK223466	GO:0016021	integral to membrane	Component
pl107934	AK223466	GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen	Function
pl107934	AK223466	GO:0020037	heme binding	Function
pl107934	AK223466	GO:0044281	small molecule metabolic process	Process
pl068994	HMlincRNA798	GO:0003677	DNA binding	Function
pl068994	HMlincRNA798	GO:0005634	nucleus	Component
pl068994	HMlincRNA798	GO:0006351	transcription, DNA-dependent	Process

pl068994	HMlincRNA798	GO:0006355	regulation of transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0016021	integral to membrane	Component
pl050273	AB209630	GO:0004385	guanylate kinase activity	Function
pl050273	AB209630	GO:0005515	protein binding	Function
pl050273	AB209630	GO:0005654	nucleoplasm	Component
pl050273	AB209630	GO:0005737	cytoplasm	Component
pl050273	AB209630	GO:0005829	cytosol	Component
pl050273	AB209630	GO:0005886	plasma membrane	Component
pl050273	AB209630	GO:0005912	adherens junction	Component
pl050273	AB209630	GO:0005923	tight junction	Component
pl050273	AB209630	GO:0006915	apoptotic process	Process
pl050273	AB209630	GO:0006921	cellular component disassembly involved in apoptotic process	Process
pl050273	AB209630	GO:0030054	cell junction	Component
pl050273	AB209630	GO:0035329	hippo signaling cascade	Process
pl069565	AK126270	GO:0016021	integral to membrane	Component
pl040361	gnl|UG|Hs	GO:0005244	voltage-gated ion channel activity	Function
pl040361	gnl|UG|Hs	GO:0005262	calcium channel activity	Function
pl040361	gnl|UG|Hs	GO:0016021	integral to membrane	Component
pl071017	uc003ymx	GO:0000421	autophagic vacuole membrane	Component
pl071017	uc003ymx	GO:0005765	lysosomal membrane	Component
pl071017	uc003ymx	GO:0006914	autophagy	Process
pl071017	uc003ymx	GO:0016021	integral to membrane	Component
pl071017	uc003ymx	GO:0031410	cytoplasmic vesicle	Component
pl109785	BC039384	GO:0005540	hyaluronic acid binding	Function
pl109785	BC039384	GO:0006954	inflammatory response	Process

pl109785	BC039384	GO:0007155	cell adhesion	Process
pl109785	BC039384	GO:0007165	signal transduction	Process
pl109785	BC039384	GO:0007267	cell-cell signaling	Process
pl088171	BC070168	GO:0004871	signal transducer activity	Function
pl088171	BC070168	GO:0005764	lysosome	Component
pl088171	BC070168	GO:0006486	protein glycosylation	Process
pl088171	BC070168	GO:0007165	signal transduction	Process
pl088171	BC070168	GO:0016021	integral to membrane	Component
pl088171	BC070168	GO:0030195	negative regulation of blood coagulation	Process
pl016931	AF086453	GO:0005515	protein binding	Function
pl016931	AF086453	GO:0005625	soluble fraction	Component
pl016931	AF086453	GO:0005813	centrosome	Component
pl016931	AF086453	GO:0005829	cytosol	Component
pl016931	AF086453	GO:0007268	synaptic transmission	Process
pl016931	AF086453	GO:0007601	visual perception	Process
pl016931	AF086453	GO:0007602	phototransduction	Process
pl016931	AF086453	GO:0008289	lipid binding	Function
pl016931	AF086453	GO:0042953	lipoprotein transport	Process
pl041707		GO:0004197	cysteine-type endopeptidase activity	Function
pl041707		GO:0004221	ubiquitin thiolesterase activity	Function
pl041707		GO:0004843	ubiquitin-specific protease activity	Function
pl041707		GO:0005515	protein binding	Function
pl041707		GO:0005575	cellular_component	Component
pl041707		GO:0006464	cellular protein modification process	Process
pl041707		GO:0006511	ubiquitin-dependent protein catabolic process	Process
pl041707		GO:0016579	protein deubiquitination	Process

pl080196	uc003ppy	GO:0004221	ubiquitin thiolesterase activity	Function
pl047883	uc003ppy	GO:0004221	ubiquitin thiolesterase activity	Function
pl080196	uc003ppy	GO:0006511	ubiquitin-dependent protein catabolic process	Process
pl047883	uc003ppy	GO:0006511	ubiquitin-dependent protein catabolic process	Process
pl080196	uc003ppy	GO:0008234	cysteine-type peptidase activity	Function
pl047883	uc003ppy	GO:0008234	cysteine-type peptidase activity	Function
pl080196	uc003ppy	GO:0008270	zinc ion binding	Function
pl047883	uc003ppy	GO:0008270	zinc ion binding	Function
pl070972	ENST00000412835	GO:0003779	actin binding	Function
pl070972	ENST00000412835	GO:0005515	protein binding	Function
pl070972	ENST00000412835	GO:0005522	profilin binding	Function
pl070972	ENST00000412835	GO:0005884	actin filament	Component
pl070972	ENST00000412835	GO:0006461	protein complex assembly	Process
pl070972	ENST00000412835	GO:0008154	actin polymerization or depolymerization	Process
pl070972	ENST00000412835	GO:0015629	actin cytoskeleton	Component
pl070972	ENST00000412835	GO:0016023	cytoplasmic membrane-bounded vesicle	Component
pl070972	ENST00000412835	GO:0030048	actin filament-based movement	Process
pl070972	ENST00000412835	GO:0046827	positive regulation of protein export from nucleus	Process
pl099742	gnl|UG|Hs	GO:0000075	cell cycle checkpoint	Process
pl099742	gnl|UG|Hs	GO:0000077	DNA damage checkpoint	Process
pl099742	gnl|UG|Hs	GO:0000186	activation of MAPKK activity	Process
pl099742	gnl|UG|Hs	GO:0000287	magnesium ion binding	Function
pl099742	gnl|UG|Hs	GO:0004674	protein serine/threonine kinase activity	Function
pl099742	gnl|UG|Hs	GO:0004709	MAP kinase kinase kinase activity	Function
pl099742	gnl|UG|Hs	GO:0005515	protein binding	Function
pl099742	gnl|UG|Hs	GO:0005524	ATP binding	Function

pl099742	gnl|UG|Hs	GO:0005634	nucleus	Component
pl099742	gnl|UG|Hs	GO:0005737	cytoplasm	Component
pl099742	gnl|UG|Hs	GO:0006468	protein phosphorylation	Process
pl099742	gnl|UG|Hs	GO:0006950	response to stress	Process
pl099742	gnl|UG|Hs	GO:0007050	cell cycle arrest	Process
pl099742	gnl|UG|Hs	GO:0007243	intracellular protein kinase cascade	Process
pl099742	gnl|UG|Hs	GO:0007257	activation of JUN kinase activity	Process
pl099742	gnl|UG|Hs	GO:0008219	cell death	Process
pl099742	gnl|UG|Hs	GO:0008283	cell proliferation	Process
pl099742	gnl|UG|Hs	GO:0009314	response to radiation	Process
pl099742	gnl|UG|Hs	GO:0030154	cell differentiation	Process
pl099742	gnl|UG|Hs	GO:0043065	positive regulation of apoptotic process	Process
pl000726	uc002fkc	GO:0003676	nucleic acid binding	Function
pl000726	uc002fkc	GO:0007154	cell communication	Process
pl000726	uc002fkc	GO:0008270	zinc ion binding	Function
pl000726	uc002fkc	GO:0035091	phosphatidylinositol binding	Function
pl089142	AK126190	GO:0008270	zinc ion binding	Function
pl089142	AK126190	GO:0016021	integral to membrane	Component
pl089142	AK126190	GO:0016409	palmitoyltransferase activity	Function
pl089142	AK126190	GO:0018345	protein palmitoylation	Process
pl090936	NR_023353	GO:0000139	Golgi membrane	Component
pl090936	NR_023353	GO:0006605	protein targeting	Process
pl090936	NR_023353	GO:0008270	zinc ion binding	Function
pl090936	NR_023353	GO:0016021	integral to membrane	Component
pl090936	NR_023353	GO:0016409	palmitoyltransferase activity	Function
pl090936	NR_023353	GO:0018345	protein palmitoylation	Process

pl080815	gnl|UG|Hs	GO:0003677	DNA binding	Function
pl080815	gnl|UG|Hs	GO:0005634	nucleus	Component
pl080815	gnl|UG|Hs	GO:0006351	transcription, DNA-dependent	Process
pl080815	gnl|UG|Hs	GO:0006355	regulation of transcription, DNA-dependent	Process
pl080815	gnl|UG|Hs	GO:0008270	zinc ion binding	Function
pl105250	NR_034060.1	GO:0003677	DNA binding	Function
pl105250	NR_034060.1	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl105250	NR_034060.1	GO:0003714	transcription corepressor activity	Function
pl105250	NR_034060.1	GO:0005634	nucleus	Component
pl105250	NR_034060.1	GO:0006351	transcription, DNA-dependent	Process
pl105250	NR_034060.1	GO:0006355	regulation of transcription, DNA-dependent	Process
pl105250	NR_034060.1	GO:0008270	zinc ion binding	Function
pl056182	ENST00000455406	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl056182	ENST00000455406	GO:0003723	RNA binding	Function
pl056182	ENST00000455406	GO:0005515	protein binding	Function
pl056182	ENST00000455406	GO:0005634	nucleus	Component
pl056182	ENST00000455406	GO:0006355	regulation of transcription, DNA-dependent	Process
pl056182	ENST00000455406	GO:0006397	mRNA processing	Process
pl056182	ENST00000455406	GO:0008270	zinc ion binding	Function
pl056182	ENST00000455406	GO:0008380	RNA splicing	Process
pl016207	ASO2077	GO:0005215	transporter activity	Function
pl016207	ASO2077	GO:0005634	nucleus	Component
pl016207	ASO2077	GO:0005730	nucleolus	Component
pl016207	ASO2077	GO:0005737	cytoplasm	Component

pl016207	ASO2077	GO:0005794	Golgi apparatus	Component
pl016207	ASO2077	GO:0006886	intracellular protein transport	Process
pl016207	ASO2077	GO:0006892	post-Golgi vesicle-mediated transport	Process
pl016207	ASO2077	GO:0006897	endocytosis	Process
pl016207	ASO2077	GO:0008565	protein transporter activity	Function
pl016207	ASO2077	GO:0030117	membrane coat	Component
pl016207	ASO2077	GO:0030137	COPI-coated vesicle	Component
pl016207	ASO2077	GO:0030665	clathrin coated vesicle membrane	Component
pl098426		GO:0000166	nucleotide binding	Function
pl098426		GO:0003953	NAD+ nucleosidase activity	Function
pl098426		GO:0005886	plasma membrane	Component
pl098426		GO:0006959	humoral immune response	Process
pl098426		GO:0007275	multicellular organismal development	Process
pl098426		GO:0019898	extrinsic to membrane	Component
pl098426		GO:0031225	anchored to membrane	Component
pl002953	NR_026717.1	GO:0004866	endopeptidase inhibitor activity	Function
pl002953	NR_026717.1	GO:0005576	extracellular region	Component
pl002953	NR_026717.1	GO:0005615	extracellular space	Component
pl002953	NR_026717.1	GO:0005886	plasma membrane	Component
pl002953	NR_026717.1	GO:0006954	inflammatory response	Process
pl002953	NR_026717.1	GO:0006956	complement activation	Process
pl002953	NR_026717.1	GO:0006958	complement activation, classical pathway	Process
pl002953	NR_026717.1	GO:0030449	regulation of complement activation	Process
pl002953	NR_026717.1	GO:0045087	innate immune response	Process
pl016873	uc002ued	GO:0003700	sequence-specific DNA binding transcription factor activity	Function

pl016873	uc002ued	GO:0005634	nucleus	Component
pl016873	uc002ued	GO:0005789	endoplasmic reticulum membrane	Component
pl016873	uc002ued	GO:0006665	sphingolipid metabolic process	Process
pl016873	uc002ued	GO:0016021	integral to membrane	Component
pl016873	uc002ued	GO:0030148	sphingolipid biosynthetic process	Process
pl016873	uc002ued	GO:0031965	nuclear membrane	Component
pl016873	uc002ued	GO:0043565	sequence-specific DNA binding	Function
pl016873	uc002ued	GO:0044281	small molecule metabolic process	Process
pl016873	uc002ued	GO:0046513	ceramide biosynthetic process	Process
pl016873	uc002ued	GO:0050291	sphingosine N-acyltransferase activity	Function
pl063538	gnl|UG|Hs	GO:0002011	morphogenesis of an epithelial sheet	Process
pl063538	gnl|UG|Hs	GO:0002224	toll-like receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0002755	MyD88-dependent toll-like receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0002756	MyD88-independent toll-like receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0004672	protein kinase activity	Function
pl063538	gnl|UG|Hs	GO:0005515	protein binding	Function
pl063538	gnl|UG|Hs	GO:0005524	ATP binding	Function
pl063538	gnl|UG|Hs	GO:0005634	nucleus	Component
pl063538	gnl|UG|Hs	GO:0005730	nucleolus	Component
pl063538	gnl|UG|Hs	GO:0005737	cytoplasm	Component
pl063538	gnl|UG|Hs	GO:0005829	cytosol	Component
pl063538	gnl|UG|Hs	GO:0006468	protein phosphorylation	Process
pl063538	gnl|UG|Hs	GO:0006954	inflammatory response	Process
pl063538	gnl|UG|Hs	GO:0006955	immune response	Process

pl063538	gnl|UG|Hs	GO:0007173	epidermal growth factor receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0007249	I-kappaB kinase/NF-kappaB cascade	Process
pl063538	gnl|UG|Hs	GO:0007252	I-kappaB phosphorylation	Process
pl063538	gnl|UG|Hs	GO:0007595	lactation	Process
pl063538	gnl|UG|Hs	GO:0008063	Toll signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0008384	IkappaB kinase activity	Function
pl063538	gnl|UG|Hs	GO:0008385	IkappaB kinase complex	Component
pl063538	gnl|UG|Hs	GO:0008543	fibroblast growth factor receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0009615	response to virus	Process
pl063538	gnl|UG|Hs	GO:0009653	anatomical structure morphogenesis	Process
pl063538	gnl|UG|Hs	GO:0009898	internal side of plasma membrane	Component
pl063538	gnl|UG|Hs	GO:0030316	osteoclast differentiation	Process
pl063538	gnl|UG|Hs	GO:0032481	positive regulation of type I interferon production	Process
pl063538	gnl|UG|Hs	GO:0033598	mammary gland epithelial cell proliferation	Process
pl063538	gnl|UG|Hs	GO:0034130	toll-like receptor 1 signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0034134	toll-like receptor 2 signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0034138	toll-like receptor 3 signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0034142	toll-like receptor 4 signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0035631	CD40 receptor complex	Component
pl063538	gnl|UG|Hs	GO:0035666	TRIF-dependent toll-like receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0042475	odontogenesis of dentin-containing tooth	Process
pl063538	gnl|UG|Hs	GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB cascade	Process
pl063538	gnl|UG|Hs	GO:0043231	intracellular membrane-bounded organelle	Component

pl063538	gnl|UG|Hs	GO:0045087	innate immune response	Process
pl063538	gnl|UG|Hs	GO:0048011	nerve growth factor receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0048015	phosphatidylinositol-mediated signaling	Process
pl063538	gnl|UG|Hs	GO:0050852	T cell receptor signaling pathway	Process
pl063538	gnl|UG|Hs	GO:0051092	positive regulation of NF-kappaB transcription factor activity	Process
pl063538	gnl|UG|Hs	GO:0060749	mammary gland alveolus development	Process
pl063538	gnl|UG|Hs	GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	Process
pl089142	AK126190	GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	Process
pl089142	AK126190	GO:0000289	nuclear-transcribed mRNA poly(A) tail shortening	Process
pl089142	AK126190	GO:0000932	cytoplasmic mRNA processing body	Component
pl089142	AK126190	GO:0003676	nucleic acid binding	Function
pl089142	AK126190	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl089142	AK126190	GO:0004871	signal transducer activity	Function
pl089142	AK126190	GO:0005515	protein binding	Function
pl089142	AK126190	GO:0005634	nucleus	Component
pl089142	AK126190	GO:0005829	cytosol	Component
pl089142	AK126190	GO:0005975	carbohydrate metabolic process	Process
pl089142	AK126190	GO:0006351	transcription, DNA-dependent	Process
pl089142	AK126190	GO:0006355	regulation of transcription, DNA-dependent	Process
pl089142	AK126190	GO:0007165	signal transduction	Process
pl089142	AK126190	GO:0010467	gene expression	Process
pl089142	AK126190	GO:0016070	RNA metabolic process	Process

pl089142	AK126190	GO:0016071	mRNA metabolic process	Process
pl089142	AK126190	GO:0030014	CCR4-NOT complex	Component
pl089142	AK126190	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl016207	ASO2077	GO:0000166	nucleotide binding	Function
pl016207	ASO2077	GO:0000932	cytoplasmic mRNA processing body	Component
pl016207	ASO2077	GO:0003723	RNA binding	Function
pl016207	ASO2077	GO:0005886	plasma membrane	Component
pl016207	ASO2077	GO:0006397	mRNA processing	Process
pl016207	ASO2077	GO:0006417	regulation of translation	Process
pl016207	ASO2077	GO:0014069	postsynaptic density	Component
pl016207	ASO2077	GO:0030054	cell junction	Component
pl016207	ASO2077	GO:0045211	postsynaptic membrane	Component
pl063538	gnl|UG|Hs	GO:0003674	molecular_function	Function
pl063538	gnl|UG|Hs	GO:0003824	catalytic activity	Function
pl063538	gnl|UG|Hs	GO:0005575	cellular_component	Component
pl063538	gnl|UG|Hs	GO:0008150	biological_process	Process
pl002953	NR_026717.1	GO:0000166	nucleotide binding	Function
pl002953	NR_026717.1	GO:0046872	metal ion binding	Function
pl112125	AK130406	GO:0005515	protein binding	Function
pl112125	AK130406	GO:0006351	transcription, DNA-dependent	Process
pl112125	AK130406	GO:0006355	regulation of transcription, DNA-dependent	Process
pl112125	AK130406	GO:0015030	Cajal body	Component
pl112125	AK130406	GO:0016607	nuclear speck	Component
pl035603	uc001jtm	GO:0003713	transcription coactivator activity	Function
pl035603	uc001jtm	GO:0005634	nucleus	Component

pl035603	uc001jtm	GO:0005737	cytoplasm	Component
pl035603	uc001jtm	GO:0006110	regulation of glycolysis	Process
pl035603	uc001jtm	GO:0006355	regulation of transcription, DNA-dependent	Process
pl035603	uc001jtm	GO:0006366	transcription from RNA polymerase II promoter	Process
pl062900	AL137436	GO:0003676	nucleic acid binding	Function
pl062900	AL137436	GO:0003924	GTPase activity	Function
pl062900	AL137436	GO:0005509	calcium ion binding	Function
pl062900	AL137436	GO:0005515	protein binding	Function
pl062900	AL137436	GO:0005524	ATP binding	Function
pl062900	AL137436	GO:0005525	GTP binding	Function
pl062900	AL137436	GO:0005634	nucleus	Component
pl062900	AL137436	GO:0005783	endoplasmic reticulum	Component
pl062900	AL137436	GO:0005886	plasma membrane	Component
pl062900	AL137436	GO:0006907	pinocytosis	Process
pl062900	AL137436	GO:0030100	regulation of endocytosis	Process
pl062900	AL137436	GO:0031901	early endosome membrane	Component
pl062900	AL137436	GO:0032456	endocytic recycling	Process
pl062900	AL137436	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	Process
pl062900	AL137436	GO:0051260	protein homooligomerization	Process
pl062900	AL137436	GO:0055038	recycling endosome membrane	Component
pl062900	AL137436	GO:0071363	cellular response to growth factor stimulus	Process
pl038713	AK129572	GO:0005543	phospholipid binding	Function
pl038713	AK129572	GO:0005737	cytoplasm	Component
pl038713	AK129572	GO:0005856	cytoskeleton	Component
pl038713	AK129572	GO:0006909	phagocytosis	Process

pl038713	AK129572	GO:0006915	apoptotic process	Process
pl038713	AK129572	GO:0017124	SH3 domain binding	Function
pl073519	AL832516	GO:0003677	DNA binding	Function
pl073519	AL832516	GO:0004386	helicase activity	Function
pl073519	AL832516	GO:0005524	ATP binding	Function
pl073519	AL832516	GO:0016607	nuclear speck	Component
pl073519	AL832516	GO:0035267	NuA4 histone acetyltransferase complex	Component
pl073519	AL832516	GO:0043967	histone H4 acetylation	Process
pl073519	AL832516	GO:0043968	histone H2A acetylation	Process
pl090936	NR_023353	GO:0000175	3'-5'-exoribonuclease activity	Function
pl090936	NR_023353	GO:0000178	exosome (RNase complex)	Component
pl090936	NR_023353	GO:0000288	nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay	Process
pl090936	NR_023353	GO:0003723	RNA binding	Function
pl090936	NR_023353	GO:0004532	exoribonuclease activity	Function
pl090936	NR_023353	GO:0005515	protein binding	Function
pl090936	NR_023353	GO:0005730	nucleolus	Component
pl090936	NR_023353	GO:0005829	cytosol	Component
pl090936	NR_023353	GO:0006364	rRNA processing	Process
pl090936	NR_023353	GO:0006401	RNA catabolic process	Process
pl090936	NR_023353	GO:0010467	gene expression	Process
pl090936	NR_023353	GO:0016070	RNA metabolic process	Process
pl090936	NR_023353	GO:0016071	mRNA metabolic process	Process
pl090936	NR_023353	GO:0043928	exonucleolytic nuclear-transcribed mRNA catabolic process involved in deadenylation-dependent decay	Process
pl098426		GO:0000151	ubiquitin ligase complex	Component

pl098426		GO:0004842	ubiquitin-protein ligase activity	Function
pl098426		GO:0005506	iron ion binding	Function
pl098426		GO:0005515	protein binding	Function
pl098426		GO:0016567	protein ubiquitination	Process
pl098426		GO:0019005	SCF ubiquitin ligase complex	Component
pl098426		GO:0031146	SCF-dependent proteasomal ubiquitin-dependent protein catabolic process	Process
pl098426		GO:0048471	perinuclear region of cytoplasm	Component
pl098426		GO:0055072	iron ion homeostasis	Process
pl016931	AF086453	GO:0002260	lymphocyte homeostasis	Process
pl016931	AF086453	GO:0003690	double-stranded DNA binding	Function
pl016931	AF086453	GO:0003705	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity	Function
pl016931	AF086453	GO:0005634	nucleus	Component
pl016931	AF086453	GO:0005667	transcription factor complex	Component
pl016931	AF086453	GO:0006357	regulation of transcription from RNA polymerase II promoter	Process
pl016931	AF086453	GO:0006366	transcription from RNA polymerase II promoter	Process
pl016931	AF086453	GO:0006952	defense response	Process
pl016931	AF086453	GO:0007389	pattern specification process	Process
pl016931	AF086453	GO:0008134	transcription factor binding	Function
pl016931	AF086453	GO:0008301	DNA binding, bending	Function
pl016931	AF086453	GO:0008544	epidermis development	Process
pl016931	AF086453	GO:0009790	embryo development	Process
pl016931	AF086453	GO:0009887	organ morphogenesis	Process

pl016931	AF086453	GO:0030216	keratinocyte differentiation	Process
pl016931	AF086453	GO:0033081	regulation of T cell differentiation in thymus	Process
pl016931	AF086453	GO:0043565	sequence-specific DNA binding	Function
pl016931	AF086453	GO:0048538	thymus development	Process
pl016931	AF086453	GO:0050673	epithelial cell proliferation	Process
pl016931	AF086453	GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	Process
pl028231	ENST00000499504	GO:0001570	vasculogenesis	Process
pl028231	ENST00000499504	GO:0004930	G-protein coupled receptor activity	Function
pl028231	ENST00000499504	GO:0005515	protein binding	Function
pl028231	ENST00000499504	GO:0005737	cytoplasm	Component
pl028231	ENST00000499504	GO:0005886	plasma membrane	Component
pl028231	ENST00000499504	GO:0005887	integral to plasma membrane	Component
pl028231	ENST00000499504	GO:0005911	cell-cell junction	Component
pl028231	ENST00000499504	GO:0007223	Wnt receptor signaling pathway, calcium modulating pathway	Process
pl028231	ENST00000499504	GO:0007420	brain development	Process
pl028231	ENST00000499504	GO:0007605	sensory perception of sound	Process
pl028231	ENST00000499504	GO:0009790	embryo development	Process
pl028231	ENST00000499504	GO:0009986	cell surface	Component
pl028231	ENST00000499504	GO:0010812	negative regulation of cell-substrate adhesion	Process
pl028231	ENST00000499504	GO:0016055	Wnt receptor signaling pathway	Process
pl028231	ENST00000499504	GO:0017147	Wnt-protein binding	Function
pl028231	ENST00000499504	GO:0019955	cytokine binding	Function
pl028231	ENST00000499504	GO:0030165	PDZ domain binding	Function
pl028231	ENST00000499504	GO:0030182	neuron differentiation	Process

pl028231	ENST00000499504	GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	Process
pl028231	ENST00000499504	GO:0031987	locomotion involved in locomotory behavior	Process
pl028231	ENST00000499504	GO:0034446	substrate adhesion-dependent cell spreading	Process
pl028231	ENST00000499504	GO:0035426	extracellular matrix-cell signaling	Process
pl028231	ENST00000499504	GO:0042701	progesterone secretion	Process
pl028231	ENST00000499504	GO:0042803	protein homodimerization activity	Function
pl028231	ENST00000499504	GO:0042813	Wnt-activated receptor activity	Function
pl028231	ENST00000499504	GO:0042995	cell projection	Component
pl028231	ENST00000499504	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl028231	ENST00000499504	GO:0046982	protein heterodimerization activity	Function
pl028231	ENST00000499504	GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	Process
pl028231	ENST00000499504	GO:0060070	canonical Wnt receptor signaling pathway	Process
pl028231	ENST00000499504	GO:0061299	retina vasculature morphogenesis in camera-type eye	Process
pl028231	ENST00000499504	GO:0061301	cerebellum vasculature morphogenesis	Process
pl028231	ENST00000499504	GO:0061304	retinal blood vessel morphogenesis	Process
pl028231	ENST00000499504	GO:0071300	cellular response to retinoic acid	Process
pl063478	NR_003698	GO:0004366	glycerol-3-phosphate O-acyltransferase activity	Function
pl063478	NR_003698	GO:0005739	mitochondrion	Component
pl063478	NR_003698	GO:0005741	mitochondrial outer membrane	Component
pl063478	NR_003698	GO:0006072	glycerol-3-phosphate metabolic process	Process
pl063478	NR_003698	GO:0016021	integral to membrane	Component
pl063478	NR_003698	GO:0016024	CDP-diacylglycerol biosynthetic process	Process
pl063478	NR_003698	GO:0019432	triglyceride biosynthetic process	Process
pl032579	NR_003187.2	GO:0003677	DNA binding	Function

pl032579	NR_003187.2	GO:0005634	nucleus	Component
pl032579	NR_003187.2	GO:0006351	transcription, DNA-dependent	Process
pl032579	NR_003187.2	GO:0006355	regulation of transcription, DNA-dependent	Process
pl032579	NR_003187.2	GO:0008270	zinc ion binding	Function
pl064191	uc004crw	GO:0003674	molecular_function	Function
pl069926	uc004crw	GO:0003674	molecular_function	Function
pl064191	uc004crw	GO:0005575	cellular_component	Component
pl069926	uc004crw	GO:0005575	cellular_component	Component
pl064191	uc004crw	GO:0008150	biological_process	Process
pl069926	uc004crw	GO:0008150	biological_process	Process
pl064191	uc004crw	GO:0009117	nucleotide metabolic process	Process
pl069926	uc004crw	GO:0009117	nucleotide metabolic process	Process
pl064191	uc004crw	GO:0016791	phosphatase activity	Function
pl069926	uc004crw	GO:0016791	phosphatase activity	Function
pl064191	uc004crw	GO:0046872	metal ion binding	Function
pl069926	uc004crw	GO:0046872	metal ion binding	Function
pl107934	AK223466	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl107934	AK223466	GO:0001102	RNA polymerase II activating transcription factor binding	Function
pl107934	AK223466	GO:0001105	RNA polymerase II transcription coactivator activity	Function
pl107934	AK223466	GO:0001654	eye development	Process
pl107934	AK223466	GO:0003714	transcription corepressor activity	Function
pl107934	AK223466	GO:0004672	protein kinase activity	Function
pl107934	AK223466	GO:0004674	protein serine/threonine kinase activity	Function
pl107934	AK223466	GO:0005515	protein binding	Function

pl107934	AK223466	GO:0005524	ATP binding	Function
pl107934	AK223466	GO:0005634	nucleus	Component
pl107934	AK223466	GO:0005737	cytoplasm	Component
pl107934	AK223466	GO:0005813	centrosome	Component
pl107934	AK223466	GO:0006468	protein phosphorylation	Process
pl107934	AK223466	GO:0006915	apoptotic process	Process
pl107934	AK223466	GO:0006978	DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator	Process
pl107934	AK223466	GO:0007179	transforming growth factor beta receptor signaling pathway	Process
pl107934	AK223466	GO:0007224	smoothened signaling pathway	Process
pl107934	AK223466	GO:0007628	adult walking behavior	Process
pl107934	AK223466	GO:0008284	positive regulation of cell proliferation	Process
pl107934	AK223466	GO:0008629	induction of apoptosis by intracellular signals	Process
pl107934	AK223466	GO:0009952	anterior/posterior pattern specification	Process
pl107934	AK223466	GO:0010842	retina layer formation	Process
pl107934	AK223466	GO:0016604	nuclear body	Component
pl107934	AK223466	GO:0016605	PML body	Component
pl107934	AK223466	GO:0018105	peptidyl-serine phosphorylation	Process
pl107934	AK223466	GO:0018107	peptidyl-threonine phosphorylation	Process
pl107934	AK223466	GO:0019048	virus-host interaction	Process
pl107934	AK223466	GO:0030182	neuron differentiation	Process
pl107934	AK223466	GO:0030218	erythrocyte differentiation	Process
pl107934	AK223466	GO:0030511	positive regulation of transforming growth factor beta receptor signaling pathway	Process

pl107934	AK223466	GO:0030514	negative regulation of BMP signaling pathway	Process
pl107934	AK223466	GO:0030578	PML body organization	Process
pl107934	AK223466	GO:0031965	nuclear membrane	Component
pl107934	AK223466	GO:0032092	positive regulation of protein binding	Process
pl107934	AK223466	GO:0042771	DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis	Process
pl107934	AK223466	GO:0043388	positive regulation of DNA binding	Process
pl107934	AK223466	GO:0043524	negative regulation of neuron apoptotic process	Process
pl107934	AK223466	GO:0045766	positive regulation of angiogenesis	Process
pl107934	AK223466	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl107934	AK223466	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl107934	AK223466	GO:0046330	positive regulation of JNK cascade	Process
pl107934	AK223466	GO:0046332	SMAD binding	Function
pl107934	AK223466	GO:0046790	virion binding	Function
pl107934	AK223466	GO:0048596	embryonic camera-type eye morphogenesis	Process
pl107934	AK223466	GO:0050882	voluntary musculoskeletal movement	Process
pl107934	AK223466	GO:0051091	positive regulation of sequence-specific DNA binding transcription factor activity	Process
pl107934	AK223466	GO:0051726	regulation of cell cycle	Process
pl107934	AK223466	GO:0060059	embryonic retina morphogenesis in camera-type eye	Process
pl107934	AK223466	GO:0060235	lens induction in camera-type eye	Process
pl107934	AK223466	GO:0060395	SMAD protein signal transduction	Process
pl107934	AK223466	GO:0061072	iris morphogenesis	Process
pl107934	AK223466	GO:0071456	cellular response to hypoxia	Process
pl045494	NR_038971.1	GO:0000166	nucleotide binding	Function

pl045494	NR_038971.1	GO:0000398	nuclear mRNA splicing, via spliceosome	Process
pl045494	NR_038971.1	GO:0003723	RNA binding	Function
pl045494	NR_038971.1	GO:0003729	mRNA binding	Function
pl045494	NR_038971.1	GO:0005515	protein binding	Function
pl045494	NR_038971.1	GO:0005654	nucleoplasm	Component
pl045494	NR_038971.1	GO:0005681	spliceosomal complex	Component
pl045494	NR_038971.1	GO:0008380	RNA splicing	Process
pl045494	NR_038971.1	GO:0010467	gene expression	Process
pl045494	NR_038971.1	GO:0042802	identical protein binding	Function
pl045494	NR_038971.1	GO:0045120	pronucleus	Component
pl045494	NR_038971.1	GO:0071013	catalytic step 2 spliceosome	Component
pl065225	uc001hox	GO:0003677	DNA binding	Function
pl065225	uc001hox	GO:0004872	receptor activity	Function
pl065225	uc001hox	GO:0005515	protein binding	Function
pl065225	uc001hox	GO:0005521	lamin binding	Function
pl065225	uc001hox	GO:0005635	nuclear envelope	Component
pl065225	uc001hox	GO:0005639	integral to nuclear inner membrane	Component
pl065225	uc001hox	GO:0005643	nuclear pore	Component
pl065225	uc001hox	GO:0006695	cholesterol biosynthetic process	Process
pl065225	uc001hox	GO:0016021	integral to membrane	Component
pl065225	uc001hox	GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	Function
pl065225	uc001hox	GO:0044281	small molecule metabolic process	Process
pl065225	uc001hox	GO:0070087	chromo shadow domain binding	Function
pl088171	BC070168	GO:0004930	G-protein coupled receptor activity	Function
pl088171	BC070168	GO:0005887	integral to plasma membrane	Component

pl088171	BC070168	GO:0007186	G-protein coupled receptor signaling pathway	Process
pl088171	BC070168	GO:0016500	protein-hormone receptor activity	Function
pl088171	BC070168	GO:0048839	inner ear development	Process
pl107503	NR_024042	GO:0005887	integral to plasma membrane	Component
pl107503	NR_024042	GO:0010628	positive regulation of gene expression	Process
pl107503	NR_024042	GO:0046007	negative regulation of activated T cell proliferation	Process
pl107503	NR_024042	GO:0050710	negative regulation of cytokine secretion	Process
pl065237	uc003png	GO:0005524	ATP binding	Function
pl065237	uc003png	GO:0005634	nucleus	Component
pl065237	uc003png	GO:0006200	ATP catabolic process	Process
pl065237	uc003png	GO:0006461	protein complex assembly	Process
pl065237	uc003png	GO:0016887	ATPase activity	Function
pl065237	uc003png	GO:0051082	unfolded protein binding	Function
pl106096		GO:0005634	nucleus	Component
pl106096		GO:0005829	cytosol	Component
pl106096		GO:0032886	regulation of microtubule-based process	Process
pl112125	AK130406	GO:0008168	methyltransferase activity	Function
pl053119	CU693173	GO:0005886	plasma membrane	Component
pl053119	CU693173	GO:0016021	integral to membrane	Component
pl095227	NR_027781.1	GO:0005507	copper ion binding	Function
pl095227	NR_027781.1	GO:0005634	nucleus	Component
pl095227	NR_027781.1	GO:0005737	cytoplasm	Component
pl095227	NR_027781.1	GO:0008270	zinc ion binding	Function
pl095227	NR_027781.1	GO:0045926	negative regulation of growth	Process
pl095227	NR_027781.1	GO:0046870	cadmium ion binding	Function
pl095227	NR_027781.1	GO:0048471	perinuclear region of cytoplasm	Component

pl095227	NR_027781.1	GO:0071294	cellular response to zinc ion	Process
pl095227	NR_027781.1	GO:0046872	metal ion binding	Function
pl042847	NR_045553.1	GO:0005739	mitochondrion	Component
pl042847	NR_045553.1	GO:0005741	mitochondrial outer membrane	Component
pl042847	NR_045553.1	GO:0005743	mitochondrial inner membrane	Component
pl042847	NR_045553.1	GO:0006626	protein targeting to mitochondrion	Process
pl042847	NR_045553.1	GO:0016021	integral to membrane	Component
pl042847	NR_045553.1	GO:0044267	cellular protein metabolic process	Process
pl082023	uc002iqz	GO:0005515	protein binding	Function
pl082023	uc002iqz	GO:0005737	cytoplasm	Component
pl082023	uc002iqz	GO:0007268	synaptic transmission	Process
pl082023	uc002iqz	GO:0007275	multicellular organismal development	Process
pl082023	uc002iqz	GO:0007283	spermatogenesis	Process
pl082023	uc002iqz	GO:0007605	sensory perception of sound	Process
pl082023	uc002iqz	GO:0016020	membrane	Component
pl082023	uc002iqz	GO:0030154	cell differentiation	Process
pl098773	ENST00000421331	GO:0005856	cytoskeleton	Component
pl098773	ENST00000421331	GO:0005924	cell-substrate adherens junction	Component
pl098773	ENST00000421331	GO:0008307	structural constituent of muscle	Function
pl098773	ENST00000421331	GO:0030018	Z disc	Component
pl098773	ENST00000421331	GO:0030334	regulation of cell migration	Process
pl098773	ENST00000421331	GO:0051015	actin filament binding	Function
pl098773	ENST00000421331	GO:0051493	regulation of cytoskeleton organization	Process
pl016873	uc002ued	GO:0005515	protein binding	Function
pl016873	uc002ued	GO:0005856	cytoskeleton	Component
pl016873	uc002ued	GO:0005886	plasma membrane	Component

pl016873	uc002ued	GO:0006897	endocytosis	Process
pl016873	uc002ued	GO:0030666	endocytic vesicle membrane	Component
pl016873	uc002ued	GO:0044281	small molecule metabolic process	Process
pl016873	uc002ued	GO:0046209	nitric oxide metabolic process	Process
pl016873	uc002ued	GO:0050999	regulation of nitric-oxide synthase activity	Process
pl071481	AK128043	GO:0004222	metalloendopeptidase activity	Function
pl071481	AK128043	GO:0005515	protein binding	Function
pl071481	AK128043	GO:0005829	cytosol	Component
pl071481	AK128043	GO:0006508	proteolysis	Process
pl071481	AK128043	GO:0007528	neuromuscular junction development	Process
pl071481	AK128043	GO:0008270	zinc ion binding	Function
pl071481	AK128043	GO:0008283	cell proliferation	Process
pl071481	AK128043	GO:0009986	cell surface	Component
pl071481	AK128043	GO:0016477	cell migration	Process
pl071481	AK128043	GO:0048408	epidermal growth factor binding	Function
pl071481	AK128043	GO:0051044	positive regulation of membrane protein ectodomain proteolysis	Process
pl071481	AK128043	GO:0052548	regulation of endopeptidase activity	Process
pl107934	AK223466	GO:0003676	nucleic acid binding	Function
pl107934	AK223466	GO:0003950	NAD+ ADP-ribosyltransferase activity	Function
pl107934	AK223466	GO:0005634	nucleus	Component
pl107934	AK223466	GO:0008270	zinc ion binding	Function
pl017442	ENST00000556070	GO:0000979	RNA polymerase II core promoter sequence-specific DNA binding	Function
pl017442	ENST00000556070	GO:0001655	urogenital system development	Process
pl017442	ENST00000556070	GO:0001658	branching involved in ureteric bud morphogenesis	Process

pl017442	ENST00000556070	GO:0001822	kidney development	Process
pl017442	ENST00000556070	GO:0001823	mesonephros development	Process
pl017442	ENST00000556070	GO:0003337	mesenchymal to epithelial transition involved in metanephros morphogenesis	Process
pl017442	ENST00000556070	GO:0003677	DNA binding	Function
pl017442	ENST00000556070	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl017442	ENST00000556070	GO:0004996	thyroid-stimulating hormone receptor activity	Function
pl017442	ENST00000556070	GO:0005515	protein binding	Function
pl017442	ENST00000556070	GO:0005634	nucleus	Component
pl017442	ENST00000556070	GO:0005654	nucleoplasm	Component
pl017442	ENST00000556070	GO:0005730	nucleolus	Component
pl017442	ENST00000556070	GO:0006351	transcription, DNA-dependent	Process
pl017442	ENST00000556070	GO:0006355	regulation of transcription, DNA-dependent	Process
pl017442	ENST00000556070	GO:0007417	central nervous system development	Process
pl017442	ENST00000556070	GO:0009653	anatomical structure morphogenesis	Process
pl017442	ENST00000556070	GO:0030878	thyroid gland development	Process
pl017442	ENST00000556070	GO:0039003	pronephric field specification	Process
pl017442	ENST00000556070	GO:0042472	inner ear morphogenesis	Process
pl017442	ENST00000556070	GO:0042981	regulation of apoptotic process	Process
pl017442	ENST00000556070	GO:0044212	transcription regulatory region DNA binding	Function
pl017442	ENST00000556070	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl017442	ENST00000556070	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl017442	ENST00000556070	GO:0048793	pronephros development	Process
pl017442	ENST00000556070	GO:0071371	cellular response to gonadotropin stimulus	Process

pl017442	ENST00000556070	GO:0071599	otic vesicle development	Process
pl017442	ENST00000556070	GO:0072108	positive regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis	Process
pl017442	ENST00000556070	GO:0072164	mesonephric tubule development	Process
pl017442	ENST00000556070	GO:0072205	metanephric collecting duct development	Process
pl017442	ENST00000556070	GO:0072207	metanephric epithelium development	Process
pl017442	ENST00000556070	GO:0072221	metanephric distal convoluted tubule development	Process
pl017442	ENST00000556070	GO:0072278	metanephric comma-shaped body morphogenesis	Process
pl017442	ENST00000556070	GO:0072284	metanephric S-shaped body morphogenesis	Process
pl017442	ENST00000556070	GO:0072289	metanephric nephron tubule formation	Process
pl017442	ENST00000556070	GO:0072305	negative regulation of mesenchymal stem cell apoptotic process involved in metanephric nephron morphogenesis	Process
pl017442	ENST00000556070	GO:0072307	regulation of metanephric nephron tubule epithelial cell differentiation	Process
pl017442	ENST00000556070	GO:0090190	positive regulation of branching involved in ureteric bud morphogenesis	Process
pl017442	ENST00000556070	GO:1900212	negative regulation of mesenchymal cell apoptotic process involved in metanephros development	Process
pl017442	ENST00000556070	GO:1900215	negative regulation of apoptotic process involved in metanephric collecting duct development	Process
pl017442	ENST00000556070	GO:1900218	negative regulation of apoptotic process involved in metanephric nephron tubule development	Process
pl017442	ENST00000556070	GO:2000594	positive regulation of metanephric DCT cell differentiation	Process
pl017442	ENST00000556070	GO:2000611	positive regulation of thyroid hormone generation	Process

pl017442	ENST00000556070	GO:2000612	regulation of thyroid-stimulating hormone secretion	Process
pl018286	uc010did	GO:0000187	activation of MAPK activity	Process
pl018286	uc010did	GO:0004857	enzyme inhibitor activity	Function
pl018286	uc010did	GO:0005829	cytosol	Component
pl018286	uc010did	GO:0007596	blood coagulation	Process
pl018286	uc010did	GO:0007601	visual perception	Process
pl018286	uc010did	GO:0030553	cGMP binding	Function
pl018286	uc010did	GO:0043086	negative regulation of catalytic activity	Process
pl018286	uc010did	GO:0045742	positive regulation of epidermal growth factor receptor signaling pathway	Process
pl018286	uc010did	GO:0045745	positive regulation of G-protein coupled receptor protein signaling pathway	Process
pl018286	uc010did	GO:0047555	3',5'-cyclic-GMP phosphodiesterase activity	Function
pl103129		GO:0001932	regulation of protein phosphorylation	Process
pl103129		GO:0005085	guanyl-nucleotide exchange factor activity	Function
pl103129		GO:0005624	membrane fraction	Component
pl103129		GO:0005886	plasma membrane	Component
pl103129		GO:0005952	cAMP-dependent protein kinase complex	Component
pl103129		GO:0006112	energy reserve metabolic process	Process
pl103129		GO:0007165	signal transduction	Process
pl103129		GO:0007264	small GTPase mediated signal transduction	Process
pl103129		GO:0007596	blood coagulation	Process
pl103129		GO:0008283	cell proliferation	Process
pl103129		GO:0008603	cAMP-dependent protein kinase regulator activity	Function
pl103129		GO:0012505	endomembrane system	Component
pl103129		GO:0030168	platelet activation	Process

pl103129		GO:0030552	cAMP binding	Function
pl103129		GO:0044281	small molecule metabolic process	Process
pl103129		GO:0050796	regulation of insulin secretion	Process
pl103129		GO:0051056	regulation of small GTPase mediated signal transduction	Process
pl081094	BC004968	GO:0004252	serine-type endopeptidase activity	Function
pl081094	BC004968	GO:0005509	calcium ion binding	Function
pl081094	BC004968	GO:0005624	membrane fraction	Component
pl081094	BC004968	GO:0005887	integral to plasma membrane	Component
pl081094	BC004968	GO:0006508	proteolysis	Process
pl081094	BC004968	GO:0007165	signal transduction	Process
pl081094	BC004968	GO:0003924	GTPase activity	Function
pl081094	BC004968	GO:0005509	calcium ion binding	Function
pl081094	BC004968	GO:0005515	protein binding	Function
pl081094	BC004968	GO:0005525	GTP binding	Function
pl081094	BC004968	GO:0005743	mitochondrial inner membrane	Component
pl081094	BC004968	GO:0005829	cytosol	Component
pl081094	BC004968	GO:0005886	plasma membrane	Component
pl081094	BC004968	GO:0006915	apoptotic process	Process
pl081094	BC004968	GO:0007264	small GTPase mediated signal transduction	Process
pl081094	BC004968	GO:0019725	cellular homeostasis	Process
pl081094	BC004968	GO:0031307	integral to mitochondrial outer membrane	Component
pl081094	BC004968	GO:0047497	mitochondrion transport along microtubule	Process
pl081094	BC004968	GO:0051056	regulation of small GTPase mediated signal transduction	Process
pl012449	BC082981	GO:0006836	neurotransmitter transport	Process

pl012449	BC082981	GO:0006887	exocytosis	Process
pl012449	BC082981	GO:0030054	cell junction	Component
pl012449	BC082981	GO:0045202	synapse	Component
pl100413	uc002nvo	GO:0005576	extracellular region	Component
pl040361	gnl|UG|Hs	GO:0005886	plasma membrane	Component
pl040361	gnl|UG|Hs	GO:0005887	integral to plasma membrane	Component
pl040361	gnl|UG|Hs	GO:0007186	G-protein coupled receptor signaling pathway	Process
pl040361	gnl|UG|Hs	GO:0007586	digestion	Process
pl040361	gnl|UG|Hs	GO:0007588	excretion	Process
pl040361	gnl|UG|Hs	GO:0015055	secretin receptor activity	Function
pl015109	uc009xxw	GO:0000164	protein phosphatase type 1 complex	Component
pl015109	uc009xxw	GO:0005634	nucleus	Component
pl015109	uc009xxw	GO:0005737	cytoplasm	Component
pl015109	uc009xxw	GO:0007265	Ras protein signal transduction	Process
pl015109	uc009xxw	GO:0008543	fibroblast growth factor receptor signaling pathway	Process
pl015109	uc009xxw	GO:0019888	protein phosphatase regulator activity	Function
pl015109	uc009xxw	GO:0019903	protein phosphatase binding	Function
pl015109	uc009xxw	GO:0046579	positive regulation of Ras protein signal transduction	Process
pl050158	uc001mmh	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl018694	uc001mmh	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl050158	uc001mmh	GO:0000902	cell morphogenesis	Process
pl018694	uc001mmh	GO:0000902	cell morphogenesis	Process
pl050158	uc001mmh	GO:0001701	in utero embryonic development	Process
pl018694	uc001mmh	GO:0001701	in utero embryonic development	Process

pl050158	uc001mmh	GO:0003677	DNA binding	Function
pl018694	uc001mmh	GO:0003677	DNA binding	Function
pl050158	uc001mmh	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl018694	uc001mmh	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl050158	uc001mmh	GO:0005515	protein binding	Function
pl018694	uc001mmh	GO:0005515	protein binding	Function
pl050158	uc001mmh	GO:0005634	nucleus	Component
pl018694	uc001mmh	GO:0005634	nucleus	Component
pl050158	uc001mmh	GO:0006351	transcription, DNA-dependent	Process
pl018694	uc001mmh	GO:0006351	transcription, DNA-dependent	Process
pl050158	uc001mmh	GO:0006355	regulation of transcription, DNA-dependent	Process
pl018694	uc001mmh	GO:0006355	regulation of transcription, DNA-dependent	Process
pl050158	uc001mmh	GO:0007517	muscle organ development	Process
pl018694	uc001mmh	GO:0007517	muscle organ development	Process
pl050158	uc001mmh	GO:0009791	post-embryonic development	Process
pl018694	uc001mmh	GO:0009791	post-embryonic development	Process
pl050158	uc001mmh	GO:0016458	gene silencing	Process
pl018694	uc001mmh	GO:0016458	gene silencing	Process
pl050158	uc001mmh	GO:0021778	oligodendrocyte cell fate specification	Process
pl018694	uc001mmh	GO:0021778	oligodendrocyte cell fate specification	Process
pl050158	uc001mmh	GO:0032332	positive regulation of chondrocyte differentiation	Process
pl018694	uc001mmh	GO:0032332	positive regulation of chondrocyte differentiation	Process
pl050158	uc001mmh	GO:0035051	cardiac cell differentiation	Process
pl018694	uc001mmh	GO:0035051	cardiac cell differentiation	Process

pl050158	uc001mmh	GO:0042692	muscle cell differentiation	Process
pl018694	uc001mmh	GO:0042692	muscle cell differentiation	Process
pl050158	uc001mmh	GO:0043565	sequence-specific DNA binding	Function
pl018694	uc001mmh	GO:0043565	sequence-specific DNA binding	Function
pl050158	uc001mmh	GO:0044212	transcription regulatory region DNA binding	Function
pl018694	uc001mmh	GO:0044212	transcription regulatory region DNA binding	Function
pl050158	uc001mmh	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl018694	uc001mmh	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl050158	uc001mmh	GO:0046982	protein heterodimerization activity	Function
pl018694	uc001mmh	GO:0046982	protein heterodimerization activity	Function
pl050158	uc001mmh	GO:0048821	erythrocyte development	Process
pl018694	uc001mmh	GO:0048821	erythrocyte development	Process
pl050158	uc001mmh	GO:0051216	cartilage development	Process
pl018694	uc001mmh	GO:0051216	cartilage development	Process
pl050158	uc001mmh	GO:0061036	positive regulation of cartilage development	Process
pl018694	uc001mmh	GO:0061036	positive regulation of cartilage development	Process
pl050158	uc001mmh	GO:0071560	cellular response to transforming growth factor beta stimulus	Process
pl018694	uc001mmh	GO:0071560	cellular response to transforming growth factor beta stimulus	Process
pl050158	uc001mmh	GO:2000741	positive regulation of mesenchymal stem cell differentiation	Process
pl018694	uc001mmh	GO:2000741	positive regulation of mesenchymal stem cell differentiation	Process
pl015535	NR_024279	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process

pl015535	NR_024279	GO:0000166	nucleotide binding	Function
pl015535	NR_024279	GO:0001085	RNA polymerase II transcription factor binding	Function
pl015535	NR_024279	GO:0001191	RNA polymerase II transcription factor binding transcription factor activity involved in negative regulation of transcription	Function
pl015535	NR_024279	GO:0003697	single-stranded DNA binding	Function
pl015535	NR_024279	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl015535	NR_024279	GO:0003714	transcription corepressor activity	Function
pl015535	NR_024279	GO:0003723	RNA binding	Function
pl015535	NR_024279	GO:0005515	protein binding	Function
pl015535	NR_024279	GO:0005634	nucleus	Component
pl015535	NR_024279	GO:0005730	nucleolus	Component
pl015535	NR_024279	GO:0007219	Notch signaling pathway	Process
pl015535	NR_024279	GO:0017053	transcriptional repressor complex	Component
pl015535	NR_024279	GO:0044419	interspecies interaction between organisms	Process
pl015535	NR_024279	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl015535	NR_024279	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl015535	NR_024279	GO:0050769	positive regulation of neurogenesis	Process
pl004774	AJ227874	GO:0000139	Golgi membrane	Component
pl004774	AJ227874	GO:0003836	beta-galactoside (CMP) alpha-2,3-sialyltransferase activity	Function
pl004774	AJ227874	GO:0005576	extracellular region	Component
pl004774	AJ227874	GO:0006486	protein glycosylation	Process
pl004774	AJ227874	GO:0016266	O-glycan processing	Process
pl004774	AJ227874	GO:0018279	protein N-linked glycosylation via asparagine	Process

pl004774	AJ227874	GO:0030173	integral to Golgi membrane	Component
pl004774	AJ227874	GO:0032580	Golgi cisterna membrane	Component
pl004774	AJ227874	GO:0043687	post-translational protein modification	Process
pl004774	AJ227874	GO:0044267	cellular protein metabolic process	Process
pl075097		GO:0005730	nucleolus	Component
pl075097		GO:0005737	cytoplasm	Component
pl075097		GO:0005794	Golgi apparatus	Component
pl075097		GO:0005815	microtubule organizing center	Component
pl075097		GO:0019904	protein domain specific binding	Function
pl075097		GO:0021987	cerebral cortex development	Process
pl075097		GO:0022008	neurogenesis	Process
pl075097		GO:0022027	interkinetic nuclear migration	Process
pl075097		GO:0030953	astral microtubule organization	Process
pl075097		GO:0032886	regulation of microtubule-based process	Process
pl075097		GO:0035257	nuclear hormone receptor binding	Function
pl068994	HMlincRNA798	GO:0003677	DNA binding	Function
pl068994	HMlincRNA798	GO:0005634	nucleus	Component
pl068994	HMlincRNA798	GO:0006366	transcription from RNA polymerase II promoter	Process
pl068994	HMlincRNA798	GO:0016021	integral to membrane	Component
pl068994	HMlincRNA798	GO:0032784	regulation of transcription elongation, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0003677	DNA binding	Function
pl068994	HMlincRNA798	GO:0005634	nucleus	Component
pl068994	HMlincRNA798	GO:0006351	transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0006355	regulation of transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0016021	integral to membrane	Component

pl068994	HMlincRNA798	GO:0003677	DNA binding	Function
pl068994	HMlincRNA798	GO:0005634	nucleus	Component
pl068994	HMlincRNA798	GO:0006351	transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0006355	regulation of transcription, DNA-dependent	Process
pl068994	HMlincRNA798	GO:0016021	integral to membrane	Component
pl042847	NR_045553.1	GO:0003417	growth plate cartilage development	Process
pl042847	NR_045553.1	GO:0005509	calcium ion binding	Function
pl042847	NR_045553.1	GO:0005576	extracellular region	Component
pl042847	NR_045553.1	GO:0007155	cell adhesion	Process
pl042847	NR_045553.1	GO:0007160	cell-matrix adhesion	Process
pl042847	NR_045553.1	GO:0008201	heparin binding	Function
pl042847	NR_045553.1	GO:0043931	ossification involved in bone maturation	Process
pl042847	NR_045553.1	GO:0048471	perinuclear region of cytoplasm	Component
pl042847	NR_045553.1	GO:0060346	bone trabecula formation	Process
pl000897	uc010jos	GO:0016021	integral to membrane	Component
pl009498	NR_024453	GO:0003674	molecular_function	Function
pl009498	NR_024453	GO:0005887	integral to plasma membrane	Component
pl009498	NR_024453	GO:0007155	cell adhesion	Process
pl009498	NR_024453	GO:0008150	biological_process	Process
pl023546	NR_037844.1	GO:0005031	tumor necrosis factor-activated receptor activity	Function
pl023546	NR_037844.1	GO:0005515	protein binding	Function
pl023546	NR_037844.1	GO:0005886	plasma membrane	Component
pl023546	NR_037844.1	GO:0005887	integral to plasma membrane	Component
pl023546	NR_037844.1	GO:0006955	immune response	Process
pl023546	NR_037844.1	GO:0007166	cell surface receptor signaling pathway	Process
pl023546	NR_037844.1	GO:0009897	external side of plasma membrane	Component

pl023546	NR_037844.1	GO:0031295	T cell costimulation	Process
pl023546	NR_037844.1	GO:0031625	ubiquitin protein ligase binding	Function
pl023546	NR_037844.1	GO:0033209	tumor necrosis factor-mediated signaling pathway	Process
pl023546	NR_037844.1	GO:0044419	interspecies interaction between organisms	Process
pl023546	NR_037844.1	GO:0046642	negative regulation of alpha-beta T cell proliferation	Process
pl023546	NR_037844.1	GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	Process
pl090489	ENST00000510238	GO:0003682	chromatin binding	Function
pl090489	ENST00000510238	GO:0005515	protein binding	Function
pl090489	ENST00000510238	GO:0005634	nucleus	Component
pl090489	ENST00000510238	GO:0006351	transcription, DNA-dependent	Process
pl090489	ENST00000510238	GO:0006915	apoptotic process	Process
pl090489	ENST00000510238	GO:0034056	estrogen response element binding	Function
pl090489	ENST00000510238	GO:0042803	protein homodimerization activity	Function
pl090489	ENST00000510238	GO:0043524	negative regulation of neuron apoptotic process	Process
pl090489	ENST00000510238	GO:0045768	positive regulation of anti-apoptosis	Process
pl090489	ENST00000510238	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl090489	ENST00000510238	GO:0051219	phosphoprotein binding	Function
pl018286	uc010did	GO:0016021	integral to membrane	Component
pl105325	ENST00000468964	GO:0000086	G2/M transition of mitotic cell cycle	Process
pl105325	ENST00000468964	GO:0000278	mitotic cell cycle	Process
pl105325	ENST00000468964	GO:0000922	spindle pole	Component
pl105325	ENST00000468964	GO:0005515	protein binding	Function
pl105325	ENST00000468964	GO:0005813	centrosome	Component
pl105325	ENST00000468964	GO:0005815	microtubule organizing center	Component
pl105325	ENST00000468964	GO:0005829	cytosol	Component

pl105325	ENST00000468964	GO:0005881	cytoplasmic microtubule	Component
pl105325	ENST00000468964	GO:0006461	protein complex assembly	Process
pl105325	ENST00000468964	GO:0007020	microtubule nucleation	Process
pl111818	gnl|UG|Hs	GO:0003674	molecular_function	Function
pl111818	gnl|UG|Hs	GO:0005730	nucleolus	Component
pl111818	gnl|UG|Hs	GO:0008150	biological_process	Process
pl081094	BC004968	GO:0005053	peroxisome matrix targeting signal-2 binding	Function
pl081094	BC004968	GO:0005777	peroxisome	Component
pl081094	BC004968	GO:0016558	protein import into peroxisome matrix	Process
pl100413	uc002nvo	GO:0003677	DNA binding	Function
pl100413	uc002nvo	GO:0005634	nucleus	Component
pl100413	uc002nvo	GO:0006351	transcription, DNA-dependent	Process
pl100413	uc002nvo	GO:0006355	regulation of transcription, DNA-dependent	Process
pl100413	uc002nvo	GO:0008270	zinc ion binding	Function
pl057456		GO:0005215	transporter activity	Function
pl057456		GO:0005524	ATP binding	Function
pl057456		GO:0005886	plasma membrane	Component
pl057456		GO:0006813	potassium ion transport	Process
pl057456		GO:0007268	synaptic transmission	Process
pl057456		GO:0008281	sulfonylurea receptor activity	Function
pl057456		GO:0008282	ATP-sensitive potassium channel complex	Component
pl057456		GO:0010107	potassium ion import	Process
pl057456		GO:0015459	potassium channel regulator activity	Function
pl057456		GO:0016020	membrane	Component
pl057456		GO:0042626	ATPase activity, coupled to transmembrane movement of substances	Function

pl057456		GO:0051607	defense response to virus	Process
pl057456		GO:0055085	transmembrane transport	Process
pl060937	AF086561	GO:0001889	liver development	Process
pl060937	AF086561	GO:0003985	acetyl-CoA C-acetyltransferase activity	Function
pl060937	AF086561	GO:0005739	mitochondrion	Component
pl060937	AF086561	GO:0005743	mitochondrial inner membrane	Component
pl060937	AF086561	GO:0005759	mitochondrial matrix	Component
pl060937	AF086561	GO:0007420	brain development	Process
pl060937	AF086561	GO:0009083	branched chain family amino acid catabolic process	Process
pl060937	AF086561	GO:0009725	response to hormone stimulus	Process
pl060937	AF086561	GO:0014070	response to organic cyclic compound	Process
pl060937	AF086561	GO:0019899	enzyme binding	Function
pl060937	AF086561	GO:0034641	cellular nitrogen compound metabolic process	Process
pl060937	AF086561	GO:0042594	response to starvation	Process
pl060937	AF086561	GO:0042803	protein homodimerization activity	Function
pl060937	AF086561	GO:0044255	cellular lipid metabolic process	Process
pl060937	AF086561	GO:0044281	small molecule metabolic process	Process
pl060937	AF086561	GO:0046872	metal ion binding	Function
pl060937	AF086561	GO:0046950	cellular ketone body metabolic process	Process
pl060937	AF086561	GO:0046951	ketone body biosynthetic process	Process
pl060937	AF086561	GO:0046952	ketone body catabolic process	Process
pl060937	AF086561	GO:0050662	coenzyme binding	Function
pl060937	AF086561	GO:0051260	protein homooligomerization	Process
pl060937	AF086561	GO:0060612	adipose tissue development	Process
pl060937	AF086561	GO:0072229	metanephric proximal convoluted tubule development	Process

pl105325	ENST00000468964	GO:0000902	cell morphogenesis	Process
pl105325	ENST00000468964	GO:0001525	angiogenesis	Process
pl105325	ENST00000468964	GO:0002102	podosome	Component
pl105325	ENST00000468964	GO:0002523	leukocyte migration involved in inflammatory response	Process
pl105325	ENST00000468964	GO:0002675	positive regulation of acute inflammatory response	Process
pl105325	ENST00000468964	GO:0004222	metalloendopeptidase activity	Function
pl105325	ENST00000468964	GO:0005509	calcium ion binding	Function
pl105325	ENST00000468964	GO:0005515	protein binding	Function
pl105325	ENST00000468964	GO:0005737	cytoplasm	Component
pl105325	ENST00000468964	GO:0005886	plasma membrane	Component
pl105325	ENST00000468964	GO:0005887	integral to plasma membrane	Component
pl105325	ENST00000468964	GO:0006508	proteolysis	Process
pl105325	ENST00000468964	GO:0006954	inflammatory response	Process
pl105325	ENST00000468964	GO:0008237	metallopeptidase activity	Function
pl105325	ENST00000468964	GO:0008270	zinc ion binding	Function
pl105325	ENST00000468964	GO:0009986	cell surface	Component
pl105325	ENST00000468964	GO:0010954	positive regulation of protein processing	Process
pl105325	ENST00000468964	GO:0022407	regulation of cell-cell adhesion	Process
pl105325	ENST00000468964	GO:0032010	phagolysosome	Component
pl105325	ENST00000468964	GO:0032127	dense core granule membrane	Component
pl105325	ENST00000468964	GO:0033089	positive regulation of T cell differentiation in thymus	Process
pl105325	ENST00000468964	GO:0035419	activation of MAPK activity involved in innate immune response	Process
pl105325	ENST00000468964	GO:0042581	specific granule	Component
pl105325	ENST00000468964	GO:0043524	negative regulation of neuron apoptotic process	Process

pl105325	ENST00000468964	GO:0043621	protein self-association	Function
pl105325	ENST00000468964	GO:0045780	positive regulation of bone resorption	Process
pl105325	ENST00000468964	GO:0045785	positive regulation of cell adhesion	Process
pl105325	ENST00000468964	GO:0048247	lymphocyte chemotaxis	Process
pl105325	ENST00000468964	GO:0050714	positive regulation of protein secretion	Process
pl105325	ENST00000468964	GO:0050839	cell adhesion molecule binding	Function
pl105325	ENST00000468964	GO:0051044	positive regulation of membrane protein ectodomain proteolysis	Process
pl105325	ENST00000468964	GO:0051092	positive regulation of NF-kappaB transcription factor activity	Process
pl105325	ENST00000468964	GO:0051897	positive regulation of protein kinase B signaling cascade	Process
pl105325	ENST00000468964	GO:0070245	positive regulation of thymocyte apoptotic process	Process
pl105325	ENST00000468964	GO:0070820	tertiary granule	Component
pl105325	ENST00000468964	GO:0071065	alpha9-beta1 integrin-vascular cell adhesion molecule-1 complex	Component
pl105325	ENST00000468964	GO:0071133	alpha9-beta1 integrin-ADAM8 complex	Component
pl105325	ENST00000468964	GO:0071456	cellular response to hypoxia	Process
pl105325	ENST00000468964	GO:2000309	positive regulation of tumor necrosis factor (ligand) superfamily member 11 production	Process
pl105325	ENST00000468964	GO:2000391	positive regulation of neutrophil extravasation	Process
pl105325	ENST00000468964	GO:2000415	positive regulation of fibronectin-dependent thymocyte migration	Process
pl105325	ENST00000468964	GO:2000418	positive regulation of eosinophil migration	Process
pl053387		GO:0003723	RNA binding	Function
pl053387		GO:0008033	tRNA processing	Process

pl053387		GO:0008251	tRNA-specific adenosine deaminase activity	Function
pl053387		GO:0046872	metal ion binding	Function
pl049503	HMlincRNA975	GO:0004859	phospholipase inhibitor activity	Function
pl049503	HMlincRNA975	GO:0005509	calcium ion binding	Function
pl049503	HMlincRNA975	GO:0005543	phospholipid binding	Function
pl049503	HMlincRNA975	GO:0005544	calcium-dependent phospholipid binding	Function
pl049503	HMlincRNA975	GO:0005622	intracellular	Component
pl049503	HMlincRNA975	GO:0005737	cytoplasm	Component
pl049503	HMlincRNA975	GO:0006916	anti-apoptosis	Process
pl049503	HMlincRNA975	GO:0007165	signal transduction	Process
pl049503	HMlincRNA975	GO:0007596	blood coagulation	Process
pl049503	HMlincRNA975	GO:0009897	external side of plasma membrane	Component
pl049503	HMlincRNA975	GO:0010033	response to organic substance	Process
pl049503	HMlincRNA975	GO:0014704	intercalated disc	Component
pl049503	HMlincRNA975	GO:0030971	receptor tyrosine kinase binding	Function
pl049503	HMlincRNA975	GO:0042383	sarcolemma	Component
pl049503	HMlincRNA975	GO:0042995	cell projection	Component
pl049503	HMlincRNA975	GO:0043065	positive regulation of apoptotic process	Process
pl049503	HMlincRNA975	GO:0043499	eukaryotic cell surface binding	Function
pl049503	HMlincRNA975	GO:0050819	negative regulation of coagulation	Process
pl049503	HMlincRNA975	GO:0051260	protein homooligomerization	Process
pl049503	HMlincRNA975	GO:0072563	endothelial microparticle	Component
pl081932	uc001jeo	GO:0005509	calcium ion binding	Function
pl074315	uc001jeo	GO:0005509	calcium ion binding	Function
pl038679	uc001jeo	GO:0005509	calcium ion binding	Function
pl081932	uc001jeo	GO:0005544	calcium-dependent phospholipid binding	Function

pl074315	uc001jeo	GO:0005544	calcium-dependent phospholipid binding	Function
pl038679	uc001jeo	GO:0005544	calcium-dependent phospholipid binding	Function
pl016207	ASO2077	GO:0005215	transporter activity	Function
pl016207	ASO2077	GO:0005634	nucleus	Component
pl016207	ASO2077	GO:0005730	nucleolus	Component
pl016207	ASO2077	GO:0005737	cytoplasm	Component
pl016207	ASO2077	GO:0005794	Golgi apparatus	Component
pl016207	ASO2077	GO:0006886	intracellular protein transport	Process
pl016207	ASO2077	GO:0006892	post-Golgi vesicle-mediated transport	Process
pl016207	ASO2077	GO:0006897	endocytosis	Process
pl016207	ASO2077	GO:0008565	protein transporter activity	Function
pl016207	ASO2077	GO:0030117	membrane coat	Component
pl016207	ASO2077	GO:0030137	COPI-coated vesicle	Component
pl016207	ASO2077	GO:0030665	clathrin coated vesicle membrane	Component
pl043625	BC031321	GO:0003677	DNA binding	Function
pl043625	BC031321	GO:0005634	nucleus	Component
pl043625	BC031321	GO:0006351	transcription, DNA-dependent	Process
pl043625	BC031321	GO:0006355	regulation of transcription, DNA-dependent	Process
pl043625	BC031321	GO:0008150	biological_process	Process
pl064191	uc004crw	GO:0006915	apoptotic process	Process
pl070257	uc010jpk	GO:0003779	actin binding	Function
pl070257	uc010jpk	GO:0005886	plasma membrane	Component
pl070257	uc010jpk	GO:0007010	cytoskeleton organization	Process
pl070257	uc010jpk	GO:0007163	establishment or maintenance of cell polarity	Process
pl070257	uc010jpk	GO:0007165	signal transduction	Process
pl070257	uc010jpk	GO:0007190	activation of adenylate cyclase activity	Process

pl070257	uc010jpk	GO:0007411	axon guidance	Process
pl112918		GO:0005737	cytoplasm	Component
pl112918		GO:0045111	intermediate filament cytoskeleton	Component
pl016873	uc002ued	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl016873	uc002ued	GO:0005634	nucleus	Component
pl016873	uc002ued	GO:0005789	endoplasmic reticulum membrane	Component
pl016873	uc002ued	GO:0006665	sphingolipid metabolic process	Process
pl016873	uc002ued	GO:0016021	integral to membrane	Component
pl016873	uc002ued	GO:0030148	sphingolipid biosynthetic process	Process
pl016873	uc002ued	GO:0031965	nuclear membrane	Component
pl016873	uc002ued	GO:0043565	sequence-specific DNA binding	Function
pl016873	uc002ued	GO:0044281	small molecule metabolic process	Process
pl016873	uc002ued	GO:0046513	ceramide biosynthetic process	Process
pl016873	uc002ued	GO:0050291	sphingosine N-acyltransferase activity	Function
pl065225	uc001hox	GO:0003777	microtubule motor activity	Function
pl065225	uc001hox	GO:0005524	ATP binding	Function
pl065225	uc001hox	GO:0005737	cytoplasm	Component
pl065225	uc001hox	GO:0005874	microtubule	Component
pl065225	uc001hox	GO:0007018	microtubule-based movement	Process
pl065225	uc001hox	GO:0030286	dynein complex	Component
pl065225	uc001hox	GO:0035085	cilium axoneme	Component
pl023122	NR_024380	GO:0001701	in utero embryonic development	Process
pl023122	NR_024380	GO:0005509	calcium ion binding	Function
pl023122	NR_024380	GO:0005576	extracellular region	Component
pl023122	NR_024380	GO:0005624	membrane fraction	Component

pl023122	NR_024380	GO:0005737	cytoplasm	Component
pl023122	NR_024380	GO:0005886	plasma membrane	Component
pl023122	NR_024380	GO:0005911	cell-cell junction	Component
pl023122	NR_024380	GO:0007155	cell adhesion	Process
pl023122	NR_024380	GO:0007156	homophilic cell adhesion	Process
pl023122	NR_024380	GO:0016021	integral to membrane	Component
pl023122	NR_024380	GO:0030057	desmosome	Component
pl023122	NR_024380	GO:0045295	gamma-catenin binding	Function
pl023122	NR_024380	GO:0050821	protein stabilization	Process
pl112125	AK130406	GO:0005515	protein binding	Function
pl112125	AK130406	GO:0006351	transcription, DNA-dependent	Process
pl112125	AK130406	GO:0006355	regulation of transcription, DNA-dependent	Process
pl112125	AK130406	GO:0015030	Cajal body	Component
pl112125	AK130406	GO:0016607	nuclear speck	Component
pl073519	AL832516	GO:0003677	DNA binding	Function
pl073519	AL832516	GO:0004386	helicase activity	Function
pl073519	AL832516	GO:0005524	ATP binding	Function
pl073519	AL832516	GO:0016607	nuclear speck	Component
pl073519	AL832516	GO:0035267	NuA4 histone acetyltransferase complex	Component
pl073519	AL832516	GO:0043967	histone H4 acetylation	Process
pl073519	AL832516	GO:0043968	histone H2A acetylation	Process
pl032441	NR_034165.1	GO:0003676	nucleic acid binding	Function
pl032441	NR_034165.1	GO:0005622	intracellular	Component
pl032441	NR_034165.1	GO:0008408	3'-5' exonuclease activity	Function
pl098426		GO:0003676	nucleic acid binding	Function
pl070063	HMlincRNA1333	GO:0000287	magnesium ion binding	Function

pl002694	HIV2736	GO:0000287	magnesium ion binding	Function
pl041707		GO:0000287	magnesium ion binding	Function
pl070063	HMlincRNA1333	GO:0003690	double-stranded DNA binding	Function
pl002694	HIV2736	GO:0003690	double-stranded DNA binding	Function
pl041707		GO:0003690	double-stranded DNA binding	Function
pl070063	HMlincRNA1333	GO:0003705	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity	Function
pl002694	HIV2736	GO:0003705	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity	Function
pl041707		GO:0003705	RNA polymerase II distal enhancer sequence-specific DNA binding transcription factor activity	Function
pl070063	HMlincRNA1333	GO:0005634	nucleus	Component
pl002694	HIV2736	GO:0005634	nucleus	Component
pl041707		GO:0005634	nucleus	Component
pl070063	HMlincRNA1333	GO:0005667	transcription factor complex	Component
pl002694	HIV2736	GO:0005667	transcription factor complex	Component
pl041707		GO:0005667	transcription factor complex	Component
pl070063	HMlincRNA1333	GO:0005730	nucleolus	Component
pl002694	HIV2736	GO:0005730	nucleolus	Component
pl041707		GO:0005730	nucleolus	Component
pl070063	HMlincRNA1333	GO:0007389	pattern specification process	Process
pl002694	HIV2736	GO:0007389	pattern specification process	Process
pl041707		GO:0007389	pattern specification process	Process

pl070063	HMlincRNA1333	GO:0007517	muscle organ development	Process
pl002694	HIV2736	GO:0007517	muscle organ development	Process
pl041707		GO:0007517	muscle organ development	Process
pl070063	HMlincRNA1333	GO:0008134	transcription factor binding	Function
pl002694	HIV2736	GO:0008134	transcription factor binding	Function
pl041707		GO:0008134	transcription factor binding	Function
pl070063	HMlincRNA1333	GO:0008301	DNA binding, bending	Function
pl002694	HIV2736	GO:0008301	DNA binding, bending	Function
pl041707		GO:0008301	DNA binding, bending	Function
pl070063	HMlincRNA1333	GO:0009790	embryo development	Process
pl002694	HIV2736	GO:0009790	embryo development	Process
pl041707		GO:0009790	embryo development	Process
pl070063	HMlincRNA1333	GO:0009888	tissue development	Process
pl002694	HIV2736	GO:0009888	tissue development	Process
pl041707		GO:0009888	tissue development	Process
pl070063	HMlincRNA1333	GO:0030154	cell differentiation	Process
pl002694	HIV2736	GO:0030154	cell differentiation	Process
pl041707		GO:0030154	cell differentiation	Process
pl070063	HMlincRNA1333	GO:0030308	negative regulation of cell growth	Process
pl002694	HIV2736	GO:0030308	negative regulation of cell growth	Process
pl041707		GO:0030308	negative regulation of cell growth	Process
pl070063	HMlincRNA1333	GO:0043565	sequence-specific DNA binding	Function
pl002694	HIV2736	GO:0043565	sequence-specific DNA binding	Function
pl041707		GO:0043565	sequence-specific DNA binding	Function
pl070063	HMlincRNA1333	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl002694	HIV2736	GO:0045892	negative regulation of transcription, DNA-dependent	Process

pl041707		GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl070063	HMlincRNA1333	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl002694	HIV2736	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl041707		GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl070063	HMlincRNA1333	GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	Process
pl002694	HIV2736	GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	Process
pl041707		GO:0051090	regulation of sequence-specific DNA binding transcription factor activity	Process
pl093750	NR_045562.1	GO:0004871	signal transducer activity	Function
pl093750	NR_045562.1	GO:0005737	cytoplasm	Component
pl093750	NR_045562.1	GO:0006869	lipid transport	Process
pl093750	NR_045562.1	GO:0006911	phagocytosis, engulfment	Process
pl093750	NR_045562.1	GO:0006915	apoptotic process	Process
pl093750	NR_045562.1	GO:0007165	signal transduction	Process
pl061285	uc003fhx	GO:0004047	aminomethyltransferase activity	Function
pl061285	uc003fhx	GO:0005739	mitochondrion	Component
pl061285	uc003fhx	GO:0006546	glycine catabolic process	Process
pl061285	uc003fhx	GO:0006783	heme biosynthetic process	Process
pl035959	NR_024380	GO:0004423	iduronate-2-sulfatase activity	Function
pl035959	NR_024380	GO:0005764	lysosome	Component
pl035959	NR_024380	GO:0008484	sulfuric ester hydrolase activity	Function
pl035959	NR_024380	GO:0046872	metal ion binding	Function
pl000897	uc010jos	GO:0000975	regulatory region DNA binding	Function
pl000897	uc010jos	GO:0002819	regulation of adaptive immune response	Process

pl000897	uc010jos	GO:0003677	DNA binding	Function
pl000897	uc010jos	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl000897	uc010jos	GO:0005515	protein binding	Function
pl000897	uc010jos	GO:0005634	nucleus	Component
pl000897	uc010jos	GO:0005654	nucleoplasm	Component
pl000897	uc010jos	GO:0005737	cytoplasm	Component
pl000897	uc010jos	GO:0005829	cytosol	Component
pl000897	uc010jos	GO:0006366	transcription from RNA polymerase II promoter	Process
pl000897	uc010jos	GO:0006468	protein phosphorylation	Process
pl000897	uc010jos	GO:0006473	protein acetylation	Process
pl000897	uc010jos	GO:0006917	induction of apoptosis	Process
pl000897	uc010jos	GO:0007050	cell cycle arrest	Process
pl000897	uc010jos	GO:0007249	I-kappaB kinase/NF-kappaB cascade	Process
pl000897	uc010jos	GO:0007565	female pregnancy	Process
pl000897	uc010jos	GO:0007596	blood coagulation	Process
pl000897	uc010jos	GO:0008285	negative regulation of cell proliferation	Process
pl000897	uc010jos	GO:0009408	response to heat	Process
pl000897	uc010jos	GO:0019221	cytokine-mediated signaling pathway	Process
pl000897	uc010jos	GO:0032481	positive regulation of type I interferon production	Process
pl000897	uc010jos	GO:0032728	positive regulation of interferon-beta production	Process
pl000897	uc010jos	GO:0034124	regulation of MyD88-dependent toll-like receptor signaling pathway	Process
pl000897	uc010jos	GO:0042512	negative regulation of tyrosine phosphorylation of Stat1 protein	Process
pl000897	uc010jos	GO:0043374	CD8-positive, alpha-beta T cell differentiation	Process

pl000897	uc010jos	GO:0043565	sequence-specific DNA binding	Function
pl000897	uc010jos	GO:0045084	positive regulation of interleukin-12 biosynthetic process	Process
pl000897	uc010jos	GO:0045088	regulation of innate immune response	Process
pl000897	uc010jos	GO:0045590	negative regulation of regulatory T cell differentiation	Process
pl000897	uc010jos	GO:0045892	negative regulation of transcription, DNA-dependent	Process
pl000897	uc010jos	GO:0045893	positive regulation of transcription, DNA-dependent	Process
pl000897	uc010jos	GO:0045944	positive regulation of transcription from RNA polymerase II promoter	Process
pl000897	uc010jos	GO:0051607	defense response to virus	Process
pl000897	uc010jos	GO:0051726	regulation of cell cycle	Process
pl000897	uc010jos	GO:0060333	interferon-gamma-mediated signaling pathway	Process
pl000897	uc010jos	GO:0060337	type I interferon-mediated signaling pathway	Process
pl000897	uc010jos	GO:0060416	response to growth hormone stimulus	Process
pl000897	uc010jos	GO:0071260	cellular response to mechanical stimulus	Process
pl000897	uc010jos	GO:0071300	cellular response to retinoic acid	Process
pl000897	uc010jos	GO:0071347	cellular response to interleukin-1	Process
pl000897	uc010jos	GO:0071356	cellular response to tumor necrosis factor	Process
pl000897	uc010jos	GO:0071359	cellular response to dsRNA	Process
pl000897	uc010jos	GO:0071375	cellular response to peptide hormone stimulus	Process
pl000897	uc010jos	GO:2000564	regulation of CD8-positive, alpha-beta T cell proliferation	Process
pl012449	BC082981	GO:0005244	voltage-gated ion channel activity	Function
pl012449	BC082981	GO:0005267	potassium channel activity	Function
pl012449	BC082981	GO:0016021	integral to membrane	Component

pl102783	HMlincRNA1153	GO:0000165	MAPK cascade	Process
pl102783	HMlincRNA1153	GO:0000186	activation of MAPKK activity	Process
pl102783	HMlincRNA1153	GO:0000287	magnesium ion binding	Function
pl102783	HMlincRNA1153	GO:0004709	MAP kinase kinase kinase activity	Function
pl102783	HMlincRNA1153	GO:0005524	ATP binding	Function
pl102783	HMlincRNA1153	GO:0006468	protein phosphorylation	Process
pl102783	HMlincRNA1153	GO:0007165	signal transduction	Process
pl102783	HMlincRNA1153	GO:0007257	activation of JUN kinase activity	Process
pl053119	CU693173	GO:0005886	plasma membrane	Component
pl053119	CU693173	GO:0016021	integral to membrane	Component
pl095227	NR_027781.1	GO:0046872	metal ion binding	Function
pl082023	uc002iqz	GO:0005515	protein binding	Function
pl082023	uc002iqz	GO:0005737	cytoplasm	Component
pl082023	uc002iqz	GO:0007268	synaptic transmission	Process
pl082023	uc002iqz	GO:0007275	multicellular organismal development	Process
pl082023	uc002iqz	GO:0007283	spermatogenesis	Process
pl082023	uc002iqz	GO:0007605	sensory perception of sound	Process
pl082023	uc002iqz	GO:0016020	membrane	Component
pl082023	uc002iqz	GO:0030154	cell differentiation	Process
pl032579	NR_003187.2	GO:0001878	response to yeast	Process
pl032579	NR_003187.2	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	Process
pl032579	NR_003187.2	GO:0002479	antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent	Process
pl032579	NR_003187.2	GO:0002679	respiratory burst involved in defense response	Process
pl032579	NR_003187.2	GO:0003924	GTPase activity	Function

pl032579	NR_003187.2	GO:0005515	protein binding	Function
pl032579	NR_003187.2	GO:0005525	GTP binding	Function
pl032579	NR_003187.2	GO:0005625	soluble fraction	Component
pl032579	NR_003187.2	GO:0005829	cytosol	Component
pl032579	NR_003187.2	GO:0006184	GTP catabolic process	Process
pl032579	NR_003187.2	GO:0006612	protein targeting to membrane	Process
pl032579	NR_003187.2	GO:0006691	leukotriene metabolic process	Process
pl032579	NR_003187.2	GO:0006801	superoxide metabolic process	Process
pl032579	NR_003187.2	GO:0006954	inflammatory response	Process
pl032579	NR_003187.2	GO:0006968	cellular defense response	Process
pl032579	NR_003187.2	GO:0007154	cell communication	Process
pl032579	NR_003187.2	GO:0008283	cell proliferation	Process
pl032579	NR_003187.2	GO:0009055	electron carrier activity	Function
pl032579	NR_003187.2	GO:0016175	superoxide-generating NADPH oxidase activity	Function
pl032579	NR_003187.2	GO:0017124	SH3 domain binding	Function
pl032579	NR_003187.2	GO:0032010	phagolysosome	Component
pl032579	NR_003187.2	GO:0035091	phosphatidylinositol binding	Function
pl032579	NR_003187.2	GO:0042554	superoxide anion generation	Process
pl032579	NR_003187.2	GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	Process
pl032579	NR_003187.2	GO:0043020	NADPH oxidase complex	Component
pl032579	NR_003187.2	GO:0045087	innate immune response	Process
pl032579	NR_003187.2	GO:0045730	respiratory burst	Process
pl032579	NR_003187.2	GO:0045986	negative regulation of smooth muscle contraction	Process
pl032579	NR_003187.2	GO:0050665	hydrogen peroxide biosynthetic process	Process
pl032579	NR_003187.2	GO:0070946	neutrophil mediated killing of gram-positive	Process

			bacterium	
pl032579	NR_003187.2	GO:0070947	neutrophil mediated killing of fungus	Process
pl070304	ENST00000441820	GO:0003779	actin binding	Function
pl070304	ENST00000441820	GO:0005100	Rho GTPase activator activity	Function
pl070304	ENST00000441820	GO:0005543	phospholipid binding	Function
pl070304	ENST00000441820	GO:0005829	cytosol	Component
pl070304	ENST00000441820	GO:0006930	substrate-dependent cell migration, cell extension	Process
pl070304	ENST00000441820	GO:0007165	signal transduction	Process
pl070304	ENST00000441820	GO:0007264	small GTPase mediated signal transduction	Process
pl070304	ENST00000441820	GO:0007399	nervous system development	Process
pl070304	ENST00000441820	GO:0007411	axon guidance	Process
pl070304	ENST00000441820	GO:0008093	cytoskeletal adaptor activity	Function
pl070304	ENST00000441820	GO:0015629	actin cytoskeleton	Component
pl070304	ENST00000441820	GO:0017124	SH3 domain binding	Function
pl070304	ENST00000441820	GO:0030036	actin cytoskeleton organization	Process
pl070304	ENST00000441820	GO:0030054	cell junction	Component
pl070304	ENST00000441820	GO:0030100	regulation of endocytosis	Process
pl070304	ENST00000441820	GO:0032321	positive regulation of Rho GTPase activity	Process
pl070304	ENST00000441820	GO:0035255	ionotropic glutamate receptor binding	Function
pl070304	ENST00000441820	GO:0043195	terminal button	Component
pl070304	ENST00000441820	GO:0043197	dendritic spine	Component
pl070304	ENST00000441820	GO:0046847	filopodium assembly	Process
pl070304	ENST00000441820	GO:0048488	synaptic vesicle endocytosis	Process
pl070304	ENST00000441820	GO:0051056	regulation of small GTPase mediated signal transduction	Process
pl070304	ENST00000441820	GO:0051966	regulation of synaptic transmission, glutamatergic	Process

pl062694	NR_033440.1	GO:0001666	response to hypoxia	Process
pl062694	NR_033440.1	GO:0004504	peptidylglycine monooxygenase activity	Function
pl062694	NR_033440.1	GO:0004598	peptidylamidoglycolate lyase activity	Function
pl062694	NR_033440.1	GO:0005507	copper ion binding	Function
pl062694	NR_033440.1	GO:0005515	protein binding	Function
pl062694	NR_033440.1	GO:0005576	extracellular region	Component
pl062694	NR_033440.1	GO:0005624	membrane fraction	Component
pl062694	NR_033440.1	GO:0006464	cellular protein modification process	Process
pl062694	NR_033440.1	GO:0006518	peptide metabolic process	Process
pl062694	NR_033440.1	GO:0007417	central nervous system development	Process
pl062694	NR_033440.1	GO:0007507	heart development	Process
pl062694	NR_033440.1	GO:0009268	response to pH	Process
pl062694	NR_033440.1	GO:0016021	integral to membrane	Component
pl062694	NR_033440.1	GO:0030141	secretory granule	Component
pl062694	NR_033440.1	GO:0031418	L-ascorbic acid binding	Function
pl062694	NR_033440.1	GO:0032355	response to estradiol stimulus	Process
pl062694	NR_033440.1	GO:0042493	response to drug	Process
pl062694	NR_033440.1	GO:0043204	perikaryon	Component
pl062694	NR_033440.1	GO:0046688	response to copper ion	Process
pl062694	NR_033440.1	GO:0051384	response to glucocorticoid stimulus	Process
pl062694	NR_033440.1	GO:0060173	limb development	Process
pl003123	ENST00000441820	GO:0000122	negative regulation of transcription from RNA polymerase II promoter	Process
pl003123	ENST00000441820	GO:0000988	protein binding transcription factor activity	Function
pl003123	ENST00000441820	GO:0004871	signal transducer activity	Function
pl003123	ENST00000441820	GO:0005634	nucleus	Component

pl003123	ENST00000441820	GO:0005737	cytoplasm	Component
pl003123	ENST00000441820	GO:0006351	transcription, DNA-dependent	Process
pl003123	ENST00000441820	GO:0007623	circadian rhythm	Process
pl115490	ENST00000424506	GO:0000166	nucleotide binding	Function
pl115490	ENST00000424506	GO:0003723	RNA binding	Function
pl115490	ENST00000424506	GO:0005634	nucleus	Component
pl115490	ENST00000424506	GO:0006396	RNA processing	Process
pl105897	uc001dbm	GO:0004714	transmembrane receptor protein tyrosine kinase activity	Function
pl105897	uc001dbm	GO:0005524	ATP binding	Function
pl105897	uc001dbm	GO:0005737	cytoplasm	Component
pl105897	uc001dbm	GO:0005886	plasma membrane	Component
pl105897	uc001dbm	GO:0005887	integral to plasma membrane	Component
pl105897	uc001dbm	GO:0007169	transmembrane receptor protein tyrosine kinase signaling pathway	Process
pl105897	uc001dbm	GO:0017147	Wnt-protein binding	Function
pl088450		GO:0000038	very long-chain fatty acid metabolic process	Process
pl088450		GO:0005524	ATP binding	Function
pl088450		GO:0005783	endoplasmic reticulum	Component
pl088450		GO:0005789	endoplasmic reticulum membrane	Component
pl088450		GO:0005792	microsome	Component
pl088450		GO:0006642	triglyceride mobilization	Process
pl088450		GO:0006699	bile acid biosynthetic process	Process
pl088450		GO:0008206	bile acid metabolic process	Process
pl088450		GO:0009925	basal plasma membrane	Component
pl088450		GO:0015245	fatty acid transporter activity	Function

pl088450	GO:0015721	bile acid and bile salt transport	Process
pl088450	GO:0015911	plasma membrane long-chain fatty acid transport	Process
pl088450	GO:0030176	integral to endoplasmic reticulum membrane	Component
pl088450	GO:0031957	very long-chain fatty acid-CoA ligase activity	Function
pl088450	GO:0032403	protein complex binding	Function
pl088450	GO:0043234	protein complex	Component
pl088450	GO:0044281	small molecule metabolic process	Process
pl088450	GO:0046951	ketone body biosynthetic process	Process
pl088450	GO:0047747	cholate-CoA ligase activity	Function
pl041833	GO:0000287	magnesium ion binding	Function
pl041833	GO:0001774	microglial cell activation	Process
pl041833	GO:0001921	positive regulation of receptor recycling	Process
pl041833	GO:0001956	positive regulation of neurotransmitter secretion	Process
pl041833	GO:0005504	fatty acid binding	Function
pl041833	GO:0005507	copper ion binding	Function
pl041833	GO:0005509	calcium ion binding	Function
pl041833	GO:0005515	protein binding	Function
pl041833	GO:0005576	extracellular region	Component
pl041833	GO:0005634	nucleus	Component
pl041833	GO:0005737	cytoplasm	Component
pl041833	GO:0005739	mitochondrion	Component
pl041833	GO:0005829	cytosol	Component
pl041833	GO:0005886	plasma membrane	Component
pl041833	GO:0005938	cell cortex	Component
pl041833	GO:0006631	fatty acid metabolic process	Process
pl041833	GO:0006638	neutral lipid metabolic process	Process

pl041833	GO:0006644	phospholipid metabolic process	Process
pl041833	GO:0006916	anti-apoptosis	Process
pl041833	GO:0006919	activation of cysteine-type endopeptidase activity involved in apoptotic process	Process
pl041833	GO:0007006	mitochondrial membrane organization	Process
pl041833	GO:0008198	ferrous iron binding	Function
pl041833	GO:0008270	zinc ion binding	Function
pl041833	GO:0008344	adult locomotory behavior	Process
pl041833	GO:0010040	response to iron(II) ion	Process
pl041833	GO:0010517	regulation of phospholipase activity	Process
pl041833	GO:0010642	negative regulation of platelet-derived growth factor receptor signaling pathway	Process
pl041833	GO:0014048	regulation of glutamate secretion	Process
pl041833	GO:0014059	regulation of dopamine secretion	Process
pl041833	GO:0015629	actin cytoskeleton	Component
pl041833	GO:0016234	inclusion body	Component
pl041833	GO:0016491	oxidoreductase activity	Function
pl041833	GO:0019717	synaptosome	Component
pl041833	GO:0019894	kinesin binding	Function
pl041833	GO:0030054	cell junction	Component
pl041833	GO:0030424	axon	Component
pl041833	GO:0030426	growth cone	Component
pl041833	GO:0030544	Hsp70 protein binding	Function
pl041833	GO:0031092	platelet alpha granule membrane	Component
pl041833	GO:0031115	negative regulation of microtubule polymerization	Process
pl041833	GO:0031623	receptor internalization	Process

pl041833	GO:0031648	protein destabilization	Process
pl041833	GO:0032026	response to magnesium ion	Process
pl041833	GO:0032410	negative regulation of transporter activity	Process
pl041833	GO:0032496	response to lipopolysaccharide	Process
pl041833	GO:0032769	negative regulation of monooxygenase activity	Process
pl041833	GO:0033138	positive regulation of peptidyl-serine phosphorylation	Process
pl041833	GO:0034341	response to interferon-gamma	Process
pl041833	GO:0034599	cellular response to oxidative stress	Process
pl041833	GO:0035067	negative regulation of histone acetylation	Process
pl041833	GO:0040012	regulation of locomotion	Process
pl041833	GO:0042393	histone binding	Function
pl041833	GO:0042416	dopamine biosynthetic process	Process
pl041833	GO:0042493	response to drug	Process
pl041833	GO:0042775	mitochondrial ATP synthesis coupled electron transport	Process
pl041833	GO:0042802	identical protein binding	Function
pl041833	GO:0043014	alpha-tubulin binding	Function
pl041833	GO:0043027	cysteine-type endopeptidase inhibitor activity involved in apoptotic process	Function
pl041833	GO:0043030	regulation of macrophage activation	Process
pl041833	GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	Process
pl041833	GO:0043205	fibril	Component
pl041833	GO:0043206	fibril organization	Process
pl041833	GO:0043524	negative regulation of neuron apoptotic process	Process

pl041833	GO:0045202	synapse	Component
pl041833	GO:0045502	dynein binding	Function
pl041833	GO:0045807	positive regulation of endocytosis	Process
pl041833	GO:0045920	negative regulation of exocytosis	Process
pl041833	GO:0048156	tau protein binding	Function
pl041833	GO:0048169	regulation of long-term neuronal synaptic plasticity	Process
pl041833	GO:0048471	perinuclear region of cytoplasm	Component
pl041833	GO:0048488	synaptic vesicle endocytosis	Process
pl041833	GO:0050812	regulation of acyl-CoA biosynthetic process	Process
pl041833	GO:0051219	phosphoprotein binding	Function
pl041833	GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	Process
pl041833	GO:0051583	dopamine uptake involved in synaptic transmission	Process
pl041833	GO:0051585	negative regulation of dopamine uptake involved in synaptic transmission	Process
pl041833	GO:0051612	negative regulation of serotonin uptake	Process
pl041833	GO:0051622	negative regulation of norepinephrine uptake	Process
pl041833	GO:0055074	calcium ion homeostasis	Process
pl041833	GO:0055114	oxidation-reduction process	Process
pl041833	GO:0060079	regulation of excitatory postsynaptic membrane potential	Process
pl041833	GO:0060291	long-term synaptic potentiation	Process
pl041833	GO:0060732	positive regulation of inositol phosphate biosynthetic process	Process
pl041833	GO:0060961	phospholipase D inhibitor activity	Function
pl041833	GO:0070495	negative regulation of thrombin receptor signaling	Process

			pathway	
pl041833		GO:0070555	response to interleukin-1	Process
pl041833		GO:0071280	cellular response to copper ion	Process
pl041833		GO:0071872	cellular response to epinephrine stimulus	Process
pl041833		GO:0071902	positive regulation of protein serine/threonine kinase activity	Process
pl002953	NR_026717.1	GO:0004674	protein serine/threonine kinase activity	Function
pl002953	NR_026717.1	GO:0005524	ATP binding	Function
pl002953	NR_026717.1	GO:0005634	nucleus	Component
pl002953	NR_026717.1	GO:0006468	protein phosphorylation	Process
pl002953	NR_026717.1	GO:0016301	kinase activity	Function
pl020232	BG200518	GO:0007049	cell cycle	Process
pl020232	BG200518	GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen	Function
pl020232	BG200518	GO:0030099	myeloid cell differentiation	Process
pl020232	BG200518	GO:0046872	metal ion binding	Function
pl020232	BG200518	GO:0070579	methylcytosine dioxygenase activity	Function
pl042847	NR_045553.1	GO:0003417	growth plate cartilage development	Process
pl042847	NR_045553.1	GO:0005509	calcium ion binding	Function
pl042847	NR_045553.1	GO:0005576	extracellular region	Component
pl042847	NR_045553.1	GO:0007155	cell adhesion	Process
pl042847	NR_045553.1	GO:0007160	cell-matrix adhesion	Process
pl042847	NR_045553.1	GO:0008201	heparin binding	Function
pl042847	NR_045553.1	GO:0043931	ossification involved in bone maturation	Process
pl042847	NR_045553.1	GO:0048471	perinuclear region of cytoplasm	Component

pl042847	NR_045553.1	GO:0060346	bone trabecula formation	Process
pl050273	AB209630	GO:0004385	guanylate kinase activity	Function
pl050273	AB209630	GO:0005515	protein binding	Function
pl050273	AB209630	GO:0005654	nucleoplasm	Component
pl050273	AB209630	GO:0005737	cytoplasm	Component
pl050273	AB209630	GO:0005829	cytosol	Component
pl050273	AB209630	GO:0005886	plasma membrane	Component
pl050273	AB209630	GO:0005912	adherens junction	Component
pl050273	AB209630	GO:0005923	tight junction	Component
pl050273	AB209630	GO:0006915	apoptotic process	Process
pl050273	AB209630	GO:0006921	cellular component disassembly involved in apoptotic process	Process
pl050273	AB209630	GO:0030054	cell junction	Component
pl050273	AB209630	GO:0035329	hippo signaling cascade	Process
pl041286	AW340752	GO:0003674	molecular_function	Function
pl041286	AW340752	GO:0005575	cellular_component	Component
pl041286	AW340752	GO:0008150	biological_process	Process
pl041286	AW340752	GO:0016021	integral to membrane	Component
pl018286	uc010did	GO:0016021	integral to membrane	Component
pl105250	NR_034060.1	GO:0003677	DNA binding	Function
pl105250	NR_034060.1	GO:0005634	nucleus	Component
pl105250	NR_034060.1	GO:0006351	transcription, DNA-dependent	Process
pl105250	NR_034060.1	GO:0006355	regulation of transcription, DNA-dependent	Process
pl105250	NR_034060.1	GO:0008270	zinc ion binding	Function
pl094413	ENST00000522129	GO:0003677	DNA binding	Function
pl094413	ENST00000522129	GO:0005634	nucleus	Component

pl094413	ENST00000522129	GO:0006351	transcription, DNA-dependent	Process
pl094413	ENST00000522129	GO:0006355	regulation of transcription, DNA-dependent	Process
pl094413	ENST00000522129	GO:0008270	zinc ion binding	Function
pl009498	NR_024453	GO:0003677	DNA binding	Function
pl009498	NR_024453	GO:0005634	nucleus	Component
pl009498	NR_024453	GO:0006351	transcription, DNA-dependent	Process
pl009498	NR_024453	GO:0006355	regulation of transcription, DNA-dependent	Process
pl009498	NR_024453	GO:0008270	zinc ion binding	Function
pl024747	uc003hho	GO:0003677	DNA binding	Function
pl024747	uc003hho	GO:0005634	nucleus	Component
pl024747	uc003hho	GO:0006351	transcription, DNA-dependent	Process
pl024747	uc003hho	GO:0006355	regulation of transcription, DNA-dependent	Process
pl024747	uc003hho	GO:0008270	zinc ion binding	Function
pl070709	BC042074	GO:0003674	molecular_function	Function
pl070709	BC042074	GO:0003677	DNA binding	Function
pl070709	BC042074	GO:0003700	sequence-specific DNA binding transcription factor activity	Function
pl070709	BC042074	GO:0005634	nucleus	Component
pl070709	BC042074	GO:0006351	transcription, DNA-dependent	Process
pl070709	BC042074	GO:0008150	biological_process	Process
pl070709	BC042074	GO:0008270	zinc ion binding	Function
pl070709	BC042074	GO:0016032	viral reproduction	Process

Supplementary Table 2-2 Information of pathways about aberrantly expressed lncRNAs by KEGG pathway analysis

LncRNAs-probe name	ID	Pathway_id	Pathway_name
pl000897	uc010jos	ar_pathway	Coregulation of Androgen receptor activity
pl000897	uc010jos	hsa05133	Pertussis
pl000897	uc010jos	reg_gr_pathway	Glucocorticoid receptor regulatory network
pl000897	uc010jos	il12_stat4pathway	IL12 signaling mediated by STAT4
pl000897	uc010jos	telomerasepathway	Regulation of Telomerase
pl000897	uc010jos	REACT_25359	RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways
pl000897	uc010jos	REACT_604	Hemostasis
pl000897	uc010jos	REACT_25162	Interferon alpha/beta signaling
pl000897	uc010jos	REACT_24970	Factors involved in megakaryocyte development and platelet production
pl000897	uc010jos	REACT_24938	TRAF6 mediated IRF7 activation
pl002694	HIV2736	trkrpathway	Neurotrophic factor-mediated Trk receptor signaling
pl002694	HIV2736	REACT_75842	Antigen processing: Ubiquitination & Proteasome degradation
pl002953	NR_026717.1	hsa05150	Staphylococcus aureus infection
pl002953	NR_026717.1	hsa05322	Systemic lupus erythematosus
pl002953	NR_026717.1	WP545	Complement Activation, Classical Pathway
pl002953	NR_026717.1	WP706	SIDS Susceptibility Pathways
pl002953	NR_026717.1	hsa03018	RNA degradation
pl002953	NR_026717.1	hsa05322	Systemic lupus erythematosus
pl002953	NR_026717.1	hsa04610	Complement and coagulation cascades
pl002953	NR_026717.1	hsa05133	Pertussis

pl002953	NR_026717.1	hsa05150	Staphylococcus aureus infection
pl002953	NR_026717.1	REACT_7972	Activation of C3 and C5
pl002953	NR_026717.1	WP706	SIDS Susceptibility Pathways
pl002953	NR_026717.1	WP545	Complement Activation, Classical Pathway
pl003123	ENST00000441820	hsa04710	Circadian rhythm - mammal
pl003123	ENST00000441820	hsa05202	Transcriptional misregulation in cancer
pl003123	ENST00000441820	REACT_24941	Circadian Clock
pl003123	ENST00000441820	REACT_111118	BMAL1:CLOCK/NPAS2 Activates Gene Expression
pl003123	ENST00000441820	WP410	Diurnally regulated genes with circadian orthologs
pl004774	AJ227874	hsa03018	RNA degradation
pl004774	AJ227874	REACT_22426	Asparagine N-linked glycosylation
pl004774	AJ227874	REACT_25208	N-glycan antennae elongation in the medial/trans-Golgi
pl004774	AJ227874	REACT_25085	N-Glycan antennae elongation
pl004774	AJ227874	REACT_22161	Post-translational protein modification
pl009498	NR_024453	HUMAN_PWY-5687	pyrimidine ribonucleotides interconversion
pl009498	NR_024453	HUMAN_PWY0-166	pyrimidine deoxyribonucleotides de novo biosynthesis I
pl009498	NR_024453	hsa00240	Pyrimidine metabolism
pl009498	NR_024453	REACT_1698	Metabolism of nucleotides
pl009498	NR_024453	REACT_21330	Synthesis and interconversion of nucleotide di- and triphosphates
pl009498	NR_024453	REACT_111217	Metabolism
pl009498	NR_024453	REACT_71	Gene Expression
pl011302	gnl|UG|Hs	hsa04623	Cytosolic DNA-sensing pathway
pl011302	gnl|UG|Hs	REACT_63	RNA Polymerase III Transcription Termination
pl011302	gnl|UG|Hs	REACT_571	RNA Polymerase III Transcription Initiation From Type 3 Promoter

pl011302	gnl|UG|Hs	REACT_1371	RNA Polymerase III Transcription
pl011302	gnl|UG|Hs	REACT_347	RNA Polymerase III Transcription Initiation From Type 1 Promoter
pl011302	gnl|UG|Hs	REACT_281	RNA Polymerase III Transcription Initiation
pl011302	gnl|UG|Hs	REACT_21352	RNA Polymerase I, RNA Polymerase III, and Mitochondrial Transcription
pl011302	gnl|UG|Hs	WP405	Eukaryotic Transcription Initiation
pl015535	NR_024279	hes_heypathway	Notch-mediated HES/HEY network
pl015535	NR_024279	notch_pathway	Notch signaling pathway
pl015535	NR_024279	WP61	Delta-Notch Signaling Pathway
pl016207	ASO2077	hsa04142	Lysosome
pl016207	ASO2077	hsa04142	Lysosome
pl016873	uc002ued	REACT_115810	Sphingolipid de novo biosynthesis
pl016873	uc002ued	REACT_12508	Metabolism of nitric oxide
pl016873	uc002ued	REACT_111217	Metabolism
pl016873	uc002ued	REACT_12541	NOSTRIN mediated eNOS trafficking
pl016873	uc002ued	REACT_12389	eNOS activation and regulation
pl016873	uc002ued	REACT_115810	Sphingolipid de novo biosynthesis
pl016992	BC114220	hdac_classii_pathway	Signaling events mediated by HDAC Class II
pl017442	ENST00000556070	hsa05202	Transcriptional misregulation in cancer
pl017442	ENST00000556070	WP53	Id Signaling Pathway
pl018286	uc010did	REACT_23876	Platelet homeostasis
pl018286	uc010did	REACT_23862	Nitric oxide stimulates guanylate cyclase
pl023546	NR_037844.1	hsa05168	Herpes simplex infection
pl023548	AK098019	hsa04728	Dopaminergic synapse
pl023548	AK098019	hsa04020	Calcium signaling pathway

pl023548	AK098019	hsa04971	Gastric acid secretion
pl023548	AK098019	hsa04726	Serotonergic synapse
pl023548	AK098019	hsa05146	Amoebiasis
pl023548	AK098019	hsa04970	Salivary secretion
pl023548	AK098019	hsa04972	Pancreatic secretion
pl023548	AK098019	hsa05142	Chagas disease (American trypanosomiasis)
pl023548	AK098019	hsa04723	Retrograde endocannabinoid signaling
pl023548	AK098019	hsa04540	Gap junction
pl023548	AK098019	arf6_pathway	Arf6 signaling events
pl023548	AK098019	lysophospholipid_pathway	LPA receptor mediated events
pl023548	AK098019	s1p_s1p3_pathway	S1P3 pathway
pl023548	AK098019	REACT_19184	GPCR downstream signaling
pl023548	AK098019	REACT_111217	Metabolism
pl023548	AK098019	REACT_604	Hemostasis
pl023548	AK098019	REACT_19193	Regulation of Insulin Secretion by Fatty Acids Bound to GPR40 (FFAR1)
pl023548	AK098019	REACT_14797	Signaling by GPCR
pl023548	AK098019	REACT_18405	Regulation of Insulin Secretion by Acetylcholine
pl023548	AK098019	REACT_111102	Signal Transduction
pl023548	AK098019	REACT_18283	G alpha (q) signalling events
pl023548	AK098019	REACT_20524	Signal amplification
pl023548	AK098019	REACT_1505	Integration of energy metabolism
pl023548	AK098019	REACT_18325	Regulation of Insulin Secretion
pl023548	AK098019	REACT_21384	Thrombin signalling through proteinase activated receptors (PARs)
pl023548	AK098019	WP289	Myometrial Relaxation and Contraction Pathways

pl023548	AK098019	WP35	G Protein Signaling Pathways
pl024747	uc003hho	hsa01100	Metabolic pathways
pl028231	ENST00000499504	hsa05200	Pathways in cancer
pl028231	ENST00000499504	hsa04916	Melanogenesis
pl028231	ENST00000499504	hsa05217	Basal cell carcinoma
pl028231	ENST00000499504	wnt_signaling_pathway	Wnt signaling network
pl028231	ENST00000499504	REACT_18372	Class B/2 (Secretin family receptors)
pl028231	ENST00000499504	REACT_21340	GPCR ligand binding
pl028231	ENST00000499504	REACT_111102	Signal Transduction
pl028231	ENST00000499504	WP399	Wnt Signaling Pathway and Pluripotency
pl028231	ENST00000499504	WP363	Wnt Signaling Pathway NetPath
pl032579	NR_003187.2	hsa04670	Leukocyte transendothelial migration
pl032579	NR_003187.2	hsa04062	Chemokine signaling pathway
pl032579	NR_003187.2	rac1_pathway	RAC1 signaling pathway
pl032579	NR_003187.2	hsa04670	Leukocyte transendothelial migration
pl032579	NR_003187.2	hsa04062	Chemokine signaling pathway
pl032579	NR_003187.2	rac1_pathway	RAC1 signaling pathway
pl035959	NR_024380	hsa00531	Glycosaminoglycan degradation
pl035959	NR_024380	hsa04142	Lysosome
pl038679	uc001jeo	WP98	Prostaglandin Synthesis and Regulation
pl038679	uc001jeo	WP98	Prostaglandin Synthesis and Regulation
pl038713	AK129572	hsa04350	TGF-beta signaling pathway
pl038713	AK129572	REACT_821	Cyclin D associated events in G1
pl038713	AK129572	REACT_111214	G0 and Early G1
pl038713	AK129572	REACT_1590	G1 Phase
pl038713	AK129572	REACT_115566	Cell Cycle

pl038713	AK129572	WP45	G1 to S cell cycle control
pl039631	DC295389	hsa04330	Notch signaling pathway
pl039631	DC295389	ps1pathway	Presenilin action in Notch and Wnt signaling
pl039631	DC295389	REACT_71	Gene Expression
pl039631	DC295389	REACT_111102	Signal Transduction
pl039631	DC295389	REACT_13673	Regulation of gene expression in late stage (branching morphogenesis) pancreatic bud precursor cells
pl039631	DC295389	REACT_14835	Notch-HLH transcription pathway
pl039631	DC295389	WP61	Delta-Notch Signaling Pathway
pl039631	DC295389	WP268	Notch Signaling Pathway
pl040361	gnl|UG|Hs	REACT_19327	G alpha (s) signalling events
pl040361	gnl|UG|Hs	REACT_18372	Class B/2 (Secretin family receptors)
pl040361	gnl|UG|Hs	REACT_14797	Signaling by GPCR
pl040361	gnl|UG|Hs	REACT_111102	Signal Transduction
pl040361	gnl|UG|Hs	REACT_19184	GPCR downstream signaling
pl041833		hsa05010	Alzheimer's disease
pl041833		alphasynuclein_pathway	Alpha-synuclein signaling
pl041833		REACT_116125	Disease
pl041833		WP437	EGFR1 Signaling Pathway
pl041833		hsa05010	Alzheimer's disease
pl041833		alphasynuclein_pathway	Alpha-synuclein signaling
pl041833		REACT_116125	Disease
pl041833		WP437	EGFR1 Signaling Pathway
pl042847	NR_045553.1	hsa04512	ECM-receptor interaction
pl042847	NR_045553.1	hsa05144	Malaria

pl042847	NR_045553.1	hsa04350	TGF-beta signaling pathway
pl042847	NR_045553.1	hsa04145	Phagosome
pl042847	NR_045553.1	REACT_16888	Signaling by PDGF
pl042847	NR_045553.1	hsa04350	TGF-beta signaling pathway
pl042847	NR_045553.1	hsa04145	Phagosome
pl042847	NR_045553.1	hsa05144	Malaria
pl042847	NR_045553.1	hsa04512	ECM-receptor interaction
pl042847	NR_045553.1	REACT_16888	Signaling by PDGF
pl045494	NR_038971.1	hsa03040	Spliceosome
pl045494	NR_038971.1	telomerasepathway	Regulation of Telomerase
pl045494	NR_038971.1	REACT_1735	mRNA Splicing
pl045494	NR_038971.1	REACT_71	Gene Expression
pl045494	NR_038971.1	WP411	mRNA processing
pl048800	HMlincRNA965	hsa05200	Pathways in cancer
pl048800	HMlincRNA965	hsa04010	MAPK signaling pathway
pl050273	AB209630	REACT_13579	Apoptotic cleavage of cell adhesion proteins
pl050273	AB209630	REACT_107	Apoptotic cleavage of cellular proteins
pl050273	AB209630	REACT_995	Apoptotic execution phase
pl050273	AB209630	REACT_13579	Apoptotic cleavage of cell adhesion proteins
pl050273	AB209630	REACT_107	Apoptotic cleavage of cellular proteins
pl050273	AB209630	REACT_995	Apoptotic execution phase
pl053131	uc001aue	HUMAN_PWY-6861	the visual cycle
pl053131	uc001aue	hsa00830	Retinol metabolism
pl053131	uc001aue	hsa01100	Metabolic pathways
pl057456		hsa02010	ABC transporters
pl057456		REACT_15480	ABC-family proteins mediated transport

pl057456		REACT_75908	Potassium Channels
pl059793	uc004cyt	REACT_1008	Glycogen breakdown (glycogenolysis)
pl059793	uc004cyt	REACT_474	Metabolism of carbohydrates
pl059793	uc004cyt	REACT_723	Glucose metabolism
pl060937	AF086561	HUMAN_ILEUDEG-PWY	isoleucine degradation I
pl060937	AF086561	HUMAN_PWY66-367	ketogenesis
pl060937	AF086561	HUMAN_TRYPTOPHAN-DEGRADATION-1	tryptophan degradation III (eukaryotic)
pl060937	AF086561	HUMAN_PWY-5910	superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate)
pl060937	AF086561	HUMAN_PWY66-368	ketolysis
pl060937	AF086561	HUMAN_PWY-922	mevalonate pathway I
pl060937	AF086561	hsa00630	Glyoxylate and dicarboxylate metabolism
pl060937	AF086561	hsa00380	Tryptophan metabolism
pl060937	AF086561	hsa00620	Pyruvate metabolism
pl060937	AF086561	hsa00280	Valine, leucine and isoleucine degradation
pl060937	AF086561	hsa00640	Propanoate metabolism
pl060937	AF086561	hsa00072	Synthesis and degradation of ketone bodies
pl060937	AF086561	REACT_59	Utilization of Ketone Bodies
pl060937	AF086561	REACT_197	Branched-chain amino acid catabolism
pl060937	AF086561	REACT_22279	Fatty acid, triacylglycerol, and ketone body metabolism
pl060937	AF086561	WP143	Fatty Acid Beta Oxidation
pl060937	AF086561	HUMAN_PWY-922	mevalonate pathway I
pl060937	AF086561	HUMAN_PWY-5910	superpathway of geranylgeranyldiphosphate biosynthesis I (via mevalonate)
pl060937	AF086561	HUMAN_PWY66-368	ketolysis
pl060937	AF086561	HUMAN_PWY66-367	ketogenesis

pl060937	AF086561	HUMAN_TRYPTOPHAN-DEGRADATION-1	tryptophan degradation III (eukaryotic)
pl060937	AF086561	HUMAN_ILEUDEG-PWY	isoleucine degradation I
pl060937	AF086561	hsa00380	Tryptophan metabolism
pl060937	AF086561	hsa00280	Valine, leucine and isoleucine degradation
pl060937	AF086561	hsa00620	Pyruvate metabolism
pl060937	AF086561	hsa00640	Propanoate metabolism
pl060937	AF086561	hsa00072	Synthesis and degradation of ketone bodies
pl060937	AF086561	hsa00630	Glyoxylate and dicarboxylate metabolism
pl060937	AF086561	REACT_197	Branched-chain amino acid catabolism
pl060937	AF086561	REACT_59	Utilization of Ketone Bodies
pl060937	AF086561	REACT_22279	Fatty acid, triacylglycerol, and ketone body metabolism
pl060937	AF086561	WP143	Fatty Acid Beta Oxidation
pl062900	AL137436	REACT_18266	Axon guidance
pl062900	AL137436	REACT_18334	NCAM signaling for neurite out-growth
pl062900	AL137436	REACT_22205	L1CAM interactions
pl062900	AL137436	REACT_22266	Interaction between L1 and Ankyrins
pl062900	AL137436	REACT_111045	Developmental Biology
pl062900	AL137436	trkrpathway	Neurotrophic factor-mediated Trk receptor signaling
pl063478	NR_003698	HUMAN_PWY4FS-8	phosphatidylglycerol biosynthesis II (non-plastidic)
pl063478	NR_003698	hsa00564	Glycerophospholipid metabolism
pl063478	NR_003698	hsa00561	Glycerolipid metabolism
pl063478	NR_003698	REACT_22279	Fatty acid, triacylglycerol, and ketone body metabolism
pl063478	NR_003698	REACT_111217	Metabolism
pl063538	gnl|UG|Hs	hsa04621	NOD-like receptor signaling pathway

pl063538	gnl|UG|Hs	hsa05160	Hepatitis C
pl063538	gnl|UG|Hs	hsa04380	Osteoclast differentiation
pl063538	gnl|UG|Hs	hsa04920	Adipocytokine signaling pathway
pl063538	gnl|UG|Hs	hsa05222	Small cell lung cancer
pl063538	gnl|UG|Hs	hsa04210	Apoptosis
pl063538	gnl|UG|Hs	hsa04662	B cell receptor signaling pathway
pl063538	gnl|UG|Hs	hsa04010	MAPK signaling pathway
pl063538	gnl|UG|Hs	hsa05142	Chagas disease (American trypanosomiasis)
pl063538	gnl|UG|Hs	hsa04062	Chemokine signaling pathway
pl063538	gnl|UG|Hs	hsa04622	RIG-I-like receptor signaling pathway
pl063538	gnl|UG|Hs	hsa04623	Cytosolic DNA-sensing pathway
pl063538	gnl|UG|Hs	hsa04660	T cell receptor signaling pathway
pl063538	gnl|UG|Hs	hsa04620	Toll-like receptor signaling pathway
pl063538	gnl|UG|Hs	hsa05120	Epithelial cell signaling in Helicobacter pylori infection
pl063538	gnl|UG|Hs	hsa05212	Pancreatic cancer
pl063538	gnl|UG|Hs	hsa05221	Acute myeloid leukemia
pl063538	gnl|UG|Hs	il1pathway	IL1-mediated signaling events
pl063538	gnl|UG|Hs	trail_pathway	TRAIL signaling pathway
pl063538	gnl|UG|Hs	nfkappabalternativepathway	Alternative NF-kappaB pathway
pl063538	gnl|UG|Hs	bcr_5pathway	BCR signaling pathway
pl063538	gnl|UG|Hs	avb3_opn_pathway	Osteopontin-mediated events
pl063538	gnl|UG|Hs	tcr_pathway	TCR signaling in naive CD4+ T cells
pl063538	gnl|UG|Hs	hivnefpathway	HIV-1 Nef: Negative effector of Fas and TNF-alpha
pl063538	gnl|UG|Hs	pi3kciaktpathway	Class I PI3K signaling events mediated by Akt
pl063538	gnl|UG|Hs	fcer1pathway	Fc-epsilon receptor I signaling in mast cells
pl063538	gnl|UG|Hs	REACT_25024	TRAF6 mediated induction of NFkB and

			MAP kinases upon TLR7/8 or 9 activation
pl063538	gnl|UG|Hs	REACT_12555	Downstream TCR signaling
pl063538	gnl|UG|Hs	REACT_116125	Disease
pl063538	gnl|UG|Hs	REACT_115961	PI3K events in ERBB4 signaling
pl063538	gnl|UG|Hs	REACT_12578	GAB1 signalosome
pl063538	gnl|UG|Hs	REACT_75913	Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways
pl063538	gnl|UG|Hs	REACT_22232	Signaling by Interleukins
pl063538	gnl|UG|Hs	REACT_21272	Downstream signaling of activated FGFR
pl063538	gnl|UG|Hs	REACT_115596	Signaling by ERBB4
pl063538	gnl|UG|Hs	REACT_22442	Interleukin-1 signaling
pl063538	gnl|UG|Hs	REACT_12526	TCR signaling
pl063538	gnl|UG|Hs	REACT_75790	Cytokine Signaling in Immune system
pl063538	gnl|UG|Hs	REACT_25039	NF-kB activation through FADD/RIP-1 pathway mediated by caspase-8 and -10
pl063538	gnl|UG|Hs	REACT_75829	PIP3 activates AKT signaling
pl063538	gnl|UG|Hs	REACT_16888	Signaling by PDGF
pl063538	gnl|UG|Hs	REACT_9047	Toll Like Receptor 9 (TLR9) Cascade
pl063538	gnl|UG|Hs	REACT_75776	NOD1/2 Signaling Pathway
pl063538	gnl|UG|Hs	REACT_25354	IRAK1 recruits IKK complex upon TLR7/8 or 9 stimulation
pl063538	gnl|UG|Hs	REACT_9020	Toll Like Receptor 7/8 (TLR7/8) Cascade
pl063538	gnl|UG|Hs	REACT_24969	TRAF6 mediated NF-kB activation
pl063538	gnl|UG|Hs	WP23	B Cell Receptor Signaling Pathway
pl064191	uc004crw	REACT_111217	Metabolism
pl064191	uc004crw	REACT_22258	Metabolism of lipids and lipoproteins

pl064191	uc004crw	REACT_116105	Glycosphingolipid metabolism
pl065225	uc001hox	HUMAN_PWY66-3	cholesterol biosynthesis II (via 24,25-dihydrolanosterol)
pl065225	uc001hox	HUMAN_PWY-6074	zymosterol biosynthesis
pl065225	uc001hox	REACT_9405	Cholesterol biosynthesis
pl068994	HMlincRNA798	hsa04630	Jak-STAT signaling pathway
pl068994	HMlincRNA798	hsa05222	Small cell lung cancer
pl068994	HMlincRNA798	ranbp2pathway	Sumoylation by RanBP2 regulates transcriptional repression
pl068994	HMlincRNA798	il12_stat4pathway	IL12 signaling mediated by STAT4
pl068994	HMlincRNA798	WP366	TGF-beta Receptor Signaling Pathway
pl068994	HMlincRNA798	WP138	Androgen Receptor Signaling Pathway
pl069409	gnl|ncrnascan|RNS1587	telomerasepathway	Regulation of Telomerase
pl069409	gnl|ncrnascan|RNS1587	hedgehog_glipathway	Hedgehog signaling events mediated by Gli proteins
pl069409	gnl|ncrnascan|RNS1587	REACT_19241	Regulation of Lipid Metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)
pl069409	gnl|ncrnascan|RNS1587	REACT_22279	Fatty acid, triacylglycerol, and ketone body metabolism
pl069926	uc004crw	REACT_111217	Metabolism
pl069926	uc004crw	REACT_22258	Metabolism of lipids and lipoproteins
pl069926	uc004crw	REACT_116105	Glycosphingolipid metabolism
pl070257	uc010jpk	REACT_19230	Role of Abl in Robo-Slit signaling
pl070257	uc010jpk	REACT_18266	Axon guidance
pl070257	uc010jpk	REACT_19230	Role of Abl in Robo-Slit signaling
pl070257	uc010jpk	REACT_18266	Axon guidance
pl070304	ENST00000441820	rhoa_reg_pathway	Regulation of RhoA activity
pl070972	ENST00000412835	fcer1pathway	Fc-epsilon receptor I signaling in mast cells

pl074315	uc001jeo	WP98	Prostaglandin Synthesis and Regulation
pl074315	uc001jeo	WP98	Prostaglandin Synthesis and Regulation
pl076250	NR_023358	hsa03013	RNA transport
pl076250	NR_023358	REACT_71	Gene Expression
pl076250	NR_023358	REACT_1014	Translation
pl076250	NR_023358	REACT_2085	GTP hydrolysis and joining of the 60S ribosomal subunit
pl076250	NR_023358	REACT_931	Ribosomal scanning and start codon recognition
pl076250	NR_023358	REACT_17015	Metabolism of proteins
pl076250	NR_023358	REACT_1979	Translation initiation complex formation
pl076250	NR_023358	REACT_1079	Formation of the ternary complex, and subsequently, the 43S complex
pl080815	gnl|UG|Hs	REACT_71	Gene Expression
pl081094	BC004968	hsa04141	Protein processing in endoplasmic reticulum
pl081094	BC004968	alphasynuclein_pathway	Alpha-synuclein signaling
pl081094	BC004968	REACT_11051	Rho GTPase cycle
pl081932	uc001jeo	WP98	Prostaglandin Synthesis and Regulation
pl081932	uc001jeo	WP98	Prostaglandin Synthesis and Regulation
pl082023	uc002iqz	hsa04144	Endocytosis
pl087848	HMlincRNA1147	hsa03320	PPAR signaling pathway
pl088450		hsa04976	Bile secretion
pl088450		hsa00120	Primary bile acid biosynthesis
pl088450		REACT_11041	Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol
pl088612	uc003hho	hsa01100	Metabolic pathways
pl089142	AK126190	hsa03018	RNA degradation
pl089142	AK126190	REACT_20514	Deadenylation of mRNA

pl089142	AK126190	REACT_71	Gene Expression
pl090173	gnl|UG|Hs	hsa00230	Purine metabolism
pl090173	gnl|UG|Hs	hsa00240	Pyrimidine metabolism
pl090173	gnl|UG|Hs	hsa03018	RNA degradation
pl090211	uc010jvv	hsa05221	Acute myeloid leukemia
pl090211	uc010jvv	hsa05200	Pathways in cancer
pl090211	uc010jvv	hsa03320	PPAR signaling pathway
pl090211	uc010jvv	ps1pathway	Presenilin action in Notch and Wnt signaling
pl090211	uc010jvv	REACT_71	Gene Expression
pl090211	uc010jvv	REACT_12627	Generic Transcription Pathway
pl090211	uc010jvv	WP399	Wnt Signaling Pathway and Pluripotency
pl090211	uc010jvv	WP170	Nuclear Receptors
pl090211	uc010jvv	WP299	Nuclear receptors in lipid metabolism and toxicity
pl090211	uc010jvv	WP236	Adipogenesis
pl090936	NR_023353	hsa03018	RNA degradation
pl090936	NR_023353	REACT_20619	mRNA Decay by 3' to 5' Exoribonuclease
pl090936	NR_023353	REACT_25064	Destabilization of mRNA by Tristetraprolin (TTP)
pl090936	NR_023353	REACT_116125	Disease
pl090936	NR_023353	REACT_15380	Diabetes pathways
pl093483	AK023559	hsa03420	Nucleotide excision repair
pl093483	AK023559	REACT_1941	Formation of transcription-coupled NER (TC-NER) repair complex
pl093483	AK023559	REACT_1628	Transcription-coupled NER (TC-NER)
pl093483	AK023559	REACT_1826	Nucleotide Excision Repair
pl093483	AK023559	REACT_21352	RNA Polymerase I, RNA Polymerase III, and Mitochondrial Transcription

pl093483	AK023559	REACT_1974	RNA Polymerase I Promoter Clearance
pl093483	AK023559	REACT_216	DNA Repair
pl093483	AK023559	REACT_2222	Dual incision reaction in TC-NER
pl093483	AK023559	REACT_71	Gene Expression
pl093483	AK023559	REACT_1941	Formation of transcription-coupled NER (TC-NER) repair complex
pl094303	AK001092	hsa04975	Fat digestion and absorption
pl094303	AK001092	hsa04666	Fc gamma R-mediated phagocytosis
pl094303	AK001092	REACT_115810	Sphingolipid de novo biosynthesis
pl094303	AK001092	REACT_22258	Metabolism of lipids and lipoproteins
pl094303	AK001092	WP325	Triacylglyceride Synthesis
pl094413	ENST00000522129	REACT_71	Gene Expression
pl095227	NR_027781.1	hsa04978	Mineral absorption
pl098426		hsa04972	Pancreatic secretion
pl098426		hsa00760	Nicotinate and nicotinamide metabolism
pl098426		REACT_17004	Chaperonin-mediated protein folding
pl098426		REACT_16907	Association of TriC/CCT with target proteins during biosynthesis
pl098426		REACT_17015	Metabolism of proteins
pl098844	AK027270	hsa00970	Aminoacyl-tRNA biosynthesis
pl098844	AK027270	REACT_15482	tRNA Aminoacylation
pl098844	AK027270	REACT_15306	Cytosolic tRNA aminoacylation
pl098844	AK027270	WP106	Alanine and aspartate metabolism
pl099742	gnl|UG|Hs	hsa04010	MAPK signaling pathway
pl100413	uc002nvo	REACT_12627	Generic Transcription Pathway
pl101461	gnl|ncrnascan|RNS1808	hsa04141	Protein processing in endoplasmic reticulum

pl101958	gnl|UG|Hs	hsa04360	Axon guidance
pl101958	gnl|UG|Hs	REACT_952	Synthesis of glycosylphosphatidylinositol (GPI)
pl101958	gnl|UG|Hs	REACT_19271	Semaphorin interactions
pl101958	gnl|UG|Hs	REACT_22161	Post-translational protein modification
pl101958	gnl|UG|Hs	REACT_111045	Developmental Biology
pl102783	HMlincRNA1153	WP382	MAPK signaling pathway
pl103129		hsa04670	Leukocyte transendothelial migration
pl103129		hsa04726	Serotonergic synapse
pl103129		REACT_15523	Integrin alphaIIb beta3 signaling
pl103129		REACT_13552	Integrin cell surface interactions
pl103129		REACT_798	Platelet activation, signaling and aggregation
pl103129		REACT_18325	Regulation of Insulin Secretion
pl103129		REACT_1505	Integration of energy metabolism
pl103129		REACT_75774	Adaptive Immune System
pl103129		REACT_23898	Rap1 signalling
pl104925	AK024129	hsa05200	Pathways in cancer
pl104925	AK024129	hsa04330	Notch signaling pathway
pl104925	AK024129	hsa05220	Chronic myeloid leukemia
pl104925	AK024129	WP363	Wnt Signaling Pathway NetPath
pl104925	AK024129	WP399	Wnt Signaling Pathway and Pluripotency
pl105093	DC295389	hsa04330	Notch signaling pathway
pl105093	DC295389	ps1pathway	Presenilin action in Notch and Wnt signaling
pl105093	DC295389	REACT_71	Gene Expression
pl105093	DC295389	REACT_111102	Signal Transduction
pl105093	DC295389	REACT_13673	Regulation of gene expression in late stage (branching morphogenesis) pancreatic bud precursor

			cells
pl105093	DC295389	REACT_14835	Notch-HLH transcription pathway
pl105093	DC295389	WP61	Delta-Notch Signaling Pathway
pl105093	DC295389	WP268	Notch Signaling Pathway
pl105250	NR_034060.1	REACT_12627	Generic Transcription Pathway
pl105325	ENST00000468964	REACT_15510	Recruitment of NuMA to mitotic centrosomes
pl105325	ENST00000468964	REACT_21391	Mitotic G2-G2/M phases
pl105325	ENST00000468964	REACT_15296	Recruitment of mitotic centrosome proteins and complexes
pl106072	BC064139	REACT_11044	Signaling by Rho GTPases
pl107934	AK223466	hsa01100	Metabolic pathways
pl107934	AK223466	REACT_13705	Phase 1 - Functionalization of compounds
pl107934	AK223466	REACT_22258	Metabolism of lipids and lipoproteins
pl107934	AK223466	REACT_111217	Metabolism
pl107934	AK223466	p53regulationpathway	p53 pathway
pl107934	AK223466	WP363	Wnt Signaling Pathway NetPath
pl112125	AK130406	hsa00340	Histidine metabolism
pl112125	AK130406	hsa00350	Tyrosine metabolism
pl115081	AK130649	hsa04666	Fc gamma R-mediated phagocytosis