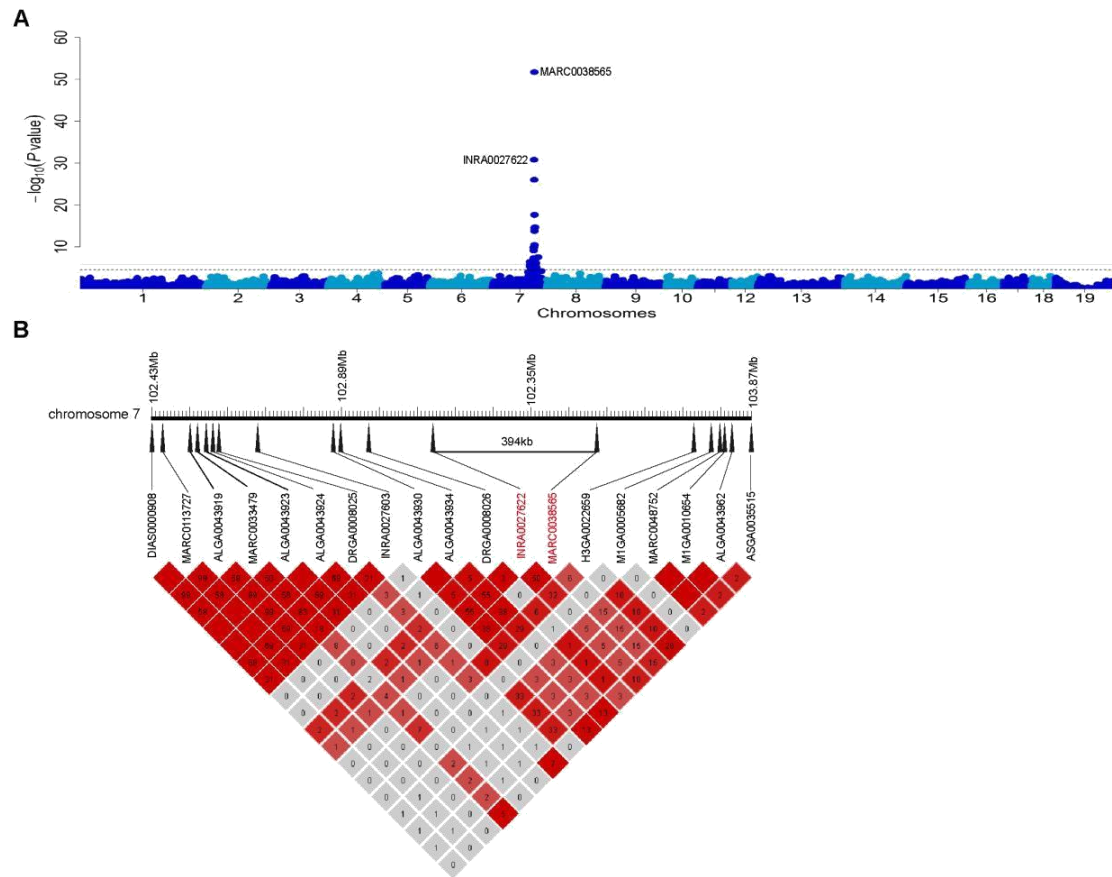
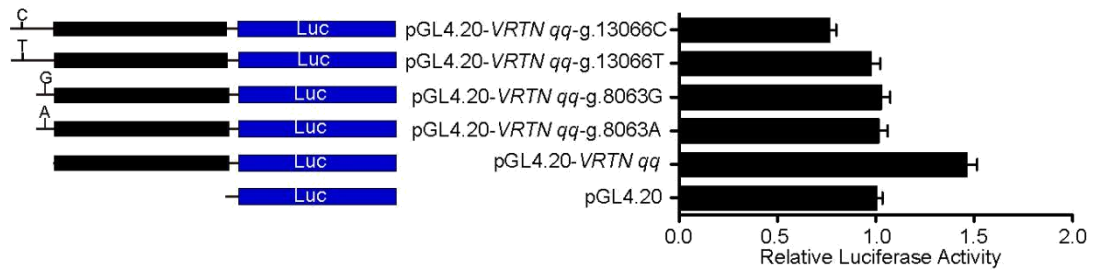


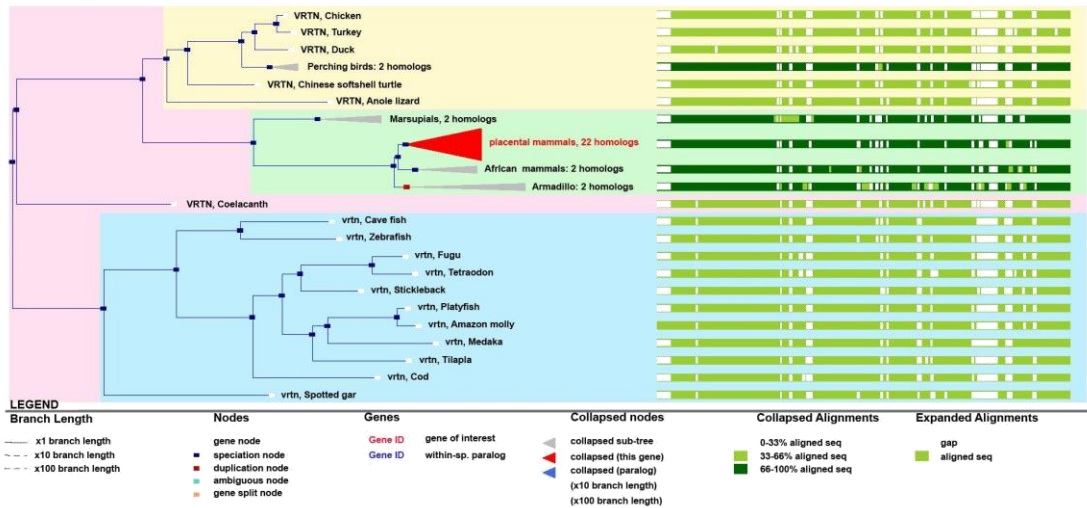
Supplementary Figure S1 Generation of TALEN-mediated *Vrtn* mutant mice. (A) Schematic representation of the genomic structure of the *Vrtn* gene (top) and TALEN targeting sequences (bottom). TALENs were constructed to target sequences in the second exon, as shown by the blue box. Sequences of TALEN recognition sites are shown at the bottom of the genomic structure. (B) DNA sequences of the target site at the *Vrtn* locus in F_0 mice identified via Sanger sequencing. ‘-’ denotes deleted nucleotides. (C) Truncated protein products that would be theoretically synthesized in the mutant mice. The scale indicates the number of nucleotides in the coding region of the *Vrtn* gene. WT, wild type.



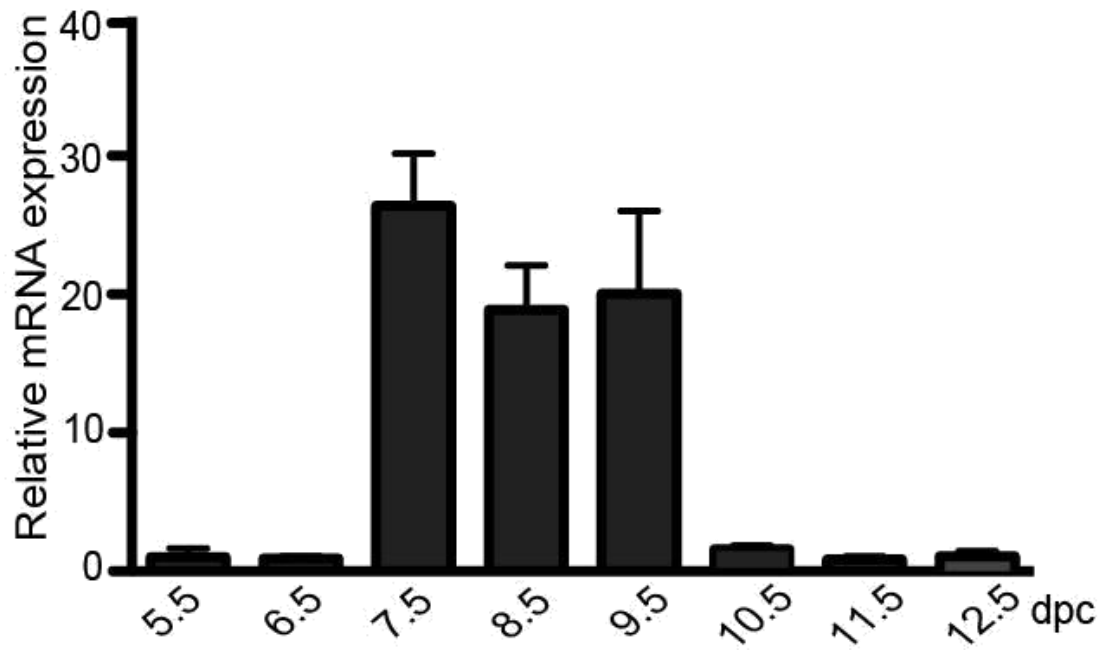
Supplementary Figure S2 Genome-wide association study (GWAS) for the number of thoracic vertebrae (TVN). (A) Manhattan plots of a GWAS for TVN in 609 European hybrid pigs. Negative \log_{10} P-values of the qualified SNPs were plotted against their genomic positions. Different colors indicate distinct chromosomes. The top SNP identified (MARC0038565) in the GWAS is indicated. (B) Regional plots for the SNPs that were associated with TVN on chromosome 7 in these 609 pigs. The top SNP (MARC0038565) is indicated in red and the surrounding SNPs in different colors represent different linkage disequilibrium extents (r^2) to the top SNP. The 394 kb confidence interval of this locus for TVN was defined by LOD drop-off 2.



Supplementary Figure S3 Two *VRTN* variants (g.8063G>A and g.13066C>T) have no effect on the expression of *VRTN*. The diagram shows the relative luciferase activity of each construct. Control indicates the wild-type *VRTN* promoter. The relative luciferase activity (i.e., firefly luciferase light units/Renilla luciferase light units) is represented as the mean \pm S.E. of triplicate experiments. No significant difference was observed between the control and other constructs ($P > 0.05$).

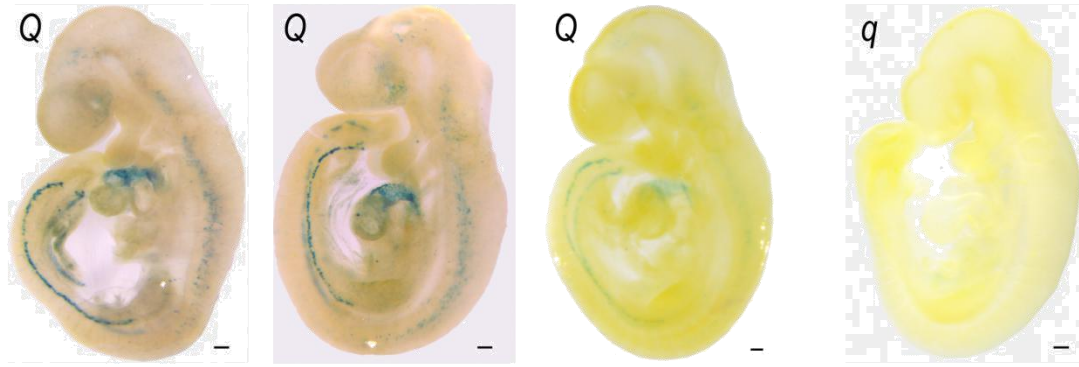


Supplementary Figure S4 Evolutionary constraint of the *VRTN* gene. The *VRTN* gene is present in all sequenced vertebrates and is conserved in mammals. The data were retrieved from the Ensembl browser (<http://asia.ensembl.org/index.html>).

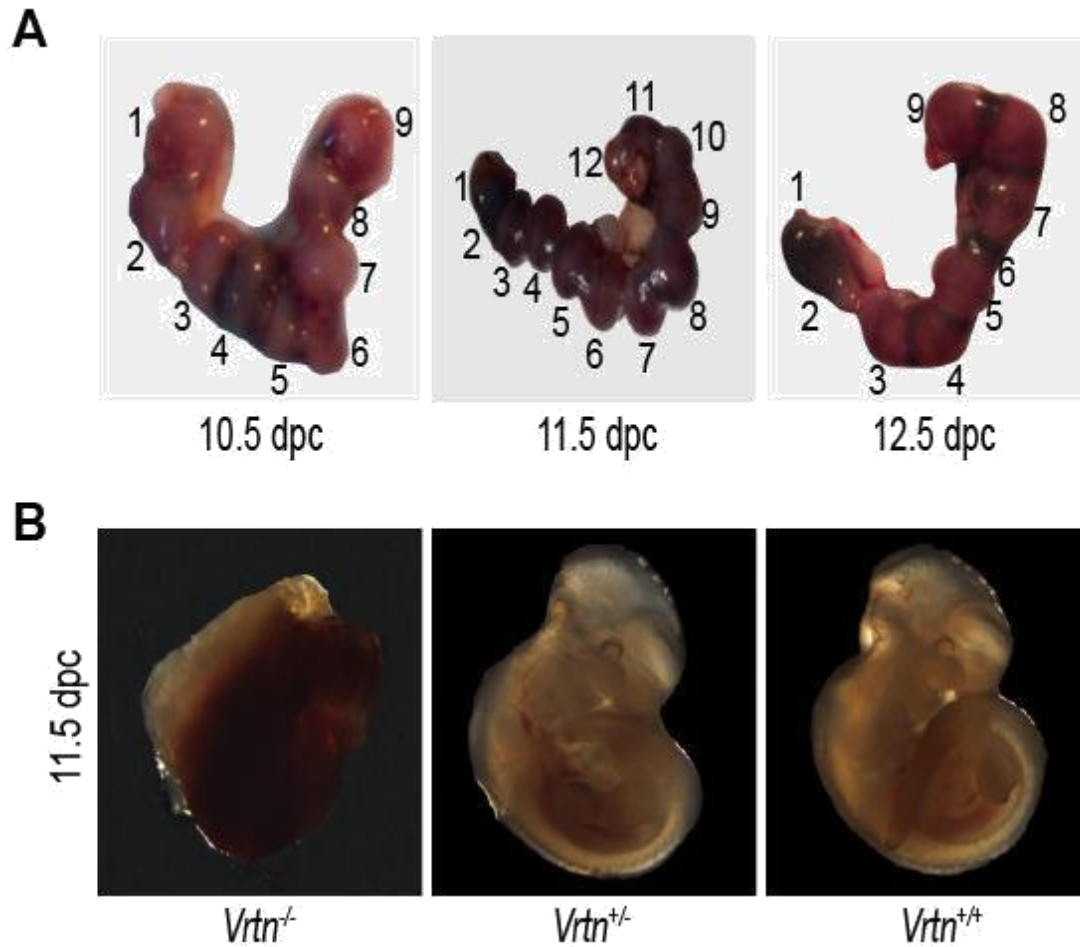


Supplementary Figure S6 *Vrtn* is expressed at the 1-28 somite stage in mice.

Temporal expression pattern of *Vrtn*. Relative mRNA levels of *Vrtn* were measured in mouse embryos at different developmental stages from 5.5 days post coitum (dpc) to 12.5 dpc using digital droplet PCR. Each sample was analyzed in triplicate, and the 18S gene was used as an internal control. Error bars correspond to the standard error of the mean computed from the triplicate measurements.



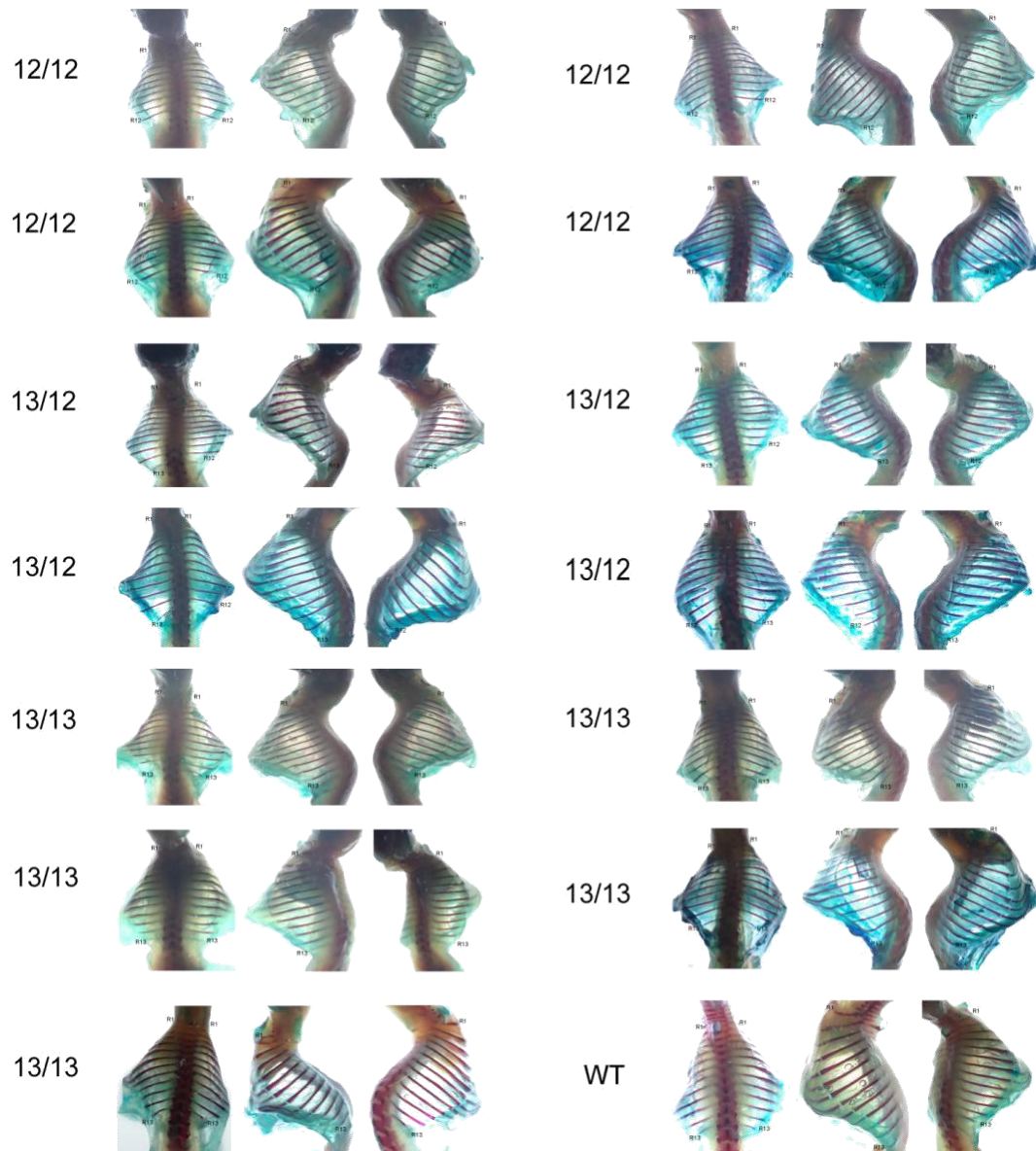
Supplementary Figure S7 Images of three embryos of *VRTN*QTN-LacZ transgenic mice at E9.5. The legend of this figure is as in Figure 2B for the left panel.



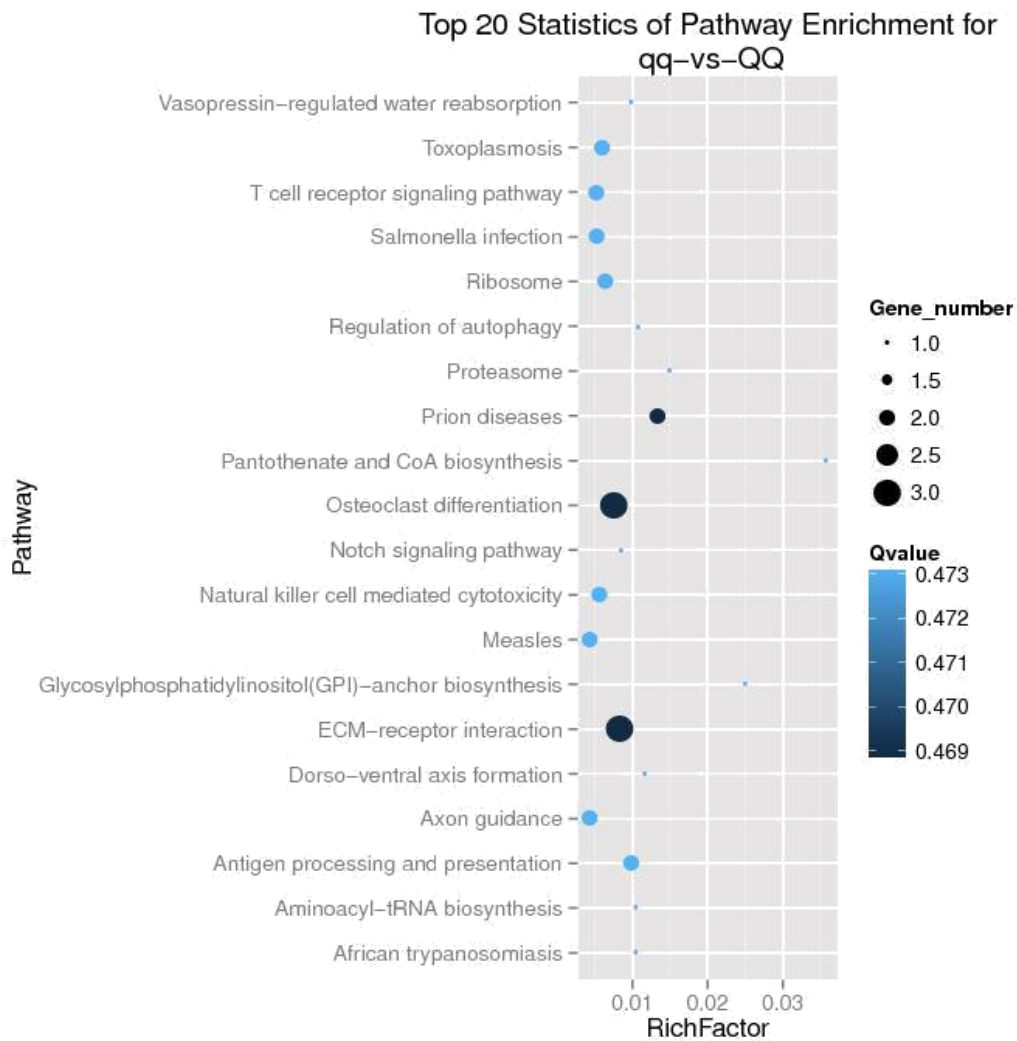
Supplementary Figure S8 *Vrtn* deficiency results in embryonic lethality in mice. (A)

Mouse uterine at 9.5, 10.5, 11.5 and 12.5 days post coitum (dpc). The embryo ball exhibits abnormal dark red at 10.5 dpc, and then display digestive atrophy at 12.5 dpc.

(B) At 11.5 dpc, *Vrtn*^{-/-} embryos are absent leaving empty yolk sac. All embryos were imaged at the same magnification (4×), and representative images are shown here.



Supplementary Figure S9 Representative images of the complete skeletons of adult *Vrtm*^{+/-} mice. 12/12, 12 thoracic vertebrae with 12 pairs of ribs; 13/12, 13 thoracic vertebrae with a rib missing from the last thoracic element on one side; 13/13, 13 thoracic vertebrae with 13 pairs of ribs. The positions of the first (R1) and last (R12 or R13) rib are labeled. WT, wild type.



Supplementary Figure S10 The scatter plot of KEGG pathways enriched for the 42 differentially expressed genes between *VRTN* mutant and wild-type pig embryos at E17.5. The y-axis indicates different KEGG pathways. The x-axis is the enrichment factor number of rich factor. The color of the circles indicates the q-value of the pathway. The range of q-values is from 0 to 1. The size of circles indicates the number of genes. The top 20 pathways are shown in this figure.

PCR primers and vectors for Plasmid construction.

No.	Primer name	Sequence (5'-3')	Amplicon (bp)	Restriction sites	Vector	Annealing Temperature(°C)
1	VRTN-cds	Synthesized by GenScript Corporation	2108	XbaI & BamHI	PUC57	
2	VRTN-cds-F1	AGATCTCGAGGGATGACATCTCGGGAGCAGCTGG	2118	XhoI	PEGFP	68/55
	VRTN-cds-R1	TTCGAAGCTTCAGCCATCGACCAGGGTGAGG		HindIII		
3	VRTN-Promotor-FP	GGAAAGCCTATGGGGATGGGGTAGAG	2663	---	pGEM-T	61.8
	VRTN-Promotor-RP	TCCCCCAGGAGGTAAGAGAAGTTCC		---		
4	291-ins	Synthesized by Sangon Biotech	519	SacI & NheI		
5	KpnI-VRTN-Promotor-FP	TTTTGGTACCAGGCACCCTGACCCCTGACAA	2191	KpnI	PGL-4.20	63
	NheI-VRTN-Promotor-RP	TTTGGCTAGCCCACCTCACCAAGACCCACC		NheI		
6	VRTN-Promotor-(A>C)-FP	ACTTTACCATTGGAAGCGCCCCCGA	1692			60
	NheI-VRTN-Promotor-RP	TTTGGCTAGCCCACCTCACCAAGACCCACC		NheI		
7	KpnI-VRTN-Promotor-FP	TTTTGGTACCAGGCACCCTGACCCCTGACAA	525	KpnI		57
	VRTN-Promotor-(A>C)-RP	TCGGGGGGCGCTTCCAATGGTAAAGT				
8	EcoRI-VRTN-cds-F	TTTTGAATTCATGACATCTCGGGAGCAGCTGG	2116	EcoRI	PNTAP-2flag	65
	HindIII-VRTN-cds-R	TTTTAAGCTTCAGCCATCGACCAGGGTGAGG		HindIII		
9	P-KpnI-hes1-FP	TTTTGGTACCTGATGTCAAACCTGCAGCTCG	1097	KpnI	PGL-4.20	62.5
	P-NheI-hes1-RP	TTTTGCTAGCGATCGGTAGCGCAATTCCAG		NheI		
10	H-KpnI-hes1-FP	TTTTGGTACCCTACGGATGAAAAGGGAAAAGGGT	847	KpnI		70/57
	H-NheI-hes1-RP	TTTTGCTAGCCCCTGGCGGCCTCTATATATA		NheI		
11	kpn1-8063-FP	TTTTGGTACCTGTGCATTGTAAAACATAAAAACTGA	194	KpnI	PGL-4.20	60
	kpn1-8063-RP	TTTTGGTACCGCAGCAGCTTCTTCAGCAAT		KpnI		
12	kpn1-13066-FP	TTTTGGTACCGGGAGGAAACTGAGTGTTGG	666	KpnI	PGL-4.20	60
	kpn1-13066-RP	TTTTGGTACCTGTCCGATTTCACTGTCTTCC		KpnI		

PCR primers for the characterization of polymorphisms in the confidence interval

No.	Mutation (chr: positiona, bp)	Primer - Sequence (5'-3')	Size (bp)	Annealing Temperature(°C)
1	c.C>T (7:103107929)	F1-AGTGTCCCCTCCATCATTGT R1-TGCACCACAAGAGAACTCCA	687	60
2	c.C>T (7:103127475)	F2-TGCTAGTCCACAATTTCCGC R2-AGCCCTTCTGATTCATGCAA	702	60
3	c.G>T (7:103148794)	F3-TGTTTGATAAAATGGCTTGGGACT R3-AGCATTGAGACAGCAAACAGA	766	60
4	c.G>A (7:103186832)	F4-GGTTTGGGTTGCTGATCTGG R4-GTCATCCTTGGCTGTGAAGT	693	60
5	c. A>G (7:103407089) c.G>A (7:103407127) c. T>C (7:103407135) c. A>C (7: 103407193) c. A>C (7: 103407222) c. A>G (7:103407263)	F5-ATGAGTCTGCCCTGAACCTC R5-AGCTCCAGAGATGGCTTTGT	974	60
6	c.G>A (7:103446430) /g.8063G>A	F6-TGTGCATTGTAAAACATAAAAACTGA R6-GCAGCAGCTTCTTCAGCAAT	173	60
7	c.C>T (7:103451433) /g.13066C>T	F7-GGGGAGGAAACTGAGTGTTGG R7-TGTCCGATTTCACTGTCTTCC	645	60
8	c.A>C(7:103457401)	F8-CATCACCCAAGGCCAGTTTC R8TCTCTCCACCTTCCAGCTTG	493	60
9	VRTN-291ins-Fp VRTN-291ins-Rp	F9-GGCAGGGAAGGTGTTTGTTA R9-GACTGGCCTCTGTCCCTTG	411/120	60

PCR primers related to construction and identification of VRTN-knockout and transgenic respectively

No.	Primer	Sequence (5'-3')	Size (bp)	Application	Annealing Temperature(°C)
1	QTN-VRTN-hsp68-LacZ-FP	CCATGAGGTTGCGGGTTC	920	Using for identifying widely reproduction of active cloning	57
	QTN-VRTN-hsp68-LacZ-RP	AATCTTCCAGCAGTTTCGCG			
2	Mouse-LacZ-FP	TTTCCATGTTGCCACTCGC	375	Amplifying QTN-VRTN-hsp68-LacZ for identifying transgenic positive mice	55
	Mouse-LacZ-RP	AACGGCTTGCCGTTTCAGCA			
3	TALEN-F	TGCACAGGCACTATTATC	52	target recognition sequence located on both sides of VRTN knockout site	57
	TALEN-R	CTCCAAGGTGATGCTGCA			
	TALEN-target	TGCAGGGCATGATCGA			
4	Mouse-TALEN-FP	GAGTCTGTACCCGGAGGAT	603	Amplifying Sequence contained Knockout site of VRTN	57
	Mouse-TALEN-RP	AGAGGACCCAGGTTTGGGA			

Primers used for genotyping of VRTN g.19034A>C and g.20311_20312ins291 Variants

No.	Primer name	Sequence (5'-3')	Size (bp)	Application	Annealing Temperature(°C)
1	VRTN-ins-Fp	GGCAGGGAAGGTGTTTGTTA	411/120	Amplifying wide-type for 411bp and mutant-type for 120bp	60
	VRTN-ins-Rp	GACTGGCCTCTGTCCCTTG			
2	VRTN-(A>C)-FP	GGGTAGAGTGGACGAGACAATAGC	79	Application with probe for VRTN g.19034A>C	60
	VRTN-(A>C)-RP	CCGAGATGAAAGAAGTGCAAATT		mutation genotyping	
3	VRTN-(A>C)-PROBE-1	CATTGGAAGTGCCC		Probe for VRTN g.19034A>C	
	VRTN-(A>C)-PROBE-2	TACCATTGGAAGTGACC		mutation genotyping	

Primers and probe used for quantitative RT-QPCR

No.	Primer name	Sequence (5'-3')	Size (bp)	notation	Annealing Temperature(°C)
1	Pig-VRTN	----	92	Ss04247759_m1- Life technology 4351372-750rxn	
2	Mouse-18S	----	115	Mm04277571_s1- Life technology 4426962-750rxn	
3	Mouse-19S	----	116	Mm04277571_s1- Life technology 4426962-751rxn	
4	Notch2-R1 Notch2-pig-P beta-actin-FP beta-actin-RP beta-actin-PROBE	AGAAGCCCTCTGGACATTTG TTGCCTACCACAATGGCACAGGAT GACAGGATGCAGAAGGAGATCAC GGAGGCGCGATGATCTTG CCCTGGCGCCCAGCACGA	68		60

Supplementary Table 2. VRTN binding sites in HEK293T cells identified using ChIP sequencing.

chr	start	end	length	summit	tags	-10*LOG10(pvalue)	fold_enrichm
chr1	569860	569973	114	66	67	891.52	120.37
chr1	2583801	2583936	136	48	15	80.63	13.81
chr1	2585064	2585212	149	46	12	54.28	9.52
chr1	2585534	2585704	171	47	18	95.16	16.03
chr1	2586281	2586477	197	101	18	87.78	14.06
chr1	2615476	2615750	275	120	22	122.82	12.77
chr1	2618913	2619015	103	44	9	50.13	10.35
chr1	2689051	2689175	125	95	9	55.73	12.77
chr1	11396770	11396898	129	70	9	53.01	8.75
chr1	15539849	15539989	141	42	9	50.01	10.59
chr1	16121683	16121852	170	54	12	50.94	7.58
chr1	16840475	16840638	164	118	14	78.78	15.55
chr1	16891927	16892065	139	94	16	55.58	7.44
chr1	16892564	16892846	283	144	27	73.7	7.23
chr1	16893409	16893554	146	80	15	52.52	6.77
chr1	16918348	16918511	164	47	14	60.85	10.08
chr1	17980255	17980428	174	104	11	58.92	10.94
chr1	21695154	21695323	170	75	10	51.98	12.77
chr1	21965146	21965256	111	35	9	60.27	10.94
chr1	27691747	27691887	141	94	9	51.21	12.77
chr1	27865069	27865211	143	96	9	50.69	9.12
chr1	28005129	28005288	160	63	12	60.06	11.57
chr1	29244540	29244691	152	64	14	52.45	6.18
chr1	30350369	30350508	140	47	11	50.59	7.27
chr1	32003853	32004011	159	97	13	57.27	9.31
chr1	36972305	36972447	143	36	9	50.69	9.12
chr1	37540229	37540364	136	89	10	58.73	12.05
chr1	43077926	43078056	131	80	9	52.12	10.42
chr1	46035826	46035954	129	45	9	50.58	9.84
chr1	51229686	51229848	163	88	11	61.83	10.94
chr1	54732314	54732501	188	108	14	50.83	7.4
chr1	57124064	57124200	137	47	12	58.18	10.71
chr1	57436982	57437117	136	84	12	51.66	6.16
chr1	59016903	59017054	152	107	13	55.27	9.62
chr1	59606680	59606823	144	47	13	55.47	9.15
chr1	65289879	65290031	153	46	12	52.03	6.98
chr1	65573882	65574041	160	62	13	52.04	8.42
chr1	68585968	68586164	197	59	18	72.24	8.13
chr1	68594400	68594549	150	41	11	51	7.86
chr1	68895809	68895956	148	103	12	52.53	7.97
chr1	72232296	72232457	162	67	11	51.06	11.34
chr1	83071017	83071151	135	95	10	50.05	9.66
chr1	85944520	85944615	96	52	9	55.41	11.11
chr1	86575517	86575645	129	81	9	50.58	11.48
chr1	86973034	86973170	137	46	11	54.63	9.11
chr1	87458566	87458721	156	84	12	50.89	8.1
chr1	87608131	87608233	103	47	10	65.46	13.79
chr1	88270573	88270709	137	60	10	50.26	9.85
chr1	90844606	90844677	72	36	9	74	10.42
chr1	91840191	91840305	115	45	9	58.91	10.94
chr1	96856487	96856620	134	45	10	50.87	8.39
chr1	99294642	99294803	162	93	11	54.09	10.64
chr1	100635921	100636047	127	80	11	53.06	8.15
chr1	101187653	101187782	130	47	11	52.29	8.19
chr1	101212487	101212657	171	59	13	53.98	8.19
chr1	101436657	101436848	192	98	14	55.51	8.29
chr1	107468909	107469030	122	54	10	53.58	9.53
chr1	117180498	117180629	132	46	9	52.46	10.59
chr1	118269930	118270068	139	73	9	51.75	10.94
chr1	120688563	120688693	131	91	9	53.07	12.46
chr1	120691031	120691141	111	67	9	56.82	10
chr1	121351896	121352033	138	61	43	252.52	18.38
chr1	121354232	121354469	238	103	69	286.02	15.84
chr1	121355646	121355807	162	122	50	218.05	14.99
chr1	121356066	121356203	138	39	48	232.77	15.88
chr1	121356859	121357011	153	117	28	79.15	10.81
chr1	121357920	121358135	216	98	93	566.45	34.5
chr1	121358412	121358601	190	93	27	71.28	10.87
chr1	121370281	121370341	61	30	14	219.47	25.53
chr1	121386256	121386345	90	45	50	696.67	91.19
chr1	121402126	121402251	126	44	9	55.43	10.94
chr1	121424976	121425065	90	45	9	65.9	16.41

chr1	121475020	121475177	158	39	34	241.38	34.01
chr1	121478607	121478796	190	56	93	631.09	38.53
chr1	121483151	121483430	280	128	119	136.11	5.2
chr1	121483522	121483596	75	37	32	51.83	3.4
chr1	121484045	121485432	1388	770	1561	3100	10.79
chr1	142537576	142537852	277	186	25	50.4	6
chr1	142537959	142538146	188	86	22	63.14	7.14
chr1	142538206	142538540	335	270	41	106.46	7.99
chr1	142538568	142539036	469	149	50	103.04	6.74
chr1	142543424	142543515	92	46	18	117.85	17.05
chr1	142584117	142584265	149	47	11	65.88	16.41
chr1	142610510	142610630	121	82	13	67.79	12
chr1	142654084	142654214	131	77	10	62.4	14.49
chr1	142806612	142806722	111	61	9	50.73	9.92
chr1	142806951	142807045	95	47	10	66.02	14.47
chr1	143537440	143537595	156	94	11	63.8	16.41
chr1	143540349	143540430	82	41	9	68.76	13.89
chr1	143543621	143543767	147	107	11	66.49	12.77
chr1	143543972	143544106	135	47	9	52.84	10.94
chr1	144528264	144528464	201	156	18	52.84	5.34
chr1	144528610	144528861	252	115	22	58.37	5.23
chr1	144826341	144826429	89	44	14	131.27	25.53
chr1	144895982	144896192	211	116	17	52.9	6.18
chr1	144982604	144982705	102	57	9	52.88	9.66
chr1	145181981	145182099	119	60	9	57.6	12.77
chr1	145200202	145200403	202	65	15	75.91	11.05
chr1	145211531	145211697	167	82	16	74.18	13.37
chr1	145247622	145247748	127	92	11	63.9	11.9
chr1	145258693	145258786	94	47	9	52.52	11.57
chr1	145290479	145290725	247	162	21	61.21	6.59
chr1	145292403	145292694	292	65	20	56.85	5.08
chr1	145395360	145395557	198	83	15	53.38	9.33
chr1	145486653	145486805	153	105	11	50.42	9.23
chr1	148241532	148241664	133	65	11	71.07	14.59
chr1	148556686	148556828	143	36	9	50.69	9.12
chr1	148676318	148676401	84	42	10	86.38	18.24
chr1	148844145	148844262	118	80	12	86.5	14.59
chr1	148846149	148846229	81	40	9	61.07	11.57
chr1	148905740	148905886	147	83	10	55.54	12.05
chr1	148928294	148928390	97	49	9	50.78	9.92
chr1	149021426	149021542	117	47	9	58.25	14.59
chr1	149034847	149035023	177	57	15	50.58	6.15
chr1	149035312	149035507	196	76	26	121.76	17.96
chr1	149204374	149204543	170	72	13	72.57	11.76
chr1	149223358	149223561	204	74	18	65.95	8.6
chr1	149658454	149658613	160	94	14	89.29	18.24
chr1	149684155	149684332	178	87	11	57.92	12.77
chr1	150208897	150209055	159	45	12	52.09	7.27
chr1	151048435	151048580	146	42	11	66.1	12.57
chr1	153643624	153643768	145	92	11	56.45	7.18
chr1	154538161	154538299	139	44	11	53.47	9
chr1	155149247	155149388	142	86	10	52.5	9.26
chr1	155989676	155989811	136	58	9	52.56	12.77
chr1	159129000	159129138	139	75	9	51.75	9.12
chr1	161162422	161162611	190	97	14	69.8	12.46
chr1	164882480	164882620	141	45	9	51.21	10.94
chr1	165613475	165613603	129	41	9	51.77	8.47
chr1	165721715	165721782	68	34	11	131.27	20.06
chr1	166178167	166178303	137	90	9	52.29	10.94
chr1	169495319	169495476	158	90	10	50.67	11.48
chr1	175201862	175201984	123	71	9	56.34	12.77
chr1	181346186	181346322	137	99	9	50.15	10.33
chr1	181922397	181922521	125	72	9	55.73	10.94
chr1	194734939	194735083	145	97	10	58.46	9.12
chr1	195114526	195114660	135	93	9	52.84	12.77
chr1	202656440	202656575	136	46	9	52.56	10.94
chr1	206718482	206718601	120	39	12	77.58	10.88
chr1	209657073	209657193	121	75	10	61.9	11.57
chr1	212050298	212050439	142	96	9	50.95	12.77
chr1	212353297	212353430	134	47	9	51.59	10.5
chr1	212740514	212740670	157	105	12	58.09	8.17
chr1	213976343	213976482	140	67	9	51.48	12.77
chr1	214698102	214698219	118	62	10	59.47	10.64
chr1	224411648	224411793	146	47	11	53.53	8.12
chr1	226102388	226102507	120	46	10	51.69	8.95
chr1	227479478	227479655	178	78	12	51.69	10.75

chr1	227538985	227539170	186	94	14	50.61	6.25
chr1	228771312	228771391	80	40	12	119.61	21.89
chr1	231262630	231262763	134	89	9	50.66	10.25
chr1	231816019	231816161	143	59	10	59.03	10.94
chr1	235247115	235247271	157	114	11	63.51	10.94
chr1	236260398	236260484	87	43	9	53.22	11.79
chr1	236260565	236260747	183	99	17	85.66	11.65
chr1	239009607	239009737	131	84	10	58.6	13.23
chr1	244114200	244114297	98	46	9	54.14	10.96
chr10	5332400	5332535	136	92	9	52.56	9.12
chr10	7030742	7030868	127	81	9	55.13	9.12
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chr10	9502745	9502907	163	90	13	79.12	16.41
chr10	11727161	11727297	137	90	11	61.15	10.57
chr10	13436110	13436260	151	103	11	60.87	11.57
chr10	17649888	17650025	138	40	9	52.01	9.12
chr10	20274518	20274644	127	92	9	55.13	10.94
chr10	38778060	38778156	97	61	21	190.85	31.09
chr10	38798217	38798374	158	89	12	71.85	16.41
chr10	38816341	38816691	351	233	29	77.77	6.18
chr10	38818089	38818601	513	329	55	208.05	12.37
chr10	38872066	38872186	121	77	11	69.83	16.15
chr10	38872627	38872712	86	43	13	105.68	18.81
chr10	38881950	38882007	58	29	15	217.64	20.7
chr10	38887041	38887127	87	43	12	108.23	21.89
chr10	39078789	39078878	90	45	13	96.07	19.07
chr10	39079394	39079524	131	88	14	86.29	14.17
chr10	39094062	39094280	219	120	13	63.73	20.06
chr10	39101970	39102041	72	36	27	384.12	38.79
chr10	39111947	39112048	102	61	11	73.28	14.67
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chr10	39121387	39121493	107	64	12	79.03	15.7
chr10	39124434	39124592	159	117	14	64.17	13.35
chr10	39125574	39125734	161	67	12	58.79	11.34
chr10	39138142	39138261	120	30	23	165.07	23.91
chr10	39139439	39139540	102	63	26	217.41	29.1
chr10	39146046	39146118	73	36	15	135.92	15.78
chr10	39149773	39149897	125	99	13	56.99	9.1
chr10	39150826	39150909	84	42	9	50.11	8.84
chr10	39151034	39151180	147	104	15	71.1	13.75
chr10	42355358	42356236	879	790	132	114.05	4.27
chr10	42356265	42356879	615	227	104	112.63	5.42
chr10	42357269	42357956	688	59	102	69.69	10.01
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chr10	42360723	42360787	65	32	34	183.44	6.39
chr10	42363321	42363620	300	66	51	66.05	6.67
chr10	42364647	42364810	164	126	59	215.22	15.37
chr10	42364969	42365254	286	208	61	118.51	9.05
chr10	42365292	42365444	153	87	36	87.42	6.94
chr10	42368985	42369526	542	422	85	149.83	8.59
chr10	42369564	42369803	240	75	35	61.6	8.55
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chr10	42379830	42379979	150	83	47	80.62	7.41
chr10	42380042	42380531	490	226	133	117.61	9.54
chr10	42384471	42384775	305	258	180	438.96	9.12
chr10	42385012	42385339	328	179	188	455.94	10.99
chr10	42385517	42385597	81	40	62	269.15	8.27
chr10	42387011	42387506	496	295	172	182.1	7.51
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chr10	42391656	42391942	287	228	88	62.51	4.04
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chr10	42398116	42398242	127	81	54	113.23	7.17
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chr10	42400116	42400525	410	237	147	308.16	10.81
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chr10	42409148	42409266	119	72	26	139.81	15.67
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chr10	42532365	42532620	256	205	57	164.48	14.86
chr10	42534703	42534861	159	38	60	322.23	24.22
chr10	42535476	42535535	60	30	26	281.91	13.51
chr10	42536285	42536365	81	40	13	66.13	8.23
chr10	42538648	42538781	134	89	13	55.1	8.45
chr10	42539026	42539251	226	165	23	90.64	10.32
chr10	42539363	42539443	81	40	13	89.31	12.2
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chr10	42597126	42597257	132	31	28	95.55	10.82
chr10	42598104	42598290	187	61	29	67.99	8.37
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chr10	42599488	42599926	439	322	104	339.91	13.94
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chr10	42614631	42614738	108	65	9	61.32	14.59
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chr10	42796902	42797044	143	78	11	53.87	12.02
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chr10	51569610	51569742	133	85	10	55.76	12.53
chr10	52664945	52665071	127	74	9	50.01	9.54
chr10	53350970	53351102	133	89	9	52.5	8.9
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chr10	104343719	104343855	137	93	11	55.46	11.94
chr10	104801167	104801280	114	67	10	58.83	10.13
chr10	111563806	111563952	147	55	10	57.9	12.77
chr10	112263939	112264078	140	65	10	51.9	10.49
chr10	112506413	112506603	191	91	13	58.28	9.99
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chr11	585479	585555	77	38	16	180.38	29.18
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chr11	30615533	30615678	146	94	10	56.16	10.42
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chr11	50689039	50689151	113	37	11	77.53	17.81
chr11	50724653	50724845	193	77	16	73.36	13.97
chr11	50725151	50725252	102	72	9	50.27	10.29
chr11	51567206	51567393	188	98	17	57.97	12.86
chr11	51568400	51568496	97	29	14	60.68	9.88
chr11	51568914	51569071	158	34	25	110.42	14.63

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chr11	51582958	51583010	53	26	12	140.67	10.46
chr11	51591255	51591368	114	69	13	98.61	18.24
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chr11	134721799	134721937	139	104	9	51.75	10.94
chr12	95433	95497	65	32	12	155.36	21.89
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chr12	14158160	14158285	126	47	9	54.21	10.59
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chr12	33234892	33235023	132	86	10	57.97	14.76
chr12	34837594	34837758	165	64	25	136.52	19.11
chr12	34841405	34841601	197	158	25	122.97	14.88
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chr12	38008591	38008764	174	46	22	161.57	33.83
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chr14	74823688	74824263	576	389	241	1188.92	25.82
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chr14	74824646	74824864	219	96	110	623.06	28.15
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chr15	100375420	100375539	120	40	9	57.28	10.94
chr15	101836398	101836535	138	53	10	56.14	11.48
chr15	102181499	102181676	178	56	14	53.87	9.57
chr15	102311335	102311478	144	45	10	54.09	8.14
chr16	134835	134952	118	74	9	57.92	10.94
chr16	544780	544891	112	42	14	110.31	23.71
chr16	1075317	1075498	182	67	17	109.38	18.24
chr16	1075554	1075690	137	89	10	60.81	12.77
chr16	1970966	1971101	136	88	9	50.11	8.54
chr16	2206514	2206646	133	86	9	53.39	12.77
chr16	2732440	2732582	143	103	10	59.03	12.77
chr16	15104212	15104314	103	46	9	55.63	11.99
chr16	17329017	17329147	131	44	9	53.96	10.94
chr16	23445707	23445845	139	47	10	60.21	10.94
chr16	27641876	27642008	133	88	9	53.39	10.94
chr16	29945185	29945344	160	114	12	53.15	7.49
chr16	29977458	29977610	153	106	11	52.36	9.66
chr16	31057425	31057572	148	64	10	52.05	7.95
chr16	32851476	32851586	111	70	9	60.27	12.77
chr16	33376593	33376715	123	42	10	65.33	16.41
chr16	33547552	33547670	119	58	9	57.6	12.77
chr16	33865179	33865365	187	78	18	100.18	14.47
chr16	33866365	33866564	200	71	16	75.43	9.53
chr16	33873979	33874149	171	111	26	193.53	36.03
chr16	33881663	33881829	167	93	19	93.61	16.84
chr16	33887624	33887770	147	60	31	222.54	26.18
chr16	33896580	33896678	99	57	20	131.45	17.21
chr16	33899847	33899968	122	46	22	127.16	17.01
chr16	33901657	33901811	155	44	13	52.61	8.25
chr16	33919299	33919430	132	44	14	73.8	12.59
chr16	33940464	33940562	99	52	9	64.7	14.59
chr16	33957541	33957656	116	69	10	63.34	13.12
chr16	33973499	33973906	408	249	99	227.34	13.42
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chr16	33983685	33983887	203	74	21	58.09	7.12
chr16	33984460	33984738	279	168	25	61.18	5.57
chr16	34002125	34002249	125	34	23	169.33	27.28
chr16	34185053	34185234	182	66	21	100.54	19.4
chr16	35215965	35216114	150	31	12	74.42	20.06
chr16	35225858	35226006	149	105	11	50.49	9
chr16	35229064	35229139	76	38	10	77.73	12.48
chr16	35229203	35229291	89	44	27	269.47	33.68
chr16	35235002	35235107	106	64	9	56.5	11.05
chr16	35239659	35239792	134	37	19	153.2	32.83
chr16	35260287	35260435	149	103	11	65.88	18.24
chr16	46385804	46386060	257	209	113	227.66	6.22
chr16	46386117	46386405	289	85	178	530.9	6.29
chr16	46386474	46386858	385	336	278	886.09	7.56
chr16	46387383	46387452	70	35	42	132.73	4.68
chr16	46388343	46388644	302	79	165	244.25	5.06
chr16	46388782	46389300	519	342	280	379.7	4.49
chr16	46390105	46390218	114	46	60	71.5	3.85
chr16	46391257	46391351	95	47	86	233.28	7.38
chr16	46391722	46392083	362	314	198	273.62	7.2
chr16	46392187	46392285	99	48	61	116.79	5.45
chr16	46392594	46392785	192	62	105	162.33	4.61
chr16	46392979	46393118	140	92	86	168.37	4.5
chr16	46393180	46393318	139	91	105	272.2	8.52
chr16	46394172	46394504	333	285	206	519.37	8.36
chr16	46395378	46395596	219	60	156	482.03	11.43
chr16	46396410	46396618	209	161	82	135.08	5.62
chr16	46396665	46396881	217	66	81	117.96	8.17
chr16	46400007	46400191	185	35	63	112.88	7.67
chr16	46401187	46401405	219	171	68	111.65	6.83
chr16	46401794	46401886	93	46	68	325.56	12.3
chr16	46402947	46403057	111	65	37	64.52	5.15
chr16	46403335	46403455	121	72	82	310.81	12.42
chr16	46403641	46403945	305	56	222	855.45	13.63
chr16	46404851	46405069	219	123	126	400.51	12.37
chr16	46405117	46405207	91	45	62	262.08	10.15
chr16	46406527	46406671	145	47	93	365.75	12.48
chr16	46406914	46407005	92	46	72	382.07	13.74

chr16	46407298	46407431	134	86	38	67.79	6.53
chr16	46407670	46407853	184	46	86	274.14	16.13
chr16	46408573	46408692	120	85	39	97.46	7.88
chr16	46410683	46410777	95	47	23	79.99	8.05
chr16	46411438	46411509	72	36	15	64.49	5.47
chr16	46411987	46412070	84	42	19	85.2	8.42
chr16	46413293	46413373	81	40	27	155.8	10.46
chr16	46416830	46417333	504	438	246	1323.81	20.07
chr16	46418300	46418421	122	82	21	53.65	7.28
chr16	46419462	46419572	111	50	24	74.51	6.31
chr16	46419783	46419907	125	47	35	127.8	7.37
chr16	46420015	46420103	89	44	22	75.42	7.28
chr16	46420233	46420372	140	106	37	125.51	11.94
chr16	46423908	46423992	85	42	24	69.4	5.61
chr16	46425330	46425586	257	174	51	66.85	6.9
chr16	46425688	46425840	153	39	32	52.4	4.23
chr16	46426177	46426369	193	145	90	357.8	15.05
chr16	46426943	46427132	190	48	69	212.31	7.46
chr16	46427313	46427774	462	77	225	880.04	9.08
chr16	46427806	46428164	359	258	96	172.44	5.78
chr16	46428982	46429213	232	117	62	113.13	9.7
chr16	46431404	46431512	109	58	33	91.01	6.15
chr16	46432710	46432787	78	39	60	525.53	20.03
chr16	46433647	46433739	93	46	24	96.27	9.42
chr16	46434296	46434524	229	111	27	50.51	10.62
chr16	46435471	46435576	106	44	73	615.78	35.89
chr16	46442780	46442892	113	52	11	53.09	9.33
chr16	46499848	46500177	330	75	42	179.24	22.52
chr16	57333163	57333306	144	90	10	52.85	7.89
chr16	60683539	60683651	113	65	9	59.58	12.77
chr16	64891560	64891718	159	96	10	54.41	12.68
chr16	78788647	78788792	146	63	10	57.9	10.87
chr16	87144965	87145098	134	92	10	55.77	9.47
chr16	87609727	87609869	143	84	9	50.69	12.77
chr17	413592	413714	123	61	9	56.34	10.94
chr17	2878739	2878848	110	43	9	56.86	9.92
chr17	4042775	4042906	132	85	9	50.32	10
chr17	4812912	4813048	137	66	9	52.29	10.94
chr17	8649341	8649477	137	38	9	52.29	9.12
chr17	8677319	8677458	140	47	9	51.48	12.77
chr17	17974505	17974635	131	52	9	53.07	12.46
chr17	21563795	21563934	140	44	10	53.38	7.77
chr17	22020644	22020813	170	83	13	76.89	20.06
chr17	22249717	22249779	63	31	24	312.78	21.65
chr17	22251412	22251506	95	47	12	62.28	10.92
chr17	22251551	22251661	111	78	15	79.24	12.85
chr17	22252042	22252115	74	37	9	55.27	8.33
chr17	22252166	22252243	78	39	26	268.11	24.07
chr17	22252730	22252859	130	82	33	244.08	29.9
chr17	22253169	22253264	96	47	69	781.2	64.1
chr17	22258330	22258478	149	38	29	176.64	23.25
chr17	22258554	22258605	52	26	9	95.22	8.05
chr17	22260032	22260121	90	45	34	315.43	31.2
chr17	22261161	22261264	104	29	11	53.17	9.56
chr17	22261469	22261643	175	125	105	1102.66	77.76
chr17	25263759	25264020	262	115	36	123.11	14.74
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chr17	25265085	25265296	212	78	22	57.44	9.3
chr17	25266306	25266601	296	173	37	106.77	10.27
chr17	25266891	25267069	179	117	32	131.4	15.3
chr17	25267761	25267995	235	46	28	73.62	7.9
chr17	25297541	25297710	170	127	15	58.75	7.86
chr17	38376050	38376191	142	96	9	50.95	10.94
chr17	38743708	38743814	107	45	9	59.15	13.66
chr17	39473177	39473312	136	41	10	56.42	8.14
chr17	41381680	41382389	710	55	120	660.01	17.11
chr17	41399851	41400243	393	102	47	98.4	6.04
chr17	41400249	41401237	989	602	249	1056.44	14.35
chr17	41466044	41466397	354	136	49	264.59	24.77
chr17	46853361	46853497	137	93	9	52.29	10.94
chr17	47062818	47062941	124	39	9	56.04	10.94
chr17	47368127	47368309	183	93	13	57.44	9.41
chr17	51350815	51350936	122	64	9	52.37	11.39
chr17	55208411	55208535	125	46	9	55.73	14.59
chr17	57082095	57082243	149	47	12	58.74	10.48
chr17	57244835	57244971	137	97	9	52.29	10.94

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chr17	57388496	57388641	146	44	12	67.54	9.26
chr17	60376944	60377090	147	70	10	51.41	10.88
chr17	60592510	60592652	143	65	9	50.69	9.12
chr17	61580601	61580758	158	94	11	56.15	9.33
chr17	63227525	63227654	130	69	11	57.75	10.62
chr17	65268706	65268843	138	91	10	56.79	11.67
chr17	67429555	67429677	123	46	10	52.47	9.35
chr17	69609991	69610171	181	107	12	52.42	11.11
chr17	72426468	72426670	203	92	16	69.93	8.84
chr17	73723249	73723381	133	77	10	62.05	10.94
chr17	77852746	77852864	119	72	9	50.76	10.64
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chr17	78090272	78090411	140	93	10	55.55	9.84
chr17	78434325	78434451	127	80	10	52.22	10.96
chr17	79242666	79242796	131	83	9	51.5	10.25
chr17	80317459	80317643	185	31	19	80.97	8.8
chr17	80317676	80317838	163	63	30	185.59	14.6
chr18	109412	109541	130	89	13	91.36	21.89
chr18	110568	110655	88	44	11	97.14	20.06
chr18	15179169	15179287	119	78	9	57.6	10.94
chr18	18510982	18511867	886	131	124	242.84	9.19
chr18	18511898	18512496	599	393	112	179.77	14.39
chr18	18512807	18512983	177	67	43	99.98	9.81
chr18	18516088	18516220	133	76	56	137.08	8.64
chr18	18516504	18516662	159	83	60	134.75	9.77
chr18	18517070	18517437	368	112	129	264.04	16.41
chr18	18518083	18518179	97	48	85	495.18	17.21
chr18	18518839	18519267	429	147	120	222.73	10.34
chr18	18519665	18520339	675	633	228	586.64	15.61
chr18	20143126	20143290	165	119	12	52.3	7.58
chr18	28197345	28197515	171	77	13	52.37	9.06
chr18	31513066	31513204	139	95	10	51.62	10.34
chr18	34302004	34302138	135	56	9	52.84	10.94
chr18	35056055	35056195	141	83	9	51.21	12.77
chr18	35876269	35876386	118	74	9	51.35	9.19
chr18	36806935	36807060	126	44	9	53.58	10.42
chr18	50319088	50319276	189	97	32	268.18	41.95
chr18	68332491	68332629	139	97	9	51.75	12.77
chr19	7515816	7516024	209	108	18	98.46	15.78
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chr19	15737308	15737428	121	38	10	62.91	11.86
chr19	27731877	27732475	599	371	342	1108.96	13.89
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chr19	27734710	27734796	87	43	43	107.37	5.63
chr19	27735295	27735443	149	60	54	72.3	5.63
chr19	27736194	27736681	488	290	123	52.18	4.17
chr19	27736696	27736856	161	47	80	167.62	8.84
chr19	27738373	27738750	378	116	103	192.2	11.01
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chr19	27906232	27906384	153	38	13	82.51	21.89
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chr19	42942734	42942868	135	47	10	59.04	10.33
chr19	42978142	42978282	141	43	9	50.33	8.9
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chr19	44712028	44712165	138	67	9	52.01	9.12
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chr19	56181766	56181933	168	98	17	114.98	20.06
chr19_gl000208_rand2	566	565	48	48	182	1138.23	24.09
chr19_gl000208_rand72805	72922	118	74	74	10	61.97	14.53
chr19_gl000208_rand75862	76038	177	100	19	19	118.63	26.43
chr19_gl000208_rand88641	88734	94	47	22	22	125.32	14.41
chr19_gl000208_rand89734	89819	86	43	43	43	404.58	28.35
chr19_gl000208_rand90075	90170	96	47	16	16	75.96	9.89
chr19_gl000208_rand90532	90708	177	61	90	90	756.91	32.68
chr19_gl000208_rand91433	91542	110	39	31	31	191.87	20.76
chr19_gl000208_rand91579	91693	115	43	21	21	106.2	13.84
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chr2	24527637	24527898	262	42	19	78.85	6.72
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chr2	36683255	36683388	134	73	9	51.9	10.59
chr2	42722130	42722256	127	89	9	54.23	10.68
chr2	59524536	59524713	178	80	12	58.42	10.88
chr2	61226116	61226256	141	46	10	52.2	9.12
chr2	62017862	62017989	128	38	9	50.01	9.62
chr2	63650506	63650654	149	56	10	55.33	12.15
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chr2	89867330	89867610	281	139	63	163.98	13.95
chr2	89867918	89868380	463	124	96	199.23	15.49
chr2	89869679	89870139	461	230	63	51.8	5.33
chr2	89872006	89872243	238	106	47	76.65	9.85
chr2	89875187	89875418	232	131	70	229.55	18.18
chr2	89878428	89878592	165	75	37	131.93	11.09
chr2	89879053	89879405	353	82	69	206.25	10.54
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chr2	90371807	90371910	104	47	14	114.77	23.71
chr2	90372314	90372393	80	40	11	108.23	20.06
chr2	90372768	90372926	159	34	29	241.92	27.36
chr2	90373354	90373421	68	34	15	206.24	27.36
chr2	90376706	90376758	53	26	9	143.19	16.41
chr2	90381346	90381432	87	43	21	232.88	38.3
chr2	91599375	91599468	94	47	28	302.45	51.07
chr2	91782287	91782664	378	290	36	50.48	4.79
chr2	91855252	91855371	120	44	9	57.28	12.77
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chr2	92268771	92269280	510	397	58	157.56	14.7
chr2	92269293	92269616	324	213	70	337.61	21.09
chr2	92276624	92276828	205	89	32	161.73	24.31
chr2	92281222	92281456	235	118	71	569.73	51.31
chr2	92281481	92281574	94	47	15	95.39	15.55
chr2	92290163	92290304	142	47	19	82.39	9.96
chr2	92290497	92290644	148	47	60	482.58	43.94
chr2	92290855	92291030	176	103	28	130.36	17.3
chr2	92291097	92291210	114	39	19	96.73	13.49
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chr2	92296385	92297177	793	490	138	518.69	27.04

chr2	92305647	92305838	192	46	73	476.29	20.33
chr2	92306064	92306246	183	47	32	131.49	18.06
chr2	92307478	92307650	173	84	27	104.23	12.91
chr2	92308035	92308175	141	32	34	178.29	19.64
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chr2	92309454	92309853	400	169	47	127.2	11.23
chr2	92312683	92312742	60	30	11	79.72	6.82
chr2	92315391	92315467	77	38	25	147.28	9.65
chr2	92315894	92316364	471	356	98	215.91	16.76
chr2	92317713	92317838	126	90	39	127.61	7.43
chr2	92318549	92318774	226	147	91	327.81	16.2
chr2	92319090	92319290	201	47	75	250.6	12.82
chr2	92320095	92320248	154	48	91	421.09	19.84
chr2	92320387	92320463	77	38	48	293.16	11.06
chr2	92320757	92320879	123	74	46	150.32	8.1
chr2	92320973	92321190	218	122	44	63.95	9.43
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chr2	92323353	92323475	123	89	26	63.39	7.41
chr2	92323548	92323623	76	38	41	278	12.24
chr2	92324175	92324296	122	48	40	183.05	11.62
chr2	92324678	92324877	200	84	35	91.18	9.43
chr2	97294579	97294744	166	93	12	61.72	12.44
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chr2	99082107	99082244	138	77	9	52.01	9.12
chr2	105126652	105126816	165	80	10	53.19	9.12
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chr2	109815907	109815974	68	34	11	122.9	17.63
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chr2	117384375	117384514	140	47	9	51.48	9.12
chr2	120867589	120867723	135	93	9	50.09	10.16
chr2	121494636	121494774	139	59	10	53.97	10.96
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chr2	128821238	128821364	127	44	9	55.13	10.94
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chr2	132996733	132996884	152	114	16	93.98	19.44
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chr2	133009420	133009548	129	71	14	62.79	8.22
chr2	133020769	133020873	105	58	10	62.54	10.2
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chr2	146796551	146796702	152	58	10	51.6	9.69
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chr2	151411134	151411264	131	55	9	50.9	10.08
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chr2	162135163	162135342	180	52	18	64.43	11.53
chr2	162135483	162135678	196	65	27	114.47	10
chr2	162135825	162135970	146	107	17	70.78	7.38
chr2	162136044	162136227	184	35	21	82.21	8.99
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chr2	180872294	180872427	134	52	9	52.54	12.57
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chr2	189183271	189183375	105	41	10	60.27	11.04
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chr20	17539443	17539593	151	103	10	52.17	14.65
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chr20	26313480	26313630	151	111	16	64.01	10.2
chr20	26318370	26318598	229	119	50	362.38	34.15
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chr20	29593400	29593488	89	44	10	52.64	10.47
chr20	29651901	29652182	282	183	23	75.59	6.81
chr20	29653466	29653614	149	69	12	51	6.65
chr20	29811854	29812032	179	107	22	119.67	22.89
chr20	29817745	29817906	162	58	22	122.79	20.4
chr20	29818340	29818481	142	96	15	70.8	13.21
chr20	29822908	29823106	199	102	17	71.24	14.64
chr20	29829314	29829429	116	69	13	72.2	13.66
chr20	29832052	29832174	123	76	19	128.88	20.96
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chr21	10084950	10085153	204	117	19	119.99	18.24
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chr21	10714698	10715666	969	555	121	53.16	3.57
chr21	10760633	10761015	383	175	45	69.5	4.62
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chr21	10807060	10807263	204	100	25	74.75	8.43
chr21	10819283	10819428	146	109	17	53.43	8.63
chr21	10819538	10819626	89	44	43	368.79	26.66
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chr21	11093021	11093503	483	177	44	79.63	6.55
chr21	11095760	11096160	401	152	33	70.22	5.43
chr21	11174868	11174979	112	64	10	59.85	10.2
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chr21	14368321	14368382	62	31	10	107.32	12.55
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chr4	49100546	49100686	141	83	35	172.39	13.89
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chr4	49633925	49634041	117	81	17	98.19	15.95
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chr4	144926515	144926656	142	42	9	50.95	9.12
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chr4_gl000193_rando89898	89987	90	45	17	17	167.76	31
chr4_gl000194_rando183293	183444	152	115	11	11	64.97	14.59
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chr5	415651	415776	126	44	13	82.4	17.99
chr5	7593085	7593225	141	98	9	51.21	10.94
chr5	11357677	11357817	141	46	9	51.21	9.12

chr5	13091736	13091878	143	40	9	50.69	9.12
chr5	17503801	17503942	142	107	9	50.95	9.12
chr5	17526809	17526899	91	45	14	119.61	25.53
chr5	23129666	23129807	142	60	9	50.95	9.12
chr5	29365440	29365552	113	47	9	59.58	14.59
chr5	34179717	34179848	132	41	11	71.42	16.41
chr5	34185786	34186055	270	42	19	85.25	9.98
chr5	34193618	34193803	186	131	17	90.64	14.17
chr5	34193970	34194083	114	70	11	66.58	8.5
chr5	36079339	36079452	114	44	9	53.19	12.44
chr5	40232387	40232529	143	60	9	50.69	10.94
chr5	40678914	40679096	183	114	13	69.57	10.25
chr5	44545520	44545688	169	61	12	57.48	8.68
chr5	46323092	46323206	115	41	10	61.15	13.89
chr5	46339515	46339678	164	88	16	106.82	25.53
chr5	46380263	46380324	62	31	9	104.07	15.24
chr5	46392826	46392971	146	34	11	64.57	12.15
chr5	49405730	49405956	227	179	49	448.96	47.42
chr5	49414407	49414482	76	38	13	143.19	23.71
chr5	49431750	49431856	107	61	23	222.1	40.12
chr5	49435145	49435220	76	38	12	123.4	19.38
chr5	49439825	49439956	132	44	10	57.01	14.42
chr5	49440058	49440228	171	39	38	335.97	58.84
chr5	49471576	49471700	125	97	11	68.34	12.92
chr5	49484778	49484973	196	101	13	62.8	17.63
chr5	55076910	55077048	139	94	10	55.21	12.92
chr5	55082930	55083073	144	44	10	58.75	9.12
chr5	68338691	68338844	154	46	11	57.93	7.89
chr5	72569309	72569443	135	60	10	61.42	10.94
chr5	75563345	75563485	141	59	9	50.97	9.06
chr5	81102932	81103064	133	35	9	50.04	8.33
chr5	83584909	83585056	148	89	10	53.3	9.84
chr5	84957435	84957574	140	101	11	68.71	18.24
chr5	90397791	90397947	157	93	10	53.2	10.42
chr5	91171172	91171301	130	47	10	63	12.77
chr5	93377061	93377224	164	68	11	53.25	10.57
chr5	94680270	94680412	143	108	10	59.03	10.94
chr5	95717200	95717347	148	90	11	53.22	8.17
chr5	102017236	102017379	144	96	10	58.75	9.12
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chr5	117727496	117727656	161	75	10	54.18	10.94
chr5	118219977	118220116	140	41	9	50.91	8.98
chr5	119901948	119902077	130	93	9	53.67	10.78
chr5	122256548	122256672	125	80	9	52.65	10.08
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chr5	134260181	134260302	122	83	35	313.04	42.42
chr5	134262720	134262822	103	28	11	62.27	11.64
chr5	137879572	137879722	151	74	10	52.17	9.77
chr5	138758023	138758156	134	91	9	53.11	10.94
chr5	141486251	141486400	150	59	10	50.31	9.26
chr5	152711883	152712004	122	82	9	56.65	10.94
chr5	154320822	154320953	132	90	9	50.62	11.76
chr5	158931536	158931724	189	97	14	78.43	12.46
chr5	161687840	161687964	125	43	9	55.73	10.94
chr5	163007565	163007702	138	95	9	52.01	10.94
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chr5	163915225	163915360	136	94	10	56.42	13.02
chr5	166712508	166712624	117	37	9	53.93	8.14
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chr5	169742397	169742515	119	47	10	54.32	9.47
chr5	171349222	171349362	141	94	10	52.79	10.8
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chr6	14560688	14560826	139	106	9	51.75	9.12
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chr6	19780027	19780163	137	95	9	50.15	8.61
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chr6	23898171	23898298	128	83	9	52.06	11.86
chr6	24730115	24730287	173	76	11	59.18	14.59
chr6	26745693	26745832	140	86	9	51.48	12.77

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chr6	41207473	41207612	140	64	11	66.47	12.15
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chr6	55502024	55502198	175	124	14	74.32	10.72
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chr6	74574762	74574912	151	66	10	50.34	9.33
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chr6	111137260	111137492	233	112	18	72.75	9.69
chr6	112538055	112538320	266	33	18	61.91	4.87
chr6	114752386	114752522	137	43	10	58.43	10.33
chr6	115215819	115215959	141	81	10	51.33	8.93
chr6	116708074	116708181	108	61	10	51.94	10.42
chr6	127431319	127431486	168	85	12	52.31	9
chr6	132138248	132138389	142	95	13	54.74	6.91
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chr6	136911022	136911159	138	96	10	51.62	10.27
chr6	137346542	137346666	125	42	10	56.5	10.49
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chr6	145159510	145159655	146	102	10	51.09	13.79
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chr6	147021260	147021423	164	68	12	54.28	9.17
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chr6	150039687	150039848	162	91	13	62.57	9.23
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chr6	153439054	153439161	108	69	9	53.04	10.27
chr6	155329145	155329240	96	47	9	57.76	11.82
chr6	157731827	157731920	94	47	12	61.05	10.64
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chr6	160341888	160342029	142	69	11	53.62	7.91
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chr6	163579165	163579305	141	38	10	52.49	9.19
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chr7	33747081	33747232	152	45	10	50.38	9.4
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chr7	45541377	45541533	157	72	10	51.88	13.44
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chr7	57995778	57995872	95	47	11	51.77	9.39
chr7	61055536	61055681	146	54	15	104.46	20.06
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chr7	61099394	61099484	91	45	12	82.47	16.45
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chr7	61739344	61739553	210	98	17	88.72	15.55
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chr7	61794547	61794698	152	57	26	151.39	22.42
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chr7	61815086	61815211	126	39	9	55.43	10.94
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chr7	61968665	61968832	168	120	53	90.31	7.24
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chr7	62000731	62000785	55	27	10	150.52	17.08
chr7	62019276	62019345	70	35	10	93.05	13.89
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chr7	105161512	105161638	127	81	9	55.13	10.94
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chr7	151981096	151981249	154	87	13	53.89	9.47
chr7	151983429	151983573	145	50	15	72.78	11.81
chr7	151997248	151997367	120	58	9	55.73	8.75
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chr7	157940197	157940501	305	45	43	271.94	24.83
chr7	157941698	157941874	177	93	17	91.72	12.34
chr7	157944038	157944195	158	118	14	68.65	12.48
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chr8	43092760	43093026	267	156	55	294.17	30.19

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chr8	43819022	43819238	217	124	17	97.26	14.59
chr8	43822418	43822565	148	29	24	198.65	38.84
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chr8	124536048	124536164	117	70	9	58.25	14.59
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chr8	142955635	142955773	139	40	10	60.21	10.94
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chr9	66512016	66512129	114	71	9	59.24	12.77
chr9	66833059	66833382	324	118	47	268.13	34.72
chr9	66833789	66834016	228	47	20	83.22	10.14
chr9	66835057	66835221	165	37	22	118.13	15.55
chr9	66843764	66843973	210	101	18	72	11.87
chr9	67320779	67320904	126	96	16	124.51	16.41
chr9	68394430	68394572	143	45	10	52.52	10.88
chr9	68398056	68398177	122	77	14	89.22	16.67

chr9	68401664	68401824	161	115	12	50.74	10.71
chr9	68403312	68403405	94	47	11	67.52	13.4
chr9	68414187	68414621	435	344	48	54.17	4.96
chr9	68415236	68415437	202	46	32	59.86	5.06
chr9	68415463	68415936	474	73	71	98.59	4.84
chr9	68419414	68421612	2199	1258	264	83.41	4.03
chr9	68425009	68426025	1017	506	120	134.15	4.16
chr9	72419274	72419406	133	88	9	52.18	12.36
chr9	72653058	72653439	382	72	66	424.4	28.9
chr9	77788982	77789107	126	46	9	55.43	14.59
chr9	78790043	78790245	203	118	42	323.77	50.11
chr9	78867646	78867791	146	101	10	58.18	12.77
chr9	81916074	81916348	275	87	21	61.91	5.56
chr9	87857108	87857235	128	46	10	56.12	10.64
chr9	90354061	90354194	134	60	9	53.11	10.94
chr9	93609638	93609766	129	98	9	54.54	9.12
chr9	94228727	94228866	140	43	9	51.48	9.12
chr9	94273175	94273304	130	87	9	51.48	8.47
chr9	101897730	101897873	144	98	11	63.35	11.67
chr9	103174070	103174211	142	53	10	55.95	10.08
chr9	106491054	106491200	147	49	11	56.77	8.8
chr9	107755128	107755262	135	30	9	52.84	9.12
chr9	110184642	110184771	130	82	9	54.25	10.94
chr9	112828436	112828536	101	54	9	63.92	14.59
chr9	127629689	127629829	141	96	9	51.21	12.77
chr9	128525583	128525777	195	122	15	53.93	8.25
chr9	128863126	128863258	133	88	9	53.39	12.77
chr9	130640621	130640755	135	92	11	68.89	12.36
chr9	134037608	134037757	150	60	10	55.05	12.15
chr9	138797731	138797864	134	88	9	51.59	10.5
chr9	138844411	138844540	130	45	9	54.25	12.77
chr9	140222412	140222597	186	44	26	139.81	17.83
chr9	140222626	140222916	291	251	40	214.16	16.45
chr9_gl000198_rando7	120	114	46	11	11	78.24	14.59
chr9_gl000198_rando139	362	224	79	18	18	103.85	10.94
chr9_gl000198_rando1818	1944	127	90	9	9	55.13	10.94
chr9_gl000198_rando1976	2145	170	40	14	14	85.81	12.77
chr9_gl000198_rando56112	56404	293	129	55	55	287.15	27.24
chr9_gl000199_rando34413	34508	96	48	93	93	1212.44	97.22
chr9_gl000199_rando34636	34711	76	38	24	24	264.57	26.04
chr9_gl000199_rando34798	35041	244	198	21	21	83.93	12.19
chr9_gl000199_rando40972	41032	61	30	14	14	219.47	25.53
chr9_gl000199_rando44259	44327	69	34	42	42	770.08	72.92
chr9_gl000199_rando47327	47417	91	45	35	35	356.89	42.15
chr9_gl000199_rando50844	50921	78	39	18	18	213.99	30.99
chr9_gl000199_rando51335	51440	106	37	33	33	354.54	53.82
chr9_gl000199_rando57114	57334	221	48	147	147	1764.44	92.87
chr9_gl000199_rando68638	68723	86	43	74	74	1217.41	134.96
chr9_gl000199_rando72927	73007	81	40	20	20	199.59	26.04
chr9_gl000199_rando73745	73805	61	30	25	25	467.74	45.59
chr9_gl000199_rando88141	88215	75	37	9	9	84.03	15.62
chr9_gl000199_rando91069	91150	82	41	18	18	202.53	31.51
chr9_gl000199_rando92704	92798	95	47	44	44	539.61	77.03
chr9_gl000199_rando93392	93480	89	44	21	21	217.19	37.39
chr9_gl000199_rando98841	99027	187	124	44	44	421.51	76.6
chr9_gl000199_rando103854	103945	92	46	9	9	65.9	16.41
chr9_gl000199_rando109777	109886	110	26	11	11	79.92	16.41
chr9_gl000199_rando110445	110507	63	31	26	26	467.74	47.42
chr9_gl000199_rando111540	111621	82	41	31	31	421.2	56.54
chr9_gl000199_rando113978	114102	125	94	17	17	135.6	27.17
chr9_gl000199_rando120777	120858	82	41	22	22	260.22	40.12
chr9_gl000199_rando125150	125219	70	35	10	10	108.23	18.24
chr9_gl000199_rando136904	136996	93	46	25	25	260.22	45.59
chr9_gl000199_rando138084	138139	56	28	18	18	331.34	32.83
chr9_gl000199_rando155659	155721	63	31	32	32	612.88	58.36
chr9_gl000199_rando159943	160082	140	98	13	13	65.38	13.25
chr9_gl000199_rando162375	162503	129	43	16	16	94.62	14.29
chr9_gl000199_rando165756	165872	117	31	30	30	223.29	30.21
chr9_gl000199_rando168210	168374	165	42	55	55	531.05	44.35
chr9_gl000199_rando169011	169181	171	90	12	12	56.29	8.56
chrM	1	1067	1067	815	1028	1084.44	3.07
chrM	1238	4152	2915	2117	2617	875.36	2.43
chrM	6174	6736	563	90	519	63.51	1.75
chrUn_gl000212	40762	40977	216	93	27	195.34	40.12
chrUn_gl000214	64294	64507	214	129	54	370.36	42.61
chrUn_gl000214	64891	65063	173	47	21	100.77	14.6

chrUn_gI000214	119392	119469	78	39	13	143.19	23.71
chrUn_gI000214	125347	125439	93	46	16	143.19	29.18
chrUn_gI000214	128990	129082	93	46	17	155.36	31
chrUn_gI000214	131670	131809	140	93	20	158.14	28.25
chrUn_gI000214	133646	133762	117	75	18	152.42	29.18
chrUn_gI000214	134470	134565	96	52	26	274.14	43.77
chrUn_gI000216	1312	1562	251	54	50	224.95	21.64
chrUn_gI000216	1762	1957	196	75	41	185.8	22.7
chrUn_gI000216	2385	2547	163	41	21	59.14	8.97
chrUn_gI000216	4922	5140	219	134	32	74.06	9.33
chrUn_gI000216	5942	6113	172	117	28	69.5	9.86
chrUn_gI000216	9503	9591	89	44	16	67.36	8.17
chrUn_gI000216	10130	10213	84	42	21	123.45	11.13
chrUn_gI000216	10391	10695	305	80	40	97.62	11.12
chrUn_gI000216	11194	11520	327	40	36	80.79	6.7
chrUn_gI000216	15123	15275	153	46	34	193.28	21.7
chrUn_gI000216	22073	22289	217	99	24	93.67	14.63
chrUn_gI000216	22452	22674	223	131	49	300.92	40.29
chrUn_gI000216	75569	75891	323	281	38	180.97	14.18
chrUn_gI000216	123581	123688	108	44	9	58.79	13.66
chrUn_gI000216	132091	132348	258	127	33	211.23	41.97
chrUn_gI000216	136767	136831	65	32	22	304.47	26.65
chrUn_gI000216	141745	141946	202	118	16	80.75	19.48
chrUn_gI000216	143154	143297	144	37	13	73.07	15.8
chrUn_gI000216	152151	152281	131	32	12	55.46	11.81
chrUn_gI000216	154355	154441	87	43	31	324.29	35.88
chrUn_gI000216	160186	160278	93	46	10	57.18	11.7
chrUn_gI000216	162428	162492	65	32	10	99.07	12.94
chrUn_gI000216	163446	163582	137	106	29	227.46	32.83
chrUn_gI000216	169565	169700	136	88	16	119.34	23.71
chrUn_gI000216	171343	171410	68	34	9	97.14	16.41
chrUn_gI000219	59377	59548	172	62	15	73.69	11.65
chrUn_gI000219	63464	63592	129	86	9	54.54	10.94
chrUn_gI000219	76710	76829	120	76	11	73.16	13.77
chrUn_gI000219	79473	79610	138	36	11	60.51	10.94
chrUn_gI000219	105542	105686	145	36	11	63.04	11.67
chrUn_gI000219	105757	105883	127	41	10	58.91	9.69
chrUn_gI000219	107049	107205	157	53	12	61.95	11.82
chrUn_gI000219	110828	110974	147	96	12	66.49	10.94
chrUn_gI000219	115927	116094	168	121	15	95.73	18.24
chrUn_gI000219	116150	116274	125	79	13	93.52	14.59
chrUn_gI000219	134242	134325	84	42	10	82.86	16.94
chrUn_gI000219	140585	140703	119	47	10	66.73	12.77
chrUn_gI000219	178764	178935	172	47	13	54.52	7.14
chrUn_gI000220	64498	64680	183	79	19	50.06	5.47
chrUn_gI000220	101701	101796	96	48	45	382.11	30.47
chrUn_gI000220	102129	102221	93	46	16	85.31	12.25
chrUn_gI000220	104223	104318	96	53	22	179.29	25
chrUn_gI000220	117828	118175	348	47	166	155.07	4.2
chrUn_gI000220	118768	125420	6653	1496	3773	888.63	2.74
chrUn_gI000220	126766	128619	1854	622	1245	104.86	1.84
chrUn_gI000220	131182	132852	1671	1341	1359	138.64	1.81
chrUn_gI000220	143521	145562	2042	1165	1289	413.83	2.52
chrUn_gI000224	1426	1515	90	45	13	96.07	19.07
chrUn_gI000224	2247	2362	116	68	28	253.52	29.34
chrUn_gI000224	3301	3567	267	225	25	122.32	14.69
chrUn_gI000224	3739	3959	221	47	43	322.37	26.71
chrUn_gI000224	4305	4475	171	47	12	53.23	12.02
chrUn_gI000224	8224	8286	63	31	14	204.85	25.14
chrUn_gI000224	15660	15726	67	33	10	119.61	18.24
chrUn_gI000225	14	144	131	28	10	62.68	14.59
chrUn_gI000225	2726	2847	122	45	10	50.31	11.3
chrUn_gI000225	2852	3006	155	44	14	70.02	15.06
chrUn_gI000225	10942	11121	180	85	19	72.56	13.5
chrUn_gI000225	17393	17510	118	84	16	57.62	8.93
chrUn_gI000225	21761	21883	123	47	21	92.03	11.78
chrUn_gI000225	26411	26729	319	39	29	75.96	9.64
chrUn_gI000225	32659	32824	166	47	19	77.05	6.64
chrUn_gI000225	33568	33799	232	167	23	80.06	10.16
chrUn_gI000225	34555	34751	197	115	22	85.27	9.17
chrUn_gI000225	37746	37820	75	37	11	71.06	8.71
chrUn_gI000225	40920	41046	127	33	12	52.81	10.81
chrUn_gI000225	50811	50981	171	84	84	664.74	31.72
chrUn_gI000225	62498	62634	137	90	18	62.62	6.7
chrUn_gI000225	66246	66353	108	60	23	102.28	8.23
chrUn_gI000225	66680	66854	175	115	27	90.26	12.89

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chrUn_gI000225	67456	67675	220	99	41	168.78	21.59
chrUn_gI000225	68161	68462	302	38	27	53.44	7.27
chrUn_gI000225	73891	74076	186	97	27	128.63	20.24
chrUn_gI000225	80539	80608	70	35	12	81.72	8.68
chrUn_gI000225	81252	81485	234	119	26	74.14	9.62
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chrUn_gI000225	85564	85756	193	108	52	333.97	31.7
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chrUn_gI000225	108227	108410	184	71	19	110.15	14.47
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chrUn_gI000226	132	293	162	48	98	1096.18	101.38
chrUn_gI000226	880	970	91	45	25	218.1	27.56
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chrUn_gI000228	116706	116800	95	47	14	119.61	25.53
chrUn_gI000228	116858	117182	325	105	21	100.54	16.41
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chrUn_gI000228	117919	118058	140	47	16	117.39	18.24
chrUn_gI000229	11901	12130	230	109	17	53.04	8.68
chrUn_gI000229	12358	12469	112	65	13	66.4	10.81
chrUn_gI000231	16512	16650	139	47	13	62.07	10.08
chrUn_gI000231	17159	17298	140	44	13	60.64	12.06
chrUn_gI000232	934	1361	428	322	35	108.01	9.26
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chrUn_gI000234	35493	35652	160	46	13	50.61	9.19
chrUn_gI000235	546	698	153	79	12	73.44	16.41
chrUn_gI000235	1719	1806	88	44	10	73.82	17.36
chrUn_gI000235	33901	34037	137	74	10	60.81	12.77
chrUn_gI000241	224	320	97	53	9	52.83	10.48
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chrX	12115666	12115788	123	39	9	56.34	9.12
chrX	13857910	13858054	145	96	10	52.87	9.54
chrX	20371064	20371197	134	59	9	50.06	10.08
chrX	36333503	36333638	136	42	9	52.56	9.12
chrX	40668530	40668663	134	47	9	53.11	12.77
chrX	42892329	42892458	130	45	9	54.25	10.94
chrX	47830815	47830930	116	30	9	58.58	14.59
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chrX	55171881	55172006	126	84	10	62.95	14.12
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chrX	58561376	58561512	137	41	60	593.4	63.26
chrX	58564993	58565096	104	43	10	60.95	12.5
chrX	61683599	61683685	87	43	17	167.76	31
chrX	61687380	61687462	83	41	23	240.71	31.11
chrX	61689610	61689728	119	83	14	90.66	18.06
chrX	61691775	61691870	96	48	32	298.28	35.88
chrX	61694683	61694820	138	40	11	57.45	10.16
chrX	61695859	61695954	96	38	13	104.07	20.33

chrX	61696547	61696642	96	47	24	238.79	38.96
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chrX	61709824	61709880	57	28	12	193.21	21.89
chrX	61715386	61715470	85	42	10	66.21	11.84
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chrX	61719775	61719831	57	28	19	257.26	16.22
chrX	61720597	61720654	58	29	20	272.32	17.51
chrX	61726478	61726677	200	115	36	166.55	22.54
chrX	61729267	61729355	89	44	13	54.07	7.48
chrX	61730984	61731114	131	87	30	150.14	16.2
chrX	61733184	61733391	208	86	22	68.04	9.15
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chrX	61799844	61800077	234	121	19	87.82	20.42
chrX	61815156	61815209	54	27	14	223.95	20.54
chrX	61823440	61823575	136	104	18	131.69	27.45
chrX	61839233	61839351	119	80	37	350.94	44.83
chrX	65924569	65924735	167	69	11	60.75	14.59
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chrX	73500512	73500696	185	73	14	56.55	9.31
chrX	74311873	74312062	190	111	13	54.34	10.48
chrX	74511782	74511895	114	44	10	50	9.31
chrX	78304575	78304727	153	51	10	51.03	11.22
chrX	83371915	83372050	136	97	10	50.12	8.33
chrX	84982851	84983023	173	93	11	59.18	10.94
chrX	87657927	87658093	167	75	11	53.1	9.19
chrX	87833847	87833974	128	85	9	51.46	10
chrX	88462368	88462491	124	79	11	74.31	14.59
chrX	89439477	89439617	141	39	9	51.21	9.12
chrX	92086427	92086567	141	73	9	51.21	10.94
chrX	94699065	94699241	177	85	13	50.71	9.06
chrX	96761838	96761984	147	62	12	51.33	9.06
chrX	98748646	98748807	162	96	14	64.15	9.42
chrX	100542628	100542752	125	44	11	50.73	8.68
chrX	101069653	101069776	124	60	10	55.1	10.06
chrX	102125244	102125379	136	45	9	50.42	10.33
chrX	102448913	102449076	164	86	15	55.8	7.18
chrX	103024769	103025031	263	57	20	65.3	6.07
chrX	104277185	104277293	109	66	9	50.66	8.33
chrX	104277834	104277957	124	81	10	53.99	9.79
chrX	104719350	104719543	194	79	16	54.74	6.51
chrX	106857276	106857433	158	117	11	53.32	8.74
chrX	107127080	107127229	150	80	11	50.2	6.43
chrX	111213121	111213258	138	38	9	52.01	10.94
chrX	114449807	114449974	168	104	13	57.98	7.49
chrX	115003375	115003468	94	47	15	105.45	18.27
chrX	115004663	115004758	96	48	40	382.21	39.44
chrX	115004847	115004937	91	45	26	216.42	25.43
chrX	115005062	115005141	80	40	23	213.8	21.98
chrX	115224395	115224487	93	46	10	59.56	12.4
chrX	117207432	117207570	139	47	11	65.67	13.55
chrX	120798396	120798515	120	36	10	59.07	10.72
chrX	123102966	123103118	153	117	12	60.56	8.39
chrX	123580907	123581050	144	104	11	57.67	10.27
chrX	124233178	124233311	134	56	10	51.14	8.45
chrX	124954408	124954551	144	46	10	54.09	9.77
chrX	126528247	126528363	117	80	11	70.32	11.05
chrX	128256555	128256667	113	47	9	51.09	8.74
chrX	128771685	128771809	125	63	10	55.34	11.66
chrX	130971278	130971415	138	105	10	50.24	9.92
chrX	139964691	139964814	124	86	9	52.95	10.08
chrX	146635120	146635261	142	84	10	59.32	9.12
chrX	149896253	149896391	139	44	9	51.17	10.78
chrY	9919469	9919523	55	27	10	155.36	18.24
chrY	9934852	9934950	99	55	10	74.62	14.59
chrY	9940691	9940808	118	45	13	85.94	14.99
chrY	9941101	9941214	114	67	14	97.19	16.37
chrY	9942861	9942974	114	53	9	55.21	11.48
chrY	9951156	9951289	134	77	9	53.11	9.12
chrY	9960285	9960419	135	90	9	52.84	10.94
chrY	9961078	9961200	123	42	9	56.34	12.77
chrY	9961487	9961605	119	38	9	57.6	12.77
chrY	10042996	10043144	149	46	12	74.75	14.59
chrY	10043659	10043817	159	105	28	229.88	29.18
chrY	13137785	13137864	80	40	20	238.79	33.88

chrY	13139252	13139305	54	27	9	135.87	14.76
chrY	13141036	13141260	225	128	23	146.41	26.26
chrY	13141741	13141837	97	48	11	84.34	15.89
chrY	13432563	13432656	94	47	9	65.9	16.41
chrY	13435604	13435742	139	42	9	51.75	12.77
chrY	13435932	13436084	153	105	11	64.68	16.41
chrY	13448617	13448757	141	92	21	68.16	8.29
chrY	13449141	13449762	622	113	58	77.78	7.51
chrY	13450125	13450328	204	37	24	50.01	4.68
chrY	13451275	13451511	237	138	29	61.73	6.58
chrY	13454525	13454597	73	36	20	128.39	9.41
chrY	13457952	13458206	255	41	30	76.2	8.98
chrY	13458359	13458495	137	98	47	304	21.37
chrY	13458617	13458775	159	93	30	138.68	9.53
chrY	13460424	13460590	167	47	18	62.74	12.65
chrY	13460944	13461034	91	45	24	162.76	17.36
chrY	13465893	13466067	175	47	26	142.62	18.76
chrY	13469369	13469540	172	47	20	104.66	20.27
chrY	13476553	13476619	67	33	11	122.41	17.49
chrY	13480256	13480446	191	97	18	98.18	17.24
chrY	13485350	13485434	85	42	9	56.49	10.36
chrY	13485505	13485696	192	78	31	195.01	28.62
chrY	13488847	13488923	77	38	9	79.52	14.2
chrY	13489078	13489203	126	61	10	59.24	11.3
chrY	13489924	13490066	143	105	9	50.12	12.57
chrY	13648122	13648196	75	37	17	206.24	31
chrY	13648940	13649018	79	39	18	206.24	32.83
chrY	13651323	13651404	82	41	23	274.14	41.95
chrY	13652113	13652200	88	44	12	108.23	21.89
chrY	13658791	13658872	82	41	17	180.38	31
chrY	13662029	13662096	68	34	18	260.22	32.83
chrY	13664657	13664764	108	66	9	61.32	14.59
chrY	13680934	13681008	75	37	32	483.47	58.36
chrY	13704309	13704389	81	40	37	531.27	67.48
chrY	13801064	13801208	145	38	31	291.04	45.59
chrY	13808669	13808792	124	31	12	83.98	18.24
chrY	13810797	13810929	133	41	15	110.34	20.06
chrY	13811047	13811181	135	32	10	61.42	10.94
chrY	13813110	13813200	91	45	18	166.56	32.33
chrY	13822612	13822664	53	26	9	143.19	16.41
chrY	13833316	13833368	53	26	10	167.76	18.24
chrY	13838442	13838516	75	37	10	97.14	18.24
chrY	13842632	13842840	209	89	54	471.47	38.89
chrY	13843912	13844041	130	45	12	71.79	11.99
chrY	13846457	13846521	65	32	26	414.1	37.62
chrY	13851948	13852094	147	67	18	134.99	27.36
chrY	13853099	13853163	65	32	18	274.14	32.83
chrY	13861899	13861953	55	27	9	131.27	16.41
chrY	13866951	13867093	143	29	17	126.41	29.18
chrY	13868370	13868441	72	36	11	119.61	20.06
chrY	13869399	13869488	90	45	10	75.95	18.24
chrY	13869722	13869872	151	115	16	112.32	25.53
chrY	28784347	28784491	145	44	11	67.11	10.94
chrY	28785699	28785787	89	44	17	167.76	31
chrY	28785919	28786062	144	37	14	95.42	23.71
chrY	28793469	28793531	63	31	9	108.23	16.41
chrY	28800208	28800282	75	37	9	86.38	16.41
chrY	58972837	58973112	276	131	27	83.4	11.01
chrY	58978652	58978833	182	134	22	50.29	8.16
chrY	58985505	58985696	192	89	21	73.34	7.58
chrY	58997019	58997172	154	83	13	58.3	11.51
chrY	59005172	59005347	176	86	15	61.26	9.69

Supplementary Table S3. The genome-wide differential expression genes (DEGs) in HEK293T cells identified after the transfection with VRTN.

ProbeSet	Gene Symbol	Geom mean of intensities in class Exp	Geom mean of intensities in class Con	Fold-change (Exp/Con)	style	Chromosome	Strand	Start	Stop
8057613	RN5S114	1779.89	554.29	3.21	up	chr2	-	1.89E+08	189141571
8034837	DNAJB1	1033.98	355.43	2.91	up	chr19	-	14625581	14629201
7975702	VRTN	73.49	34.84	2.11	up	chr14	+	74815195	74826711
7970864	HSPH1	3502.7	1801.27	1.94	up	chr13	-	31710762	31736502
7906775	HSPA6	568.93	307.84	1.85	up	chr1	+	1.62E+08	161576821
8008644	---	40.24	65.78	0.61	down	chr17	+	54948531	54948637
7965322	KITLG	140.68	208.98	0.67	down	chr12	-	88886566	88974238
8137709	ZFAND2A	619.21	276.48	2.24	up	chr7	-	1192543	1199798
8103206	FBXW7	191.33	269.38	0.71	down	chr4	-	1.53E+08	153456172
7963567	KRT8	498.54	239.3	2.08	up	chr12	-	53290971	53298860
8095744	AREG	36.14	14.25	2.54	up	chr4	+	75480839	75490482
8167763	TSPYL2	651.08	420.38	1.55	up	chrX	+	53111549	53117722
7951662	CRYAB	63.69	21.39	2.98	up	chr11	-	1.12E+08	111782494
8030007	EMP3	548.5	386.9	1.42	up	chr19	+	48828629	48833811
8065410	CST4	283.08	173.92	1.63	up	chr20	-	23666269	23669677
7942596	SERPINH1	1146.71	498.41	2.3	up	chr11	+	75273170	75283846
8047441	---	35.29	18.21	1.94	up	chr2	+	2.02E+08	202288329
8117583	---	522.81	723.56	0.72	down	chr6	+	27775970	27778623
8149927	CLU	668.91	320.05	2.09	up	chr8	-	27454434	27472371
8096845	EGF	48	31.61	1.52	up	chr4	+	1.11E+08	110933419
7974212	---	23.69	17.7	1.34	up	chr14	+	50151262	50151379
8170013	ZNF75D	45.86	27.47	1.67	up	chrX	+	1.34E+08	134257528
8175317	ZNF75D	45.86	27.47	1.67	up	chrX	-	1.34E+08	134383198
8095986	ANXA3	98.76	58.24	1.7	up	chr4	+	79472742	79531605
8092886	---	10.23	7.65	1.34	up	chr3	-	1.94E+08	194254309
8097335	HSPA4L	2440.61	1851.2	1.32	up	chr4	+	1.29E+08	128754530

8140534	SEMA3C	134.31	189.15	0.71	down	chr7	-	80371854	80548667
8136161	RN5S245	31.62	51.1	0.62	down	chr7	+	1.3E+08	129667237
8164252	SH2D3C	208.54	152.8	1.36	up	chr9	-	1.31E+08	130541048
7946288	ZNF214	74.83	107.74	0.69	down	chr11	-	7020549	7041541
8151917	MTERFD1	242.16	323.56	0.75	down	chr8	-	97251645	97273817
7964602	LRIG3	185.05	257.49	0.72	down	chr12	-	59265937	59314262
7959102	HSPB8	210.57	94.84	2.22	up	chr12	+	1.2E+08	119632777
7935058	MYOF	87.47	59.6	1.47	up	chr10	-	95065703	95242074
8117589	---	199.08	284.56	0.7	down	chr6	+	27777714	27779078
7989130	---	19.89	26.88	0.74	down	chr15	-	56321883	56322179
8016494	TTLL6	60.73	45.11	1.35	up	chr17	-	46839602	46871686
7937335	IFITM1	614.05	396.18	1.55	up	chr11	+	313853	315272
8033736	OR7G1	33.38	23.69	1.41	up	chr19	-	9225274	9226439
7949021	RCOR2	132.33	95.04	1.39	up	chr11	-	63678702	63684316
8123148	MRPL18	1416.34	1019.05	1.39	up	chr6	+	1.6E+08	160219468
7973618	IRF9	136.02	89.63	1.52	up	chr14	+	24630422	24636611
8117054	CAP2	944.97	720.57	1.31	up	chr6	+	17393736	17558023
7905147	C1orf54	150.53	108.99	1.38	up	chr1	+	1.5E+08	150253327
8146401	---	23.48	17.84	1.32	up	chr8	+	50242769	50243105
8118682	PHF1	280.39	200.08	1.4	up	chr6	+	33378740	33384309
7906764	HSPA6	261.2	93.58	2.79	up	chr1	+	1.61E+08	161496700
8008321	ACSF2	335.75	260.29	1.29	up	chr17	+	48503591	48552198
7981333	---	60.46	31.34	1.93	up	chr14	-	1.03E+08	102543806
8095736	AREG	71.22	41.55	1.71	up	chr4	+	75310853	75320727
8038126	CA11	295.34	174.18	1.7	up	chr19	-	49141272	49149451
7920333	---	69.97	44.27	1.58	up	chr1	-	1.54E+08	153698829
8124437	HIST1H3F	271.14	378.96	0.72	down	chr6	-	26250369	26250835
7963631	RARG	205.77	161.45	1.27	up	chr12	-	53604353	53626036
8091867	BCHE	28.74	37.2	0.77	down	chr3	-	1.65E+08	165555250
7956522	KIF5A	267.04	201.33	1.33	up	chr12	+	57978689	57979697

8117321	TRIM38	153.3	111.63	1.37 up	chr6	+	25963059	25985531
8102328	CFI	39.47	28.8	1.37 up	chr4	-	1.11E+08	110723196
8174554	RN5S512	41.51	28.74	1.44 up	chrX	-	1.11E+08	110913176
8091998	---	12.81	18.18	0.7 down	chr3	-	1.69E+08	169438081
8126093	---	30.97	22.69	1.36 up	chr6	-	37218982	37219081
8022488	ABHD3	277.12	208.36	1.33 up	chr18	-	19230858	19284726
8038213	HSD17B14	143.44	112.59	1.27 up	chr19	-	49316274	49339934
8084818	CCDC50	313.38	397.71	0.79 down	chr3	+	1.91E+08	191109964
7902541	IFI44L	73.93	39.56	1.87 up	chr1	+	79086116	79108484
8024120	ABCA7	160.55	128.63	1.25 up	chr19	+	1041245	1065571
8126402	TRERF1	68.01	54.38	1.25 up	chr6	-	42192963	42419783
8072876	LGALS1	519.74	351.86	1.48 up	chr22	+	38071613	38075809
8037001	TRNAK38P	28.85	41.88	0.69 down	chr19	-	41748142	41748214
8035304	BST2	43.53	32.69	1.33 up	chr19	-	17513755	17516457
8175871	L1CAM	73.8	54.33	1.36 up	chrX	-	1.53E+08	153151608
8140668	SEMA3A	156.8	212.6	0.74 down	chr7	-	83587659	83824217
8096704	NPNT	144.9	112.45	1.29 up	chr4	+	1.07E+08	106892828
8141768	RASA4	395.31	291.83	1.35 up	chr7	-	1.02E+08	102158234
8124502	ZNF184	248.4	354.56	0.7 down	chr6	-	27418527	27440879
8098006	GLRB	63.05	47.76	1.32 up	chr4	+	1.58E+08	158092854
8147057	CHMP4C	84.98	105.85	0.8 down	chr8	+	82644686	82671750
8025893	---	15.6	9.24	1.69 up	chr19	+	11519447	11519554
8016387	PRR15L	38.26	28.72	1.33 up	chr17	-	46029333	46035110
8125091	VARS	449.61	582.41	0.77 down	chr6	-	31745295	31763712
8178609	VARS	449.61	582.41	0.77 down	chr6	-	31745295	31763712
7981960	SNORD116-6	11.71	8.29	1.41 up	chr15	+	25310173	25310268
7971913	PPP1R2P10	11.72	19.61	0.6 down	chr13	-	64385499	64385740
7985493	TM6SF1	42.14	33.09	1.27 up	chr15	+	83776324	83806111
7936201	WDR96	58.12	41.51	1.4 up	chr10	-	1.06E+08	105992120
8104930	SLC1A3	216	267.18	0.81 down	chr5	+	36606689	36688436

8096091	THAP9	122.18	165.86	0.74	down	chr4	+	83821837	83841438
7922152	C1orf114	93.11	118.51	0.79	down	chr1	-	1.69E+08	169396721
7911276	OR2T6	14.33	10.99	1.3	up	chr1	+	2.49E+08	248551847
7989132	RFX7	410.03	321.74	1.27	up	chr15	-	56379478	56471510
8170196	---	21.43	17	1.26	up	chrX	+	1.36E+08	135856259
8136790	---	29	22.84	1.27	up	chr7	+	1.42E+08	142456642
7914557	SYNC	113.04	87.8	1.29	up	chr1	-	33145961	33160873
8004940	C17orf48	50.72	62.1	0.82	down	chr17	+	10600927	10614875
8018791	---	48.7	34.42	1.42	up	chr17	-	74699716	74699808
8097080	SYNPO2	52.92	39.62	1.34	up	chr4	+	1.2E+08	119982402
8020354	OR4K15	14.45	11.65	1.24	up	chr18	+	14613296	14614135
7969179	RNASEH2B	274.85	337.16	0.82	down	chr13	+	51483814	51530901
8083429	MBNL1	856.39	1070.83	0.8	down	chr3	+	1.52E+08	152183569
8124798	PPP1R18	109.6	86.87	1.26	up	chr6	-	30644133	30655672
7947147	SVIP	241.42	295.39	0.82	down	chr11	-	22841857	22851381
7994675	ASPHD1	120.11	93.1	1.29	up	chr16	+	29912147	29931178
7922018	ILDR2	105.76	76.76	1.38	up	chr1	-	1.67E+08	166944561
8139270	RASA4CP	466.33	307.91	1.51	up	chr7	-	44066569	44078607
8046755	RN5S113	101.24	125.51	0.81	down	chr2	+	1.83E+08	182913639
8133721	HSPB1	178.85	130.59	1.37	up	chr7	+	75931923	75933614
8124413	HIST1H4D	713.46	891.9	0.8	down	chr6	-	26188938	26189304
7929919	SFXN3	185.12	145.99	1.27	up	chr10	+	1.03E+08	102800998
8096335	HERC6	150.43	116.6	1.29	up	chr4	+	89299891	89364249
8124240	KIAA0319	69.94	56.54	1.24	up	chr6	-	24544332	24646383
8100893	COX18	167.44	211.78	0.79	down	chr4	-	73920415	73935472
8027860	FFAR3	28.75	35.12	0.82	down	chr19	+	35862262	35863302
8105220	ISL1	110.53	145.24	0.76	down	chr5	+	50678958	50690564
8108447	CXXC5	310.95	229.97	1.35	up	chr5	+	1.39E+08	139063467
8126729	CLIC5	35.46	25.92	1.37	up	chr6	-	45866188	46048132
8121510	RPF2	1072.43	1320.95	0.81	down	chr6	+	1.11E+08	111347303

7952205	MCAM	185.65	147.95	1.25	up	chr11	-	1.19E+08	119187840
8066482	WFDC5	57.45	46.74	1.23	up	chr20	-	43738093	43743813
8034199	---	61.09	45.4	1.35	up	chr19	-	11411543	11431999
8113073	ARRDC3	413.47	564.42	0.73	down	chr5	-	90664541	90679121
8160981	FAM214B	169.81	134.53	1.26	up	chr9	-	35104109	35115893
7957627	---	8.09	5.31	1.52	up	chr12	+	95669546	95669646
8038117	DBP	437.67	332.02	1.32	up	chr19	-	49133820	49140623
7926728	MYO3A	64.23	48.16	1.33	up	chr10	+	26223196	26501459
8021101	HAUS1	200.81	255.1	0.79	down	chr18	+	43684298	43708299
8037657	DMPK	211.24	174.62	1.21	up	chr19	-	46272975	46285810
8089112	FILIP1L	99.4	67.52	1.47	up	chr3	-	99551988	99833357
7929047	IFIT2	33.13	21.35	1.55	up	chr10	+	91061712	91069033
8160900	FAM205B	21.85	17.78	1.23	up	chr9	-	34830265	34838583
7934838	RPL7AP8	40.45	49.87	0.81	down	chr10	-	88390582	88391367
7947540	TRAF6	252.92	338.39	0.75	down	chr11	-	36510723	36531822
8109333	GPX3	519.2	349.84	1.48	up	chr5	+	1.5E+08	150409051
8157450	ORM2	42.57	30.93	1.38	up	chr9	+	1.17E+08	117096021
7918753	---	25.31	36.39	0.7	down	chr1	-	1.15E+08	115087969
7965206	SLC6A15	248.68	308.41	0.81	down	chr12	-	85253267	85306574
8015412	JUP	780.39	624.59	1.25	up	chr17	-	39910864	39942950
8057803	TMEFF2	27.92	22.73	1.23	up	chr2	-	1.93E+08	193059659
8113039	MEF2C	216.7	280.15	0.77	down	chr5	-	88016154	88179062
8151756	TMEM55A	116.2	90.68	1.28	up	chr8	-	92006499	92053066
7914202	SNHG12	908.7	1280.54	0.71	down	chr1	-	28905050	28909495
7912515	NPPA	23.5	30.15	0.78	down	chr1	-	11905766	11908402
7983189	---	6.83	10.53	0.65	down	chr15	+	43539878	43539977
8098707	HSP90AA4P	154.53	124.08	1.25	up	chr4	+	1.9E+08	190396344
8117535	HIST1H2AG	342.76	434.93	0.79	down	chr6	+	27100821	27103071
8163109	FRRS1L	161.69	133.95	1.21	up	chr9	-	1.12E+08	111929571
7991932	FAM195A	80.04	97.33	0.82	down	chr16	+	691849	698474

8099696	SEPSECS	113.24	149.73	0.76	down	chr4	-	25121636	25162064
8142019	ORC5	595.04	745.84	0.8	down	chr7	-	1.04E+08	103848495
8117580	HIST1H2AI	794.93	981.54	0.81	down	chr6	+	27775899	27776479
8116760	RIOK1	782.59	951.24	0.82	down	chr6	+	7390026	7418270
7964484	B4GALNT1	155.15	128.4	1.21	up	chr12	-	58017193	58026985
8113369	SLCO4C1	379.39	303.21	1.25	up	chr5	-	1.02E+08	101632253
7965979	ALDH1L2	202.67	301.67	0.67	down	chr12	-	1.05E+08	105478241
8024888	MIR7-3HG	105.43	78.59	1.34	up	chr19	+	4769152	4772531
7946115	OR52L1	21.83	17.98	1.21	up	chr11	-	6007171	6008160
7905154	C1orf51	120.9	78.88	1.53	up	chr1	+	1.5E+08	150259505
8063531	FAM209B	68.11	53.15	1.28	up	chr20	+	55108302	55111576
8024687	TJP3	154.42	126.82	1.22	up	chr19	+	3728374	3750810
8021470	PMAIP1	537.36	666.76	0.81	down	chr18	+	57567234	57571537
8103834	AGA	113.76	150.01	0.76	down	chr4	-	1.78E+08	178363591
8118310	HSPA1A	3104.45	2525.81	1.23	up	chr6	+	31783320	31785719
8161829	C9orf41	328.39	399.13	0.82	down	chr9	-	77595934	77643339
8160405	KLHL9	681.85	821.53	0.83	down	chr9	-	21324054	21335429
8168672	---	10.39	8.2	1.27	up	chrX	+	91053092	91053282
8061847	BPIFA2	34.91	28.46	1.23	up	chr20	+	31749654	31769223
8086344	CX3CR1	16.72	13.45	1.24	up	chr3	-	39304985	39323186
8179322	HSPA1A	2996.69	2437.84	1.23	up	chr6	+	31783337	31785719
8061019	NDUFAF5	138.21	180.71	0.76	down	chr20	+	13765596	13799067
7954398	C12orf39	79.41	56.52	1.4	up	chr12	+	21679241	21685457
8041853	EPCAM	65.54	44.45	1.47	up	chr2	+	47596446	47614159
8085912	---	8.94	11.4	0.78	down	chr3	-	27307070	27307174
8074020	SELO	196.84	237.88	0.83	down	chr22	+	50639408	50656045
8057744	STAT1	686.38	552.02	1.24	up	chr2	-	1.92E+08	191878936
7981324	---	12.82	9.71	1.32	up	chr14	-	1.02E+08	101612032
8079422	TDGF1	6.53	8.12	0.8	down	chr3	+	46619213	46623953
8117655	ZNF193	106.49	134	0.79	down	chr6	+	28193067	28201260

7981978	SNORD116-15	18.91	27.33	0.69	down	chr15	+	25326434	25326525
7950269	---	36.15	26.5	1.36	up	chr11	-	72580588	72580695
7929511	ENTPD1	36.2	28.84	1.26	up	chr10	+	97471536	97629452
7904726	TXNIP	951.93	610.28	1.56	up	chr1	+	1.45E+08	145442635
8126820	GPR110	18.15	14.38	1.26	up	chr6	-	46967117	47010082
8113124	---	32.99	45.33	0.73	down	chr5	-	93979044	93989091
8002379	RNU6-23	46.44	68.61	0.68	down	chr16	-	70479198	70479302
7956488	KIF5A	343.03	266.81	1.29	up	chr12	+	57943840	57980415
8116635	BPHL	202.15	245.47	0.82	down	chr6	+	3118610	3153430
7968883	LACC1	96.3	69.49	1.39	up	chr13	+	44453969	44466438
7901110	AKR1A1	329.66	397.93	0.83	down	chr1	+	46016215	46035722
8085579	---	12.43	20.82	0.6	down	chr3	-	15474617	15474723
7952810	IGSF9B	44.34	61.78	0.72	down	chr11	-	1.34E+08	133786330
7980327	ANGEL1	279.01	339.47	0.82	down	chr14	-	77253586	77279231
8034315	ZNF823	147.97	121.98	1.21	up	chr19	-	11832081	11849736
7977440	KIAA0125	205.36	158.9	1.29	up	chr14	+	1.06E+08	106388531
8098439	EPCAM	58.66	29.72	1.97	up	chr4	+	1.82E+08	182444154
8124610	TRIM27	349.53	446.79	0.78	down	chr6	-	28870779	28891768
8179575	TRIM27	349.53	446.79	0.78	down	chr6	-	28870779	28891768
8099967	RBM47	127.27	87.46	1.46	up	chr4	-	40425284	40631881
7986246	HMG1P38	298.15	358.75	0.83	down	chr15	+	93254977	93256105
8024111	CNN2	710.95	569.48	1.25	up	chr19	+	1026298	1039064
7953409	PTMS	625.76	490.23	1.28	up	chr12	+	6875541	6880118
7958759	---	52.94	40.3	1.31	up	chr12	+	1.12E+08	112019618
8001529	---	145.44	117.5	1.24	up	chr16	-	56696148	56696745
8013529	---	18.13	25.08	0.72	down	chr17	-	22026590	22026632
7952350	SCN3B	88.16	71.58	1.23	up	chr11	-	1.23E+08	123525315
7949275	MIR194-2	140.21	99.36	1.41	up	chr11	-	64658827	64658911
7914342	FABP3	52.42	35.77	1.47	up	chr1	-	31838100	31845923
8126770	CYP39A1	49.7	64.53	0.77	down	chr6	-	46517445	46620523

7917199	TTLL7	438.07	343.21	1.28	up	chr1	-	84330711	84464833
8048370	BCS1L	482.27	598.89	0.81	down	chr2	+	2.2E+08	219528166
7963923	SARNP	474.76	575.01	0.83	down	chr12	-	56146364	56211506
8074606	USP41	203.54	245.33	0.83	down	chr22	-	20717911	20782479
8043835	C2orf15	109.9	79.29	1.39	up	chr2	+	99758185	99767950
8000791	YPEL3	365.75	290.73	1.26	up	chr16	-	30103635	30107528
8169015	TCEAL7	48.33	37.49	1.29	up	chrX	+	1.03E+08	102587254
8137700	C7orf50	315.04	397.78	0.79	down	chr7	-	1036642	1177893
8065612	C20orf112	121.3	100.54	1.21	up	chr20	-	31030862	31172875
8009277	RGS9	115.36	87.7	1.32	up	chr17	+	63133572	63223817
8077931	MKRN2	614.69	738.62	0.83	down	chr3	+	12598571	12625212
8093130	RNF168	386.22	464.75	0.83	down	chr3	-	1.96E+08	196230582
7927732	ARID5B	451.78	565.02	0.8	down	chr10	+	63661059	63856703
8008201	NGFR	183.52	145.39	1.26	up	chr17	+	47572655	47592372
7905510	LCE4A	86.37	65.77	1.31	up	chr1	+	1.53E+08	152681967
8110620	BTNL3	9.33	11.46	0.81	down	chr5	+	1.8E+08	180433727
8099051	NOP14	563.19	681.23	0.83	down	chr4	-	2939663	2965123
8138454	TWISTNB	323.24	389.94	0.83	down	chr7	-	19735085	19748660
7906948	RN5S63	23.6	33.88	0.7	down	chr1	+	1.63E+08	163479362
7974029	TTC6	12.73	10.28	1.24	up	chr14	+	38264472	38311890
8088958	GBE1	360.99	277.81	1.3	up	chr3	-	81538852	81811312
8121559	---	10.37	12.8	0.81	down	chr6	+	1.13E+08	113292794
8126428	TRERF1	33.54	26.92	1.25	up	chr6	-	42193435	42194982
8037144	DEDD2	463.52	365.7	1.27	up	chr19	-	42702750	42724275
7921713	F11R	217.85	180.61	1.21	up	chr1	-	1.61E+08	161008780
8169056	TMEM31	48.94	39.86	1.23	up	chrX	+	1.03E+08	102968960
7965200	CCDC59	621.26	754.84	0.82	down	chr12	-	82746618	82752172
7972546	GAPDHP22	87.5	108.64	0.81	down	chr13	-	99843030	99843239
7931643	CYP2E1	85.1	69.3	1.23	up	chr10	+	1.35E+08	135374724
7938263	EIF3F	419.19	322.24	1.3	up	chr11	+	8008867	8019707

8034589	FARSA	1128.46	1358.55	0.83	down	chr19	-	13033293	13044536
7996819	CDH3	79.51	64.25	1.24	up	chr16	+	68678739	68732942
7970513	SKA3	351.67	440.49	0.8	down	chr13	-	21727734	21750710
8097128	EXOSC9	839.77	1031.63	0.81	down	chr4	+	1.23E+08	122738176
8043564	FAHD2A	294.13	382.08	0.77	down	chr2	+	96068448	96078879
7923972	---	25.38	20.88	1.22	up	chr1	-	2.08E+08	207595059
8012466	KRBA2	73.01	59.57	1.23	up	chr17	-	8271973	8274858
8145977	PLEKHA2	93.92	73.89	1.27	up	chr8	+	38758829	38827299
8006668	MRM1	92.71	115.74	0.8	down	chr17	+	34958025	34965407
7913858	PAQR7	55.23	44.09	1.25	up	chr1	-	26187701	26197744
8142061	PUS7	274.23	331.71	0.83	down	chr7	-	1.05E+08	105162685
8088996	---	21.43	37.74	0.57	down	chr3	-	87381210	87381282
7946695	RN5S331	14.41	9.68	1.49	up	chr11	-	13929032	13929133
8154962	DNAJB5	392.27	321.58	1.22	up	chr9	+	34989742	34998428
8111201	RN5S180	28.87	17.29	1.67	up	chr5	-	17157101	17157182
8083592	---	31.77	23.7	1.34	up	chr3	+	1.57E+08	156871428
8129872	OLIG3	33.3	40.65	0.82	down	chr6	-	1.38E+08	137815531
7908003	NPL	64.9	49.69	1.31	up	chr1	+	1.83E+08	182799519
7996219	NDRG4	349.43	283.34	1.23	up	chr16	+	58497617	58547523
8147516	MATN2	63.79	51.01	1.25	up	chr8	+	98881307	99048948
8141803	RASA4	337.22	244.91	1.38	up	chr7	-	1.02E+08	102257176
7917359	ZNHIT6	466.85	568.96	0.82	down	chr1	-	86118489	86174103
7902227	GADD45A	663.16	855.58	0.78	down	chr1	+	68150744	68154021
8126184	KIF6	48.44	59.37	0.82	down	chr6	-	39303926	39693182
8162696	XPA	282.56	352.83	0.8	down	chr9	-	1E+08	100459649
7910369	HIST3H2BB	145.38	180.54	0.81	down	chr1	+	2.29E+08	228648171
8156759	---	21.19	16.85	1.26	up	chr9	+	1.01E+08	100794616
7938072	OR56B4	21.47	16.76	1.28	up	chr11	+	6129009	6129968
8128001	CGA	48.05	37.68	1.28	up	chr6	-	87795216	87804850
8127872	SNAP91	121.7	98.74	1.23	up	chr6	-	84262604	84419111

7981046	IFI27L2	315.18	245.74	1.28	up	chr14	-	94594118	94595957
8026900	KCNN1	169.36	134.02	1.26	up	chr19	+	18062111	18109930
8150439	ANK1	119.92	98.52	1.22	up	chr8	-	41510744	41754280
8151711	NBN	221.7	270.8	0.82	down	chr8	-	90945559	90996899
8018646	FOXJ1	81.68	57.96	1.41	up	chr17	-	74132414	74137371
7905067	HIST2H4B	1000.4	1400.88	0.71	down	chr1	+	1.5E+08	149806194
7919627	HIST2H4B	1000.4	1400.88	0.71	down	chr1	-	1.5E+08	149832734
8015301	KRT35	31.45	38.06	0.83	down	chr17	-	39632941	39637668
8178090	C6orf48	672.65	878.46	0.77	down	chr6	+	31802645	31807538
8179326	C6orf48	672.65	878.46	0.77	down	chr6	+	31802645	31807541
8090529	RAB43	47.15	57.01	0.83	down	chr3	-	1.29E+08	128840625
8048761	---	115.09	148.01	0.78	down	chr2	+	2.26E+08	225798884
7917468	RN5S52	91.15	62.52	1.46	up	chr1	-	87918945	87919056
8082583	ARVP6125	29.43	21.71	1.36	up	chr3	+	1.3E+08	129763668
8097957	GUCY1A3	96.15	119.49	0.8	down	chr4	+	1.57E+08	156653485
8010983	ABR	299.83	245.9	1.22	up	chr17	-	906758	1090616
8001564	DOK4	164.66	136.25	1.21	up	chr16	-	57505870	57520327
7909127	MFSD4	69.97	57.89	1.21	up	chr1	+	2.06E+08	205572046
8041519	FAM82A1	42.29	32.97	1.28	up	chr2	+	38152462	38294280
8054329	RNF149	274.13	329.03	0.83	down	chr2	-	1.02E+08	101925152
7965723	UHRF1BP1L	261.06	315.44	0.83	down	chr12	-	1E+08	100536642
7983763	MAPK6	194.58	237.95	0.82	down	chr15	+	52311447	52358462
8000930	---	30.76	22.97	1.34	up	chr16	-	30712678	30712755
8083061	---	12.82	15.88	0.81	down	chr3	+	1.41E+08	140621512
7963774	ZNF385A	316.61	254.4	1.24	up	chr12	-	54762920	54785070
7964360	STAT6	222.04	180.43	1.23	up	chr12	-	57489191	57505161
8102792	PCDH18	179.16	231.92	0.77	down	chr4	-	1.38E+08	138453637
8012883	HS3ST3A1	206.63	249.61	0.83	down	chr17	-	13399006	13505244
8082827	CEP63	120.86	153.25	0.79	down	chr3	+	1.34E+08	134293855
7923501	---	196.2	153.23	1.28	up	chr1	-	2.03E+08	202884108

8155508	---	12.9	10.31	1.25	up	chr9	+	45661987	45662270
8016868	---	74.21	59.43	1.25	up	chr17	-	55868619	55868752
8174047	TIMM8A	309.86	418.37	0.74	down	chrX	-	1.01E+08	100604184
7952036	MPZL3	96.59	76.37	1.26	up	chr11	-	1.18E+08	118123065
8038326	SLC6A16	79.78	65.62	1.22	up	chr19	-	49792889	49828661
7979416	TIMM9	232.31	296.36	0.78	down	chr14	-	58875212	58894232
8117395	HIST1H2BF	411.03	497.96	0.83	down	chr6	+	26199748	26200942
8042503	MXD1	362.1	299.44	1.21	up	chr2	+	70142203	70170077
8028652	ZFP36	122.62	95.8	1.28	up	chr19	+	39897453	39900047
8103646	NEK1	415.97	499.32	0.83	down	chr4	-	1.7E+08	170533733
7926807	PDSS1	430.4	544.79	0.79	down	chr10	+	26986588	27035727
8022606	RN5S452	41.94	57.37	0.73	down	chr18	-	21750469	21750587
7973306	ABHD4	392.49	322.54	1.22	up	chr14	+	23067146	23081265
7929065	IFIT1	106.41	63.32	1.68	up	chr10	+	91152303	91163745
8073022	CBY1	184.71	226.85	0.81	down	chr22	+	39052647	39069855
8012054	DLG4	122.29	86.21	1.42	up	chr17	-	7093209	7123030
8119386	TDRG1	48.18	28.49	1.69	up	chr6	+	40346076	40347638
8050423	MYCNOS	71.11	88.49	0.8	down	chr2	-	16080035	16080364
8166607	---	45.58	61.46	0.74	down	chrX	+	28988853	28988926
8178220	---	318.25	392.46	0.81	down	chr6	+	33043748	33043918
8035795	ZNF626	53.98	44.03	1.23	up	chr19	-	20802285	20844406
8052399	BCL11A	207.47	249.88	0.83	down	chr2	-	60678302	60780768
7910636	RNY4P16	49.64	37.42	1.33	up	chr1	+	2.35E+08	234973821
8083569	TIPARP	444.64	561.13	0.79	down	chr3	+	1.56E+08	156424559
7977761	SALL2	225.74	182.38	1.24	up	chr14	-	21989231	22005337
8020724	DSG1	19.85	16.26	1.22	up	chr18	+	28898052	28936459
7987310	GJD2	147.97	121.01	1.22	up	chr15	-	35044642	35046784
8094609	FAM114A1	67.61	54.12	1.25	up	chr4	+	38869437	38947360
8143749	ZNF467	122.53	100.77	1.22	up	chr7	-	1.49E+08	149470295
8140085	MLXIPL	220.7	171.42	1.29	up	chr7	-	73007524	73038870

8030133	NUCB1	1067.08	880.31	1.21 up	chr19	+	49403600	49426528
8134415	ACN9	114.79	139.57	0.82 down	chr7	+	96745900	96811075
7959298	TMEM120B	338.29	405.83	0.83 down	chr12	+	1.22E+08	122216356
8001178	C16orf87	362.69	445.95	0.81 down	chr16	-	46835959	46865074
8120335	FAM83B	139.89	107.61	1.3 up	chr6	+	54711564	54806883
7905283	ANXA9	68.08	81.91	0.83 down	chr1	+	1.51E+08	150968114
8148149	ZHX2	365.43	298.24	1.23 up	chr8	+	1.24E+08	123986755
7907893	MR1	100.46	81.23	1.24 up	chr1	+	1.81E+08	181025689
7941749	SYT12	88.11	72.69	1.21 up	chr11	+	66774249	66818330
7908597	NR5A2	57.34	46.13	1.24 up	chr1	+	2E+08	200146552
7964460	DDIT3	163.88	129.56	1.26 up	chr12	-	57910371	57914300
8047677	CD28	31.91	38.24	0.83 down	chr2	+	2.05E+08	204602556
8140650	SEMA3E	49.01	60.28	0.81 down	chr7	-	82993222	83278324
8010295	ENGASE	185.9	152.25	1.22 up	chr17	+	77071019	77084681
7982955	---	6.33	8.04	0.79 down	chr15	+	41907429	41907497
8143448	FLJ40852	36.09	43.77	0.82 down	chr7	-	1.41E+08	141438030
7938301	AKIP1	217.33	261.41	0.83 down	chr11	+	8932701	8941626
7937934	SSU72P5	27.92	33.77	0.83 down	chr11	+	4351095	4351679
7945954	SSU72P5	27.92	33.77	0.83 down	chr11	-	4263286	4263870
8115600	C5orf54	59.18	73.85	0.8 down	chr5	-	1.6E+08	159827060
7930148	SFXN2	332.37	434.14	0.77 down	chr10	+	1.04E+08	104498951
7946328	---	64.38	84.11	0.77 down	chr11	-	7910756	7910826
8156126	RMI1	232.4	283.66	0.82 down	chr9	+	86595697	86618989
8139121	---	22.24	18.22	1.22 up	chr7	-	38396908	38398763
8174576	AMOT	919.95	1232.88	0.75 down	chrX	-	1.12E+08	112084043
8169352	NXT2	232.25	177.18	1.31 up	chrX	+	1.09E+08	108787919
8010021	TEN1-CDK3	104.1	86.15	1.21 up	chr17	+	73997409	74002078
8064864	RN5-8S7	9.05	10.99	0.82 down	chr20	-	5326702	5326772
8086451	HIGD1A	544.96	656.18	0.83 down	chr3	-	42825790	42845993
8005679	CCDC144B	101.07	83.7	1.21 up	chr17	+	20224475	20241399

8010560	PP13	46.37	33.94	1.37	up	chr17	+	78977135	78978932
8043055	DNAH6	86.51	68.23	1.27	up	chr2	+	84852098	84864410
8147744	---	24.18	18.23	1.33	up	chr8	+	1.04E+08	104095934
7948133	OR5M3	13.35	11.06	1.21	up	chr11	-	56237050	56237973
7918876	---	61.57	50.86	1.21	up	chr1	-	1.16E+08	116164623
7932598	ENKUR	8.67	11.25	0.77	down	chr10	-	25270908	25305095
8125461	HLA-DQB1	20.94	27.76	0.75	down	chr6	-	32626434	32627216
8045795	KCNJ3	52.57	41.7	1.26	up	chr2	+	1.56E+08	155713014
7959925	RN5S376	35	42.38	0.83	down	chr12	+	1.32E+08	132145704
7967705	RN5S376	35	42.38	0.83	down	chr12	-	1.32E+08	131784296
7943288	SRSF8	266.71	370.6	0.72	down	chr11	+	94800055	94804388
7997662	KIAA0513	172.16	132.7	1.3	up	chr16	+	85061410	85127836
8034217	EPOR	178.04	146.24	1.22	up	chr19	-	11487883	11495019
8031196	LAIR2	113	88.46	1.28	up	chr19	+	55014013	55021897
8073603	RNU12	169.94	207.08	0.82	down	chr22	+	43011251	43011399
8113346	---	25.05	31.98	0.78	down	chr5	-	99384562	99384619
7985224	TBC1D2B	112.94	139.87	0.81	down	chr15	+	79045450	79045650
7929052	IFIT3	37.02	27.66	1.34	up	chr10	+	91087651	91100728
7954899	CNTN1	177.73	142.39	1.25	up	chr12	+	41086356	41464094
7949956	MTL5	71.42	58.92	1.21	up	chr11	-	68474908	68519163
8147970	EBAG9	157.89	194.15	0.81	down	chr8	+	1.11E+08	110578225
8100001	---	69.83	57.41	1.22	up	chr4	-	40828674	40828782
8095758	RCHY1	16.68	20.12	0.83	down	chr4	+	76407466	76407663
8120600	---	20.82	25.55	0.81	down	chr6	+	71892315	71892421
8010285	---	81.29	66.81	1.22	up	chr17	+	76396016	76396144
8089986	---	13.36	10.59	1.26	up	chr3	-	1.22E+08	121744151
8075401	GAL3ST1	121.72	94.39	1.29	up	chr22	-	30950622	30960884
8046792	DUSP19	55.12	66.17	0.83	down	chr2	+	1.84E+08	183965371
7907601	FAM5B	26.09	32.01	0.82	down	chr1	+	1.77E+08	177251558
8135544	FOXP2	116.33	157.27	0.74	down	chr7	+	1.14E+08	114330155

8165888	---	18.01	22.29	0.81	down	chrX	+	7922621	7924183
8124524	HIST1H2AK	246.43	296.74	0.83	down	chr6	-	27805658	27806117
8143710	TRNAY17P	50.78	30.87	1.64	up	chr7	-	1.49E+08	149053820
8131944	NFE2L3	116.52	150.27	0.78	down	chr7	+	26191860	26225936
8028213	ZNF568	54.97	76.03	0.72	down	chr19	+	37407245	37443645
8121622	RSPH4A	58.98	40.69	1.45	up	chr6	+	1.17E+08	116954141
7908940	ATP2B4	465.56	384.23	1.21	up	chr1	+	2.04E+08	203713209
8059951	---	37.47	45.93	0.82	down	chr2	-	2.38E+08	238432151
8059955	RAB17	60.07	49.06	1.22	up	chr2	-	2.38E+08	238499738
7923027	GLRX2	129.42	160.65	0.81	down	chr1	-	1.93E+08	193075244
7943317	RN5S347	28.42	23.19	1.23	up	chr11	+	97528464	97528582
8100530	---	16.1	13.27	1.21	up	chr4	-	57684386	57684480
7970404	TPTE2	17.74	23.39	0.76	down	chr13	-	19997017	20110903
8118963	FANCE	212.05	258.89	0.82	down	chr6	+	35420132	35434881
7931353	PTPRE	42.71	51.41	0.83	down	chr10	+	1.3E+08	129884165
8151686	MMP16	46.01	59.4	0.77	down	chr8	-	89049460	89339776
7914127	IFI6	1027.04	793.4	1.29	up	chr1	-	27992572	27998729
7930921	---	464.21	334.9	1.39	up	chr10	+	1.21E+08	121437331
8044764	---	50.21	41.15	1.22	up	chr2	+	1.19E+08	118774245
8171297	MID1	841.13	1020.49	0.82	down	chrX	-	10413596	10851773
8028219	ZNF420	158.01	196.18	0.81	down	chr19	+	37569337	37621212
7938788	LDHC	37.3	30.47	1.22	up	chr11	+	18433853	18472793
7965166	PPFIA2	39.5	31.78	1.24	up	chr12	-	81653356	82153109
8004416	CHRNB1	172.45	138.17	1.25	up	chr17	+	7348380	7361026
7996837	CDH1	177.43	141.09	1.26	up	chr16	+	68771195	68869444
7976065	---	9.36	11.98	0.78	down	chr14	+	84640021	84640079
8016994	RNF43	182.28	220.68	0.83	down	chr17	-	56429861	56494899
8031669	ZNF470	97.8	123.04	0.79	down	chr19	+	57079377	57090119
8106978	RFESD	59.26	71.58	0.83	down	chr5	+	94982483	94993786
8085714	TRNAC31P	179.82	142.47	1.26	up	chr3	-	17741391	17741464

8142685	TMEM229A	47.12	37.02	1.27	up	chr7	-	1.24E+08	123672238
7953532	ENO2	715.02	484.58	1.48	up	chr12	+	7023614	7032860
7951008	TAF1D	1193.56	1514.16	0.79	down	chr11	-	93463146	93474662
8016213	RN5S443	143.18	186.2	0.77	down	chr17	-	43404742	43404861
7907010	FMO8P	63.88	42.28	1.51	up	chr1	+	1.67E+08	166543011
7924058	IRF6	44.23	35.09	1.26	up	chr1	-	2.1E+08	209979479
8103494	NPY1R	28.49	20.96	1.36	up	chr4	-	1.64E+08	164253748
8039645	ZNF772	66.28	81.24	0.82	down	chr19	-	57980954	57988938
7971671	GUCY1B2	72.82	56.1	1.3	up	chr13	-	51568647	51640142
7901314	---	50.7	60.78	0.83	down	chr1	+	48569306	48569878
8136347	CALD1	295.8	360.06	0.82	down	chr7	+	1.34E+08	134655474
7919382	---	28.34	23.47	1.21	up	chr1	-	1.48E+08	147716809
8007446	IFI35	99.04	77.32	1.28	up	chr17	+	41158814	41166473
8149396	OR7E8P	15.66	11.29	1.39	up	chr8	-	12541778	12544523
8056376	SCN3A	19	15.67	1.21	up	chr2	-	1.66E+08	166060553
7905503	LCE2C	25.37	17.81	1.42	up	chr1	+	1.53E+08	152649050
8051411	RN5S91	24.77	30.67	0.81	down	chr2	-	33510866	33510954
7957032	YEATS4	327.68	405.46	0.81	down	chr12	+	69753532	69784576
7909390	CR1L	14.7	11.7	1.26	up	chr1	+	2.08E+08	207911885
7936567	RAB11FIP2	286.85	345.69	0.83	down	chr10	-	1.2E+08	119806114
7899499	RAB42	32.37	25.53	1.27	up	chr1	+	28918712	28921955
7902290	CTH	308.01	400.62	0.77	down	chr1	+	70876955	70905643
8097811	DKFZP434I0714	91.29	112.87	0.81	down	chr4	+	1.53E+08	153460412
8005683	---	11.6	9.31	1.25	up	chr17	+	20226313	20226422
8037444	ZNF235	67.69	85.13	0.8	down	chr19	-	44790600	44809170
8084266	HTR3D	28.61	35.59	0.8	down	chr3	+	1.84E+08	183757157
7986068	BLM	786.51	986.36	0.8	down	chr15	+	91260579	91358686
8095545	RUFY3	293.42	368.36	0.8	down	chr4	+	71570871	71672925
7900461	ZNF684	87.04	105.32	0.83	down	chr1	+	40997233	41013841
7991904	PIGQ	162.55	199.46	0.81	down	chr16	+	620001	634109

7956097	SUOX	159.1	130.78	1.22	up	chr12	+	56391043	56399309
8104926	---	25.98	34.16	0.76	down	chr5	+	36155221	36155322
7935188	SORBS1	163.22	132.57	1.23	up	chr10	-	97071528	97321171
7952673	FLJ45950	25.29	36.55	0.69	down	chr11	-	1.29E+08	129107006
8153664	BOP1	224.65	271.48	0.83	down	chr8	-	1.45E+08	145319977
7952549	RPUSD4	180.77	218.04	0.83	down	chr11	-	1.26E+08	126081548
8040522	MFSD2B	23.87	32.05	0.74	down	chr2	+	24244676	24246600
7898916	GRHL3	98.43	73.03	1.35	up	chr1	+	24645881	24690972
7899265	SFN	140.63	116.6	1.21	up	chr1	+	27189629	27190948
8007848	LOC644172	221.36	176.74	1.25	up	chr17	+	44321463	44322413
7973748	C14orf23	72.31	88.43	0.82	down	chr14	+	29242003	29262375
8067932	LINC00478	28.12	38.36	0.73	down	chr21	+	17442842	17979542
8047403	CASP10	73.55	58.39	1.26	up	chr2	+	2.02E+08	202094127
7919303	---	56.76	75.48	0.75	down	chr1	-	1.47E+08	146556303
8081241	C3orf26	593.72	752.58	0.79	down	chr3	+	99536681	99897447
8012931	CDRT1	54.84	66.72	0.82	down	chr17	-	15491977	15502111
7933933	DNAJC12	132.84	161.67	0.82	down	chr10	-	69556048	69597937
7951032	TAF1D	106.19	134.35	0.79	down	chr11	-	93465170	93465299
8117120	ID4	238.58	288.4	0.83	down	chr6	+	19837617	19840915
8117372	HIST1H2AC	574.75	693.53	0.83	down	chr6	+	26124373	26139337
7898736	LINC00339	93.1	112.07	0.83	down	chr1	+	22351684	22357712
7977801	---	8.8	15.16	0.58	down	chr14	-	23321828	23321937
8018522	FBF1	285.26	344.26	0.83	down	chr17	-	73905925	73937221
7961363	---	45.04	56.16	0.8	down	chr12	-	12442161	12442263
8031570	RFPL4A	20.94	25.98	0.81	down	chr19	+	56273166	56274541
8042381	PNO1	411.86	531.83	0.77	down	chr2	+	68384997	68403091
7931346	---	18.42	25.48	0.72	down	chr10	+	1.29E+08	128609475
7915238	NT5C1A	116.68	94.28	1.24	up	chr1	-	40124793	40137710
8081454	---	28.27	22.93	1.23	up	chr3	+	1.06E+08	106407625
8061112	---	24.26	30.11	0.81	down	chr20	+	17469615	17470086

7997525	MLYCD	76.22	92	0.83	down	chr16	+	83932730	83949793
7980344	ZDHC2	78.39	94.39	0.83	down	chr14	-	77597621	77608137
7940582	BEST1	107.3	82.89	1.29	up	chr11	+	61717356	61732405
8132302	PP13004	60.03	49.14	1.22	up	chr7	+	36118694	36125340
7963826	PPP1R1A	191.56	158.31	1.21	up	chr12	-	54971172	54982456
8091239	RN5S143	7.17	11.29	0.63	down	chr3	-	1.42E+08	142310634
8131612	---	17.44	14.03	1.24	up	chr7	+	17245276	17245552
8138363	SOSTDC1	32.45	39.62	0.82	down	chr7	-	16501106	16505474
8138995	---	29.7	24.41	1.22	up	chr7	-	35189065	35189144
7974811	---	15.22	21.15	0.72	down	chr14	+	61246696	61247086
7918449	KCNA2	58.97	45.25	1.3	up	chr1	-	1.11E+08	111174096
8019231	PDE6G	78.66	64.2	1.23	up	chr17	-	79617250	79623615
8158823	---	16.87	13.66	1.23	up	chr9	+	1.34E+08	134002474
7929012	STAMBPL1	65.39	78.72	0.83	down	chr10	+	90639491	90734910
7969202	---	31.91	26.43	1.21	up	chr13	+	52043886	52044183
7909350	CR2	20.34	24.68	0.82	down	chr1	+	2.08E+08	207663240
8111533	LMBRD2	281.69	341.41	0.83	down	chr5	-	36103414	36152015
8118111	HCP5	87.27	70.22	1.24	up	chr6	+	31430959	31433586
7913642	---	45.17	36.74	1.23	up	chr1	-	23801082	23803135
7977497	CCNB1IP1	538.12	672.23	0.8	down	chr14	-	20779529	20801457
7937330	IFITM2	508.18	415.13	1.22	up	chr11	+	307915	309395
7944989	---	37.27	47.68	0.78	down	chr11	+	1.25E+08	125444712
7912535	---	38.21	50.86	0.75	down	chr1	-	12590392	12590475
8131379	---	326.74	400.14	0.82	down	chr7	+	6056511	6056642
8084810	---	21.86	16.61	1.32	up	chr3	+	1.9E+08	190360277
7922404	GAS5	687.67	850.95	0.81	down	chr1	-	1.74E+08	173834042
7975602	ACOT2	161.66	195.52	0.83	down	chr14	+	74035763	74042360
8057416	---	13.36	16.57	0.81	down	chr2	-	1.8E+08	179990364
8068157	KRTAP20-4	28.91	34.88	0.83	down	chr21	+	31992946	31993169
8133215	STAG3L4	182.89	225.67	0.81	down	chr7	+	66767659	66785388

8140686	SEMA3D	144.2	174.91	0.82	down	chr7	-	84624869	84782989
7992789	TNFRSF12A	651.88	514.08	1.27	up	chr16	+	3070333	3072384
8053231	LOXL3	186.5	154.05	1.21	up	chr2	-	74759385	74781085
7917850	ARHGAP29	164.34	201.81	0.81	down	chr1	-	94637307	94713133
8015031	CCR7	62.86	49.15	1.28	up	chr17	-	38710021	38721724
8167161	---	36.45	28.97	1.26	up	chrX	+	47335061	47335179
8057463	CERKL	58.95	47.79	1.23	up	chr2	-	1.82E+08	182521762
7960889	FAM86FP	243.97	293.91	0.83	down	chr12	-	8385103	8391297
8016261	LOC644172	250.64	201.22	1.25	up	chr17	-	43678235	43679197
8168790	TMEM35	67.61	54.47	1.24	up	chrX	+	1E+08	100351353
7957433	LRRIQ1	78.23	63.67	1.23	up	chr12	+	85430099	85518636
8117822	ZNRD1	80.52	99.19	0.81	down	chr6	+	30026676	30032686
8139840	ERV3-1	200.46	164.41	1.22	up	chr7	-	64451590	64453404
8105663	NLN	295.58	366.45	0.81	down	chr5	+	65018023	65125111
8174664	---	48.87	31.63	1.54	up	chrX	-	1.17E+08	117048308
8139125	TARP	41.53	31.67	1.31	up	chr7	-	38402261	38403119
8006736	DUSP14	114.6	145.81	0.79	down	chr17	+	35849951	35873598
8049075	B3GNT7	94.17	76.45	1.23	up	chr2	+	2.32E+08	232263684
7963670	MAP3K12	152.57	125.32	1.22	up	chr12	-	53874279	53893444
8043436	IGKV2D-29	21.43	28.36	0.76	down	chr2	+	89986777	89987115
8131374	AIMP2	433.07	568.58	0.76	down	chr7	+	6048882	6063465
8129108	ZUFSP	249.1	308.72	0.81	down	chr6	-	1.17E+08	116989959
7919645	SV2A	320.71	260.03	1.23	up	chr1	-	1.5E+08	149889434
8100347	SCFD2	364.71	444.93	0.82	down	chr4	-	53739149	54232242
7933204	C10orf10	114.38	92.85	1.23	up	chr10	-	45471577	45474258
7944803	VWA5A	40.9	33.49	1.22	up	chr11	+	1.24E+08	124017619
7952436	ESAM	61.68	47.89	1.29	up	chr11	-	1.25E+08	124632186
7905039	---	7.32	6.02	1.22	up	chr1	+	1.49E+08	149187682
8112196	---	14.79	10.89	1.36	up	chr5	-	56464937	56465036
7927167	---	31.19	25	1.25	up	chr10	+	43879179	43879418

8136967	OR2A5	21.49	25.98	0.83	down	chr7	+	1.44E+08	143748430
7924508	SUSD4	79.49	62.91	1.26	up	chr1	-	2.23E+08	223537520
8112672	ANKRD31	31.39	37.79	0.83	down	chr5	-	74443061	74532703
7910186	---	71.36	57.53	1.24	up	chr1	+	2.28E+08	227681557
7945952	---	54.77	66.1	0.83	down	chr11	-	4010387	4010692
7974737	LRRC9	39.26	31.57	1.24	up	chr14	+	60386431	60530277
8005636	---	39.19	53.01	0.74	down	chr17	+	19506660	19506727
7976000	ADCK1	163.6	196.36	0.83	down	chr14	+	78266469	78400294
8150580	MTND1P7	20.71	14.47	1.43	up	chr8	-	47739518	47739585
7920238	S100A12	13.48	16.41	0.82	down	chr1	-	1.53E+08	153348125
7929533	LOC100653119	9.7	7.38	1.31	up	chr10	+	97741700	97743704
8065194	---	105.63	76.48	1.38	up	chr20	-	18094113	18094223
8036744	EID2B	110.68	141.08	0.78	down	chr19	-	40021630	40023495
8145795	---	681.53	840.15	0.81	down	chr8	+	33397529	33397655
7972674	TEX30	127.28	156.42	0.81	down	chr13	-	1.03E+08	103426161
7982070	SNORD115-32	15.76	12.96	1.22	up	chr15	+	25474114	25474195
8139158	---	95.7	77.64	1.23	up	chr7	-	38570642	38570939
7963052	---	21.17	25.68	0.82	down	chr12	-	49526638	49526730
7916167	ORC1	465.6	570.2	0.82	down	chr1	-	52838501	52870131
8031640	ZNF583	115.99	155.08	0.75	down	chr19	+	56915718	56936400
8156261	---	14.36	20.23	0.71	down	chr9	+	90989184	90989272
8085193	LOC440944	33.06	44.98	0.73	down	chr3	-	9438147	9438668
8076329	---	14.81	19.25	0.77	down	chr22	-	41773183	41773287
8156160	KIF27	161.29	206.48	0.78	down	chr9	+	88388756	88401092
8065278	LOC643659	52.76	43.72	1.21	up	chr20	-	20056619	20057068
7898721	---	23.34	17	1.37	up	chr1	+	22313974	22314270
7897441	H6PD	78.19	95.34	0.82	down	chr1	+	9294834	9331396
7962137	---	9.05	12.61	0.72	down	chr12	-	31229801	31229907
7955448	---	9.54	7.86	1.21	up	chr12	+	51431282	51431388
8108180	---	1278.62	1694.86	0.75	down	chr5	+	1.34E+08	134259812

8005048	MYOCD	36.15	29.28	1.23	up	chr17	+	12569214	12667020
7918755	---	52.94	66.43	0.8	down	chr1	-	1.15E+08	115088855
8069700	N6AMT1	103.44	124.77	0.83	down	chr21	-	30244513	30257766
7929814	---	11.5	9.55	1.21	up	chr10	+	1.02E+08	102018431
8172086	---	255.87	308.1	0.83	down	chrX	-	39645778	39646077
7919390	---	227.36	291.39	0.78	down	chr1	-	1.48E+08	147806891
7983228	MAP1A	182.64	142.91	1.28	up	chr15	+	43803156	43823818
7960771	CD163L1	55.75	45.85	1.22	up	chr12	-	7597556	7596753
7979904	ADAM21	20.75	25.87	0.8	down	chr14	-	70712470	70714518
7921358	OR10T1P	28.33	23.44	1.21	up	chr1	-	1.58E+08	158415804
7901495	---	15.65	12.25	1.28	up	chr1	+	53267886	53268008
7993776	LOC81691	254.59	310.21	0.82	down	chr16	+	20817821	20860990
8007605	---	9.64	7.98	1.21	up	chr17	+	42384473	42384540
7947322	DCDC1	35.39	28.78	1.23	up	chr11	-	31284171	31391321
8175261	MIR503	91.17	74.16	1.23	up	chrX	-	1.34E+08	133680428
8140620	PCLO	74.2	92.07	0.81	down	chr7	-	82387891	82791908
8101673	---	82.39	55.46	1.49	up	chr4	-	88665106	88665205
7901710	---	8.24	6.66	1.24	up	chr1	+	55839110	55839177
8058927	TMBIM1	153.06	119.53	1.28	up	chr2	-	2.19E+08	219157280
7964596	---	46.49	60.69	0.77	down	chr12	-	58371731	58372056
8106931	ANKRD32	151.4	186.79	0.81	down	chr5	+	93954052	94033326
8107321	EPB41L4A-AS1	576.12	691.26	0.83	down	chr5	+	1.11E+08	111498004
8096959	ANK2	112.98	139.13	0.81	down	chr4	+	1.14E+08	114304891
8109177	---	40.18	31.81	1.26	up	chr5	+	1.49E+08	149101935
7905490	LCE3C	46.16	56.06	0.82	down	chr1	+	1.53E+08	152573492
7896759	LOC643837	88.06	108.5	0.81	down	chr1	+	791391	793751
7986567	---	24.15	30.27	0.8	down	chr15	-	20300986	20301282
7986633	---	24.15	30.27	0.8	down	chr15	-	21308172	21308467
8115666	NUDCD2	91.98	111.64	0.82	down	chr5	-	1.63E+08	162887143
8100734	UGT2B17	11.88	8.81	1.35	up	chr4	-	69402902	69434245

7906777	FCGR2B	19.88	15.44	1.29	up	chr1	+	1.62E+08	161648444
7998927	TRNAP24P	430.14	200.29	2.15	up	chr16	-	3202609	3202680
7974052	---	13.15	16.71	0.79	down	chr14	+	39456485	39456585
7951413	CARD17	14.43	11.69	1.23	up	chr11	-	1.05E+08	104972158
8102800	SLC7A11	175.53	273.04	0.64	down	chr4	-	1.39E+08	139163503
7929612	---	32.38	26.23	1.23	up	chr10	+	99057051	99057314
7982337	---	39.37	50.25	0.78	down	chr15	+	32220506	32220637
8128383	COQ3	138.58	168.32	0.82	down	chr6	-	99817276	99842080
8174983	RN5S513	67.09	80.36	0.83	down	chrX	-	1.29E+08	128570624
7957467	C12orf29	686.04	824.58	0.83	down	chr12	+	88429268	88443937
8021666	---	16.43	13.57	1.21	up	chr18	+	63339339	63339866
8031566	---	17.48	13.6	1.28	up	chr19	+	56218943	56219248
8134252	GNGT1	18.05	22.26	0.81	down	chr7	+	93535820	93540485
7930775	---	7.07	5.85	1.21	up	chr10	+	1.18E+08	118297814
8178590	DDAH2	209.61	166.72	1.26	up	chr6	-	31694817	31698039
8179819	DDAH2	209.61	166.72	1.26	up	chr6	-	31694817	31698039
8062480	SNHG11	153	184.5	0.83	down	chr20	+	37075325	37079564
7939613	MAPK8IP1	210.74	164.3	1.28	up	chr11	+	45907202	45928016
8124416	HIST1H3D	302.94	385.99	0.78	down	chr6	-	26196129	26199513
7911339	---	1541.69	1984.25	0.78	down	chr1	-	566207	566280
8165698	---	1541.69	1984.25	0.78	down	chrM	-	5658	5731
8132992	---	71.05	86.15	0.82	down	chr7	+	57238552	57238610
8157300	BSPRY	137.69	111.37	1.24	up	chr9	+	1.16E+08	116133513
8034097	LOC147727	85.77	112.98	0.76	down	chr19	-	10762829	10763104
7923173	MIR181B1	34.89	44.99	0.78	down	chr1	-	1.99E+08	198828111
7920877	ARHGEF2	295.73	236.83	1.25	up	chr1	-	1.56E+08	155959864
7948397	---	402.2	489.51	0.82	down	chr11	-	59394420	59394491
8039892	KIR2DS5	21.22	16.55	1.28	up	chr19_gl000209_random	+	98088	113132
7996260	---	1878.99	2282.3	0.82	down	chr16	+	59765259	59765358
7996891	CIRH1A	1973.62	2398.55	0.82	down	chr16	+	69166533	69202924

8124500	LOC439938	17.64	21.24	0.83	down	chr6	-	27373747	27374112
7969241	RNY4P24	33.2	44.9	0.74	down	chr13	+	52974139	52974232
7986675	NIPA1	294.53	239.65	1.23	up	chr15	-	23043279	23086436
8031759	ZNF773	138.31	174.83	0.79	down	chr19	+	58011309	58024436
8088915	---	11.17	8.84	1.26	up	chr3	-	76014124	76014220
8031750	ZNF419	75.55	91.52	0.83	down	chr19	+	57999109	58006048
7948101	OR4A47	9.64	12.14	0.79	down	chr11	-	51458714	51459613
7926979	---	96.15	74.69	1.29	up	chr10	+	35215702	35215810
8057954	C2orf66	22.7	18.53	1.23	up	chr2	-	1.98E+08	197675000
8159846	---	12.14	9.48	1.28	up	chr9	-	1001863	1001963
8110569	SQSTM1	656.23	539.16	1.22	up	chr5	+	1.79E+08	179265078
8139113	---	22.27	17.68	1.26	up	chr7	-	38372736	38375237
8035083	CYP4F2	28.81	36.36	0.79	down	chr19	-	15988834	16008885
8131996	LOC401317	465.08	575.92	0.81	down	chr7	+	28338940	28865511
8037433	ZNF45	60.61	80.96	0.75	down	chr19	-	44416781	44429562
8044473	POLR1B	339.91	413.52	0.82	down	chr2	+	1.13E+08	113335408
8068361	SLC5A3	572.25	456	1.25	up	chr21	+	35467162	35478561
7944152	IL10RA	62.11	51.2	1.21	up	chr11	+	1.18E+08	117872194
7989951	LOC100131796	12.75	16.36	0.78	down	chr15	-	67336562	67336915
8153258	SLC45A4	60.45	74.12	0.82	down	chr8	-	1.42E+08	142218782
8166563	SCARNA23	167.64	204.68	0.82	down	chrX	+	24762558	24762687
8154765	DNAJA1	1621.36	1231.09	1.32	up	chr9	+	33025209	33039905
8081878	---	85.91	110.29	0.78	down	chr3	+	1.19E+08	119248323
7971905	PCDH20	78.55	61.43	1.28	up	chr13	-	61983818	61989396
7990652	---	39.53	47.85	0.83	down	chr15	-	78209090	78209254
8179055	ZNRD1	192.44	238.42	0.81	down	chr6	+	30029117	30032678
8173428	---	236.72	194.7	1.22	up	chrX	-	70240126	70240283
8025124	FLJ25758	40.85	31.26	1.31	up	chr19	+	7011514	7013338
7956989	MDM2	2117.02	2537.66	0.83	down	chr12	+	69201971	69234214
7948364	MPEG1	41.84	33.73	1.24	up	chr11	-	58978136	58980359

7922029	GPA33	70.34	56.55	1.24	up	chr1	-	1.67E+08	167059868
8043043	DNAH6	123.52	98.53	1.25	up	chr2	+	84743579	84811978
7957715	NEDD1	1165.04	1491.21	0.78	down	chr12	+	97301016	97347128

Supplementary Table S4. Embryos at 9.5 and 10.5 dpc recovered from *VRTN*^{+/-}

Embryonic day		intercrosses No. of offspring of genotype			
		+/+	+/-	-/-	Total
9.5	Predicted	15	30	15	60
	Observed	12	32	17	61
10.5	Predicted	18	36	18	72
	Observed	23	35	16	74

Supplementary Table S5. Enriched GO categories of 42 differentially expressed genes between VRTN mutant (QQ) and wild-type pig (qq) embryos at E17.5.

Ontology	Class	Number	Gene
biological_process	biological regulation	10	ENSSSCT00000009803;ENSSSCT00000002199;ENSSSCT00000000519;ENSSSCT00000017456;ENSSSCT00000007658;ENSSSCT00000006012;ENSSSCT00000015009;ENSSSCT00000012911;ENSSSCT00000032249;ENSSSCT00000029810
biological_process	cell killing	1	ENSSSCT00000000519
biological_process	cellular component organization or biogenesis	4	ENSSSCT00000007658;ENSSSCT00000012911;ENSSSCT00000028216;ENSSSCT00000002818
biological_process	cellular process	21	ENSSSCT00000002818;ENSSSCT00000009803;ENSSSCT00000025335;ENSSSCT00000026904;ENSSSCT00000002199;ENSSSCT0000000519;ENSSSCT0000004953;ENSSSCT00000005787;ENSSSCT00000017456;ENSSSCT00000031443;ENSSSCT00000007658;ENSSSCT00000013588;ENSSSCT00000032249;ENSSSCT00000015009;ENSSSCT00000012911;ENSSSCT00000018526;ENSSSCT00000006012;ENSSSCT00000026299;ENSSSCT00000031124;ENSSSCT00000029810;ENSSSCT0000003052
biological_process	developmental process	8	ENSSSCT00000009803;ENSSSCT00000012911;ENSSSCT00000017456;ENSSSCT00000007658;ENSSSCT00000015009;ENSSSCT00000006012;ENSSSCT00000013588;ENSSSCT00000004953
biological_process	establishment of localization	8	ENSSSCT0000000519;ENSSSCT00000016077;ENSSSCT00000031443;ENSSSCT00000025335;ENSSSCT00000012911;ENSSSCT00000026904;ENSSSCT00000009803;ENSSSCT00000002818
biological_process	growth	1	ENSSSCT00000032249
biological_process	immune system process	2	ENSSSCT0000000519;ENSSSCT00000015009
biological_process	localization	9	ENSSSCT0000000519;ENSSSCT00000016077;ENSSSCT00000031443;ENSSSCT00000025335;ENSSSCT00000007658;ENSSSCT00000012911;ENSSSCT00000026904;ENSSSCT00000009803;ENSSSCT00000002818
biological_process	metabolic process	18	ENSSSCT00000025335;ENSSSCT00000026904;ENSSSCT0000000519;ENSSSCT00000028216;ENSSSCT00000007658;ENSSSCT00000031443;ENSSSCT00000013588;ENSSSCT00000032249;ENSSSCT00000015009;ENSSSCT00000029021;ENSSSCT00000018526;ENSSSCT00000009803;ENSSSCT00000006012;ENSSSCT00000026299;ENSSSCT00000031124;ENSSSCT00000003052;ENSSSCT00000012911;ENSSSCT0000002199
biological_process	multi-organism process	3	ENSSSCT0000000519;ENSSSCT00000013588;ENSSSCT00000023548
biological_process	multicellular organismal process	9	ENSSSCT00000015009;ENSSSCT00000009803;ENSSSCT00000017456;ENSSSCT00000012911;ENSSSCT00000013588;ENSSSCT0000004953;ENSSSCT0000003052;ENSSSCT00000007658;ENSSSCT00000000519
biological_process	negative regulation of biological process	5	ENSSSCT0000000519;ENSSSCT00000007658;ENSSSCT00000017456;ENSSSCT00000012911;ENSSSCT00000032249
biological_process	positive regulation of biological process	4	ENSSSCT0000000519;ENSSSCT00000017456;ENSSSCT00000015009;ENSSSCT00000012911
biological_process	regulation of biological process	10	ENSSSCT00000009803;ENSSSCT00000002199;ENSSSCT0000000519;ENSSSCT00000017456;ENSSSCT00000007658;ENSSSCT00000006012;ENSSSCT00000015009;ENSSSCT00000012911;ENSSSCT00000032249;ENSSSCT00000029810
biological_process	reproduction	3	ENSSSCT00000015009;ENSSSCT00000009803;ENSSSCT00000013588
biological_process	reproductive process	3	ENSSSCT00000015009;ENSSSCT00000009803;ENSSSCT00000013588
biological_process	response to stimulus	8	ENSSSCT00000009803;ENSSSCT00000002199;ENSSSCT00000015009;ENSSSCT00000032249;ENSSSCT00000017456;ENSSSCT0000000519;ENSSSCT00000012911;ENSSSCT00000029810
biological_process	rhythmic process	1	ENSSSCT00000009803
biological_process	signaling	7	ENSSSCT00000009803;ENSSSCT00000002199;ENSSSCT00000017456;ENSSSCT0000000519;ENSSSCT00000029810;ENSSSCT00000012911;ENSSSCT0000003052
biological_process	single-organism process	15	ENSSSCT00000002818;ENSSSCT00000009803;ENSSSCT00000017456;ENSSSCT00000002199;ENSSSCT00000012911;ENSSSCT0000000519;ENSSSCT00000032249;ENSSSCT00000015009;ENSSSCT00000016077;ENSSSCT00000007658;ENSSSCT00000025335;ENSSSCT00000013588;ENSSSCT00000004953;ENSSSCT00000003052;ENSSSCT00000029810
cellular_component	cell	22	ENSSSCT00000013588;ENSSSCT00000028216;ENSSSCT00000002818;ENSSSCT00000015009;ENSSSCT00000026904;ENSSSCT00000018331;ENSSSCT0000003052;ENSSSCT00000019357;ENSSSCT00000006012;ENSSSCT00000023548;ENSSSCT00000032249;ENSSSCT00000007658;ENSSSCT00000016884;ENSSSCT00000009803;ENSSSCT00000029791;ENSSSCT00000029810;ENSSSCT00000025335;ENSSSCT00000002199;ENSSSCT00000031443;ENSSSCT00000029021;ENSSSCT00000016643;ENSSSCT00000018526
cellular_component	cell part	22	ENSSSCT00000013588;ENSSSCT00000028216;ENSSSCT00000002818;ENSSSCT00000015009;ENSSSCT00000026904;ENSSSCT00000018331;ENSSSCT0000003052;ENSSSCT00000019357;ENSSSCT00000006012;ENSSSCT00000023548;ENSSSCT00000032249;ENSSSCT00000007658;ENSSSCT00000016884;ENSSSCT00000009803;ENSSSCT00000029791;ENSSSCT00000029810;ENSSSCT00000025335;ENSSSCT00000002199;ENSSSCT00000031443;ENSSSCT00000029021;ENSSSCT00000016643;ENSSSCT00000018526
cellular_component	extracellular matrix	1	ENSSSCT00000004953
cellular_component	extracellular region	6	ENSSSCT00000026299;ENSSSCT00000009803;ENSSSCT00000012911;ENSSSCT00000031124;ENSSSCT0000000519;ENSSSCT00000004953
cellular_component	extracellular region part	6	ENSSSCT00000026299;ENSSSCT00000009803;ENSSSCT00000012911;ENSSSCT00000031124;ENSSSCT0000000519;ENSSSCT00000004953
cellular_component	macromolecular complex	7	ENSSSCT00000013588;ENSSSCT00000028216;ENSSSCT00000002818;ENSSSCT00000026904;ENSSSCT00000019357;ENSSSCT00000016077;ENSSSCT00000032249
cellular_component	membrane	7	ENSSSCT00000026904;ENSSSCT00000026299;ENSSSCT000000031124;ENSSSCT00000017456;ENSSSCT00000025335;ENSSSCT00000016407;ENSSSCT00000023548
cellular_component	membrane part	5	ENSSSCT00000026904;ENSSSCT00000017456;ENSSSCT00000025335;ENSSSCT00000016407;ENSSSCT00000023548
cellular_component	membrane-enclosed lumen	6	ENSSSCT00000032249;ENSSSCT00000029021;ENSSSCT00000016643;ENSSSCT00000013588;ENSSSCT00000018526;ENSSSCT00000015009
cellular_component	organelle	17	ENSSSCT00000002818;ENSSSCT00000015009;ENSSSCT00000026904;ENSSSCT00000018331;ENSSSCT0000003052;ENSSSCT00000019357;ENSSSCT00000006012;ENSSSCT00000023548;ENSSSCT00000032249;ENSSSCT00000007658;ENSSSCT00000025335;ENSSSCT00000031443;ENSSSCT00000029791;ENSSSCT00000029021;ENSSSCT00000016643;ENSSSCT00000013588;ENSSSCT00000018526
cellular_component	organelle part	11	ENSSSCT00000002818;ENSSSCT00000015009;ENSSSCT00000026904;ENSSSCT00000032249;ENSSSCT00000007658;ENSSSCT00000025335;ENSSSCT00000031443;ENSSSCT00000029021;ENSSSCT00000016643;ENSSSCT00000013588;ENSSSCT00000018526
molecular_function	binding	21	ENSSSCT00000032249;ENSSSCT00000012911;ENSSSCT00000004785;ENSSSCT00000029791;ENSSSCT00000016884;ENSSSCT00000016643;ENSSSCT00000019357;ENSSSCT00000006012;ENSSSCT00000007658;ENSSSCT00000026299;ENSSSCT00000031124;ENSSSCT00000023548;ENSSSCT00000016077;ENSSSCT00000018526;ENSSSCT00000002818;ENSSSCT0000002199;ENSSSCT0000000519;ENSSSCT00000015009;ENSSSCT00000029810;ENSSSCT00000009803;ENSSSCT00000013588
molecular_function	catalytic activity	11	ENSSSCT00000031443;ENSSSCT00000005787;ENSSSCT00000002199;ENSSSCT00000026904;ENSSSCT00000029791;ENSSSCT00000002818;ENSSSCT00000018331;ENSSSCT00000018526;ENSSSCT00000029021;ENSSSCT00000025335;ENSSSCT00000023548
molecular_function	enzyme regulator activity	2	ENSSSCT00000002199;ENSSSCT00000012911
molecular_function	molecular transducer activity	1	ENSSSCT00000017456
molecular_function	nucleic acid binding transcription factor activity	2	ENSSSCT00000003052;ENSSSCT00000015009
molecular_function	protein binding transcription factor activity	1	ENSSSCT00000015009
molecular_function	receptor activity	1	ENSSSCT00000017456
molecular_function	structural molecule activity	3	ENSSSCT00000013588;ENSSSCT00000028216;ENSSSCT00000004953
molecular_function	transporter activity	2	ENSSSCT00000026904;ENSSSCT00000016077

Supplementary Table S6. Two differentially expressed genes – NOTCH2 and HSPG2 – between VRTN mutant (QQ) and wild-type (qq) pig embryos at the thoracic somite stage (E17.5) are directly relevant to abnormal vertebral segmentation in human and model animals

Genes	Ensembl ID	Syndromes	OMIM reference
<i>NOTCH2</i>	ENSSSCT00000024449	Alagille	118450
<i>HSPG2</i>	ENSSSCT00000003907	Silverman	224410
	ENSSSCT00000026299		
	ENSSSCT00000031124		