

Supplementary Table 7. Differential expressed genes between TALEN-edited pigs and wild type strain control

Order	Tran	TranAcc	GeneName	Chr	Start	End	Strand	Type	Status	Desc	Num_of_Samples	EXP:C1:PKM	EXP:C1:PKM	EXP:C3:PKM	EXP:WT:PKM	C1/WT	C3/WT	Rseq-WGS (TranAcc)	Rseq-WGS (GeneName)	
12851	TBIG01285	ENSSSCG0	MS4A8B		2	1057287	10573067	-	CODING	KNOWN	Uncharacter	7	993.712	2175.65	169.184	6486.59	-6.52764	-2.98145	-38.3404	-
25850	TBIG02585	XLOC_025f	Brf1	GL892627	61598	64554	-	CODING	NOVEL	Transcripti	7	5844.93	5147.78	596.764	14674.7	-2.51067	-2.50669	-24.5905	-	
21241	TBIG02124	ENSSSCG0	SLA-5		7	24643495	24685566	+	CODING	NOVEL	Uncharacter	7	2469.65	1117.89	633.824	13588.6	-5.50224	-12.1556	-21.4391	-
26453	TBIG02645	XLOC_026f	ALAD	GL893446	1	256	+	CODING	NOVEL	Delta-amir	7	18092.1	11315.1	4975.5	94831.2	-5.24158	-8.38094	-19.0596	-	
28902	TBIG02890	XLOC_028f	Mark4	GL896419	25788	25980	-	CODING	NOVEL	MAP/micr	7	1224.94	2334.19	543.951	9744.39	-7.95499	-4.17463	-17.9141	-	
26029	TBIG02602	XLOC_026f	Lrrc61	GL892911	272446	272602	-	CODING	NOVEL	Leucine-ric	7	1343.4	12552.7	3278.29	52643.9	-39.1871	-4.19383	-16.0583	-	
7248	TBIG00724	ENSSSCG0	USMG5		14	50545515	50545776	+	CODING	KNOWN	up-regulat	7	1735.83	4383.96	940.426	13295	-7.65916	-3.03265	-14.1372	-
28708	TBIG02870	XLOC_028f	IL3RA	GL896347	6795	7293	-	CODING	NOVEL	Interleukin	7	343.757	535.83	148.954	1996.01	-5.80646	-3.72508	-13.4002	-	
3163	TBIG00316	XLOC_003f	plxdc2		10	60033512	60033722	-	CODING	NOVEL	Plexin dom	7	466.216	413.47	89.2053	1100.18	-2.35981	-2.66085	-12.3331	-
26519	TBIG02651	XLOC_026f	IL10RB	GL893534	34	249	-	CODING	NOVEL	Interleukin	7	444.221	897.454	178.531	2135.31	-4.80686	-2.3793	-11.9604	-	
1358	TBIG00135	ENSSSCG0	CSNK1G1		1	1.19E+08	1.19E+08	-	CODING	KNOWN	Uncharacter	7	185.684	281274	63.8625	621.448	-3.3468	-22.094	-9.73103	-
27071	TBIG02707	XLOC_027f	Klc3	GL894198	17666	17856	-	CODING	NOVEL	Kinesin lig	7	1785.26	2045.74	876.138	7911.74	-4.4317	-3.86742	-9.03024	-	
26368	TBIG02636	XLOC_026f	PLEKH1	GL893315	20220	20387	-	CODING	NOVEL	Pleckstrin l	7	1024.25	807.283	452.041	4043	-3.94728	-5.00816	-8.94388	-	
25530	TBIG02553	XLOC_025f	Dnm3		9	1.26E+08	1.26E+08	-	CODING	NOVEL	Dynamin-2	7	236.256	93.8751	183.984	1641.89	-6.94962	-17.4902	-8.92409	-
3726	TBIG00372	XLOC_003f	VWA8		11	26081870	26082015	-	CODING	NOVEL	von Willeb	7	9889.72	1107.1	556.956	4939.05	2.002353	-4.6125	-8.86794	-
28459	TBIG02845	XLOC_028f	YBEY	GL896243	11753	13386	-	CODING	NOVEL	Putative ri	7	11671.8	9993.06	3216.59	28354.6	-2.42933	-2.83743	-8.81511	-	
3103	TBIG00310	XLOC_003f	Rpi7		10	38814256	38814448	-	CODING	NOVEL	60S riboso	7	36830	28929.8	10280.7	89110.3	-2.27831	-2.90047	-8.1619	-
28677	TBIG02867	XLOC_028f	UBAC1	GL896332	34809	35168	-	CODING	NOVEL	Ubiquitin-i	7	896.056	487.796	387.436	3118.89	-3.48069	-6.39384	-8.05008	-	
26632	TBIG02663	XLOC_026f	ALAD	GL893668	1	205	-	CODING	NOVEL	Delta-amir	7	508.509	213.068	144.345	1032.23	-2.02991	-4.8446	-7.15113	-	
29618	TBIG02961	ENSSSCG0	Inmt	JH118806	24194	29094	-	CODING	NEW_AS	Uncharacter	7	51.2178	12.9122	19.7954	131.443	-2.56635	-10.1798	-6.64008	-	
28310	TBIG02831	XLOC_028f	Aspscr1	GL896186	4539	5283	-	CODING	NOVEL	Tether con	7	111101	427287	133790	887772	-7.99068	-2.07669	-6.63556	-	
28755	TBIG02875	XLOC_028f	SLC2A4RG	GL896364	17152	17420	-	CODING	NOVEL	SLC2A4 re	7	529.225	1680.01	684.833	4442.35	-8.39407	-2.64424	-6.48676	-	
28760	TBIG02876	XLOC_028f	RTEL1	GL896364	44051	44631	-	CODING	NOVEL	Regulator i	7	2544.08	5045.32	2144.24	13675.2	-5.3753	-2.71047	-6.37764	-	
10113	TBIG01011	XLOC_010f	NDUF4F2		16	42680451	42680654	-	CODING	NOVEL	Mimitin, m	7	1021.82	566.254	447.605	2677.44	-2.62027	-4.72834	-5.9817	-
29136	TBIG02913	XLOC_029f	MUCM_RA	GL896545	5	1258	-	CODING	NOVEL	Ig mu chai	7	1902.74	3482.87	2616.84	15150.9	-7.96267	-4.35012	-5.78977	-	
26170	TBIG02617	XLOC_026f	FCGR3	GL893101	2	233	-	CODING	NOVEL	Low affin	7	21882.7	20977.6	10363.2	54871.7	-2.50754	-2.61573	-5.29486	-	
20022	TBIG02002	XLOC_020f	SORCS2		8	3950581	3957905	-	CODING	NOVEL	VPS10 dor	6	141.638	30.0105	109.574	565.652	-3.99365	-18.8485	-5.16228	-
32033	TBIG00700	XLOC_007f	Pde9a		13	2.16E+08	2.16E+08	-	CODING	NOVEL	High affini	7	6734.99	10161	6118.63	31554.9	-4.68522	-3.10549	-5.15718	-
28498	TBIG02849	XLOC_028f	ANAPC2	GL896260	5047	5903	-	CODING	NOVEL	Anaphase-	7	5632.6	4455.65	2653.28	13344.2	-2.3691	-2.99489	-5.02932	-	
28944	TBIG02894	ENSSSCG0	LSM2	GL896442	6429	6878	-	CODING	KNOWN	Sus scrofa	7	2764.95	2160.36	1509.04	7535.84	-2.72549	-3.48823	-4.9938	-	
2436	TBIG00243	XLOC_002f	SHB		1	2.67E+08	2.67E+08	-	CODING	NOVEL	SH2 doma	7	458.985	203.963	249.52	1207.42	-2.63063	-5.9198	-4.83897	-
7176	TBIG00717	ENSSSCG0	PLBD2		14	40832763	40853776	+	CODING	NEW_AS	phospholip	7	290.154	277.52	255.526	114.423	2.535801	2.425387	-4.47794	-
1163	TBIG01166	ENSSSCG0	Inmt		18	46637157	46641921	+	CODING	NOVEL	Indolethyl	7	86.2352	30.2503	70.6645	315.744	-3.66143	-10.4377	-4.46821	-
28832	TBIG02883	XLOC_028f	Id3	GL896386	13540	13725	-	CODING	NOVEL	DNA-bindi	7	3118.86	7254.2	12690.4	53577.3	-17.1875	-7.38569	-4.22188	-	
21952	TBIG02195	ENSSSCG0	TMP-CH24		7	24706220	24722563	-	CODING	NOVEL	-	7	44834.2	26013.1	30648.3	126113	-2.17288	-4.84806	-11.1484	-
25078	TBIG02507	ENSSSCG0	STAP4		9	74981686	75048318	-	CODING	NEW_AS	Sus scrofa	7	534.424	630.743	55.8317	227.229	2.351918	2.775803	-4.06989	-
12695	TBIG01269	XLOC_012f	gag-pol		2	742220	747473	-	CODING	NOVEL	Gag-Pol pi	7	28.239	18.9851	16.1817	64.6756	-2.29029	-3.40665	-3.99684	-
28985	TBIG02898	ENSSSCG0	CDC137	GL896467	17073	19084	+	CODING	NOVEL	coiled-coil	7	45.3546	21.9816	27.73	107.236	-2.36439	-4.87844	-3.86715	-	
9846	TBIG00984	XLOC_009f	Lilrb3		16	86105298	86420144	+	CODING	NEW_AS	Leukoocyte	7	15.815	18.5381	10.4448	38.1865	-2.41457	-2.05989	-3.65603	-
11666	TBIG01166	ENSSSCG0	Polr2l		2	142435	143584	-	CODING	KNOWN	Uncharacter	7	434.073	383.895	252.755	912.007	-2.10105	-2.37567	-3.60826	-
28298	TBIG02829	XLOC_028f	CXB	GL896176	1	516	-	CODING	NOVEL	Creatine ki	7	8803.22	15344.7	10522.1	37111.1	-4.21563	-2.4185	-3.52697	-	
26282	TBIG02628	XLOC_026f	TMEM50A	GL893200	4	247	-	CODING	NOVEL	Transmeml	7	250.389	125.967	197.585	687.195	-2.74451	-5.45536	-3.47797	-	
14008	TBIG01400	XLOC_014f	skp1		2	1.46E+08	1.46E+08	-	CODING	NOVEL	S-phase ki	7	495282	508346	388191	1309070	-2.64308	-2.57136	-3.37223	-
28427	TBIG02842	XLOC_028f	Notch1	GL896225	29279	29470	-	CODING	NOVEL	Neurogeni	7	341.54	4103.8	3043.43	9855.52	-2.88561	-2.40156	-3.23829	-	
25707	TBIG02570	XLOC_025f	ALAD	GL892357	1	153	-	CODING	NOVEL	Delta-amir	7	4997.38	7484.45	4885.37	15294	-3.0604	-2.04344	-3.13057	-	
29719	TBIG02971	XLOC_029f	DHODH	JH118898	117287	117660	-	CODING	NOVEL	Dihydrooro	7	19.9777	39.4171	48.8822	152.807	-7.64888	-3.87667	-3.12603	-	
11812	TBIG01181	ENSSSCG0	FTH1		2	8983277	8986090	+	CODING	KNOWN	Sus scrofa	7	2699.56	2302.27	1858.38	5776.74	-2.13988	-2.50913	-3.10848	-
26017	TBIG02601	XLOC_026f	Atp6v0e2	GL892911	249005	252536	+	CODING	NOVEL	V-type pro	7	1802.02	912.166	1340.96	4077.25	-2.2626	-4.46986	-3.04055	-	
8245	TBIG00824	ENSSSCG0	UROS		14	1.47E+08	1.47E+08	-	CODING	NEW_AS	uroporph	7	92.8593	37.3737	68.2353	203.717	-2.19382	-5.45081	-2.98551	-
28476	TBIG02847	XLOC_028f	OGFR	GL896248	17478	17712	-	CODING	NOVEL	Opioid rec	7	64.4559	424.353	320.956	945.201	-1.64643	-2.27379	-2.94496	-	
14314	TBIG01431	ENSSSCG0	HBM		3	40948175	40948852	+	CODING	KNOWN	hemoglobi	7	123.249	1175.84	4474.71	13125.1	-106.493	-11.1623	-2.93317	-
18556	TBIG01855	XLOC_018f	TPT1		5	16183353	16183667	-	CODING	NOVEL	Translation	7	4311.82	3349.63	4702.8	13772.9	-3.19422	-4.11177	-2.92866	-
18253	TBIG01825	ENSSSCG0	Itr2		5	51068458	51115752	-	CODING	NEW_AS	Uncharacter	7	394.53	253.902	409.283	1196.59	-3.03295	-4.7128	-2.92362	-
14478	TBIG01447	ENSSSCG0	RNF181		3	62044672	62046534	+	CODING	NEW_AS	Uncharacter	7	12.0065	14.9899	11.8412	33.6444	-2.80218	-2.24447	-2.8413	-
28284	TBIG02828	XLOC_028f	NAPRT1	GL896158	3	235	-	CODING	NOVEL	Nicotinate	7	357.39	511.042	690.025	1916.85	-5.36347	-3.75087	-2.77794	-	
19785	TBIG01978	ENSSSCG0	KARS		6	11913750	11914466	-	CODING	KNOWN	Uncharacter	7	73.3252	74.9938	77.6953	213.652	-2.91376	-2.86805	-2.74987	-
26332	TBIG02633	XLOC_026f	Ube2m	GL893268	2	136	-	CODING	NOVEL	NEDB8-co	7	6588.11	41615.5	5228.5	14337.8	-2.17631	2.902502	-2.74224	-	
23878	TBIG02387	XLOC_023f	Pol		6	64377465	64377626	-	CODING	NOVEL	Retrovirus	6	3454.52	3828.55	411.104	1080.51	3.19712	3.54328	-2.62831	-
29556	TBIG02955	ENSSSCG0	C18orf8	JH118750	12529	14226	-	CODING	KNOWN	Uncharacter	7	200.381	236.421	222.718	581.38	-2.90137	-2.45909	-2.61039	-	
21950	TBIG02195	ENSSSCG0	SLA-5		7	24684421	24749212	-	CODING	NOVEL	Uncharacter	7	25.0326	22.7202	24.6405	64.2552	-2.56686	-2.82811	-2.60771	-
24971	TBIG02497	ENSSSCG0	SORL1		9	53829400	53908876	-	CODING	NEW_AS	Uncharacter	7	128.003	94.3783	14.1043	36.4657	3.51023	2.588139	-2.58453	-

26863	TB1G02686 XLOC_0261 SENP3	GL893964.	2	1393	+	CODING	NOVEL	Sentrin-spr	7	30.0942	28.351	30.6696	14.167	2.124246	2.0012	2.164862	-	-	
8976	TB1G00897 ENSSSCG0 NMI		15	3600	29467	-	CODING	NEW_AS	N-myc (an	7	25.4716	25.908	26.6202	12.2474	2.079756	2.115388	2.173539	-	-
28672	TB1G02867 XLOC_0281 Kpn4	GL896327.	9685	13278	+	CODING	NOVEL	Importin s	7	101.307	5223.81	4254.56	1957.14	5.176278	2.669104	2.173866	-	-	
849	TB1G00084 ENSSSCG0 PRPF4		1	2.85E+08	2.85E+08	+	CODING	NEW_AS	pre-mRNA	7	53.261	41.1012	37.7856	17.3289	3.073536	2.37183	2.180496	-	-
26730	TB1G02673 ENSSSCG0 KDELR2	GL893800.	7054	17355	+	CODING	NEW_AS	KDEL (Lys-	7	45.8798	45.7896	42.4378	19.3699	2.368613	2.363956	2.190915	-	-	
6156	TB1G00615 ENSSSCG0 COPB2		13	87895226	87930998	-	CODING	NEW_AS	coatomer 1	7	74.2013	65.1686	67.5623	30.7361	2.414142	2.120262	2.198142	-	-
25095	TB1G02509 ENSSSCG0 SAMD9		9	79679765	79714213	-	CODING	NEW_AS	sterile like	7	58.1417	61.0172	49.9107	22.6889	2.562651	2.689297	2.199785	-	-
23067	TB1G02306 ENSSSCG0 TBC1D1		8	30778696	30793855	-	CODING	NEW_AS	Uncharact	7	45.979	48.4195	43.8218	19.8785	2.313001	2.435772	2.204482	-	-
9682	TB1G00968 ENSSSCG0 IL7R		16	22278436	22314407	+	CODING	NEW_AS	interleukin	7	103.834	64.531	65.7059	29.8034	3.483965	2.165223	2.204644	-	-
3957	TB1G00395 ENSSSCG0 NBR1		12	20093103	20126422	+	CODING	NEW_AS	neighbor c	7	36.1676	27.5106	29.4027	13.3027	2.718816	2.068046	2.210281	-	-
26515	TB1G02651 XLOC_0261 HSPA6	GL893523.	1	293	-	CODING	NOVEL	Heat shoel	7	103.493	93.2129	82.0541	36.9707	2.799325	2.521264	2.219436	-	-	
21900	TB1G02190 XLOC_0211 FAM65B		7	20752463	20990945	-	CODING	NEW_AS	Protein FA	7	142.59	124.416	119.218	53.5648	2.662009	2.322719	2.225678	-	-
19813	TB1G01981 ENSSSCG0 IST1		6	14464800	14489691	-	CODING	NEW_AS	Uncharact	7	51.0404	38.8494	37.9261	16.9292	3.014933	2.294816	2.240277	-	-
24530	TB1G02453 ENSSSCG0 PDI4A		9	1.2E+08	1.2E+08	+	CODING	NEW_AS	protein dis	7	88.6251	115.53	83.4976	37.0335	2.393106	3.119608	2.254651	-	-
28296	TB1G02829 XLOC_0281 IGHG4	GL896171.	5	540	+	CODING	NOVEL	Ig gamma	7	247.21	661.85	276.828	121.593	2.033094	5.443159	2.276677	-	-	
7854	TB1G00785 ENSSSCG0 ANKRD13		14	43479365	43506038	-	CODING	NEW_AS	Ankyrin rej	7	53.4606	38.9802	41.5515	18.2352	2.931725	2.137635	2.278642	-	-
21865	TB1G02186 ENSSSCG0 F13A1		7	3721329	4102833	-	CODING	NEW_AS	Uncharact	7	349.897	277.55	213.936	93.4317	3.74495	2.970619	2.289758	-	-
19841	TB1G01984 ENSSSCG0 GOT2		6	18501596	18507494	-	CODING	NEW_AS	glutamic-o	7	34.05	29.3039	32.9471	14.3514	2.372591	2.041884	2.295741	-	-
5846	TB1G00584 ENSSSCG0 CMTM6		13	20261322	20287139	-	CODING	NEW_AS	CKL-like 1	7	48.8546	39.7929	38.4579	16.647	2.934739	2.390395	2.3102	-	-
26357	TB1G02635 ENSSSCG0 HA1B_BOV	GL893304.	28077	43963	-	CODING	NEW_AS	BOLA class	7	76.7646	55.8364	57.9475	25.0711	3.061876	2.227122	2.311327	-	-	
8519	TB1G00851 ENSSSCG0 DARS		15	18269639	18344270	+	CODING	NEW_AS	aspartyl-tR	7	54.9954	43.8047	44.5019	19.1791	2.867465	2.283981	2.320333	-	-
28137	TB1G02813 ENSSSCG0 CTDSP2	GL895994.	29300	45360	-	CODING	NEW_AS	CTD (carb	7	96.8499	75.802	83.4617	35.876	2.699574	2.112889	2.326394	-	-	
5269	TB1G00526 ENSSSCG0 Nbeal2		13	33122342	33133683	+	CODING	NEW_AS	Uncharact	7	83.186	65.6626	53.316	22.8995	3.632656	2.867425	2.32826	-	-
2766	TB1G00276 ENSSSCG0 KLF6		10	72992249	73001823	+	CODING	NEW_AS	Kruppel-lik	7	54.4766	36.1548	40.2427	17.2591	3.156399	2.094825	2.33168	-	-
22050	TB1G02205 ENSSSCG0 SLA-DRB*H		7	29113063	29125516	-	CODING	NEW_AS	Sus scrofa	7	145.019	176.295	136.157	58.0712	2.497262	3.035842	2.344656	-	-
10297	TB1G01029 XLOC_0101 gag-pro		17	36964339	36974782	+	CODING	NOVEL	Gag-Pro p	7	53.1501	43.9935	42.6527	18.0607	2.942859	2.435669	2.361631	-	-
29142	TB1G02914 ENSSSCG0 VPS35	GL896549.	6363	23585	-	CODING	NEW_AS	vacuolar p	7	40.8995	35.8611	38.9961	16.4955	2.479434	2.173993	2.364045	-	-	
10710	TB1G01071 ENSSSCG0 NDRG3		17	45359657	45427454	-	CODING	NEW_AS	NDRG fam	7	29.3645	26.1356	28.4647	12.0392	2.439074	2.170875	2.364335	-	-
9804	TB1G00980 ENSSSCG0 RNF145		16	70068344	70121376	+	CODING	NEW_AS	ring finger	7	68.0868	48.5401	46.4501	19.524	3.487339	2.486176	2.379128	-	-
17806	TB1G01780 ENSSSCG0 LRRK2		5	74510800	74657314	+	CODING	NEW_AS	Sus scrofa	7	42.6593	32.0993	35.5483	14.8942	2.864155	2.155154	2.386721	-	-
19760	TB1G01976 XLOC_0191 Irf8		6	3330963	3340067	-	CODING	NOVEL	Interferon	7	51.2276	62.8791	33.162	13.8726	3.692718	4.532611	2.390468	-	-
11031	TB1G01103 ENSSSCG0 GIMAP4		18	6609767	6621208	+	CODING	NEW_AS	GM2 gang	7	68.199	61.324	63.577	26.4872	2.574791	2.315549	2.399994	-	-
28410	TB1G02841 ENSSSCG0 SURF4	GL896220.	574	4799	-	CODING	NEW_AS	surfeit 4 [S	7	53.658	62.036	59.3858	24.6938	2.172934	2.51221	2.404887	-	-	
7831	TB1G00783 ENSSSCG0 CLC8B1		14	41244220	41251489	-	CODING	NOVEL	solute car	7	95.9113	107.421	50.6975	20.9724	4.573215	5.122018	2.417344	-	-
10034	TB1G01003 ENSSSCG0 GM2A		16	77974389	77987652	-	CODING	NEW_AS	GM2 gang	7	84.9733	80.5477	62.3129	25.6403	3.314052	3.141449	2.430272	-	-
7292	TB1G00729 ENSSSCG0 MAPK1		14	53599167	53615840	+	CODING	NEW_AS	mitogen-a	7	94.8376	76.3225	76.2807	31.1684	3.042748	2.448714	2.447373	-	-
12463	TB1G01246 ENSSSCG0 REEP5		2	1.21E+08	1.22E+08	+	CODING	NEW_AS	receptor a1	7	107.834	79.594	97.9111	39.7888	2.71016	2.000412	2.46077	-	-
21799	TB1G02179 ENSSSCG0 PAPLA		7	1.25E+08	1.25E+08	+	CODING	NEW_AS	poly(A) po	7	55.3282	43.4424	51.6498	20.9783	2.637402	2.070826	2.462058	-	-
6699	TB1G00696 ENSSSCG0 PTPN12		1	2.26E+08	2.26E+08	+	CODING	NEW_AS	protein ty	7	39.2649	33.3557	27.0746	19.9855	3.574248	3.063339	2.464576	-	-
283	TB1G00283 ENSSSCG0 NARS		1	1.17E+08	1.18E+08	+	CODING	NEW_AS	asparagine	7	56.5282	41.5603	50.6499	20.5254	2.754061	2.024823	2.469862	-	-
26677	TB1G02667 ENSSSCG0 APMAP	GL893705.	64290	67208	-	CODING	KNOWN	Adipocyte	7	72.161	67.4088	50.6346	20.4636	3.52631	3.294083	2.474374	-	-	
7800	TB1G00780 ENSSSCG0 ANAPC7		14	33669495	33718033	-	CODING	NEW_AS	anaphase 1	7	26.7281	23.1358	27.8188	11.2345	2.379109	2.059353	2.476194	-	-
16321	TB1G01632 XLOC_0161 ARNT		4	1.08E+08	1.08E+08	+	CODING	NEW_AS	Aryl hydro	7	36.3501	25.9563	31.7854	12.8186	2.835731	2.024894	2.479631	-	-
29769	TB1G02976 ENSSSCG0 TXNDC11	JH118940.	20412	78632	-	CODING	NEW_AS	Uncharact	7	28.6043	29.7805	27.3208	11.0172	2.596331	2.703092	2.479832	-	-	
17615	TB1G01761 ENSSSCG0 GLB1	GL894277.	5160	12749	-	CODING	KNOWN	Uncharact	7	75.0143	62.4706	75.7414	30.5424	2.456071	2.045373	2.479877	-	-	
20161	TB1G01061 ENSSSCG0 ACS51		17	34949431	34988723	-	CODING	NEW_AS	acyl-CoA s	7	41.1264	43.7668	45.6065	18.3511	2.241086	2.384969	2.485219	-	-
21149	TB1G02114 ENSSSCG0 BLOC1C55		7	5327730	5546412	+	CODING	NOVEL	biogenesis	7	105.903	220.49	125.448	50.0105	2.117615	4.408874	2.508433	-	-
2781	TB1G00278 ENSSSCG0 DCTN5		10	2661	17242	-	CODING	KNOWN	dynactin 5	7	44.4534	43.0362	51.9809	20.7122	2.146242	2.077819	2.509675	-	-
7201	TB1G00720 ENSSSCG0 MLEC		14	43069385	43084765	-	CODING	NEW_AS	malleatin [7	24.1558	20.7292	25.9667	10.2856	2.348507	2.051361	2.524568	-	-
5193	TB1G00519 ENSSSCG0 UBP1		13	20784893	20832356	-	CODING	NEW_AS	upstream 1	7	44.4955	31.7645	38.3249	15.1034	2.946509	2.103136	2.537501	-	-
5228	TB1G00522 ENSSSCG0 CTNNB1		13	27623074	27667302	+	CODING	NEW_AS	Sus scrofa	7	74.8559	55.7844	64.5247	25.4027	2.946769	2.196003	2.540073	-	-
1806	TB1G00180 ENSSSCG0 ROD1		1	2.84E+08	2.84E+08	-	CODING	NEW_AS	Sus scrofa	7	48.5353	37.1763	44.8866	17.5447	2.76638	2.118948	2.558414	-	-
9319	TB1G00931 ENSSSCG0 AGFG1		15	1.43E+08	1.43E+08	-	CODING	NEW_AS	ArfGAP w/	7	26.7001	27.9922	30.6422	11.9064	2.24251	2.351021	2.573591	-	-
28741	TB1G02874 XLOC_0281 Exoc3	GL896361.	60175	62637	-	CODING	NOVEL	Exocyst co	7	27.9099	30.1452	34.8522	13.5323	2.062465	2.227648	2.575482	-	-	
9345	TB1G00934 ENSSSCG0 Inpp5d		15	1.48E+08	1.48E+08	-	CODING	NEW_AS	Uncharact	7	61.8168	54.6138	68.8704	26.6813	2.316859	2.046894	2.581224	-	-
9153	TB1G00915 ENSSSCG0 WIPF1		15	89757199	89837471	-	CODING	NEW_AS	WAS/WAS	7	102.675	77.0715	92.5996	35.8474	2.864224	2.149989	2.583161	-	-
3323	TB1G00332 ENSSSCG0 ELF1		11	26327366	26385565	+	CODING	NEW_AS	E74-like fa	7	91.1587	66.9882	71.7486	27.7247	3.287996	2.416192	2.587895	-	-
30616	TB1G03061 ENSSSCG0 ARHGFE6	X	1	1.28E+08	1.28E+08	-	CODING	NEW_AS	Rac/Cdc42	7	36.0784	29.9378	31.1084	11.9858	3.010095	2.477752	2.595438	-	-
10713	TB1G01071 ENSSSCG0 SAMHD1		17	45556581	45582808	-	CODING	NEW_AS	Uncharact	7	87.8642	60.2169	74.5792	28.5531	3.077221	2.108944	2.611948	-	-
19651	TB1G01965 ENSSSCG0 EPS15		6	1.48E+08	1.48E+08	+	CODING	NEW_AS	epidermal	7	31.4888	22.646	26.6061	10.1686	3.09667	2.227052	2.616496	-	-
27156	TB1G02715 ENSSSCG0 NLRC5	GL894265.	7198	10643	-	CODING	NEW_AS	Protein NL	7	214.497	167.438	180.653	68.9464	3.111069	2.428524	2.620195	-	-	
15176	TB1G01517 ENSSSCG0 RPIA		3	59834045	59864868	-	CODING	NEW_AS	ribose 5-1										

5736	TBIG00573 XLOC_005	GBE1	13	1.84E+08	1.84E+08	+	CODING	NOVEL	1.4-alpha-i	7	74.1595	70.6589	78.2403	25.4132	2.918149	2.780402	3.078727	-	-
13370	TBIG01337 ENSSSCG0	CANX	2	8.0445609	80482509	-	CODING	KNOWN	calnexin [S	7	54.6557	40.8975	51.797	16.8076	3.251844	2.433274	3.081761	-	-
16477	TBIG01647 ENSSSCG0	GBP1	4	1.39E+08	1.4E+08	+	CODING	NEW_AS	Sus scrofa	7	191.634	131.65	180.467	57.8376	3.313312	2.726201	3.120237	-	-
20551	TBIG02055 ENSSSCG0	JAK1	6	1.36E+08	1.36E+08	-	CODING	NEW_AS	Janus kina	7	200.684	127.755	143.562	45.9455	4.367871	2.780577	3.124615	-	-
17433	TBIG01743 ENSSSCG0	IL2RB	5	8.223890	8249820	-	CODING	NEW_AS	Uncharact	7	83.5944	53.3671	79.5051	25.4298	3.287261	2.098605	3.126454	-	-
14174	TBIG01417 XLOC_014	GBAS	3	1.7205926	17219756	+	CODING	NOVEL	Protein Nij	7	57.5279	47.9816	62.7497	19.8058	2.904599	2.422603	3.168249	-	-
27593	TBIG02759 ENSSSCG0	ELP3	GL894948.	1037	6292	+	CODING	KNOWN	Uncharact	7	36.4931	26.4841	37.4437	11.7946	3.094052	2.254543	3.174648	-	-
22505	TBIG02250 ENSSSCG0	TMED10	7	1.04E+08	1.04E+08	-	CODING	NEW_AS	transmemt	7	56.1532	42.405	55.4414	17.3964	3.227863	2.437573	3.186947	-	-
27159	TBIG02715 XLOC_027	Jak1	GL894267.	3	422	-	CODING	NOVEL	Tyrosine-p	7	148.38	95.8767	127.726	40.0643	3.703547	2.393071	3.188025	-	-
6206	TBIG00620 ENSSSCG0	CCNL1	13	1.05E+08	1.05E+08	-	CODING	NEW_AS	cyclin LI [!	7	42.4061	32.4785	43.9096	13.742	3.085875	2.363448	3.195285	-	-
15270	TBIG01527 ENSSSCG0	ACTR2	3	80487337	80525402	-	CODING	KNOWN	Sus scrofa	7	192.817	125.065	198.3	61.4546	3.137552	2.03508	3.226772	-	-
16714	TBIG01671 ENSSSCG0	RCS2D1	4	90996577	91079847	-	CODING	NEW_AS	RCS2 dom	7	69.7956	53.0808	79.5734	24.592	2.838142	2.158458	3.235743	-	-
14375	TBIG01437 ENSSSCG0	FAM120A	3	44107429	44330948	+	CODING	NEW_AS	family with	7	36.7947	26.4047	41.9108	12.9051	2.851175	2.046067	3.247615	-	-
1532	TBIG00153 ENSSSCG0	VPS4B	1	1.76E+08	1.76E+08	-	CODING	NEW_AS	vacuolar p	7	38.9495	28.78	45.7719	14.0411	2.773964	2.049697	3.259851	-	-
23467	TBIG02346 XLOC_023	TLR6	8	31625693	31660825	-	CODING	NEW_AS	Toll-like re	7	30.051	24.2306	35.6839	10.9276	2.750009	2.217376	3.265484	-	-
6363	TBIG00636 ENSSSCG0	ATP6V1A	13	1.56E+08	1.56E+08	-	CODING	NEW_AS	ATPase, H-	7	30.805	24.7878	34.899	10.6734	2.886147	2.32239	3.269717	-	-
23594	TBIG02359 ENSSSCG0	G3BP2	8	75410919	75499534	-	CODING	NEW_AS	GTPase acti	7	33.475	21.596	35.01	10.5393	3.176207	2.049092	3.321852	-	-
28212	TBIG02821 ENSSSCG0	YIPF5	GL896100.	827	9421	-	CODING	KNOWN	protein YIF	7	41.5617	32.426	51.9762	15.5571	2.671558	2.084322	3.340895	-	-
30078	TBIG03007 ENSSSCG0	OGT	X	64962766	65000187	+	CODING	NEW_AS	Sus scrofa	7	111.033	75.2087	117.309	35.0493	3.167909	2.145797	3.346971	-	-
15358	TBIG01535 ENSSSCG0	PRKD3	3	1.09E+08	1.1E+08	-	CODING	NEW_AS	protein kin	7	44.5871	28.3631	39.2181	11.67	3.82066	2.430428	3.360591	-	-
1479	TBIG00147 ENSSSCG0	THBS1	1	1.47E+08	1.47E+08	-	CODING	NEW_AS	Sus scrofa	7	79.0614	46.4264	40.2191	11.9141	6.635952	3.896761	3.375756	-	-
9990	TBIG00999 XLOC_009	DOCK2	16	58744789	58751935	+	CODING	NOVEL	Dedicator	7	78.0226	63.5007	94.6406	27.8784	2.798676	2.277774	3.394764	-	-
27870	TBIG02787 ENSSSCG0	HIATL1	GL895478.	11241	49084	-	CODING	NEW_AS	Sus scrofa	7	47.1809	37.9099	34.7135	10.0602	4.689857	3.768305	3.450578	-	-
5459	TBIG00545 ENSSSCG0	SRPRB	13	82474461	82496616	+	CODING	KNOWN	signal rec	7	51.5088	40.1247	54.1702	15.4301	3.338203	2.600417	3.510684	-	-
2860	TBIG00286 ENSSSCG0	PTPRC	10	26246556	26287845	+	CODING	NEW_AS	Uncharact	7	393.984	274.914	396.897	112.639	3.497758	2.414031	3.52362	-	-
3345	TBIG00334 ENSSSCG0	NDFIP2	11	56246092	56312418	+	CODING	NEW_AS	Nedd4 fru	7	54.5985	29.9039	49.7824	14.115	3.868119	2.11859	3.526915	-	-
9201	TBIG00920 ENSSSCG0	STK17B	15	1.11E+08	1.11E+08	-	CODING	NEW_AS	serine/thre	7	122.075	71.9184	115.152	32.107	3.80213	2.23996	3.586508	-	-
27266	TBIG02726 XLOC_027	Dync1h1	GL894475.	19	942	+	CODING	NOVEL	Cytoplasm	7	27.1342	20.8042	36.3496	10.0862	2.69023	2.02624	3.603894	-	-
29714	TBIG02971 XLOC_029	TM9SF2	JH118897.	8484	27691	+	CODING	NOVEL	Transmeml	7	55.1815	44.7188	68.8485	19.0685	2.893856	2.345166	3.610588	-	-
873	TBIG00087 ENSSSCG0	RAB14	1	2.93E+08	2.94E+08	+	CODING	NEW_AS	RAB14, me	7	37.8024	30.173	44.1384	12.1287	3.116773	2.487736	3.639197	-	-
10459	TBIG01045 ENSSSCG0	CSE1L	17	57095159	57109228	-	CODING	KNOWN	CSE1 chroi	7	79.6241	39.0217	59.4584	15.9775	4.983514	2.442291	3.721383	-	-
16083	TBIG01608 ENSSSCG0	TRAM1	4	70399155	70431004	+	CODING	NEW_AS	translocati	7	80.5535	63.1363	90.0989	24.0047	3.355739	2.630164	3.753386	-	-
5535	TBIG00553 ENSSSCG0	NLRP1	13	1.08E+08	1.08E+08	+	CODING	KNOWN	Uncharact	7	46.6606	26.0405	48.6281	12.8257	3.638055	2.030338	3.791458	-	-
27758	TBIG02775 XLOC_027	Tbk1	GL895245.	669	795	-	CODING	NOVEL	Serine/thre	7	239.69	317.129	321.825	84.848	2.837078	3.753681	3.809265	-	-
15977	TBIG01597 ENSSSCG0	KIAA0196	4	15149903	15246609	+	CODING	NEW_AS	WASH con	7	37.1102	31.7119	44.7795	11.649	3.185698	2.722285	3.844064	-	-
30599	TBIG03059 ENSSSCG0	MS14	X	1.24E+08	1.24E+08	-	CODING	NEW_AS	Serine/thre	7	39.8961	20.2312	38.4758	10.0046	3.987776	2.02219	3.845811	-	-
10742	TBIG01074 ENSSSCG0	STK4	17	52872154	52878619	-	CODING	KNOWN	serine/thre	7	73.6392	51.4528	77.8127	19.9957	3.682752	2.573193	3.891472	-	-
23575	TBIG02357 ENSSSCG0	Igj	8	71347284	71358511	-	CODING	KNOWN	immunogl	7	442.434	585.16	476.436	122.085	3.623983	4.793054	3.902494	-	-
26699	TBIG02669 XLOC_026	INTS12	GL893739.	1798	12539	+	CODING	NOVEL	Integrator	7	53.9285	59.7287	72.6546	18.2814	2.949111	3.267184	3.974236	-	-
20352	TBIG02035 ENSSSCG0	ARID1A	6	77607451	77612795	+	CODING	KNOWN	AT rich int	7	39.2487	24.6264	40.7517	10.186	3.8532	2.417671	4.000756	-	-
2928	TBIG02928 ENSSSCG0	RAB5A	JH118496.	1977	24283	-	CODING	KNOWN	RAB5A, me	7	34.2504	28.9413	54.9243	13.7102	2.498169	2.110932	4.00609	-	-
5283	TBIG00528 XLOC_000	Zwilch	1	1.82E+08	1.82E+08	+	CODING	NOVEL	Protein zw	7	22.4381	21.2835	42.6459	10.5359	2.12968	2.020093	4.047675	-	-
16950	TBIG01695 ENSSSCG0	ST7L	4	1.18E+08	1.18E+08	-	CODING	NOVEL	suppressio	7	59.0845	28.5359	46.1817	11.266	5.244497	2.532922	4.09921	-	-
30491	TBIG03049 ENSSSCG0	MAGT1	X	70812442	70877254	+	CODING	NEW_AS	magnesiun	7	43.3067	32.2748	51.1111	12.4321	3.483458	2.596086	4.11122	-	-
29419	TBIG02941 ENSSSCG0	ZCCHC4	JH118638.	93888	288709	+	CODING	NEW_AS	Uncharact	7	85.9682	12.3849	157.937	38.3551	2.241376	-3.09692	4.117757	-	-
29981	TBIG02998 ENSSSCG0	DDX3X	X	41161892	41177782	+	CODING	KNOWN	Uncharact	7	51.7024	29.5464	60.9819	14.6258	3.535013	2.020156	4.169474	-	-
136	TBIG00013 ENSSSCG0	SERINC1	1	44519709	44540322	+	CODING	NEW_AS	Uncharact	7	161.371	77.035	130.549	30.9315	5.217044	2.490503	4.220584	-	-
15750	TBIG01575 XLOC_015	EXOC6B	3	73146787	73147018	-	CODING	NOVEL	Exocyst co	7	259.786	156.403	312.54	73.951	3.512948	2.114954	4.226312	-	-
27152	TBIG02715 XLOC_027	Nomo1	GL894264.	4444	10080	-	CODING	NOVEL	Nodal mo	7	62.8315	51.9085	92.2525	21.3114	2.948258	2.435715	4.328786	-	-
17904	TBIG01790 XLOC_017	PPP1R12A	5	1.06E+08	1.07E+08	+	CODING	NOVEL	Protein ph	7	70.0987	44.0703	71.446	15.8748	4.415722	2.776117	4.500592	-	-
16023	TBIG00602 ENSSSCG0	HIF1A	1	2.12E+08	2.12E+08	+	CODING	NEW_AS	Sus scrofa	7	51.869	33.759	57.0442	12.5835	4.121985	2.682799	4.533254	-	-
1266	TBIG00126 ENSSSCG0	CD164	1	84719535	84736132	-	CODING	NEW_AS	Sialomucin	7	85.3405	63.603	120.15	25.3557	3.365732	2.50843	4.738579	-	-
13463	TBIG01346 ENSSSCG0	ERAP2	2	1.07E+08	1.07E+08	-	CODING	NEW_AS	Uncharact	7	57.3708	32.2542	58.4791	12.2971	4.665393	2.622911	4.75552	-	-
10150	TBIG01015 XLOC_010	Dock2	16	58655196	58655489	-	CODING	NOVEL	Dedicator	7	77.1889	59.9841	103.385	21.7224	3.553424	2.761394	4.759373	-	-
25929	TBIG02592 XLOC_025	MCM6	GL892768.	76	196	-	CODING	NOVEL	DNA replic	7	200063	361204	135128	281582	7.104964	12.82767	4.798886	-	-
15175	TBIG01517 ENSSSCG0	IGKV1-5	3	59753693	59754231	-	CODING	KNOWN	Uncharact	7	292.246	311.217	338.211	69.6683	4.19482	4.467125	4.85459	-	-
24877	TBIG02487 XLOC_024	TMEM123	9	37031495	37080859	-	CODING	NOVEL	Porinim [S	7	85.9356	43.0955	105.712	21.3824	4.018988	2.015466	4.943879	-	-
18202	TBIG01820 ENSSSCG0	GNS	5	32134175	32173480	-	CODING	KNOWN	glucosamir	7	43.081	37.3886	55.5237	11.1391	3.867548	3.356519	4.984577	-	-
11082	TBIG01108 XLOC_011	Mtpn	18	14099503	14151591	+	CODING	NOVEL	Myotroph	7	45.4978	29.1578	73.1138	14.3838	3.163128	2.027128	5.083066	-	-
2977	TBIG00297 ENSSSCG0	ITGB1	10	61450695	61521893	+	CODING	NEW_AS	integrin, b	7	96.9823	52.3312	89.0997	16.9243	5.730358	3.039275	5.264602	-	-
9208	TBIG00920 ENSSSCG0	SF3B1	15	1.12E+08	1.13E+08	-	CODING	NEW_AS	splicing fa	7	108.572	59.6028	131.111	24.4846	4.434297	2.434297	5.354835	-	-
7577	TBIG00757 ENSSSCG0	ADD3	14	1.31E+08	1.31E+08	+	CODING	NEW_AS	adducin 3	7	76.7192	41.1507	85.1385	15.7562					