Table S1 Definition and method of traits

Traits	Definitions[1]	Unit	Methods
STO (%)	Percentage of slow-twitch-oxidative fiber (STO)	%	[2,3]The cryopreserved muscle samples were cutting into slices of 12μm thickness after equilibration to -20°C. NADH tetrazolium reductase and Myofibrillar ATPase were stained to identify the muscle fiber types. 3 sections were used for calculating the percentage of STO, FTO and FTG by relating the number of counted fibers of each type to the total counted fiber number.
FTO (%)	Percentage of fast-twitch-oxidative fiber (FTO)	%	
FTG (%)	Percentage of fast-twitch-glycolytic fiber (FTG)	%	
State 3 Pyruvate	State 3 mitochondrial respiratory activity (MRA) analyzed with substrate combination pyruvate/malate	pmol O_2/sec*mg sample weight	[2]Samples were dissected and muscle fibers were mechanically permeabilized, dried on filter paper and weighted. The MRA was measured using Oxygraph equipped with a Clark-electrode. The weight-specific oxygen consumption (pmol O_2 /sec*mg sample weight) was calculated as the time derivative of oxygen concentration. State 3 respiration was initiated with 5mM ADP. State 4 respiration was initiated with 28 μM CAT. RCI Pyruvate was calculated by dividing the state 3 Pyruvate and state 4 respiration rate. Each experiment was repeated three times.
State 3 Succinate	State 3 mitochondrial respiratory activity (MRA) analyzed with substrate combination succinate/rotenone	pmol O_2/sec*mg sample weight	
State 4 CAT	State 4 mitochondrial respiratory activity initiated with carboxy-atractyloside (CAT)	pmol O_2/sec*mg sample weight	
RCI Pyruvate	Respiratory control index (RCI) when considering substrates pyruvate/malate	no	
RCI Succinate	Respiratory control index (RCI) when considering substrates succinate/rotenone	no	

GP	Enzyme activity of glycogen phosphorylase (GP)	U/g Protein	[3,4]Muscle samples were homogenized and all the experiments were finished within 2h in duplicate. **GP** catalyzed the degradation of glycogen to glucose-1-phosphate followed by the isomerization to glucose-6-phosphate (G-6-P). GP activity was determined spectrophotometrically by the reduction of NADP$^+$ to NADPH at 340nm and PH 6.8 when G-6-P dehydrogenase catalyzed G-6-P to gluconate-6-phosphate. **PFK** catalyzes fructose-6-phosphate to fructose 1,6-bis-phosphate, which is split to glyceraldehyde-3-phosphate and dihydroxyacetonephosphate (DHAP). PFK activity was determined by the oxidation of NADH to NAD$^+$ at 340nm and PH 8.0 when glycerol-3-phosphate dehydrogenase/triosephosphate isomerase catalyzed DHAP to glycerol-3-phosphate. **LDH** activity was determined by the oxidation of NADH to NAD$^+$ at 340nm when LDH catalyzed pyruvate to lactate. **CS** catalyzes acetyl-CoA and oxaloacetate to citrate to liberating CoA. CS activity was determined by the irreversible reaction of CoA with 5,5’-Dithiobis-(2-
PFK	Enzyme activity of phosphofructokinase (PFK)	U/g Protein	
LDH	Enzyme activity of lactate dehydrogenase (LDH)	U/g Protein	
CS	Enzyme activity of citrate synthase (CS)	U/g Protein	
Complex I	Enzyme activity of NADH-ubiquinone oxidoreductase (also called Complex I)	U/g Protein	

Complex II	Enzyme activity of succinate dehydrogenase (also called Complex II)	U/g Protein	nitrobenzoic acid) to thionitrobenzoic acid at 412nm. **Complex I** was spectrophotometrically determined by following the oxidation of NADH to NAD^+ at 340nm. **Complex II** was determined at 600nm following the reduction of 2, 6-dichlorophenolindophenol (DCPIP) by ubiquinol resulting from this reaction. **COX** was determined by following the oxidation of reduced cytochrome c to the oxidized form at 550nm and PH7.0.
COX	Enzyme activity of cytochrome c oxidase (COX)	U/g Protein	
IMP	Inosine 5′-monophosphate (IMP) concentration	µmol/g muscle	[4]Each sample was homogenized with 5% ice-cold TCA in the ratio of 1:4 (w/v) followed by centrifugation for 5min at 20,000g. The supernatant was neutralized with potassium hydroxide and centrifugation again. The supernatant was stored at -80°C until further analysis. The concentration of ATP, ADP, AMP and IMP were measured by High-performance liquid chromatography (HPLC) system. The degassed isocratic mobile phase consisted of 100mM KH_2PO_4, 1.44mM retrabutylammonium hydrogen sulfate and 0.5% methanol adjusted to PH7.0.
AMP	Adenosine 5'-monophosphate (AMP) concentration	µmol/g muscle	
ADP	Adenosine diphosphate (ADP) concentration	µmol/g muscle	
ATP	Adenosine triphosphate (ATP) concentration	µmol/g muscle	

[1] longissimus muscle (LM) between the 13/14th thoracic vertebra (Th) 24h ante mortem

[2] (Werner *et al.* 2010a)

[3] (Werner *et al.* 2010b)

[4] (Krischek *et al.* 2011)

Krischek C., Natter R., Wigger R. & Wicke M. (2011) Adenine nucleotide concentrations and glycolytic enzyme activities in longissimus muscle samples of different pig genotypes collected before and after slaughter. *Meat Sci* **89**, 217-20.

Werner C., Natter R., Schellander K. & Wicke M. (2010a) Mitochondrial respiratory activity in porcine longissimus muscle fibers of different pig genetics in relation to their meat quality. *Meat Sci* **85**, 127-33.

Werner C., Natter R. & Wicke M. (2010b) Changes of the activities of glycolytic and oxidative enzymes before and after slaughter in the longissimus muscle of Pietrain and Duroc pigs and a Duroc-Pietrain crossbreed. *J Anim Sci* **88**, 4016-25.

Table S2 The primer sequences in qRT-PCR

Gene Symbol	Gene description	Primer	Sequence 5´-3´
ATP6V1C1	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	Forward	TGTACGGTGGCTGAAAGTGA
		Reverse	TTGGGTTGAAGGAGCATTGC
ATP6V1E1	ATPase, H+ transporting, lysosomal 31kDa, V1 subunit E1	Forward	ATACCTTAGAGAGCCGGCTG
		Reverse	GCGGGTGTCTTCAAATGTCA
COX10	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	Forward	TCTGGAAGGGTCTCTCTCGA
		Reverse	CCTTCTCCTTTGGCCTCAGA
COX7A2	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)	Forward	TGCATCTGAAGGGAGGGATC
		Reverse	CTAACTGAGTGCTGGGAGGA
CYB5A	cytochrome b5 type A (microsomal)	Forward	TTAGCTTCTGGTGATGGGCC
		Reverse	CATCTAGCACGCCAATGGAC
NDUFS1	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	Forward	GCTGATCCACTTGTTCCACC
		Reverse	AGCAAAACTGGGTCCTGGTA
NDUFS6	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)	Forward	CGTCAGAAGGAGGTGAATGAG
		Reverse	CGTCTTCGTTTCCTTGTCCA
PPA1	pyrophosphatase (inorganic) 1	Forward	AGGGTGAAAGTTCTGGGCAT
		Reverse	GTCCACAGTAGCTTCCAGGT
ACTB[1]	actin, beta	Forward	GAGAAGCTCTGCTACGTCGC
		Reverse	CCTGATGTCCACGTCGCACT
RPL32[1]	Ribosomal protein L32	Forward	AGCCCAAGATCGTCAAAAAG
		Reverse	TGTTGCTCCCATAACCAATG
RPS11[1]	Ribosomal protein S11	Forward	GAAACTGGCAAGGAGAAG
		Reverse	TTCGGATGTAGTGGAGGTAG

[1] Reference genes

Table S3 Differentially expressed probes identified in porcine LD muscle between Duroc and PiNN breed types at adult stage

Gene symbol	Probeset	Description	Lsmean Duroc	Lsmean PiNN	P-Value for Duroc-PiNN	FDR for Duroc-PiNN	Fold change	Regulation
C16orf65	SNOWBALL_004478_st	PDZ domain containing 9	10.231	7.199	4.228E-15	7.53E-11	8.18	Duroc-up
PLCE1	SNOWBALL_024947_st	PREDICTED: Sus scrofa similar to pancreas-enriched phospholipase C (LOC100155331), mRNA	6.399	5.382	4.644E-10	4.14E-06	2.02	Duroc-up
TJP2	SNOWBALL_003043_st	tight junction protein 2 (zona occludens 2)	6.119	5.521	3.070E-08	1.82E-04	1.51	Duroc-up
BCL7B	SNOWBALL_004398_st	B-cell CLL/lymphoma 7B	6.863	7.410	5.893E-08	2.63E-04	-1.46	PiNN-up
SLC35B2	SNOWBALL_010049_st	solute carrier family 35, member B2	5.700	6.111	1.178E-07	3.37E-04	-1.33	PiNN-up
VGLL3	SNOWBALL_023047_s_st	vestigial like 3 (Drosophila)	7.230	6.469	1.324E-07	3.37E-04	1.69	Duroc-up
PLCE1	SNOWBALL_017086_s_st	phospholipase C, epsilon 1	7.316	6.274	1.259E-07	3.37E-04	2.06	Duroc-up
MAPKAPK3	SNOWBALL_015399_s_st	mitogen-activated protein kinase-activated protein kinase 3	6.693	7.482	2.872E-07	6.40E-04	-1.73	PiNN-up
FZD7	SNOWBALL_044919_st	frizzled homolog 7 (Drosophila)	5.209	6.421	3.552E-07	6.74E-04	-2.32	PiNN-up
TTC3	SNOWBALL_016228_st	tetratricopeptide repeat domain 3	8.064	7.252	3.784E-07	6.74E-04	1.76	Duroc-up
NT5DC1	SNOWBALL_047365_st	5'-nucleotidase domain-containing protein 1-like	5.912	4.927	4.695E-07	7.61E-04	1.98	Duroc-up
MAPKAPK3	SNOWBALL_023101_st	mitogen-activated protein kinase-activated protein kinase 3	6.441	7.021	5.746E-07	8.53E-04	-1.49	PiNN-up
KRTCAP2	SNOWBALL_005809_st	keratinocyte associated protein 2	7.601	7.976	6.451E-07	8.84E-04	-1.30	PiNN-up
MRPL2	SNOWBALL_009857_st	mitochondrial ribosomal protein L2	6.701	7.364	9.069E-07	1.14E-03	-1.58	PiNN-up
CDC27	SNOWBALL_014383_st	cell division cycle 27 homolog (S. cerevisiae)	8.085	7.405	9.616E-07	1.14E-03	1.60	Duroc-up
PEX19	SNOWBALL_000847_st	peroxisomal biogenesis factor 19	6.069	6.723	1.110E-06	1.16E-03	-1.57	PiNN-up
C16orf5	SNOWBALL_004928_st	chromosome 16 open reading frame 5	7.204	7.533	1.062E-06	1.16E-03	-1.26	PiNN-up
TEX264	SNOWBALL_037264_st	testis expressed 264	5.993	6.555	1.365E-06	1.28E-03	-1.48	PiNN-up
LOC100508851	SNOWBALL_032753_st	Ssc_hash_S18270885 BP167376 full-length enriched swine cDNA library, adult thymus Sus scrofa cDNA clone THY010029G06 5prime, mRNA	5.777	4.888	1.358E-06	1.28E-03	1.85	Duroc-up
PCM1	SNOWBALL_018996_st	pericentriolar material 1	8.668	7.715	1.564E-06	1.39E-03	1.94	Duroc-up
LOC100517759	SNOWBALL_033588_st	Ssc_hash_S29969254 PDUts1023H02 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1023H02 5prime, mRNA	4.162	4.833	1.662E-06	1.41E-03	-1.59	PiNN-up
MTMR3	SNOWBALL_024268_s_st	myotubularin related protein 3	7.934	8.307	2.037E-06	1.65E-03	-1.30	PiNN-up
UBE3A	SNOWBALL_003291_s_st	ubiquitin-protein ligase E3A-like	9.341	8.563	2.159E-06	1.67E-03	1.71	Duroc-up
PAK2	SNOWBALL_015816_st	p21 protein (Cdc42/Rac)-activated kinase 2	8.549	8.049	2.425E-06	1.80E-03	1.41	Duroc-up

BAT3	SNOWBALL_001236_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	7.170	7.616	2.540E-06	1.81E-03	-1.36	PiNN-up
DUSP12	SNOWBALL_006005_st	dual specificity phosphatase 12	6.418	7.404	3.744E-06	1.86E-03	-1.98	PiNN-up
	SNOWBALL_041873_st		4.399	4.827	3.590E-06	1.86E-03	-1.35	PiNN-up
CSNK1E	SNOWBALL_006793_st	casein kinase 1, epsilon	7.269	7.695	3.502E-06	1.86E-03	-1.34	PiNN-up
MTHFR	SNOWBALL_009016_st	methylenetetrahydrofolate reductase (NAD(P)H)	5.934	6.187	3.262E-06	1.86E-03	-1.19	PiNN-up
NEB	SNOWBALL_024019_st	PREDICTED: Sus scrofa similar to nebulin (LOC100154210), mRNA	11.978	11.626	2.750E-06	1.86E-03	1.28	Duroc-up
NT5DC1	SNOWBALL_000037_st	5'-nucleotidase domain containing 1	7.129	6.519	3.210E-06	1.86E-03	1.53	Duroc-up
PCM1	SNOWBALL_019000_st	pericentriolar material 1 protein-like	9.320	8.673	3.148E-06	1.86E-03	1.57	Duroc-up
APLF	SNOWBALL_005427_st	aprataxin and PNKP like factor	6.572	5.839	3.144E-06	1.86E-03	1.66	Duroc-up
DMD	SNOWBALL_020157_s_st	dystrophin	10.466	9.647	3.176E-06	1.86E-03	1.76	Duroc-up
PCM1	SNOWBALL_031582_st	pericentriolar material 1	9.571	8.686	3.758E-06	1.86E-03	1.85	Duroc-up
ZCCHC11	SNOWBALL_009000_st	zinc finger, CCHC domain containing 11	9.182	8.290	3.692E-06	1.86E-03	1.86	Duroc-up
PEX19	SNOWBALL_000849_st	peroxisomal biogenesis factor 19	8.176	8.921	4.476E-06	1.87E-03	-1.68	PiNN-up
PATL1	SNOWBALL_034902_st	protein associated with topoisomerase II homolog 1 (yeast)	3.826	4.472	4.490E-06	1.87E-03	-1.56	PiNN-up
DCTN4	SNOWBALL_025366_st	dynactin 4 (p62)	8.305	8.615	4.512E-06	1.87E-03	-1.24	PiNN-up
ZNF829	SNOWBALL_024496_x_st	PREDICTED: Sus scrofa hypothetical protein LOC100151774 (LOC100151774), mRNA	11.943	11.723	4.498E-06	1.87E-03	1.17	Duroc-up
SCAPER	SNOWBALL_010485_st	S-phase cyclin A-associated protein in the ER	7.026	6.291	4.042E-06	1.87E-03	1.66	Duroc-up
	SNOWBALL_035867_st	Ssc_hash_S40238181 rpliv0133_j19.y1 liv Sus scrofa cDNA 5prime, mRNA	8.464	7.607	4.523E-06	1.87E-03	1.81	Duroc-up
LARP1B	SNOWBALL_011715_st	La ribonucleoprotein domain family, member 1B	6.511	5.509	4.447E-06	1.87E-03	2.00	Duroc-up
LOC100511711	SNOWBALL_012742_s_st	islet cell autoantigen 1-like	6.875	5.804	4.755E-06	1.93E-03	2.10	Duroc-up
GGTA1	SNOWBALL_003366_st	N-acetyllactosaminide alpha-1,3-galactosyltransferase (EC 2.4.1.87)(UDP-galactose:beta-D-galactosyl-1,4-N-acetyl-D-glucosaminide alpha-1,3-galactosyltransferase)(Galactosyltransferase)	7.086	6.387	4.921E-06	1.95E-03	1.62	Duroc-up
ZHX1	SNOWBALL_045012_st	zinc fingers and homeoboxes protein 1-like	5.707	4.875	5.076E-06	1.97E-03	1.78	Duroc-up
	SNOWBALL_035396_st	Ssc_hash_S40179924 rjca10c_a7.y1 jca Sus scrofa cDNA 5prime, mRNA	6.504	7.262	5.323E-06	2.02E-03	-1.69	PiNN-up
ATG9A	SNOWBALL_017966_st	ATG9 autophagy related 9 homolog A (S. cerevisiae)	8.234	8.642	5.882E-06	2.06E-03	-1.33	PiNN-up
hsa-mir-544b	bta-mir-544b-2_st	MI0009861	7.316	6.678	5.760E-06	2.06E-03	1.56	Duroc-up
PNRC2	SNOWBALL_025636_s_st	proline-rich nuclear receptor coactivator 2	8.436	7.533	5.903E-06	2.06E-03	1.87	Duroc-up
ARHGAP5	SNOWBALL_010866_st	Rho GTPase activating protein 5	8.680	7.722	5.621E-06	2.06E-03	1.94	Duroc-up

EIF3F	SNOWBALL_047508_st	eukaryotic translation initiation factor 3, subunit F	8.716	9.112	6.294E-06	2.06E-03	-1.32	PiNN-up
CIZ1	SNOWBALL_003756_st	CDKN1A interacting zinc finger protein 1	7.178	7.422	6.385E-06	2.06E-03	-1.18	PiNN-up
ZNF292	SNOWBALL_002285_st	zinc finger protein 292	7.498	6.712	6.487E-06	2.06E-03	1.72	Duroc-up
ARHGAP5	SNOWBALL_010167_st	Rho GTPase activating protein 5	6.474	5.665	6.120E-06	2.06E-03	1.75	Duroc-up
VGLL3	SNOWBALL_037138_st	vestigial like 3 (Drosophila)	6.228	5.258	6.469E-06	2.06E-03	1.96	Duroc-up
DGCR2	SNOWBALL_016830_st	DiGeorge syndrome critical region gene 2	7.605	7.888	6.781E-06	2.12E-03	-1.22	PiNN-up
CD164	SNOWBALL_002669_st	CD164 molecule, sialomucin	10.017	9.669	7.190E-06	2.15E-03	1.27	Duroc-up
FAM120A	SNOWBALL_004907_st	family with sequence similarity 120A	8.282	7.858	7.289E-06	2.15E-03	1.34	Duroc-up
SCYL2	SNOWBALL_007695_st	SCY1-like 2 (S. cerevisiae)	7.429	6.873	7.351E-06	2.15E-03	1.47	Duroc-up
AGTPBP1	SNOWBALL_013414_st	ATP/GTP binding protein 1	6.402	5.591	6.991E-06	2.15E-03	1.75	Duroc-up
TWISTNB	SNOWBALL_012814_st	TWIST neighbor	6.931	6.354	7.577E-06	2.18E-03	1.49	Duroc-up
NMNAT1	SNOWBALL_009111_st	nicotinamide nucleotide adenylyltransferase 1	6.781	7.693	8.292E-06	2.18E-03	-1.88	PiNN-up
PPAPDC3	SNOWBALL_031389_st	phosphatidic acid phosphatase type 2 domain containing 3	7.851	8.353	8.120E-06	2.18E-03	-1.42	PiNN-up
KIAA2013	SNOWBALL_009354_st	KIAA2013	7.537	7.940	8.097E-06	2.18E-03	-1.32	PiNN-up
LOC100511498	SNOWBALL_004308_s_st	7SK snRNA methylphosphate capping enzyme-like	6.544	6.865	8.456E-06	2.18E-03	-1.25	PiNN-up
TTLL7	SNOWBALL_009297_st	tubulin tyrosine ligase-like family, member 7	8.213	7.601	7.847E-06	2.18E-03	1.53	Duroc-up
DMD	SNOWBALL_020132_s_st	dystrophin	11.033	10.395	7.797E-06	2.18E-03	1.56	Duroc-up
NIPBL	SNOWBALL_018593_st	Nipped-B homolog (Drosophila)	7.589	6.867	8.384E-06	2.18E-03	1.65	Duroc-up
PPP1R12A	SNOWBALL_037422_st	protein phosphatase 1, regulatory (inhibitor) subunit 12A	9.124	8.386	8.571E-06	2.18E-03	1.67	Duroc-up
LOC100525009	SNOWBALL_026081_st	Sus scrofa mRNA, clone:OVRM10083F10, expressed in ovary	5.542	5.961	8.697E-06	2.18E-03	-1.34	PiNN-up
HECTD3	SNOWBALL_009324_st	HECT domain containing 3	6.495	6.865	9.048E-06	2.19E-03	-1.29	PiNN-up
USP15	SNOWBALL_000925_st	ubiquitin specific peptidase 15	6.701	6.146	8.923E-06	2.19E-03	1.47	Duroc-up
ABCE1	SNOWBALL_011653_st	ATP-binding cassette, sub-family E (OABP), member 1	7.917	7.080	9.086E-06	2.19E-03	1.79	Duroc-up
FAM171A1	SNOWBALL_028073_st	family with sequence similarity 171, member A1	5.496	6.056	9.549E-06	2.21E-03	-1.48	PiNN-up
CACNA2D1	SNOWBALL_012512_st	calcium channel, voltage-dependent, alpha 2/delta subunit 1	11.093	10.373	9.528E-06	2.21E-03	1.65	Duroc-up
HLTF	SNOWBALL_015548_st	helicase-like transcription factor	5.966	5.165	9.514E-06	2.21E-03	1.74	Duroc-up
MGC155219	SNOWBALL_047523_st	hypothetical LOC531855	7.976	8.352	9.741E-06	2.23E-03	-1.30	PiNN-up
PLCE1	SNOWBALL_024946_st	PREDICTED: Sus scrofa similar to Phospholipase C, epsilon 1 (LOC100157745), mRNA	6.417	5.578	9.940E-06	2.24E-03	1.79	Duroc-up
SPRY2	SNOWBALL_014044_st	sprouty homolog 2 (Drosophila)	6.593	6.942	1.065E-05	2.35E-03	-1.27	PiNN-up

PCGF5	SNOWBALL_024603_st	PREDICTED: Sus scrofa similar to polycomb group ring finger 5 (LOC100154083), mRNA	6.493	5.932	1.070E-05	2.35E-03	1.48	Duroc-up
FAM169A	SNOWBALL_020612_x_st	U6 spliceosomal RNA [Source: RFAM;Acc:RF00026]	7.625	8.630	1.127E-05	2.42E-03	-2.01	PiNN-up
BSCL2	SNOWBALL_023008_s_st	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	6.351	6.870	1.166E-05	2.42E-03	-1.43	PiNN-up
NFIA	SNOWBALL_047369_st	nuclear factor I/A	9.778	9.349	1.125E-05	2.42E-03	1.35	Duroc-up
NFIA	SNOWBALL_047373_s_st	nuclear factor I/A	7.375	6.931	1.161E-05	2.42E-03	1.36	Duroc-up
	SNOWBALL_040488_st		4.428	3.797	1.152E-05	2.42E-03	1.55	Duroc-up
ANKRD34A	SNOWBALL_039269_st	ankyrin repeat domain 34A	6.087	6.738	1.314E-05	2.45E-03	-1.57	PiNN-up
COL6A3	SNOWBALL_018429_s_st	collagen, type VI, alpha 3	6.938	7.360	1.375E-05	2.45E-03	-1.34	PiNN-up
FAM107A	SNOWBALL_015494_st	family with sequence similarity 107, member A	6.663	6.957	1.367E-05	2.45E-03	-1.23	PiNN-up
SPI1	SNOWBALL_000614_s_st	spleen focus forming virus (SFFV) proviral integration oncogene spi1	5.480	5.749	1.245E-05	2.45E-03	-1.20	PiNN-up
PDS5B	SNOWBALL_013777_st	PDS5, regulator of cohesion maintenance, homolog B (S. cerevisiae)	7.208	6.748	1.369E-05	2.45E-03	1.38	Duroc-up
PRRC2C	SNOWBALL_013016_st	putative vascular inducible G protein-coupled receptor	9.013	8.482	1.281E-05	2.45E-03	1.45	Duroc-up
ACSL3	SNOWBALL_023103_st	acyl-CoA synthetase long-chain family member 3	7.683	7.094	1.255E-05	2.45E-03	1.50	Duroc-up
PRPF40A	SNOWBALL_017938_st	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	7.648	7.002	1.225E-05	2.45E-03	1.56	Duroc-up
EHBP1	SNOWBALL_005311_st	EH domain binding protein 1	6.848	6.201	1.213E-05	2.45E-03	1.57	Duroc-up
SSFA2	SNOWBALL_018143_s_st	sperm specific antigen 2	6.775	6.092	1.233E-05	2.45E-03	1.61	Duroc-up
ACSL3	SNOWBALL_017987_s_st	acyl-CoA synthetase long-chain family member 3	7.924	7.170	1.318E-05	2.45E-03	1.69	Duroc-up
PRPF40A	SNOWBALL_023851_st	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)	7.648	6.894	1.278E-05	2.45E-03	1.69	Duroc-up
RSF1	SNOWBALL_012291_s_st	remodeling and spacing factor 1	7.021	6.219	1.342E-05	2.45E-03	1.74	Duroc-up
Nhlrc2	SNOWBALL_024798_s_st	PREDICTED: Sus scrofa similar to NHL repeat containing 2 (LOC100155569), mRNA	5.865	5.039	1.330E-05	2.45E-03	1.77	Duroc-up
KCNJ11	SNOWBALL_032203_st	potassium inwardly-rectifying channel, subfamily J, member 11	6.591	6.894	1.416E-05	2.46E-03	-1.23	PiNN-up
KCTD9	SNOWBALL_016278_st	potassium channel tetramerisation domain containing 9	7.499	7.005	1.407E-05	2.46E-03	1.41	Duroc-up
SMCHD1	SNOWBALL_033045_st	structural maintenance of chromosomes flexible hinge domain containing 1	7.275	6.317	1.424E-05	2.46E-03	1.94	Duroc-up
RNASEK	SNOWBALL_015124_st	ribonuclease, RNase K	6.076	6.562	1.447E-05	2.48E-03	-1.40	PiNN-up
PFN1	SNOWBALL_014985_st	profilin 1	7.236	7.687	1.460E-05	2.48E-03	-1.37	PiNN-up
PNRC2	SNOWBALL_022340_s_st	proline-rich nuclear receptor coactivator 2	9.126	8.575	1.483E-05	2.49E-03	1.47	Duroc-up
MLSTD2	SNOWBALL_033073_st	fatty acyl CoA reductase 1	7.240	6.679	1.543E-05	2.57E-03	1.48	Duroc-up

PITPNB	SNOWBALL_016550_s_st	phosphatidylinositol transfer protein, beta	7.476	6.969	1.566E-05	2.58E-03	1.42	Duroc-up
ATP6V0C	SNOWBALL_004906_st	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	7.927	8.273	1.666E-05	2.72E-03	-1.27	PiNN-up
APPL1	SNOWBALL_023364_st	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	8.573	7.974	1.691E-05	2.74E-03	1.51	Duroc-up
RAB19	SNOWBALL_019696_st	RAB19, member RAS oncogene family	4.983	5.448	1.737E-05	2.75E-03	-1.38	PiNN-up
PAK2	SNOWBALL_015861_st	p21 protein (Cdc42/Rac)-activated kinase 2	8.889	8.529	1.759E-05	2.75E-03	1.28	Duroc-up
KIAA1715	SNOWBALL_018183_s_st	protein lunapark-like	8.599	7.958	1.732E-05	2.75E-03	1.56	Duroc-up
LRRC40	SNOWBALL_009329_st	leucine rich repeat containing 40	6.170	5.429	1.749E-05	2.75E-03	1.67	Duroc-up
UPF2	SNOWBALL_013690_st	UPF2 regulator of nonsense transcripts homolog (yeast)	7.345	6.641	1.821E-05	2.82E-03	1.63	Duroc-up
TRIM8	SNOWBALL_024853_st	tripartite motif containing 8	6.830	7.164	1.842E-05	2.83E-03	-1.26	PiNN-up
Dvir\GJ14580	SNOWBALL_035784_st	Ssc_hash_S40268747 rmas940b_b7.y1 mas Sus scrofa cDNA 5prime, mRNA	5.470	6.527	1.897E-05	2.84E-03	-2.08	PiNN-up
ZER1	SNOWBALL_003667_st	zer-1 homolog (C. elegans)	7.967	8.439	1.881E-05	2.84E-03	-1.39	PiNN-up
PARD3B	SNOWBALL_021828_s_st	par-3 partitioning defective 3 homolog B (C. elegans)	5.148	4.412	1.882E-05	2.84E-03	1.67	Duroc-up
SMARCA5	SNOWBALL_011803_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	7.187	6.720	1.924E-05	2.86E-03	1.38	Duroc-up
ALG3	SNOWBALL_047238_st	asparagine-linked glycosylation 3, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	6.768	7.166	1.948E-05	2.87E-03	-1.32	PiNN-up
7SK	SNOWBALL_006358_st	7SK RNA	5.559	6.066	1.967E-05	2.87E-03	-1.42	PiNN-up
UBAP2	SNOWBALL_013511_s_st	ubiquitin associated protein 2	9.347	9.763	1.985E-05	2.88E-03	-1.33	PiNN-up
KIAA0427	SNOWBALL_002491_st	KIAA0427	7.444	7.801	2.068E-05	2.88E-03	-1.28	PiNN-up
ZFP161	SNOWBALL_038506_st	zinc finger protein 161 homolog (mouse)	5.153	5.329	2.076E-05	2.88E-03	-1.13	PiNN-up
DCAF10	SNOWBALL_003876_st	DDB1 and CUL4 associated factor 10	7.463	7.088	2.015E-05	2.88E-03	1.30	Duroc-up
MYSM1	SNOWBALL_009226_st	Myb-like, SWIRM and MPN domains 1	7.044	6.480	2.051E-05	2.88E-03	1.48	Duroc-up
NCOA7	SNOWBALL_002213_st	nuclear receptor coactivator 7	5.686	5.058	2.050E-05	2.88E-03	1.55	Duroc-up
DMD	SNOWBALL_023267_st	dystrophin	10.635	9.988	2.086E-05	2.88E-03	1.57	Duroc-up
HOOK3	SNOWBALL_026216_st	hook homolog 3 (Drosophila)	8.401	7.569	2.108E-05	2.89E-03	1.78	Duroc-up
PPP4C	SNOWBALL_047775_st	protein phosphatase 4, catalytic subunit	5.798	6.119	2.157E-05	2.91E-03	-1.25	PiNN-up
PAK2	SNOWBALL_032940_st	p21 protein (Cdc42/Rac)-activated kinase 2	7.809	7.214	2.146E-05	2.91E-03	1.51	Duroc-up
ZFP36	SNOWBALL_017388_st	zinc finger protein 36, C3H type, homolog (mouse)	6.370	6.853	2.245E-05	2.95E-03	-1.40	PiNN-up
DISP1	SNOWBALL_021756_st	dispatched homolog 1 (Drosophila)	7.250	7.715	2.256E-05	2.95E-03	-1.38	PiNN-up
SURF4	SNOWBALL_025905_s_st	surfeit 4	7.449	7.869	2.232E-05	2.95E-03	-1.34	PiNN-up
C12orf29	SNOWBALL_007722_st	chromosome 12 open reading frame 29	6.900	6.320	2.266E-05	2.95E-03	1.49	Duroc-up
JMJD1C	SNOWBALL_024490_st	jumonji domain containing 1C	7.759	7.013	2.245E-05	2.95E-03	1.68	Duroc-up
DIS3L2	SNOWBALL_000918_st	DIS3 mitotic control homolog (S. cerevisiae)-like 2	7.593	8.145	2.348E-05	3.00E-03	-1.47	PiNN-up

NFE2L1	SNOWBALL_022120_st	nuclear factor (erythroid-derived 2)-like 1	8.434	8.893	2.372E-05	3.00E-03	-1.37	PiNN-up
DMD	SNOWBALL_001674_s_st	dystrophin	10.035	9.305	2.363E-05	3.00E-03	1.66	Duroc-up
MANEA	SNOWBALL_002272_st	mannosidase, endo-alpha	7.235	6.349	2.348E-05	3.00E-03	1.85	Duroc-up
MFSD11	SNOWBALL_041734_st	major facilitator superfamily domain containing 11	5.301	5.694	2.430E-05	3.03E-03	-1.31	PiNN-up
COX10	SNOWBALL_014724_st	protoheme IX farnesyltransferase, mitochondrial-like	6.245	6.632	2.474E-05	3.03E-03	-1.31	PiNN-up
RSRC1	SNOWBALL_021797_st	arginine/serine-rich coiled-coil 1	5.663	5.288	2.435E-05	3.03E-03	1.30	Duroc-up
GRSF1	SNOWBALL_011500_st	G-rich RNA sequence binding factor 1	8.794	8.335	2.483E-05	3.03E-03	1.37	Duroc-up
LOC100518209	SNOWBALL_028054_st	Ssc_hash_S17526441 BX676641 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0028.o.07 3prim, mRNA	5.931	5.204	2.474E-05	3.03E-03	1.66	Duroc-up
TUBA8	SNOWBALL_007682_st	tubulin, alpha 8	10.362	10.788	2.624E-05	3.10E-03	-1.34	PiNN-up
MTMR3	SNOWBALL_016629_st	myotubularin related protein 3	8.042	8.373	2.608E-05	3.10E-03	-1.26	PiNN-up
PTEN	SNOWBALL_017268_s_st	phosphatase and tensin homolog	8.213	7.660	2.583E-05	3.10E-03	1.47	Duroc-up
RIF1	SNOWBALL_018395_s_st	RAP1 interacting factor homolog (yeast)	6.796	6.187	2.590E-05	3.10E-03	1.53	Duroc-up
KIAA1033	SNOWBALL_007539_st	KIAA1033	7.808	7.178	2.606E-05	3.10E-03	1.55	Duroc-up
PEX19	SNOWBALL_000848_s_st	peroxisomal biogenesis factor 19	7.270	7.787	2.689E-05	3.10E-03	-1.43	PiNN-up
DHRS7B	SNOWBALL_030473_st	dehydrogenase/reductase (SDR family) member 7B	6.797	7.113	2.724E-05	3.10E-03	-1.24	PiNN-up
MRPS35	SNOWBALL_007347_st	mitochondrial ribosomal protein S35	7.466	6.935	2.692E-05	3.10E-03	1.45	Duroc-up
LOC100426506	SNOWBALL_017201_st	hypothetical LOC100426506	7.525	6.979	2.680E-05	3.10E-03	1.46	Duroc-up
LOC100520104	SNOWBALL_037541_st	hypothetical LOC100520104	5.954	5.221	2.708E-05	3.10E-03	1.66	Duroc-up
BIRC2	SNOWBALL_021970_st	baculoviral IAP repeat containing 2	7.458	6.676	2.733E-05	3.10E-03	1.72	Duroc-up
NCKAP1	SNOWBALL_018039_s_st	NCK-associated protein 1	9.135	8.688	2.774E-05	3.12E-03	1.36	Duroc-up
KIAA0528	SNOWBALL_034188_st	KIAA0528	6.321	5.809	2.781E-05	3.12E-03	1.43	Duroc-up
SCARB2	SNOWBALL_011528_st	scavenger receptor class B, member 2	8.369	8.937	2.843E-05	3.15E-03	-1.48	PiNN-up
RGS5	SNOWBALL_038043_st	regulator of G-protein signaling 5	8.828	8.044	2.827E-05	3.15E-03	1.72	Duroc-up
SRPK2	SNOWBALL_038054_st	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	4.409	3.506	2.885E-05	3.17E-03	1.87	Duroc-up
CAND1	SNOWBALL_007469_st	cullin-associated NEDD8-dissociated protein 1-like	6.686	6.150	2.907E-05	3.18E-03	1.45	Duroc-up
C7orf26	SNOWBALL_026553_st	chromosome 7 open reading frame 26	5.932	6.521	2.937E-05	3.19E-03	-1.50	PiNN-up
EFTUD1	SNOWBALL_010910_st	elongation factor Tu GTP binding domain containing 1	7.625	7.100	2.969E-05	3.21E-03	1.44	Duroc-up
AKAP1	SNOWBALL_042830_st		7.757	8.118	3.019E-05	3.22E-03	-1.28	PiNN-up
NUDT4	SNOWBALL_007706_st	nudix (nucleoside diphosphate linked moiety X)-type motif 4	10.524	10.006	3.031E-05	3.22E-03	1.43	Duroc-up
ALMS1	SNOWBALL_046481_st	Alstrom syndrome 1	5.746	5.069	3.003E-05	3.22E-03	1.60	Duroc-up
ZC3H11A	SNOWBALL_026182_s_st	zinc finger CCCH-type containing 11A	10.441	9.894	3.068E-05	3.23E-03	1.46	Duroc-up

ERBB2IP	SNOWBALL_018709_st	erbb2 interacting protein	9.087	8.529	3.100E-05	3.25E-03	1.47	Duroc-up
GPBP1	SNOWBALL_018834_st	vasculin-like	8.395	7.731	3.268E-05	3.41E-03	1.59	Duroc-up
HCFC1	SNOWBALL_020413_st	host cell factor C1 (VP16-accessory protein)	6.626	6.887	3.298E-05	3.42E-03	-1.20	PiNN-up
THOC2	SNOWBALL_001898_s_st	THO complex 2	7.012	6.406	3.325E-05	3.43E-03	1.52	Duroc-up
C1orf51	SNOWBALL_006337_st	chromosome 1 open reading frame 51	6.481	7.395	3.355E-05	3.44E-03	-1.88	PiNN-up
ATF6	SNOWBALL_029743_st	activating transcription factor 6	7.263	6.635	3.376E-05	3.44E-03	1.55	Duroc-up
XPA	SNOWBALL_003595_st	xeroderma pigmentosum, complementation group A	5.646	5.218	3.475E-05	3.50E-03	1.35	Duroc-up
AHR	SNOWBALL_012870_st	aryl hydrocarbon receptor	6.002	5.559	3.470E-05	3.50E-03	1.36	Duroc-up
LPP	SNOWBALL_033867_st	LIM domain containing preferred translocation partner in lipoma	8.351	7.534	3.508E-05	3.51E-03	1.76	Duroc-up
ASXL1	SNOWBALL_019158_st	additional sex combs like 1 (Drosophila)	6.399	6.747	3.606E-05	3.57E-03	-1.27	PiNN-up
OXR1	SNOWBALL_005673_st	oxidation resistance 1	8.231	7.518	3.592E-05	3.57E-03	1.64	Duroc-up
PCBP1	SNOWBALL_004982_st	poly(rC) binding protein 1	10.142	10.514	3.635E-05	3.58E-03	-1.29	PiNN-up
CLCN1	SNOWBALL_019637_st	chloride channel 1, skeletal muscle	6.917	7.356	3.757E-05	3.67E-03	-1.36	PiNN-up
CDKAL1	SNOWBALL_009553_st	CDK5 regulatory subunit associated protein 1-like 1	7.650	7.282	3.805E-05	3.67E-03	1.29	Duroc-up
TAF2	SNOWBALL_005597_s_st	TAF2 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 150kDa	7.539	6.905	3.796E-05	3.67E-03	1.55	Duroc-up
LOC100524197	SNOWBALL_020855_st	hypothetical LOC100524197	10.992	7.131	3.812E-05	3.67E-03	14.53	Duroc-up
ELMOD3	SNOWBALL_005381_st	ELMO/CED-12 domain containing 3	7.124	7.638	3.844E-05	3.68E-03	-1.43	PiNN-up
LIMCH1	SNOWBALL_011383_st	LIM and calponin homology domains 1	10.275	9.784	3.889E-05	3.70E-03	1.41	Duroc-up
USP45	SNOWBALL_002608_st	ubiquitin specific peptidase 45	7.031	6.312	3.898E-05	3.70E-03	1.65	Duroc-up
STYX	SNOWBALL_003304_st	serine/threonine/tyrosine interacting protein	8.158	7.538	3.948E-05	3.70E-03	1.54	Duroc-up
C3orf63	SNOWBALL_045669_st	chromosome 3 open reading frame 63	6.555	5.907	3.939E-05	3.70E-03	1.57	Duroc-up
NCK2	SNOWBALL_023285_s_st	NCK adaptor protein 2	7.506	7.929	4.231E-05	3.73E-03	-1.34	PiNN-up
KDELR2	SNOWBALL_034130_st	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	5.238	5.611	4.184E-05	3.73E-03	-1.30	PiNN-up
PSKH1	SNOWBALL_033205_st	protein serine kinase H1	6.920	7.276	4.192E-05	3.73E-03	-1.28	PiNN-up
RNF40	SNOWBALL_004447_s_st	e3 ubiquitin-protein ligase BRE1B-like	5.883	6.126	4.059E-05	3.73E-03	-1.18	PiNN-up
CDC5L	SNOWBALL_009908_st	CDC5 cell division cycle 5-like (S. pombe)	7.594	7.148	4.227E-05	3.73E-03	1.36	Duroc-up
ASH1L	SNOWBALL_005994_st	ash1 (absent, small, or homeotic)-like (Drosophila)	9.736	9.222	4.167E-05	3.73E-03	1.43	Duroc-up
LMBRD2	SNOWBALL_018580_st	LMBR1 domain containing 2	7.920	7.350	4.175E-05	3.73E-03	1.48	Duroc-up
BBX	SNOWBALL_021494_s_st	bobby sox homolog (Drosophila)	7.037	6.463	4.017E-05	3.73E-03	1.49	Duroc-up
LOC100518043	SNOWBALL_023867_st	PREDICTED: Sus scrofa hypothetical protein LOC100155710 (LOC100155710), mRNA	6.542	5.920	4.088E-05	3.73E-03	1.54	Duroc-up
ZHX1	SNOWBALL_005613_st	zinc fingers and homeoboxes 1	8.414	7.727	4.075E-05	3.73E-03	1.61	Duroc-up
KIF5B	SNOWBALL_013456_st	kinesin family member 5B	9.585	8.808	4.039E-05	3.73E-03	1.71	Duroc-up
DMD	SNOWBALL_020169_s_st	dystrophin	10.080	9.294	4.162E-05	3.73E-03	1.72	Duroc-up

DCUN1D1	SNOWBALL_015792_s_st	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	10.292	9.655	4.253E-05	3.73E-03	1.56	Duroc-up
FRYL	SNOWBALL_028938_st	FRY-like	5.535	4.978	4.296E-05	3.75E-03	1.47	Duroc-up
ZFP106	SNOWBALL_002930_st	zinc finger protein 106 homolog (mouse)	11.847	11.312	4.347E-05	3.77E-03	1.45	Duroc-up
TBL1XR1	SNOWBALL_032334_st	transducin (beta)-like 1 X-linked receptor 1	6.334	5.485	4.356E-05	3.77E-03	1.80	Duroc-up
NAT15	SNOWBALL_034407_st	N-acetyltransferase 15 (GCN5-related, putative)	8.813	9.269	4.410E-05	3.78E-03	-1.37	PiNN-up
SNX13	SNOWBALL_012627_st	sorting nexin 13	6.963	6.155	4.408E-05	3.78E-03	1.75	Duroc-up
	SNOWBALL_043762_st		5.170	5.663	4.526E-05	3.81E-03	-1.41	PiNN-up
HIST1H2AC	SNOWBALL_009572_st	histone cluster 1, H2ac	8.763	9.163	4.563E-05	3.81E-03	-1.32	PiNN-up
SLAIN2	SNOWBALL_011368_st	SLAIN motif family, member 2	9.863	9.525	4.636E-05	3.81E-03	1.26	Duroc-up
ZC3H11A	SNOWBALL_021969_st	zinc finger CCCH-type containing 11A	10.424	9.984	4.627E-05	3.81E-03	1.36	Duroc-up
CAPN7	SNOWBALL_021072_s_st	calpain 7	7.013	6.495	4.577E-05	3.81E-03	1.43	Duroc-up
GTDC1	SNOWBALL_024064_st	glycosyltransferase-like domain containing 1	7.257	6.589	4.568E-05	3.81E-03	1.59	Duroc-up
DLG1	SNOWBALL_000264_s_st	discs, large homolog 1 (Drosophila)	7.020	6.336	4.548E-05	3.81E-03	1.61	Duroc-up
FGFR1OP2	SNOWBALL_007346_st	FGFR1 oncogene partner 2	7.525	6.788	4.594E-05	3.81E-03	1.67	Duroc-up
CCDC142	SNOWBALL_033461_st	coiled-coil domain containing 142	5.050	4.284	4.598E-05	3.81E-03	1.70	Duroc-up
FRYL	SNOWBALL_011379_st	FRY-like	7.252	6.740	4.805E-05	3.89E-03	1.43	Duroc-up
	SNOWBALL_037997_st		5.479	4.948	4.798E-05	3.89E-03	1.44	Duroc-up
RGS5	SNOWBALL_005974_st	regulator of G-protein signaling 5	10.237	9.395	4.764E-05	3.89E-03	1.79	Duroc-up
ARPC4	SNOWBALL_023380_s_st	Sus scrofa actin related protein 2/3 complex subunit 4 mRNA, complete cds	7.535	8.009	4.849E-05	3.89E-03	-1.39	PiNN-up
SDCCAG8	SNOWBALL_013274_st	serologically defined colon cancer antigen 8	6.294	5.522	4.828E-05	3.89E-03	1.71	Duroc-up
KIAA1161	SNOWBALL_013446_st	KIAA1161	8.857	9.246	4.896E-05	3.91E-03	-1.31	PiNN-up
HBS1L	SNOWBALL_002152_s_st	HBS1-like protein-like	5.600	4.732	4.978E-05	3.96E-03	1.82	Duroc-up
BAT3	SNOWBALL_001250_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	8.243	8.502	5.060E-05	3.97E-03	-1.20	PiNN-up
ARHGEF10L	SNOWBALL_009210_st	Rho guanine nucleotide exchange factor (GEF) 10-like	6.721	6.975	5.043E-05	3.97E-03	-1.19	PiNN-up
N4BP2L2	SNOWBALL_013774_st	NEDD4 binding protein 2-like 2	6.968	6.248	5.044E-05	3.97E-03	1.65	Duroc-up
WAC	SNOWBALL_013390_st	WW domain containing adaptor with coiled-coil	9.058	8.588	5.207E-05	4.07E-03	1.38	Duroc-up
KIF21A	SNOWBALL_007808_st	kinesin family member 21A	5.564	5.005	5.224E-05	4.07E-03	1.47	Duroc-up
PCYT2	SNOWBALL_021437_s_st	phosphate cytidylyltransferase 2, ethanolamine	6.055	6.264	5.292E-05	4.09E-03	-1.16	PiNN-up
HSP90B1	SNOWBALL_007684_st	//heat shock protein 90kDa beta (Grp94), member 2 (pseudogene)	8.183	7.506	5.306E-05	4.09E-03	1.60	Duroc-up
	SNOWBALL_035910_st	Ssc_hash_S29980115 PDUts1156B07 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1156B07 5prime, mRNA	5.455	6.064	5.391E-05	4.14E-03	-1.52	PiNN-up

KLHL31	SNOWBALL_030831_st	kelch-like 31 (Drosophila)	11.166	10.584	5.429E-05	4.15E-03	1.50	Duroc-up
G3BP1	SNOWBALL_018698_st	glycine receptor subunit alpha-1-like	8.622	8.342	5.491E-05	4.16E-03	1.21	Duroc-up
DPYD	SNOWBALL_006409_st	dihydropyrimidine dehydrogenase	6.962	6.439	5.487E-05	4.16E-03	1.44	Duroc-up
RFC1	SNOWBALL_011407_st	replication factor C (activator 1) 1, 145kDa	6.187	5.542	5.544E-05	4.19E-03	1.56	Duroc-up
BBX	SNOWBALL_016182_st	bobby sox homolog (Drosophila)	7.004	6.462	5.620E-05	4.19E-03	1.46	Duroc-up
CCDC132	SNOWBALL_035433_st	coiled-coil domain containing 132	7.875	7.254	5.617E-05	4.19E-03	1.54	Duroc-up
LCORL	SNOWBALL_011309_st	ligand dependent nuclear receptor corepressor-like	5.138	4.485	5.595E-05	4.19E-03	1.57	Duroc-up
CTAGE5	SNOWBALL_003120_st	CTAGE family, member 5	7.127	6.443	5.793E-05	4.30E-03	1.61	Duroc-up
PLCB4	SNOWBALL_019071_st	phospholipase C, beta 4	6.851	6.324	5.995E-05	4.36E-03	1.44	Duroc-up
N4BP2L2	SNOWBALL_013782_st	NEDD4-binding protein 2-like 2-like	8.206	7.653	5.937E-05	4.36E-03	1.47	Duroc-up
NKTR	SNOWBALL_015244_st	natural killer-tumor recognition sequence	7.089	6.443	5.978E-05	4.36E-03	1.56	Duroc-up
RAB30	SNOWBALL_035965_st	RAB30, member RAS oncogene family	5.455	4.706	5.979E-05	4.36E-03	1.68	Duroc-up
MSH2	SNOWBALL_005485_st	mutS homolog 2, colon cancer, nonpolyposis type 1 (E. coli)	5.753	4.946	5.974E-05	4.36E-03	1.75	Duroc-up
SCN1B	SNOWBALL_008193_st	sodium channel, voltage-gated, type I, beta	9.642	10.308	6.088E-05	4.39E-03	-1.59	PiNN-up
ADD3	SNOWBALL_024818_s_st	adducin 3 (gamma)	6.050	5.512	6.115E-05	4.39E-03	1.45	Duroc-up
USP15	SNOWBALL_033181_st	ubiquitin specific peptidase 15	7.968	7.107	6.103E-05	4.39E-03	1.82	Duroc-up
LETM1	SNOWBALL_011260_st	leucine zipper-EF-hand containing transmembrane protein 1	6.364	6.605	6.234E-05	4.46E-03	-1.18	PiNN-up
CSPP1	SNOWBALL_005707_st	centrosome and spindle pole associated protein 1	6.472	5.935	6.262E-05	4.46E-03	1.45	Duroc-up
TSC22D1	SNOWBALL_013842_st	TSC22 domain family, member 1	8.819	9.189	6.360E-05	4.48E-03	-1.29	PiNN-up
SSFA2	SNOWBALL_023905_st	PREDICTED: Sus scrofa similar to sperm specific antigen 2 (LOC100155630), mRNA	7.186	6.733	6.344E-05	4.48E-03	1.37	Duroc-up
DLG1	SNOWBALL_000265_s_st	discs, large homolog 1 (Drosophila)	7.142	6.355	6.309E-05	4.48E-03	1.73	Duroc-up
RNF185	SNOWBALL_024239_st	PREDICTED: Sus scrofa similar to ring finger protein 185, transcript variant 3 (LOC100157569), mRNA	6.437	7.093	6.422E-05	4.51E-03	-1.57	PiNN-up
NT5DC3	SNOWBALL_007548_st	5'-nucleotidase domain containing 3	7.417	7.969	6.507E-05	4.53E-03	-1.47	PiNN-up
UBE3A	SNOWBALL_002807_st	ubiquitin protein ligase E3A	8.616	8.082	6.499E-05	4.53E-03	1.45	Duroc-up
SFRS2IP	SNOWBALL_007608_st	splicing factor, arginine/serine-rich 2, interacting protein	7.678	6.863	6.565E-05	4.54E-03	1.76	Duroc-up
VPS26A	SNOWBALL_017432_s_st	vacuolar protein sorting 26 homolog A (S. pombe)	9.141	8.286	6.580E-05	4.54E-03	1.81	Duroc-up
MTRF1	SNOWBALL_013818_st	mitochondrial translational release factor 1	6.200	5.617	6.658E-05	4.58E-03	1.50	Duroc-up
UBE2D2	SNOWBALL_011784_st	ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast)	9.802	9.401	6.712E-05	4.60E-03	1.32	Duroc-up
BAT3	SNOWBALL_001244_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	7.638	8.231	7.018E-05	4.71E-03	-1.51	PiNN-up
YIPF3	SNOWBALL_009933_s_st	Yip1 domain family, member 3	6.280	6.708	6.996E-05	4.71E-03	-1.35	PiNN-up

MUC13	SNOWBALL_024178_x_st	mucin 13, cell surface associated	12.783	12.617	6.997E-05	4.71E-03	1.12	Duroc-up
CLINT1	SNOWBALL_018799_st	clathrin interactor 1	9.708	9.203	7.029E-05	4.71E-03	1.42	Duroc-up
TIA1	SNOWBALL_027995_st	Ssc_hash_S18548660 BX917311 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0037.m.19 5prim, mRNA	5.712	5.120	6.945E-05	4.71E-03	1.51	Duroc-up
SMC2	SNOWBALL_003473_st	structural maintenance of chromosomes 2	5.465	4.489	6.977E-05	4.71E-03	1.97	Duroc-up
SPPL3	SNOWBALL_016794_st	signal peptide peptidase-like 3-like	7.626	7.989	7.059E-05	4.71E-03	-1.29	PiNN-up
ILK	SNOWBALL_025936_st	integrin-linked kinase	6.438	7.015	7.128E-05	4.74E-03	-1.49	PiNN-up
TRAPPC8	SNOWBALL_009254_st	//trafficking protein particle complex 8	7.626	7.001	7.153E-05	4.74E-03	1.54	Duroc-up
SYNPO	SNOWBALL_030397_st	synaptopodin	8.470	8.815	7.245E-05	4.78E-03	-1.27	PiNN-up
ZNF252	SNOWBALL_008689_st	zinc finger protein 271-like	4.544	3.927	7.273E-05	4.78E-03	1.53	Duroc-up
LEO1	SNOWBALL_002445_st	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	6.716	6.286	7.359E-05	4.82E-03	1.35	Duroc-up
TIPRL	SNOWBALL_005984_st	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)	7.796	7.337	7.474E-05	4.88E-03	1.38	Duroc-up
GPBP1	SNOWBALL_018864_s_st	vasculin-like	8.552	8.024	7.514E-05	4.89E-03	1.44	Duroc-up
GNG3	SNOWBALL_021293_s_st	guanine nucleotide binding protein (G protein), gamma 3	6.016	6.566	7.612E-05	4.91E-03	-1.46	PiNN-up
UTRN	SNOWBALL_002114_st	utrophin	7.601	7.032	7.588E-05	4.91E-03	1.48	Duroc-up
CEP350	SNOWBALL_012882_st	centrosomal protein 350kDa	8.756	8.180	7.678E-05	4.94E-03	1.49	Duroc-up
TESK1	SNOWBALL_003839_st	testis-specific kinase 1	8.174	8.563	7.707E-05	4.94E-03	-1.31	PiNN-up
DENND4A	SNOWBALL_002689_st	DENN/MADD domain containing 4A	7.126	6.587	7.864E-05	4.99E-03	1.45	Duroc-up
GPR155	SNOWBALL_017887_st	G protein-coupled receptor 155	6.449	5.898	7.872E-05	4.99E-03	1.46	Duroc-up
EBAG9	SNOWBALL_005590_st	receptor-binding cancer antigen expressed on SiSo cells-like	7.297	6.700	7.864E-05	4.99E-03	1.51	Duroc-up
EDC3	SNOWBALL_010638_st	enhancer of mRNA decapping 3 homolog (S. cerevisiae)	6.895	7.213	7.921E-05	5.01E-03	-1.25	PiNN-up
ZBTB11	SNOWBALL_015865_st	zinc finger and BTB domain containing 11	6.301	6.606	8.011E-05	5.04E-03	-1.24	PiNN-up
ATP9A	SNOWBALL_000455_st	ATPase, class II, type 9A	6.751	7.021	8.090E-05	5.05E-03	-1.21	PiNN-up
SOS2	SNOWBALL_003104_st	son of sevenless homolog 2 (Drosophila)	8.968	8.440	8.128E-05	5.05E-03	1.44	Duroc-up
AHI1	SNOWBALL_002148_st	Abelson helper integration site 1	6.528	5.919	8.141E-05	5.05E-03	1.53	Duroc-up
TRPM7	SNOWBALL_002897_st	transient receptor potential cation channel, subfamily M, member 7	7.615	6.976	8.109E-05	5.05E-03	1.56	Duroc-up
NBEAL1	SNOWBALL_041990_st	neurobeachin-like 1	6.238	5.641	8.225E-05	5.07E-03	1.51	Duroc-up
SMEK2	SNOWBALL_004988_st	SMEK homolog 2, suppressor of mek1 (Dictyostelium)	7.186	6.476	8.199E-05	5.07E-03	1.64	Duroc-up
DLG1	SNOWBALL_000263_s_st	discs, large homolog 1 (Drosophila)	8.014	7.378	8.274E-05	5.08E-03	1.55	Duroc-up

CUTA	SNOWBALL_010040_st	cutA divalent cation tolerance homolog (E. coli)	6.786	7.312	8.388E-05	5.12E-03	-1.44	PiNN-up
TM9SF1	SNOWBALL_010777_st	transmembrane 9 superfamily member 1	6.557	6.952	8.478E-05	5.12E-03	-1.31	PiNN-up
TCF25	SNOWBALL_007846_s_st	transcription factor 25 (basic helix-loop-helix)	7.011	7.302	8.459E-05	5.12E-03	-1.22	PiNN-up
C5orf42	SNOWBALL_018649_st	chromosome 5 open reading frame 42	5.236	4.769	8.506E-05	5.12E-03	1.38	Duroc-up
PDK1	SNOWBALL_017931_st	pyruvate dehydrogenase kinase, isozyme 1	6.962	6.434	8.443E-05	5.12E-03	1.44	Duroc-up
C18orf54	SNOWBALL_002442_st	chromosome 18 open reading frame 54	4.541	3.764	8.416E-05	5.12E-03	1.71	Duroc-up
ADAMTS20	SNOWBALL_007681_s_st	ADAM metallopeptidase with thrombospondin type 1 motif, 20	6.031	5.327	8.733E-05	5.24E-03	1.63	Duroc-up
RB1	SNOWBALL_013869_st	retinoblastoma 1	8.284	7.846	8.980E-05	5.36E-03	1.35	Duroc-up
SENP6	SNOWBALL_042664_st	sentrin-specific protease 6-like	8.013	7.472	9.043E-05	5.36E-03	1.45	Duroc-up
CUL4B	SNOWBALL_001839_st	cullin 4B	6.439	5.835	8.994E-05	5.36E-03	1.52	Duroc-up
CLIC4	SNOWBALL_028685_st	chloride intracellular channel 4	7.559	6.919	9.050E-05	5.36E-03	1.56	Duroc-up
FUNDC2	SNOWBALL_001998_st	FUN14 domain containing 2	7.817	8.412	9.149E-05	5.38E-03	-1.51	PiNN-up
RBM26	SNOWBALL_013979_st	RNA binding motif protein 26	7.343	6.952	9.177E-05	5.38E-03	1.31	Duroc-up
SNX14	SNOWBALL_002345_st	sorting nexin 14	7.205	6.730	9.151E-05	5.38E-03	1.39	Duroc-up
TUBG2	SNOWBALL_014373_st	tubulin, gamma 2	8.995	9.418	9.224E-05	5.39E-03	-1.34	PiNN-up
TIAL1	SNOWBALL_013222_s_st	TIA1 cytotoxic granule-associated RNA binding protein-like 1	8.406	8.032	9.273E-05	5.40E-03	1.30	Duroc-up
SFRS18	SNOWBALL_002543_st	splicing factor, arginine/serine-rich 18 [Source:HGNC Symbol;Acc:21222]//UPF0471 protein C1orf63	8.131	7.516	9.344E-05	5.42E-03	1.53	Duroc-up
C1QA	SNOWBALL_009028_st	complement component 1, q subcomponent, A chain	6.474	6.925	9.443E-05	5.43E-03	-1.37	PiNN-up
SLC8A3	SNOWBALL_010150_st	solute carrier family 8 (sodium/calcium exchanger), member 3	8.238	7.746	9.410E-05	5.43E-03	1.41	Duroc-up
CCDC88A	SNOWBALL_005294_st	coiled-coil domain containing 88A	5.904	5.186	9.450E-05	5.43E-03	1.65	Duroc-up
CTAGE5	SNOWBALL_002876_st	CTAGE family, member 5	4.791	4.316	9.507E-05	5.45E-03	1.39	Duroc-up
LPP	SNOWBALL_033791_st	LIM domain containing preferred translocation partner in lipoma	9.037	8.408	9.553E-05	5.46E-03	1.55	Duroc-up
	SNOWBALL_005082_st		8.864	8.209	9.588E-05	5.46E-03	1.58	Duroc-up
PLOD1	SNOWBALL_009295_st	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1	6.938	7.246	9.755E-05	5.52E-03	-1.24	PiNN-up
SMC2	SNOWBALL_004085_st	structural maintenance of chromosomes 2	5.518	4.621	9.741E-05	5.52E-03	1.86	Duroc-up
RPP30	SNOWBALL_017084_st	ribonuclease P/MRP 30kDa subunit	5.881	5.315	9.969E-05	5.62E-03	1.48	Duroc-up
SKIV2L2	SNOWBALL_018601_st	superkiller viralicidic activity 2-like 2 (S. cerevisiae)	7.189	6.595	1.001E-04	5.63E-03	1.51	Duroc-up
THRA	SNOWBALL_014500_s_st	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	6.706	7.064	1.005E-04	5.63E-03	-1.28	PiNN-up
CXCL12	SNOWBALL_000343_st	chemokine (C-X-C motif) ligand 12	7.654	8.139	1.016E-04	5.66E-03	-1.40	PiNN-up
USP34	SNOWBALL_005147_st	ubiquitin specific peptidase 34	8.738	8.250	1.014E-04	5.66E-03	1.40	Duroc-up

CCNT2	SNOWBALL_031904_st	cyclin T2	5.461	4.950	1.034E-04	5.74E-03	1.43	Duroc-up
PLEKHF2	SNOWBALL_035373_st	pleckstrin homology domain containing, family F (with FYVE domain) member 2	7.617	7.083	1.038E-04	5.74E-03	1.45	Duroc-up
FILIP1	SNOWBALL_002562_st	filamin A interacting protein 1	9.191	8.331	1.046E-04	5.77E-03	1.82	Duroc-up
	SNOWBALL_046201_st		5.336	5.659	1.059E-04	5.77E-03	-1.25	PiNN-up
ATF6	SNOWBALL_005836_st	activating transcription factor 6	9.003	8.594	1.060E-04	5.77E-03	1.33	Duroc-up
SLC10A5	SNOWBALL_025229_st	solute carrier family 10 (sodium/bile acid cotransporter family), member 5	4.280	3.768	1.059E-04	5.77E-03	1.43	Duroc-up
PBRM1	SNOWBALL_015336_st	polybromo 1	8.213	7.631	1.057E-04	5.77E-03	1.50	Duroc-up
PLCD1	SNOWBALL_047539_st	phospholipase C, delta 1	6.773	7.144	1.077E-04	5.85E-03	-1.29	PiNN-up
	SNOWBALL_034933_st	Ssc_hash_S17512141 BX666984 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0027.c.20 3prim, mRNA	4.518	4.030	1.081E-04	5.85E-03	1.40	Duroc-up
CCNT2	SNOWBALL_017680_st	cyclin T2	7.004	6.504	1.095E-04	5.86E-03	1.41	Duroc-up
ADAM9	SNOWBALL_017775_st	ADAM metallopeptidase domain 9	7.108	6.596	1.093E-04	5.86E-03	1.43	Duroc-up
FRYL	SNOWBALL_011345_s_st	FRY-like	7.032	6.470	1.088E-04	5.86E-03	1.48	Duroc-up
SUZ12	SNOWBALL_014612_s_st	suppressor of zeste 12 homolog (Drosophila)	6.990	6.380	1.089E-04	5.86E-03	1.53	Duroc-up
PPP3CA	SNOWBALL_011654_s_st	protein phosphatase 3, catalytic subunit, alpha isozyme	8.755	8.328	1.105E-04	5.90E-03	1.34	Duroc-up
LMF2	SNOWBALL_007482_st	lipase maturation factor 2	6.253	6.603	1.109E-04	5.90E-03	-1.27	PiNN-up
FAM168B	SNOWBALL_043094_st	hypothetical LOC505853	6.944	7.374	1.121E-04	5.95E-03	-1.35	PiNN-up
FNTB	SNOWBALL_010176_st	farnesyltransferase, CAAX box, beta	6.722	7.755	1.150E-04	5.96E-03	-2.05	PiNN-up
RNF157	SNOWBALL_000118_st	ring finger protein 157	8.077	8.494	1.135E-04	5.96E-03	-1.34	PiNN-up
EIF5A	SNOWBALL_014984_st	eukaryotic translation initiation factor 5A	10.191	10.556	1.138E-04	5.96E-03	-1.29	PiNN-up
PARD3B	SNOWBALL_018041_s_st	partitioning defective 3 homolog B-like	5.818	5.414	1.153E-04	5.96E-03	1.32	Duroc-up
BDP1	SNOWBALL_018827_st	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	6.976	6.554	1.148E-04	5.96E-03	1.34	Duroc-up
RUFY2	SNOWBALL_024686_st	RUN and FYVE domain containing 2	6.708	6.070	1.132E-04	5.96E-03	1.56	Duroc-up
JMJD1C	SNOWBALL_017161_s_st	jumonji domain containing 1C	7.795	7.078	1.151E-04	5.96E-03	1.64	Duroc-up
CLIC4	SNOWBALL_047572_st	chloride intracellular channel 4	5.794	5.024	1.146E-04	5.96E-03	1.71	Duroc-up
PDE7B	SNOWBALL_046168_st		5.619	3.955	1.155E-04	5.96E-03	3.17	Duroc-up
NCKAP1	SNOWBALL_023903_s_st	PREDICTED: Sus scrofa similar to Nck-associated protein 1 (NAP 1) (p125Nap1) (Membrane-associated protein HEM-2), transcript variant 1 (LOC100158033), mRNA	9.376	8.932	1.163E-04	5.99E-03	1.36	Duroc-up
LTBP1	SNOWBALL_005514_st	latent transforming growth factor beta binding protein 1	6.687	7.032	1.182E-04	6.04E-03	-1.27	PiNN-up

BLZF1	SNOWBALL_025731_s_st	basic leucine zipper nuclear factor 1	7.439	6.875	1.180E-04	6.04E-03	1.48	Duroc-up
N4BP2	SNOWBALL_011336_st	NEDD4 binding protein 2	6.000	5.264	1.178E-04	6.04E-03	1.67	Duroc-up
PRRC2C	SNOWBALL_026577_st	proline-rich coiled-coil 2C	8.428	7.823	1.187E-04	6.04E-03	1.52	Duroc-up
VCPIP1	SNOWBALL_028062_st	valosin containing protein (p97)/p47 complex interacting protein 1	6.169	5.407	1.197E-04	6.08E-03	1.70	Duroc-up
COL6A3	SNOWBALL_024027_s_st	collagen, type VI, alpha 3	7.473	8.099	1.202E-04	6.08E-03	-1.54	PiNN-up
	SNOWBALL_035959_st	Ssc_hash_S29987646 PDUts2064E05 Porcine testis cDNA library II Sus scrofa cDNA clone PDUts2064E05 5prime, mRNA	4.701	5.550	1.206E-04	6.09E-03	-1.80	PiNN-up
LOC100517018	SNOWBALL_002374_st	activating signal cointegrator 1 complex subunit 3-like	7.664	6.882	1.215E-04	6.12E-03	1.72	Duroc-up
CGRRF1	SNOWBALL_003143_st	cell growth regulator with ring finger domain 1	6.130	5.568	1.224E-04	6.13E-03	1.48	Duroc-up
ADAMTS20	SNOWBALL_007516_st	ADAM metallopeptidase with thrombospondin type 1 motif, 20	6.441	5.776	1.223E-04	6.13E-03	1.58	Duroc-up
U2SURP	SNOWBALL_015543_st	U2-associated protein SR140 (140 kDa Ser/Arg-rich domain protein)	7.504	6.767	1.228E-04	6.13E-03	1.67	Duroc-up
AKAP9	SNOWBALL_012691_st	A kinase (PRKA) anchor protein (yotiao) 9	7.898	7.156	1.237E-04	6.16E-03	1.67	Duroc-up
COL6A3	SNOWBALL_018441_s_st	collagen, type VI, alpha 3	8.917	9.332	1.253E-04	6.19E-03	-1.33	PiNN-up
DGCR2	SNOWBALL_024166_st	DiGeorge syndrome critical region gene 2	6.215	6.484	1.253E-04	6.19E-03	-1.21	PiNN-up
FERMT2	SNOWBALL_002730_st	//fermitin family member 2	8.884	8.427	1.251E-04	6.19E-03	1.37	Duroc-up
LOC100515048	SNOWBALL_013312_st	uncharacterized protein C9orf102 homolog	7.925	7.430	1.265E-04	6.19E-03	1.41	Duroc-up
RECQL	SNOWBALL_007189_st	RecQ protein-like (DNA helicase Q1-like)	5.353	4.711	1.261E-04	6.19E-03	1.56	Duroc-up
RPS6KA3	SNOWBALL_032337_st	ribosomal protein S6 kinase, 90kDa, polypeptide 3	8.301	7.642	1.265E-04	6.19E-03	1.58	Duroc-up
FZD7	SNOWBALL_046663_st	frizzled homolog 7 (Drosophila)	7.016	7.731	1.275E-04	6.21E-03	-1.64	PiNN-up
PNRC2	SNOWBALL_026968_s_st	Sus scrofa clone Clu_4823.scr.msk.p1.Contig4, mRNA sequence	7.227	6.538	1.275E-04	6.21E-03	1.61	Duroc-up
SLC37A3	SNOWBALL_019708_st	solute carrier family 37 (glycerol-3-phosphate transporter), member 3	5.445	5.821	1.290E-04	6.26E-03	-1.30	PiNN-up
CAPN6	SNOWBALL_020725_st	calpain 6	8.136	8.732	1.295E-04	6.27E-03	-1.51	PiNN-up
C1orf9	SNOWBALL_013216_st	chromosome 1 open reading frame 9	6.471	5.754	1.341E-04	6.44E-03	1.64	Duroc-up
LPP	SNOWBALL_032698_st	LIM domain containing preferred translocation partner in lipoma	7.002	6.227	1.339E-04	6.44E-03	1.71	Duroc-up
CPEB2	SNOWBALL_033059_st	cytoplasmic polyadenylation element binding protein 2	4.963	4.055	1.337E-04	6.44E-03	1.88	Duroc-up
MLXIP	SNOWBALL_024405_s_st	MLX interacting protein	9.264	9.653	1.345E-04	6.44E-03	-1.31	PiNN-up
KIAA1009	SNOWBALL_002250_st	KIAA1009	4.739	4.189	1.360E-04	6.49E-03	1.46	Duroc-up

SREK1	SNOWBALL_018808_st	splicing factor, arginine/serine-rich 12 //splicing regulatory glutamine/lysine-rich protein 1	7.047	6.428	1.363E-04	6.49E-03	1.54	Duroc-up
RNF160	SNOWBALL_040115_st	listerin E3 ubiquitin protein ligase 1	5.825	5.376	1.389E-04	6.60E-03	1.36	Duroc-up
CCNG1	SNOWBALL_018791_st	cyclin G1	11.128	10.514	1.392E-04	6.60E-03	1.53	Duroc-up
PREX2	SNOWBALL_005791_st	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exchange factor 2	6.577	6.093	1.411E-04	6.67E-03	1.40	Duroc-up
TECPR2	SNOWBALL_011113_st	tectonin beta-propeller repeat containing 2	5.620	5.846	1.417E-04	6.68E-03	-1.17	PiNN-up
ACSL3	SNOWBALL_018193_s_st	acyl-CoA synthetase long-chain family member 3	8.075	7.460	1.426E-04	6.68E-03	1.53	Duroc-up
FAM115A	SNOWBALL_019632_st	protein FAM115A-like	5.833	4.928	1.425E-04	6.68E-03	1.87	Duroc-up
	SNOWBALL_036631_st	Ssc_hash_S40152599 rhyp01c_e19.y1 hyp Sus scrofa cDNA 5prime, mRNA	5.516	6.268	1.432E-04	6.70E-03	-1.68	PiNN-up
MPDZ	SNOWBALL_003021_st	multiple PDZ domain protein	7.408	7.016	1.435E-04	6.70E-03	1.31	Duroc-up
C18H19orf54	SNOWBALL_034109_st	Ssc_hash_S35332857 SusFleck_BF_0097_0100_5_pCNS_L06 SusFleck Backfat Sus scrofa cDNA clone 0097_0100_L06 5prime, mRNA	4.239	4.612	1.470E-04	6.80E-03	-1.29	PiNN-up
ATP11A	SNOWBALL_035589_st	ATPase, class VI, type 11A	7.258	7.488	1.468E-04	6.80E-03	-1.17	PiNN-up
MYO1B	SNOWBALL_018101_st	myosin IB	6.484	6.084	1.468E-04	6.80E-03	1.32	Duroc-up
ACSM5	SNOWBALL_042513_st	acyl-CoA synthetase medium-chain family member 5	6.548	7.200	1.477E-04	6.82E-03	-1.57	PiNN-up
CCDC76	SNOWBALL_006291_st	coiled-coil domain containing 76	6.678	6.054	1.501E-04	6.91E-03	1.54	Duroc-up
CDC25B	SNOWBALL_019173_st	cell division cycle 25 homolog B (S. pombe)	5.568	5.956	1.511E-04	6.92E-03	-1.31	PiNN-up
EDC4	SNOWBALL_007944_st	enhancer of mRNA decapping 4	6.562	6.857	1.514E-04	6.92E-03	-1.23	PiNN-up
ZNF219	SNOWBALL_034119_st	zinc finger protein 219	6.635	6.894	1.518E-04	6.92E-03	-1.20	PiNN-up
PPP2R5E	SNOWBALL_003092_st	protein phosphatase 2, regulatory subunit B', epsilon isoform	7.612	7.169	1.513E-04	6.92E-03	1.36	Duroc-up
HIPK2	SNOWBALL_033736_st	homeodomain interacting protein kinase 2	7.080	7.455	1.554E-04	7.06E-03	-1.30	PiNN-up
PPFIBP1	SNOWBALL_007319_st	PTPRF interacting protein, binding protein 1 (liprin beta 1)	8.104	7.553	1.559E-04	7.07E-03	1.47	Duroc-up
DNM1L	SNOWBALL_007165_st	dynamin 1-like	7.467	6.724	1.564E-04	7.07E-03	1.67	Duroc-up
MRPL37	SNOWBALL_035186_st	mitochondrial ribosomal protein L37	5.538	5.746	1.580E-04	7.09E-03	-1.16	PiNN-up
ATR	SNOWBALL_015667_st	ataxia telangiectasia and Rad3 related	5.917	5.359	1.578E-04	7.09E-03	1.47	Duroc-up
RICTOR	SNOWBALL_036078_st	RPTOR independent companion of MTOR, complex 2	5.163	4.412	1.574E-04	7.09E-03	1.68	Duroc-up
HNRNPA2B1	SNOWBALL_037281_st	heterogeneous nuclear ribonucleoprotein A2/B1	6.090	5.279	1.602E-04	7.17E-03	1.75	Duroc-up
MOSPD2	SNOWBALL_020046_s_st	motile sperm domain containing 2	5.877	5.440	1.611E-04	7.17E-03	1.35	Duroc-up
KIAA1826	SNOWBALL_012331_st	KIAA1826	5.910	5.184	1.614E-04	7.17E-03	1.65	Duroc-up
LOC100445169	SNOWBALL_035842_st	Ssc_hash_S23760501 1117844 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.813	4.859	1.609E-04	7.17E-03	1.94	Duroc-up

PPP2R3A	SNOWBALL_015660_st	protein phosphatase 2, regulatory subunit B'', alpha	6.962	6.508	1.624E-04	7.19E-03	1.37	Duroc-up
ECT2	SNOWBALL_045163_st	epithelial cell transforming sequence 2 oncogene	4.109	3.483	1.626E-04	7.19E-03	1.54	Duroc-up
PICALM	SNOWBALL_012407_st	phosphatidylinositol binding clathrin assembly protein	8.591	8.252	1.636E-04	7.22E-03	1.27	Duroc-up
CEBPB	SNOWBALL_000431_st	CCAAT/enhancer binding protein (C/EBP), beta	7.353	7.918	1.647E-04	7.24E-03	-1.48	PiNN-up
RPL19	SNOWBALL_032620_st	ribosomal protein L19	7.275	7.612	1.653E-04	7.24E-03	-1.26	PiNN-up
MBNL2	SNOWBALL_014006_st	muscleblind-like 2 (Drosophila)	9.876	9.464	1.651E-04	7.24E-03	1.33	Duroc-up
HTRA3	SNOWBALL_011327_st	HtrA serine peptidase 3	6.189	6.494	1.666E-04	7.26E-03	-1.24	PiNN-up
ZNF644	SNOWBALL_006265_st	zinc finger protein 644	9.818	9.091	1.663E-04	7.26E-03	1.66	Duroc-up
AKAP2	SNOWBALL_033138_st	A kinase (PRKA) anchor protein 2	7.714	7.144	1.673E-04	7.27E-03	1.48	Duroc-up
APOD	SNOWBALL_000254_st	apolipoprotein D	6.745	7.354	1.680E-04	7.28E-03	-1.53	PiNN-up
MLL2	SNOWBALL_006930_st	myeloid/lymphoid or mixed-lineage leukemia 2	6.703	6.985	1.702E-04	7.36E-03	-1.22	PiNN-up
SMARCC2	SNOWBALL_007069_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	8.323	8.627	1.737E-04	7.48E-03	-1.23	PiNN-up
PLOD2	SNOWBALL_015458_st	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	7.108	6.408	1.736E-04	7.48E-03	1.62	Duroc-up
WIPF3	SNOWBALL_029530_st	WAS/WASL interacting protein family, member 3	7.078	7.844	1.750E-04	7.48E-03	-1.70	PiNN-up
RPS6KA3	SNOWBALL_020067_st	ribosomal protein S6 kinase, 90kDa, polypeptide 3	9.842	9.338	1.744E-04	7.48E-03	1.42	Duroc-up
ARFGEF1	SNOWBALL_000828_st	ADP-ribosylation factor guanine nucleotide-exchange factor 1(brefeldin A-inhibited)	7.325	6.786	1.751E-04	7.48E-03	1.45	Duroc-up
LOC100519755	SNOWBALL_002910_s_st	tRNA (guanine-N(1)-)-methyltransferase-like	6.159	5.397	1.758E-04	7.50E-03	1.70	Duroc-up
DUS1L	SNOWBALL_022160_st	dihydrouridine synthase 1-like (S. cerevisiae)	7.112	7.459	1.773E-04	7.52E-03	-1.27	PiNN-up
KPNA3	SNOWBALL_013887_st	importin subunit alpha-3-like	11.406	11.034	1.798E-04	7.52E-03	1.29	Duroc-up
DDX10	SNOWBALL_012416_st	DEAD (Asp-Glu-Ala-Asp) box polypeptide 10	6.921	6.459	1.784E-04	7.52E-03	1.38	Duroc-up
LOC100512871	SNOWBALL_018863_s_st	peptidylprolyl isomerase domain and WD repeat-containing protein 1-like	6.374	5.823	1.792E-04	7.52E-03	1.46	Duroc-up
NUDT4	SNOWBALL_027221_st	nudix (nucleoside diphosphate linked moiety X)-type motif 4	10.770	10.167	1.788E-04	7.52E-03	1.52	Duroc-up
C5H12orf11	SNOWBALL_022055_s_st	Sus scrofa mRNA, clone:AMP010006A02, expressed in alveolar macrophages	6.861	6.192	1.798E-04	7.52E-03	1.59	Duroc-up
PDS5A	SNOWBALL_033687_st	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	7.110	6.421	1.791E-04	7.52E-03	1.61	Duroc-up
DYNC2LI1	SNOWBALL_005041_st	dynein, cytoplasmic 2, light intermediate chain 1	4.601	3.874	1.793E-04	7.52E-03	1.66	Duroc-up
LOC100523150	SNOWBALL_019076_st	hypothetical protein LOC100523150	7.443	7.637	1.809E-04	7.55E-03	-1.14	PiNN-up
CIB1	SNOWBALL_010830_s_st	calcium and integrin binding 1 (calmyrin)	6.569	6.965	1.816E-04	7.56E-03	-1.32	PiNN-up
TMEM65	SNOWBALL_005616_st	transmembrane protein 65	7.938	7.551	1.820E-04	7.56E-03	1.31	Duroc-up
SPIRE1	SNOWBALL_034389_st	spire homolog 1 (Drosophila)	5.071	5.567	1.854E-04	7.63E-03	-1.41	PiNN-up

CAPZA1	SNOWBALL_006379_st	capping protein (actin filament) muscle Z-line, alpha 1	6.332	5.925	1.848E-04	7.63E-03	1.33	Duroc-up
PPM1A	SNOWBALL_044070_st	protein phosphatase, Mg2+/Mn2+ dependent, 1A	5.862	5.240	1.858E-04	7.63E-03	1.54	Duroc-up
RPGRIP1L	SNOWBALL_008102_st	RPGRIP1-like	5.544	4.886	1.844E-04	7.63E-03	1.58	Duroc-up
TMTC4	SNOWBALL_014087_st	transmembrane and tetratricopeptide repeat containing 4	6.369	5.506	1.858E-04	7.63E-03	1.82	Duroc-up
MPP1	SNOWBALL_002009_s_st	membrane protein, palmitoylated 1, 55kDa	6.678	7.170	1.893E-04	7.63E-03	-1.41	PiNN-up
LOC100336808	SNOWBALL_040837_st	phosphorylase kinase, alpha 1 (muscle)-like	6.973	7.383	1.889E-04	7.63E-03	-1.33	PiNN-up
LCMT1	SNOWBALL_004514_st	leucine carboxyl methyltransferase 1	7.075	7.416	1.872E-04	7.63E-03	-1.27	PiNN-up
LOC100511636	SNOWBALL_008109_st	protein LSM14 homolog A-like	9.499	9.231	1.880E-04	7.63E-03	1.20	Duroc-up
PRKAA1	SNOWBALL_018605_st	protein kinase, AMP-activated, alpha 1 catalytic subunit	6.451	6.006	1.879E-04	7.63E-03	1.36	Duroc-up
PARG	SNOWBALL_017462_s_st	poly(ADP-ribose) glycohydrolase-like	6.756	6.198	1.886E-04	7.63E-03	1.47	Duroc-up
SBNO1	SNOWBALL_016419_s_st	strawberry notch homolog 1 (Drosophila)	7.297	6.737	1.873E-04	7.63E-03	1.47	Duroc-up
	SNOWBALL_045420_st		5.938	5.087	1.881E-04	7.63E-03	1.80	Duroc-up
GTF3C4	SNOWBALL_003423_st	general transcription factor IIIC, polypeptide 4, 90kDa	5.983	6.331	1.917E-04	7.71E-03	-1.27	PiNN-up
SYVN1	SNOWBALL_044790_st	e3 ubiquitin-protein ligase synoviolin-like	6.680	6.968	1.942E-04	7.74E-03	-1.22	PiNN-up
CSGALNACT2	SNOWBALL_017019_st	chondroitin sulfate N-acetylgalactosaminyltransferase 2	7.432	7.077	1.930E-04	7.74E-03	1.28	Duroc-up
SOS1	SNOWBALL_005470_st	son of sevenless homolog 1 (Drosophila)	8.412	7.930	1.935E-04	7.74E-03	1.40	Duroc-up
Fert2	SNOWBALL_028781_st	Ssc_hash_S41574905 PIC-A-1151 Sus Scrofa Adipocyte Zap Express Library After differentiation Sus scrofa cDNA clone SS-AA-4-1a-T3_M09, mRNA	6.001	5.212	1.939E-04	7.74E-03	1.73	Duroc-up
APH1A	SNOWBALL_006288_st	anterior pharynx defective 1 homolog A (C. elegans)	7.106	7.745	1.988E-04	7.85E-03	-1.56	PiNN-up
KCNJ11	SNOWBALL_023187_st	potassium inwardly-rectifying channel, subfamily J, member 11	7.594	8.058	1.985E-04	7.85E-03	-1.38	PiNN-up
NRF1	SNOWBALL_019714_st	nuclear respiratory factor 1	6.610	6.847	1.997E-04	7.85E-03	-1.18	PiNN-up
	SNOWBALL_031179_st	Ssc_hash_S18280413 BP436310 full-length enriched swine cDNA library, adult lung Sus scrofa cDNA clone LNG010047D05 5prime, mRNA	5.988	5.210	1.975E-04	7.85E-03	1.71	Duroc-up
RHOBTB3	SNOWBALL_029911_st	Ssc_hash_S17512158 BX667001 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0027.d.23 3prim, mRNA	5.353	4.491	2.000E-04	7.85E-03	1.82	Duroc-up
EIF1AX	SNOWBALL_026465_s_st	ring finger protein 8	7.748	6.882	1.996E-04	7.85E-03	1.82	Duroc-up
ETNK1	SNOWBALL_025733_st	ethanolamine kinase 1	5.116	4.212	1.981E-04	7.85E-03	1.87	Duroc-up
MPI	SNOWBALL_010612_s_st	mannose phosphate isomerase	6.067	6.764	2.006E-04	7.86E-03	-1.62	PiNN-up

NFIA	SNOWBALL_029948_st	Ssc_hash_S23693254 1100140 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	8.260	7.562	2.014E-04	7.87E-03	1.62	Duroc-up
TCEA1	SNOWBALL_005964_st	transcription elongation factor A (SII), 1	6.641	6.125	2.020E-04	7.88E-03	1.43	Duroc-up
HSD17B8	SNOWBALL_001440_s_st	OTTSUSG00000001394 hydroxysteroid (17-beta) dehydrogenase 8	6.167	6.595	2.040E-04	7.89E-03	-1.35	PiNN-up
LOC100522188	SNOWBALL_025425_s_st	Sus scrofa mRNA, clone:MLN010011C09, expressed in mesenteric lymph node	7.523	7.947	2.054E-04	7.89E-03	-1.34	PiNN-up
AMIGO1	SNOWBALL_006664_st	adhesion molecule with Ig-like domain 1	8.125	8.481	2.063E-04	7.89E-03	-1.28	PiNN-up
C19orf12	SNOWBALL_008198_st	chromosome 19 open reading frame 12	6.369	6.717	2.067E-04	7.89E-03	-1.27	PiNN-up
PBRM1	SNOWBALL_025087_st	polybromo 1	6.778	6.470	2.048E-04	7.89E-03	1.24	Duroc-up
DBT	SNOWBALL_006465_st	dihydrolipoamide branched chain transacylase E2	7.353	6.929	2.046E-04	7.89E-03	1.34	Duroc-up
NCKAP1	SNOWBALL_023902_s_st	PREDICTED: Sus scrofa similar to Nck-associated protein 1 (NAP 1) (p125Nap1) (Membrane-associated protein HEM-2), transcript variant 2 (LOC100158033), mRNA	8.676	8.194	2.066E-04	7.89E-03	1.40	Duroc-up
CCDC150	SNOWBALL_018130_st	coiled-coil domain containing 150	4.879	4.357	2.066E-04	7.89E-03	1.44	Duroc-up
SPON1	SNOWBALL_028750_st	spondin 1, extracellular matrix protein	5.207	4.626	2.056E-04	7.89E-03	1.50	Duroc-up
SDCCAG1	SNOWBALL_002870_st	serologically defined colon cancer antigen 1 [Source:HGNC Symbol;Acc:10663]	6.763	6.059	2.041E-04	7.89E-03	1.63	Duroc-up
STRN	SNOWBALL_005129_st	striatin, calmodulin binding protein	7.090	6.592	2.082E-04	7.93E-03	1.41	Duroc-up
	SNOWBALL_032470_st	Ssc_hash_S23689621 1000101 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	4.718	4.271	2.093E-04	7.95E-03	1.36	Duroc-up
LOC100518162	SNOWBALL_011708_st	Transposase	6.467	5.968	2.117E-04	8.03E-03	1.41	Duroc-up
PDE8A	SNOWBALL_010728_s_st	high affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A-like	6.814	6.252	2.123E-04	8.03E-03	1.48	Duroc-up
EIF1AX	SNOWBALL_026256_st	Sus scrofa mRNA, clone:OVRM10037F04, expressed in ovary	7.544	6.809	2.128E-04	8.04E-03	1.66	Duroc-up
LPIN1	SNOWBALL_037456_st	lipin 1	3.611	3.977	2.156E-04	8.12E-03	-1.29	PiNN-up
SCRN3	SNOWBALL_017874_st	secernin 3	8.291	7.623	2.206E-04	8.29E-03	1.59	Duroc-up
BCL7A	SNOWBALL_016407_st	B-cell CLL/lymphoma 7A	6.637	6.990	2.227E-04	8.35E-03	-1.28	PiNN-up
CNPPD1	SNOWBALL_023968_s_st	PREDICTED: Sus scrofa similar to CG40191 CG40191-PB (LOC100157604), mRNA	5.397	5.731	2.230E-04	8.35E-03	-1.26	PiNN-up
NPNT	SNOWBALL_028326_st	nephronectin	3.568	4.183	2.321E-04	8.37E-03	-1.53	PiNN-up
BHLHE40	SNOWBALL_015699_st	basic helix-loop-helix family, member e40	9.554	10.160	2.278E-04	8.37E-03	-1.52	PiNN-up
ZNF592	SNOWBALL_042134_st	zinc finger protein 592	5.430	5.886	2.367E-04	8.37E-03	-1.37	PiNN-up
ZNRD1	SNOWBALL_001063_s_st	OTTSUSG00000001257 zinc ribbon domain containing, 1	5.578	5.997	2.339E-04	8.37E-03	-1.34	PiNN-up

ATF7	SNOWBALL_047233_st	activating transcription factor 7	6.786	7.117	2.352E-04	8.37E-03	-1.26	PiNN-up
HCFC1	SNOWBALL_025676_st	host cell factor C1 (VP16-accessory protein)	6.252	6.571	2.352E-04	8.37E-03	-1.25	PiNN-up
SRL	SNOWBALL_004823_st	sarcalumenin	9.610	9.922	2.293E-04	8.37E-03	-1.24	PiNN-up
NUP62	SNOWBALL_008584_st	nucleoporin 62kDa	6.213	6.507	2.267E-04	8.37E-03	-1.23	PiNN-up
WFDC2	SNOWBALL_025833_st	WAP four-disulfide core domain 2	5.862	6.139	2.248E-04	8.37E-03	-1.21	PiNN-up
DIDO1	SNOWBALL_037231_st	death inducer-obliterator 1	5.989	6.256	2.281E-04	8.37E-03	-1.20	PiNN-up
DUSP28	SNOWBALL_018503_st	dual specificity phosphatase 28	7.161	7.418	2.266E-04	8.37E-03	-1.19	PiNN-up
LOC100448878	SNOWBALL_011491_st	hypothetical protein LOC100448878	6.529	6.738	2.373E-04	8.37E-03	-1.16	PiNN-up
ATP2A1	SNOWBALL_004436_st	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	13.077	13.257	2.248E-04	8.37E-03	-1.13	PiNN-up
MYO6	SNOWBALL_002402_st	myosin VI	5.141	4.745	2.381E-04	8.37E-03	1.32	Duroc-up
NFE2L2	SNOWBALL_018036_st	nuclear factor (erythroid-derived 2)-like 2	9.154	8.732	2.268E-04	8.37E-03	1.34	Duroc-up
C1orf27	SNOWBALL_012978_st	chromosome 1 open reading frame 27	6.940	6.516	2.371E-04	8.37E-03	1.34	Duroc-up
USP38	SNOWBALL_040111_st	ubiquitin specific peptidase 38	6.321	5.886	2.358E-04	8.37E-03	1.35	Duroc-up
C9orf41	SNOWBALL_003998_st	chromosome 9 open reading frame 41	7.129	6.657	2.380E-04	8.37E-03	1.39	Duroc-up
TMED5	SNOWBALL_006235_st	transmembrane emp24 protein transport domain containing 5	7.653	7.159	2.283E-04	8.37E-03	1.41	Duroc-up
THAP6	SNOWBALL_011560_st	THAP domain containing 6	5.655	5.160	2.254E-04	8.37E-03	1.41	Duroc-up
NKTR	SNOWBALL_015236_s_st	natural killer-tumor recognition sequence	7.560	7.047	2.300E-04	8.37E-03	1.43	Duroc-up
LPP	SNOWBALL_041041_st	LIM domain containing preferred translocation partner in lipoma	7.186	6.644	2.342E-04	8.37E-03	1.46	Duroc-up
RNPC3	SNOWBALL_006284_st	RNA-binding region (RNP1, RRM) containing 3	7.830	7.274	2.361E-04	8.37E-03	1.47	Duroc-up
ZNF583	SNOWBALL_008526_st	zinc finger protein 583	5.909	5.243	2.362E-04	8.37E-03	1.59	Duroc-up
MTDH	SNOWBALL_005709_st	metadherin	9.250	8.581	2.296E-04	8.37E-03	1.59	Duroc-up
LPP	SNOWBALL_047048_st	LIM domain containing preferred translocation partner in lipoma	8.237	7.552	2.295E-04	8.37E-03	1.61	Duroc-up
NARG2	SNOWBALL_002495_st	NMDA receptor regulated 2	6.115	5.425	2.330E-04	8.37E-03	1.61	Duroc-up
SUV39H2	SNOWBALL_031085_st	suppressor of variegation 3-9 homolog 2 (Drosophila)	4.723	3.992	2.317E-04	8.37E-03	1.66	Duroc-up
PCNX	SNOWBALL_036738_st	pecanex homolog (Drosophila)	5.927	5.149	2.331E-04	8.37E-03	1.71	Duroc-up
TBC1D15	SNOWBALL_007178_st	TBC1 domain family, member 15	6.324	5.481	2.379E-04	8.37E-03	1.79	Duroc-up
DMXL1	SNOWBALL_027788_st	Dmx-like 1	5.589	4.431	2.331E-04	8.37E-03	2.23	Duroc-up
UBE2J2	SNOWBALL_008293_st	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)	7.146	7.618	2.395E-04	8.38E-03	-1.39	PiNN-up
PAPOLA	SNOWBALL_010921_st	poly(A) polymerase alpha	8.460	8.004	2.394E-04	8.38E-03	1.37	Duroc-up
USP7	SNOWBALL_004807_st	ubiquitin specific peptidase 7 (herpes virus-associated)	8.433	8.041	2.403E-04	8.40E-03	1.31	Duroc-up

SPRYD4	SNOWBALL_007384_st	SPRY domain containing 4	5.727	6.156	2.433E-04	8.41E-03	-1.35	PiNN-up
FAM134A	SNOWBALL_023966_st	PREDICTED: Sus scrofa similar to chromosome 2 open reading frame 17 (LOC100156393), mRNA	6.669	7.032	2.431E-04	8.41E-03	-1.29	PiNN-up
PGS1	SNOWBALL_022426_s_st	phosphatidylglycerophosphate synthase 1	6.147	6.449	2.418E-04	8.41E-03	-1.23	PiNN-up
PARP8	SNOWBALL_018675_st	poly (ADP-ribose) polymerase family, member 8	5.533	5.179	2.435E-04	8.41E-03	1.28	Duroc-up
WHSC1L1	SNOWBALL_030376_st	Wolf-Hirschhorn syndrome candidate 1-like 1	7.531	7.114	2.421E-04	8.41E-03	1.34	Duroc-up
NARG1	SNOWBALL_011650_st	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	7.837	7.206	2.433E-04	8.41E-03	1.55	Duroc-up
PREPL	SNOWBALL_005338_st	prolyl endopeptidase-like	7.643	7.139	2.444E-04	8.42E-03	1.42	Duroc-up
CCDC39	SNOWBALL_025126_s_st	coiled-coil domain containing 39	9.081	8.268	2.453E-04	8.44E-03	1.76	Duroc-up
MAX	SNOWBALL_010853_st	MYC associated factor X	8.692	9.231	2.466E-04	8.44E-03	-1.45	PiNN-up
ZEB2	SNOWBALL_030717_st	zinc finger E-box binding homeobox 2	6.668	5.986	2.469E-04	8.44E-03	1.60	Duroc-up
	SNOWBALL_038638_st		5.406	4.688	2.460E-04	8.44E-03	1.64	Duroc-up
ITSN2	SNOWBALL_025736_s_st	intersectin 2	7.557	6.988	2.475E-04	8.45E-03	1.48	Duroc-up
PHTF2	SNOWBALL_012520_st	putative homeodomain transcription factor 2	9.473	9.046	2.480E-04	8.45E-03	1.34	Duroc-up
TMEM63A	SNOWBALL_013267_st	transmembrane protein 63A	6.026	6.307	2.491E-04	8.46E-03	-1.21	PiNN-up
	SNOWBALL_040924_st		3.437	2.839	2.496E-04	8.46E-03	1.51	Duroc-up
VPS13A	SNOWBALL_003687_st	vacuolar protein sorting 13 homolog A (S. cerevisiae)	7.961	7.341	2.497E-04	8.46E-03	1.54	Duroc-up
UBE2K	SNOWBALL_027313_st	ubiquitin-conjugating enzyme E2K (UBC1 homolog, yeast)	7.359	6.726	2.522E-04	8.53E-03	1.55	Duroc-up
UBR1	SNOWBALL_002752_st	ubiquitin protein ligase E3 component n-recognin 1	8.288	7.883	2.527E-04	8.53E-03	1.32	Duroc-up
GMPPA	SNOWBALL_025854_st	Sus scrofa mRNA, clone:LVR010101B04, expressed in liver	6.663	7.169	2.542E-04	8.56E-03	-1.42	PiNN-up
AGL	SNOWBALL_033719_st	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	10.451	9.734	2.557E-04	8.60E-03	1.64	Duroc-up
FAM160B2	SNOWBALL_016256_st	family with sequence similarity 160, member B2	6.086	6.385	2.572E-04	8.63E-03	-1.23	PiNN-up
VPS13C	SNOWBALL_002554_st	vacuolar protein sorting 13 homolog C (S. cerevisiae)	8.098	7.504	2.584E-04	8.65E-03	1.51	Duroc-up
BIRC3	SNOWBALL_021793_st	baculoviral IAP repeat containing 3	7.359	6.491	2.604E-04	8.71E-03	1.83	Duroc-up
	SNOWBALL_020863_st		8.291	6.421	2.610E-04	8.71E-03	3.65	Duroc-up
EIF3A	SNOWBALL_017004_s_st	eukaryotic translation initiation factor 3, subunit A	8.508	8.047	2.617E-04	8.72E-03	1.38	Duroc-up
REEP3	SNOWBALL_024488_st	PREDICTED: Sus scrofa similar to MGC165949 protein (LOC100158143), mRNA	6.764	5.895	2.644E-04	8.79E-03	1.83	Duroc-up
TBC1D7	SNOWBALL_009517_st	TBC1 domain family, member 7	5.725	6.174	2.684E-04	8.81E-03	-1.36	PiNN-up
DCTN4	SNOWBALL_026053_s_st	dynactin 4 (p62)	7.856	8.262	2.685E-04	8.81E-03	-1.32	PiNN-up
MTMR3	SNOWBALL_035953_st	Ssc_hash_S50197117 susfleck_FC_N_32_A03 SUSFLECK Fat Cell Normalized Sus scrofa cDNA clone 32_A03, mRNA	7.755	8.083	2.670E-04	8.81E-03	-1.25	PiNN-up
REPIN1	SNOWBALL_031066_st	replication initiator 1	6.827	7.131	2.680E-04	8.81E-03	-1.23	PiNN-up

LTBP4	SNOWBALL_031132_st	latent transforming growth factor beta binding protein 4	7.418	7.710	2.682E-04	8.81E-03	-1.22	PiNN-up
ITGAV	SNOWBALL_018091_st	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	7.060	6.557	2.658E-04	8.81E-03	1.42	Duroc-up
MIOS	SNOWBALL_012588_st	missing oocyte, meiosis regulator, homolog (Drosophila)	6.898	6.340	2.679E-04	8.81E-03	1.47	Duroc-up
KDM4A	SNOWBALL_031356_st	lysine (K)-specific demethylase 4A	5.648	5.956	2.704E-04	8.86E-03	-1.24	PiNN-up
MLXIP	SNOWBALL_016466_st	MLX interacting protein	7.937	8.331	2.731E-04	8.91E-03	-1.31	PiNN-up
IBTK	SNOWBALL_002440_st	inhibitor of Bruton agammaglobulinemia tyrosine kinase	6.924	6.419	2.735E-04	8.91E-03	1.42	Duroc-up
AR	SNOWBALL_030412_st	Ssc_hash_S18556206 BX924857 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0025.k.15 5prim, mRNA	4.361	3.789	2.739E-04	8.91E-03	1.49	Duroc-up
ZC3H11A	SNOWBALL_021806_s_st	zinc finger CCCH-type containing 11A	9.168	8.590	2.736E-04	8.91E-03	1.49	Duroc-up
SGPP1	SNOWBALL_003227_st	sphingosine-1-phosphate phosphatase 1	7.350	6.851	2.759E-04	8.94E-03	1.41	Duroc-up
GMFB	SNOWBALL_029690_st	glia maturation factor, beta	4.393	3.649	2.754E-04	8.94E-03	1.67	Duroc-up
TAB3	SNOWBALL_027934_st	TGF-beta activated kinase 1/MAP3K7 binding protein 3	5.874	5.108	2.764E-04	8.94E-03	1.70	Duroc-up
SDAD1	SNOWBALL_011454_st	SDA1 domain containing 1	6.195	5.589	2.773E-04	8.95E-03	1.52	Duroc-up
ANXA10	SNOWBALL_018753_st	annexin A6-like	7.070	7.453	2.788E-04	8.97E-03	-1.30	PiNN-up
PTEN	SNOWBALL_037155_st	Ssc_hash_S29974063 PDUts1082G08 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1082G08 5prime similar to homologue to ref	6.818	5.983	2.790E-04	8.97E-03	1.78	Duroc-up
ABCF3	SNOWBALL_025845_s_st	ATP-binding cassette, sub-family F (GCN20), member 3	6.543	6.887	2.796E-04	8.98E-03	-1.27	PiNN-up
GTPBP1	SNOWBALL_006836_st	GTP binding protein 1	6.843	7.084	2.807E-04	8.98E-03	-1.18	PiNN-up
ATP2B1	SNOWBALL_007705_s_st	ATPase, Ca++ transporting, plasma membrane 1	9.322	8.800	2.807E-04	8.98E-03	1.44	Duroc-up
QKI	SNOWBALL_030765_st	quaking homolog, KH domain RNA binding (mouse)	8.490	7.858	2.820E-04	9.01E-03	1.55	Duroc-up
PICK1	SNOWBALL_006795_st	protein interacting with PRKCA 1	6.567	7.091	2.832E-04	9.01E-03	-1.44	PiNN-up
AUP1	SNOWBALL_005240_st	ancient ubiquitous protein 1	8.589	8.877	2.833E-04	9.01E-03	-1.22	PiNN-up
LOC100152425	SNOWBALL_010567_s_st	envelope glycoprotein-like	6.556	5.282	2.838E-04	9.01E-03	2.42	Duroc-up
CTNS	SNOWBALL_015056_st	cystinosis, nephropathic	5.258	5.713	2.864E-04	9.04E-03	-1.37	PiNN-up
OGDH	SNOWBALL_019926_st	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	9.392	9.794	2.859E-04	9.04E-03	-1.32	PiNN-up
MOCS1	SNOWBALL_025194_s_st	molybdenum cofactor synthesis 1	6.077	6.455	2.867E-04	9.04E-03	-1.30	PiNN-up
PJA2	SNOWBALL_034888_st	praja ring finger 2	7.346	6.639	2.859E-04	9.04E-03	1.63	Duroc-up

	SNOWBALL_035691_st	Ssc_hash_S18557668 BX926319 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0021.c.05 5prim, mRNA	5.730	5.053	2.884E-04	9.08E-03	1.60	Duroc-up
IBTK	SNOWBALL_002456_s_st	inhibitor of Bruton agammaglobulinemia tyrosine kinase	7.578	7.068	2.910E-04	9.14E-03	1.42	Duroc-up
RAB11FIP2	SNOWBALL_016856_s_st	RAB11 family interacting protein 2 (class I)	7.519	6.942	2.912E-04	9.14E-03	1.49	Duroc-up
C18orf8	SNOWBALL_008665_st	chromosome 18 open reading frame 8	6.101	6.397	2.928E-04	9.17E-03	-1.23	PiNN-up
EIF1AX	SNOWBALL_020065_st	eukaryotic translation initiation factor 1A, Y-linked	9.298	8.662	2.941E-04	9.19E-03	1.55	Duroc-up
TGS1	SNOWBALL_005820_st	trimethylguanosine synthase 1	6.091	5.868	2.994E-04	9.33E-03	1.17	Duroc-up
HAUS6	SNOWBALL_003221_st	HAUS augmin-like complex, subunit 6	5.579	5.119	2.993E-04	9.33E-03	1.38	Duroc-up
IL6ST	SNOWBALL_045321_st	interleukin 6 signal transducer (gp130, oncostatin M receptor)	7.642	7.022	3.021E-04	9.40E-03	1.54	Duroc-up
NID1	SNOWBALL_047565_st	nidogen 1	7.159	7.535	3.029E-04	9.40E-03	-1.30	PiNN-up
TMEM47	SNOWBALL_035530_st	transmembrane protein 47	7.643	6.820	3.043E-04	9.43E-03	1.77	Duroc-up
FASTKD1	SNOWBALL_017854_st	FAST kinase domains 1	6.234	5.708	3.068E-04	9.48E-03	1.44	Duroc-up
SNX16	SNOWBALL_005681_st	sorting nexin 16	6.456	5.686	3.069E-04	9.48E-03	1.71	Duroc-up
LOC100301250	SNOWBALL_022089_s_st	Sus scrofa mRNA, clone:SMG010007H12, expressed in submaxillary gland	6.453	7.684	3.084E-04	9.51E-03	-2.35	PiNN-up
C20orf32	SNOWBALL_000495_st	OTTSUSG00000000585 orthologue of H. sapiens chromsome 20 open reading frame 32 (C20orf32)	4.536	4.972	3.096E-04	9.53E-03	-1.35	PiNN-up
ACVR1B	SNOWBALL_033995_st	activin A receptor, type IB	5.878	6.522	3.108E-04	9.54E-03	-1.56	PiNN-up
LTBP1	SNOWBALL_005459_s_st	latent transforming growth factor beta binding protein 1	6.358	6.738	3.117E-04	9.54E-03	-1.30	PiNN-up
GSK3A	SNOWBALL_008261_st	glycogen synthase kinase 3 alpha	8.313	8.590	3.121E-04	9.54E-03	-1.21	PiNN-up
GOLT1B	SNOWBALL_007334_st	golgi transport 1B	6.576	6.207	3.113E-04	9.54E-03	1.29	Duroc-up
PRRC2C	SNOWBALL_035536_st	proline-rich coiled-coil 2C	9.312	8.957	3.143E-04	9.59E-03	1.28	Duroc-up
MRPS18B	SNOWBALL_001142_s_st	OTTSUSG00000001284 mitochondrial ribosomal protein S18B	5.487	5.862	3.169E-04	9.62E-03	-1.30	PiNN-up
LMNA	SNOWBALL_006043_st	lamin A/C	6.805	7.054	3.169E-04	9.62E-03	-1.19	PiNN-up
PAPOLG	SNOWBALL_005382_st	poly(A) polymerase gamma	5.938	5.483	3.169E-04	9.62E-03	1.37	Duroc-up
	SNOWBALL_039449_st		4.067	3.554	3.198E-04	9.69E-03	1.43	Duroc-up
AGPS	SNOWBALL_018048_st	alkylglycerone phosphate synthase	8.029	7.430	3.220E-04	9.73E-03	1.51	Duroc-up
ZEB2	SNOWBALL_033397_st	Ssc_hash_S26724500 AJ960584 KN404_2 Sus scrofa cDNA clone C0007751p11 5prime, mRNA	6.670	6.068	3.218E-04	9.73E-03	1.52	Duroc-up
TSC22D1	SNOWBALL_013893_st	TSC22 domain family, member 1	7.029	7.421	3.267E-04	9.76E-03	-1.31	PiNN-up
GGA2	SNOWBALL_013224_st	golgi-associated, gamma adaptin ear containing, ARF binding protein 2	6.580	6.972	3.255E-04	9.76E-03	-1.31	PiNN-up

KLHL29	SNOWBALL_045545_st	kelch-like 29 (Drosophila)	6.739	7.120	3.270E-04	9.76E-03	-1.30	PiNN-up
CENPP	SNOWBALL_004690_st	centromere protein P	5.856	5.442	3.267E-04	9.76E-03	1.33	Duroc-up
ASCC3	SNOWBALL_002617_st	Activating signal cointegrator 1 complex subunit 3 (EC 3.6.1.-)(ASC-1 complex subunit p200)(Trip4 complex subunit p200)(Helicase, ATP binding 1)	6.881	6.410	3.275E-04	9.76E-03	1.39	Duroc-up
DNAJC13	SNOWBALL_015652_st	DnaJ (Hsp40) homolog, subfamily C, member 13	7.158	6.664	3.276E-04	9.76E-03	1.41	Duroc-up
TPX2	SNOWBALL_019270_s_st	TPX2, microtubule-associated, homolog (Xenopus laevis)	5.681	5.151	3.248E-04	9.76E-03	1.44	Duroc-up
EEA1	SNOWBALL_007751_st	early endosome antigen 1	7.633	6.831	3.260E-04	9.76E-03	1.74	Duroc-up
KIAA1429	SNOWBALL_005631_st	KIAA1429	8.272	7.843	3.299E-04	9.80E-03	1.35	Duroc-up
THOC2	SNOWBALL_023523_st	THO complex 2	7.017	6.341	3.301E-04	9.80E-03	1.60	Duroc-up
METTL14	SNOWBALL_011785_st	methyltransferase like 14	5.782	5.438	3.307E-04	9.81E-03	1.27	Duroc-up
HMCN1	SNOWBALL_012880_st	hemicentin 1	6.750	6.340	3.345E-04	9.90E-03	1.33	Duroc-up
SNORA42	SNOWBALL_006246_st	Small nucleolar RNA SNORA42/SNORA80 family [Source: RFAM;Acc:RF00406]	7.161	7.686	3.359E-04	9.90E-03	-1.44	PiNN-up
C17orf80	SNOWBALL_014220_st	chromosome 17 open reading frame 80	6.102	6.427	3.359E-04	9.90E-03	-1.25	PiNN-up
COX4NB	SNOWBALL_029094_st	COX4 neighbor	7.408	7.722	3.363E-04	9.90E-03	-1.24	PiNN-up
RTN3	SNOWBALL_038062_st	reticulon 3	6.310	5.826	3.368E-04	9.90E-03	1.40	Duroc-up
KPNA4	SNOWBALL_034883_st	karyopherin alpha 4 (importin alpha 3)	4.841	4.213	3.396E-04	9.97E-03	1.55	Duroc-up
LMAN1	SNOWBALL_028676_st	Ssc_hash_S29976328 PDUts1109C03 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1109C03 5prime similar to homologue to gb	6.641	5.952	3.405E-04	9.98E-03	1.61	Duroc-up
	SNOWBALL_031048_st	Ssc_hash_S16766791 834332 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	6.675	7.376	3.414E-04	9.99E-03	-1.63	PiNN-up
PDK3	SNOWBALL_031432_st	pyruvate dehydrogenase kinase, isozyme 3	6.588	5.795	3.426E-04	9.99E-03	1.73	Duroc-up
USP15	SNOWBALL_025225_st	PREDICTED: Sus scrofa similar to ubiquitin specific peptidase 15 (LOC100152172), mRNA	7.047	6.005	3.426E-04	9.99E-03	2.06	Duroc-up
SLMAP	SNOWBALL_015567_st	sarcolemma associated protein	8.678	8.113	3.435E-04	1.00E-02	1.48	Duroc-up
SLC48A1	SNOWBALL_034650_st	solute carrier family 48 (heme transporter), member 1	6.347	6.693	3.450E-04	1.00E-02	-1.27	PiNN-up
SEL1L	SNOWBALL_036127_st	sel-1 suppressor of lin-12-like (C. elegans)	7.179	6.712	3.453E-04	1.00E-02	1.38	Duroc-up
FTSJ1	SNOWBALL_016308_s_st	FtsJ homolog 1 (E. coli)	11.063	10.651	3.464E-04	1.00E-02	1.33	Duroc-up
KIAA1731	SNOWBALL_012459_st	KIAA1731	5.423	5.079	3.473E-04	1.00E-02	1.27	Duroc-up
PIK3R1	SNOWBALL_018737_st	phosphoinositide-3-kinase, regulatory subunit 1 (alpha)	8.786	8.245	3.479E-04	1.00E-02	1.45	Duroc-up
UBR3	SNOWBALL_017932_st	ubiquitin protein ligase E3 component n-recognin 3 (putative)	10.157	9.680	3.546E-04	1.02E-02	1.39	Duroc-up

XIRP2	SNOWBALL_031422_st	xin actin-binding repeat containing 2	12.434	11.732	3.543E-04	1.02E-02	1.63	Duroc-up
ATRX	SNOWBALL_033081_st	alpha thalassemia/mental retardation syndrome X-linked	6.676	5.898	3.538E-04	1.02E-02	1.72	Duroc-up
CMYA5	SNOWBALL_030400_st	cardiomyopathy associated 5	12.403	12.057	3.556E-04	1.02E-02	1.27	Duroc-up
DNAJB6	SNOWBALL_019579_st	DnaJ (Hsp40) homolog, subfamily B, member 6	5.987	6.315	3.571E-04	1.02E-02	-1.26	PiNN-up
ITGA6	SNOWBALL_017934_st	integrin, alpha 6	7.056	6.430	3.578E-04	1.02E-02	1.54	Duroc-up
ECHDC1	SNOWBALL_002346_st	enoyl CoA hydratase domain containing 1	6.537	5.674	3.576E-04	1.02E-02	1.82	Duroc-up
MED15	SNOWBALL_016733_s_st	mediator complex subunit 15	6.809	7.166	3.597E-04	1.02E-02	-1.28	PiNN-up
MATN2	SNOWBALL_005777_st	matrilin 2	6.635	6.313	3.593E-04	1.02E-02	1.25	Duroc-up
GKAP1	SNOWBALL_031654_st	G kinase anchoring protein 1	7.250	6.465	3.588E-04	1.02E-02	1.72	Duroc-up
LOC100152287	SNOWBALL_010708_st	telomerase protein component 1-like	6.742	7.183	3.615E-04	1.03E-02	-1.36	PiNN-up
DPP9	SNOWBALL_029945_st	dipeptidyl-peptidase 9	6.967	7.241	3.659E-04	1.03E-02	-1.21	PiNN-up
GSPT1	SNOWBALL_031743_st	G1 to S phase transition 1	6.577	5.876	3.658E-04	1.03E-02	1.63	Duroc-up
LOC100155995	SNOWBALL_034174_st	Ssc_hash_S40064881 rfat0122_m21.y1 fat Sus scrofa cDNA 5prime, mRNA	7.843	7.071	3.652E-04	1.03E-02	1.71	Duroc-up
	SNOWBALL_041955_st		6.492	5.989	3.666E-04	1.03E-02	1.42	Duroc-up
CTSD	SNOWBALL_023340_st	cathepsin D	8.433	8.860	3.680E-04	1.03E-02	-1.34	PiNN-up
RSF1	SNOWBALL_023065_s_st	remodeling and spacing factor 1	6.681	6.099	3.680E-04	1.03E-02	1.50	Duroc-up
GLS	SNOWBALL_023891_st	glutaminase	6.449	5.657	3.721E-04	1.04E-02	1.73	Duroc-up
R3HDM2	SNOWBALL_040857_st	R3H domain containing 2	10.375	10.167	3.744E-04	1.05E-02	1.15	Duroc-up
LMAN1	SNOWBALL_003065_st	lectin, mannose-binding, 1	7.722	7.253	3.739E-04	1.05E-02	1.38	Duroc-up
PLCB4	SNOWBALL_032655_st	Ssc_hash_S40439733 rret27_f14.y1 ret Sus scrofa cDNA 5prime, mRNA	5.128	4.178	3.741E-04	1.05E-02	1.93	Duroc-up
OPA1	SNOWBALL_016209_st	optic atrophy 1 (autosomal dominant)	7.599	7.114	3.756E-04	1.05E-02	1.40	Duroc-up
KIAA0776	SNOWBALL_002367_st	KIAA0776	7.829	7.133	3.783E-04	1.05E-02	1.62	Duroc-up
IKZF2	SNOWBALL_036690_st	IKAROS family zinc finger 2 (Helios)	7.881	6.949	3.783E-04	1.05E-02	1.91	Duroc-up
EPHX2	SNOWBALL_016316_st	epoxide hydrolase 2, cytoplasmic	5.652	6.722	3.793E-04	1.05E-02	-2.10	PiNN-up
CDK11A	SNOWBALL_008533_st	cyclin-dependent kinase 11A	6.179	6.375	3.797E-04	1.05E-02	-1.15	PiNN-up
RUFY2	SNOWBALL_017165_s_st	RUN and FYVE domain containing 2	6.610	5.858	3.805E-04	1.05E-02	1.68	Duroc-up
PGPEP1	SNOWBALL_031120_st	pyroglutamyl-peptidase I	7.735	8.131	3.829E-04	1.06E-02	-1.32	PiNN-up
USP1	SNOWBALL_009163_st	ubiquitin specific peptidase 1	5.908	5.143	3.824E-04	1.06E-02	1.70	Duroc-up
TMEM115	SNOWBALL_015426_st	transmembrane protein 115	6.659	7.052	3.838E-04	1.06E-02	-1.31	PiNN-up
LOC220906	SNOWBALL_008863_x_st	hypothetical LOC220906	5.350	5.019	3.852E-04	1.06E-02	1.26	Duroc-up
TLK1	SNOWBALL_023938_st	tousled-like kinase 1	4.005	3.514	3.862E-04	1.06E-02	1.41	Duroc-up
PUM2	SNOWBALL_033869_st	pumilio homolog 2 (Drosophila)	7.291	6.690	3.859E-04	1.06E-02	1.52	Duroc-up
LPP	SNOWBALL_044892_s_st	hypothetical LOC100520104	7.798	7.046	3.861E-04	1.06E-02	1.68	Duroc-up
LARP4	SNOWBALL_007080_st	La ribonucleoprotein domain family, member 4	8.460	8.223	3.872E-04	1.06E-02	1.18	Duroc-up

MRPS24	SNOWBALL_019875_st	mitochondrial ribosomal protein S24	7.460	7.916	3.888E-04	1.06E-02	-1.37	PiNN-up
DNAJC21	SNOWBALL_018581_st	DnaJ (Hsp40) homolog, subfamily C, member 21	9.099	8.395	3.885E-04	1.06E-02	1.63	Duroc-up
ZBTB38	SNOWBALL_028237_st	zinc finger and BTB domain containing 38	5.784	5.073	3.891E-04	1.06E-02	1.64	Duroc-up
HTRA1	SNOWBALL_025015_s_st	PREDICTED: Sus scrofa similar to Serine protease HTRA1 precursor (L56) (Serine protease 11) (LOC100156868), mRNA	8.152	8.479	3.923E-04	1.06E-02	-1.26	PiNN-up
ZER1	SNOWBALL_039543_st	protein zer-1 homolog	6.162	6.472	3.930E-04	1.06E-02	-1.24	PiNN-up
PRAF2	SNOWBALL_020336_st	PRA1 domain family, member 2	6.958	7.258	3.922E-04	1.06E-02	-1.23	PiNN-up
ZDHHC21	SNOWBALL_003155_st	zinc finger, DHHC-type containing 21	6.311	5.695	3.918E-04	1.06E-02	1.53	Duroc-up
SNX6	SNOWBALL_010669_st	sorting nexin 6	7.129	6.479	3.924E-04	1.06E-02	1.57	Duroc-up
CNIH	SNOWBALL_047527_st	cornichon homolog (Drosophila)	4.483	4.086	3.939E-04	1.06E-02	1.32	Duroc-up
BAT4	SNOWBALL_001255_s_st	OTTSUSG00000001331 HLA-B associated transcript 4	7.022	7.334	3.953E-04	1.06E-02	-1.24	PiNN-up
FADD	SNOWBALL_040044_st	Fas (TNFRSF6)-associated via death domain	5.723	6.017	3.958E-04	1.06E-02	-1.23	PiNN-up
PLBD2	SNOWBALL_016644_st	phospholipase B domain containing 2	6.430	6.713	3.950E-04	1.06E-02	-1.22	PiNN-up
RNF138	SNOWBALL_009212_st	ring finger protein 138	6.375	5.959	3.970E-04	1.06E-02	1.33	Duroc-up
NFIA	SNOWBALL_047424_st	nuclear factor 1 A-type-like	6.285	5.702	3.974E-04	1.06E-02	1.50	Duroc-up
LOC100518573	SNOWBALL_028095_st	Ssc_hash_S18291732 BP143457 full-length enriched swine cDNA library, adult ovary Sus scrofa cDNA clone OVR010031E12 5prime, mRNA	6.019	5.712	3.987E-04	1.07E-02	1.24	Duroc-up
ATXN1	SNOWBALL_025441_st	ataxin 1	5.661	6.116	4.016E-04	1.07E-02	-1.37	PiNN-up
PPM1H	SNOWBALL_025224_st	protein phosphatase, Mg2+/Mn2+ dependent, 1H	3.458	3.798	4.012E-04	1.07E-02	-1.27	PiNN-up
TRAPPC1	SNOWBALL_014845_s_st	trafficking protein particle complex subunit 1-like	6.909	7.234	4.004E-04	1.07E-02	-1.25	PiNN-up
SPAST	SNOWBALL_005093_s_st	spastin	8.458	8.049	4.014E-04	1.07E-02	1.33	Duroc-up
WDR70	SNOWBALL_018623_st	WD repeat domain 70	7.562	7.165	4.031E-04	1.07E-02	1.32	Duroc-up
PLA2G15	SNOWBALL_007952_st	phospholipase A2, group XV	5.815	6.199	4.038E-04	1.07E-02	-1.30	PiNN-up
ZNF518B	SNOWBALL_041202_st	zinc finger protein 518B	5.750	6.137	4.068E-04	1.07E-02	-1.31	PiNN-up
RAD21	SNOWBALL_000791_s_st	RAD21 homolog (S. pombe)	7.379	6.931	4.063E-04	1.07E-02	1.36	Duroc-up
ADARB1	SNOWBALL_015876_st	adenosine deaminase, RNA-specific, B1	6.389	6.751	4.131E-04	1.09E-02	-1.29	PiNN-up
SRF	SNOWBALL_042602_s_st	serum response factor (c-fos serum response element-binding transcription factor)	5.225	5.566	4.136E-04	1.09E-02	-1.27	PiNN-up
EML4	SNOWBALL_005046_st	echinoderm microtubule associated protein like 4	6.181	5.915	4.144E-04	1.09E-02	1.20	Duroc-up
TMEM87A	SNOWBALL_003302_st	transmembrane protein 87A	7.431	7.090	4.141E-04	1.09E-02	1.27	Duroc-up
CD2AP	SNOWBALL_010069_st	CD2-associated protein	6.108	5.561	4.133E-04	1.09E-02	1.46	Duroc-up
THOC1	SNOWBALL_026487_s_st	THO complex 1	6.488	5.939	4.168E-04	1.09E-02	1.46	Duroc-up
LOC100519047	SNOWBALL_014151_s_st	ubiquitin-conjugating enzyme E2 O-like	6.558	7.103	4.203E-04	1.10E-02	-1.46	PiNN-up
Mtmr6	SNOWBALL_035945_st	myotubularin related protein 6	6.662	6.898	4.270E-04	1.11E-02	-1.18	PiNN-up

PDE8A	SNOWBALL_010849_s_st	phosphodiesterase 8A	6.759	6.329	4.277E-04	1.11E-02	1.35	Duroc-up
UPF2	SNOWBALL_031131_st	Ssc_hash_S20948340 AJ660063 KN277 Sus scrofa cDNA clone C0005218_P16, mRNA	7.270	6.518	4.304E-04	1.12E-02	1.68	Duroc-up
ERLEC1	SNOWBALL_004980_st	endoplasmic reticulum lectin 1	7.731	7.188	4.335E-04	1.13E-02	1.46	Duroc-up
SNX29P2	SNOWBALL_004593_st	RUN domain containing 2A	6.360	6.625	4.371E-04	1.13E-02	-1.20	PiNN-up
CSF1	SNOWBALL_006352_st	colony stimulating factor 1 (macrophage)	5.709	6.186	4.400E-04	1.14E-02	-1.39	PiNN-up
DDR2	SNOWBALL_021949_st	discoidin domain receptor tyrosine kinase 2	5.208	4.672	4.399E-04	1.14E-02	1.45	Duroc-up
DCTN5	SNOWBALL_013227_st	dynactin 5 (p25)	6.965	7.365	4.435E-04	1.15E-02	-1.32	PiNN-up
	SNOWBALL_041706_st		4.974	5.404	4.452E-04	1.15E-02	-1.35	PiNN-up
PPM1A	SNOWBALL_003240_st	protein phosphatase, Mg2+/Mn2+ dependent, 1A	9.884	9.478	4.450E-04	1.15E-02	1.33	Duroc-up
CYHR1	SNOWBALL_005543_st	cysteine/histidine-rich 1	5.990	6.370	4.480E-04	1.15E-02	-1.30	PiNN-up
CEP110	SNOWBALL_046851_st	centrosomal protein 110kDa	5.681	4.951	4.492E-04	1.15E-02	1.66	Duroc-up
MAP3K7	SNOWBALL_000026_s_st	OTTSUSG00000001552	7.752	7.347	4.500E-04	1.15E-02	1.32	Duroc-up
CALCRL	SNOWBALL_018225_st	calcitonin receptor-like	7.905	7.402	4.510E-04	1.15E-02	1.42	Duroc-up
CAB39	SNOWBALL_018357_st	calcium binding protein 39	8.681	8.388	4.533E-04	1.16E-02	1.22	Duroc-up
RNF103-CHMP3	SNOWBALL_004833_st	charged multivesicular body protein 3-like	5.008	5.437	4.543E-04	1.16E-02	-1.35	PiNN-up
KCNJ12	SNOWBALL_033774_st	potassium inwardly-rectifying channel, subfamily J, member 12	6.552	7.027	4.552E-04	1.16E-02	-1.39	PiNN-up
	SNOWBALL_045569_st		5.681	6.140	4.637E-04	1.16E-02	-1.38	PiNN-up
GYS1	SNOWBALL_008279_st	glycogen synthase 1 (muscle)	10.303	10.712	4.646E-04	1.16E-02	-1.33	PiNN-up
LMAN2L	SNOWBALL_004742_st	lectin, mannose-binding 2-like	6.890	7.259	4.626E-04	1.16E-02	-1.29	PiNN-up
GPS2	SNOWBALL_014898_st	G protein pathway suppressor 2	7.895	8.191	4.654E-04	1.16E-02	-1.23	PiNN-up
TTLL12	SNOWBALL_006731_st	tubulin tyrosine ligase-like family, member 12	6.721	6.992	4.643E-04	1.16E-02	-1.21	PiNN-up
	SNOWBALL_032803_st	Ssc_hash_S50175297 susfleck_LV_N_62_B04 SUSFLECK Liver Normalized Sus scrofa cDNA clone 62_B04, mRNA	4.402	4.656	4.623E-04	1.16E-02	-1.19	PiNN-up
MTFR1	SNOWBALL_006020_st	mitochondrial fission regulator 1	5.684	5.315	4.657E-04	1.16E-02	1.29	Duroc-up
TLK1	SNOWBALL_017886_s_st	tousled-like kinase 1	6.697	6.237	4.567E-04	1.16E-02	1.38	Duroc-up
FAM190B	SNOWBALL_017354_s_st	family with sequence similarity 190, member B	7.698	7.193	4.609E-04	1.16E-02	1.42	Duroc-up
TOP2B	SNOWBALL_015214_st	topoisomerase (DNA) II beta 180kDa	7.279	6.753	4.618E-04	1.16E-02	1.44	Duroc-up
KBTBD3	SNOWBALL_012394_st	kelch repeat and BTB (POZ) domain containing 3	5.913	5.357	4.601E-04	1.16E-02	1.47	Duroc-up
	SNOWBALL_040151_st		5.495	4.919	4.611E-04	1.16E-02	1.49	Duroc-up
PMS1	SNOWBALL_018232_st	PMS1 postmeiotic segregation increased 1 (S. cerevisiae)	6.182	5.574	4.628E-04	1.16E-02	1.52	Duroc-up
LMBRD2	SNOWBALL_031733_st	LMBR1 domain containing 2	5.698	5.070	4.584E-04	1.16E-02	1.55	Duroc-up
METAP2	SNOWBALL_007760_st	methionyl aminopeptidase 2	8.371	7.716	4.655E-04	1.16E-02	1.57	Duroc-up

PPP2R5E	SNOWBALL_003015_st	serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit epsilon isoform-like	7.703	7.184	4.665E-04	1.16E-02	1.43	Duroc-up
MIER3	SNOWBALL_033875_st	mesoderm induction early response 1, family member 3	6.027	5.291	4.680E-04	1.16E-02	1.67	Duroc-up
CWC22	SNOWBALL_018061_st	pre-mRNA-splicing factor CWC22 homolog	5.951	5.425	4.687E-04	1.17E-02	1.44	Duroc-up
DUS2L	SNOWBALL_047216_s_st	dihydrouridine synthase 2-like, SMM1 homolog (S. cerevisiae)	6.129	6.624	4.725E-04	1.17E-02	-1.41	PiNN-up
ACSS1	SNOWBALL_019135_s_st	acyl-CoA synthetase short-chain family member 1	6.480	6.818	4.714E-04	1.17E-02	-1.26	PiNN-up
LOC476297	SNOWBALL_013361_st	similar to RAD26L hypothetical protein	8.078	7.577	4.722E-04	1.17E-02	1.41	Duroc-up
THAP5	SNOWBALL_019878_st	THAP domain containing 5	6.442	5.576	4.721E-04	1.17E-02	1.82	Duroc-up
HIG2	SNOWBALL_019749_st	hypoxia-inducible protein	6.402	6.697	4.745E-04	1.17E-02	-1.23	PiNN-up
PKN2	SNOWBALL_006668_st	protein kinase N2	9.122	8.769	4.740E-04	1.17E-02	1.28	Duroc-up
KCNJ8	SNOWBALL_023188_s_st	potassium inwardly-rectifying channel, subfamily J, member 8	5.820	5.414	4.762E-04	1.17E-02	1.33	Duroc-up
AP4E1	SNOWBALL_002668_st	adaptor-related protein complex 4, epsilon 1 subunit	8.095	7.590	4.787E-04	1.18E-02	1.42	Duroc-up
SMC4	SNOWBALL_015460_st	structural maintenance of chromosomes 4	5.170	4.500	4.802E-04	1.18E-02	1.59	Duroc-up
TOR1B	SNOWBALL_003485_s_st	Torsin 1B Fragment [Source:UniProtKB/TrEMBL;Acc:B6VD07]	7.007	7.311	4.840E-04	1.18E-02	-1.23	PiNN-up
DLG1	SNOWBALL_000262_st	discs, large homolog 1 (Drosophila)	8.070	7.658	4.836E-04	1.18E-02	1.33	Duroc-up
DNASE1L1	SNOWBALL_026518_st	deoxyribonuclease I-like 1	6.954	7.452	4.873E-04	1.19E-02	-1.41	PiNN-up
CASZ1	SNOWBALL_008683_st	castor zinc finger 1	7.293	7.617	4.866E-04	1.19E-02	-1.25	PiNN-up
ITIH5	SNOWBALL_013567_st	inter-alpha (globulin) inhibitor H5	7.577	7.811	4.870E-04	1.19E-02	-1.18	PiNN-up
TIAL1	SNOWBALL_024758_st	TIA1 cytotoxic granule-associated RNA binding protein-like 1	6.638	5.974	4.882E-04	1.19E-02	1.58	Duroc-up
GPR107	SNOWBALL_034141_st	G protein-coupled receptor 107	5.824	6.120	4.917E-04	1.20E-02	-1.23	PiNN-up
hsa-mir-1	bta-mir-1-1_x_st	MI0009719	5.278	6.206	4.936E-04	1.20E-02	-1.90	PiNN-up
NPEPL1	SNOWBALL_000543_st	aminopeptidase-like 1	7.628	8.170	4.954E-04	1.20E-02	-1.46	PiNN-up
TMEM131	SNOWBALL_004921_st	transmembrane protein 131	9.167	8.863	4.946E-04	1.20E-02	1.23	Duroc-up
WHSC1L1	SNOWBALL_017808_st	Wolf-Hirschhorn syndrome candidate 1-like 1	6.789	6.436	4.957E-04	1.20E-02	1.28	Duroc-up
PIK3C2A	SNOWBALL_035694_st	phosphoinositide-3-kinase, class 2, alpha polypeptide	4.709	4.077	4.946E-04	1.20E-02	1.55	Duroc-up
MYH14	SNOWBALL_038110_st	myosin-14-like	6.400	6.632	4.967E-04	1.20E-02	-1.17	PiNN-up
NCK2	SNOWBALL_004838_s_st	NCK adaptor protein 2	7.348	7.603	4.978E-04	1.20E-02	-1.19	PiNN-up
SLC22A16	SNOWBALL_002401_st	solute carrier family 22 (organic cation/carnitine transporter), member 16	5.936	6.772	5.002E-04	1.20E-02	-1.78	PiNN-up
PTOV1	SNOWBALL_008590_st	prostate tumor overexpressed 1	7.337	7.722	5.007E-04	1.20E-02	-1.31	PiNN-up
WDR67	SNOWBALL_005609_st	WD repeat domain 67	5.986	5.396	5.007E-04	1.20E-02	1.51	Duroc-up

EIF2B2	SNOWBALL_010798_st	eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa	7.884	8.268	5.021E-04	1.20E-02	-1.31	PiNN-up
CTDP1	SNOWBALL_003745_st	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	5.968	6.157	5.035E-04	1.20E-02	-1.14	PiNN-up
NBN	SNOWBALL_000821_st	OTTSUSG00000000677 Nibrin,partialCDS	4.410	3.463	5.033E-04	1.20E-02	1.93	Duroc-up
HDLBP	SNOWBALL_023113_s_st	high density lipoprotein binding protein	9.495	9.764	5.047E-04	1.20E-02	-1.20	PiNN-up
	SNOWBALL_038984_st		4.362	3.684	5.087E-04	1.21E-02	1.60	Duroc-up
TBL1XR1	SNOWBALL_032404_st	transducin (beta)-like 1 X-linked receptor 1	7.016	6.278	5.081E-04	1.21E-02	1.67	Duroc-up
ATRX	SNOWBALL_020332_st	alpha thalassemia/mental retardation syndrome X-linked	7.219	6.414	5.081E-04	1.21E-02	1.75	Duroc-up
SNTB2	SNOWBALL_033556_st	syntrophin, beta 2 (dystrophin-associated protein A1, 59kDa, basic component 2)	6.074	5.158	5.071E-04	1.21E-02	1.89	Duroc-up
ZNF529	SNOWBALL_008046_st	zinc finger protein 780B	4.642	4.059	5.122E-04	1.21E-02	1.50	Duroc-up
TMF1	SNOWBALL_015722_s_st	TATA element modulatory factor-like	5.662	4.992	5.160E-04	1.22E-02	1.59	Duroc-up
C3orf58	SNOWBALL_015526_st	chromosome 3 open reading frame 58	6.445	6.001	5.180E-04	1.22E-02	1.36	Duroc-up
BPTF	SNOWBALL_014398_st	bromodomain PHD finger transcription factor	8.161	7.678	5.192E-04	1.22E-02	1.40	Duroc-up
FOXN2	SNOWBALL_031798_st	forkhead box N2	6.661	5.921	5.189E-04	1.22E-02	1.67	Duroc-up
ZNF638	SNOWBALL_034970_st	zinc finger protein 638	7.078	6.317	5.185E-04	1.22E-02	1.69	Duroc-up
UBXN7	SNOWBALL_046402_st	UBX domain protein 7	6.082	5.537	5.206E-04	1.22E-02	1.46	Duroc-up
PUS7	SNOWBALL_012847_st	pseudouridylate synthase 7 homolog (S. cerevisiae)	6.640	6.195	5.219E-04	1.23E-02	1.36	Duroc-up
SCN4B	SNOWBALL_012409_st	sodium channel, voltage-gated, type IV, beta	7.662	8.484	5.231E-04	1.23E-02	-1.77	PiNN-up
LOC396781	SNOWBALL_021340_x_st	Sus scrofa mRNA, clone:MLN010055E01, expressed in mesenteric lymph nodes	7.948	8.608	5.282E-04	1.23E-02	-1.58	PiNN-up
COL6A3	SNOWBALL_018275_s_st	collagen, type VI, alpha 3	8.499	8.928	5.268E-04	1.23E-02	-1.35	PiNN-up
MEF2D	SNOWBALL_025652_st	myocyte enhancer factor 2D	7.892	8.223	5.304E-04	1.23E-02	-1.26	PiNN-up
NID1	SNOWBALL_016832_st	nidogen 1	7.211	7.540	5.306E-04	1.23E-02	-1.26	PiNN-up
BAT3	SNOWBALL_001239_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	7.598	7.875	5.268E-04	1.23E-02	-1.21	PiNN-up
TMCO1	SNOWBALL_006139_st	transmembrane and coiled-coil domains 1	6.862	6.437	5.258E-04	1.23E-02	1.34	Duroc-up
R3HDM1	SNOWBALL_017687_st	R3H domain containing 1	9.241	8.813	5.247E-04	1.23E-02	1.35	Duroc-up
CNOT6L	SNOWBALL_033993_st	CCR4-NOT transcription complex, subunit 6-like	3.958	3.455	5.279E-04	1.23E-02	1.42	Duroc-up
U6	SNOWBALL_012990_st	U6 spliceosomal RNA [Source: RFAM;Acc:RF00026]	6.649	5.999	5.300E-04	1.23E-02	1.57	Duroc-up
USP8	SNOWBALL_003198_st	ubiquitin specific peptidase 8	6.752	6.095	5.305E-04	1.23E-02	1.58	Duroc-up
LNPEP	SNOWBALL_027402_st	leucyl/cystinyl aminopeptidase	8.463	7.662	5.238E-04	1.23E-02	1.74	Duroc-up
LOC100062646	SNOWBALL_042069_st	hypothetical protein LOC100062646	5.576	6.056	5.325E-04	1.23E-02	-1.39	PiNN-up
	SNOWBALL_044936_st		10.016	10.568	5.339E-04	1.23E-02	-1.47	PiNN-up
NEK1	SNOWBALL_016335_st	NIMA (never in mitosis gene a)-related kinase 1	5.657	5.313	5.353E-04	1.23E-02	1.27	Duroc-up

CUL3	SNOWBALL_017967_st	cullin 3	9.939	9.478	5.379E-04	1.24E-02	1.38	Duroc-up
SLMAP	SNOWBALL_027270_st	sarcolemma associated protein	6.138	5.632	5.379E-04	1.24E-02	1.42	Duroc-up
	SNOWBALL_028275_st	Ssc_hash_S23768594 1140128 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.510	5.895	5.410E-04	1.24E-02	-1.31	PiNN-up
TAOK3	SNOWBALL_016450_st	TAO kinase 3	6.235	5.840	5.420E-04	1.24E-02	1.31	Duroc-up
TRIM24	SNOWBALL_019735_st	tripartite motif containing 24	6.921	6.354	5.406E-04	1.24E-02	1.48	Duroc-up
DNAJC1	SNOWBALL_013441_st	DnaJ (Hsp40) homolog, subfamily C, member 1	5.721	5.036	5.400E-04	1.24E-02	1.61	Duroc-up
SSPN	SNOWBALL_030407_st	sarcospan (Kras oncogene-associated gene)	8.448	7.689	5.420E-04	1.24E-02	1.69	Duroc-up
PPP2R3A	SNOWBALL_015536_st	protein phosphatase 2, regulatory subunit B'', alpha	8.441	7.981	5.441E-04	1.24E-02	1.38	Duroc-up
MDP1	SNOWBALL_010542_st	magnesium-dependent phosphatase 1	5.237	5.617	5.463E-04	1.24E-02	-1.30	PiNN-up
ZMYM4	SNOWBALL_008670_st	zinc finger, MYM-type 4	8.444	7.988	5.489E-04	1.25E-02	1.37	Duroc-up
FTSJ1	SNOWBALL_007243_s_st	FtsJ homolog 1 (E. coli)	10.836	10.489	5.516E-04	1.25E-02	1.27	Duroc-up
C14orf106	SNOWBALL_003297_st	Kinetochore-associated protein KNL-2 homolog (HsKNL-2)(Mis18-binding protein 1)(P243)	5.430	4.899	5.518E-04	1.25E-02	1.44	Duroc-up
COPS2	SNOWBALL_003260_st	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	9.055	8.294	5.527E-04	1.25E-02	1.69	Duroc-up
ZBTB33	SNOWBALL_001861_st	zinc finger and BTB domain containing 33	5.598	5.186	5.563E-04	1.26E-02	1.33	Duroc-up
SRCAP	SNOWBALL_004559_st	Snf2-related CREBBP activator protein	7.368	7.659	5.584E-04	1.26E-02	-1.22	PiNN-up
PPP2R5E	SNOWBALL_030028_st	Ssc_hash_S23759053 1116260 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.828	5.008	5.583E-04	1.26E-02	1.77	Duroc-up
CSE1L	SNOWBALL_025974_st	CSE1 chromosome segregation 1-like (yeast)	8.874	8.514	5.618E-04	1.26E-02	1.28	Duroc-up
NOP58	SNOWBALL_024004_s_st	NOP58 ribonucleoprotein homolog (yeast)	7.737	7.321	5.617E-04	1.26E-02	1.33	Duroc-up
AP3S2	SNOWBALL_025155_st	adaptor-related protein complex 3, sigma 2 subunit	5.691	6.021	5.647E-04	1.27E-02	-1.26	PiNN-up
NRBP1	SNOWBALL_025924_st	nuclear receptor binding protein 1	7.531	7.818	5.637E-04	1.27E-02	-1.22	PiNN-up
ASPA	SNOWBALL_014969_st	aspartoacylase	6.235	5.731	5.652E-04	1.27E-02	1.42	Duroc-up
TPR	SNOWBALL_013055_st	translocated promoter region (to activated MET oncogene)	6.927	6.209	5.642E-04	1.27E-02	1.65	Duroc-up
ASH2L	SNOWBALL_026072_st	ash2 (absent, small, or homeotic)-like (Drosophila)	7.016	7.350	5.670E-04	1.27E-02	-1.26	PiNN-up
HSPG2	SNOWBALL_009343_st	basement membrane-specific heparan sulfate proteoglycan core protein-like	8.449	8.749	5.665E-04	1.27E-02	-1.23	PiNN-up
KIAA1715	SNOWBALL_018110_st	KIAA1715	8.016	7.597	5.675E-04	1.27E-02	1.34	Duroc-up
TGOLN2	SNOWBALL_005420_st	trans-golgi network protein 2	7.207	7.534	5.695E-04	1.27E-02	-1.25	PiNN-up
ERGIC2	SNOWBALL_007442_st	ERGIC and golgi 2	8.969	8.262	5.700E-04	1.27E-02	1.63	Duroc-up
ZFP91	SNOWBALL_042555_st	zinc finger protein 91 homolog (mouse)	9.209	8.712	5.741E-04	1.28E-02	1.41	Duroc-up
DMXL1	SNOWBALL_031649_st	Dmx-like 1	6.341	5.508	5.750E-04	1.28E-02	1.78	Duroc-up
USP28	SNOWBALL_012499_st	ubiquitin specific peptidase 28	9.692	9.412	5.773E-04	1.28E-02	1.21	Duroc-up
BTBD1	SNOWBALL_010882_st	BTB (POZ) domain containing 1	10.834	10.314	5.767E-04	1.28E-02	1.43	Duroc-up

PPAP2B	SNOWBALL_009058_st	phosphatidic acid phosphatase type 2B	7.765	8.139	5.808E-04	1.28E-02	-1.30	PiNN-up
NAPA	SNOWBALL_008303_st	N-ethylmaleimide-sensitive factor attachment protein, alpha	7.233	7.545	5.807E-04	1.28E-02	-1.24	PiNN-up
ZMYM1	SNOWBALL_032465_st	zinc finger, MYM-type 1	4.690	3.928	5.833E-04	1.29E-02	1.70	Duroc-up
AGL	SNOWBALL_025236_st	PREDICTED: Sus scrofa similar to glycogen debranching enzyme (LOC100156497), mRNA	11.731	11.286	5.858E-04	1.29E-02	1.36	Duroc-up
TAF5L	SNOWBALL_017259_s_st	TAF5-like RNA polymerase II, p300/CBP-associated factor (PCAF)-associated factor, 65kDa	6.797	6.983	5.891E-04	1.30E-02	-1.14	PiNN-up
Rnu7	SNOWBALL_035441_st	Ssc_hash_S17510311 BX665337 Sus Scrofa library (scag) Sus scrofa cDNA clone scag0006.d.04 5prim, mRNA	7.753	8.051	5.911E-04	1.30E-02	-1.23	PiNN-up
LOC100512762	SNOWBALL_022054_x_st	Sus scrofa mRNA, clone:AMP010007E02, expressed in alveolar macrophages	11.598	10.422	5.930E-04	1.30E-02	2.26	Duroc-up
LOC100431909	SNOWBALL_043883_st	ras-specific guanine nucleotide-releasing factor RalGPS1-like	5.221	5.684	5.955E-04	1.30E-02	-1.38	PiNN-up
RNY1	SNOWBALL_013109_st	Y RNA [Source: RFAM;Acc:RF00019]	10.862	11.200	5.962E-04	1.30E-02	-1.26	PiNN-up
MEF2D	SNOWBALL_006069_st	myocyte enhancer factor 2D	8.981	9.288	5.950E-04	1.30E-02	-1.24	PiNN-up
RRP15	SNOWBALL_026105_st	ribosomal RNA processing 15 homolog (S. cerevisiae)	6.628	6.089	5.970E-04	1.30E-02	1.45	Duroc-up
PDK3	SNOWBALL_026530_st	pyruvate dehydrogenase kinase, isozyme 3	7.164	6.609	5.967E-04	1.30E-02	1.47	Duroc-up
TBC1D17	SNOWBALL_008517_st	TBC1 domain family, member 17	6.896	7.296	5.993E-04	1.31E-02	-1.32	PiNN-up
NR1D1	SNOWBALL_014660_st	nuclear receptor subfamily 1, group D, member 1	6.743	7.209	6.018E-04	1.31E-02	-1.38	PiNN-up
MPHOSPH10	SNOWBALL_003040_st	u3 small nucleolar ribonucleoprotein protein MPP10-like	5.415	4.710	6.012E-04	1.31E-02	1.63	Duroc-up
C10orf118	SNOWBALL_040165_st	chromosome 10 open reading frame 118	5.195	4.393	6.029E-04	1.31E-02	1.74	Duroc-up
ATRX	SNOWBALL_035127_st	alpha thalassemia/mental retardation syndrome X-linked	6.295	5.587	6.057E-04	1.31E-02	1.63	Duroc-up
UNC45B	SNOWBALL_014428_s_st	unc-45 homolog B (C. elegans)	7.889	8.232	6.138E-04	1.33E-02	-1.27	PiNN-up
XPO1	SNOWBALL_022666_st	exportin 1 (CRM1 homolog, yeast)	7.425	6.650	6.140E-04	1.33E-02	1.71	Duroc-up
ITCH	SNOWBALL_019149_st	itchy E3 ubiquitin protein ligase homolog (mouse)	8.151	7.820	6.151E-04	1.33E-02	1.26	Duroc-up
TMBIM1	SNOWBALL_018176_st	transmembrane BAX inhibitor motif containing 1	7.110	7.580	6.206E-04	1.34E-02	-1.38	PiNN-up
GNAQ	SNOWBALL_047469_st	guanine nucleotide binding protein (G protein), q polypeptide	5.437	5.005	6.197E-04	1.34E-02	1.35	Duroc-up
BIRC3	SNOWBALL_020919_s_st	SSU79142 Sus scrofa putative inhibitor of apoptosis (PIAP) mRNA, complete cds	7.679	6.897	6.203E-04	1.34E-02	1.72	Duroc-up
DCTN4	SNOWBALL_026230_s_st	dynactin 4 (p62)	8.905	9.315	6.244E-04	1.34E-02	-1.33	PiNN-up

PLCE1	SNOWBALL_024945_s_st	PREDICTED: Sus scrofa similar to pancreas-enriched phospholipase C (LOC100152908), mRNA	5.576	5.088	6.243E-04	1.34E-02	1.40	Duroc-up
BMPR1A	SNOWBALL_024694_st	bone morphogenetic protein receptor, type IA	6.658	5.982	6.238E-04	1.34E-02	1.60	Duroc-up
XIAP	SNOWBALL_001899_st	X-linked inhibitor of apoptosis	7.639	7.174	6.253E-04	1.34E-02	1.38	Duroc-up
SERINC2	SNOWBALL_040035_st	serine incorporator 2	4.940	5.282	6.276E-04	1.34E-02	-1.27	PiNN-up
NPLOC4	SNOWBALL_022312_st	nuclear protein localization 4 homolog (S. cerevisiae)	5.956	6.272	6.288E-04	1.34E-02	-1.24	PiNN-up
TOPORS	SNOWBALL_013444_st	topoisomerase I binding, arginine/serine-rich, E3 ubiquitin protein ligase	6.718	6.319	6.337E-04	1.35E-02	1.32	Duroc-up
MAB21L2	SNOWBALL_011902_st	mab-21-like 2 (C. elegans)	4.002	4.501	6.407E-04	1.37E-02	-1.41	PiNN-up
LOC100520104	SNOWBALL_027592_st	Ssc_hash_S18359470 915432 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	7.216	6.249	6.421E-04	1.37E-02	1.95	Duroc-up
CYTB	SNOWBALL_026815_st	cytochrome b reductase 1	7.033	7.494	6.458E-04	1.37E-02	-1.38	PiNN-up
REEP1	SNOWBALL_004739_st	receptor accessory protein 1	7.022	7.388	6.462E-04	1.37E-02	-1.29	PiNN-up
GSK3B	SNOWBALL_029878_st	glycogen synthase kinase 3 beta	6.468	5.835	6.446E-04	1.37E-02	1.55	Duroc-up
TNIK	SNOWBALL_044905_st	TRAF2 and NCK interacting kinase	5.365	4.615	6.455E-04	1.37E-02	1.68	Duroc-up
TAX1BP1	SNOWBALL_019906_st	Tax1 (human T-cell leukemia virus type I) binding protein 1	8.396	7.557	6.475E-04	1.37E-02	1.79	Duroc-up
FITM2	SNOWBALL_019437_s_st	fat storage-inducing transmembrane protein 2	6.354	6.675	6.510E-04	1.37E-02	-1.25	PiNN-up
SEPT7	SNOWBALL_019887_st	septin 7	8.048	7.455	6.498E-04	1.37E-02	1.51	Duroc-up
CDADC1	SNOWBALL_013819_st	cytidine and dCMP deaminase domain containing 1	6.584	5.901	6.508E-04	1.37E-02	1.61	Duroc-up
RAD54B	SNOWBALL_005789_st	DNA repair and recombination protein RAD54B-like	5.532	4.815	6.501E-04	1.37E-02	1.64	Duroc-up
RBM25	SNOWBALL_010269_s_st	RNA-binding protein 25-like	8.000	7.535	6.529E-04	1.37E-02	1.38	Duroc-up
ZHX3	SNOWBALL_019407_st	zinc fingers and homeoboxes 3	6.746	7.031	6.552E-04	1.38E-02	-1.22	PiNN-up
HERPUD1	SNOWBALL_025839_st	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	6.155	6.593	6.602E-04	1.38E-02	-1.35	PiNN-up
CDIPT	SNOWBALL_021101_s_st	CDP-diacylglycerol--inositol 3-phosphatidyltransferase	6.308	6.669	6.604E-04	1.38E-02	-1.29	PiNN-up
COL6A1	SNOWBALL_026602_st	collagen, type VI, alpha 1	7.060	7.282	6.597E-04	1.38E-02	-1.17	PiNN-up
ZNF26	SNOWBALL_024098_st	zinc finger protein 26	5.617	5.203	6.600E-04	1.38E-02	1.33	Duroc-up
BCLAF1	SNOWBALL_002095_st	BCL2-associated transcription factor 1	8.400	7.776	6.569E-04	1.38E-02	1.54	Duroc-up
DYNC1LI1	SNOWBALL_015213_st	dynein, cytoplasmic 1, light intermediate chain 1	6.737	6.044	6.586E-04	1.38E-02	1.62	Duroc-up
CEBPZ	SNOWBALL_005475_st	CCAAT/enhancer binding protein (C/EBP), zeta	6.846	6.119	6.644E-04	1.38E-02	1.66	Duroc-up
PTPN4	SNOWBALL_036158_st	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	5.846	4.839	6.672E-04	1.39E-02	2.01	Duroc-up
HDLBP	SNOWBALL_018318_st	high density lipoprotein binding protein	9.343	9.590	6.687E-04	1.39E-02	-1.19	PiNN-up
ASB1	SNOWBALL_037807_st	ankyrin repeat and SOCS box containing 1	5.809	6.280	6.706E-04	1.39E-02	-1.39	PiNN-up

FAM3C	SNOWBALL_019861_st	family with sequence similarity 3, member C	7.338	6.823	6.706E-04	1.39E-02	1.43	Duroc-up
FGD4	SNOWBALL_043646_st	FYVE, RhoGEF and PH domain containing 4	3.658	3.204	6.734E-04	1.39E-02	1.37	Duroc-up
SNRNP200	SNOWBALL_002586_st	U5 small nuclear ribonucleoprotein 200 kDa helicase (EC 3.6.1.-)(U5 snRNP-specific 200 kDa protein)(U5-200KD)(Activating signal cointegrator 1 complex subunit 3-like 1)(BRR2 homolog)	6.797	6.310	6.736E-04	1.39E-02	1.40	Duroc-up
RNF185	SNOWBALL_024240_st	PREDICTED: Sus scrofa similar to ring finger protein 185, transcript variant 2 (LOC100157569), mRNA	5.656	6.007	6.746E-04	1.39E-02	-1.28	PiNN-up
RPS6KB1	SNOWBALL_014473_st	ribosomal protein S6 kinase, 70kDa, polypeptide 1	8.305	7.918	6.791E-04	1.40E-02	1.31	Duroc-up
WDR49	SNOWBALL_023725_st	PREDICTED: Sus scrofa similar to WD repeat domain 49 (LOC100152270), mRNA	5.477	5.781	6.840E-04	1.41E-02	-1.23	PiNN-up
SHISA3	SNOWBALL_044370_st	Shisa homolog 3 (Xenopus laevis)-like	4.591	4.997	6.869E-04	1.42E-02	-1.33	PiNN-up
TRMT2A	SNOWBALL_016564_st	TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae)	6.285	6.630	6.897E-04	1.42E-02	-1.27	PiNN-up
PTPN14	SNOWBALL_013151_st	protein tyrosine phosphatase, non-receptor type 14	8.212	8.480	6.893E-04	1.42E-02	-1.20	PiNN-up
MYOC	SNOWBALL_012997_st	myocilin, trabecular meshwork inducible glucocorticoid response	6.571	7.411	6.934E-04	1.42E-02	-1.79	PiNN-up
CASZ1	SNOWBALL_032734_st	castor zinc finger 1	6.653	6.913	6.934E-04	1.42E-02	-1.20	PiNN-up
TRIP12	SNOWBALL_025738_st	thyroid hormone receptor interactor 12	9.069	8.643	6.940E-04	1.42E-02	1.34	Duroc-up
ADAM10	SNOWBALL_002391_st	ADAM metallopeptidase domain 10	6.456	5.997	6.910E-04	1.42E-02	1.37	Duroc-up
GTF2H3	SNOWBALL_016525_st	general transcription factor IIH, polypeptide 3, 34kDa	6.348	5.775	6.940E-04	1.42E-02	1.49	Duroc-up
38412	SNOWBALL_024598_st	membrane-associated ring finger (C3HC4) 5	8.620	8.147	6.977E-04	1.42E-02	1.39	Duroc-up
LSM14A	SNOWBALL_008134_st	LSM14A, SCD6 homolog A (S. cerevisiae)	8.579	8.209	7.031E-04	1.43E-02	1.29	Duroc-up
	SNOWBALL_042962_st		4.635	3.805	7.061E-04	1.44E-02	1.78	Duroc-up
KIAA2026	SNOWBALL_002945_st	KIAA2026	7.669	7.192	7.084E-04	1.44E-02	1.39	Duroc-up
NSMAF	SNOWBALL_005990_st	neutral sphingomyelinase (N-SMase) activation associated factor	5.662	5.983	7.100E-04	1.44E-02	-1.25	PiNN-up
C6orf204	SNOWBALL_002261_st	chromosome 6 open reading frame 204	7.902	7.310	7.132E-04	1.45E-02	1.51	Duroc-up
C10orf26	SNOWBALL_024851_st	chromosome 10 open reading frame 26	9.601	9.971	7.180E-04	1.45E-02	-1.29	PiNN-up
ENO1	SNOWBALL_009095_st	enolase 1, (alpha)	7.760	8.104	7.182E-04	1.45E-02	-1.27	PiNN-up
ADSL	SNOWBALL_006787_st	adenylosuccinate lyase	7.980	8.520	7.229E-04	1.46E-02	-1.45	PiNN-up
NF2	SNOWBALL_024272_st	PREDICTED: Sus scrofa similar to neurofibromatosis 2, transcript variant 1 (LOC100158071), mRNA	5.718	5.923	7.238E-04	1.46E-02	-1.15	PiNN-up
VIT	SNOWBALL_005131_st	vitrin	5.995	6.435	7.247E-04	1.46E-02	-1.36	PiNN-up
XRN1	SNOWBALL_015557_s_st	5'-3' exoribonuclease 1	7.457	6.956	7.266E-04	1.46E-02	1.42	Duroc-up
	SNOWBALL_045673_st		4.306	3.635	7.274E-04	1.46E-02	1.59	Duroc-up

LOC100523558	SNOWBALL_029124_st	Ssc_hash_S17514573 BX669142 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0030.g.23 3prim, mRNA	7.050	6.635	7.284E-04	1.47E-02	1.33	Duroc-up
PHF20L1	SNOWBALL_000744_st	PHD finger protein 20-like 1	8.116	7.734	7.324E-04	1.47E-02	1.30	Duroc-up
SMAD4	SNOWBALL_002510_st	SMAD family member 4	8.500	8.043	7.347E-04	1.47E-02	1.37	Duroc-up
FAM190B	SNOWBALL_024715_st	family with sequence similarity 190, member B	8.338	7.889	7.362E-04	1.48E-02	1.36	Duroc-up
CDK9	SNOWBALL_003866_st	cyclin-dependent kinase 9	7.212	7.449	7.416E-04	1.48E-02	-1.18	PiNN-up
VGLL3	SNOWBALL_023048_s_st	vestigial like 3 (Drosophila)	7.082	6.202	7.422E-04	1.48E-02	1.84	Duroc-up
CASZ1	SNOWBALL_009138_st	zinc finger protein castor homolog 1-like	7.103	7.383	7.452E-04	1.49E-02	-1.21	PiNN-up
GULP1	SNOWBALL_018007_st	GULP, engulfment adaptor PTB domain containing 1	7.835	7.107	7.468E-04	1.49E-02	1.66	Duroc-up
PER1	SNOWBALL_015143_st	period homolog 1 (Drosophila)	6.914	7.398	7.527E-04	1.50E-02	-1.40	PiNN-up
ZNF512	SNOWBALL_005315_st	zinc finger protein 512	5.315	5.643	7.521E-04	1.50E-02	-1.26	PiNN-up
WWP1	SNOWBALL_005714_st	WW domain containing E3 ubiquitin protein ligase 1	10.945	10.436	7.532E-04	1.50E-02	1.42	Duroc-up
REEP3	SNOWBALL_016948_s_st	receptor accessory protein 3	6.055	5.290	7.519E-04	1.50E-02	1.70	Duroc-up
RAB32	SNOWBALL_002150_st	RAB32, member RAS oncogene family	6.931	7.275	7.551E-04	1.50E-02	-1.27	PiNN-up
FBXO11	SNOWBALL_027972_st	F-box protein 11	7.157	6.650	7.564E-04	1.50E-02	1.42	Duroc-up
HIST1H2AB	SNOWBALL_009649_st	histone H2A type 1-like	4.898	5.236	7.583E-04	1.50E-02	-1.26	PiNN-up
ERBB4	SNOWBALL_018071_s_st	receptor tyrosine-protein kinase erbB-4-like	6.535	5.897	7.597E-04	1.50E-02	1.56	Duroc-up
VPS11	SNOWBALL_012801_st	vacuolar protein sorting 11 homolog (S. cerevisiae)	7.167	7.491	7.619E-04	1.51E-02	-1.25	PiNN-up
SMAD3	SNOWBALL_002983_st	SMAD family member 3	6.949	7.227	7.672E-04	1.51E-02	-1.21	PiNN-up
SPATA5	SNOWBALL_011678_st	spermatogenesis associated 5	6.478	6.127	7.689E-04	1.51E-02	1.28	Duroc-up
XIAP	SNOWBALL_001900_st	X-linked inhibitor of apoptosis	6.117	5.575	7.696E-04	1.51E-02	1.46	Duroc-up
PNPLA8	SNOWBALL_012667_s_st	patatin-like phospholipase domain containing 8	7.036	6.473	7.691E-04	1.51E-02	1.48	Duroc-up
SCFD1	SNOWBALL_010797_st	sec1 family domain containing 1	7.256	6.651	7.678E-04	1.51E-02	1.52	Duroc-up
TRIM65	SNOWBALL_028103_st	tripartite motif containing 65	3.448	4.132	7.718E-04	1.51E-02	-1.61	PiNN-up
VPS18	SNOWBALL_002818_st	vacuolar protein sorting 18 homolog (S. cerevisiae)	5.741	6.023	7.724E-04	1.51E-02	-1.22	PiNN-up
ARIH1	SNOWBALL_010587_st	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	9.446	8.979	7.773E-04	1.52E-02	1.38	Duroc-up
SNORA58	SNOWBALL_006634_st	Small nucleolar RNA SNORA58 [Source: RFAM;Acc:RF00418]	6.446	7.630	7.797E-04	1.52E-02	-2.27	PiNN-up
RNF217	SNOWBALL_002207_st	ring finger protein 217	7.526	7.136	7.807E-04	1.52E-02	1.31	Duroc-up
SFT	SNOWBALL_024634_st	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	7.704	7.164	7.804E-04	1.52E-02	1.45	Duroc-up
BC026181	SNOWBALL_027012_st	zinc finger protein 639	7.040	6.474	7.796E-04	1.52E-02	1.48	Duroc-up
SRPK3	SNOWBALL_020396_s_st	Serine/arginine-rich protein specific kinase 3 [Source:UniProtKB/TrEMBL;Acc:B8Y466]	7.128	7.377	7.828E-04	1.52E-02	-1.19	PiNN-up
SRPK2	SNOWBALL_037354_st	SRSF protein kinase 2	5.749	5.435	7.854E-04	1.53E-02	1.24	Duroc-up

SETD1B	SNOWBALL_047614_st	SET domain containing 1B	4.416	4.742	7.864E-04	1.53E-02	-1.25	PiNN-up
STIM1	SNOWBALL_012194_st	stromal interaction molecule 1	6.859	7.126	7.899E-04	1.53E-02	-1.20	PiNN-up
	SNOWBALL_044231_st		6.057	6.668	7.918E-04	1.54E-02	-1.53	PiNN-up
RNPC1	SNOWBALL_000518_s_st	OTTSUSG00000000596 RNA-binding region (RNP1, RRM) containing 1	8.145	8.460	7.948E-04	1.54E-02	-1.24	PiNN-up
EIF2A	SNOWBALL_015704_st	eukaryotic translation initiation factor 2A, 65kDa	9.990	9.331	7.934E-04	1.54E-02	1.58	Duroc-up
ACAP2	SNOWBALL_039924_st	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	5.187	4.446	7.941E-04	1.54E-02	1.67	Duroc-up
NEURL	SNOWBALL_016921_s_st	neuralized homolog (Drosophila)	8.513	8.929	7.989E-04	1.54E-02	-1.33	PiNN-up
BAZ1B	SNOWBALL_029556_st	bromodomain adjacent to zinc finger domain, 1B	8.363	7.931	7.981E-04	1.54E-02	1.35	Duroc-up
EXOC5	SNOWBALL_003110_st	exocyst complex component 5	8.139	7.535	7.996E-04	1.54E-02	1.52	Duroc-up
	SNOWBALL_043972_st		5.195	4.827	8.035E-04	1.54E-02	1.29	Duroc-up
	SNOWBALL_033496_st	Ssc_hash_S26725150 AJ961234 KN404_2 Sus scrofa cDNA clone C0007757j19 5prime, mRNA	5.466	5.016	8.070E-04	1.54E-02	1.37	Duroc-up
BRWD3	SNOWBALL_045407_st	bromodomain and WD repeat-containing protein 3-like	4.112	3.647	8.030E-04	1.54E-02	1.38	Duroc-up
ARIH1	SNOWBALL_042422_st	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	6.575	6.083	8.048E-04	1.54E-02	1.41	Duroc-up
ITPR2	SNOWBALL_007306_st	inositol 1,4,5-trisphosphate receptor, type 2	7.732	7.194	8.041E-04	1.54E-02	1.45	Duroc-up
XIRP2	SNOWBALL_000376_st	xin actin-binding repeat containing 2	12.222	11.591	8.052E-04	1.54E-02	1.55	Duroc-up
SMC6	SNOWBALL_005116_st	structural maintenance of chromosomes 6	6.683	6.036	8.066E-04	1.54E-02	1.57	Duroc-up
ROCK2	SNOWBALL_005170_st	Rho-associated, coiled-coil containing protein kinase 2	9.041	8.354	8.063E-04	1.54E-02	1.61	Duroc-up
RDX	SNOWBALL_012341_st	radixin	9.609	8.965	8.102E-04	1.55E-02	1.56	Duroc-up
COL6A3	SNOWBALL_024029_s_st	collagen, type VI, alpha 3	8.984	9.416	8.158E-04	1.55E-02	-1.35	PiNN-up
TMEM184B	SNOWBALL_006846_st	transmembrane protein 184B	7.274	7.572	8.133E-04	1.55E-02	-1.23	PiNN-up
VPS4A	SNOWBALL_040064_st	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	3.369	3.589	8.170E-04	1.55E-02	-1.16	PiNN-up
PCF11	SNOWBALL_012281_st	PCF11, cleavage and polyadenylation factor subunit, homolog (S. cerevisiae)	7.383	6.910	8.152E-04	1.55E-02	1.39	Duroc-up
ZNF280B	SNOWBALL_024219_s_st	PREDICTED: Sus scrofa similar to Suppressor of hairy wing homolog 2 (LOC100153096), mRNA	6.328	5.853	8.167E-04	1.55E-02	1.39	Duroc-up
	SNOWBALL_045372_st		5.824	5.229	8.168E-04	1.55E-02	1.51	Duroc-up
KLHL24	SNOWBALL_033099_st	kelch-like 24 (Drosophila)	3.881	3.188	8.203E-04	1.55E-02	1.62	Duroc-up
TSC1	SNOWBALL_004177_st	tuberous sclerosis 1	7.457	7.780	8.236E-04	1.56E-02	-1.25	PiNN-up
SNORD18	SNOWBALL_003535_st	Small nucleolar RNA SNORD18 [Source: RFAM;Acc:RF00093]	6.591	7.446	8.250E-04	1.56E-02	-1.81	PiNN-up
CRAT	SNOWBALL_003987_st	carnitine O-acetyltransferase	9.688	10.300	8.283E-04	1.56E-02	-1.53	PiNN-up

	SNOWBALL_032303_st	Ssc_hash_S23764572 1122379 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.024	4.716	8.266E-04	1.56E-02	1.24	Duroc-up
ZNF287	SNOWBALL_014965_st	zinc finger protein 287	5.430	5.077	8.275E-04	1.56E-02	1.28	Duroc-up
MDM2	SNOWBALL_035853_st	Mdm2 p53 binding protein homolog (mouse)	8.332	7.664	8.276E-04	1.56E-02	1.59	Duroc-up
TMED4	SNOWBALL_019957_st	transmembrane emp24 protein transport domain containing 4	7.801	8.243	8.308E-04	1.56E-02	-1.36	PiNN-up
KPNB1	SNOWBALL_014712_st	karyopherin (importin) beta 1	9.355	9.114	8.299E-04	1.56E-02	1.18	Duroc-up
ZEB2	SNOWBALL_026213_st	zinc finger E-box binding homeobox 2	6.010	5.598	8.321E-04	1.56E-02	1.33	Duroc-up
WDR75	SNOWBALL_018050_st	WD repeat domain 75	6.244	5.814	8.314E-04	1.56E-02	1.35	Duroc-up
G2E3	SNOWBALL_010918_st	G2/M-phase specific E3 ubiquitin protein ligase	5.696	5.264	8.337E-04	1.56E-02	1.35	Duroc-up
MUM1L1	SNOWBALL_020783_st	melanoma associated antigen (mutated) 1-like 1	5.899	5.144	8.340E-04	1.56E-02	1.69	Duroc-up
ITPR2	SNOWBALL_007122_st	inositol 1,4,5-trisphosphate receptor, type 2	8.573	8.154	8.355E-04	1.56E-02	1.34	Duroc-up
	SNOWBALL_027613_st	Ssc_hash_S6013640 359859 MARC 1PIG Sus scrofa cDNA 5prime, mRNA	4.936	4.094	8.378E-04	1.56E-02	1.79	Duroc-up
SPATA7	SNOWBALL_010480_st	spermatogenesis associated 7	5.230	4.796	8.409E-04	1.57E-02	1.35	Duroc-up
PIK3CA	SNOWBALL_033103_st	phosphoinositide-3-kinase, catalytic, alpha polypeptide	7.427	6.927	8.417E-04	1.57E-02	1.41	Duroc-up
IPO13	SNOWBALL_037462_st	importin 13	6.860	7.324	8.483E-04	1.58E-02	-1.38	PiNN-up
SPATA5	SNOWBALL_011863_st	spermatogenesis associated 5	3.989	3.582	8.527E-04	1.58E-02	1.33	Duroc-up
ANK2	SNOWBALL_030114_st	ankyrin 2, neuronal	8.149	7.620	8.577E-04	1.59E-02	1.44	Duroc-up
MED18	SNOWBALL_021453_st	mediator complex subunit 18	5.186	5.727	8.610E-04	1.60E-02	-1.46	PiNN-up
EIF4G3	SNOWBALL_008688_st	eukaryotic translation initiation factor 4 gamma, 3	9.391	9.000	8.641E-04	1.60E-02	1.31	Duroc-up
PHF3	SNOWBALL_002314_st	PHD finger protein 3	7.595	6.969	8.708E-04	1.61E-02	1.54	Duroc-up
THAP11	SNOWBALL_008019_st	THAP domain containing 11	7.899	8.192	8.722E-04	1.61E-02	-1.23	PiNN-up
CTSA	SNOWBALL_019356_st	cathepsin A	7.232	7.564	8.761E-04	1.62E-02	-1.26	PiNN-up
NHLRC2	SNOWBALL_016871_st	NHL repeat containing 2	7.670	7.292	8.867E-04	1.64E-02	1.30	Duroc-up
PRKAR2A	SNOWBALL_015406_st	protein kinase, cAMP-dependent, regulatory, type II, alpha	11.240	10.863	8.916E-04	1.64E-02	1.30	Duroc-up
C5H12orf35	SNOWBALL_007316_st	uncharacterized protein C12orf35-like	7.489	6.793	8.943E-04	1.65E-02	1.62	Duroc-up
HIPK3	SNOWBALL_044937_st	homeodomain interacting protein kinase 3	9.193	8.714	8.978E-04	1.65E-02	1.39	Duroc-up
LRPPRC	SNOWBALL_004953_st	leucine-rich PPR-motif containing	8.612	8.118	8.995E-04	1.65E-02	1.41	Duroc-up
UBAP2L	SNOWBALL_005889_st	ubiquitin associated protein 2-like	9.462	9.648	9.033E-04	1.66E-02	-1.14	PiNN-up
RB1CC1	SNOWBALL_025669_st	RB1-inducible coiled-coil 1	8.636	8.168	9.040E-04	1.66E-02	1.38	Duroc-up
MIPOL1	SNOWBALL_010714_st	mirror-image polydactyly 1	4.322	3.540	9.041E-04	1.66E-02	1.72	Duroc-up
EXOC7	SNOWBALL_014146_st	exocyst complex component 7	8.215	8.646	9.053E-04	1.66E-02	-1.35	PiNN-up
SNORA1	SNOWBALL_012902_st	Small nucleolar RNA SNORA1	7.132	7.701	9.106E-04	1.66E-02	-1.48	PiNN-up
AUTS2	SNOWBALL_004554_st	autism susceptibility candidate 2	6.410	6.696	9.111E-04	1.66E-02	-1.22	PiNN-up

RFK	SNOWBALL_003655_st	riboflavin kinase-like	5.891	5.416	9.095E-04	1.66E-02	1.39	Duroc-up
USO1	SNOWBALL_011545_st	USO1 vesicle docking protein homolog (yeast)	8.865	8.227	9.084E-04	1.66E-02	1.56	Duroc-up
PCYOX1	SNOWBALL_005332_st	prenylcysteine oxidase 1	9.805	9.317	9.121E-04	1.66E-02	1.40	Duroc-up
SECISBP2L	SNOWBALL_002912_st	SECIS binding protein 2-like	7.389	6.960	9.183E-04	1.67E-02	1.35	Duroc-up
ROCK2	SNOWBALL_047256_st	Rho-associated, coiled-coil containing protein kinase 2	5.223	4.691	9.180E-04	1.67E-02	1.45	Duroc-up
CLASP2	SNOWBALL_015189_st	cytoplasmic linker associated protein 2	8.014	7.697	9.227E-04	1.67E-02	1.25	Duroc-up
MAK16	SNOWBALL_017847_st	Protein MAK16 homolog (Protein RBM13)(NNP78)	7.080	6.608	9.222E-04	1.67E-02	1.39	Duroc-up
LOC100454352	SNOWBALL_035763_st	Ssc_hash_S40192600 rjej10b_f23.y1 jej Sus scrofa cDNA 5prime, mRNA	5.992	5.461	9.254E-04	1.68E-02	1.44	Duroc-up
TOP3A	SNOWBALL_030832_st	topoisomerase (DNA) III alpha	6.601	6.930	9.285E-04	1.68E-02	-1.26	PiNN-up
BRD4	SNOWBALL_047822_st		8.073	8.251	9.286E-04	1.68E-02	-1.13	PiNN-up
POLH	SNOWBALL_010036_st	GTP-binding protein 2-like	5.963	6.212	9.297E-04	1.68E-02	-1.19	PiNN-up
USP2	SNOWBALL_012631_st	ubiquitin specific peptidase 2	8.569	8.915	9.324E-04	1.68E-02	-1.27	PiNN-up
jerky	SNOWBALL_040503_st	hypothetical protein LOC100068958	6.342	6.600	9.322E-04	1.68E-02	-1.20	PiNN-up
SNORA63	SNOWBALL_016136_st	Small nucleolar RNA SNORA63 [Source: RFAM;Acc:RF00092]	7.432	8.417	9.359E-04	1.68E-02	-1.98	PiNN-up
INPP4B	SNOWBALL_041760_st	inositol polyphosphate-4-phosphatase, type II, 105kDa	4.845	4.121	9.369E-04	1.68E-02	1.65	Duroc-up
SMEK2	SNOWBALL_005073_s_st	serine/threonine-protein phosphatase 4 regulatory subunit 3B-like	7.966	7.109	9.362E-04	1.68E-02	1.81	Duroc-up
ZCCHC10	SNOWBALL_027826_st	zinc finger, CCHC domain containing 10	5.835	5.284	9.380E-04	1.68E-02	1.47	Duroc-up
HSPG2	SNOWBALL_008880_st	heparan sulfate proteoglycan 2	8.211	8.477	9.408E-04	1.69E-02	-1.20	PiNN-up
ATXN7L3	SNOWBALL_014275_st	ataxin 7-like 3	5.657	6.036	9.432E-04	1.69E-02	-1.30	PiNN-up
SPEG	SNOWBALL_029611_st	SPEG complex locus	5.413	5.793	9.475E-04	1.70E-02	-1.30	PiNN-up
C1orf26	SNOWBALL_013157_st	Uncharacterized protein C1orf26 [Source:UniProtKB/Swiss-Prot;Acc:Q5T5J6]	5.464	4.818	9.495E-04	1.70E-02	1.56	Duroc-up
XIRP2	SNOWBALL_000375_st	OTTSUSG00000001584 xin actin-binding repeat containing 2	11.329	10.563	9.508E-04	1.70E-02	1.70	Duroc-up
NIN	SNOWBALL_003032_st	ninein (GSK3B interacting protein)	6.418	5.979	9.553E-04	1.70E-02	1.36	Duroc-up
SEC22A	SNOWBALL_015974_st	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	6.290	5.805	9.555E-04	1.70E-02	1.40	Duroc-up
CCDC97	SNOWBALL_008596_st	coiled-coil domain containing 97	6.763	7.012	9.605E-04	1.71E-02	-1.19	PiNN-up
IGJ	SNOWBALL_011427_st	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	5.648	5.002	9.616E-04	1.71E-02	1.57	Duroc-up
GNAQ	SNOWBALL_033564_st	guanine nucleotide binding protein (G protein), q polypeptide	4.820	4.209	9.633E-04	1.71E-02	1.53	Duroc-up

EDF1	SNOWBALL_003622_s_st	endothelial differentiation-related factor 1	8.193	8.397	9.677E-04	1.72E-02	-1.15	PiNN-up
ARMC8	SNOWBALL_036979_st	armadillo repeat containing 8	6.581	6.197	9.696E-04	1.72E-02	1.30	Duroc-up
PHF23	SNOWBALL_014725_st	PHD finger protein 23	5.356	5.671	9.717E-04	1.72E-02	-1.24	PiNN-up
PSENEN	SNOWBALL_008101_st	presenilin enhancer 2 homolog (C. elegans)	9.087	9.480	9.731E-04	1.72E-02	-1.31	PiNN-up
BZW1	SNOWBALL_024011_s_st	basic leucine zipper and W2 domains 1	7.368	6.865	9.769E-04	1.73E-02	1.42	Duroc-up
MYEF2	SNOWBALL_003156_st	myelin expression factor 2	4.833	4.527	9.792E-04	1.73E-02	1.24	Duroc-up
COL6A3	SNOWBALL_024025_s_st	collagen, type VI, alpha 3	7.469	7.868	9.874E-04	1.74E-02	-1.32	PiNN-up
NARG1L	SNOWBALL_013859_st	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	7.188	6.749	9.895E-04	1.74E-02	1.36	Duroc-up
BAT3	SNOWBALL_001234_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	8.052	8.398	9.950E-04	1.75E-02	-1.27	PiNN-up
TFIP11	SNOWBALL_016614_st	tuftelin interacting protein 11	5.676	6.056	9.993E-04	1.75E-02	-1.30	PiNN-up
CHTOP	SNOWBALL_006376_s_st	Friend of PRMT1 protein-like	7.887	8.181	9.984E-04	1.75E-02	-1.23	PiNN-up
APPBP2	SNOWBALL_014444_st	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	8.321	7.989	9.995E-04	1.75E-02	1.26	Duroc-up
SUCLG2	SNOWBALL_015641_st	succinate-CoA ligase, GDP-forming, beta subunit	8.532	7.762	9.974E-04	1.75E-02	1.71	Duroc-up
DCTN4	SNOWBALL_022377_s_st	dynactin 4 (p62)	8.233	8.584	1.002E-03	1.75E-02	-1.28	PiNN-up
TXNDC4	SNOWBALL_023307_st	endoplasmic reticulum protein 44	8.359	8.119	1.002E-03	1.75E-02	1.18	Duroc-up
RIF1	SNOWBALL_018454_s_st	RAP1 interacting factor homolog (yeast)	5.717	5.233	1.003E-03	1.75E-02	1.40	Duroc-up
ARHGAP17	SNOWBALL_004489_st	Rho GTPase activating protein 17	7.169	7.370	1.006E-03	1.76E-02	-1.15	PiNN-up
SPPL2A	SNOWBALL_002607_st	signal peptide peptidase-like 2A-like	7.354	6.951	1.007E-03	1.76E-02	1.32	Duroc-up
BMPR2	SNOWBALL_029908_st	bone morphogenetic protein receptor, type II (serine/threonine kinase)	7.862	7.330	1.008E-03	1.76E-02	1.45	Duroc-up
SLC38A4	SNOWBALL_037243_st	solute carrier family 38, member 4	6.113	5.204	1.009E-03	1.76E-02	1.88	Duroc-up
C12orf4	SNOWBALL_007380_st	chromosome 12 open reading frame 4	7.447	7.160	1.011E-03	1.76E-02	1.22	Duroc-up
CD99L2	SNOWBALL_020712_st	CD99 molecule-like 2	6.805	7.076	1.012E-03	1.76E-02	-1.21	PiNN-up
CAMK2D	SNOWBALL_011802_st	calcium/calmodulin-dependent protein kinase II delta	9.786	9.423	1.014E-03	1.76E-02	1.29	Duroc-up
NANOS1	SNOWBALL_017147_s_st	nanos homolog 1 (Drosophila)	7.028	7.332	1.020E-03	1.77E-02	-1.23	PiNN-up
hsa-mir-3141	hsa-mir-3141_st	MI0014165	6.924	7.316	1.021E-03	1.77E-02	-1.31	PiNN-up
STX16	SNOWBALL_000540_s_st	syntaxin 16	6.540	6.859	1.022E-03	1.77E-02	-1.25	PiNN-up
LOC100507119	SNOWBALL_016279_s_st	hypothetical LOC100507119	6.855	7.222	1.025E-03	1.77E-02	-1.29	PiNN-up
ARMC1	SNOWBALL_005862_st	armadillo repeat containing 1	6.690	6.210	1.026E-03	1.77E-02	1.39	Duroc-up
TEX9	SNOWBALL_002506_st	testis expressed 9	8.985	8.201	1.027E-03	1.77E-02	1.72	Duroc-up
KIAA1107	SNOWBALL_006313_st	KIAA1107	6.675	5.715	1.033E-03	1.78E-02	1.95	Duroc-up
bys1	SNOWBALL_023400_st	Sus scrofa bystin-like (bys1) mRNA, complete cds	5.721	6.188	1.040E-03	1.79E-02	-1.38	PiNN-up
CDH29	SNOWBALL_015391_st	cadherin-related family member 4	3.692	4.027	1.039E-03	1.79E-02	-1.26	PiNN-up
MTDH	SNOWBALL_005685_st	metadherin	7.620	7.446	1.039E-03	1.79E-02	1.13	Duroc-up

PKN2	SNOWBALL_040010_st	protein kinase N2	8.351	7.923	1.041E-03	1.79E-02	1.35	Duroc-up
	SNOWBALL_040601_st		7.493	6.986	1.040E-03	1.79E-02	1.42	Duroc-up
	SNOWBALL_039637_st		4.101	3.513	1.039E-03	1.79E-02	1.50	Duroc-up
CHD1	SNOWBALL_028214_st	chromodomain helicase DNA binding protein 1	4.853	4.199	1.043E-03	1.79E-02	1.57	Duroc-up
LYST	SNOWBALL_000316_s_st	lysosomal trafficking regulator	6.832	6.444	1.049E-03	1.79E-02	1.31	Duroc-up
SELT	SNOWBALL_027312_st	Ssc_hash_S17517335 BX671904 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0035.h.17 5prim, mRNA	6.192	5.710	1.049E-03	1.79E-02	1.40	Duroc-up
PCNP	SNOWBALL_016122_st	PEST proteolytic signal containing nuclear protein	7.885	7.219	1.055E-03	1.80E-02	1.59	Duroc-up
ABCB6	SNOWBALL_023965_st	PREDICTED: Sus scrofa similar to ATP-binding cassette, sub-family B, member 6 (LOC100155585), mRNA	6.172	6.937	1.060E-03	1.81E-02	-1.70	PiNN-up
TSC22D1	SNOWBALL_013875_st	TSC22 domain family, member 1	7.805	8.138	1.066E-03	1.81E-02	-1.26	PiNN-up
PCGF1	SNOWBALL_005496_st	polycomb group ring finger 1	6.158	6.469	1.065E-03	1.81E-02	-1.24	PiNN-up
C4orf21	SNOWBALL_042404_st	chromosome 4 open reading frame 21	4.404	4.680	1.062E-03	1.81E-02	-1.21	PiNN-up
SLC44A1	SNOWBALL_004156_st	solute carrier family 44, member 1	8.473	8.123	1.060E-03	1.81E-02	1.28	Duroc-up
WDR43	SNOWBALL_005211_st	WD repeat domain 43	6.997	6.484	1.065E-03	1.81E-02	1.43	Duroc-up
BAZ2B	SNOWBALL_017895_st	bromodomain adjacent to zinc finger domain, 2B	7.292	6.725	1.065E-03	1.81E-02	1.48	Duroc-up
ZRANB2	SNOWBALL_009071_st	zinc finger, RAN-binding domain containing 2	6.943	6.292	1.061E-03	1.81E-02	1.57	Duroc-up
CCDC82	SNOWBALL_012402_st	coiled-coil domain containing 82	5.398	4.635	1.066E-03	1.81E-02	1.70	Duroc-up
LYST	SNOWBALL_000318_s_st	lysosomal trafficking regulator	6.706	6.391	1.069E-03	1.81E-02	1.24	Duroc-up
PRKAA2	SNOWBALL_037953_st	protein kinase, AMP-activated, alpha 2 catalytic subunit	8.848	8.317	1.080E-03	1.83E-02	1.44	Duroc-up
BTD	SNOWBALL_015174_st	biotinidase	6.488	6.914	1.082E-03	1.83E-02	-1.34	PiNN-up
NUDCD3	SNOWBALL_019960_st	NudC domain containing 3	6.967	7.276	1.083E-03	1.83E-02	-1.24	PiNN-up
CSTF1	SNOWBALL_000491_st	cleavage stimulation factor, 3' pre-RNA, subunit 1, 50kDa	6.947	7.161	1.085E-03	1.83E-02	-1.16	PiNN-up
ADAMTS20	SNOWBALL_007474_st	ADAM metallopeptidase with thrombospondin type 1 motif, 20	7.331	6.620	1.085E-03	1.83E-02	1.64	Duroc-up
DHRS1	SNOWBALL_010395_st	dehydrogenase/reductase (SDR family) member 1	5.763	6.236	1.089E-03	1.83E-02	-1.39	PiNN-up
WAPAL	SNOWBALL_017482_st	wings apart-like homolog (Drosophila)	7.592	7.113	1.090E-03	1.83E-02	1.39	Duroc-up
STT3B	SNOWBALL_015191_st	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	9.364	8.979	1.097E-03	1.84E-02	1.31	Duroc-up
IDE	SNOWBALL_017063_s_st	insulin-degrading enzyme	8.903	8.476	1.098E-03	1.84E-02	1.34	Duroc-up
RIOK3	SNOWBALL_026217_st	RIO kinase 3 (yeast)	8.645	8.091	1.097E-03	1.84E-02	1.47	Duroc-up
CRYAB	SNOWBALL_012382_st	crystallin, alpha B	9.068	9.625	1.099E-03	1.84E-02	-1.47	PiNN-up
LAMP2	SNOWBALL_001846_s_st	lysosomal-associated membrane protein 2	8.121	7.747	1.108E-03	1.85E-02	1.30	Duroc-up

CEBPB	SNOWBALL_022898_s_st	CCAAT/enhancer binding protein (C/EBP), beta	8.224	8.778	1.113E-03	1.86E-02	-1.47	PiNN-up
FAM100A	SNOWBALL_004606_st	family with sequence similarity 100, member A	7.510	7.826	1.116E-03	1.86E-02	-1.24	PiNN-up
STARD7	SNOWBALL_004676_st	StAR-related lipid transfer (START) domain containing 7	8.018	8.348	1.123E-03	1.87E-02	-1.26	PiNN-up
SLTM	SNOWBALL_002433_s_st	SAFB-like, transcription modulator	8.319	7.937	1.124E-03	1.87E-02	1.30	Duroc-up
AR	SNOWBALL_020241_st	androgen receptor	6.965	6.502	1.123E-03	1.87E-02	1.38	Duroc-up
ATAD2B	SNOWBALL_005424_st	ATPase family, AAA domain containing 2B	7.360	6.880	1.120E-03	1.87E-02	1.39	Duroc-up
ZNF800	SNOWBALL_030158_st	zinc finger protein 800	3.722	3.098	1.123E-03	1.87E-02	1.54	Duroc-up
ADD3	SNOWBALL_024819_s_st	adducin 3 (gamma)	7.590	7.187	1.128E-03	1.87E-02	1.32	Duroc-up
GGA1	SNOWBALL_029086_st	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	6.689	6.902	1.130E-03	1.87E-02	-1.16	PiNN-up
C3H1orf212	SNOWBALL_022243_st	Sus scrofa mRNA, clone:PBL010107C11, expressed in peripheral blood mononuclear cells	6.385	6.850	1.138E-03	1.88E-02	-1.38	PiNN-up
NISCH	SNOWBALL_021780_s_st	nischarin	5.739	6.146	1.137E-03	1.88E-02	-1.33	PiNN-up
HN1	SNOWBALL_028679_st	Ssc_hash_S40002491 rece40_e16.y1 ece Sus scrofa cDNA 5prime, mRNA	3.567	3.931	1.142E-03	1.88E-02	-1.29	PiNN-up
ZNF384	SNOWBALL_007430_st	zinc finger protein 384	7.595	7.919	1.143E-03	1.88E-02	-1.25	PiNN-up
ADRM1	SNOWBALL_027392_st	adhesion regulating molecule 1	7.475	7.708	1.140E-03	1.88E-02	-1.18	PiNN-up
STAU2	SNOWBALL_005672_st	staufen, RNA binding protein, homolog 2 (Drosophila)	9.466	9.150	1.140E-03	1.88E-02	1.24	Duroc-up
SMARCA5	SNOWBALL_011895_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	7.839	7.395	1.143E-03	1.88E-02	1.36	Duroc-up
NBN	SNOWBALL_000820_s_st	OTTSUSG00000000691 NBN_genefragment	6.369	5.605	1.148E-03	1.89E-02	1.70	Duroc-up
SPARCL1	SNOWBALL_011628_s_st	SPARC-like 1 (hevin)	9.278	8.800	1.158E-03	1.91E-02	1.39	Duroc-up
TTC11	SNOWBALL_026926_st	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)	7.760	8.138	1.166E-03	1.91E-02	-1.30	PiNN-up
MUDENG	SNOWBALL_003269_st	MU-2/AP1M2 domain containing, death-inducing	6.945	6.546	1.163E-03	1.91E-02	1.32	Duroc-up
DR1	SNOWBALL_006331_st	down-regulator of transcription 1, TBP-binding (negative cofactor 2)	8.417	7.996	1.165E-03	1.91E-02	1.34	Duroc-up
ORC4L	SNOWBALL_017670_st	origin recognition complex, subunit 4-like (yeast) //origin recognition complex, subunit 4-like (S. cerevisiae)	6.129	5.488	1.163E-03	1.91E-02	1.56	Duroc-up
LOC465540	SNOWBALL_046556_st	similar to translation initiation factor eIF-2 gamma subunit	6.157	5.514	1.164E-03	1.91E-02	1.56	Duroc-up
AASS	SNOWBALL_019880_st	aminoadipate-semialdehyde synthase	6.906	6.204	1.168E-03	1.91E-02	1.63	Duroc-up
ZNF677	SNOWBALL_042315_st	zinc finger protein 677	3.992	5.266	1.177E-03	1.92E-02	-2.42	PiNN-up
DSTYK	SNOWBALL_012582_st	dual serine/threonine and tyrosine protein kinase	5.375	5.591	1.178E-03	1.92E-02	-1.16	PiNN-up

STAG1	SNOWBALL_015507_st	stromal antigen 1	5.554	5.270	1.176E-03	1.92E-02	1.22	Duroc-up
ZC3H12C	SNOWBALL_042457_st	zinc finger CCCH-type containing 12C	5.912	5.613	1.177E-03	1.92E-02	1.23	Duroc-up
NEURL	SNOWBALL_024839_st	PREDICTED: Sus scrofa similar to Neuralized-like protein 1 (h-neuralized 1) (h-neu) (RING finger protein 67) (LOC100155006), mRNA	7.438	7.804	1.180E-03	1.92E-02	-1.29	PiNN-up
C12orf52	SNOWBALL_016643_st	chromosome 12 open reading frame 52	6.235	6.482	1.182E-03	1.92E-02	-1.19	PiNN-up
TAB2	SNOWBALL_000020_st	TGF-beta activated kinase 1/MAP3K7 binding protein 2	10.407	10.141	1.181E-03	1.92E-02	1.20	Duroc-up
MAGT1	SNOWBALL_020272_st	magnesium transporter 1	6.997	6.651	1.180E-03	1.92E-02	1.27	Duroc-up
FGD4	SNOWBALL_000939_st	FYVE, RhoGEF and PH domain containing 4	6.019	5.450	1.189E-03	1.93E-02	1.48	Duroc-up
SYS1	SNOWBALL_023632_s_st	PREDICTED: Sus scrofa similar to SYS1 Golgi-localized integral membrane protein homolog (LOC100153534), mRNA	6.433	6.680	1.193E-03	1.93E-02	-1.19	PiNN-up
PHF20L1	SNOWBALL_038293_st	PHD finger protein 20-like 1	4.446	3.786	1.196E-03	1.94E-02	1.58	Duroc-up
AB020966	SNOWBALL_027001_st	RNA (guanine-7-) methyltransferase	6.404	5.960	1.199E-03	1.94E-02	1.36	Duroc-up
LOC100525934	SNOWBALL_029681_st	Ssc_hash_S27603983 EST-AR109C04 Porcine Lymph node cDNA library Sus scrofa cDNA clone AR109C04, mRNA	6.446	5.652	1.200E-03	1.94E-02	1.73	Duroc-up
PIGO	SNOWBALL_031122_st	phosphatidylinositol glycan anchor biosynthesis, class O	6.140	6.455	1.202E-03	1.94E-02	-1.24	PiNN-up
FAM135A	SNOWBALL_002233_st	family with sequence similarity 135, member A	6.371	5.882	1.202E-03	1.94E-02	1.40	Duroc-up
CEP63	SNOWBALL_037044_st	Ssc_hash_S19546008 951455 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	6.169	5.781	1.209E-03	1.95E-02	1.31	Duroc-up
ERBB2IP	SNOWBALL_018686_st	leucine-rich repeats and IQ motif containing 4	7.777	7.167	1.212E-03	1.95E-02	1.53	Duroc-up
CHMP2A	SNOWBALL_026015_st	chromatin modifying protein 2A	7.152	7.401	1.215E-03	1.95E-02	-1.19	PiNN-up
SHOC2	SNOWBALL_017176_s_st	soc-2 suppressor of clear homolog (C. elegans)	8.133	7.713	1.214E-03	1.95E-02	1.34	Duroc-up
SEPX1	SNOWBALL_021122_s_st	selenoprotein X, 1	5.996	6.540	1.222E-03	1.96E-02	-1.46	PiNN-up
STAG2	SNOWBALL_023525_st	stromal antigen 2	7.059	6.671	1.228E-03	1.97E-02	1.31	Duroc-up
NDUFB10	SNOWBALL_042338_st	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa	4.677	5.004	1.229E-03	1.97E-02	-1.25	PiNN-up
GTF2A1	SNOWBALL_010391_st	general transcription factor IIA, 1, 19/37kDa	6.770	6.336	1.232E-03	1.97E-02	1.35	Duroc-up
TRDN	SNOWBALL_045840_st		5.787	5.322	1.244E-03	1.99E-02	1.38	Duroc-up
RASIP1	SNOWBALL_042530_st	ras-interacting protein 1-like	5.539	5.853	1.250E-03	2.00E-02	-1.24	PiNN-up
PDE8A	SNOWBALL_010365_st	high affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic phosphodiesterase 8A-like	6.968	6.612	1.247E-03	2.00E-02	1.28	Duroc-up
C21orf55	SNOWBALL_037747_st	DnaJ (Hsp40) homolog, subfamily C, member 28	5.991	5.562	1.251E-03	2.00E-02	1.35	Duroc-up
ASB15	SNOWBALL_032671_st	ankyrin repeat and SOCS box containing 15	7.406	6.653	1.251E-03	2.00E-02	1.68	Duroc-up

CREM	SNOWBALL_000012_s_st	cAMP responsive element modulator	5.656	4.697	1.252E-03	2.00E-02	1.94	Duroc-up
UTP20	SNOWBALL_007487_st	UTP20, small subunit (SSU) processome component, homolog (yeast)	6.843	6.425	1.257E-03	2.00E-02	1.34	Duroc-up
TM9SF3	SNOWBALL_024929_st	transmembrane 9 superfamily member 3	6.999	6.568	1.259E-03	2.00E-02	1.35	Duroc-up
SEC63	SNOWBALL_002639_s_st	SEC63 homolog (S. cerevisiae)	7.376	6.935	1.259E-03	2.00E-02	1.36	Duroc-up
PKN2	SNOWBALL_040007_s_st	protein kinase N2	7.881	7.331	1.262E-03	2.00E-02	1.46	Duroc-up
AR	SNOWBALL_023434_st	PREDICTED: Sus scrofa hypothetical protein LOC100156251 (LOC100156251), mRNA	7.107	6.480	1.265E-03	2.01E-02	1.54	Duroc-up
SLC48A1	SNOWBALL_030932_st	solute carrier family 48 (heme transporter), member 1	6.528	6.839	1.266E-03	2.01E-02	-1.24	PiNN-up
MLL5	SNOWBALL_026290_st	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	8.375	8.101	1.269E-03	2.01E-02	1.21	Duroc-up
HNRNPL	SNOWBALL_029080_st	heterogeneous nuclear ribonucleoprotein L	9.175	9.528	1.273E-03	2.01E-02	-1.28	PiNN-up
VGLL3	SNOWBALL_015803_s_st	vestigial like 3 (Drosophila)	7.396	7.062	1.273E-03	2.01E-02	1.26	Duroc-up
MSTN	SNOWBALL_018138_st	myostatin	7.781	7.009	1.275E-03	2.01E-02	1.71	Duroc-up
ADARB1	SNOWBALL_037622_st	adenosine deaminase, RNA-specific, B1	6.249	6.657	1.278E-03	2.02E-02	-1.33	PiNN-up
Zbtb20	SNOWBALL_042295_st	zinc finger and BTB domain containing 20	7.181	6.729	1.277E-03	2.02E-02	1.37	Duroc-up
NOC3L	SNOWBALL_023034_st	nucleolar complex associated 3 homolog (S. cerevisiae)	6.032	5.380	1.284E-03	2.02E-02	1.57	Duroc-up
NFE2L1	SNOWBALL_021455_s_st	nuclear factor (erythroid-derived 2)-like 1	5.938	6.378	1.286E-03	2.02E-02	-1.36	PiNN-up
C7orf10	SNOWBALL_019925_st	similar to Protein C7orf10 (Dermal papilla-derived protein 13)	6.375	6.631	1.290E-03	2.02E-02	-1.19	PiNN-up
RBM39	SNOWBALL_019231_s_st	RNA binding motif protein 39	8.279	7.828	1.288E-03	2.02E-02	1.37	Duroc-up
ATP13A3	SNOWBALL_027229_st	ATPase type 13A3	4.488	3.952	1.289E-03	2.02E-02	1.45	Duroc-up
CUL5	SNOWBALL_028232_st	cullin 5	7.943	7.152	1.287E-03	2.02E-02	1.73	Duroc-up
LOC100465737	SNOWBALL_032857_st	Ssc_hash_S18548197 BX916848 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0034.c.15 5prim, mRNA	3.992	3.638	1.292E-03	2.02E-02	1.28	Duroc-up
BMPR2	SNOWBALL_022802_st	bone morphogenetic protein receptor, type II (serine/threonine kinase)	4.881	4.307	1.293E-03	2.02E-02	1.49	Duroc-up
TM9SF2	SNOWBALL_021425_st	transmembrane 9 superfamily member 2	8.689	8.317	1.304E-03	2.04E-02	1.29	Duroc-up
ORAI1	SNOWBALL_016445_st	ORAI calcium release-activated calcium modulator 1	8.837	9.295	1.309E-03	2.04E-02	-1.37	PiNN-up
CHD7	SNOWBALL_005937_st	chromodomain helicase DNA binding protein 7	7.003	6.695	1.308E-03	2.04E-02	1.24	Duroc-up
PIGC	SNOWBALL_047330_st	phosphatidylinositol glycan anchor biosynthesis, class C	4.616	4.976	1.313E-03	2.05E-02	-1.28	PiNN-up
DNAJC30	SNOWBALL_004351_st	DnaJ (Hsp40) homolog, subfamily C, member 30	5.426	5.699	1.313E-03	2.05E-02	-1.21	PiNN-up

MICAL2	SNOWBALL_031086_st	microtubule associated monoxygenase, calponin and LIM domain containing 2	4.251	4.637	1.320E-03	2.06E-02	-1.31	PiNN-up
HIST1H1C	SNOWBALL_009648_st	histone cluster 1, H1c	7.691	8.182	1.321E-03	2.06E-02	-1.41	PiNN-up
CLIC5	SNOWBALL_023207_st	chloride intracellular channel 5	9.236	9.699	1.327E-03	2.06E-02	-1.38	PiNN-up
EIF4A3	SNOWBALL_043613_st	eukaryotic translation initiation factor 4A3	5.170	5.498	1.326E-03	2.06E-02	-1.26	PiNN-up
EXOC2	SNOWBALL_001025_s_st	exocyst complex component 2	7.749	7.938	1.328E-03	2.06E-02	-1.14	PiNN-up
LMBRD2	SNOWBALL_030053_st	LMBR1 domain containing 2	5.360	4.459	1.326E-03	2.06E-02	1.87	Duroc-up
JSRP1	SNOWBALL_036971_st	junctional sarcoplasmic reticulum protein 1	7.015	7.351	1.330E-03	2.06E-02	-1.26	PiNN-up
TBC1D2B	SNOWBALL_010420_st	TBC1 domain family, member 2B	5.624	5.914	1.334E-03	2.06E-02	-1.22	PiNN-up
RING1	SNOWBALL_001445_s_st	OTTSUSG00000001395 ring finger protein 1	6.331	6.602	1.332E-03	2.06E-02	-1.21	PiNN-up
C14orf135	SNOWBALL_003002_st	chromosome 14 open reading frame 135	3.860	3.372	1.333E-03	2.06E-02	1.40	Duroc-up
RG9MTD2	SNOWBALL_011955_st	RNA (guanine-9-)-methyltransferase domain-containing protein 2-like	5.302	4.928	1.337E-03	2.07E-02	1.30	Duroc-up
PCM1	SNOWBALL_028843_st	pericentriolar material 1	6.841	6.101	1.340E-03	2.07E-02	1.67	Duroc-up
E2F6	SNOWBALL_005499_st	E2F transcription factor 6	8.169	8.483	1.345E-03	2.07E-02	-1.24	PiNN-up
KIDINS220	SNOWBALL_021847_s_st	kinase D-interacting substrate, 220kDa	7.730	7.288	1.345E-03	2.07E-02	1.36	Duroc-up
LOC100450734	SNOWBALL_028021_st	Ssc_hash_S18386573 937918 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.494	4.787	1.346E-03	2.07E-02	1.63	Duroc-up
EFHA2	SNOWBALL_018974_st	EF-hand domain family, member A2	6.222	5.647	1.350E-03	2.08E-02	1.49	Duroc-up
P4HB	SNOWBALL_022137_st	prolyl 4-hydroxylase, beta polypeptide	6.642	7.066	1.353E-03	2.08E-02	-1.34	PiNN-up
TAF6	SNOWBALL_037543_st	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	6.792	7.088	1.355E-03	2.08E-02	-1.23	PiNN-up
LOC100515086	SNOWBALL_027634_st	Ssc_hash_S18548122 BX916773 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0035.j.21 5prim, mRNA	3.255	2.883	1.357E-03	2.08E-02	1.29	Duroc-up
RLF	SNOWBALL_008916_st	rearranged L-myc fusion	7.386	6.947	1.353E-03	2.08E-02	1.36	Duroc-up
SNX4	SNOWBALL_021844_st	sorting nexin 4	5.036	4.490	1.357E-03	2.08E-02	1.46	Duroc-up
FAM118A	SNOWBALL_006707_st	family with sequence similarity 118, member A	6.130	6.432	1.367E-03	2.08E-02	-1.23	PiNN-up
ZBTB5	SNOWBALL_004010_st	zinc finger and BTB domain containing 5	6.340	6.565	1.366E-03	2.08E-02	-1.17	PiNN-up
LOC100513915	SNOWBALL_035391_st	Ssc_hash_S31121510 1544279 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	6.565	6.159	1.366E-03	2.08E-02	1.33	Duroc-up
PDS5A	SNOWBALL_022165_st	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	6.758	6.266	1.365E-03	2.08E-02	1.41	Duroc-up
ARRDC4	SNOWBALL_001498_st	arrestin domain containing 4	6.173	5.665	1.368E-03	2.08E-02	1.42	Duroc-up
UBXN7	SNOWBALL_031415_st	UBX domain protein 7	4.795	4.112	1.363E-03	2.08E-02	1.60	Duroc-up
HDGFRP3	SNOWBALL_010717_st	hepatoma-derived growth factor, related protein 3	6.434	6.107	1.371E-03	2.08E-02	1.25	Duroc-up
KLHL24	SNOWBALL_015924_st	kelch-like 24 (Drosophila)	9.655	9.169	1.370E-03	2.08E-02	1.40	Duroc-up

DYNC2H1	SNOWBALL_012440_st	dynein, cytoplasmic 2, heavy chain 1	4.606	4.278	1.374E-03	2.09E-02	1.26	Duroc-up
RN7SK	SNOWBALL_011073_x_st	7SK RNA [Source: RFAM;Acc:RF00100]	9.523	9.632	1.381E-03	2.09E-02	-1.08	PiNN-up
	SNOWBALL_032881_st	Ssc_hash_S17516219 BX670788 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0033.o.06 3prim, mRNA	9.800	9.322	1.381E-03	2.09E-02	1.39	Duroc-up
FAM164A	SNOWBALL_005713_st	family with sequence similarity 164, member A	5.579	4.966	1.387E-03	2.10E-02	1.53	Duroc-up
RPRD1A	SNOWBALL_042692_st	regulation of nuclear pre-mRNA domain containing 1A	6.407	5.857	1.389E-03	2.10E-02	1.46	Duroc-up
ABCC5	SNOWBALL_016156_st	ATP-binding cassette, sub-family C (CFTR/MRP), member 5	7.390	7.755	1.390E-03	2.10E-02	-1.29	PiNN-up
C4orf32	SNOWBALL_011711_st	chromosome 4 open reading frame 32	5.861	5.103	1.397E-03	2.11E-02	1.69	Duroc-up
SFRS18	SNOWBALL_037510_st	splicing factor, arginine/serine-rich 18	8.826	8.506	1.398E-03	2.11E-02	1.25	Duroc-up
LOC100520850	SNOWBALL_021397_st	Sus scrofa mRNA, clone:MLN010030D12, expressed in mesenteric lymph nodes	6.141	6.402	1.402E-03	2.11E-02	-1.20	PiNN-up
ATF2	SNOWBALL_018015_st	activating transcription factor 2	7.438	7.205	1.402E-03	2.11E-02	1.18	Duroc-up
REL	SNOWBALL_000694_st	v-rel reticuloendotheliosis viral oncogene homolog (avian)	5.904	5.413	1.402E-03	2.11E-02	1.40	Duroc-up
COLEC12	SNOWBALL_043349_st	collectin sub-family member 12	7.358	7.814	1.404E-03	2.11E-02	-1.37	PiNN-up
GPR107	SNOWBALL_003503_st	G protein-coupled receptor 107	6.677	7.032	1.407E-03	2.11E-02	-1.28	PiNN-up
JMY	SNOWBALL_032330_st	junction mediating and regulatory protein, p53 cofactor	5.948	5.488	1.407E-03	2.11E-02	1.38	Duroc-up
	SNOWBALL_044635_st		5.090	5.651	1.411E-03	2.12E-02	-1.48	PiNN-up
SRF	SNOWBALL_009984_s_st	serum response factor-like	8.366	8.649	1.411E-03	2.12E-02	-1.22	PiNN-up
PPP1R12A	SNOWBALL_007822_st	protein phosphatase 1, regulatory (inhibitor) subunit 12A	6.763	6.463	1.413E-03	2.12E-02	1.23	Duroc-up
LRRN3	SNOWBALL_000597_st	leucine rich repeat neuronal 3	3.537	3.135	1.414E-03	2.12E-02	1.32	Duroc-up
RLF	SNOWBALL_033329_st	rearranged L-myc fusion	4.764	4.214	1.414E-03	2.12E-02	1.46	Duroc-up
RARRES2	SNOWBALL_021040_s_st	retinoic acid receptor responder (tazarotene induced) 2	6.083	6.393	1.421E-03	2.12E-02	-1.24	PiNN-up
TMPO	SNOWBALL_007801_st	thymopoietin	6.919	6.596	1.422E-03	2.12E-02	1.25	Duroc-up
LOC100517404	SNOWBALL_009377_st	protein TRS85 homolog	8.225	7.826	1.419E-03	2.12E-02	1.32	Duroc-up
GMFB	SNOWBALL_003164_st	glia maturation factor, beta	5.292	4.872	1.422E-03	2.12E-02	1.34	Duroc-up
ZNF839	SNOWBALL_011069_st	zinc finger protein 839	6.254	6.501	1.427E-03	2.13E-02	-1.19	PiNN-up
GOSR1	SNOWBALL_031338_st	golgi SNAP receptor complex member 1	5.932	5.381	1.430E-03	2.13E-02	1.47	Duroc-up
LOC100526182	SNOWBALL_033994_st	Ssc_hash_S6015093 362211 MARC 1PIG Sus scrofa cDNA 5prime, mRNA	6.588	6.034	1.430E-03	2.13E-02	1.47	Duroc-up

AR	SNOWBALL_037187_st	Ssc_hash_S50206475 susfleck_AF_N_52_G05 SUSFLECK Abdominal Fat Normalized Sus scrofa cDNA clone 52_G05, mRNA	6.229	5.620	1.435E-03	2.13E-02	1.53	Duroc-up
MMRN2	SNOWBALL_016909_s_st	multimerin 2	6.112	6.341	1.440E-03	2.13E-02	-1.17	PiNN-up
ARL15	SNOWBALL_018636_st	ADP-ribosylation factor-like protein 15-like	7.365	6.993	1.438E-03	2.13E-02	1.29	Duroc-up
MYO9A	SNOWBALL_002924_st	myosin IXA	7.507	6.965	1.439E-03	2.13E-02	1.46	Duroc-up
ANKRD12	SNOWBALL_009235_st	ankyrin repeat domain 12	7.409	6.829	1.440E-03	2.13E-02	1.49	Duroc-up
LOC152217	SNOWBALL_015984_st	hypothetical LOC152217	7.274	7.656	1.444E-03	2.14E-02	-1.30	PiNN-up
COG8	SNOWBALL_007985_st	component of oligomeric golgi complex 8	7.069	7.292	1.447E-03	2.14E-02	-1.17	PiNN-up
ZNF432	SNOWBALL_008504_st	zinc finger protein 432	5.363	4.845	1.449E-03	2.14E-02	1.43	Duroc-up
XRN1	SNOWBALL_015743_s_st	5'-3' exoribonuclease 1	6.558	6.039	1.450E-03	2.14E-02	1.43	Duroc-up
PPIL2	SNOWBALL_024184_s_st	peptidylprolyl isomerase (cyclophilin)-like 2	6.542	6.859	1.453E-03	2.14E-02	-1.25	PiNN-up
ALG2	SNOWBALL_003750_st	asparagine-linked glycosylation 2, alpha-1,3-mannosyltransferase homolog (S. cerevisiae)	6.138	6.435	1.456E-03	2.15E-02	-1.23	PiNN-up
ZNF740	SNOWBALL_006944_st	zinc finger protein 740	6.128	6.468	1.467E-03	2.15E-02	-1.27	PiNN-up
COL6A2	SNOWBALL_036068_st	collagen, type VI, alpha 2	7.758	8.058	1.462E-03	2.15E-02	-1.23	PiNN-up
MANBAL	SNOWBALL_040098_st	mannosidase, beta A, lysosomal-like	5.322	5.545	1.460E-03	2.15E-02	-1.17	PiNN-up
TAF4	SNOWBALL_031097_st	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	7.511	7.665	1.465E-03	2.15E-02	-1.11	PiNN-up
KPNA3	SNOWBALL_013829_s_st	karyopherin alpha 3 (importin alpha 4)	10.652	10.355	1.467E-03	2.15E-02	1.23	Duroc-up
PTAR1	SNOWBALL_002994_st	protein prenyltransferase alpha subunit repeat containing 1	7.330	6.974	1.463E-03	2.15E-02	1.28	Duroc-up
AKR1A1	SNOWBALL_020933_s_st	aldo-keto reductase family 1, member A1 (aldehyde reductase)	5.903	5.378	1.465E-03	2.15E-02	1.44	Duroc-up
GSK3A	SNOWBALL_028610_st	glycogen synthase kinase 3 alpha	3.748	4.256	1.469E-03	2.15E-02	-1.42	PiNN-up
FAM160B1	SNOWBALL_024790_st	PREDICTED: Sus scrofa similar to Uncharacterized protein KIAA1600 (LOC100153060), mRNA	7.732	7.415	1.468E-03	2.15E-02	1.25	Duroc-up
SF3B4	SNOWBALL_006616_st	splicing factor 3b, subunit 4, 49kDa	6.107	6.447	1.470E-03	2.15E-02	-1.27	PiNN-up
SH3GLB2	SNOWBALL_003662_st	SH3-domain GRB2-like endophilin B2	6.127	6.535	1.474E-03	2.15E-02	-1.33	PiNN-up
SLC30A9	SNOWBALL_011415_s_st	solute carrier family 30 (zinc transporter), member 9	7.507	6.963	1.480E-03	2.16E-02	1.46	Duroc-up
EPC2	SNOWBALL_017661_st	enhancer of polycomb homolog 2 (Drosophila)	6.413	5.861	1.483E-03	2.16E-02	1.47	Duroc-up
MECP2	SNOWBALL_020634_st	methyl CpG binding protein 2 (Rett syndrome)	6.669	6.889	1.485E-03	2.16E-02	-1.16	PiNN-up
ATP11C	SNOWBALL_001945_st	ATPase, class VI, type 11C	5.778	5.309	1.486E-03	2.16E-02	1.38	Duroc-up
CRISPLD2	SNOWBALL_007878_st	cysteine-rich secretory protein LCCL domain containing 2	6.365	6.689	1.492E-03	2.17E-02	-1.25	PiNN-up
GGA1	SNOWBALL_047600_st	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	5.989	6.238	1.492E-03	2.17E-02	-1.19	PiNN-up

MPHOSPH9	SNOWBALL_016431_st	M-phase phosphoprotein 9	5.811	5.366	1.489E-03	2.17E-02	1.36	Duroc-up
NBN	SNOWBALL_005761_st	nibrin	6.152	5.683	1.492E-03	2.17E-02	1.38	Duroc-up
SNX2	SNOWBALL_025742_st	sorting nexin 2	6.906	6.404	1.495E-03	2.17E-02	1.42	Duroc-up
USP30	SNOWBALL_024311_s_st	ubiquitin specific peptidase 30	7.125	7.632	1.499E-03	2.17E-02	-1.42	PiNN-up
PTPN12	SNOWBALL_012694_st	protein tyrosine phosphatase, non-receptor type 12	6.342	6.005	1.500E-03	2.17E-02	1.26	Duroc-up
ATRX	SNOWBALL_020212_s_st	alpha thalassemia/mental retardation syndrome X-linked	6.102	5.520	1.502E-03	2.17E-02	1.50	Duroc-up
NFRKB	SNOWBALL_042477_st	nuclear factor related to kappaB binding protein	6.633	6.942	1.504E-03	2.17E-02	-1.24	PiNN-up
SLC38A4	SNOWBALL_022950_st	solute carrier family 38, member 4	5.866	4.731	1.505E-03	2.17E-02	2.20	Duroc-up
RC3H2	SNOWBALL_036488_st	ring finger and CCCH-type domains 2	6.598	6.055	1.507E-03	2.17E-02	1.46	Duroc-up
CNIH	SNOWBALL_025848_st	cornichon homolog (Drosophila)	5.575	5.179	1.508E-03	2.17E-02	1.32	Duroc-up
RBM12B	SNOWBALL_005741_st	RNA binding motif protein 12B	6.248	5.799	1.512E-03	2.18E-02	1.36	Duroc-up
LMBRD2	SNOWBALL_028933_st	LMBR1 domain containing 2	4.271	3.625	1.512E-03	2.18E-02	1.57	Duroc-up
ATRX	SNOWBALL_043032_st	alpha thalassemia/mental retardation syndrome X-linked	5.878	5.368	1.517E-03	2.18E-02	1.42	Duroc-up
SNX6	SNOWBALL_047372_st	sorting nexin-6	6.532	5.883	1.517E-03	2.18E-02	1.57	Duroc-up
VCAM1	SNOWBALL_006538_st	vascular cell adhesion molecule 1	6.200	6.584	1.521E-03	2.18E-02	-1.30	PiNN-up
PLEKHM1	SNOWBALL_014405_st	pleckstrin homology domain containing, family M (with RUN domain) member 1	5.996	6.180	1.521E-03	2.18E-02	-1.14	PiNN-up
KLHL24	SNOWBALL_022020_st	Sus scrofa mRNA, clone:AMP010025C11, expressed in alveolar macrophages	8.773	8.018	1.519E-03	2.18E-02	1.69	Duroc-up
CCNT2	SNOWBALL_017685_s_st	cyclin T2	7.210	6.920	1.531E-03	2.19E-02	1.22	Duroc-up
CEP290	SNOWBALL_007510_s_st	centrosomal protein of 290 kDa-like	4.367	4.051	1.531E-03	2.19E-02	1.24	Duroc-up
	SNOWBALL_039392_st		4.208	3.659	1.531E-03	2.19E-02	1.46	Duroc-up
LOC100512504	SNOWBALL_034579_st	Ssc_hash_S23698123 1106795 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	4.922	4.118	1.531E-03	2.19E-02	1.75	Duroc-up
CCPG1	SNOWBALL_002380_st	cell cycle progression 1	8.202	7.398	1.532E-03	2.19E-02	1.75	Duroc-up
THRA	SNOWBALL_014562_st	thyroid hormone receptor, alpha (erythroblastic leukemia viral (v-erb-a) oncogene homolog, avian)	9.305	9.707	1.541E-03	2.20E-02	-1.32	PiNN-up
OPG	SNOWBALL_005586_s_st	tumor necrosis factor receptor superfamily, member 11b	6.893	7.554	1.547E-03	2.21E-02	-1.58	PiNN-up
C1QB	SNOWBALL_008804_st	Complement C1qB Fragment	6.232	6.695	1.549E-03	2.21E-02	-1.38	PiNN-up
SRP68	SNOWBALL_014155_st	signal recognition particle 68kDa	7.710	7.975	1.555E-03	2.21E-02	-1.20	PiNN-up
UTRN	SNOWBALL_002141_st	utrophin	6.846	6.481	1.561E-03	2.22E-02	1.29	Duroc-up
RNF185	SNOWBALL_024238_s_st	PREDICTED: Sus scrofa similar to ring finger protein 185, transcript variant 1 (LOC100157569), mRNA	6.921	7.350	1.571E-03	2.23E-02	-1.35	PiNN-up

PIGW	SNOWBALL_040195_st	phosphatidylinositol glycan anchor biosynthesis, class W	3.790	3.378	1.570E-03	2.23E-02	1.33	Duroc-up
SP3	SNOWBALL_017930_s_st	Sp3 transcription factor	7.937	7.626	1.573E-03	2.23E-02	1.24	Duroc-up
DCAF5	SNOWBALL_010518_st	DDB1 and CUL4 associated factor 5	9.441	9.929	1.580E-03	2.24E-02	-1.40	PiNN-up
ITSN1	SNOWBALL_039098_st	intersectin 1 (SH3 domain protein)	6.557	6.264	1.582E-03	2.24E-02	1.23	Duroc-up
ZCCHC6	SNOWBALL_000003_st	zinc finger, CCHC domain containing 6	6.465	6.031	1.582E-03	2.24E-02	1.35	Duroc-up
AMIGO1	SNOWBALL_038924_st	adhesion molecule with Ig-like domain 1	7.543	7.955	1.587E-03	2.24E-02	-1.33	PiNN-up
DDHD1	SNOWBALL_003268_st	DDHD domain containing 1	6.301	5.875	1.587E-03	2.24E-02	1.34	Duroc-up
TBL3	SNOWBALL_047312_st	transducin (beta)-like 3	3.179	3.359	1.594E-03	2.25E-02	-1.13	PiNN-up
GPM6B	SNOWBALL_023601_s_st	glycoprotein M6B	3.997	3.645	1.596E-03	2.25E-02	1.28	Duroc-up
KIAA1671	SNOWBALL_024298_st	PREDICTED: Sus scrofa similar to Uncharacterized protein KIAA1671 (LOC100154475), mRNA	8.171	8.425	1.601E-03	2.26E-02	-1.19	PiNN-up
ASB1	SNOWBALL_042239_s_st	ankyrin repeat and SOCS box containing 1	6.908	7.385	1.603E-03	2.26E-02	-1.39	PiNN-up
DDR1	SNOWBALL_001164_s_st	OTTSUSG00000001299 discoidin domain receptor family, member 1	5.938	6.315	1.607E-03	2.26E-02	-1.30	PiNN-up
ETNK1	SNOWBALL_030632_st	Ssc_hash_S19545927 951368 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.329	4.644	1.606E-03	2.26E-02	1.61	Duroc-up
PDE4D	SNOWBALL_030982_st	phosphodiesterase 4D, cAMP-specific	6.608	5.890	1.607E-03	2.26E-02	1.64	Duroc-up
ACACB	SNOWBALL_024312_st	PREDICTED: Sus scrofa similar to Acetyl-CoA carboxylase 2 (ACC-beta) (LOC100154993), mRNA	7.631	8.116	1.609E-03	2.26E-02	-1.40	PiNN-up
SEL1L	SNOWBALL_033563_st	sel-1 suppressor of lin-12-like (C. elegans)	7.547	6.982	1.610E-03	2.26E-02	1.48	Duroc-up
LOC100523712	SNOWBALL_037099_st	Ssc_hash_S29969549 PDUts1027C02 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1027C02 5prime, mRNA	5.149	5.615	1.624E-03	2.27E-02	-1.38	PiNN-up
BCL9	SNOWBALL_006399_st	B-cell CLL/lymphoma 9	6.246	6.513	1.625E-03	2.27E-02	-1.20	PiNN-up
SLC38A2	SNOWBALL_044960_st	solute carrier family 38, member 2	3.863	3.671	1.623E-03	2.27E-02	1.14	Duroc-up
DTWD1	SNOWBALL_002763_st	DTW domain containing 1	5.630	5.092	1.625E-03	2.27E-02	1.45	Duroc-up
PLOD2	SNOWBALL_035014_st	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	5.736	4.756	1.626E-03	2.27E-02	1.97	Duroc-up
ARRDC4	SNOWBALL_001499_s_st	arrestin domain containing 4	6.008	5.555	1.628E-03	2.27E-02	1.37	Duroc-up
POLR1E	SNOWBALL_003768_st	polymerase (RNA) I polypeptide E, 53kDa	6.445	6.761	1.631E-03	2.28E-02	-1.25	PiNN-up
TPX2	SNOWBALL_021785_s_st	TPX2, microtubule-associated, homolog (Xenopus laevis)	5.183	4.612	1.632E-03	2.28E-02	1.49	Duroc-up
PPP5C	SNOWBALL_008214_st	protein phosphatase 5, catalytic subunit	6.314	6.496	1.634E-03	2.28E-02	-1.13	PiNN-up
ZNF829	SNOWBALL_016135_st	zinc finger protein 829	4.779	4.444	1.635E-03	2.28E-02	1.26	Duroc-up
FAM160B1	SNOWBALL_017042_s_st	family with sequence similarity 160, member B1	8.798	8.388	1.639E-03	2.28E-02	1.33	Duroc-up
RPAP3	SNOWBALL_027507_st	RNA polymerase II associated protein 3	7.067	6.601	1.639E-03	2.28E-02	1.38	Duroc-up

	SNOWBALL_031402_st	Ssc_hash_S31113340 1531061 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	4.776	5.323	1.654E-03	2.28E-02	-1.46	PiNN-up
ADPRHL1	SNOWBALL_035151_st	ADP-ribosylhydrolase like 1	8.669	9.097	1.650E-03	2.28E-02	-1.35	PiNN-up
BECN1	SNOWBALL_014387_st	beclin 1, autophagy related	8.265	8.660	1.647E-03	2.28E-02	-1.31	PiNN-up
LOC100515757	SNOWBALL_015614_st	fibulin-2-like	7.348	7.664	1.655E-03	2.28E-02	-1.24	PiNN-up
FAM127A	SNOWBALL_037401_st	protein FAM127-like	6.302	6.603	1.648E-03	2.28E-02	-1.23	PiNN-up
FAM134C	SNOWBALL_014352_st	family with sequence similarity 134, member C	6.640	6.924	1.648E-03	2.28E-02	-1.22	PiNN-up
MORC3	SNOWBALL_015911_st	MORC family CW-type zinc finger 3	5.823	5.409	1.655E-03	2.28E-02	1.33	Duroc-up
GTF3C6	SNOWBALL_002446_st	general transcription factor IIIC, polypeptide 6, alpha 35kDa	5.562	5.090	1.642E-03	2.28E-02	1.39	Duroc-up
KIF21A	SNOWBALL_007481_st	kinesin family member 21A	6.161	5.677	1.643E-03	2.28E-02	1.40	Duroc-up
MRPL1	SNOWBALL_011557_st	mitochondrial ribosomal protein L1	7.173	6.571	1.646E-03	2.28E-02	1.52	Duroc-up
	SNOWBALL_030380_st	Ssc_hash_S18551108 BX919759 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0008.g.13 5prim, mRNA	3.896	3.233	1.653E-03	2.28E-02	1.58	Duroc-up
TNIK	SNOWBALL_046640_st	TRAF2 and NCK interacting kinase	6.840	5.915	1.654E-03	2.28E-02	1.90	Duroc-up
LRRC41	SNOWBALL_009157_st	leucine rich repeat containing 41	6.793	7.079	1.658E-03	2.28E-02	-1.22	PiNN-up
LOC100512504	SNOWBALL_028279_st	Ssc_hash_S16514274 806268 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	4.274	3.457	1.661E-03	2.28E-02	1.76	Duroc-up
GSK3B	SNOWBALL_016204_st	glycogen synthase kinase 3 beta	8.711	8.414	1.672E-03	2.30E-02	1.23	Duroc-up
RASGEF1B	SNOWBALL_034789_st	RasGEF domain family, member 1B	6.585	5.937	1.674E-03	2.30E-02	1.57	Duroc-up
CMTM6	SNOWBALL_015200_st	CKLF-like MARVEL transmembrane domain containing 6	6.505	6.184	1.686E-03	2.31E-02	1.25	Duroc-up
	SNOWBALL_033597_st	Ssc_hash_S16514845 807386 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	4.671	5.183	1.698E-03	2.31E-02	-1.43	PiNN-up
ASB2	SNOWBALL_010198_st	ankyrin repeat and SOCS box containing 2	9.426	9.870	1.698E-03	2.31E-02	-1.36	PiNN-up
CCDC71	SNOWBALL_015331_st	coiled-coil domain containing 71	6.227	6.564	1.697E-03	2.31E-02	-1.26	PiNN-up
FBXO17	SNOWBALL_008055_st	F-box protein 17	6.229	6.466	1.699E-03	2.31E-02	-1.18	PiNN-up
TRIM28	SNOWBALL_021593_s_st	tripartite motif containing 28	7.549	7.770	1.689E-03	2.31E-02	-1.17	PiNN-up
VLDLR	SNOWBALL_003098_st	very low density lipoprotein receptor	9.900	9.728	1.691E-03	2.31E-02	1.13	Duroc-up
ARMCX5	SNOWBALL_020439_st	armadillo repeat containing, X-linked 5	5.060	4.652	1.694E-03	2.31E-02	1.33	Duroc-up
SMARCA5	SNOWBALL_023005_s_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	8.375	7.876	1.694E-03	2.31E-02	1.41	Duroc-up
UHMK1	SNOWBALL_036179_st	U2AF homology motif (UHM) kinase 1	6.625	6.066	1.698E-03	2.31E-02	1.47	Duroc-up
ZNF26	SNOWBALL_016338_s_st	zinc finger protein 26	6.245	5.681	1.702E-03	2.32E-02	1.48	Duroc-up
KRT75	SNOWBALL_007110_st	keratin 75	5.272	5.498	1.710E-03	2.32E-02	-1.17	PiNN-up
CEP57	SNOWBALL_012417_s_st	hypothetical protein LOC100518322	5.902	5.504	1.710E-03	2.32E-02	1.32	Duroc-up

SCLT1	SNOWBALL_011830_st	sodium channel and clathrin linker 1	5.173	4.520	1.707E-03	2.32E-02	1.57	Duroc-up
DNM1L	SNOWBALL_035928_st	dynamin 1-like	6.265	5.237	1.710E-03	2.32E-02	2.04	Duroc-up
RNF13	SNOWBALL_026466_s_st	ring finger protein 13	7.950	7.433	1.715E-03	2.33E-02	1.43	Duroc-up
KCNN3	SNOWBALL_042313_st	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	5.974	5.383	1.716E-03	2.33E-02	1.51	Duroc-up
DPP4	SNOWBALL_000370_st	dipeptidyl-peptidase 4	6.068	5.582	1.736E-03	2.35E-02	1.40	Duroc-up
SPOPL	SNOWBALL_017669_s_st	speckle-type POZ protein-like	8.915	8.352	1.737E-03	2.35E-02	1.48	Duroc-up
HIGD2A	SNOWBALL_021738_s_st	HIG1 hypoxia inducible domain family, member 2A	5.254	5.607	1.741E-03	2.35E-02	-1.28	PiNN-up
GSDMB	SNOWBALL_014519_s_st	ORM1-like protein 3-like	6.065	6.428	1.744E-03	2.36E-02	-1.29	PiNN-up
TMEM11	SNOWBALL_027611_st	transmembrane protein 11	7.442	7.928	1.746E-03	2.36E-02	-1.40	PiNN-up
SON	SNOWBALL_034189_st	SON DNA binding protein	6.205	5.368	1.746E-03	2.36E-02	1.79	Duroc-up
NUDT7	SNOWBALL_007907_st	nudix (nucleoside diphosphate linked moiety X)-type motif 7	6.419	6.805	1.752E-03	2.36E-02	-1.31	PiNN-up
ZZZ3	SNOWBALL_009206_st	zinc finger, ZZ-type containing 3	7.513	7.105	1.753E-03	2.36E-02	1.33	Duroc-up
ZC3H8	SNOWBALL_004696_st	zinc finger CCCH-type containing 8	5.682	5.200	1.753E-03	2.36E-02	1.40	Duroc-up
FEM1B	SNOWBALL_031297_st	fem-1 homolog b (C. elegans)	7.087	6.419	1.751E-03	2.36E-02	1.59	Duroc-up
LOC100151784	SNOWBALL_034591_st	Ssc_hash_S19540375 943873 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	7.306	6.563	1.757E-03	2.36E-02	1.67	Duroc-up
MAMLD1	SNOWBALL_020686_st	mastermind-like domain containing 1	5.854	6.212	1.767E-03	2.36E-02	-1.28	PiNN-up
DLG5	SNOWBALL_000329_st	discs, large homolog 5 (Drosophila)	6.503	6.813	1.764E-03	2.36E-02	-1.24	PiNN-up
Prdm2	SNOWBALL_038755_st	PR domain containing 2, with ZNF domain	8.037	8.296	1.767E-03	2.36E-02	-1.20	PiNN-up
GUCY1A2	SNOWBALL_039174_st	guanylate cyclase 1, soluble, alpha 2	4.945	4.527	1.768E-03	2.36E-02	1.34	Duroc-up
PARG	SNOWBALL_024649_st	PREDICTED: Sus scrofa similar to poly(ADP-ribose) glycohydrolase (LOC100158204), mRNA	5.988	5.497	1.767E-03	2.36E-02	1.41	Duroc-up
CCNT2	SNOWBALL_036468_st	cyclin T2	6.545	5.796	1.767E-03	2.36E-02	1.68	Duroc-up
mir-2366	bta-mir-2366_st	MI0011397	6.602	6.202	1.772E-03	2.37E-02	1.32	Duroc-up
RPS23	SNOWBALL_001668_s_st	OTTSUSG00000001875 ribosomal protein S23 (RPS23) pseudogene	7.423	8.206	1.779E-03	2.37E-02	-1.72	PiNN-up
LOC721475	SNOWBALL_041987_st	hypothetical protein LOC100156282	4.428	4.665	1.779E-03	2.37E-02	-1.18	PiNN-up
ERO1L	SNOWBALL_023306_s_st	ERO1-like (S. cerevisiae)	5.367	5.010	1.779E-03	2.37E-02	1.28	Duroc-up
	SNOWBALL_036079_st	Ssc_hash_S34525268 DB799544 full-length enriched swine cDNA library, adult immature dendritic cell Sus scrofa cDNA clone DCI010113A04 5prime, mRNA	3.886	3.283	1.779E-03	2.37E-02	1.52	Duroc-up
UTRN	SNOWBALL_030113_st	utrophin	5.708	4.976	1.775E-03	2.37E-02	1.66	Duroc-up
GPS1	SNOWBALL_025440_st	G protein pathway suppressor 1	7.954	8.344	1.787E-03	2.37E-02	-1.31	PiNN-up
BIRC6	SNOWBALL_005122_s_st	baculoviral IAP repeat containing 6	7.437	7.107	1.785E-03	2.37E-02	1.26	Duroc-up
SRPK1	SNOWBALL_010008_s_st	SRSF protein kinase 1	7.592	7.147	1.786E-03	2.37E-02	1.36	Duroc-up

GNPDA2	SNOWBALL_011412_st	glucosamine-6-phosphate deaminase 2	5.868	5.307	1.787E-03	2.37E-02	1.48	Duroc-up
C11orf57	SNOWBALL_012500_s_st	uncharacterized protein C11orf57-like	6.327	5.679	1.791E-03	2.38E-02	1.57	Duroc-up
CYP2B6	SNOWBALL_008515_st	cytochrome P450, family 2, subfamily B, polypeptide 6	6.633	7.337	1.794E-03	2.38E-02	-1.63	PiNN-up
N4BP1	SNOWBALL_008067_st	NEDD4 binding protein 1	8.142	7.739	1.795E-03	2.38E-02	1.32	Duroc-up
PRUNE2	SNOWBALL_027558_st	prune homolog 2 (Drosophila)	6.800	6.026	1.796E-03	2.38E-02	1.71	Duroc-up
OPTN	SNOWBALL_021134_s_st	optineurin	10.437	9.935	1.798E-03	2.38E-02	1.42	Duroc-up
NLN	SNOWBALL_018543_st	neurolysin (metallopeptidase M3 family)	5.965	5.485	1.801E-03	2.38E-02	1.39	Duroc-up
SREK1IP1	SNOWBALL_022023_s_st	SREK1-interacting protein 1	5.313	4.538	1.806E-03	2.39E-02	1.71	Duroc-up
MAP3K3	SNOWBALL_000126_st	mitogen-activated protein kinase kinase kinase 3	7.377	7.607	1.813E-03	2.39E-02	-1.17	PiNN-up
SUV39H2	SNOWBALL_013475_st	suppressor of variegation 3-9 homolog 2 (Drosophila)	5.673	5.242	1.813E-03	2.39E-02	1.35	Duroc-up
FOXN2	SNOWBALL_004946_st	forkhead box N2	8.049	7.586	1.814E-03	2.39E-02	1.38	Duroc-up
ITGAV	SNOWBALL_047637_st	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)	5.100	4.192	1.811E-03	2.39E-02	1.88	Duroc-up
LOC100522353	SNOWBALL_021990_st	Sus scrofa mRNA, clone:SPL010027D01, expressed in spleen	5.402	5.634	1.822E-03	2.39E-02	-1.17	PiNN-up
CLEC16A	SNOWBALL_021315_st	C-type lectin domain family 16, member A	6.845	7.050	1.821E-03	2.39E-02	-1.15	PiNN-up
SFRS13A	SNOWBALL_027575_st	Ssc_hash_S34521072 DB797722 full-length enriched swine cDNA library, adult immature dendritic cell Sus scrofa cDNA clone DCI010092C10 5prime, mRNA	6.001	5.328	1.822E-03	2.39E-02	1.59	Duroc-up
SCAP	SNOWBALL_015271_s_st	Sterol regulatory element-binding protein cleavage-activating protein (SREBP cleavage-activating protein)(SCAP)	6.647	6.875	1.831E-03	2.40E-02	-1.17	PiNN-up
CASP8AP2	SNOWBALL_002224_st	CASP8-associated protein 2-like	5.292	4.867	1.831E-03	2.40E-02	1.34	Duroc-up
STAG2	SNOWBALL_023524_s_st	stromal antigen 2	7.498	6.992	1.831E-03	2.40E-02	1.42	Duroc-up
PPP3CA	SNOWBALL_025551_s_st	protein phosphatase 3, catalytic subunit, alpha isozyme	9.388	8.680	1.852E-03	2.43E-02	1.63	Duroc-up
	SNOWBALL_039173_st		5.785	4.964	1.856E-03	2.43E-02	1.77	Duroc-up
XPC	SNOWBALL_015583_st	xeroderma pigmentosum, complementation group C	5.649	5.833	1.864E-03	2.44E-02	-1.14	PiNN-up
QKI	SNOWBALL_047830_st	quaking homolog, KH domain RNA binding (mouse)	7.590	7.066	1.865E-03	2.44E-02	1.44	Duroc-up
DNAJC5	SNOWBALL_021175_st	DnaJ (Hsp40) homolog, subfamily C, member 5	8.870	9.173	1.870E-03	2.44E-02	-1.23	PiNN-up
KIAA0100	SNOWBALL_041601_st	transcription elongation factor SPT6-like	9.019	9.331	1.878E-03	2.45E-02	-1.24	PiNN-up
ARX	SNOWBALL_029905_st	aristaless related homeobox	6.812	7.185	1.880E-03	2.45E-02	-1.30	PiNN-up
MYST2	SNOWBALL_014494_s_st	MYST histone acetyltransferase 2	7.567	7.833	1.888E-03	2.46E-02	-1.20	PiNN-up
CHORDC1	SNOWBALL_012422_st	cysteine and histidine-rich domain (CHORD) containing 1	8.270	7.527	1.896E-03	2.47E-02	1.67	Duroc-up

STAUFEN	SNOWBALL_005652_s_st	RNA binding protein homolog Fragment [Source:UniProtKB/TrEMBL;Acc:Q50HU4]	6.083	5.564	1.900E-03	2.47E-02	1.43	Duroc-up
GTF3A	SNOWBALL_013729_st	general transcription factor IIIA	6.083	6.547	1.908E-03	2.48E-02	-1.38	PiNN-up
RPS9	SNOWBALL_013488_st	ribosomal protein S9	9.832	10.271	1.910E-03	2.48E-02	-1.36	PiNN-up
CCDC97	SNOWBALL_030056_st	coiled-coil domain containing 97	5.357	5.701	1.911E-03	2.48E-02	-1.27	PiNN-up
INADL	SNOWBALL_027292_st	InaD-like (Drosophila)	7.242	6.654	1.910E-03	2.48E-02	1.50	Duroc-up
ZBED6	SNOWBALL_012564_st	zinc finger BED domain-containing protein 6-like	9.917	9.534	1.918E-03	2.49E-02	1.30	Duroc-up
KLHL31	SNOWBALL_010066_st	kelch-like 31 (Drosophila)	11.033	10.848	1.923E-03	2.49E-02	1.14	Duroc-up
KRTCAP2	SNOWBALL_006124_s_st	keratinocyte associated protein 2	7.703	8.083	1.940E-03	2.51E-02	-1.30	PiNN-up
MTHFD1	SNOWBALL_010618_st	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1, methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase	8.080	8.442	1.945E-03	2.51E-02	-1.29	PiNN-up
AMIGO1	SNOWBALL_038058_st	adhesion molecule with Ig-like domain 1	6.508	6.820	1.945E-03	2.51E-02	-1.24	PiNN-up
CASC4	SNOWBALL_003158_st	cancer susceptibility candidate 4	7.145	6.750	1.937E-03	2.51E-02	1.31	Duroc-up
OBFC2A	SNOWBALL_023889_s_st	oligonucleotide/oligosaccharide-binding fold containing 2A	5.201	4.668	1.938E-03	2.51E-02	1.45	Duroc-up
MAP4K3	SNOWBALL_005118_st	mitogen-activated protein kinase kinase kinase kinase 3-like	6.861	6.325	1.945E-03	2.51E-02	1.45	Duroc-up
C10orf84	SNOWBALL_016996_st	chromosome 10 open reading frame 84	4.758	4.102	1.944E-03	2.51E-02	1.58	Duroc-up
FAM171A1	SNOWBALL_013528_st	family with sequence similarity 171, member A1	6.294	6.508	1.948E-03	2.51E-02	-1.16	PiNN-up
MDFIC	SNOWBALL_019899_st	MyoD family inhibitor domain containing	6.354	5.869	1.947E-03	2.51E-02	1.40	Duroc-up
CH242-124P4.2	SNOWBALL_001902_st	OTTSUSG00000000986 putative novel transcript	4.827	4.587	1.956E-03	2.51E-02	1.18	Duroc-up
WDHD1	SNOWBALL_002773_st	WD repeat and HMG-box DNA binding protein 1	3.759	3.462	1.956E-03	2.51E-02	1.23	Duroc-up
TMEM45A	SNOWBALL_005939_st	transmembrane protein 45A	9.712	9.365	1.954E-03	2.51E-02	1.27	Duroc-up
CCDC132	SNOWBALL_012515_st	coiled-coil domain containing 132	6.938	6.242	1.957E-03	2.51E-02	1.62	Duroc-up
ZNF25	SNOWBALL_017178_st	zinc finger protein 25	5.890	5.163	1.958E-03	2.51E-02	1.66	Duroc-up
MMP2	SNOWBALL_022948_st	matrix metallopeptidase 2 (gelatinase A, 72kDa gelatinase, 72kDa type IV collagenase)	7.108	7.489	1.961E-03	2.51E-02	-1.30	PiNN-up
	SNOWBALL_046915_st		4.869	5.324	1.963E-03	2.52E-02	-1.37	PiNN-up
FAM73A	SNOWBALL_009178_st	family with sequence similarity 73, member A	6.134	5.700	1.968E-03	2.52E-02	1.35	Duroc-up
CDK19	SNOWBALL_026387_st	cyclin-dependent kinase 19	6.118	5.668	1.967E-03	2.52E-02	1.37	Duroc-up
ASAH1	SNOWBALL_018994_s_st	acid ceramidase-like	6.541	6.966	1.974E-03	2.52E-02	-1.34	PiNN-up
C1orf109	SNOWBALL_033229_st	chromosome 1 open reading frame 109	5.392	5.669	1.975E-03	2.52E-02	-1.21	PiNN-up
KITLG	SNOWBALL_007554_st	KIT ligand	4.863	4.458	1.976E-03	2.52E-02	1.32	Duroc-up
LOC100156275	SNOWBALL_005730_s_st	receptor-binding cancer antigen expressed on SiSo cells-like	6.719	6.284	1.974E-03	2.52E-02	1.35	Duroc-up

MOBKL3	SNOWBALL_018118_st	MOB1, Mps One Binder kinase activator-like 3 (yeast)	7.411	6.931	1.976E-03	2.52E-02	1.39	Duroc-up
TMX3	SNOWBALL_003318_st	thioredoxin-related transmembrane protein 3	7.861	7.435	1.978E-03	2.52E-02	1.34	Duroc-up
SMARCD2	SNOWBALL_014333_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	6.053	6.308	1.981E-03	2.52E-02	-1.19	PiNN-up
RAB10	SNOWBALL_005133_st	RAB10, member RAS oncogene family	9.267	8.917	1.983E-03	2.52E-02	1.27	Duroc-up
LAGE3	SNOWBALL_014661_s_st	L antigen family, member 3	5.676	5.951	1.985E-03	2.52E-02	-1.21	PiNN-up
NUFIP2	SNOWBALL_040013_st	nuclear fragile X mental retardation protein interacting protein 2	6.224	5.687	1.993E-03	2.53E-02	1.45	Duroc-up
FZD4	SNOWBALL_025435_st	frizzled homolog 4 (Drosophila)	6.283	6.694	1.997E-03	2.53E-02	-1.33	PiNN-up
ELL	SNOWBALL_040239_st	elongation factor RNA polymerase II	6.288	6.580	1.997E-03	2.53E-02	-1.22	PiNN-up
DHX29	SNOWBALL_018633_st	DEAH (Asp-Glu-Ala-His) box polypeptide 29	6.813	6.110	1.994E-03	2.53E-02	1.63	Duroc-up
NFKBIL1	SNOWBALL_001209_st	OTTSUSG00000001320 nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor-like 1	6.184	6.444	2.000E-03	2.53E-02	-1.20	PiNN-up
GAA	SNOWBALL_014130_st	glucosidase, alpha; acid	6.223	6.484	2.001E-03	2.53E-02	-1.20	PiNN-up
NEB	SNOWBALL_024018_st	nebulin	12.911	12.770	2.006E-03	2.53E-02	1.10	Duroc-up
Smarca2	SNOWBALL_023007_s_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	9.181	8.830	2.004E-03	2.53E-02	1.28	Duroc-up
BRWD1	SNOWBALL_032731_st	bromodomain and WD repeat domain containing 1	7.207	6.721	2.006E-03	2.53E-02	1.40	Duroc-up
EXOSC9	SNOWBALL_011824_st	exosome component 9	8.472	8.090	2.014E-03	2.54E-02	1.30	Duroc-up
CYP51A1	SNOWBALL_012601_st	cytochrome P450, family 51, subfamily A, polypeptide 1	5.807	5.375	2.015E-03	2.54E-02	1.35	Duroc-up
	SNOWBALL_039564_st		5.713	5.047	2.014E-03	2.54E-02	1.59	Duroc-up
INPP4A	SNOWBALL_004613_s_st	inositol polyphosphate-4-phosphatase, type I, 107kDa	6.924	7.196	2.020E-03	2.54E-02	-1.21	PiNN-up
BAT2	SNOWBALL_001232_s_st	OTTSUSG00000001328 HLA-B associated transcript 2	7.669	7.945	2.024E-03	2.55E-02	-1.21	PiNN-up
MRPS18A	SNOWBALL_009860_s_st	mitochondrial ribosomal protein S18A	6.285	6.753	2.030E-03	2.55E-02	-1.38	PiNN-up
TCF4	SNOWBALL_002386_st	transcription factor 4	7.926	7.587	2.030E-03	2.55E-02	1.27	Duroc-up
VPS8	SNOWBALL_029583_st	vacuolar protein sorting 8 homolog (S. cerevisiae)	6.614	6.239	2.031E-03	2.55E-02	1.30	Duroc-up
ZDHHC2	SNOWBALL_023834_st	PREDICTED: Sus scrofa similar to Palmitoyltransferase ZDHHC2 (Zinc finger DHHC domain-containing protein 2) (DHHC-2) (LOC100155681), mRNA	5.781	5.266	2.031E-03	2.55E-02	1.43	Duroc-up
U6	SNOWBALL_015993_st	U6 spliceosomal RNA [Source: RFAM;Acc:RF00026]	4.808	4.066	2.037E-03	2.55E-02	1.67	Duroc-up
MTHFD2L	SNOWBALL_011548_st	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	6.568	6.922	2.039E-03	2.56E-02	-1.28	PiNN-up

RYBP	SNOWBALL_035593_st	Ssc_hash_S29967747 PDUts1005D07 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1005D07 5prime similar to homologue to ref	4.177	3.721	2.046E-03	2.56E-02	1.37	Duroc-up
LOC100512583	SNOWBALL_034343_st	Ssc_hash_S26711180 AJ947264 KN404_1 Sus scrofa cDNA clone C0007739n12 3prime, mRNA	7.109	7.645	2.053E-03	2.56E-02	-1.45	PiNN-up
ANKRD52	SNOWBALL_006992_st	ankyrin repeat domain 52	7.530	7.848	2.050E-03	2.56E-02	-1.25	PiNN-up
PHC2	SNOWBALL_047495_st	polyhomeotic homolog 2 (Drosophila)	6.752	6.988	2.050E-03	2.56E-02	-1.18	PiNN-up
SHOC2	SNOWBALL_024813_st	soc-2 suppressor of clear homolog (C. elegans)	7.005	6.520	2.053E-03	2.56E-02	1.40	Duroc-up
TNIK	SNOWBALL_027610_st	TRAF2 and NCK interacting kinase	4.990	4.023	2.054E-03	2.56E-02	1.95	Duroc-up
PRRC2C	SNOWBALL_013054_st	proline-rich coiled-coil 2C	8.799	8.608	2.058E-03	2.57E-02	1.14	Duroc-up
STK3	SNOWBALL_005670_st	serine/threonine kinase 3	6.955	6.529	2.061E-03	2.57E-02	1.34	Duroc-up
ZC3H13	SNOWBALL_013834_st	zinc finger CCCH-type containing 13	7.170	6.797	2.064E-03	2.57E-02	1.30	Duroc-up
SLC30A5	SNOWBALL_021064_s_st	solute carrier family 30 (zinc transporter), member 5	6.545	6.119	2.072E-03	2.58E-02	1.34	Duroc-up
AFF4	SNOWBALL_039748_st	AF4/FMR2 family, member 4	3.613	3.393	2.075E-03	2.58E-02	1.16	Duroc-up
ZSWIM6	SNOWBALL_027508_st	zinc finger, SWIM-type containing 6	4.139	3.646	2.077E-03	2.58E-02	1.41	Duroc-up
NFIB	SNOWBALL_003181_st	nuclear factor I/B	8.849	8.408	2.079E-03	2.58E-02	1.36	Duroc-up
BCS1L	SNOWBALL_026568_st	BCS1-like (S. cerevisiae)	6.927	7.379	2.086E-03	2.58E-02	-1.37	PiNN-up
MAMLD1	SNOWBALL_036200_st	mastermind-like domain containing 1	4.801	5.232	2.084E-03	2.58E-02	-1.35	PiNN-up
ANKMY2	SNOWBALL_012822_st	ankyrin repeat and MYND domain containing 2	7.906	7.327	2.085E-03	2.58E-02	1.49	Duroc-up
PLCB4	SNOWBALL_023812_s_st	PREDICTED: Sus scrofa similar to phospholipase C beta 4 (LOC100153085), partial mRNA	6.625	5.975	2.085E-03	2.58E-02	1.57	Duroc-up
NEURL4	SNOWBALL_036041_st	neuralized homolog 4 (Drosophila)	4.422	4.705	2.090E-03	2.59E-02	-1.22	PiNN-up
42522	SNOWBALL_023403_st	interferon, alpha-inducible protein 6	5.922	6.499	2.103E-03	2.59E-02	-1.49	PiNN-up
SCARB2	SNOWBALL_034531_st	scavenger receptor class B, member 2	7.458	7.907	2.105E-03	2.59E-02	-1.36	PiNN-up
GYS1	SNOWBALL_008473_s_st	glycogen synthase 1 (muscle)	10.654	10.949	2.104E-03	2.59E-02	-1.23	PiNN-up
TFEB	SNOWBALL_009956_st	transcription factor EB	7.249	7.440	2.104E-03	2.59E-02	-1.14	PiNN-up
ZNF148	SNOWBALL_016173_st	zinc finger protein 148	7.466	7.025	2.096E-03	2.59E-02	1.36	Duroc-up
HMCN1	SNOWBALL_012908_st	hemicentin 1	5.842	5.371	2.105E-03	2.59E-02	1.39	Duroc-up
C13orf31	SNOWBALL_013867_st	chromosome 13 open reading frame 31	7.094	6.583	2.105E-03	2.59E-02	1.43	Duroc-up
SOS1	SNOWBALL_043045_st	son of sevenless homolog 1 (Drosophila)	6.314	5.676	2.099E-03	2.59E-02	1.56	Duroc-up
TAX1BP1	SNOWBALL_000598_st	Tax1 (human T-cell leukemia virus type I) binding protein 1	7.216	6.540	2.101E-03	2.59E-02	1.60	Duroc-up
TET2	SNOWBALL_030156_st	Ssc_hash_S18383383 934401 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.339	4.652	2.095E-03	2.59E-02	1.61	Duroc-up
USP19	SNOWBALL_015380_st	ubiquitin specific peptidase 19	6.835	7.118	2.107E-03	2.59E-02	-1.22	PiNN-up
OSBPL8	SNOWBALL_007291_st	oxysterol binding protein-like 8	7.128	6.439	2.108E-03	2.59E-02	1.61	Duroc-up

TIAL1	SNOWBALL_017093_s_st	TIA1 cytotoxic granule-associated RNA binding protein-like 1	7.140	6.786	2.118E-03	2.60E-02	1.28	Duroc-up
	SNOWBALL_031528_st	Ssc_hash_S29989431 PDUts2083H08 Porcine testis cDNA library II Sus scrofa cDNA clone PDUts2083H08 5prime, mRNA	4.963	5.160	2.120E-03	2.60E-02	-1.15	PiNN-up
ENO3	SNOWBALL_014754_st	enolase 3 (beta, muscle)	13.036	13.262	2.133E-03	2.61E-02	-1.17	PiNN-up
BOD1L	SNOWBALL_011290_st	biorientation of chromosomes in cell division 1-like	7.565	7.129	2.134E-03	2.61E-02	1.35	Duroc-up
SERBP1	SNOWBALL_047404_st	plasminogen activator inhibitor 1 RNA-binding protein-like	7.085	6.458	2.140E-03	2.62E-02	1.54	Duroc-up
ANKRD52	SNOWBALL_007071_s_st	ankyrin repeat domain 52	7.975	8.276	2.149E-03	2.62E-02	-1.23	PiNN-up
OXR1	SNOWBALL_035056_st	Ssc_hash_S40204141 ruio10_a4.y1 kid Sus scrofa cDNA 5prime, mRNA	6.487	5.694	2.148E-03	2.62E-02	1.73	Duroc-up
TBC1D23	SNOWBALL_021976_s_st	TBC1 domain family, member 23	7.202	6.896	2.157E-03	2.63E-02	1.24	Duroc-up
ELAC2	SNOWBALL_030789_st	Ssc_hash_S23700375 1110606 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	6.608	6.836	2.177E-03	2.65E-02	-1.17	PiNN-up
PPP2R5A	SNOWBALL_013177_st	protein phosphatase 2, regulatory subunit B', alpha	7.806	7.461	2.176E-03	2.65E-02	1.27	Duroc-up
AASDHPPT	SNOWBALL_012360_st	aminoadipate-semialdehyde dehydrogenase-phosphopantetheinyl transferase	5.688	5.336	2.175E-03	2.65E-02	1.28	Duroc-up
SYNPO2L	SNOWBALL_024443_st	synaptopodin 2-like	8.154	8.430	2.179E-03	2.65E-02	-1.21	PiNN-up
FARP1	SNOWBALL_014039_st	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	7.055	7.356	2.189E-03	2.66E-02	-1.23	PiNN-up
PIAS3	SNOWBALL_006515_st	protein inhibitor of activated STAT, 3	5.872	6.158	2.193E-03	2.66E-02	-1.22	PiNN-up
IPO9	SNOWBALL_013386_st	importin 9	7.459	7.712	2.195E-03	2.66E-02	-1.19	PiNN-up
MUL1	SNOWBALL_008759_st	mitochondrial ubiquitin ligase activator of NFKB 1-like	6.334	6.540	2.194E-03	2.66E-02	-1.15	PiNN-up
PIGQ	SNOWBALL_004778_st	phosphatidylinositol glycan anchor biosynthesis, class Q	5.911	6.105	2.188E-03	2.66E-02	-1.14	PiNN-up
BCAP29	SNOWBALL_045075_st	B-cell receptor-associated protein 29	5.981	5.395	2.192E-03	2.66E-02	1.50	Duroc-up
APOOL	SNOWBALL_023475_st	zinc finger protein 711	4.759	4.374	2.197E-03	2.66E-02	1.31	Duroc-up
DYT1	SNOWBALL_023029_s_st	Sus scrofa torsin A (DYT1) mRNA, complete cds	6.370	6.653	2.199E-03	2.66E-02	-1.22	PiNN-up
CASP10	SNOWBALL_022866_st	Sus scrofa CASP10 mRNA for caspase 10, complete cds	6.993	6.714	2.201E-03	2.66E-02	1.21	Duroc-up
ERRFI1	SNOWBALL_034410_st	ERBB receptor feedback inhibitor 1	5.885	6.338	2.205E-03	2.66E-02	-1.37	PiNN-up
UBE2D1	SNOWBALL_023169_s_st	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	10.537	10.130	2.204E-03	2.66E-02	1.33	Duroc-up
PURB	SNOWBALL_019830_st	purine-rich element binding protein B	7.802	7.994	2.207E-03	2.66E-02	-1.14	PiNN-up
MLXIP	SNOWBALL_036193_st	MLX interacting protein	8.208	8.495	2.212E-03	2.67E-02	-1.22	PiNN-up

RYBP	SNOWBALL_030452_st	RING1 and YY1 binding protein	5.100	4.648	2.213E-03	2.67E-02	1.37	Duroc-up
NFE2L1	SNOWBALL_014655_st	nuclear factor (erythroid-derived 2)-like 1	9.328	9.715	2.224E-03	2.68E-02	-1.31	PiNN-up
VCPIP1	SNOWBALL_032137_st	valosin containing protein (p97)/p47 complex interacting protein 1	6.081	5.381	2.222E-03	2.68E-02	1.62	Duroc-up
STYX	SNOWBALL_029762_st	serine/threonine/tyrosine interacting protein	5.135	4.420	2.223E-03	2.68E-02	1.64	Duroc-up
CAMTA2	SNOWBALL_014751_st	calmodulin binding transcription activator 2	6.843	7.099	2.226E-03	2.68E-02	-1.19	PiNN-up
SEC62	SNOWBALL_021020_s_st	SEC62 homolog (S. cerevisiae)	7.565	6.880	2.231E-03	2.68E-02	1.61	Duroc-up
TBCC	SNOWBALL_009870_s_st	tubulin folding cofactor C	8.042	8.484	2.248E-03	2.69E-02	-1.36	PiNN-up
DOCK8	SNOWBALL_002741_st	dedicator of cytokinesis 8	5.590	5.897	2.244E-03	2.69E-02	-1.24	PiNN-up
ILK	SNOWBALL_025602_s_st	integrin-linked kinase	7.511	7.815	2.247E-03	2.69E-02	-1.23	PiNN-up
RAPGEF1	SNOWBALL_003326_st	Rap guanine nucleotide exchange factor (GEF) 1	8.343	8.631	2.244E-03	2.69E-02	-1.22	PiNN-up
CHSY1	SNOWBALL_003130_st	chondroitin sulfate synthase 1	6.685	6.497	2.241E-03	2.69E-02	1.14	Duroc-up
VAMP4	SNOWBALL_012989_st	vesicle-associated membrane protein 4	5.925	5.627	2.251E-03	2.69E-02	1.23	Duroc-up
FMN1	SNOWBALL_002778_st	formin 1	5.586	5.151	2.237E-03	2.69E-02	1.35	Duroc-up
ATP13A3	SNOWBALL_047791_st	ATPase type 13A3	5.381	4.844	2.251E-03	2.69E-02	1.45	Duroc-up
MMADHC	SNOWBALL_027023_s_st	Sus scrofa clone Clu_12475.scr.msk.p1.Contig2, mRNA sequence	7.148	6.585	2.248E-03	2.69E-02	1.48	Duroc-up
CAND1	SNOWBALL_036890_st	cullin-associated and neddylation-dissociated 1	4.018	3.427	2.244E-03	2.69E-02	1.51	Duroc-up
VKORC1	SNOWBALL_004530_st	vitamin K epoxide reductase complex, subunit 1	7.243	7.569	2.252E-03	2.69E-02	-1.25	PiNN-up
LRRC47	SNOWBALL_037323_st	leucine rich repeat containing 47	5.785	6.136	2.258E-03	2.69E-02	-1.28	PiNN-up
STXBP3	SNOWBALL_006396_st	syntaxin binding protein 3	7.559	7.149	2.263E-03	2.70E-02	1.33	Duroc-up
TGFBR1	SNOWBALL_025740_s_st	transforming growth factor, beta receptor 1	6.205	5.621	2.285E-03	2.72E-02	1.50	Duroc-up
SLC41A1	SNOWBALL_040103_st	solute carrier family 41, member 1	7.041	7.452	2.288E-03	2.72E-02	-1.33	PiNN-up
RNF144A	SNOWBALL_022438_st	ring finger protein 144A	5.067	5.515	2.300E-03	2.73E-02	-1.36	PiNN-up
COL6A3	SNOWBALL_024026_st	collagen, type VI, alpha 3	6.761	7.190	2.297E-03	2.73E-02	-1.35	PiNN-up
DNAJB14	SNOWBALL_011738_st	DnaJ (Hsp40) homolog, subfamily B, member 14	5.164	4.768	2.301E-03	2.73E-02	1.32	Duroc-up
ZBTB1	SNOWBALL_010455_s_st	zinc finger and BTB domain containing 1	6.385	5.905	2.299E-03	2.73E-02	1.39	Duroc-up
PB103351.00.0	SNOWBALL_035129_st	Ssc_hash_S40156924 rhyp33c_p6.y1 hyp Sus scrofa cDNA 5prime, mRNA	7.765	7.062	2.301E-03	2.73E-02	1.63	Duroc-up
STAG2	SNOWBALL_020553_st	stromal antigen 2	7.592	7.105	2.304E-03	2.73E-02	1.40	Duroc-up
DUSP3	SNOWBALL_014369_st	dual specificity phosphatase 3	8.327	8.818	2.311E-03	2.73E-02	-1.41	PiNN-up
TGFBRAP1	SNOWBALL_047347_st	transforming growth factor, beta receptor associated protein 1	6.265	6.560	2.310E-03	2.73E-02	-1.23	PiNN-up
CBFA2T2	SNOWBALL_019277_st	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	6.743	7.027	2.312E-03	2.73E-02	-1.22	PiNN-up
PIGN	SNOWBALL_003313_st	phosphatidylinositol glycan anchor biosynthesis, class N	7.011	6.723	2.314E-03	2.73E-02	1.22	Duroc-up

OSBPL2	SNOWBALL_025655_st	oxysterol binding protein-like 2	6.294	6.881	2.319E-03	2.74E-02	-1.50	PiNN-up
NPRL3	SNOWBALL_004721_st	nitrogen permease regulator 3-like protein-like	5.870	6.184	2.330E-03	2.75E-02	-1.24	PiNN-up
CAND2	SNOWBALL_015695_st	cullin-associated and neddylation-dissociated 2 (putative)	8.321	8.552	2.332E-03	2.75E-02	-1.17	PiNN-up
ITCH	SNOWBALL_044148_st	itchy E3 ubiquitin protein ligase homolog (mouse)	4.822	4.402	2.330E-03	2.75E-02	1.34	Duroc-up
KIAA0247	SNOWBALL_010673_st	KIAA0247	6.105	6.381	2.338E-03	2.75E-02	-1.21	PiNN-up
zgc:136817	SNOWBALL_041865_st	zgc:136817	5.184	5.516	2.343E-03	2.76E-02	-1.26	PiNN-up
CILP	SNOWBALL_002993_s_st	Cartilage intermediate layer protein 1 Fragment (CILP-1) [Contains Cartilage intermediate layer protein 1 C2]	7.160	7.700	2.353E-03	2.77E-02	-1.45	PiNN-up
CLOCK	SNOWBALL_011599_st	clock homolog (mouse)	8.012	7.782	2.372E-03	2.79E-02	1.17	Duroc-up
TM9SF3	SNOWBALL_017436_s_st	transmembrane 9 superfamily member 3	8.235	7.908	2.375E-03	2.79E-02	1.25	Duroc-up
RNF141	SNOWBALL_021841_st	ring finger protein 141	7.500	7.053	2.376E-03	2.79E-02	1.36	Duroc-up
NUDCD1	SNOWBALL_005768_st	NudC domain containing 1	6.823	6.282	2.376E-03	2.79E-02	1.46	Duroc-up
RRAGD	SNOWBALL_029012_st	Ras-related GTP binding D	5.320	4.763	2.373E-03	2.79E-02	1.47	Duroc-up
NDUFS7	SNOWBALL_037404_st	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)	4.366	4.746	2.380E-03	2.79E-02	-1.30	PiNN-up
LOC100523549	SNOWBALL_005539_s_st	COMM domain-containing protein 5-like	5.709	5.992	2.381E-03	2.79E-02	-1.22	PiNN-up
CU468856.2	SNOWBALL_000245_st	OTTSUSG00000000786	8.883	9.127	2.382E-03	2.79E-02	-1.18	PiNN-up
CDC25B	SNOWBALL_021168_st	cell division cycle 25 homolog B (S. pombe)	5.289	5.650	2.389E-03	2.79E-02	-1.28	PiNN-up
EIF4A3	SNOWBALL_014141_s_st	eukaryotic translation initiation factor 4A3	7.267	7.587	2.389E-03	2.79E-02	-1.25	PiNN-up
BEST3	SNOWBALL_007206_st	bestrophin 3	7.619	7.208	2.393E-03	2.79E-02	1.33	Duroc-up
UCHL3	SNOWBALL_014014_s_st	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	8.669	8.246	2.394E-03	2.79E-02	1.34	Duroc-up
TMEM185A	SNOWBALL_020825_st	transmembrane protein 185A	6.795	7.219	2.398E-03	2.79E-02	-1.34	PiNN-up
ADRBK2	SNOWBALL_047165_st	adrenergic, beta, receptor kinase 2	4.102	3.749	2.396E-03	2.79E-02	1.28	Duroc-up
LOC100521180	SNOWBALL_034625_st	Ssc_hash_S40024521 reje18b_h2.y1 eje Sus scrofa cDNA 5prime, mRNA	6.289	6.501	2.400E-03	2.80E-02	-1.16	PiNN-up
IMP2	SNOWBALL_024324_s_st	PREDICTED: Sus scrofa similar to Signal peptide peptidase-like 3 (SPP-like 3 protein) (Intramembrane protease 2) (IMP2) (Presenilin-like protein 4) (LOC100153784), mRNA	6.511	6.897	2.412E-03	2.80E-02	-1.31	PiNN-up
CCDC149	SNOWBALL_031609_st	coiled-coil domain containing 149	6.494	6.850	2.407E-03	2.80E-02	-1.28	PiNN-up
CASC3	SNOWBALL_014666_st	cancer susceptibility candidate 3	7.609	7.946	2.414E-03	2.80E-02	-1.26	PiNN-up
ZKSCAN1	SNOWBALL_040348_st	zinc finger with KRAB and SCAN domains 1	5.597	5.255	2.414E-03	2.80E-02	1.27	Duroc-up
TBL1XR1	SNOWBALL_015613_st	transducin (beta)-like 1 X-linked receptor 1	9.213	8.862	2.403E-03	2.80E-02	1.28	Duroc-up
DDX21	SNOWBALL_024679_s_st	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	6.562	6.079	2.410E-03	2.80E-02	1.40	Duroc-up

ZFR	SNOWBALL_034800_st	zinc finger RNA binding protein	6.854	6.334	2.406E-03	2.80E-02	1.43	Duroc-up
SLC39A10	SNOWBALL_038164_st	solute carrier family 39 (zinc transporter), member 10	5.377	4.780	2.408E-03	2.80E-02	1.51	Duroc-up
DDX50	SNOWBALL_016963_s_st	DEAD (Asp-Glu-Ala-Asp) box polypeptide 50	5.633	5.330	2.428E-03	2.81E-02	1.23	Duroc-up
LOC100152991	SNOWBALL_027663_st	Ssc_hash_S27600602 EST-AR127A11 Infected Porcine Thymus cDNA library Sus scrofa cDNA clone AR127A11, mRNA	6.155	6.492	2.430E-03	2.81E-02	-1.26	PiNN-up
C7H1orf27	SNOWBALL_047556_st	odorant response abnormal 4	6.041	5.389	2.433E-03	2.81E-02	1.57	Duroc-up
C10orf118	SNOWBALL_047201_st	chromosome 10 open reading frame 118	6.063	5.518	2.437E-03	2.82E-02	1.46	Duroc-up
ERBB2	SNOWBALL_014480_st	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	6.357	6.768	2.450E-03	2.82E-02	-1.33	PiNN-up
HLA-A	SNOWBALL_022996_x_st	Sus scrofa MHC class I antigen (SLA-3) mRNA, SLA-3*Wu05 allele, partial cds	7.825	8.083	2.450E-03	2.82E-02	-1.20	PiNN-up
GSPT1	SNOWBALL_004623_st	G1 to S phase transition 1	8.358	8.068	2.448E-03	2.82E-02	1.22	Duroc-up
MGEA5	SNOWBALL_024875_s_st	meningioma expressed antigen 5 (hyaluronidase)	9.910	9.519	2.444E-03	2.82E-02	1.31	Duroc-up
STEAP4	SNOWBALL_012859_st	STEAP family member 4	5.024	4.560	2.441E-03	2.82E-02	1.38	Duroc-up
MSL2	SNOWBALL_045061_st	male-specific lethal 2 homolog (Drosophila)	4.224	3.698	2.450E-03	2.82E-02	1.44	Duroc-up
	SNOWBALL_035714_st	Ssc_hash_S19545684 951101 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	6.520	5.979	2.443E-03	2.82E-02	1.45	Duroc-up
SYS1	SNOWBALL_023642_s_st	PREDICTED: Sus scrofa similar to SYS1 Golgi-localized integral membrane protein homolog, transcript variant 1 (LOC100153558), mRNA	7.282	7.651	2.477E-03	2.84E-02	-1.29	PiNN-up
SDF2	SNOWBALL_015126_st	stromal cell-derived factor 2	5.771	6.130	2.474E-03	2.84E-02	-1.28	PiNN-up
CNNM3	SNOWBALL_004918_st	cyclin M3	6.177	6.345	2.474E-03	2.84E-02	-1.12	PiNN-up
MAPK8IP3	SNOWBALL_004651_st	mitogen-activated protein kinase 8 interacting protein 3	6.089	6.240	2.476E-03	2.84E-02	-1.11	PiNN-up
FBXL17	SNOWBALL_030918_st	F-box and leucine-rich repeat protein 17	5.231	4.640	2.474E-03	2.84E-02	1.51	Duroc-up
	SNOWBALL_032519_st	Ssc_hash_S22284237 CJ026967 full-length enriched swine cDNA library, adult trachea Sus scrofa cDNA clone TCH01H040063 5prime, mRNA	5.909	6.248	2.479E-03	2.84E-02	-1.27	PiNN-up
GTDC1	SNOWBALL_017651_s_st	glycosyltransferase-like domain containing 1	6.791	6.299	2.492E-03	2.85E-02	1.41	Duroc-up
KCTD9	SNOWBALL_029797_st	potassium channel tetramerisation domain containing 9	6.050	5.494	2.491E-03	2.85E-02	1.47	Duroc-up
	SNOWBALL_036156_st	Ssc_hash_S39807366 rcbl0_010631.y1 cbl Sus scrofa cDNA 5prime, mRNA	4.725	4.121	2.491E-03	2.85E-02	1.52	Duroc-up
AEBP2	SNOWBALL_007279_st	AE binding protein 2	8.072	7.857	2.494E-03	2.85E-02	1.16	Duroc-up

QRICH1	SNOWBALL_015409_st	glutamine-rich 1	8.284	8.491	2.502E-03	2.85E-02	-1.15	PiNN-up
FXR1	SNOWBALL_046193_st	fragile X mental retardation, autosomal homolog 1	4.784	4.341	2.501E-03	2.85E-02	1.36	Duroc-up
HNRNPH3	SNOWBALL_017020_s_st	heterogeneous nuclear ribonucleoprotein H3 (2H9)	8.170	7.674	2.499E-03	2.85E-02	1.41	Duroc-up
USP25	SNOWBALL_030088_st	ubiquitin specific peptidase 25	10.126	9.629	2.501E-03	2.85E-02	1.41	Duroc-up
MECOM	SNOWBALL_015751_st	MDS1 and EVI1 complex locus	5.956	5.534	2.506E-03	2.86E-02	1.34	Duroc-up
HN1	SNOWBALL_014221_st	hematological and neurological expressed 1	8.033	8.449	2.508E-03	2.86E-02	-1.33	PiNN-up
HERC4	SNOWBALL_024482_st	PREDICTED: Sus scrofa similar to hect domain and RLD 4 (LOC100155982), mRNA	6.475	6.181	2.509E-03	2.86E-02	1.23	Duroc-up
NOL3	SNOWBALL_007979_st	nucleolar protein 3 (apoptosis repressor with CARD domain)	7.597	8.098	2.519E-03	2.86E-02	-1.42	PiNN-up
ERRFI1	SNOWBALL_027184_st	ERBB receptor feedback inhibitor 1	4.982	5.357	2.519E-03	2.86E-02	-1.30	PiNN-up
FAM185A	SNOWBALL_012698_s_st	family with sequence similarity 185, member A	6.489	6.190	2.516E-03	2.86E-02	1.23	Duroc-up
	SNOWBALL_029461_st	Ssc_hash_S16769993 842347 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	4.550	4.114	2.518E-03	2.86E-02	1.35	Duroc-up
THOC1	SNOWBALL_026399_s_st	THO complex 1	5.990	5.541	2.520E-03	2.86E-02	1.36	Duroc-up
TNIK	SNOWBALL_046714_st	TRAF2 and NCK interacting kinase	5.450	4.858	2.514E-03	2.86E-02	1.51	Duroc-up
HOOK3	SNOWBALL_041889_st	hook homolog 3 (Drosophila)	7.362	6.778	2.522E-03	2.86E-02	1.50	Duroc-up
ODZ3	SNOWBALL_017783_st	odz, odd Oz/ten-m homolog 3 (Drosophila)	5.304	5.614	2.528E-03	2.86E-02	-1.24	PiNN-up
SNORD33	SNOWBALL_009043_s_st	Small nucleolar RNA Z195/SNORD33/SNORD32 family	13.403	13.583	2.539E-03	2.87E-02	-1.13	PiNN-up
PPP2R2A	SNOWBALL_016329_st	protein phosphatase 2, regulatory subunit B, alpha	8.173	7.854	2.535E-03	2.87E-02	1.25	Duroc-up
NUCKS1	SNOWBALL_025756_st	nuclear casein kinase and cyclin-dependent kinase substrate 1	7.316	6.944	2.539E-03	2.87E-02	1.29	Duroc-up
ABCC9	SNOWBALL_029936_st	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	8.673	8.117	2.534E-03	2.87E-02	1.47	Duroc-up
NEDD1	SNOWBALL_007596_st	protein NEDD1-like	5.637	4.889	2.536E-03	2.87E-02	1.68	Duroc-up
CCAR1	SNOWBALL_017076_st	cell division cycle and apoptosis regulator 1	7.463	7.196	2.541E-03	2.87E-02	1.20	Duroc-up
ZXDC	SNOWBALL_021682_st	ZXD family zinc finger C	6.454	6.809	2.545E-03	2.87E-02	-1.28	PiNN-up
RBL1	SNOWBALL_019519_st	retinoblastoma-like protein 1-like	6.558	6.092	2.544E-03	2.87E-02	1.38	Duroc-up
ZEB1	SNOWBALL_046309_st		5.124	4.461	2.548E-03	2.87E-02	1.58	Duroc-up
MTOR	SNOWBALL_009348_st	mechanistic target of rapamycin (serine/threonine kinase)	7.729	7.980	2.551E-03	2.87E-02	-1.19	PiNN-up
CNOT7	SNOWBALL_023833_st	CCR4-NOT transcription complex, subunit 7	6.778	6.239	2.552E-03	2.87E-02	1.45	Duroc-up
EIF3E	SNOWBALL_000797_st	eukaryotic translation initiation factor 3, subunit E	9.564	8.956	2.553E-03	2.87E-02	1.52	Duroc-up
ZBTB47	SNOWBALL_015237_st	zinc finger and BTB domain containing 47	7.874	8.178	2.562E-03	2.88E-02	-1.23	PiNN-up
MYST1	SNOWBALL_000668_st	MYST histone acetyltransferase 1	8.151	8.367	2.566E-03	2.88E-02	-1.16	PiNN-up
EAF1	SNOWBALL_015164_st	ELL associated factor 1	6.484	6.693	2.565E-03	2.88E-02	-1.16	PiNN-up

TTC7B	SNOWBALL_010635_st	tetratricopeptide repeat domain 7B	8.970	8.710	2.563E-03	2.88E-02	1.20	Duroc-up
P2RX6	SNOWBALL_016817_st	purinergic receptor P2X, ligand-gated ion channel, 6	6.273	6.488	2.569E-03	2.88E-02	-1.16	PiNN-up
PRKG1	SNOWBALL_040450_st	protein kinase, cGMP-dependent, type I	4.637	3.804	2.577E-03	2.88E-02	1.78	Duroc-up
TRIP11	SNOWBALL_010657_st	thyroid hormone receptor interactor 11	7.023	6.443	2.583E-03	2.89E-02	1.49	Duroc-up
FEM1C	SNOWBALL_026494_st	fem-1 homolog c (C. elegans)	6.313	5.705	2.586E-03	2.89E-02	1.52	Duroc-up
MAPT	SNOWBALL_014356_st	microtubule-associated protein tau	6.623	6.928	2.592E-03	2.89E-02	-1.24	PiNN-up
LOC100473202	SNOWBALL_028250_st	Ssc_hash_S18378606 923113 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	7.201	6.508	2.592E-03	2.89E-02	1.62	Duroc-up
PRKCA	SNOWBALL_040027_st	protein kinase C, alpha	3.800	4.107	2.595E-03	2.90E-02	-1.24	PiNN-up
WDR44	SNOWBALL_020666_s_st	WD repeat domain 44	7.446	7.026	2.597E-03	2.90E-02	1.34	Duroc-up
	SNOWBALL_039190_st		5.009	5.405	2.600E-03	2.90E-02	-1.32	PiNN-up
AHNAK	SNOWBALL_047518_st	AHNAK nucleoprotein	8.595	8.259	2.604E-03	2.90E-02	1.26	Duroc-up
HLA-L	SNOWBALL_035136_st	Ssc_hash_S50211341 susfleck_AF_N_18_B07 SUSFLECK Abdominal Fat Normalized Sus scrofa cDNA clone 18_B07, mRNA	5.665	5.161	2.611E-03	2.91E-02	1.42	Duroc-up
DPM3	SNOWBALL_005835_st	dolichyl-phosphate mannosyltransferase polypeptide 3	6.496	6.658	2.622E-03	2.92E-02	-1.12	PiNN-up
SLC6A8	SNOWBALL_020813_st	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	10.097	10.438	2.641E-03	2.92E-02	-1.27	PiNN-up
LRP1	SNOWBALL_035537_st	Ssc_hash_S18353841 892841 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	7.463	7.766	2.640E-03	2.92E-02	-1.23	PiNN-up
DNMBP	SNOWBALL_017212_s_st	dynamin binding protein	6.164	6.458	2.640E-03	2.92E-02	-1.23	PiNN-up
LOC100518162	SNOWBALL_003282_s_st	hypothetical protein LOC100518162	8.773	8.331	2.633E-03	2.92E-02	1.36	Duroc-up
RABEP1	SNOWBALL_015008_st	rabaptin, RAB GTPase binding effector protein 1	8.437	7.970	2.641E-03	2.92E-02	1.38	Duroc-up
JMY	SNOWBALL_028512_st	junction mediating and regulatory protein, p53 cofactor	6.069	5.472	2.638E-03	2.92E-02	1.51	Duroc-up
C2orf69	SNOWBALL_018151_st	chromosome 2 open reading frame 69	5.753	5.153	2.636E-03	2.92E-02	1.52	Duroc-up
	SNOWBALL_041568_st		4.494	3.868	2.633E-03	2.92E-02	1.54	Duroc-up
C7orf58	SNOWBALL_019811_st	chromosome 7 open reading frame 58	8.470	8.141	2.645E-03	2.93E-02	1.26	Duroc-up
NOX4	SNOWBALL_012347_st	NADPH oxidase 4	6.474	6.828	2.649E-03	2.93E-02	-1.28	PiNN-up
ART1	SNOWBALL_012138_s_st	GPI-linked NAD(P)(+)--arginine ADP-ribosyltransferase 1-like	6.991	7.298	2.653E-03	2.93E-02	-1.24	PiNN-up
YTHDC1	SNOWBALL_044888_st	YTH domain containing 1	4.375	3.750	2.657E-03	2.93E-02	1.54	Duroc-up
GNB5	SNOWBALL_002638_st	guanine nucleotide binding protein (G protein), beta 5	5.383	5.941	2.664E-03	2.94E-02	-1.47	PiNN-up
RPGRIP1L	SNOWBALL_032157_st	RPGRIP1-like	4.620	3.971	2.665E-03	2.94E-02	1.57	Duroc-up
COMMD4	SNOWBALL_022205_st	COMM domain containing 4	6.414	6.718	2.674E-03	2.95E-02	-1.23	PiNN-up

RNF185	SNOWBALL_016656_s_st	RING finger protein 185-like	6.749	7.128	2.680E-03	2.95E-02	-1.30	PiNN-up
ZFYVE1	SNOWBALL_010861_st	zinc finger, FYVE domain containing 1	6.789	7.046	2.680E-03	2.95E-02	-1.19	PiNN-up
TECRL	SNOWBALL_026998_st	trans-2,3-enoyl-CoA reductase-like	7.264	6.230	2.706E-03	2.98E-02	2.05	Duroc-up
TMEM47	SNOWBALL_020115_s_st	transmembrane protein 47	8.303	7.959	2.712E-03	2.98E-02	1.27	Duroc-up
KIAA1279	SNOWBALL_017008_s_st	KIAA1279	10.181	10.645	2.716E-03	2.98E-02	-1.38	PiNN-up
TRAFD1	SNOWBALL_000301_s_st	TRAF-type zinc finger domain containing 1	5.499	5.942	2.717E-03	2.98E-02	-1.36	PiNN-up
ENTPD5	SNOWBALL_036847_st	ectonucleoside triphosphate diphosphohydrolase 5	5.960	5.604	2.718E-03	2.98E-02	1.28	Duroc-up
RXRA	SNOWBALL_004095_st	retinoid X receptor, alpha	8.051	8.311	2.733E-03	3.00E-02	-1.20	PiNN-up
PRSS23	SNOWBALL_012505_st	serine protease 23-like	6.781	7.418	2.747E-03	3.01E-02	-1.56	PiNN-up
HGSNAT	SNOWBALL_019001_st	heparan-alpha-glucosaminide N-acetyltransferase	7.703	8.037	2.748E-03	3.01E-02	-1.26	PiNN-up
ZNF643	SNOWBALL_009247_st	zinc finger protein 643	5.228	4.875	2.744E-03	3.01E-02	1.28	Duroc-up
BRD1	SNOWBALL_031694_st	bromodomain containing 1	6.196	6.437	2.754E-03	3.01E-02	-1.18	PiNN-up
CNOT4	SNOWBALL_019730_st	CCR4-NOT transcription complex, subunit 4	8.734	8.485	2.753E-03	3.01E-02	1.19	Duroc-up
TRAK2	SNOWBALL_028004_st	trafficking protein, kinesin binding 2	4.498	3.932	2.757E-03	3.01E-02	1.48	Duroc-up
H41	SNOWBALL_035058_st	CDV3 homolog (mouse)	9.304	8.991	2.765E-03	3.02E-02	1.24	Duroc-up
RAB11FIP2	SNOWBALL_024772_st	RAB11 family interacting protein 2 (class I)	7.555	7.020	2.763E-03	3.02E-02	1.45	Duroc-up
Mospd2	SNOWBALL_023597_s_st	motile sperm domain containing 2	4.682	4.147	2.766E-03	3.02E-02	1.45	Duroc-up
BHLHE40	SNOWBALL_028257_st	Ssc_hash_S31123110 1546058 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	7.242	7.943	2.777E-03	3.02E-02	-1.62	PiNN-up
FBXW7	SNOWBALL_011455_st	F-box and WD repeat domain containing 7	6.823	6.577	2.772E-03	3.02E-02	1.19	Duroc-up
CNOT2	SNOWBALL_007285_st	CCR4-NOT transcription complex, subunit 2	8.015	7.610	2.777E-03	3.02E-02	1.32	Duroc-up
KTN1	SNOWBALL_003193_st	kinectin 1 (kinesin receptor)	8.438	7.658	2.777E-03	3.02E-02	1.72	Duroc-up
CAV3	SNOWBALL_026813_st	caveolin 3	7.351	7.733	2.782E-03	3.03E-02	-1.30	PiNN-up
GAPDH	SNOWBALL_023145_st	Sus scrofa glyceraldehyde-3-phosphate dehydrogenase mRNA, partial cds	13.941	14.033	2.792E-03	3.03E-02	-1.07	PiNN-up
COX10	SNOWBALL_014952_st	COX10 homolog, cytochrome c oxidase assembly protein, heme A: farnesyltransferase (yeast)	6.964	7.341	2.796E-03	3.04E-02	-1.30	PiNN-up
MT-ND2	SNOWBALL_020862_st	mitochondrially encoded NADH dehydrogenase 2	13.392	13.221	2.808E-03	3.05E-02	1.13	Duroc-up
	SNOWBALL_041044_st		4.540	4.052	2.808E-03	3.05E-02	1.40	Duroc-up
	SNOWBALL_044046_st		6.604	7.470	2.818E-03	3.05E-02	-1.82	PiNN-up
SCARB2	SNOWBALL_037566_st	scavenger receptor class B, member 2	5.846	6.342	2.816E-03	3.05E-02	-1.41	PiNN-up
CCDC101	SNOWBALL_026050_st	coiled-coil domain containing 101	5.888	6.233	2.815E-03	3.05E-02	-1.27	PiNN-up
C6orf142	SNOWBALL_009877_st	Uncharacterized protein C6orf142 [Source:UniProtKB/Swiss-Prot;Acc:Q5VWP3]	9.329	9.598	2.812E-03	3.05E-02	-1.20	PiNN-up
PPIL4	SNOWBALL_002125_st	peptidylprolyl isomerase (cyclophilin)-like 4	5.332	5.033	2.815E-03	3.05E-02	1.23	Duroc-up
RBM18	SNOWBALL_003695_st	RNA binding motif protein 18	7.513	6.949	2.821E-03	3.05E-02	1.48	Duroc-up
TTC7B	SNOWBALL_040175_st	tetratricopeptide repeat domain 7B	5.971	5.325	2.823E-03	3.05E-02	1.56	Duroc-up

	SNOWBALL_031194_st	Ssc_hash_S19539424 942824 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.507	4.722	2.822E-03	3.05E-02	1.72	Duroc-up
LOC100154493	SNOWBALL_009760_s_st	olfactory receptor 2G3-like	5.142	5.835	2.833E-03	3.05E-02	-1.62	PiNN-up
ACPT	SNOWBALL_029983_st	Ssc_hash_S18276682 BP173173 full-length enriched swine cDNA library, adult uterus Sus scrofa cDNA clone UTR010035H02 5prime, mRNA	6.137	6.571	2.841E-03	3.05E-02	-1.35	PiNN-up
ZNF529	SNOWBALL_008124_st	zinc finger protein 780B	6.094	6.500	2.846E-03	3.05E-02	-1.33	PiNN-up
ZBTB47	SNOWBALL_042432_st	zinc finger and BTB domain containing 47	5.142	5.488	2.838E-03	3.05E-02	-1.27	PiNN-up
MKRN1	SNOWBALL_019668_st	makorin ring finger protein 1	7.711	8.002	2.845E-03	3.05E-02	-1.22	PiNN-up
DENND4B	SNOWBALL_006191_st	DENN/MADD domain containing 4B	7.265	7.480	2.851E-03	3.05E-02	-1.16	PiNN-up
ARF3	SNOWBALL_022840_st	ADP-ribosylation factor 3	5.677	5.868	2.851E-03	3.05E-02	-1.14	PiNN-up
PPP1R11	SNOWBALL_001060_st	OTTSUSG00000001258 protein phosphatase 1, regulatory (inhibitor) subunit 11	7.373	7.128	2.842E-03	3.05E-02	1.19	Duroc-up
PWWP2A	SNOWBALL_030213_st	PWWP domain containing 2A	4.708	4.400	2.843E-03	3.05E-02	1.24	Duroc-up
LGR5	SNOWBALL_007292_st	leucine-rich repeat containing G protein-coupled receptor 5	6.439	5.966	2.853E-03	3.05E-02	1.39	Duroc-up
KIAA1731	SNOWBALL_012474_s_st	KIAA1731	6.155	5.599	2.840E-03	3.05E-02	1.47	Duroc-up
ZDHHC21	SNOWBALL_040592_st	zinc finger, DHHC-type containing 21	4.719	4.034	2.839E-03	3.05E-02	1.61	Duroc-up
NCK1	SNOWBALL_026590_st	NCK adaptor protein 1	4.212	3.525	2.849E-03	3.05E-02	1.61	Duroc-up
RHOQ	SNOWBALL_005220_st	ras homolog gene family, member Q	9.846	9.123	2.835E-03	3.05E-02	1.65	Duroc-up
CCDC149	SNOWBALL_033620_st	coiled-coil domain containing 149	6.272	6.770	2.854E-03	3.05E-02	-1.41	PiNN-up
PPP1CC	SNOWBALL_016522_st	protein phosphatase 1, catalytic subunit, gamma isozyme	10.318	9.868	2.857E-03	3.05E-02	1.37	Duroc-up
ZFP91	SNOWBALL_027511_st	zinc finger protein 91 homolog (mouse)	9.705	9.212	2.862E-03	3.06E-02	1.41	Duroc-up
PAFAH1B1	SNOWBALL_014933_st	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	8.562	8.325	2.874E-03	3.07E-02	1.18	Duroc-up
GPSM2	SNOWBALL_028854_st	G-protein signaling modulator 2	4.567	4.135	2.873E-03	3.07E-02	1.35	Duroc-up
KLHL22	SNOWBALL_026514_s_st	kelch-like 22 (Drosophila)	6.840	8.218	2.877E-03	3.07E-02	-2.60	PiNN-up
MT-ND3	SNOWBALL_020875_st	mitochondrially encoded NADH dehydrogenase 3	12.527	12.278	2.882E-03	3.07E-02	1.19	Duroc-up
NANOG	SNOWBALL_003205_st	Nanog homeobox	5.654	5.158	2.884E-03	3.07E-02	1.41	Duroc-up
C2orf29	SNOWBALL_004784_st	chromosome 2 open reading frame 29	7.873	8.084	2.890E-03	3.08E-02	-1.16	PiNN-up
GLUD1	SNOWBALL_024695_s_st	PREDICTED: Sus scrofa similar to glutamate dehydrogenase 1 (LOC100157162), partial mRNA	9.190	8.624	2.898E-03	3.08E-02	1.48	Duroc-up
hsa-mir-1268	hsa-mir-1268_st	MI0006405	7.620	8.136	2.912E-03	3.09E-02	-1.43	PiNN-up
TMEM164	SNOWBALL_020633_st	transmembrane protein 164	6.621	7.014	2.911E-03	3.09E-02	-1.31	PiNN-up
PHF12	SNOWBALL_014776_st	PHD finger protein 12	6.720	6.952	2.907E-03	3.09E-02	-1.17	PiNN-up

BAP1	SNOWBALL_025092_s_st	BRCA1 associated protein-1 (ubiquitin carboxy-terminal hydrolase)	6.882	7.112	2.904E-03	3.09E-02	-1.17	PiNN-up
KIFAP3	SNOWBALL_006155_st	kinesin-associated protein 3	7.018	6.699	2.915E-03	3.09E-02	1.25	Duroc-up
KPNA5	SNOWBALL_002206_st	karyopherin alpha 5 (importin alpha 6)	5.978	5.538	2.914E-03	3.09E-02	1.36	Duroc-up
INTS6	SNOWBALL_013821_st	integrator complex subunit 6	7.283	6.795	2.913E-03	3.09E-02	1.40	Duroc-up
DEK	SNOWBALL_009561_st	DEK oncogene	9.547	8.888	2.907E-03	3.09E-02	1.58	Duroc-up
AMOT	SNOWBALL_023541_s_st	PREDICTED: Sus scrofa similar to angiomotin (LOC100158213), mRNA	9.153	9.400	2.920E-03	3.09E-02	-1.19	PiNN-up
FNBP1	SNOWBALL_003554_st	formin binding protein 1	5.587	5.321	2.921E-03	3.09E-02	1.20	Duroc-up
PEBP4	SNOWBALL_022814_s_st	phosphatidylethanolamine-binding protein 4	9.305	9.867	2.922E-03	3.09E-02	-1.48	PiNN-up
ESR1	SNOWBALL_002174_s_st	estrogen receptor 1	5.119	5.570	2.930E-03	3.10E-02	-1.37	PiNN-up
MAN2B2	SNOWBALL_027322_st	mannosidase, alpha, class 2B, member 2	5.600	6.107	2.935E-03	3.10E-02	-1.42	PiNN-up
CTIF	SNOWBALL_034080_st	CBP80/20-dependent translation initiation factor	6.190	6.527	2.934E-03	3.10E-02	-1.26	PiNN-up
EIF4G3	SNOWBALL_002264_s_st	eukaryotic translation initiation factor 4 gamma, 3	9.461	9.002	2.935E-03	3.10E-02	1.37	Duroc-up
	SNOWBALL_041876_st		3.619	3.211	2.938E-03	3.10E-02	1.33	Duroc-up
HSPB2	SNOWBALL_012338_st	heat shock 27kDa protein 2	6.985	7.485	2.943E-03	3.10E-02	-1.41	PiNN-up
BRWD1	SNOWBALL_044418_st	similar to WDR9 protein, form A	7.508	7.131	2.946E-03	3.10E-02	1.30	Duroc-up
EXOC5	SNOWBALL_021891_st	exocyst complex component 5	4.745	4.118	2.944E-03	3.10E-02	1.54	Duroc-up
CIDEA	SNOWBALL_022824_s_st	cell death-inducing DFFA-like effector a	5.029	5.342	2.959E-03	3.11E-02	-1.24	PiNN-up
KIAA1109	SNOWBALL_011891_st	KIAA1109	8.355	7.860	2.958E-03	3.11E-02	1.41	Duroc-up
UST	SNOWBALL_002151_st	uronyl-2-sulfotransferase	6.534	6.816	2.972E-03	3.12E-02	-1.22	PiNN-up
BCL2L13	SNOWBALL_007585_st	BCL2-like 13 (apoptosis facilitator)	8.371	8.645	2.974E-03	3.12E-02	-1.21	PiNN-up
POMT2	SNOWBALL_010614_st	protein-O-mannosyltransferase 2	6.212	6.468	2.972E-03	3.12E-02	-1.19	PiNN-up
ZNF277	SNOWBALL_019900_st	zinc finger protein 277	7.951	7.228	2.970E-03	3.12E-02	1.65	Duroc-up
	SNOWBALL_032766_st	Ssc_hash_S34520616 DB790924 full-length enriched swine cDNA library, adult immature dendritic cell Sus scrofa cDNA clone DCI010005E04 5prime, mRNA	4.702	3.948	2.971E-03	3.12E-02	1.69	Duroc-up
PTPN11	SNOWBALL_025264_st	protein tyrosine phosphatase, non-receptor type 11	9.356	9.000	2.990E-03	3.13E-02	1.28	Duroc-up
XYLT1	SNOWBALL_004457_st	xylosyltransferase I	5.624	5.886	2.999E-03	3.14E-02	-1.20	PiNN-up
ENO1	SNOWBALL_042600_st	alpha-enolase-like	7.005	7.335	3.006E-03	3.14E-02	-1.26	PiNN-up
C7orf60	SNOWBALL_027660_st	chromosome 7 open reading frame 60	5.883	5.076	3.011E-03	3.15E-02	1.75	Duroc-up
HBA1	SNOWBALL_000676_st	hemoglobin, alpha 1	7.192	7.977	3.014E-03	3.15E-02	-1.72	PiNN-up
UBN1	SNOWBALL_025452_st	Sus scrofa mRNA, clone:PBL010103A04, expressed in periphral blood mononuclear cell	6.048	6.337	3.025E-03	3.15E-02	-1.22	PiNN-up
POLH	SNOWBALL_018393_s_st	GTP-binding protein 2-like	6.259	6.540	3.025E-03	3.15E-02	-1.21	PiNN-up
PBX1	SNOWBALL_033966_st	pre-B-cell leukemia homeobox 1	6.979	6.556	3.025E-03	3.15E-02	1.34	Duroc-up
MRPL22	SNOWBALL_018696_st	mitochondrial ribosomal protein L22	7.059	7.391	3.029E-03	3.16E-02	-1.26	PiNN-up

	SNOWBALL_029222_st	Ssc_hash_S50208407 susfleck_AF_N_31_C07 SUSFLECK Abdominal Fat Normalized Sus scrofa cDNA clone 31_C07, mRNA	4.519	4.965	3.039E-03	3.17E-02	-1.36	PiNN-up
CCDC55	SNOWBALL_014734_st	coiled-coil domain containing 55	7.085	6.425	3.045E-03	3.17E-02	1.58	Duroc-up
PER3	SNOWBALL_038420_st	period homolog 3 (Drosophila)	4.175	4.798	3.053E-03	3.18E-02	-1.54	PiNN-up
MGRN1	SNOWBALL_004806_st	mahogunin, ring finger 1	6.336	6.654	3.059E-03	3.18E-02	-1.25	PiNN-up
DIP2C	SNOWBALL_013625_st	DIP2 disco-interacting protein 2 homolog C (Drosophila)	8.390	8.618	3.060E-03	3.18E-02	-1.17	PiNN-up
ZNF570	SNOWBALL_008049_st	zinc finger protein 570	5.242	4.787	3.060E-03	3.18E-02	1.37	Duroc-up
SKP1	SNOWBALL_025379_st	Sus scrofa mRNA, clone:MLN010078H04, expressed in mesenteric lymph node	6.057	5.711	3.073E-03	3.19E-02	1.27	Duroc-up
VRK3	SNOWBALL_008404_st	vaccinia related kinase 3	5.652	6.051	3.076E-03	3.19E-02	-1.32	PiNN-up
ASB15	SNOWBALL_019856_st	ankyrin repeat and SOCS box containing 15	9.669	9.158	3.077E-03	3.19E-02	1.43	Duroc-up
DDX52	SNOWBALL_026181_st	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	5.713	5.198	3.083E-03	3.19E-02	1.43	Duroc-up
CCDC127	SNOWBALL_026177_s_st	coiled-coil domain containing 127	7.126	7.640	3.105E-03	3.21E-02	-1.43	PiNN-up
	SNOWBALL_037704_st		5.225	5.481	3.101E-03	3.21E-02	-1.19	PiNN-up
SHPRH	SNOWBALL_002168_st	SNF2 histone linker PHD RING helicase	7.142	6.807	3.105E-03	3.21E-02	1.26	Duroc-up
AEBP2	SNOWBALL_035206_st	AE binding protein 2	4.477	3.765	3.120E-03	3.22E-02	1.64	Duroc-up
GTF3C4	SNOWBALL_045053_st	general transcription factor IIIC, polypeptide 4, 90kDa	4.008	4.233	3.123E-03	3.23E-02	-1.17	PiNN-up
LIX1L	SNOWBALL_030611_st	Lix1 homolog (mouse)-like	6.078	6.454	3.130E-03	3.23E-02	-1.30	PiNN-up
RS1	SNOWBALL_029660_st	Ssc_hash_S17517906 BX672475 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0034.i.08 5prim, mRNA	5.018	5.449	3.139E-03	3.24E-02	-1.35	PiNN-up
PIK3IP1	SNOWBALL_016764_s_st	phosphoinositide-3-kinase interacting protein 1	6.636	6.884	3.151E-03	3.25E-02	-1.19	PiNN-up
BMS1	SNOWBALL_017271_s_st	BMS1 homolog, ribosome assembly protein (yeast)	6.661	6.293	3.153E-03	3.25E-02	1.29	Duroc-up
PPARGC1A	SNOWBALL_025989_st	Sus scrofa mRNA, clone:OVRM10103G06, expressed in ovary	7.963	7.547	3.153E-03	3.25E-02	1.33	Duroc-up
ENG	SNOWBALL_000112_s_st	OTTSUSG00000001884 endoglin pseudogene	6.787	7.017	3.158E-03	3.25E-02	-1.17	PiNN-up
PTPN4	SNOWBALL_035270_st	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	7.781	6.980	3.161E-03	3.25E-02	1.74	Duroc-up
MGRN1	SNOWBALL_026449_st	Sus scrofa mRNA, clone:OVR010068F07, expressed in ovary	6.800	7.022	3.163E-03	3.25E-02	-1.17	PiNN-up
TMEM214	SNOWBALL_005444_st	transmembrane protein 214	7.468	7.690	3.165E-03	3.25E-02	-1.17	PiNN-up
LRCH4	SNOWBALL_045011_st	leucine-rich repeats and calponin homology (CH) domain containing 4	6.591	6.793	3.170E-03	3.26E-02	-1.15	PiNN-up
FUBP1	SNOWBALL_009335_s_st	far upstream element (FUSE) binding protein 1	8.059	7.642	3.175E-03	3.26E-02	1.33	Duroc-up

WWP1	SNOWBALL_025778_st	WW domain containing E3 ubiquitin protein ligase 1	7.895	7.355	3.173E-03	3.26E-02	1.45	Duroc-up
PARM1	SNOWBALL_011533_st	prostate androgen-regulated mucin-like protein 1	6.830	7.115	3.186E-03	3.27E-02	-1.22	PiNN-up
BRIX1	SNOWBALL_018590_st	BRX1, biogenesis of ribosomes, homolog (S. cerevisiae)	6.458	6.000	3.189E-03	3.27E-02	1.37	Duroc-up
MAZ	SNOWBALL_022428_s_st	MYC-associated zinc finger protein (purine-binding transcription factor)	6.837	7.149	3.198E-03	3.27E-02	-1.24	PiNN-up
DIDO1	SNOWBALL_044459_st	death inducer-obliterator 1	5.389	5.692	3.201E-03	3.27E-02	-1.23	PiNN-up
ZNF652	SNOWBALL_026270_s_st	zinc finger protein 652	7.247	6.908	3.201E-03	3.27E-02	1.26	Duroc-up
PFKFB2	SNOWBALL_036957_st	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	4.573	5.097	3.218E-03	3.29E-02	-1.44	PiNN-up
NAT6	SNOWBALL_015322_st	N-acetyltransferase 6 (GCN5-related)	6.292	6.557	3.229E-03	3.30E-02	-1.20	PiNN-up
ZC3H11A	SNOWBALL_036894_st	zinc finger CCCH-type containing 11A	7.686	7.226	3.230E-03	3.30E-02	1.38	Duroc-up
KLHL33	SNOWBALL_010791_st	kelch-like 33 (Drosophila)	6.947	7.229	3.233E-03	3.30E-02	-1.22	PiNN-up
RIC8B	SNOWBALL_006838_st	resistance to inhibitors of cholinesterase 8 homolog B (C. elegans)	7.691	7.369	3.241E-03	3.31E-02	1.25	Duroc-up
OSBPL2	SNOWBALL_021694_s_st	oxysterol binding protein-like 2	6.299	6.612	3.244E-03	3.31E-02	-1.24	PiNN-up
TMEM170B	SNOWBALL_036017_st	transmembrane protein 170B	5.232	4.729	3.248E-03	3.31E-02	1.42	Duroc-up
Sulfurtransferase	SNOWBALL_002369_st	heat shock protein 67B2-like	7.062	6.165	3.253E-03	3.31E-02	1.86	Duroc-up
	SNOWBALL_045175_st		6.606	6.075	3.260E-03	3.32E-02	1.45	Duroc-up
PPP2R1A	SNOWBALL_021010_s_st	protein phosphatase 2, regulatory subunit A, alpha	6.743	7.032	3.264E-03	3.32E-02	-1.22	PiNN-up
FOXN3	SNOWBALL_025604_st	forkhead box N3	8.887	8.590	3.265E-03	3.32E-02	1.23	Duroc-up
LOC100155390	SNOWBALL_019672_st	Sorting nexin 5	5.589	5.279	3.277E-03	3.33E-02	1.24	Duroc-up
LACTB2	SNOWBALL_005725_st	lactamase, beta 2	6.781	6.170	3.288E-03	3.34E-02	1.53	Duroc-up
TNFRSF1B	SNOWBALL_022345_s_st	tumor necrosis factor receptor superfamily, member 1B	6.170	6.418	3.301E-03	3.35E-02	-1.19	PiNN-up
RALGAPA1	SNOWBALL_010299_st	Ral GTPase activating protein, alpha subunit 1 (catalytic)	8.696	8.191	3.307E-03	3.35E-02	1.42	Duroc-up
GPRC5B	SNOWBALL_004591_st	G protein-coupled receptor, family C, group 5, member B	7.228	7.719	3.321E-03	3.37E-02	-1.41	PiNN-up
RABEP1	SNOWBALL_025858_st	rabaptin, RAB GTPase binding effector protein 1	8.246	7.685	3.325E-03	3.37E-02	1.48	Duroc-up
ADCY9	SNOWBALL_004878_st	adenylate cyclase 9	7.912	8.222	3.333E-03	3.37E-02	-1.24	PiNN-up
GNL1	SNOWBALL_001093_st	OTTSUSG00000001276 guanine nucleotide binding protein-like 1	6.038	6.312	3.336E-03	3.37E-02	-1.21	PiNN-up
KIRREL	SNOWBALL_000862_s_st	OTTSUSG00000001789 PREDICTED: similar to putative kin of IRRE-like protein	6.588	6.803	3.335E-03	3.37E-02	-1.16	PiNN-up
NMD3	SNOWBALL_026398_st	NMD3 homolog (S. cerevisiae)	6.935	6.485	3.330E-03	3.37E-02	1.37	Duroc-up

RG9MTD1	SNOWBALL_016196_st	RNA (guanine-9-) methyltransferase domain containing 1	4.829	4.347	3.335E-03	3.37E-02	1.40	Duroc-up
C22orf13	SNOWBALL_016712_s_st	chromosome 22 open reading frame 13	6.750	6.955	3.347E-03	3.37E-02	-1.15	PiNN-up
EIF2C1	SNOWBALL_008633_st	eukaryotic translation initiation factor 2C, 1	6.906	7.064	3.345E-03	3.37E-02	-1.12	PiNN-up
CNGB1	SNOWBALL_007343_s_st	cyclic nucleotide gated channel beta 1	10.399	10.083	3.342E-03	3.37E-02	1.24	Duroc-up
C12orf23	SNOWBALL_037415_st	chromosome 12 open reading frame 23	7.804	7.271	3.347E-03	3.37E-02	1.45	Duroc-up
	SNOWBALL_040363_st		5.288	5.005	3.355E-03	3.38E-02	1.22	Duroc-up
CFL1	SNOWBALL_000608_s_st	cofilin 1 (non-muscle)	8.356	7.952	3.352E-03	3.38E-02	1.32	Duroc-up
KMO	SNOWBALL_026392_st	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	6.425	5.866	3.353E-03	3.38E-02	1.47	Duroc-up
SRRM1	SNOWBALL_047419_st	serine/arginine repetitive matrix 1	6.484	5.974	3.360E-03	3.38E-02	1.42	Duroc-up
RICTOR	SNOWBALL_018629_st	RPTOR independent companion of MTOR, complex 2	7.628	7.113	3.361E-03	3.38E-02	1.43	Duroc-up
MDM2	SNOWBALL_007304_st	Mdm2 p53 binding protein homolog (mouse)	8.691	8.362	3.364E-03	3.38E-02	1.26	Duroc-up
TAF9B	SNOWBALL_023485_s_st	PREDICTED: Sus scrofa similar to transcription associated factor 9B (LOC100155451), mRNA	7.612	7.207	3.366E-03	3.38E-02	1.32	Duroc-up
CSTF2T	SNOWBALL_016640_s_st	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa, tau variant	6.007	5.816	3.375E-03	3.39E-02	1.14	Duroc-up
CUL2	SNOWBALL_013404_st	cullin 2	7.243	6.843	3.383E-03	3.39E-02	1.32	Duroc-up
	SNOWBALL_017385_s_st	membrane-associated ring finger (C3HC4) 5	8.586	8.223	3.387E-03	3.39E-02	1.29	Duroc-up
SURF4	SNOWBALL_026052_s_st	surfeit 4	6.706	7.203	3.389E-03	3.40E-02	-1.41	PiNN-up
TBRG4	SNOWBALL_019783_st	cell cycle progression 2 protein	6.541	6.767	3.393E-03	3.40E-02	-1.17	PiNN-up
TWF1	SNOWBALL_007512_st	twinfilin, actin-binding protein, homolog 1 (Drosophila)	6.000	5.558	3.391E-03	3.40E-02	1.36	Duroc-up
DNAJC10	SNOWBALL_018112_st	DnaJ (Hsp40) homolog, subfamily C, member 10	8.030	7.426	3.395E-03	3.40E-02	1.52	Duroc-up
MARCH8	SNOWBALL_017393_st	membrane-associated ring finger (C3HC4) 8	5.350	5.617	3.404E-03	3.40E-02	-1.20	PiNN-up
TTC14	SNOWBALL_025128_s_st	tetratricopeptide repeat domain 14	4.650	4.215	3.410E-03	3.41E-02	1.35	Duroc-up
ADPRHL1	SNOWBALL_031033_st	ADP-ribosylhydrolase like 1	6.707	7.138	3.419E-03	3.41E-02	-1.35	PiNN-up
UBR4	SNOWBALL_009353_s_st	ubiquitin protein ligase E3 component n-recognin 4	9.221	9.489	3.420E-03	3.41E-02	-1.20	PiNN-up
ZCCHC11	SNOWBALL_008702_st	zinc finger, CCHC domain containing 11	7.690	7.283	3.428E-03	3.42E-02	1.33	Duroc-up
COL6A1	SNOWBALL_026603_st	collagen, type VI, alpha 1	8.897	9.197	3.438E-03	3.42E-02	-1.23	PiNN-up
JMJD6	SNOWBALL_022388_s_st	jumonji domain containing 6	6.100	6.347	3.437E-03	3.42E-02	-1.19	PiNN-up
ZC3H14	SNOWBALL_010688_st	zinc finger CCCH-type containing 14	7.304	6.991	3.434E-03	3.42E-02	1.24	Duroc-up
ZNF674	SNOWBALL_020159_st	zinc finger protein 674	6.033	5.572	3.436E-03	3.42E-02	1.38	Duroc-up
C6orf174	SNOWBALL_036056_st	chromosome 6 open reading frame 174	7.309	6.488	3.434E-03	3.42E-02	1.77	Duroc-up
CILP	SNOWBALL_003039_s_st	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	7.282	7.842	3.446E-03	3.42E-02	-1.47	PiNN-up
DCAF5	SNOWBALL_010324_s_st	DDB1 and CUL4 associated factor 5	7.716	8.041	3.445E-03	3.42E-02	-1.25	PiNN-up

SNORD24	SNOWBALL_013170_st	Small nucleolar RNA SNORD24	10.646	10.980	3.464E-03	3.43E-02	-1.26	PiNN-up
GGCX	SNOWBALL_046907_st	gamma-glutamyl carboxylase	6.545	6.819	3.465E-03	3.43E-02	-1.21	PiNN-up
AMOT	SNOWBALL_001813_s_st	angiomotin	9.367	9.637	3.457E-03	3.43E-02	-1.21	PiNN-up
BCAR3	SNOWBALL_006605_st	breast cancer anti-estrogen resistance 3	5.495	5.696	3.458E-03	3.43E-02	-1.15	PiNN-up
QKI	SNOWBALL_002033_st	quaking homolog, KH domain RNA binding (mouse)	9.949	9.676	3.467E-03	3.43E-02	1.21	Duroc-up
STAU2	SNOWBALL_033483_st	staufen, RNA binding protein, homolog 2 (Drosophila)	7.416	7.037	3.467E-03	3.43E-02	1.30	Duroc-up
SUSD1	SNOWBALL_003822_st	sushi domain containing 1	7.610	7.110	3.468E-03	3.43E-02	1.41	Duroc-up
CD36	SNOWBALL_001574_s_st	CD36 molecule (thrombospondin receptor)	10.415	9.870	3.458E-03	3.43E-02	1.46	Duroc-up
PHTF2	SNOWBALL_034859_st	putative homeodomain transcription factor 2	7.824	7.198	3.475E-03	3.43E-02	1.54	Duroc-up
Orc4	SNOWBALL_024065_s_st	PREDICTED: Sus scrofa similar to Origin recognition complex, subunit 4-like (yeast) (LOC100153297), mRNA	6.765	6.438	3.481E-03	3.44E-02	1.25	Duroc-up
MEF2D	SNOWBALL_035307_st	myocyte enhancer factor 2D	6.835	7.055	3.485E-03	3.44E-02	-1.16	PiNN-up
CACNG6	SNOWBALL_008611_st	calcium channel, voltage-dependent, gamma subunit 6	6.678	7.036	3.489E-03	3.44E-02	-1.28	PiNN-up
GCN1L1	SNOWBALL_016803_st	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	7.353	7.585	3.496E-03	3.45E-02	-1.17	PiNN-up
APPL1	SNOWBALL_028945_st	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	7.001	6.271	3.495E-03	3.45E-02	1.66	Duroc-up
DYNLRB1	SNOWBALL_019212_st	dynein, light chain, roadblock-type 1	9.673	9.994	3.499E-03	3.45E-02	-1.25	PiNN-up
UBR3	SNOWBALL_032943_st	ubiquitin protein ligase E3 component n-recognin 3 (putative)	8.579	7.968	3.500E-03	3.45E-02	1.53	Duroc-up
PEBP4	SNOWBALL_016309_s_st	phosphatidylethanolamine-binding protein 4	7.083	7.797	3.511E-03	3.45E-02	-1.64	PiNN-up
APOD	SNOWBALL_000258_s_st	apolipoprotein D	6.444	7.057	3.514E-03	3.45E-02	-1.53	PiNN-up
BNIP2	SNOWBALL_029582_st	BCL2/adenovirus E1B 19kDa interacting protein 2	5.205	4.695	3.512E-03	3.45E-02	1.42	Duroc-up
SLC39A10	SNOWBALL_032815_st	solute carrier family 39 (zinc transporter), member 10	5.197	4.777	3.516E-03	3.45E-02	1.34	Duroc-up
CAB39	SNOWBALL_024047_s_st	PREDICTED: Sus scrofa similar to Calcium-binding protein 39 (Protein Mo25) (LOC100157453), mRNA	10.199	9.922	3.525E-03	3.46E-02	1.21	Duroc-up
EEPD1	SNOWBALL_027626_st	endonuclease/exonuclease/phosphatase family domain containing 1	7.113	7.395	3.527E-03	3.46E-02	-1.22	PiNN-up
KIAA1166	SNOWBALL_023436_st	PREDICTED: Sus scrofa similar to KIAA1166 protein (LOC100151781), mRNA	4.100	4.530	3.532E-03	3.46E-02	-1.35	PiNN-up
ANKRD27	SNOWBALL_008173_st	ankyrin repeat domain 27 (VPS9 domain)	6.345	6.552	3.538E-03	3.47E-02	-1.15	PiNN-up
TMEM106B	SNOWBALL_012681_st	transmembrane protein 106B	8.416	7.928	3.547E-03	3.47E-02	1.40	Duroc-up
XIAP	SNOWBALL_001901_s_st	X-linked inhibitor of apoptosis	7.589	7.047	3.553E-03	3.48E-02	1.46	Duroc-up

NIF3L1	SNOWBALL_018069_st	NIF3 NGG1 interacting factor 3-like 1 (S. pombe)	5.439	4.835	3.551E-03	3.48E-02	1.52	Duroc-up
WDTC1	SNOWBALL_009244_st	WD and tetratricopeptide repeats 1	8.030	8.320	3.564E-03	3.49E-02	-1.22	PiNN-up
ATP11C	SNOWBALL_001947_s_st	ATPase, class VI, type 11C	5.048	4.370	3.571E-03	3.49E-02	1.60	Duroc-up
HERPUD1	SNOWBALL_021538_s_st	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	7.566	8.088	3.578E-03	3.49E-02	-1.44	PiNN-up
AKT1	SNOWBALL_022895_st	v-akt murine thymoma viral oncogene homolog 1	7.714	8.048	3.580E-03	3.49E-02	-1.26	PiNN-up
VKORC1L1	SNOWBALL_047282_st	vitamin K epoxide reductase complex, subunit 1-like 1	8.596	8.117	3.579E-03	3.49E-02	1.39	Duroc-up
ASAP3	SNOWBALL_008631_st	ArfGAP with SH3 domain, ankyrin repeat and PH domain 3	6.075	6.285	3.583E-03	3.50E-02	-1.16	PiNN-up
ZNF507	SNOWBALL_044909_st	zinc finger protein 507	5.889	5.243	3.593E-03	3.50E-02	1.57	Duroc-up
ZNF638	SNOWBALL_026469_st	zinc finger protein 638	8.849	8.387	3.598E-03	3.51E-02	1.38	Duroc-up
KIAA0664	SNOWBALL_015052_st	KIAA0664	7.481	7.740	3.601E-03	3.51E-02	-1.20	PiNN-up
SMG5	SNOWBALL_006134_st	Smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	8.002	8.353	3.604E-03	3.51E-02	-1.28	PiNN-up
ZNF697	SNOWBALL_034083_st	zinc finger protein 697	5.470	5.859	3.607E-03	3.51E-02	-1.31	PiNN-up
SLTM	SNOWBALL_002527_s_st	SAFB-like, transcription modulator	8.201	7.604	3.610E-03	3.51E-02	1.51	Duroc-up
TBC1D12	SNOWBALL_024944_st	TBC1 domain family, member 12	4.188	3.789	3.615E-03	3.51E-02	1.32	Duroc-up
STON1	SNOWBALL_005111_st	general transcription factor IIA, 1-like	5.779	5.530	3.621E-03	3.52E-02	1.19	Duroc-up
ACLY	SNOWBALL_014704_s_st	ATP citrate lyase	6.220	6.454	3.628E-03	3.52E-02	-1.18	PiNN-up
TIMM9	SNOWBALL_002911_st	translocase of inner mitochondrial membrane 9 homolog (yeast)	5.546	5.054	3.630E-03	3.52E-02	1.41	Duroc-up
COPS2	SNOWBALL_029805_st	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)	6.948	6.202	3.627E-03	3.52E-02	1.68	Duroc-up
Gsk3b	SNOWBALL_042995_st	glycogen synthase kinase 3 beta	8.172	7.831	3.633E-03	3.52E-02	1.27	Duroc-up
NM_138428.2	SNOWBALL_026914_s_st	Sus scrofa clone reje29b_j2.y1.abd, mRNA sequence	7.589	8.044	3.640E-03	3.52E-02	-1.37	PiNN-up
MLF2	SNOWBALL_007431_st	myeloid leukemia factor 2	7.827	8.151	3.643E-03	3.53E-02	-1.25	PiNN-up
DIRC2	SNOWBALL_047342_st	disrupted in renal carcinoma 2	7.819	8.066	3.651E-03	3.53E-02	-1.19	PiNN-up
PKP1	SNOWBALL_043944_st	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome)	4.523	4.768	3.654E-03	3.53E-02	-1.18	PiNN-up
ANKRD17	SNOWBALL_037640_st	ankyrin repeat domain 17	7.981	7.711	3.653E-03	3.53E-02	1.21	Duroc-up
ATP8B1	SNOWBALL_002985_st	ATPase, aminophospholipid transporter, class I, type 8B, member 1	5.807	5.401	3.660E-03	3.53E-02	1.33	Duroc-up
PIK3C2A	SNOWBALL_047051_st	phosphoinositide-3-kinase, class 2, alpha polypeptide	6.843	6.230	3.660E-03	3.53E-02	1.53	Duroc-up
C6orf174	SNOWBALL_002305_st	chromosome 6 open reading frame 174	8.083	7.394	3.659E-03	3.53E-02	1.61	Duroc-up
PBRM1	SNOWBALL_021608_s_st	polybromo 1	8.225	7.943	3.672E-03	3.53E-02	1.22	Duroc-up

FYTTD1	SNOWBALL_033624_st	forty-two-three domain containing 1	8.834	8.457	3.670E-03	3.53E-02	1.30	Duroc-up
TTC35	SNOWBALL_005793_st	tetratricopeptide repeat domain 35	8.352	7.949	3.669E-03	3.53E-02	1.32	Duroc-up
LOC100152449	SNOWBALL_016197_st	Protease Fragment [Source:UniProtKB/TrEMBL;Acc:O62629]	5.705	5.148	3.664E-03	3.53E-02	1.47	Duroc-up
KPNA5	SNOWBALL_027945_st	karyopherin alpha 5 (importin alpha 6)	4.435	3.783	3.672E-03	3.53E-02	1.57	Duroc-up
	SNOWBALL_038462_st		3.871	3.640	3.684E-03	3.54E-02	1.17	Duroc-up
ZNF181	SNOWBALL_008202_st	zinc finger protein 181	4.502	3.779	3.685E-03	3.54E-02	1.65	Duroc-up
	SNOWBALL_045692_st		3.186	3.486	3.688E-03	3.54E-02	-1.23	PiNN-up
VPS26B	SNOWBALL_023282_st	vacuolar protein sorting 26 homolog B (S. pombe)	6.378	6.666	3.702E-03	3.55E-02	-1.22	PiNN-up
EPB41	SNOWBALL_009137_st	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	8.719	8.387	3.710E-03	3.56E-02	1.26	Duroc-up
AP2S1	SNOWBALL_008280_st	adaptor-related protein complex 2, sigma 1 subunit	6.375	6.679	3.715E-03	3.56E-02	-1.23	PiNN-up
	SNOWBALL_044642_st		6.034	6.387	3.723E-03	3.57E-02	-1.28	PiNN-up
SRRD	SNOWBALL_024291_s_st	SRR1 domain containing	5.453	5.793	3.724E-03	3.57E-02	-1.27	PiNN-up
	SNOWBALL_038833_st		6.315	5.850	3.725E-03	3.57E-02	1.38	Duroc-up
HERPUD1	SNOWBALL_025840_s_st	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	8.658	9.232	3.738E-03	3.58E-02	-1.49	PiNN-up
RABEP1	SNOWBALL_015154_s_st	rabaptin, RAB GTPase binding effector protein 1	8.941	8.454	3.738E-03	3.58E-02	1.40	Duroc-up
KIAA0355	SNOWBALL_008103_st	KIAA0355	8.031	7.749	3.749E-03	3.58E-02	1.22	Duroc-up
	SNOWBALL_034239_st	Ssc_hash_S26645717 BW984308 full-length enriched swine cDNA library, adult intestine Sus scrofa cDNA clone ITT010094A01 5prime, mRNA	5.041	4.514	3.748E-03	3.58E-02	1.44	Duroc-up
HCFC2	SNOWBALL_007504_st	host cell factor C2	7.800	7.386	3.756E-03	3.59E-02	1.33	Duroc-up
	SNOWBALL_044867_st		6.471	6.014	3.763E-03	3.59E-02	1.37	Duroc-up
IFRD2	SNOWBALL_025100_st	interferon-related developmental regulator 2	6.465	6.747	3.765E-03	3.59E-02	-1.22	PiNN-up
ANTXR2	SNOWBALL_022383_st	anthrax toxin receptor 2	6.473	6.785	3.770E-03	3.59E-02	-1.24	PiNN-up
FIGF	SNOWBALL_020039_s_st	c-fos induced growth factor (vascular endothelial growth factor D)	5.425	5.831	3.776E-03	3.60E-02	-1.32	PiNN-up
TTLL7	SNOWBALL_035161_st	tubulin tyrosine ligase-like family, member 7	5.253	4.482	3.780E-03	3.60E-02	1.71	Duroc-up
SEMA3C	SNOWBALL_012790_st	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C	8.259	7.899	3.784E-03	3.60E-02	1.28	Duroc-up
LTBR	SNOWBALL_007183_st	lymphotoxin beta receptor (TNFR superfamily, member 3)	6.748	6.974	3.792E-03	3.61E-02	-1.17	PiNN-up
CRBN	SNOWBALL_029068_st	cereblon	6.769	5.984	3.797E-03	3.61E-02	1.72	Duroc-up
NOL8	SNOWBALL_004735_st	nucleolar protein 8	5.530	5.062	3.800E-03	3.61E-02	1.38	Duroc-up

LOC695826	SNOWBALL_033709_st	Ssc_hash_S29974692 PDUts1090D02 Porcine testis cDNA library I Sus scrofa cDNA clone PDUts1090D02 5prime similar to homologue to emb	5.040	4.386	3.802E-03	3.61E-02	1.57	Duroc-up
XPO1	SNOWBALL_005164_st	exportin 1 (CRM1 homolog, yeast)	7.709	7.159	3.806E-03	3.61E-02	1.46	Duroc-up
MEF2A	SNOWBALL_002794_st	myocyte enhancer factor 2A	9.167	8.822	3.817E-03	3.62E-02	1.27	Duroc-up
CROT	SNOWBALL_012647_st	carnitine O-octanoyltransferase	6.569	6.205	3.817E-03	3.62E-02	1.29	Duroc-up
R3HCC1	SNOWBALL_040122_st	R3H domain and coiled-coil containing 1	4.905	5.324	3.828E-03	3.63E-02	-1.34	PiNN-up
ANKRD13C	SNOWBALL_008667_st	ankyrin repeat domain 13C	7.685	7.305	3.833E-03	3.63E-02	1.30	Duroc-up
MIB1	SNOWBALL_031725_st	Ssc_hash_S50198822 susfleck_FC_N_20_D05 SUSFLECK Fat Cell Normalized Sus scrofa cDNA clone 20_D05, mRNA	7.547	7.268	3.841E-03	3.64E-02	1.21	Duroc-up
SEC61A2	SNOWBALL_013676_st	Sec61 alpha 2 subunit (S. cerevisiae)	7.394	7.845	3.843E-03	3.64E-02	-1.37	PiNN-up
PPAP2B	SNOWBALL_047804_st	phosphatidic acid phosphatase type 2B	3.320	3.637	3.852E-03	3.64E-02	-1.25	PiNN-up
NT5E	SNOWBALL_002358_s_st	5 nucleotidase, ecto	6.045	6.339	3.851E-03	3.64E-02	-1.23	PiNN-up
PIGL	SNOWBALL_015019_st	phosphatidylinositol glycan anchor biosynthesis, class L	5.267	5.601	3.869E-03	3.64E-02	-1.26	PiNN-up
NFAT5	SNOWBALL_035224_st	nuclear factor of activated T-cells 5, tonicity-responsive	8.083	7.726	3.869E-03	3.64E-02	1.28	Duroc-up
FBXO30	SNOWBALL_002167_st	F-box protein 30	8.285	7.910	3.866E-03	3.64E-02	1.30	Duroc-up
WBP4	SNOWBALL_013896_st	WW domain binding protein 4 (formin binding protein 21)	6.351	5.952	3.866E-03	3.64E-02	1.32	Duroc-up
IDE	SNOWBALL_024596_st	insulin-degrading enzyme	8.625	8.226	3.862E-03	3.64E-02	1.32	Duroc-up
MMADHC	SNOWBALL_022011_s_st	Sus scrofa mRNA, clone:AMP010045A08, expressed in alveolar macrophages	9.203	8.763	3.861E-03	3.64E-02	1.36	Duroc-up
UHMK1	SNOWBALL_029474_st	U2AF homology motif (UHM) kinase 1	7.511	7.056	3.855E-03	3.64E-02	1.37	Duroc-up
RASSF8	SNOWBALL_007314_st	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	7.742	7.193	3.859E-03	3.64E-02	1.46	Duroc-up
TMBIM4	SNOWBALL_007125_st	transmembrane BAX inhibitor motif containing 4	6.977	6.506	3.876E-03	3.65E-02	1.39	Duroc-up
ZC3H6	SNOWBALL_032910_st	zinc finger CCCH-type containing 6	4.109	3.676	3.881E-03	3.65E-02	1.35	Duroc-up
PROX1	SNOWBALL_044815_st	prospero homeobox 1	4.610	3.707	3.913E-03	3.68E-02	1.87	Duroc-up
Rnu2-10	SNOWBALL_011694_x_st	U2 spliceosomal RNA [Source: RFAM;Acc:RF00004]	6.246	5.810	3.919E-03	3.68E-02	1.35	Duroc-up
CHMP2B	SNOWBALL_015872_st	chromatin modifying protein 2B	6.836	6.229	3.920E-03	3.68E-02	1.52	Duroc-up
THTPA	SNOWBALL_010261_st	thiamine triphosphatase	6.036	6.369	3.923E-03	3.68E-02	-1.26	PiNN-up
GTF2F2	SNOWBALL_026373_s_st	general transcription factor IIF, polypeptide 2, 30kDa	6.828	6.251	3.926E-03	3.68E-02	1.49	Duroc-up
TRIM9	SNOWBALL_044377_st	tripartite motif containing 9	5.663	5.222	3.936E-03	3.69E-02	1.36	Duroc-up
LRPAP1	SNOWBALL_037798_st	low density lipoprotein receptor-related protein 1	7.420	7.677	3.954E-03	3.70E-02	-1.19	PiNN-up
UBN1	SNOWBALL_004809_st	ubinuclein 1	6.457	6.735	3.968E-03	3.71E-02	-1.21	PiNN-up

SGSM3	SNOWBALL_006742_st	small G protein signaling modulator 3	6.097	6.318	3.985E-03	3.71E-02	-1.17	PiNN-up
MOCS3	SNOWBALL_000448_st	molybdenum cofactor synthesis 3	5.342	5.540	3.981E-03	3.71E-02	-1.15	PiNN-up
SEL1L	SNOWBALL_010676_st	sel-1 suppressor of lin-12-like (C. elegans)	7.761	7.474	3.984E-03	3.71E-02	1.22	Duroc-up
ARHGAP29	SNOWBALL_006364_st	Rho GTPase activating protein 29	6.513	6.224	3.966E-03	3.71E-02	1.22	Duroc-up
GABPA	SNOWBALL_035452_st	GA binding protein transcription factor, alpha subunit 60kDa	6.953	6.593	3.974E-03	3.71E-02	1.28	Duroc-up
ALG11	SNOWBALL_013873_st	asparagine-linked glycosylation 11, alpha-1,2-mannosyltransferase homolog (yeast)	6.140	5.715	3.977E-03	3.71E-02	1.34	Duroc-up
KRIT1	SNOWBALL_012813_st	KRIT1, ankyrin repeat containing	6.381	5.929	3.972E-03	3.71E-02	1.37	Duroc-up
BIRC6	SNOWBALL_005341_st	baculoviral IAP repeat containing 6	6.687	6.228	3.977E-03	3.71E-02	1.37	Duroc-up
GPRIN3	SNOWBALL_046620_st	GPRIN family member 3	5.843	5.255	3.985E-03	3.71E-02	1.50	Duroc-up
	SNOWBALL_032574_st	Ssc_hash_S22280195 CJ022925 full-length enriched swine cDNA library, adult trachea Sus scrofa cDNA clone TCH01H100006 5prime, mRNA	5.818	5.156	3.980E-03	3.71E-02	1.58	Duroc-up
LOC100517562	SNOWBALL_042364_st	heparan-alpha-glucosaminide N-acetyltransferase-like	6.874	7.194	3.990E-03	3.71E-02	-1.25	PiNN-up
EIF2AK2	SNOWBALL_004948_st	eukaryotic translation initiation factor 2-alpha kinase 2	5.758	5.319	3.993E-03	3.72E-02	1.36	Duroc-up
EXOC6	SNOWBALL_017043_st	exocyst complex component 6	4.925	4.412	3.996E-03	3.72E-02	1.43	Duroc-up
ACVR1B	SNOWBALL_007062_st	activin A receptor, type IB	6.478	6.939	4.003E-03	3.72E-02	-1.38	PiNN-up
COPS7A	SNOWBALL_007228_st	COP9 constitutive photomorphogenic homolog subunit 7A (Arabidopsis)	7.521	7.923	4.015E-03	3.73E-02	-1.32	PiNN-up
WNK1	SNOWBALL_007756_st	WNK lysine deficient protein kinase 1	9.545	9.333	4.015E-03	3.73E-02	1.16	Duroc-up
ZNF518B	SNOWBALL_043525_st	zinc finger protein 518B	5.953	6.188	4.024E-03	3.73E-02	-1.18	PiNN-up
NUDT7	SNOWBALL_007910_st	nudix (nucleoside diphosphate linked moiety X)-type motif 7	6.117	6.775	4.027E-03	3.74E-02	-1.58	PiNN-up
ARPC2	SNOWBALL_018102_st	actin related protein 2/3 complex, subunit 2, 34kDa	5.069	5.471	4.032E-03	3.74E-02	-1.32	PiNN-up
	SNOWBALL_046109_st		4.943	5.730	4.037E-03	3.74E-02	-1.73	PiNN-up
SUZ12	SNOWBALL_014445_s_st	suppressor of zeste 12 homolog (Drosophila)	6.261	5.729	4.041E-03	3.74E-02	1.45	Duroc-up
	SNOWBALL_039209_st		4.657	4.004	4.042E-03	3.74E-02	1.57	Duroc-up
PRPF8	SNOWBALL_015014_st	PRP8 pre-mRNA processing factor 8 homolog (S. cerevisiae)	8.786	9.040	4.061E-03	3.76E-02	-1.19	PiNN-up
CYP24A1	SNOWBALL_000478_st	cytochrome P450, family 24, subfamily A, polypeptide 1	2.797	3.042	4.065E-03	3.76E-02	-1.18	PiNN-up
SPATA2	SNOWBALL_022336_st	spermatogenesis associated 2	6.397	6.662	4.072E-03	3.76E-02	-1.20	PiNN-up
SCAMP3	SNOWBALL_005858_s_st	secretory carrier membrane protein 3	8.022	8.253	4.074E-03	3.76E-02	-1.17	PiNN-up
CCDC59	SNOWBALL_007536_st	coiled-coil domain containing 59	5.911	5.428	4.072E-03	3.76E-02	1.40	Duroc-up

VRK2	SNOWBALL_005400_st	vaccinia related kinase 2	4.778	4.224	4.080E-03	3.77E-02	1.47	Duroc-up
	SNOWBALL_041499_st		5.255	5.743	4.095E-03	3.77E-02	-1.40	PiNN-up
TRIM68	SNOWBALL_030996_st	tripartite motif containing 68	4.669	5.069	4.098E-03	3.77E-02	-1.32	PiNN-up
BAT3	SNOWBALL_001242_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	7.573	7.908	4.094E-03	3.77E-02	-1.26	PiNN-up
TXLNB	SNOWBALL_035918_st	taxilin beta	7.748	7.185	4.097E-03	3.77E-02	1.48	Duroc-up
LOC100513974	SNOWBALL_025396_st	Sus scrofa mRNA, clone:UTR010057A01, expressed in uterus	6.148	6.425	4.103E-03	3.78E-02	-1.21	PiNN-up
ERO1LB	SNOWBALL_016653_s_st	ERO1-like beta (S. cerevisiae)	5.729	5.305	4.114E-03	3.78E-02	1.34	Duroc-up
ACACB	SNOWBALL_016843_s_st	acetyl-CoA carboxylase beta	7.784	8.154	4.123E-03	3.79E-02	-1.29	PiNN-up
CTNNAL1	SNOWBALL_004161_st	catenin (cadherin-associated protein), alpha-like 1	6.504	5.930	4.124E-03	3.79E-02	1.49	Duroc-up
PPP3CA	SNOWBALL_025699_s_st	protein phosphatase 3, catalytic subunit, alpha isozyme	9.222	8.481	4.124E-03	3.79E-02	1.67	Duroc-up
ATAD1	SNOWBALL_024618_s_st	ATPase family, AAA domain containing 1	6.755	6.294	4.133E-03	3.79E-02	1.38	Duroc-up
	SNOWBALL_035514_st	Ssc_hash_S16769907 842259 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	4.504	4.940	4.144E-03	3.80E-02	-1.35	PiNN-up
POLR3A	SNOWBALL_038903_st	polymerase (RNA) III (DNA directed) polypeptide A, 155kDa	5.535	5.931	4.154E-03	3.81E-02	-1.32	PiNN-up
ATAD1	SNOWBALL_017139_s_st	ATPase family, AAA domain containing 1	8.378	8.128	4.157E-03	3.81E-02	1.19	Duroc-up
ITGB6	SNOWBALL_017817_st	integrin, beta 6	7.515	7.155	4.157E-03	3.81E-02	1.28	Duroc-up
	SNOWBALL_032705_st	Ssc_hash_S22301407 CJ000765 full-length enriched swine cDNA library, adult liver Sus scrofa cDNA clone LVR01A070092 5prime, mRNA s	6.613	6.117	4.153E-03	3.81E-02	1.41	Duroc-up
MRS2	SNOWBALL_009546_st	MRS2 magnesium homeostasis factor homolog (S. cerevisiae)	7.197	6.829	4.160E-03	3.81E-02	1.29	Duroc-up
CYS1	SNOWBALL_028537_st	cystin 1	7.460	8.074	4.169E-03	3.81E-02	-1.53	PiNN-up
EIF2C1	SNOWBALL_027263_st	eukaryotic translation initiation factor 2C, 1	6.417	6.654	4.168E-03	3.81E-02	-1.18	PiNN-up
NM_015934.3	SNOWBALL_026960_s_st	NOP58 ribonucleoprotein homolog (yeast)	7.223	6.650	4.169E-03	3.81E-02	1.49	Duroc-up
	SNOWBALL_027892_st	Ssc_hash_S19541420 946228 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	6.384	5.781	4.176E-03	3.81E-02	1.52	Duroc-up
COL6A1	SNOWBALL_027821_st	collagen, type VI, alpha 1	8.337	8.712	4.184E-03	3.82E-02	-1.30	PiNN-up
TMEM127	SNOWBALL_004915_st	transmembrane protein 127	6.760	7.073	4.183E-03	3.82E-02	-1.24	PiNN-up
SPG7	SNOWBALL_042449_st	spastic paraplegia 7 (pure and complicated autosomal recessive)	6.458	6.707	4.195E-03	3.83E-02	-1.19	PiNN-up
CLN6	SNOWBALL_002792_st	ceroid-lipofuscinosis, neuronal 6, late infantile, variant	6.014	6.614	4.199E-03	3.83E-02	-1.52	PiNN-up
LOC100525406	SNOWBALL_008819_st	non-histone chromosomal protein HMG-14-like	4.535	4.785	4.198E-03	3.83E-02	-1.19	PiNN-up

DUS2L	SNOWBALL_047232_st	DEAD (Asp-Glu-Ala-Asp) box polypeptide 28	5.854	6.150	4.202E-03	3.83E-02	-1.23	PiNN-up
SLC3A2	SNOWBALL_025433_st	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	6.927	7.209	4.215E-03	3.84E-02	-1.22	PiNN-up
ICMT	SNOWBALL_008273_st	isoprenylcysteine carboxyl methyltransferase	7.453	7.713	4.223E-03	3.84E-02	-1.20	PiNN-up
	SNOWBALL_034981_st	Ssc_hash_S18556585 BX925236 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0017.a.03 5prim, mRNA	4.350	4.813	4.232E-03	3.84E-02	-1.38	PiNN-up
SNORA16A	SNOWBALL_042494_st	small nucleolar RNA, H/ACA box 16A	6.025	6.272	4.236E-03	3.84E-02	-1.19	PiNN-up
PRKAR2A	SNOWBALL_022894_s_st	protein kinase, cAMP-dependent, regulatory, type II, alpha	9.699	9.441	4.235E-03	3.84E-02	1.20	Duroc-up
ARMC8	SNOWBALL_022058_s_st	armadillo repeat containing 8	7.474	7.134	4.233E-03	3.84E-02	1.27	Duroc-up
RSRC2	SNOWBALL_024408_s_st	arginine/serine-rich coiled-coil 2	5.755	5.346	4.233E-03	3.84E-02	1.33	Duroc-up
SLC16A5	SNOWBALL_014259_st	solute carrier family 16, member 5 (monocarboxylic acid transporter 6)	8.288	8.825	4.241E-03	3.85E-02	-1.45	PiNN-up
MEF2D	SNOWBALL_023377_s_st	myocyte enhancer factor 2D	9.629	9.867	4.243E-03	3.85E-02	-1.18	PiNN-up
LRP10	SNOWBALL_036123_st	low density lipoprotein receptor-related protein 10	4.431	4.884	4.252E-03	3.85E-02	-1.37	PiNN-up
LOC735715	SNOWBALL_038819_st	hypothetical protein LOC735715	4.763	5.057	4.266E-03	3.85E-02	-1.23	PiNN-up
RPS20	SNOWBALL_000484_st	OTTSUSG00000000579 ribosomal protein S20 (RPS20) pseudogene	4.913	5.179	4.259E-03	3.85E-02	-1.20	PiNN-up
TOMM34	SNOWBALL_019367_s_st	translocase of outer mitochondrial membrane 34	5.714	5.944	4.266E-03	3.85E-02	-1.17	PiNN-up
FXR2	SNOWBALL_000215_st	fragile X mental retardation, autosomal homolog 2	8.260	8.454	4.264E-03	3.85E-02	-1.14	PiNN-up
VKORC1L1	SNOWBALL_032633_st	vitamin K epoxide reductase complex, subunit 1-like 1	8.462	8.023	4.261E-03	3.85E-02	1.36	Duroc-up
DDO	SNOWBALL_002652_s_st	d-aspartate oxidase-like	6.474	5.627	4.259E-03	3.85E-02	1.80	Duroc-up
GLS	SNOWBALL_023892_st	glutaminase	5.784	5.549	4.274E-03	3.86E-02	1.18	Duroc-up
PPM1K	SNOWBALL_028536_st	protein phosphatase, Mg2+/Mn2+ dependent, 1K	6.028	5.409	4.273E-03	3.86E-02	1.54	Duroc-up
CP	SNOWBALL_000250_s_st	ceruloplasmin (ferroxidase)	5.879	5.673	4.282E-03	3.86E-02	1.15	Duroc-up
NUS1	SNOWBALL_002278_st	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	7.351	7.073	4.281E-03	3.86E-02	1.21	Duroc-up
CASC4	SNOWBALL_003068_st	protein CASC4-like	5.861	5.376	4.278E-03	3.86E-02	1.40	Duroc-up
ARPP19	SNOWBALL_002534_st	cAMP-regulated phosphoprotein, 19kDa	8.475	7.955	4.285E-03	3.86E-02	1.43	Duroc-up
SCAMP3	SNOWBALL_005899_s_st	secretory carrier membrane protein 3	8.208	8.617	4.293E-03	3.86E-02	-1.33	PiNN-up
MXD4	SNOWBALL_011253_st	MAX dimerization protein 4	6.759	6.955	4.292E-03	3.86E-02	-1.15	PiNN-up
LOC100512762	SNOWBALL_026474_st	Sus scrofa mRNA, clone:AMP010075A12, expressed in alveolar macrophage	12.589	12.342	4.294E-03	3.86E-02	1.19	Duroc-up
BPGM	SNOWBALL_019685_st	2,3-bisphosphoglycerate mutase	8.573	9.288	4.298E-03	3.86E-02	-1.64	PiNN-up

UBR3	SNOWBALL_028973_st	ubiquitin protein ligase E3 component n-recognin 3 (putative)	6.560	5.896	4.299E-03	3.86E-02	1.58	Duroc-up
LOC100521864	SNOWBALL_034948_st	Ssc_hash_S17527502 BX676460 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0031.h.14 3prim, mRNA	5.201	5.406	4.305E-03	3.86E-02	-1.15	PiNN-up
SNAPC1	SNOWBALL_003276_st	small nuclear RNA activating complex, polypeptide 1, 43kDa	6.321	5.937	4.304E-03	3.86E-02	1.31	Duroc-up
LRP1B	SNOWBALL_007126_st	low density lipoprotein receptor-related protein 1B	7.359	7.620	4.309E-03	3.86E-02	-1.20	PiNN-up
SPEG	SNOWBALL_013478_st	SPEG complex locus	5.432	5.676	4.310E-03	3.86E-02	-1.18	PiNN-up
	SNOWBALL_041500_st		3.537	3.730	4.313E-03	3.86E-02	-1.14	PiNN-up
SP100	SNOWBALL_003026_st	SP100 nuclear antigen	8.282	7.908	4.314E-03	3.86E-02	1.30	Duroc-up
LOC100525416	SNOWBALL_012215_st	GPI-linked NAD(P)(+)--arginine ADP-ribosyltransferase 1-like	7.669	8.092	4.322E-03	3.87E-02	-1.34	PiNN-up
OGFR	SNOWBALL_037479_s_st	opioid growth factor receptor	5.186	5.542	4.320E-03	3.87E-02	-1.28	PiNN-up
RBM22	SNOWBALL_025431_st	RNA binding motif protein 22	6.592	6.844	4.347E-03	3.88E-02	-1.19	PiNN-up
NVL	SNOWBALL_027983_st	nuclear VCP-like	5.370	5.065	4.347E-03	3.88E-02	1.23	Duroc-up
TNIK	SNOWBALL_023077_st	TRAF2 and NCK interacting kinase	6.921	6.558	4.349E-03	3.88E-02	1.29	Duroc-up
PPFIA1	SNOWBALL_045858_st	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 1	5.220	5.545	4.360E-03	3.89E-02	-1.25	PiNN-up
POLI	SNOWBALL_002529_st	polymerase (DNA directed) iota	6.381	6.015	4.361E-03	3.89E-02	1.29	Duroc-up
USP13	SNOWBALL_015573_st	ubiquitin specific peptidase 13 (isopeptidase T-3)	10.505	10.289	4.369E-03	3.90E-02	1.16	Duroc-up
FOLR2	SNOWBALL_012178_st	folate receptor 3 (gamma)	6.405	6.953	4.380E-03	3.90E-02	-1.46	PiNN-up
AMD1	SNOWBALL_002637_st	adenosylmethionine decarboxylase 1	9.078	8.668	4.382E-03	3.90E-02	1.33	Duroc-up
C1orf21	SNOWBALL_035524_st	chromosome 1 open reading frame 21	6.725	6.482	4.393E-03	3.91E-02	1.18	Duroc-up
CUL3	SNOWBALL_017995_st	cullin-3-like	7.964	7.446	4.393E-03	3.91E-02	1.43	Duroc-up
PTPRK	SNOWBALL_002222_st	protein tyrosine phosphatase, receptor type, K	6.532	6.011	4.390E-03	3.91E-02	1.44	Duroc-up
C2orf69	SNOWBALL_035943_st	chromosome 2 open reading frame 69	3.751	3.132	4.397E-03	3.91E-02	1.54	Duroc-up
RNF125	SNOWBALL_039405_st	ring finger protein 125	4.875	4.383	4.402E-03	3.91E-02	1.41	Duroc-up
CD52	SNOWBALL_021837_st	CD52 molecule	5.470	5.985	4.409E-03	3.92E-02	-1.43	PiNN-up
SMCHD1	SNOWBALL_030292_st	structural maintenance of chromosomes flexible hinge domain containing 1	7.468	6.958	4.412E-03	3.92E-02	1.42	Duroc-up
MAF	SNOWBALL_021586_s_st	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	8.724	9.046	4.418E-03	3.92E-02	-1.25	PiNN-up
GAPDH	SNOWBALL_007200_st	glyceraldehyde-3-phosphate dehydrogenase	13.758	13.843	4.423E-03	3.92E-02	-1.06	PiNN-up
ESF1	SNOWBALL_019046_s_st	ESF1 homolog	6.464	5.878	4.423E-03	3.92E-02	1.50	Duroc-up
LOC100157940	SNOWBALL_009951_s_st	transcription factor EB-like	6.646	6.851	4.428E-03	3.92E-02	-1.15	PiNN-up

LARP4	SNOWBALL_032580_st	La ribonucleoprotein domain family, member 4	6.439	5.742	4.430E-03	3.92E-02	1.62	Duroc-up
GAB2	SNOWBALL_030527_st	GRB2-associated binding protein 2	6.244	6.397	4.435E-03	3.93E-02	-1.11	PiNN-up
PRMT7	SNOWBALL_007971_s_st	protein arginine methyltransferase 7	6.249	6.581	4.461E-03	3.94E-02	-1.26	PiNN-up
SLC1A3	SNOWBALL_018599_st	solute carrier family 1 (glial high affinity glutamate transporter), member 3	6.571	6.266	4.458E-03	3.94E-02	1.24	Duroc-up
CSE1L	SNOWBALL_025413_st	CSE1 chromosome segregation 1-like (yeast)	7.848	7.369	4.461E-03	3.94E-02	1.39	Duroc-up
	SNOWBALL_037094_st	Ssc_hash_S50200199 susfleck_FC_N_15_F04 SUSFLECK Fat Cell Normalized Sus scrofa cDNA clone 15_F04, mRNA	3.843	3.244	4.455E-03	3.94E-02	1.51	Duroc-up
CBR4	SNOWBALL_024112_s_st	PREDICTED: Sus scrofa similar to MGC138958 protein (LOC100153608), mRNA	6.219	5.539	4.458E-03	3.94E-02	1.60	Duroc-up
DARS	SNOWBALL_017662_st	aspartyl-tRNA synthetase	7.873	7.355	4.472E-03	3.94E-02	1.43	Duroc-up
CCAR1	SNOWBALL_017434_s_st	cell division cycle and apoptosis regulator 1	7.504	6.915	4.471E-03	3.94E-02	1.50	Duroc-up
RUVBL2	SNOWBALL_008378_st	RuvB-like 2 (E. coli)	6.107	6.339	4.488E-03	3.96E-02	-1.17	PiNN-up
ZNF740	SNOWBALL_030467_st	zinc finger protein 740	5.405	5.615	4.487E-03	3.96E-02	-1.16	PiNN-up
ABHD13	SNOWBALL_029786_st	abhydrolase domain containing 13	6.066	5.587	4.499E-03	3.96E-02	1.39	Duroc-up
RWDD1	SNOWBALL_016710_st	RWD domain containing 1	6.864	6.316	4.499E-03	3.96E-02	1.46	Duroc-up
TAF1B	SNOWBALL_004962_st	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	5.402	4.976	4.507E-03	3.97E-02	1.34	Duroc-up
LOC100520695	SNOWBALL_014717_st	spindle and kinetochore-associated protein 2-like	6.222	5.699	4.511E-03	3.97E-02	1.44	Duroc-up
PPAPDC3	SNOWBALL_003660_st	phosphatidic acid phosphatase type 2 domain containing 3	6.791	7.136	4.529E-03	3.98E-02	-1.27	PiNN-up
ERP44	SNOWBALL_003949_s_st	endoplasmic reticulum protein 44	7.071	6.776	4.530E-03	3.98E-02	1.23	Duroc-up
RSBN1L	SNOWBALL_026922_s_st	round spermatid basic protein 1-like	6.518	6.281	4.540E-03	3.98E-02	1.18	Duroc-up
CHUK	SNOWBALL_017391_s_st	conserved helix-loop-helix ubiquitous kinase	7.686	7.385	4.541E-03	3.98E-02	1.23	Duroc-up
	SNOWBALL_036111_st	Ssc_hash_S39800433 rcbe24_p14.y1 cbe Sus scrofa cDNA 5prime, mRNA	5.550	5.074	4.539E-03	3.98E-02	1.39	Duroc-up
MTERFD3	SNOWBALL_006849_st	MTERF domain containing 3	5.637	5.097	4.534E-03	3.98E-02	1.45	Duroc-up
C5orf41	SNOWBALL_030137_st	chromosome 5 open reading frame 41	5.123	4.809	4.545E-03	3.98E-02	1.24	Duroc-up
CNOT6L	SNOWBALL_028358_st	CCR4-NOT transcription complex, subunit 6-like	6.363	5.864	4.555E-03	3.99E-02	1.41	Duroc-up
Hook3	SNOWBALL_047673_st	hook homolog 3 (Drosophila)	5.223	4.940	4.560E-03	3.99E-02	1.22	Duroc-up
ABCF3	SNOWBALL_022411_st	ATP-binding cassette, sub-family F (GCN20), member 3	7.868	8.149	4.570E-03	4.00E-02	-1.21	PiNN-up
FAM122A	SNOWBALL_027486_st	family with sequence similarity 122A	6.946	6.435	4.580E-03	4.01E-02	1.42	Duroc-up
	SNOWBALL_046733_st		4.652	3.988	4.585E-03	4.01E-02	1.59	Duroc-up
RAB35	SNOWBALL_016630_st	Ras-related protein Rab-18	6.352	6.685	4.593E-03	4.01E-02	-1.26	PiNN-up
ZFP36L1	SNOWBALL_047306_st	zinc finger protein 36, C3H1 type-like 1-like	4.018	4.411	4.605E-03	4.02E-02	-1.31	PiNN-up

ZNF828	SNOWBALL_035412_st	zinc finger protein 828	6.251	6.531	4.611E-03	4.02E-02	-1.21	PiNN-up
ZFHX3	SNOWBALL_032769_st	zinc finger homeobox 3	5.165	4.817	4.609E-03	4.02E-02	1.27	Duroc-up
TBL1XR1	SNOWBALL_036623_st	transducin (beta)-like 1 X-linked receptor 1	3.876	3.303	4.610E-03	4.02E-02	1.49	Duroc-up
ZNF423	SNOWBALL_008083_st	zinc finger protein 423	6.758	7.034	4.622E-03	4.03E-02	-1.21	PiNN-up
RUFY3	SNOWBALL_042564_st	RUN and FYVE domain containing 3	7.093	6.672	4.620E-03	4.03E-02	1.34	Duroc-up
MAP3K7	SNOWBALL_000027_s_st	mitogen-activated protein kinase kinase kinase 7	6.632	6.179	4.621E-03	4.03E-02	1.37	Duroc-up
NET1	SNOWBALL_034803_st	Ssc_hash_S18551801 BX920452 Sus Scrofa library (scan) Sus scrofa cDNA clone scan0009.d.05 5prim, mRNA	5.069	4.637	4.624E-03	4.03E-02	1.35	Duroc-up
POLG	SNOWBALL_010642_st	polymerase (DNA directed), gamma	6.826	7.002	4.638E-03	4.03E-02	-1.13	PiNN-up
KDM5C	SNOWBALL_020197_s_st	lysine (K)-specific demethylase 5C	6.139	6.300	4.636E-03	4.03E-02	-1.12	PiNN-up
MTERF	SNOWBALL_012768_st	mitochondrial transcription termination factor	5.536	5.041	4.640E-03	4.03E-02	1.41	Duroc-up
LOC100520105	SNOWBALL_016175_st	protein EURL homolog	5.929	5.436	4.647E-03	4.04E-02	1.41	Duroc-up
KIF1B	SNOWBALL_047802_st	kinesin family member 1B	7.970	7.542	4.656E-03	4.04E-02	1.34	Duroc-up
FAM133B	SNOWBALL_012580_st	hypothetical protein LOC100519438	6.080	5.604	4.655E-03	4.04E-02	1.39	Duroc-up
TRAM1	SNOWBALL_005783_st	translocation associated membrane protein 1	8.468	8.069	4.667E-03	4.05E-02	1.32	Duroc-up
PRKD3	SNOWBALL_005002_st	protein kinase D3	7.549	7.175	4.669E-03	4.05E-02	1.30	Duroc-up
PAFAH1B1	SNOWBALL_026576_st	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	8.205	7.788	4.671E-03	4.05E-02	1.34	Duroc-up
C1QB	SNOWBALL_009008_s_st	Complement C1qB Fragment	6.331	6.873	4.680E-03	4.05E-02	-1.46	PiNN-up
NACA	SNOWBALL_040157_st	nascent polypeptide-associated complex alpha subunit	7.786	8.161	4.684E-03	4.06E-02	-1.30	PiNN-up
NIPSNAP3B	SNOWBALL_003509_s_st	nipsnap homolog 3A	5.648	5.381	4.688E-03	4.06E-02	1.20	Duroc-up
CTDSPL2	SNOWBALL_002942_st	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	5.682	5.176	4.686E-03	4.06E-02	1.42	Duroc-up
RAB10	SNOWBALL_005468_st	RAB10, member RAS oncogene family	8.676	8.439	4.696E-03	4.06E-02	1.18	Duroc-up
CLPX	SNOWBALL_002817_st	ClpX caseinolytic peptidase X homolog (E. coli)	8.869	8.439	4.715E-03	4.07E-02	1.35	Duroc-up
hsa-mir-1208	hsa-mir-1208_st	MI0006341	4.122	4.721	4.728E-03	4.08E-02	-1.51	PiNN-up
FAM40A	SNOWBALL_006444_st	family with sequence similarity 40, member A	6.031	6.332	4.732E-03	4.09E-02	-1.23	PiNN-up
UBE2W	SNOWBALL_005688_st	ubiquitin-conjugating enzyme E2W (putative)	7.259	6.851	4.736E-03	4.09E-02	1.33	Duroc-up
DDX21	SNOWBALL_017324_s_st	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	7.601	7.226	4.744E-03	4.09E-02	1.30	Duroc-up
AFTPH	SNOWBALL_005034_st	aftiphilin	8.060	7.702	4.750E-03	4.10E-02	1.28	Duroc-up
SPG11	SNOWBALL_002793_st	spatacsin-like	6.554	6.283	4.764E-03	4.10E-02	1.21	Duroc-up
FAM177A1	SNOWBALL_010662_st	family with sequence similarity 177, member A1	5.912	5.549	4.765E-03	4.10E-02	1.29	Duroc-up
	SNOWBALL_036538_st	Ssc_hash_S41575013 PIC-A-1239 Sus Scrofa Adipocyte Zap Express Library After differentiation Sus scrofa cDNA clone SS-AA-4-2a-T3_M18, mRNA	5.485	4.931	4.777E-03	4.11E-02	1.47	Duroc-up

PP2D1	SNOWBALL_040030_st	caveolin 1, caveolae protein, 22kDa	5.587	5.269	4.786E-03	4.12E-02	1.25	Duroc-up
HLA-A	SNOWBALL_009808_s_st	MHC class I antigen 8	5.648	6.119	4.793E-03	4.12E-02	-1.39	PiNN-up
SUFU	SNOWBALL_017281_s_st	suppressor of fused homolog (Drosophila)	6.025	6.265	4.793E-03	4.12E-02	-1.18	PiNN-up
PI4KB	SNOWBALL_006564_st	phosphatidylinositol 4-kinase, catalytic, beta	7.446	7.683	4.796E-03	4.12E-02	-1.18	PiNN-up
RBL2	SNOWBALL_031636_st	retinoblastoma-like 2 (p130)	7.151	6.784	4.808E-03	4.13E-02	1.29	Duroc-up
TCP11L2	SNOWBALL_006798_st	t-complex 11 (mouse)-like 2	7.854	7.552	4.815E-03	4.13E-02	1.23	Duroc-up
LOC100510500	SNOWBALL_028379_st	Ssc_hash_S34511316 DB789786 full-length enriched swine cDNA library, adult adrenal gland Sus scrofa cDNA clone ADR010093F08 5prime, mRNA	6.565	6.810	4.835E-03	4.14E-02	-1.18	PiNN-up
DIMT1L	SNOWBALL_025859_s_st	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	6.727	6.210	4.836E-03	4.14E-02	1.43	Duroc-up
SLC35F5	SNOWBALL_024058_st	PREDICTED: Sus scrofa similar to Solute carrier family 35 member F5 (LOC100157997), mRNA	8.299	7.726	4.835E-03	4.14E-02	1.49	Duroc-up
AGXT2L2	SNOWBALL_046302_st	alanine-glyoxylate aminotransferase 2-like 2	6.389	6.682	4.840E-03	4.15E-02	-1.22	PiNN-up
CU302278.2	SNOWBALL_000810_st	OTTSUSG00000000742	5.795	5.654	4.842E-03	4.15E-02	1.10	Duroc-up
TRMT1L	SNOWBALL_027289_st	TRM1 tRNA methyltransferase 1-like	5.712	5.037	4.849E-03	4.15E-02	1.60	Duroc-up
PARP3	SNOWBALL_021632_st	poly (ADP-ribose) polymerase family, member 3	6.493	6.717	4.854E-03	4.15E-02	-1.17	PiNN-up
C1orf55	SNOWBALL_013293_st	chromosome 1 open reading frame 55	6.543	6.848	4.868E-03	4.16E-02	-1.24	PiNN-up
CLSTN1	SNOWBALL_009072_st	calsyntenin 1	6.883	7.058	4.876E-03	4.17E-02	-1.13	PiNN-up
ALKBH8	SNOWBALL_047047_st	alkB, alkylation repair homolog 8 (E. coli)	5.684	5.318	4.885E-03	4.17E-02	1.29	Duroc-up
EMILIN2	SNOWBALL_009052_st	elastin microfibril interfacer 2	5.664	5.941	4.892E-03	4.18E-02	-1.21	PiNN-up
ZNF142	SNOWBALL_017960_st	zinc finger protein 142	6.103	6.342	4.902E-03	4.18E-02	-1.18	PiNN-up
	SNOWBALL_039731_st		3.279	3.833	4.911E-03	4.19E-02	-1.47	PiNN-up
C10orf76	SNOWBALL_017319_st	chromosome 10 open reading frame 76	8.001	8.256	4.910E-03	4.19E-02	-1.19	PiNN-up
NUAK1	SNOWBALL_045972_st	NUAK family, SNF1-like kinase, 1	3.375	3.625	4.916E-03	4.19E-02	-1.19	PiNN-up
JAK1	SNOWBALL_008653_st	Janus kinase 1	9.552	9.377	4.914E-03	4.19E-02	1.13	Duroc-up
SLC29A1	SNOWBALL_010085_s_st	solute carrier family 29 (nucleoside transporters), member 1	8.845	9.215	4.922E-03	4.19E-02	-1.29	PiNN-up
SETD1A	SNOWBALL_004592_st	SET domain containing 1A	5.647	5.871	4.928E-03	4.19E-02	-1.17	PiNN-up
LACE1	SNOWBALL_037010_st	lactation elevated 1	6.087	5.660	4.928E-03	4.19E-02	1.34	Duroc-up
IL6ST	SNOWBALL_035411_st	interleukin 6 signal transducer (gp130, oncostatin M receptor)	6.273	5.597	4.933E-03	4.19E-02	1.60	Duroc-up
SPOPL	SNOWBALL_030110_st	speckle-type POZ protein-like	6.226	5.706	4.947E-03	4.20E-02	1.43	Duroc-up
INPP4B	SNOWBALL_011664_st	inositol polyphosphate-4-phosphatase, type II, 105kDa	7.338	6.948	4.959E-03	4.21E-02	1.31	Duroc-up
RNF19A	SNOWBALL_005779_st	ring finger protein 19A	7.809	7.414	4.960E-03	4.21E-02	1.32	Duroc-up

UBE2D1	SNOWBALL_017022_st	ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast)	8.872	8.443	4.956E-03	4.21E-02	1.35	Duroc-up
PM20D2	SNOWBALL_002353_st	peptidase M20 domain containing 2	7.342	6.856	4.961E-03	4.21E-02	1.40	Duroc-up
SUSD4	SNOWBALL_013341_st	sushi domain containing 4	5.788	6.140	4.969E-03	4.21E-02	-1.28	PiNN-up
MAP3K2	SNOWBALL_028282_st	mitogen-activated protein kinase kinase kinase 2	5.551	5.150	4.974E-03	4.21E-02	1.32	Duroc-up
CFL2	SNOWBALL_010443_st	cofilin 2 (muscle)	9.049	8.661	4.985E-03	4.22E-02	1.31	Duroc-up
MRPL46	SNOWBALL_002853_st	mitochondrial ribosomal protein L46	7.082	7.399	4.989E-03	4.22E-02	-1.25	PiNN-up
DNASE1L1	SNOWBALL_022443_s_st	deoxyribonuclease I-like 1	7.294	7.661	4.994E-03	4.22E-02	-1.29	PiNN-up
TELO2	SNOWBALL_004640_st	TEL2, telomere maintenance 2, homolog (S. cerevisiae)	5.950	6.148	4.994E-03	4.22E-02	-1.15	PiNN-up
MAP3K2	SNOWBALL_040179_st	mitogen-activated protein kinase kinase kinase 2	4.210	3.820	5.002E-03	4.23E-02	1.31	Duroc-up
C7orf10	SNOWBALL_019935_st	chromosome 7 open reading frame 10	7.521	7.804	5.020E-03	4.24E-02	-1.22	PiNN-up
CBX6	SNOWBALL_027233_st	chromobox homolog 6	5.442	5.800	5.025E-03	4.24E-02	-1.28	PiNN-up
CREG1	SNOWBALL_006066_st	cellular repressor of E1A-stimulated genes 1	7.702	7.401	5.029E-03	4.25E-02	1.23	Duroc-up
LDOC1L	SNOWBALL_006718_st	leucine zipper, down-regulated in cancer 1-like	6.206	6.412	5.046E-03	4.26E-02	-1.15	PiNN-up
TMEM59	SNOWBALL_026406_s_st	transmembrane protein 59	7.525	7.016	5.044E-03	4.26E-02	1.42	Duroc-up
NAPG	SNOWBALL_022039_st	N-ethylmaleimide-sensitive factor attachment protein, gamma	6.419	6.690	5.056E-03	4.26E-02	-1.21	PiNN-up
DMTF1	SNOWBALL_012838_st	cyclin D binding myb-like transcription factor 1	6.337	6.037	5.067E-03	4.27E-02	1.23	Duroc-up
MLL5	SNOWBALL_037369_st	myeloid/lymphoid or mixed-lineage leukemia 5 (trithorax homolog, Drosophila)	5.626	5.174	5.082E-03	4.28E-02	1.37	Duroc-up
CALCRL	SNOWBALL_035843_st	calcitonin receptor-like	5.694	4.852	5.087E-03	4.28E-02	1.79	Duroc-up
SMARCB1	SNOWBALL_024194_s_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	4.859	5.292	5.099E-03	4.29E-02	-1.35	PiNN-up
AKAP7	SNOWBALL_002203_st	A kinase (PRKA) anchor protein 7	5.480	5.813	5.101E-03	4.29E-02	-1.26	PiNN-up
PABPC3	SNOWBALL_005739_st	poly(A) binding protein, cytoplasmic 3//poly(A) binding protein, cytoplasmic 1	9.418	9.131	5.106E-03	4.29E-02	1.22	Duroc-up
ANXA6	SNOWBALL_018728_st	annexin A6	8.671	8.931	5.115E-03	4.29E-02	-1.20	PiNN-up
CUL9	SNOWBALL_009880_s_st	cullin-9-like	5.907	6.121	5.113E-03	4.29E-02	-1.16	PiNN-up
	SNOWBALL_038262_st		8.625	8.298	5.111E-03	4.29E-02	1.25	Duroc-up
LGR5	SNOWBALL_007173_st	leucine-rich repeat containing G protein-coupled receptor 5	6.245	5.883	5.120E-03	4.29E-02	1.29	Duroc-up
LOC100519981	SNOWBALL_028240_st	Ssc_hash_S31108241 1516895 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	6.127	5.487	5.119E-03	4.29E-02	1.56	Duroc-up
FAM175B	SNOWBALL_017371_st	family with sequence similarity 175, member B	5.802	5.401	5.124E-03	4.29E-02	1.32	Duroc-up
CA14	SNOWBALL_006521_st	carbonic anhydrase XIV	6.555	7.379	5.136E-03	4.30E-02	-1.77	PiNN-up

BAT3	SNOWBALL_001237_s_st	OTTSUSG00000001329 HLA-B associated transcript 3	7.353	7.832	5.142E-03	4.30E-02	-1.39	PiNN-up
PEX11B	SNOWBALL_006182_st	peroxisomal biogenesis factor 11 beta	6.490	6.883	5.136E-03	4.30E-02	-1.31	PiNN-up
FTSJD2	SNOWBALL_010024_st	FtsJ methyltransferase domain containing 2	5.630	5.960	5.141E-03	4.30E-02	-1.26	PiNN-up
ARHGAP19	SNOWBALL_016986_st	Rho GTPase activating protein 19	6.523	6.211	5.143E-03	4.30E-02	1.24	Duroc-up
	SNOWBALL_035385_st	Ssc_hash_S39814050 rcbl0_008774.y1 cbl Sus scrofa cDNA 5prime, mRNA	5.497	5.011	5.142E-03	4.30E-02	1.40	Duroc-up
ZNF248	SNOWBALL_016971_s_st	zinc finger protein 248	6.366	5.840	5.135E-03	4.30E-02	1.44	Duroc-up
CAD	SNOWBALL_045831_st	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	5.811	6.043	5.167E-03	4.31E-02	-1.17	PiNN-up
	SNOWBALL_046469_st		3.819	3.412	5.169E-03	4.31E-02	1.33	Duroc-up
FARP1	SNOWBALL_027252_st	Ssc_hash_S19543678 948919 MARC 4PIG Sus scrofa cDNA 3prime, mRNA	5.415	5.673	5.174E-03	4.32E-02	-1.20	PiNN-up
LOC100461822	SNOWBALL_035577_st	Ssc_hash_S17524644 BX673785 Sus Scrofa library (scac) Sus scrofa cDNA clone scac0040.c.24 5prim, mRNA	8.832	8.557	5.178E-03	4.32E-02	1.21	Duroc-up
ZNF451	SNOWBALL_010051_st	zinc finger protein 451	6.557	6.271	5.187E-03	4.32E-02	1.22	Duroc-up
UBA2	SNOWBALL_008069_st	ubiquitin-like modifier activating enzyme 2	6.801	6.553	5.202E-03	4.33E-02	1.19	Duroc-up
LOC100137763	SNOWBALL_012523_st	hypothetical protein LOC100137763	6.454	6.054	5.202E-03	4.33E-02	1.32	Duroc-up
UQCRC1	SNOWBALL_015401_st	ubiquinol-cytochrome c reductase core protein I	8.889	9.308	5.210E-03	4.33E-02	-1.34	PiNN-up
TMEM33	SNOWBALL_011332_st	transmembrane protein 33	7.396	6.955	5.210E-03	4.33E-02	1.36	Duroc-up
LOC100335177	SNOWBALL_036019_st	Ssc_hash_S31120558 1543173 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	5.162	4.654	5.217E-03	4.34E-02	1.42	Duroc-up
ZFYVE9	SNOWBALL_009060_st	zinc finger, FYVE domain containing 9	7.123	6.813	5.224E-03	4.34E-02	1.24	Duroc-up
RBM39	SNOWBALL_023701_s_st	RNA binding motif protein 39	8.414	7.959	5.225E-03	4.34E-02	1.37	Duroc-up
TMX3	SNOWBALL_027197_st	thioredoxin-related transmembrane protein 3	5.900	5.343	5.224E-03	4.34E-02	1.47	Duroc-up
RBM39	SNOWBALL_023700_s_st	RNA binding motif protein 39	8.200	7.872	5.229E-03	4.34E-02	1.26	Duroc-up
ATRX	SNOWBALL_020357_s_st	alpha thalassemia/mental retardation syndrome X-linked	6.433	5.800	5.235E-03	4.34E-02	1.55	Duroc-up
TLR5	SNOWBALL_022949_st	toll-like receptor 5	5.607	5.982	5.251E-03	4.35E-02	-1.30	PiNN-up
ACVR2B	SNOWBALL_047323_st	activin A receptor, type IIB	7.672	8.028	5.251E-03	4.35E-02	-1.28	PiNN-up
LOC100506346	SNOWBALL_029774_st	Ssc_hash_S23763825 1121553 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	7.101	6.593	5.268E-03	4.36E-02	1.42	Duroc-up
TMF1	SNOWBALL_015636_s_st	TATA element modulatory factor-like	5.819	5.459	5.284E-03	4.38E-02	1.28	Duroc-up
ERCC3	SNOWBALL_017723_st	TFIIH basal transcription factor complex helicase XPB subunit-like	6.352	6.779	5.293E-03	4.38E-02	-1.34	PiNN-up

IL23R	SNOWBALL_023237_s_st	Sus scrofa interleukin 23 receptor alpha (IL23RA), mRNA	3.371	3.603	5.311E-03	4.39E-02	-1.17	PiNN-up
LOC100157614	SNOWBALL_023634_s_st	PREDICTED: Sus scrofa similar to LOC507590 protein, transcript variant 2 (LOC100156401), mRNA	10.579	10.209	5.310E-03	4.39E-02	1.29	Duroc-up
LOC100517174	SNOWBALL_019463_s_st	mps one binder kinase activator-like 1A-like	5.569	5.841	5.318E-03	4.40E-02	-1.21	PiNN-up
MAP4K4	SNOWBALL_021938_st	mitogen-activated protein kinase kinase kinase kinase 4	5.075	5.233	5.321E-03	4.40E-02	-1.12	PiNN-up
DPF2	SNOWBALL_047452_st	D4, zinc and double PHD fingers family 2	4.758	5.182	5.335E-03	4.40E-02	-1.34	PiNN-up
RNMT	SNOWBALL_026489_st	RNA (guanine-7-) methyltransferase	5.931	5.478	5.335E-03	4.40E-02	1.37	Duroc-up
SKIL	SNOWBALL_015688_st	SKI-like oncogene	6.810	6.282	5.331E-03	4.40E-02	1.44	Duroc-up
MIER1	SNOWBALL_008930_st	mesoderm induction early response 1 homolog (Xenopus laevis)	5.918	5.324	5.332E-03	4.40E-02	1.51	Duroc-up
	SNOWBALL_035881_st	Ssc_hash_S26720631 AJ956715 KN404_2 Sus scrofa cDNA clone C0007757l02 5prime, mRNA	4.700	5.034	5.339E-03	4.40E-02	-1.26	PiNN-up
SURF4	SNOWBALL_047575_st	surfeit 4	5.083	5.404	5.352E-03	4.41E-02	-1.25	PiNN-up
CALCOCO1	SNOWBALL_047598_st	calcium binding and coiled-coil domain 1	5.408	5.721	5.354E-03	4.41E-02	-1.24	PiNN-up
LOC100513958	SNOWBALL_018751_s_st	e3 ubiquitin-protein ligase TRIM23-like	8.259	7.871	5.354E-03	4.41E-02	1.31	Duroc-up
ATXN7	SNOWBALL_030610_st	ataxin 7	5.303	4.750	5.354E-03	4.41E-02	1.47	Duroc-up
MPRIP	SNOWBALL_047530_st	myosin phosphatase Rho interacting protein	6.814	7.142	5.365E-03	4.41E-02	-1.26	PiNN-up
MGEA5	SNOWBALL_017193_s_st	meningioma expressed antigen 5 (hyaluronidase)	8.684	8.306	5.368E-03	4.41E-02	1.30	Duroc-up
ZNF142	SNOWBALL_018168_s_st	zinc finger protein 142	6.473	6.648	5.379E-03	4.41E-02	-1.13	PiNN-up
NEB	SNOWBALL_018312_st	nebulin	13.168	13.005	5.374E-03	4.41E-02	1.12	Duroc-up
MALT1	SNOWBALL_003222_s_st	mucosa associated lymphoid tissue lymphoma translocation gene 1	6.698	6.386	5.374E-03	4.41E-02	1.24	Duroc-up
SEC22A	SNOWBALL_036963_st	SEC22 vesicle trafficking protein homolog A (S. cerevisiae)	5.708	5.066	5.379E-03	4.41E-02	1.56	Duroc-up
PLA2G7	SNOWBALL_038639_st	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	5.551	5.021	5.382E-03	4.41E-02	1.44	Duroc-up
GOLGA4	SNOWBALL_015216_st	golgin A4	9.207	8.653	5.385E-03	4.41E-02	1.47	Duroc-up
LPHN2	SNOWBALL_030297_st	latrophilin 2	4.925	4.495	5.388E-03	4.41E-02	1.35	Duroc-up
M6PR	SNOWBALL_007296_st	mannose-6-phosphate receptor (cation dependent)	6.734	6.962	5.408E-03	4.43E-02	-1.17	PiNN-up
EEPD1	SNOWBALL_042631_st	endonuclease/exonuclease/phosphatase family domain containing 1	6.274	6.554	5.426E-03	4.44E-02	-1.21	PiNN-up
HEXIM1	SNOWBALL_014379_st	hexamethylene bis-acetamide inducible 1	7.589	7.874	5.432E-03	4.44E-02	-1.22	PiNN-up
CSDE1	SNOWBALL_006282_st	cold shock domain containing E1, RNA-binding	12.138	11.717	5.437E-03	4.44E-02	1.34	Duroc-up
KCNAB1	SNOWBALL_045060_st	potassium voltage-gated channel, shaker-related subfamily, beta member 1	6.787	6.253	5.435E-03	4.44E-02	1.45	Duroc-up

STAM2	SNOWBALL_018518_s_st	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	6.310	5.923	5.471E-03	4.47E-02	1.31	Duroc-up
ZBTB5	SNOWBALL_027869_st	zinc finger and BTB domain containing 5	5.761	6.081	5.481E-03	4.47E-02	-1.25	PiNN-up
ACBD5	SNOWBALL_013415_st	acyl-CoA binding domain containing 5	8.352	7.934	5.479E-03	4.47E-02	1.34	Duroc-up
CRKL	SNOWBALL_016646_st	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	9.170	9.390	5.487E-03	4.48E-02	-1.16	PiNN-up
YAF2	SNOWBALL_027320_st	YY1 associated factor 2	6.706	6.359	5.503E-03	4.49E-02	1.27	Duroc-up
CNOT7	SNOWBALL_018976_s_st	hypothetical LOC100514258	8.087	7.608	5.508E-03	4.49E-02	1.39	Duroc-up
IL6ST	SNOWBALL_000388_st	interleukin 6 signal transducer (gp130, oncostatin M receptor)	9.175	8.755	5.516E-03	4.49E-02	1.34	Duroc-up
UBE2W	SNOWBALL_035393_st	ubiquitin-conjugating enzyme E2W (putative)	4.681	4.007	5.517E-03	4.49E-02	1.60	Duroc-up
RNF10	SNOWBALL_016673_st	hypothetical protein LOC100521584	8.235	8.400	5.522E-03	4.49E-02	-1.12	PiNN-up
CTNNA3	SNOWBALL_024485_st	catenin (cadherin-associated protein), alpha 3	6.784	6.447	5.523E-03	4.49E-02	1.26	Duroc-up
GIT1	SNOWBALL_015095_st	G protein-coupled receptor kinase interacting ArfGAP 1	6.190	6.407	5.528E-03	4.50E-02	-1.16	PiNN-up
LOC100519100	SNOWBALL_012961_st	rab GTPase-activating protein 1-like	5.328	4.923	5.543E-03	4.51E-02	1.32	Duroc-up
ICK	SNOWBALL_031469_st	intestinal cell (MAK-like) kinase	6.271	5.878	5.547E-03	4.51E-02	1.31	Duroc-up
ABL2	SNOWBALL_039469_st	v-abl Abelson murine leukemia viral oncogene homolog 2	4.004	3.408	5.552E-03	4.51E-02	1.51	Duroc-up
VPS26A	SNOWBALL_024675_st	PREDICTED: Sus scrofa similar to vacuolar protein sorting 26 (LOC100155086), mRNA	9.342	8.728	5.551E-03	4.51E-02	1.53	Duroc-up
TNS1	SNOWBALL_027428_st	tensin 1	6.475	6.895	5.558E-03	4.51E-02	-1.34	PiNN-up
ARPC4	SNOWBALL_015534_st	actin related protein 2/3 complex, subunit 4, 20kDa	6.855	7.148	5.557E-03	4.51E-02	-1.22	PiNN-up
ADSL	SNOWBALL_023388_s_st	adenylosuccinate lyase	9.033	9.540	5.568E-03	4.51E-02	-1.42	PiNN-up
	SNOWBALL_041624_st		5.743	5.267	5.570E-03	4.51E-02	1.39	Duroc-up
TNRC6A	SNOWBALL_034041_st	trinucleotide repeat containing 6A	6.728	6.326	5.584E-03	4.52E-02	1.32	Duroc-up
GTPBP10	SNOWBALL_012709_s_st	GTP-binding protein 10 (putative)	5.443	4.900	5.584E-03	4.52E-02	1.46	Duroc-up
TUBGCP2	SNOWBALL_017129_st	tubulin, gamma complex associated protein 2	6.832	7.170	5.588E-03	4.52E-02	-1.26	PiNN-up
PPP1R16B	SNOWBALL_047038_st	protein phosphatase 1, regulatory (inhibitor) subunit 16B	4.125	4.359	5.592E-03	4.52E-02	-1.18	PiNN-up
	SNOWBALL_040225_st		4.988	5.263	5.599E-03	4.53E-02	-1.21	PiNN-up
LOC779492	SNOWBALL_037208_st	Ssc_hash_S50180997 susfleck_LM_17_F04 SUSFLECK Loin Muscle Sus scrofa cDNA clone 17_F04, mRNA	4.442	3.853	5.602E-03	4.53E-02	1.50	Duroc-up
TLE1	SNOWBALL_004073_st	transducin-like enhancer of split 1 (E(sp1) homolog, Drosophila)	6.004	6.426	5.627E-03	4.55E-02	-1.34	PiNN-up
MRPL47	SNOWBALL_015562_st	mitochondrial ribosomal protein L47	6.965	6.496	5.644E-03	4.56E-02	1.38	Duroc-up

C17orf39	SNOWBALL_035526_st	chromosome 17 open reading frame 39	5.913	5.730	5.662E-03	4.57E-02	1.14	Duroc-up
NR3C1	SNOWBALL_025369_st	Sus scrofa mRNA, clone:MLN010099F07, expressed in mesenteric lymph node	7.025	6.548	5.664E-03	4.57E-02	1.39	Duroc-up
ZNF574	SNOWBALL_008377_st	zinc finger protein 574	6.350	6.525	5.673E-03	4.57E-02	-1.13	PiNN-up
CCNDBP1	SNOWBALL_042113_st	cyclin-D1-binding protein 1-like	7.195	7.309	5.677E-03	4.58E-02	-1.08	PiNN-up
BHLHE41	SNOWBALL_039973_st	class E basic helix-loop-helix protein 40-like	8.399	8.923	5.680E-03	4.58E-02	-1.44	PiNN-up
C16orf62	SNOWBALL_026327_st	chromosome 16 open reading frame 62	6.468	6.819	5.683E-03	4.58E-02	-1.28	PiNN-up
FLII	SNOWBALL_045448_st	flightless I homolog (Drosophila)	8.188	8.428	5.694E-03	4.58E-02	-1.18	PiNN-up
POGZ	SNOWBALL_006663_st	pogo transposable element with ZNF domain	7.623	7.816	5.721E-03	4.60E-02	-1.14	PiNN-up
OPTN	SNOWBALL_025914_st	optineurin	10.604	10.160	5.725E-03	4.60E-02	1.36	Duroc-up
SNORD65	SNOWBALL_014882_st	Small nucleolar RNA SNORD65	5.842	6.313	5.729E-03	4.61E-02	-1.39	PiNN-up
SMARCC1	SNOWBALL_015368_st	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	7.254	7.091	5.743E-03	4.61E-02	1.12	Duroc-up
ITCH	SNOWBALL_047213_s_st	itchy E3 ubiquitin protein ligase homolog (mouse)	4.044	3.532	5.743E-03	4.61E-02	1.43	Duroc-up
TTI1	SNOWBALL_019498_s_st	KIAA0406 [Source:HGNC Symbol;Acc:29029]//Tel2 interacting protein 1 homolog (S. pombe) [Source:HGNC Symbol;Acc:29029]	6.640	6.931	5.765E-03	4.63E-02	-1.22	PiNN-up
	SNOWBALL_031030_st	Ssc_hash_S22312452 CJ020192 full-length enriched swine cDNA library, adult spleen Sus scrofa cDNA clone SPL01B020080 5prime, mRNA	5.079	5.410	5.770E-03	4.63E-02	-1.26	PiNN-up
LOC100471890	SNOWBALL_028272_st	Ssc_hash_S50167008 susfleck_PG_N_25_F12 SUSFLECK Pituitary Gland Normalized Sus scrofa cDNA clone 25_F12, mRNA	6.099	6.278	5.776E-03	4.63E-02	-1.13	PiNN-up
IMPACT	SNOWBALL_009013_s_st	Impact homolog (mouse)	5.942	5.501	5.783E-03	4.64E-02	1.36	Duroc-up
LOC100522038	SNOWBALL_017463_s_st	poly(ADP-ribose) glycohydrolase-like	5.541	5.041	5.789E-03	4.64E-02	1.41	Duroc-up
ZEB2	SNOWBALL_025550_s_st	Sus scrofa mRNA, clone:PBL010030B09, expressed in periphral blood mononuclear cell	5.608	5.104	5.786E-03	4.64E-02	1.42	Duroc-up
AZI2	SNOWBALL_015210_st	5-azacytidine induced 2	7.156	6.606	5.795E-03	4.64E-02	1.46	Duroc-up
DHRS3	SNOWBALL_009033_s_st	dehydrogenase/reductase (SDR family) member 3	8.041	8.565	5.804E-03	4.64E-02	-1.44	PiNN-up
	SNOWBALL_046864_st		5.216	5.488	5.825E-03	4.66E-02	-1.21	PiNN-up
DLG5	SNOWBALL_000328_st	discs, large homolog 5 (Drosophila)	5.657	5.907	5.834E-03	4.66E-02	-1.19	PiNN-up
ZNF24	SNOWBALL_028515_st	zinc finger protein 24	4.875	4.619	5.840E-03	4.67E-02	1.19	Duroc-up
	SNOWBALL_031172_st	Ssc_hash_S22277612 CJ013973 full-length enriched swine cDNA library, adult mesenteric lymph node Sus scrofa cDNA clone MLN01A060080 5prime, mRNA	3.939	3.199	5.849E-03	4.67E-02	1.67	Duroc-up
KLHL38	SNOWBALL_000777_st	OTTSUSG00000000774	7.475	7.771	5.852E-03	4.67E-02	-1.23	PiNN-up

EFTUD2	SNOWBALL_014291_st	elongation factor Tu GTP binding domain containing 2	8.063	8.364	5.855E-03	4.67E-02	-1.23	PiNN-up
MAK10	SNOWBALL_013489_st	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	7.350	6.990	5.863E-03	4.68E-02	1.28	Duroc-up
FAM120B	SNOWBALL_038563_st	family with sequence similarity 120B	5.859	6.117	5.867E-03	4.68E-02	-1.20	PiNN-up
FAM160A1	SNOWBALL_011517_st	family with sequence similarity 160, member A1	7.394	7.635	5.879E-03	4.69E-02	-1.18	PiNN-up
RRAGA	SNOWBALL_003277_st	Ras-related GTP binding A	9.812	10.189	5.892E-03	4.69E-02	-1.30	PiNN-up
EXOSC4	SNOWBALL_005580_st	exosome component 4	7.351	7.678	5.893E-03	4.69E-02	-1.25	PiNN-up
ZC3H15	SNOWBALL_023898_s_st	PREDICTED: Sus scrofa similar to erythropoietin 4 immediate early response (LOC100158058), partial mRNA	7.918	7.367	5.890E-03	4.69E-02	1.47	Duroc-up
RSL24D1	SNOWBALL_002622_st	ribosomal L24 domain containing 1	5.613	5.039	5.892E-03	4.69E-02	1.49	Duroc-up
AMBP	SNOWBALL_000102_st	alpha-1-microglobulin/bikunin precursor	5.075	5.389	5.901E-03	4.69E-02	-1.24	PiNN-up
PLA2G7	SNOWBALL_043514_st	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	4.446	4.720	5.902E-03	4.69E-02	-1.21	PiNN-up
BRD7	SNOWBALL_027692_st	bromodomain containing 7	7.565	7.240	5.907E-03	4.69E-02	1.25	Duroc-up
CEBPZ	SNOWBALL_005155_st	CCAAT/enhancer binding protein (C/EBP), zeta	7.986	7.521	5.907E-03	4.69E-02	1.38	Duroc-up
TRAPPC2	SNOWBALL_001638_st	trafficking protein particle complex 2	4.453	4.836	5.913E-03	4.69E-02	-1.30	PiNN-up
SRSF12	SNOWBALL_031113_st	serine/arginine-rich splicing factor 12	4.618	3.549	5.910E-03	4.69E-02	2.10	Duroc-up
DIAPH2	SNOWBALL_026309_st	diaphanous homolog 2 (Drosophila)	6.506	6.089	5.917E-03	4.69E-02	1.33	Duroc-up
UBXN1	SNOWBALL_026547_st	UBX domain protein 1	7.935	8.165	5.920E-03	4.69E-02	-1.17	PiNN-up
EIF5B	SNOWBALL_004876_st	eukaryotic translation initiation factor 5B	7.961	7.394	5.925E-03	4.69E-02	1.48	Duroc-up
	SNOWBALL_046577_st		5.528	5.145	5.936E-03	4.70E-02	1.30	Duroc-up
PHIP	SNOWBALL_002489_st	pleckstrin homology domain interacting protein	6.863	6.445	5.941E-03	4.70E-02	1.34	Duroc-up
RAB11FIP2	SNOWBALL_047669_st	RAB11 family interacting protein 2 (class I)	7.129	6.510	5.946E-03	4.70E-02	1.54	Duroc-up
SMC5	SNOWBALL_002760_st	structural maintenance of chromosomes 5	5.325	4.668	5.946E-03	4.70E-02	1.58	Duroc-up
SYPL2	SNOWBALL_006173_st	synaptophysin-like 2	10.635	10.905	5.949E-03	4.70E-02	-1.21	PiNN-up
LOC100152884	SNOWBALL_030280_st	Ssc_hash_S18379353 929650 MARC 4PIG Sus scrofa cDNA 5prime, mRNA	5.742	5.244	5.951E-03	4.70E-02	1.41	Duroc-up
CHR12Putative ORF001	SNOWBALL_000161_st	OTTSUSG00000000846 Putative Open Reading Frame 001 on pig chromosme 12	6.892	6.745	5.962E-03	4.71E-02	1.11	Duroc-up
AP2M1	SNOWBALL_026209_st	adaptor-related protein complex 2, mu 1 subunit	7.033	7.223	5.967E-03	4.71E-02	-1.14	PiNN-up
FOXN2	SNOWBALL_029062_st	forkhead box N2	5.716	5.200	5.971E-03	4.71E-02	1.43	Duroc-up
	SNOWBALL_042957_st		4.022	3.797	5.980E-03	4.72E-02	1.17	Duroc-up
SH3KBP1	SNOWBALL_020068_st	SH3-domain kinase binding protein 1	7.209	6.732	6.000E-03	4.73E-02	1.39	Duroc-up
SKP2	SNOWBALL_029941_st	S-phase kinase-associated protein 2 (p45)	7.288	6.854	6.012E-03	4.74E-02	1.35	Duroc-up
C17orf48	SNOWBALL_015071_st	chromosome 17 open reading frame 48	5.863	6.283	6.023E-03	4.74E-02	-1.34	PiNN-up
RABGGTA	SNOWBALL_010852_st	Rab geranylgeranyltransferase, alpha subunit	7.025	7.568	6.052E-03	4.76E-02	-1.46	PiNN-up

MYNN	SNOWBALL_029772_st	myoneurin	6.361	5.909	6.052E-03	4.76E-02	1.37	Duroc-up
KSR1	SNOWBALL_014651_st	kinase suppressor of ras 1	7.081	7.340	6.061E-03	4.77E-02	-1.20	PiNN-up
	SNOWBALL_045479_st		5.319	5.683	6.070E-03	4.77E-02	-1.29	PiNN-up
AF102147	SNOWBALL_026970_s_st	DIM1 dimethyladenosine transferase 1-like (S. cerevisiae)	8.065	7.664	6.071E-03	4.77E-02	1.32	Duroc-up
BHLHE41	SNOWBALL_007251_st	basic helix-loop-helix family, member e41	7.981	8.331	6.087E-03	4.78E-02	-1.27	PiNN-up
BAT3	SNOWBALL_001247_st	OTTSUSG00000001329 HLA-B associated transcript 3	8.220	8.496	6.094E-03	4.78E-02	-1.21	PiNN-up
RNF41	SNOWBALL_007060_st	ring finger protein 41	6.978	7.182	6.094E-03	4.78E-02	-1.15	PiNN-up
CASK	SNOWBALL_020147_st	calcium/calmodulin-dependent serine protein kinase (MAGUK family)	7.751	7.490	6.107E-03	4.79E-02	1.20	Duroc-up
KIAA2018	SNOWBALL_035802_st	KIAA2018	6.978	6.576	6.107E-03	4.79E-02	1.32	Duroc-up
RBBP5	SNOWBALL_012535_st	retinoblastoma binding protein 5	7.760	7.876	6.134E-03	4.81E-02	-1.08	PiNN-up
	SNOWBALL_034025_st	Ssc_hash_S50172903 susfleck_LV_71_H06 SUSFLECK Liver Sus scrofa cDNA clone 71_H06, mRNA	5.544	5.845	6.138E-03	4.81E-02	-1.23	PiNN-up
Rnu3b2	SNOWBALL_015142_st	Small nucleolar RNA U3	6.380	7.092	6.153E-03	4.82E-02	-1.64	PiNN-up
USP42	SNOWBALL_037444_st	ubiquitin specific peptidase 42	5.603	5.951	6.152E-03	4.82E-02	-1.27	PiNN-up
ZFR	SNOWBALL_034299_st	zinc finger RNA binding protein	8.720	8.451	6.164E-03	4.82E-02	1.20	Duroc-up
ITGB8	SNOWBALL_012533_st	integrin, beta 8	6.295	5.872	6.160E-03	4.82E-02	1.34	Duroc-up
RNF128	SNOWBALL_001796_s_st	ring finger protein 128	6.045	5.409	6.164E-03	4.82E-02	1.55	Duroc-up
	SNOWBALL_046748_st		4.257	4.562	6.200E-03	4.85E-02	-1.24	PiNN-up
	SNOWBALL_030481_st	Ssc_hash_S19543825 949098 MARC 4PIG Sus scrofa cDNA 3prime, mRNA	4.226	4.457	6.205E-03	4.85E-02	-1.17	PiNN-up
DHX8	SNOWBALL_014289_st	DEAH (Asp-Glu-Ala-His) box polypeptide 8	6.401	6.620	6.219E-03	4.86E-02	-1.16	PiNN-up
WASF2	SNOWBALL_009251_st	WAS protein family, member 2	7.041	7.166	6.223E-03	4.86E-02	-1.09	PiNN-up
HIF1A	SNOWBALL_002788_s_st	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	7.205	6.923	6.220E-03	4.86E-02	1.22	Duroc-up
TOLLIP	SNOWBALL_025575_st	toll interacting protein	7.468	7.845	6.246E-03	4.87E-02	-1.30	PiNN-up
ACTR2	SNOWBALL_005206_st	ARP2 actin-related protein 2 homolog (yeast)	8.319	7.978	6.244E-03	4.87E-02	1.27	Duroc-up
DUSP1	SNOWBALL_000392_st	dual specificity phosphatase 1	7.142	7.664	6.258E-03	4.87E-02	-1.44	PiNN-up
	SNOWBALL_043179_st		4.645	4.961	6.262E-03	4.87E-02	-1.24	PiNN-up
NLK	SNOWBALL_014678_st	nemo-like kinase	7.171	6.924	6.255E-03	4.87E-02	1.19	Duroc-up
LOC521363	SNOWBALL_036059_st	Ssc_hash_S31133510 1573537 MARC 3PIG Sus scrofa cDNA 5prime, mRNA	4.976	4.470	6.260E-03	4.87E-02	1.42	Duroc-up
PTP4A2	SNOWBALL_009179_st	protein tyrosine phosphatase type IVA, member 2	10.876	10.560	6.276E-03	4.88E-02	1.25	Duroc-up

NCOA4	SNOWBALL_024648_s_st	PREDICTED: Sus scrofa similar to nuclear receptor coactivator 4 (LOC100156184), mRNA	9.099	8.601	6.275E-03	4.88E-02	1.41	Duroc-up
LRP6	SNOWBALL_028089_st	low density lipoprotein receptor-related protein 6	4.996	4.333	6.291E-03	4.89E-02	1.58	Duroc-up
ATP1A4	SNOWBALL_025659_st	ATPase, Na+/K+ transporting, alpha 4 polypeptide	6.398	6.715	6.304E-03	4.90E-02	-1.25	PiNN-up
IFIT5	SNOWBALL_017481_s_st	interferon-induced protein with tetratricopeptide repeats 5	6.021	5.333	6.303E-03	4.90E-02	1.61	Duroc-up
	SNOWBALL_035964_st	Ssc_hash_S39840041 rche18_b14.y1 che Sus scrofa cDNA 5prime, mRNA	4.428	4.837	6.339E-03	4.90E-02	-1.33	PiNN-up
E2F6	SNOWBALL_038659_st	E2F transcription factor 6	5.340	5.638	6.322E-03	4.90E-02	-1.23	PiNN-up
CDK5	SNOWBALL_047363_st	cyclin-dependent kinase 5	5.697	5.987	6.330E-03	4.90E-02	-1.22	PiNN-up
TLN1	SNOWBALL_003651_st	talin 1	6.958	7.223	6.334E-03	4.90E-02	-1.20	PiNN-up
AVEN	SNOWBALL_010153_st	apoptosis, caspase activation inhibitor	7.910	8.145	6.330E-03	4.90E-02	-1.18	PiNN-up
UBTF	SNOWBALL_014278_st	upstream binding transcription factor, RNA polymerase I	7.826	8.039	6.327E-03	4.90E-02	-1.16	PiNN-up
MPP7	SNOWBALL_013458_st	membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7)	6.516	6.204	6.347E-03	4.90E-02	1.24	Duroc-up
XBP1	SNOWBALL_023150_st	Sus scrofa X-box-binding protein 1 (XBP1) mRNA, complete cds, alternatively spliced	7.580	7.267	6.348E-03	4.90E-02	1.24	Duroc-up
FAM126A	SNOWBALL_038001_st	family with sequence similarity 126, member A	5.599	5.283	6.317E-03	4.90E-02	1.24	Duroc-up
NRIP1	SNOWBALL_029056_st	nuclear receptor interacting protein 1	5.902	5.453	6.338E-03	4.90E-02	1.37	Duroc-up
TDRD3	SNOWBALL_013920_st	tudor domain containing 3	6.658	6.173	6.340E-03	4.90E-02	1.40	Duroc-up
SMC3	SNOWBALL_017382_st	structural maintenance of chromosomes 3	7.398	6.865	6.348E-03	4.90E-02	1.45	Duroc-up
OSGEPL1	SNOWBALL_018171_s_st	O-sialoglycoprotein endopeptidase-like 1	6.659	6.109	6.346E-03	4.90E-02	1.46	Duroc-up
ENAH	SNOWBALL_027534_st	enabled homolog (Drosophila)	8.035	7.185	6.331E-03	4.90E-02	1.80	Duroc-up
LIN54	SNOWBALL_030283_st	lin-54 homolog (C. elegans)	5.433	4.840	6.358E-03	4.90E-02	1.51	Duroc-up
CAPN3	SNOWBALL_002943_s_st	calpain 3, (p94)	7.672	8.028	6.377E-03	4.92E-02	-1.28	PiNN-up
GUCY1A3	SNOWBALL_028222_st	guanylate cyclase 1, soluble, alpha 3	4.873	4.283	6.375E-03	4.92E-02	1.50	Duroc-up
UBIAD1	SNOWBALL_031201_st	UbiA prenyltransferase domain containing 1	5.312	5.537	6.396E-03	4.93E-02	-1.17	PiNN-up
	SNOWBALL_046461_st		5.239	4.792	6.394E-03	4.93E-02	1.36	Duroc-up
MUT	SNOWBALL_009919_s_st	methylmalonyl CoA mutase	8.153	7.597	6.399E-03	4.93E-02	1.47	Duroc-up
C8orf59	SNOWBALL_005721_st	chromosome 8 open reading frame 59	5.391	4.943	6.415E-03	4.94E-02	1.36	Duroc-up
YTHDC1	SNOWBALL_022247_st	YTH domain containing 1	5.861	6.048	6.423E-03	4.94E-02	-1.14	PiNN-up
VAPA	SNOWBALL_035140_st	VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa	7.409	7.118	6.426E-03	4.94E-02	1.22	Duroc-up
SCRN3	SNOWBALL_036245_st	secernin 3	5.644	5.024	6.428E-03	4.94E-02	1.54	Duroc-up
ZNF641	SNOWBALL_035199_st	zinc finger protein 641	5.858	6.345	6.434E-03	4.94E-02	-1.40	PiNN-up
	SNOWBALL_046966_st		4.838	4.482	6.435E-03	4.94E-02	1.28	Duroc-up

ATP2B2	SNOWBALL_015601_st	ATPase, Ca++ transporting, plasma membrane 2	7.621	7.910	6.439E-03	4.94E-02	-1.22	PiNN-up
ZZEF1	SNOWBALL_046968_st	ATPase, Ca++ transporting, ubiquitous	7.185	7.516	6.444E-03	4.94E-02	-1.26	PiNN-up
SLC16A6	SNOWBALL_014202_st	Monocarboxylate transporter 7 (MCT 7)(Monocarboxylate transporter 6)(MCT 6)(Solute carrier family 16 member 6)	4.862	5.292	6.453E-03	4.95E-02	-1.35	PiNN-up
TNXB	SNOWBALL_001312_s_st	OTTSUSG00000001348 tenascin XB	6.638	6.960	6.472E-03	4.95E-02	-1.25	PiNN-up
GCN1L1	SNOWBALL_024335_s_st	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	7.567	7.824	6.471E-03	4.95E-02	-1.19	PiNN-up
UBR4	SNOWBALL_009065_st	ubiquitin protein ligase E3 component n-recognin 4	8.760	8.977	6.474E-03	4.95E-02	-1.16	PiNN-up
LPHN2	SNOWBALL_008878_st	latrophilin 2	8.083	7.843	6.461E-03	4.95E-02	1.18	Duroc-up
C10orf46	SNOWBALL_016953_s_st	chromosome 10 open reading frame 46	8.236	7.938	6.468E-03	4.95E-02	1.23	Duroc-up
ZRANB1	SNOWBALL_031671_st	zinc finger, RAN-binding domain containing 1	6.156	5.778	6.467E-03	4.95E-02	1.30	Duroc-up
PITPNB	SNOWBALL_024288_s_st	phosphatidylinositol transfer protein, beta	6.375	5.690	6.461E-03	4.95E-02	1.61	Duroc-up
KREMEN1	SNOWBALL_027782_st	kringle containing transmembrane protein 1	4.870	5.168	6.484E-03	4.95E-02	-1.23	PiNN-up
SYNE1	SNOWBALL_032850_st	spectrin repeat containing, nuclear envelope 1	8.109	7.732	6.482E-03	4.95E-02	1.30	Duroc-up
TRAPPC8	SNOWBALL_042898_st	protein TRS85 homolog	6.886	6.565	6.511E-03	4.97E-02	1.25	Duroc-up
IKZF4	SNOWBALL_027600_st	IKAROS family zinc finger 4 (Eos)	5.959	6.206	6.522E-03	4.98E-02	-1.19	PiNN-up
ARID1B	SNOWBALL_035787_st	Ssc_hash_S40387945 rova008_i12.y1 ova Sus scrofa cDNA 5prime, mRNA	4.509	4.100	6.537E-03	4.99E-02	1.33	Duroc-up
MRPS10	SNOWBALL_009962_s_st	mitochondrial ribosomal protein S10	8.045	7.602	6.539E-03	4.99E-02	1.36	Duroc-up
DIP2C	SNOWBALL_034712_st	DIP2 disco-interacting protein 2 homolog C (Drosophila)	6.512	6.916	6.543E-03	4.99E-02	-1.32	PiNN-up
PIP4K2B	SNOWBALL_040046_st	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	8.273	8.571	6.552E-03	4.99E-02	-1.23	PiNN-up
GCLC	SNOWBALL_001450_st	glutamate-cysteine ligase, catalytic subunit	5.530	5.158	6.554E-03	4.99E-02	1.29	Duroc-up
MSL3	SNOWBALL_001625_st	male-specific lethal 3 homolog (Drosophila)	5.846	6.255	6.568E-03	4.99E-02	-1.33	PiNN-up
KIAA1310	SNOWBALL_040002_st	KIAA1310	6.297	6.555	6.563E-03	4.99E-02	-1.20	PiNN-up
PIGB	SNOWBALL_025568_st	phosphatidylinositol glycan anchor biosynthesis, class B	5.112	5.317	6.568E-03	4.99E-02	-1.15	PiNN-up
PPP1R2	SNOWBALL_015958_st	protein phosphatase 1, regulatory (inhibitor) subunit 2	9.989	9.532	6.564E-03	4.99E-02	1.37	Duroc-up
DNAJC3	SNOWBALL_021707_st	DnaJ (Hsp40) homolog, subfamily C, member 3	6.392	5.739	6.558E-03	4.99E-02	1.57	Duroc-up

Table S4 The gene list in the top Go terms in biologically meaningful clusters for each module of Duroc

Module	No.genes/ Module	Go Term	Count[1]	% Count[2]	P-Value	Genes
magenta	770	GO:0031981~nuclear lumen	96	12.47	1.23E-06	EIF6, CCNT2, **RNMT**, ***BTD*** , E2F7, RBM5, NFKB2, MED22, RNGTT, PRIM1, RBM4B, **G2E3**, RRN3, **GTF2A1**, ANG, SRRM2, FOXF1, CDK12, CIRH1A, OGT, TSEN15, CUL1, STX5, GTPBP4, **SP100**, EXOSC7, POLR1D, YY1, FMR1, ANAPC4, CCNL1, SF1, TOPBP1, LAS1L, MCM2, SFRS1, MBD2, **NVL**, RFWD2, **XPA**, ***EIF4A3*** , **HIF1A**, **CFL1**, NEK4, FUS, POLR2G, **STON1**, TH1L, **DIMT1L**, POLR2B, NR2C2, CXXC1, EXOSC10, ERCC8, SF3B1, ORC2L, ERCC5, VRK1, **MORC3**, FIGN, HAND2, HNRNPF, HINFP, **GPSM2**, SUPT7L, **PRKAA2**, ***ERCC3*** , GTF3C2, ERCC4, CHD4, ***RBM22*** , DHX9, PDCD11, MLL, MAFB, CREBBP, **SFRS13A**, ***POLR3A*** , ***CASC3*** , INTS10, **CDC27**, APPL2, CDC25A, ***CDC25B*** , ***MEF2D*** , **SON**, ORC3L, SFPQ, **WHSC1L1**, THRAP3, JAZF1, TDG, ALKBH3, PBX2, CBS, CALM1
skyblue	231	GO:0005524~ATP binding	39	16.88	3.02E-05	UBE2Z, **NEK1**, DICER1, STK17B, UBA6, ATP10D, SPO11, ABCA1, ACSF2, EPHB2, ***ATP2B2*** , MKKS, DHX16, DYRK2, POLG2, ENTPD1, IP6K1, SIK2, KIAA0232, CDC7, ***PRKCA*** , LIMK1, DDX1, PI4KA, ACACA, PFKP, **HLTF**, SARS2, MARK1, CDKL5, ABCG2, RFC5, EPHA4, ***ATP9A*** , ***ATP2A1*** , ABCC1, TSSK1B, SMC1A, UBE2S
royalblue	271	GO:0044265~cellular macromolecule catabolic process	23	8.49	6.25E-04	***ZFP36*** , ***NPLOC4*** , ***EIF2C1*** , ***LRRC41*** , PABPC4, UBE2V1, SOCS7, ZNRF1, EDEM1, ATM, TRIM11, SENP1, ***CUL9*** , UBE2M, FBXO28, USP37, FBXW2, **CAND1**, FBXL14, **USP15**, EIF2C3, **TRIP12**, ASB6
saddlebrown	232	GO:0004672~protein kinase activity	18	7.76	4.78E-03	***PRKCA*** , NRP2, FASTKD3, IRAK1, OBSCN, BCKDK, TAOK2, BRAF, STK38, **ADRBK2**, POLR2B, ***DDR1*** , ***MAP4K4*** , ***MAP3K3*** , MAPK14, NEK9, LRRK2, BMPR1B
black	468	GO:0006793~phosphorus metabolic process	44	9.40	3.61E-04	NDUFB3, ADORA2B, PTPLAD1, SSH3, **CASK**, TFG, **PRKG1**, LATS2, EPHB1, **VRK2**, **MAP3K2**, C1QTNF2, CDK12, **PIK3CA**, ***BRD4*** , EGF, **PIK3R1**, MAP2K5, CSNK1A1, NDUFA4, TAF1, SGK3, PIK3CB, RYK, **PTPN4**, PDK4, PTPRS, CDK7, **ATR**, OXSR1, CDC25A, GAK, RPS6KA5, **ICK**, SGK196, SCYL1, COX3, DUSP27, COX1, NDUFV2, BMP2K, **EIF2AK2**, DUSP8, **ABL2**
midnightblue	551	GO:0010629~negative regulation of gene expression	36	6.53	6.55E-06	**GCLC**, HSD3B7, TSG101, RBM3, TH1L, TP63, **ZEB2**, PDX1, REST, RBM9, PDCD4, SORBS3, DGCR8, LANCL2, BCL6, TNRC6B, SUPT5H, **TNRC6A**, ***ZNF423*** , SATB2, TRIM27, ***SMAD3*** , SPEN, WWTR1, MBD1, STAT3, MSX1, HDAC1, TRPS1, NAB1, DNMT1, CELF1, TBL1X, COMMD7, ***DNAJB6*** , EIF2C4

darkred	1238	GO:0000139~Golgi membrane	30	2.42	9.21E-06	GLG1, FUT8, **CNIH**, AP1G1, ***CLSTN1*** , ST8SIA2, SGMS1, CLTC, ARFGEF2, **TMF1**, B2M, ST3GAL1, ST6GALNAC6, GBF1, INPP5E, PCSK7, PDGFD, SEC24D, GOLGA3, ACER3, BSG, ***SCAMP3*** , MAN1A2, ***HLA-A*** , CHST3, LDLRAP1, MAN2A2, GNAS, **GOSR1**, TRAPPC3
blue	1979	GO:0005739~mitochondrion	182	9.20	5.98E-10	GRPEL1, PDP2, EHHADH, RNASEH1, ROMO1, ***COX4NB*** , MRPS30, HIBADH, FAHD1, PECR, ***ACSS1*** , CISD1, **AGPS**, SLC25A24, SLC25A22, ***MRPL37*** , ***DNAJC5*** , PDHA1, HADH, WWOX, MTUS1, MRPL34, MRPL35, **OXR1**, MRPL53, FECH, **OPA1**, SYNJ2BP, BCL2L11, TIMM8A, SLC25A35, ATP5C1, ATPIF1, MRPL45, MDH2, CAV2, HSD17B10, CAV1, ACADSB, FDX1, **GLUD1**, MTX2, CHCHD3, **KMO**, BCL2L1, ELK3, ACAT1, TK2, DTD1, MTCH2, TOMM6, GFM1, DIABLO, LIAS, HSPE1, ***AP2M1*** , FH, CXORF23, **MMADHC**, ***MRPS24*** , AK2, ***CIDEA*** , IDH3B, ***REEP1*** , AFG3L2, VDAC3, MMAB, **PTPN11**, SLC25A12, TRNT1, NDUFV3, KIAA1279, PSMC4, TOMM70A, PTCD3, **GLS**, NDUFV2, C2ORF47, HSPD1, MRP63, ABCF2, CYP11B2, PRDX4, BNIP3, TIMM50, PRDX3, **PTEN**, ***KCNJ11*** , CDS2, ACOT9, ***NDUFS7*** , TRIAP1, MCCC2, NDUFS6, IMMP2L, CASP3, NDUFS4, AGPAT5, TPP1, GPX4, GBAS, ATP5L, GHR, ATP5J, ***TOMM34*** , ***PRKCA*** , ***PPP2R1A*** , NDUFB11, SLC25A4, AIFM1, CYCS, COX4I1, TMEM70, **CBR4**, COQ9, CDK7, TIMM23, NDUFA10, ACADL, NDUFA11, LAP3, **KIF1B**, MRPS9, **CLIC4**, **PPM1K**, TOMM20, ***CTSD*** , CTSB, PMPCA, NDUFB3, **APOOL**, ***USP30*** , NDUFB4, SAMM50, NDUFB8, UROS, NFS1, TIMM10, **AASS**, HK1, ATP5G2, ATP5G3, GRAMD4, NDUFB2, TSC22D3, ACSL1, SH3GLB1, VDAC1P5, MRPL19, PPP3CB, MARS2, ***MLXIP*** , **PPP3CA**, HSD17B4, ACSL4, MLLT6, **ACSL3**, AGK, ENOSF1, ACSL5, TXNIP, C6ORF168, NDUFA5, **DNM1L**, COX7A1, IMMT, PSAP, **PDK3**, ILF3, SOD1, MSRB3, CAPRIN2, SDHA, SDHB, **ABCC9**, ***MRPL22*** , GOLPH3, **WHSC1L1**, **NLN**, HIBCH, ALKBH3, MGST1, VPS25
greenyellow	656	GO:0044429~mitochondrial part	45	6.86	5.81E-06	SAMM50, QARS, TOMM20L, IARS2, ***OGDH*** , UQCRFS1, HADHB, GOT2, ***NDUFS7*** , FAHD1, MFF, HTRA2, IVD, CPOX, GSTK1, BCL2, DHODH, MRPL32, HADH, NDUFS1, HMGCL, COX16, SCO1, SUOX, FECH, MRPS22, ACADS, CBR4, CYB5A, DLAT, SOD2, SDHA, MFN2, SDHB, NNT, CYP27A1, PSEN1, TOMM70A, PHB2, TMLHE, POLDIP2, TOMM20, TOMM22, ATP5A1, PCCA
lightcyan	331	GO:0044420~extracellular matrix part	9	2.72	1.57E-03	VEGFA, COL3A1, NTN4, ***COL6A1*** , COL12A1, SPARC, TIMP2, COL5A2, FN1
darkgrey	251	GO:0031410~cytoplasmic vesicle	17	6.77	2.10E-02	ESD, YWHAE, GHRHR, DVL1, **LAMP2**, SLC2A4, ***CRISPLD2*** , ANXA11, BACE1, MYH11, TRAPPC4, YIPF5, COPG, PHLDA1, SCAMP5, PATE4, HIP1

white	260	GO:0005856~cytoskeleton	31	11.92	6.49E-03	**ENAH**, SHROOM4, TLN2, AURKB, AKAP11, **SEC62**, KLHL5, PTK2, TUBB, ***PSKH1*** , SORBS1, MYBPH, TUBA3E, DDX20, ***VPS11*** , ***NF2*** , INPPL1, ***MICAL2*** , BFSP1, PSD3, DRG1, MID1IP1, ***DCTN4*** , ***DNMBP*** , TACC2, ACTRT2, MYO10, ARHGAP32, NAV1, JAK2, SEPT6
lightyellow	277	GO:0030029~actin filament-based process	15	5.42	2.97E-05	MYL6, **TRPM7**, LMO7, DAAM1, DAAM2, LLGL1, ***PFN1*** , CORO1A, ***NISCH*** , PFN4, MYL6B, GHRL, WIPF1, PLS3, MYH10
paleturquoise	204	GO:0008092~cytoskeletal protein binding	17	8.33	3.98E-04	MTSS1, PHACTR2, PTPN3, **UTRN**, FRMD3, EPB41L2, **SYNE1**, **NEB**, SORBS1, FYN, SORBS2, ***MAPT*** , SNTB1, SPTBN1, MSN, WIPF1, SPTB
violet	167	GO:0043408~regulation of MAPKKK cascade	6	3.59	3.04E-03	***CAV3*** , **TAOK3**, ***MUL1*** , IGF2, IL6R, **FGD4**
darkorange	246	GO:0070013~intracellular organelle lumen	33	13.41	7.40E-03	MRPL40, RBM15B, LMO4, PRKDC, NR2C2, **RTN3**, HNRNPA3, MCCC2, PARN, SRRM2, YAP1, BDH1, ETFB, ***GTF3C4*** , PDPR, HMG20A, **YTHDC1**, POLR1C, MED13L, WWTR1, **APPL1**, ZBTB43, ATM, ***ATXN7L3*** , ***ATXN1*** , HDAC4, MAPK1, ATF3, HIPK1, CFL1, ***FLII*** , USP22, ***ACSM5***
purple	368	GO:0006350~transcription	79	21.47	1.27E-07	***THRA*** , STAT5A, FOXK2, ZNF530, HOXD10, MAMSTR, PAX7, ATOH8, MKL2, AKIRIN2, ***MLL2*** , CCNK, ***ESR1*** , MED12, ADNP, ***ZNF142*** , RXRG, ZHX2, ZNF687, ZNF7, SPEN, ZFP28, MCM6, EYA3, NCOA3, NCOA6, ***ZNF384*** , ***CAND2*** , ***EDF1*** , CARM1, IRAK1BP1, **CLOCK**, CRTC2, ***CAMTA2*** , ZNF516, ETV7, ***NACA*** , ***HCFC1*** , SOX4, C17ORF79, ***TSC22D1*** , TSPYL2, **XBP1**, HOXA5, TEAD4, RQCD1, BCL9L, MAML3, ***ZNF423*** , ERCC2, ***MAF*** , ASXL2, TAF1, ***TAF4*** , ZMYM2, ***ZBTB47*** , IKZF1, MAFB, TP53BP1, ***TRIM28*** , ***ASXL1*** , SMAD5, CREBBP, PPP1R10, TEAD1, POLR3A, ***MEF2D*** , NOTCH2, CSRNP3, **PNRC2**, ***ATF7*** , GRLF1, KDM4C, ZNF318, HIVEP1, NCOR1, HDAC8, NCOR2, HDAC6
grey60	787	GO:0051603~proteolysis involved in cellular protein catabolic process	61	7.75	3.07E-09	USPL1, BTRC, **RNF217**, RNF216, SENP5, WWP2, KLHL9, KLHL21, RANBP2, **ITCH**, RNF149, FBXO21, **VCPIP1**, **TBL1XR1**, **SKP2**, GAN, UBE2N, WDR48, SENP3, ***PIAS3*** , KLHL15, UBR5, ADAM17, UBD, PIAS2, PIAS1, FBXO15, NEURL2, USP24, **USP7**, CUEDC2, OTUD5, DERL2, ***APH1A*** , USP3, UBE2QL1, EDEM3, ZBTB16, PSMA7, MYCBP2, CYLD, USP37, OTUD7A, ZMPSTE24, **USP34**, FBXW11, **TRIP12**, USP31, ***UBXN1*** , **SHPRH**, HACE1, PARK2, SUGT1, URM1, TULP4, TOM1L1, NEDD4, FBXO34, HDAC6, ***RNF41*** , RNF111
salmon	337	GO:0046907~intracellular transport	26	7.72	9.90E-04	SNX9, NCBP1, YWHAZ, XPO5, ***LMAN2L*** , MYL1, ***NAPA*** , GLI3, TAPBP, ***STX16*** , PPP3CB, RAB11A, STAM, WIPF1, AGAP3, **RHOBTB3**, ARHGEF2, SMG1, ***ICMT*** , MYH9, AP4S1, ATXN1, ***KIAA1279*** , ARCN1, RAB14, SORT1
cyan	341	GO:0042325~regulation of phosphorylation	23	6.74	9.28E-05	EGFR, **CCNT2**, PTPRC, ADCY2, VAV3, HCLS1, ***PFKFB2*** , MET, TGFBR2, **ZEB2**, IL6R, LPAR1, ADIPOQ, APLP2, ATXN1, ***ACVR2B*** , APP, ERCC6, ***NUP62*** , NPM1, ADAM17, CDK5RAP1, **BMPR1A**

pink	437	GO:0043232~intracellular non-membrane-bounded organelle	90	20.59	7.21E-06	***TGOLN2*** , GYPC, LIMA1, ***TLN1*** , ***RPL19*** , GAR1, CCNT1, PRRX2, TTN, RPS2, **RTN3**, VCL, ARHGAP6, CDC45, SIN3A, **ANK2**, RHOA, DYNC1H1, ***MYST2*** , FTL, SYMPK, ***CRYAB*** , EXOSC5, ***UBR4*** , PSD3, APTX, ***PURB*** , UXT, CCDC6, ARHGAP32, NME2, EPB41L1, EP300, **CEP350**, HUWE1, HIST2H2BF, **LYST**, ***HIPK2*** , CSTB, NOL10, RPS12, BIN1, DST, EP400, UBA52, XRN2, **CLOCK**, STON2, KRT6C, TRIOBP, MIDN, RABGAP1, SSH1, DAG1, POLA1, AHCTF1, ABI1, **NR3C1**, MYL9, NPHP3, CHD8, **CHD7**, RPL31, RPL6, HIST1H4E, EXOC4, CLASP1, TINF2, TAF1, ***TBL3*** , HIST1H2BD, **CENPP**, ***PTPN14*** , ITPR1, ATXN1, MEF2D, **SYNE1**, HILS1, SP1, ***SMARCC2*** , MCPH1, TMOD2, PSPC1, MYH11, **JAK1**, SPTBN1, **UTP20**, **ALG11**, NCOR1, CBS

[1] Number of genes in term

[2] (Number of genes in term / Number of genes in Module)×100

[3] In bold genes that are members of the respective trait-associated modules and up-regulated expressed in Duroc

[4] In bold and italic genes that are members of the respective trait-associated modules and down-regulated expressed in Duroc

Table S5 The gene list in the top Go terms in biologically meaningful clusters for each module of PiNN

Module	No.genes/ Module	Go Term	Count[1]	% Count[2]	P-Value	Genes
orangered3	63	No Significant Term				
white	112	GO:0019899~enzyme binding	8	7.14	3.96E-02	EGFR, PHRF1, CCND2, **AKAP2**, CAMK2N1, POT1, FLNA, LLGL1
mediumpurple2	88	GO:0019318~hexose metabolic process	5	5.68	1.74E-02	PHKA2, PPP1R3D, **AKR1A1**, GPT, PMM2
paleturquoise	660	GO:0031981~nuclear lumen	80	12.12	5.72E-05	***TGOLN2*** , MEF2B, TSG101, HMGN5, CBX5, **RTN3**, MEN1, ***PSKH1*** , CSNK2A1, FOXF1, DHX33, MSN, SUPT5H, **TPR**, FTSJ2, PITX1, BRD8, **SRPK2**, GTPBP4, **RBL2**, RCOR3, EMG1, **RBL1**, MTA1, LAS1L, HDAC11, SPEN, ZCCHC17, TAF12, RPAIN, PTRF, RFC2, ZMIZ1, ***HIPK2*** , MAPK3, CSTB, CPSF1, POLR2H, POLR2G, ***SYVN1*** , TSHZ1, ***ELL*** , ELK3, ZBTB16, UBAC1, POLR2C, POLR2A, RPA3, MINA, SRRT, SF3B1, **SFRS18,** SET, ISY1, LIAS, GTF3C2, ETV6, XPOT, DNMT3A, SSRP1, ***ADARB1*** , MLL, MKI67, ***TAF6*** , CREBBP, ***SMAD3*** , ILF3, NXF1, **APPL1**, CDC27, STAT3, **ATF6**, ***ATXN1*** , **GTF2F2**, PCNA, CALM3, JAK2, WRB, DUSP7, VPS25
palevioletred1	43	No Significant Term				
blue2	2004	GO:0009057~macromolecule catabolic process	159	7.93	2.75E-15	NCBP2, NCBP1, ***EIF2C1*** , BTRC, PPP2R5C, RNF216, **ERLEC1**, ISG15, WIBG, FBXO28, RABGEF1, RNF149, **ITCH**, FBXO21, FBXO22, CUL1, ANAPC2, MAGOH, ZHX2, UBE2J1, ***UBR4*** , **UBR3**, UBR2, **CLPX**, GNS, PSMA2, ADAMTS9, **CD36**, ***PIAS3*** , RNF139, FBXL5, ***ASB1*** , FBXL4, ASB5, XRN2, EIF2C4, FBXO11, ASB6, RAD23B, FBXO40, PABPC4, UBA5, **ASB15**, **ARIH1**, **FBXW7**, UBE2D3, HECTD2, HNRNPD, OTUD7B, FBXW2, RNF168, FBXO3, HECTD1, SPOP, UFSP2, SMG1, **MALT1**, ***CASC3*** , MARCH11, PSMC6, P2RX7, CBLB, NEDD4, RNF2, **UBA2**, **PNRC2**, UBA3, TDG, FBXO33, UBE2E1, ***SPG7*** , USPL1, HECW2, UBE2G1, SENP5, ***MGRN1*** , TPP1, PSMD1, PSMD2, PSMD5, FBXL14, USP16, **USP15**, KLHL20, **USP13**, FBXL18, **VCPIP1**, **ABCE1**, SPACA3, BRCC3, **ZCCHC11**, FBXL20, EXOSC7, CYCS, MBD4, ERLIN1, HERC3, LRRC29, HERC2, CDK7, UBE2H, GTF2H2, UBE2N, SENP2, RFWD2, WDR48, SENP3, PRKCQ, ***XPC*** , PSEN1, SIAH3, **MGEA5**, USP21, UCHL5, **MDM2**, **UCHL3**, SIAH1, **PCYOX1**, USP24, CLN5, **USP7**, OTUD5, ***USP30*** , USP6, UBE3B, ATG12, ZBTB16, C12ORF51, **RNF125**, ZFP36L2, SUMO2, CYLD, ERCC5, SUMO1, **RNF128**, PPP2CB, **USP38**, USP36, PRSS16, NEDD4L, FBXW11, **TRIP12**, FEN1, ***RNF144A*** , RNF144B, BIRC6, ***MARCH8*** , UBE2Q2, SELS, PSMD14, KCMF1, **GSPT1**, PSMD12, TOM1L1, ACE2, USP48, FAF1, TBL1X, ***USP42***

darkolivegreen2	58	GO:0005730~nucleolus	9	15.52	1.46E-03	EXOSC10, ELP3, DHX9, ELP2, YPEL2, SPTBN1, **PBX1**, ACIN1, BUB3
darkolivegreen4	336	GO:0070013~intracellular organelle lumen	56	16.67	2.54E-05	RBM4, INTS3, ACSS2, ***OGDH*** , GHRHR, **RTN3**, RBM4B, SIN3A, P4HA1, SRRM2, INTS7, NARS2, **SRRM1**, ***BRD4*** , **TPR**, PDPR, **MYO6**, FECH, YY1, PRKAB2, ***RING1*** , HMG20A, MCM2, ISG20L2, RFC5, ***EIF4A3*** , RFC3, ***MED15*** , JUN, RNF20, CPSF3L, TDRD7, FKBP4, ***SRL*** , ***SETD1A*** , COIL, TSPYL1, ***HNRNPL*** , NOM1, WDR12, THAP1, HIST1H4C, TERF2, DHX9, DLST, RBM23, **MPHOSPH10**, SAP18, ***POLR3A*** , WRN, DDX5, SF3A1, CDC25A, ATM, ***MEF2D*** , PHF5A
brown2	70	GO:0016702~oxidoreductase activity	3	4.29	3.18E-02	HIF1AN, ***KDM4A*** , ***KDM5C***
palevioletred2	70	GO:0048008~platelet-derived growth factor receptor signaling pathway	3	4.29	1.86E-03	PDGFA, CSRNP1, PDGFRA
deeppink	42	GO:0010647~positive regulation of cell communication	7	16.67	1.05E-04	TMED7, UBC, ***ESR1*** , **ZEB2**, IGF2, ***FADD*** , CITED2
black	252	GO:0044265~cellular macromolecule catabolic process	25	9.92	1.94E-04	***SYVN1*** , **C10ORF46**, ATG12, **XIAP**, UBA6, RLIM, ***ZFP36L1*** , LONP1, ERCC5, KLHL9, **VCPIP1**, USP40, **SHPRH**, PARK2, HERC1, **CDC27**, ATM, NEDD4, DCP1A, SIAH1, PIAS2, **CUL4B**, **SPOPL**, *USP42* , USP24
darkgreen	963	GO:0043632~modification-dependent macromolecule catabolic process	73	7.58	1.06E-11	KIAA0368, UBE2G1, BTRC, VPRBP, SENP5, **SENP6**, **CUL3**, **CUL2**, **G2E3**, **CUL5**, ATG7, **WWP1**, KLHL9, FBXO28, USP12, DDA1, RANBP2, **ITCH**, FBXO22, USP14, **USP13**, **TBL1XR1**, SOCS7, **UBR3**, **TOPORS**, SOCS5, WDR48, **DCUN1D1**, SENP1, HUWE1, MIB2, **MDM2**, **UBE2W**, PIAS2, TGFB1I1, **SPOPL**, **USP25**, USP24, FBXL2, **FBXO11**, **USP7**, **XIAP**, FBXO40, **UBE3A**, USP9X, EDEM3, MYCBP2, **ARIH1**, CYLD, **USP38**, USP37, ZMPSTE24, NEDD4L, **USP34**, **UBE2D1**, USP32, **TRIP12**, **MYSM1**, HECTD1, **RNF19A**, HACE1, *MUL1* , **BIRC6**, **MALT1**, SUGT1, ATE1, NEDD4, **FBXO30**, **ZRANB1**, CUL4B, USP48, **USP45**, RNF111
greenyellow	128	GO:0015629~actin cytoskeleton	16	12.50	1.93E-10	MYL6, ABLIM1, MYL2, TNNC1, MYL3, ACTN2, MYH7, MYOZ2, MYH6, MYL12A, TNNI1, TPM3, TNNT1, MYL6B, FILIP1L, MYH7B
green	640	GO:0016563~transcription activator activity	35	5.47	2.61E-06	SUPT3H, RSF1, ZBTB9, MITF, CDH1, MED23, TRRAP, FOXO3, **ZEB1**, NFYA, TGFB1, CXXC1, HSF2, POU3F3, ABRA, MKL1, MYST4, NFATC1, ZNF281, IRAK1, TAF1, **SP100**, TP53BP1, CREBBP, SMAD5, **SMAD4**, TEAD1, NR4A3, SPEN, ***MEF2D*** , RNF4, THRAP3, ***ZNF384*** , **CAND1**, PIAS1
grey60	709	GO:0051254~positive regulation of RNA metabolic process	40	5.64	1.49E-05	NCBP1, ELF1, THRB, NAA15, SOX4, FOXO1, RORA, ***SRF*** , **ZBTB38**, EPC1, CHD8, **MLL5**, MRPL12, **MDFIC**, MKL2, **TCF4**, KLF6, **TBL1XR1**, KLF7, **AR**, KLF12, EPAS1, MAFB, KLF13, ***SMAD3*** , TEAD1, CREB5, **RB1**, **ARID1B**, **PPARGC1A**, **NRIP1**, *ATXN1* , **ATF6**, NCOA2, SP1, **ATXN7**, FOXC2, PIAS2, PIAS1, **SMARCA2**

lightsteelblue	165	GO:0008270~zinc ion binding	36	21.82	6.31E-04	SEC24B, PPARD, **RSF1**, USP3, RBM6, **WBP4**, ZNF34, ZNRF3, **CNOT4**, PPP3CB, ZNF407, PATZ1, RNF121, DNAJA2, NFX1, EHMT1, ***ZNF592*** , TADA2A, CRIP3, ZMYM5, MOBKL1A, PRKCI, BIRC5, RBBP6, **ZFR**, ZNF140, **SUZ12**, MNAT1, MTF1, HNF4A, UBR5, **ACAP2**, ZNHIT6, **CHORDC1**, ZNF410, KLF3
mediumorchid	511	GO:0005524~ATP binding	64	12.52	7.57E-04	***SPG7*** , XRCC2, ADCY2, ATP6AP1, ATP5B, INO80, PPIP5K1, MOV10L1, QARS, CCT3, TTL, ACTR3, MAP3K5, ***PSKH1*** , **MAP3K4**, DDX24, MKKS, FIGNL2, POLG2, SIK3, IRAK1, **PIK3C2A**, **TPX2**, OLA1, MAPK1, ACVR2A, PDIK1L, **KIF1B**, **RFK**, **UBE2K**, ***ATP9A*** , BMP2K, MYH7B, EP400, GPN1, MAPKAPK5, C9ORF98, CETN2, CTPS2, STK17A, PFAS, SGK223, DDX47, PTK2, CHD1L, MAP3K2, TEK, SUPV3L1, SNRNP35, HSPA8, TCP1, **PDK3**, **NLK**, MYO1G, GARS, LARS2, EPHA1, **SMC3**, **ATRX**, RPS6KA6, **ICK**, ***GSK3A*** , DDX59, RAD54L2
orange	181	GO:0048598~embryonic morphogenesis	10	5.52	2.84E-03	WNT3, HOXA4, ***TSC1*** , MAFB, FBXW4, RAB23, **LRP6**, **MECOM**, GLI3, SHANK3
thistle1	282	GO:0051276~chromosome organization	18	6.38	1.35E-03	HIST1H2BF, RCOR1, EZH1, ***SETD1B*** , MORF4L2, SOX6, ARID1B, **SMC4**, **SUV39H2**, **MLL5**, EP300, **NIPBL**, **BPTF**, HIST1H3C, **JMJD1C**, HDAC9, MYST3, APC

[1] Number of genes in term

[2] (Number of genes in term / Number of genes in Module)×100

[3] In bold genes that are members of the respective trait-associated modules and down-regulated expressed in PiNN

[4] In bold and italic genes that are members of the respective trait-associated modules and up-regulated expressed in PiNN