

Table S1. Positional candidate genes within QTL support interval region (SW38-S0215) on SSC13

Gene	Locus (Start – Stop)*		Accession No.	Description
<i>LOC100152482</i>	206661900	206663813	XM_003358929.1	oligodendrocyte transcription factor 2-like
<i>LOC100620095</i>	206713880	206714794	XM_003358931.1	oligodendrocyte transcription factor 1-like
<i>LOC100620748</i>	206922534	206924684	XM_003358936.1	dnaI homolog subfamily C member 28-like
<i>LOC100620652</i>	206941093	206969505	XM_003358935.1	trifunctionalpurine biosynthetic protein adenosine-3-like
<i>DBP-5</i>	206972831	207005201	XM_003358932.1	son3 protein
<i>DONSON</i>	207004326	207014612	XM_003358934.1	downstream neighbor of SON
<i>CRYZL1</i>	207015352	207077229	NM_001098596.1	crystallin, zeta (quinone reductase)-like 1
<i>LOC100622454</i>	207143842	207200200	XM_003358946.2	intersectin-1-like
<i>LOC100737549</i>	207203154	207280868	XM_003483356.1	intersectin-1-like
<i>LOC100622563</i>	207293970	207316331	XM_003358947.2	intersectin-1-like
<i>LOC733678</i>	207336292	207346559	NM_001044606.2	ATP synthase H ⁺ -transporting mitochondrial F1 complex O subunit
<i>LOC100510984</i>	207517599	207586370	XM_003132757.3	uncharacterized LOC100510984
<i>SLC5A3</i>	207541715	207543871	XM_003358937.1	solute carrier family 5 (sodium/myo-inositolcotransporter), member 3
<i>KCNE2</i>	207808671	207809042	XM_001927946.2	potassium voltage-gated channel, Isk-related family, member 2
<i>LOC100511159</i>	207813875	207846766	XM_003132758.1	protein FAM165B-like
<i>LOC100621502</i>	207879824	207887836	XM_003358939.1	potassium voltage-gated channel subfamily E member 1-like
<i>RCAN1</i>	207934802	207945091	NM_001243913.1	regulator of calcineurin 1
<i>CLIC6</i>	208080351	208130617	XM_003358948.1	chloride intracellular channel 6
<i>LOC100621586</i>	208163975	208164559		60S ribosomal protein L19-like
<i>RUNX1</i>	208205560	208300127	NM_001246252.1	runt-related transcription factor 1
<i>LOC100622010</i>	208453631	208456395	XR_131030.1	uncharacterized LOC100622010
<i>LOC100737721</i>	209379479	209383643	XM_003483357.1	uncharacterized LOC100737721
<i>LOC100623043</i>	209458533	209458912		proteasome assembly chaperone 4-like
<i>LOC100622064</i>	209699367	209703864	XM_003358942.1	uncharacterized LOC100622064
<i>SETD4</i>	209715202	209740272	XM_003358943.1	SET domain containing 4
<i>LOC100622246</i>	209751977	209758101	XM_003358944.1	carbonyl reductase [NADPH] 1-like
<i>CBR3</i>	209842863	209852618	NM_001244732.1	carbonyl reductase 3
<i>DOPEY2</i>	209882344	210009502	XM_003132763.1	dopey family member 2
<i>MORC3</i>	210024240	210066421	XM_003132764.1	MORC family CW-type zinc finger 3
<i>CHAF1B</i>	210075155	210099935	XM_003132765.1	chromatin assembly factor 1, subunit B (p60)
<i>LOC100513760</i>	210106849	210130608	XM_003132766.3	uncharacterized LOC100513760
<i>CLDN14</i>	210156559	210157513	NM_001161642.1	claudin 14
<i>LOC100623917</i>	210439397	210478671	XM_003358951.2	single-minded homolog 2-like
<i>HLCS</i>	210483855	210670282	XM_003132771.3	Holocarboxylasesynthetase (biotin-(propionyl-CoA-carboxylase (ATP-hydrolysing)) ligase)
<i>LOC100624407</i>	210670289	210684639	XM_003358954.1	uncharacterized LOC100624407
<i>LOC100153272</i>	210717956	210727523	XM_001928073.2	protein ripply3-like
<i>PIGP</i>	210760413	210769136	NM_001243520.1	phosphatidylinositolglycan anchor biosynthesis, class P
<i>TTC3</i>	210781584	210880629	XM_003358955.2	tetratricopeptide repeat domain 3
<i>LOC100738307</i>	210988730	211046114	XM_003483358.1	Down syndrome critical region protein 3-like
<i>DYRK1A</i>	211098364	211248171	XM_003132770.3	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1A
<i>LOC100738376</i>	211406307	211406865		60S ribosomal protein L15-like
<i>LOC100515928</i>	211425031	211613214	XM_003132774.3	G protein-activated inward rectifier potassium channel 2-like
<i>KCNJ15</i>	211979422	212022415	XM_001928412.2	potassium inwardly-rectifying channel, subfamily J, member 15
<i>ERG</i>	212086250	212156873	NM_001244456.1	v-etserythroblastosis virus E26 oncogene homolog (avian)

* SNP position derived from the *Sus scrofa* 10.2 assembly (NCBI).

Table S2. Primer sets for exonic sequence variants in the *RUNX1*, *DYRK1A*, and *KCNJ15* genes

Gene	SNP	Region	Primer		Size (bp)	T_m (°C)	Restriction enzyme
			Name	Sequences (5' → 3')			
<i>RUNX1</i>	SNP1	Exon6 (c.1331 C<G)	R1F	GATCACAGATCACGTTCACTGC	380	62	
			R1R	<i>Biotin</i> -CGTCCTACCACCTCTACTACGG			
			RM1	AGCCTCAGTAGGGCCGCCAT			
	SNP2	Exon6 (c.1319 A<G)	R2F	<i>Biotin</i> -GATCACAGATCACGTTCACTGC	380	62	
			R2R	CGTCCTACCACCTCTACTACGG			
			RM2	CAACATGGCGCCTGCCGCGC			
<i>DYRK1A</i>	SNP1	Exon11 (c.2989 G<A)	D1F	GGTGGGAAGTTTGGTTTTTTG	588	62	<i>Bam</i> HI
			D1R	TGTGACCTTCAACCAATAAGGA			
			D2F	GCCAATAACCTGTTCAAAA			
	D2R	<i>Biotin</i> -CAGGCCTGACATTTGGTTAC					
	DM1	GAACAAAAGCAGGTTTTTAT					
	SNP3	Exon11 (c.5070 C<A)	D3F	<i>Biotin</i> -GTCCTCAGACTCTTTACTATGCTT	298	64	
			D3R	ACAAACTATTCGCACTCTGAATC			
			DM2	CTAGTTTGCTTTTTACACAC			
	<i>KCNJ15</i>	SNP1	Exon2 (g.-293 C<G)	K1F	<i>Biotin</i> -TTCCTTCAGGTAAATCCTACCC	297	
K1R				GTGCACGATTTAAGTCACTTTT			
KM1				ACGCTGGCTGGATGTGAAG			
SNP2		Exon3 (g.-207 G<A)	K2F	<i>Biotin</i> -CCTTTACTACTACTGCCTCTGAA	260	62	
			K2R	GCAAAGCAAAAGGCTCCTC			
			KM2	CTTTTCTCTCTGTCAACTC			
SNP3		Exon5 (g.1029 T<C)	K3F	CTCTCCAAAACCGCAAGTAC	486	64	
			K3R	<i>Biotin</i> -CCCTCCACCAAGTTCTTTGA			
			KM3	AAGTACAGGCAGGAGGATCA			
SNP4		Exon5 (g.1161 T<C)	KM4	CGCCTCAGCTTAGCTCCTTC			
SNP5		Exon5 (g.1232 G<A)	KM5	GAAAACAAAACCTGCGTGGCC			

Table S3. Genotype and allele frequencies of the SNPs detected in RUNX1, DYRK1A, and KCNJ15 genes in a resource population between Landrace and KNP

	Genotype frequencies			Allele frequencies		MAF Minor allele
RUNX1-SNP1 (c.1331 C<G)	CC	CG	GG	C	G	
KNP	0.053	0.579	0.368	0.342	0.658	0.1983
Landrace	-	0.176	0.824	0.088	0.912	C
F ₂	0.085	0.427	0.489	0.298	0.702	
RUNX1-SNP2 (c.1319 A<G)	AA	AG	GG	A	G	
KNP	-	0.316	0.684	0.158	0.842	0.1293
Landrace	-	0.059	0.941	0.029	0.971	A
F ₂	0.012	0.160	0.828	0.092	0.908	
DYRK1A-SNP1 (c.2989 G<A)	GG	GA	AA	G	A	
KNP	-	-	1.000	-	1.000	0.3707
Landrace	0.588	0.412	-	0.794	0.206	G
F ₂	0.112	0.510	0.377	0.367	0.633	
DYRK1A-SNP2 (c.4332 C<T)	CC	CT	TT	C	T	
KNP	-	-	1.000	-	1.000	0.0431
Landrace	-	0.059	0.941	0.029	0.971	C
F ₂	-	0.061	0.939	0.030	0.970	
DYRK1A-SNP3 (c.5070 C<A)	CC	CA	AA	C	A	
KNP	0.111	0.444	0.444	0.333	0.667	0.1667
Landrace	-	-	1.000	-	1.000	C
F ₂	0.019	0.222	0.759	0.130	0.870	
KCNJ15-SNP1 (g.-293 C<G)	CC	CG	GG	C	G	
KNP	0.158	0.579	0.263	0.447	0.553	0.2241
Landrace	-	-	1.000	-	1.000	C
F ₂	0.039	0.357	0.605	0.217	0.783	
KCNJ15-SNP2 (g.-207 G<A)	GG	GA	AA	G	A	
KNP	0.158	0.632	0.211	0.474	0.526	0.2328
Landrace	-	-	1.000	-	1.000	G
F ₂	0.032	0.304	0.664	0.184	0.816	
KCNJ15-SNP3 (g.1029 T<C)	TT	TC	CC	T	C	
KNP	0.158	0.632	0.211	0.474	0.526	0.2328
Landrace	-	-	1.000	-	1.000	T
F ₂	0.035	0.337	0.628	0.204	0.796	
KCNJ15-SNP4 (g.1161 T<C)	TT	TC	CC	T	C	
KNP	0.105	0.474	0.421	0.342	0.658	0.4397
Landrace	0.176	0.529	0.294	0.441	0.559	T
F ₂	0.141	0.590	0.269	0.436	0.564	
KCNJ15-SNP5 (g.1232 G<A)	GG	GA	AA	G	A	
KNP	-	0.053	0.947	0.026	0.974	0.2586
Landrace	0.294	0.529	0.176	0.559	0.441	G
F ₂	0.037	0.387	0.576	0.230	0.770	