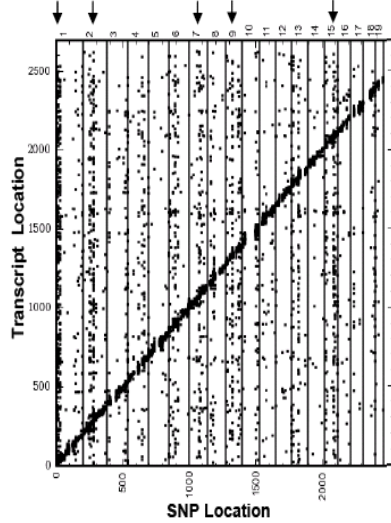


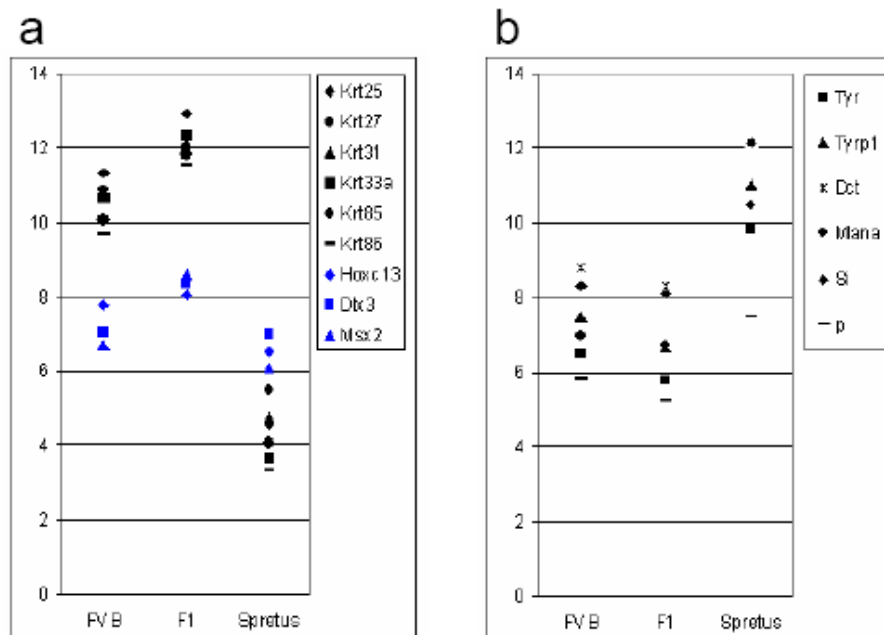
Genetic architecture of murine skin inflammation and tumor susceptibility (Supplementary data)

Supplementary Figure 1



Distribution of significant trans-eQTL in FVBB tail epidermis. This figure plots the distribution of all eQTL measured in skin ($\leq 5\%$ FDR). Genomic location of SNPs across all chromosomes is plotted on the horizontal axis; location of probes is plotted on the vertical axis. No eQTL were calculated on the X or Y chromosomes. Solid vertical lines separate chromosomes. The dark line along the diagonal are putative *cis*-eQTL. Arrows indicate significant hot-spots (chi-squared test, Bonferroni correction for 223 tests). Total trans-eQTL count = 1034. (see Supplementary Tables 1,2 for specific chromosome and SNP breakdowns).

Supplementary Figure 2



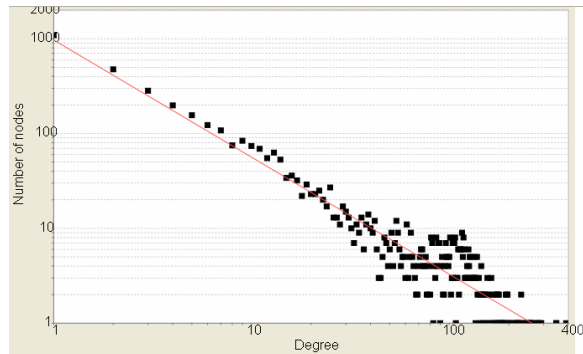
Gene expression in parental mice shows genetic influence on functionally related genes

The Y-axis is the log-transformed mean of four biological replicate gene expression values measured in FVB/N, SPRET/Ei, and FVB x SPRET F1 animals with Affymetrix arrays. All genes are significantly different between strains (FDR q -value = 0 for all genes).

(A) Gene expression of representative hair follicle genes. Structural genes are shown in black; transcription factors *Hoxc13*, *Dlx3*, and *Msx2* are shown in blue.

(B) Gene expression of melanin biosynthesis genes.

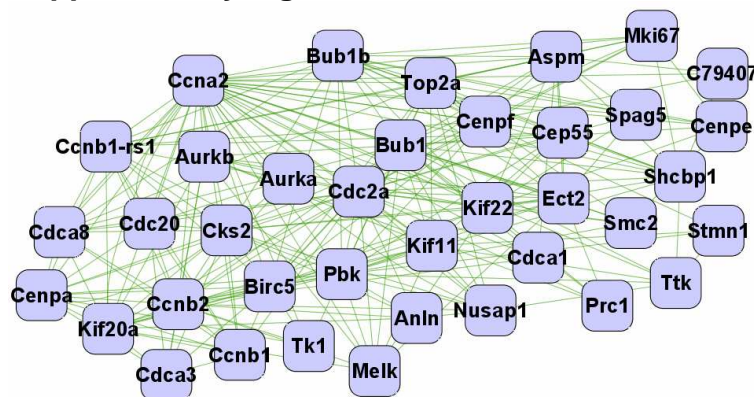
Supplementary Figure 3



Degree Distribution of FVBBX correlation network.

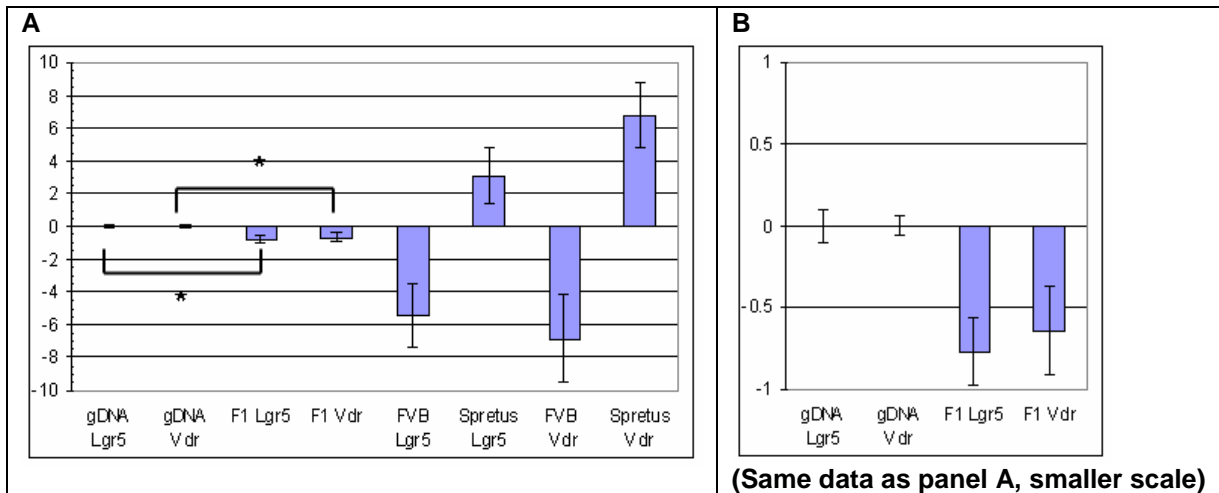
Structural characteristics of the FVBBX relevance network were calculated using the NetworkAnalyzer³¹ plug-in for Cytoscape. The correlation coefficient cut-off for the relevance network was 0.8. The network contains 3933 nodes and 40,335 edges. The mean number of neighbors is 19.3 and the mean clustering coefficient is 0.35. The network is plausibly scale-free, as a linear least-squares fit of the log degree to log number of nodes had an r -squared value of 0.88 for a power law of the form $y=969.25x^{-1.235}$.

Supplementary Figure 4



Cell Cycle gene correlation network in FVBBX. Edges indicate correlation $r^2 \geq 0.64$. This clique was automatically identified from the FVBBX tail epidermal gene expression.

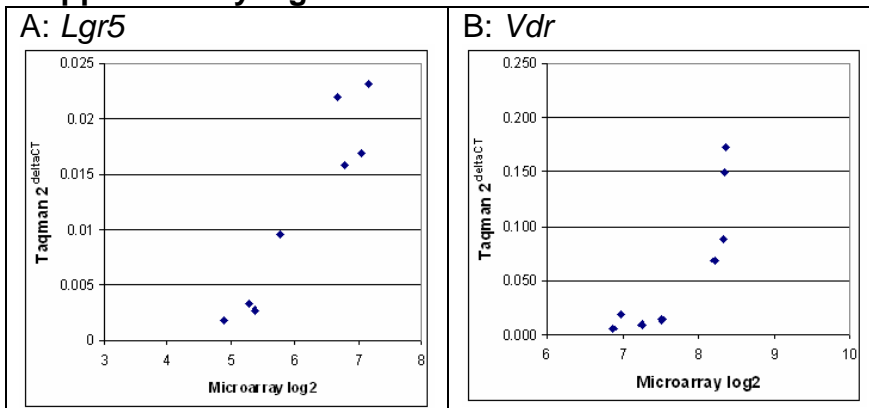
Supplementary Figure 5



Taqman validation of allele-specific expression of *Lgr5* and *Vdr* in parental and F1 animals.

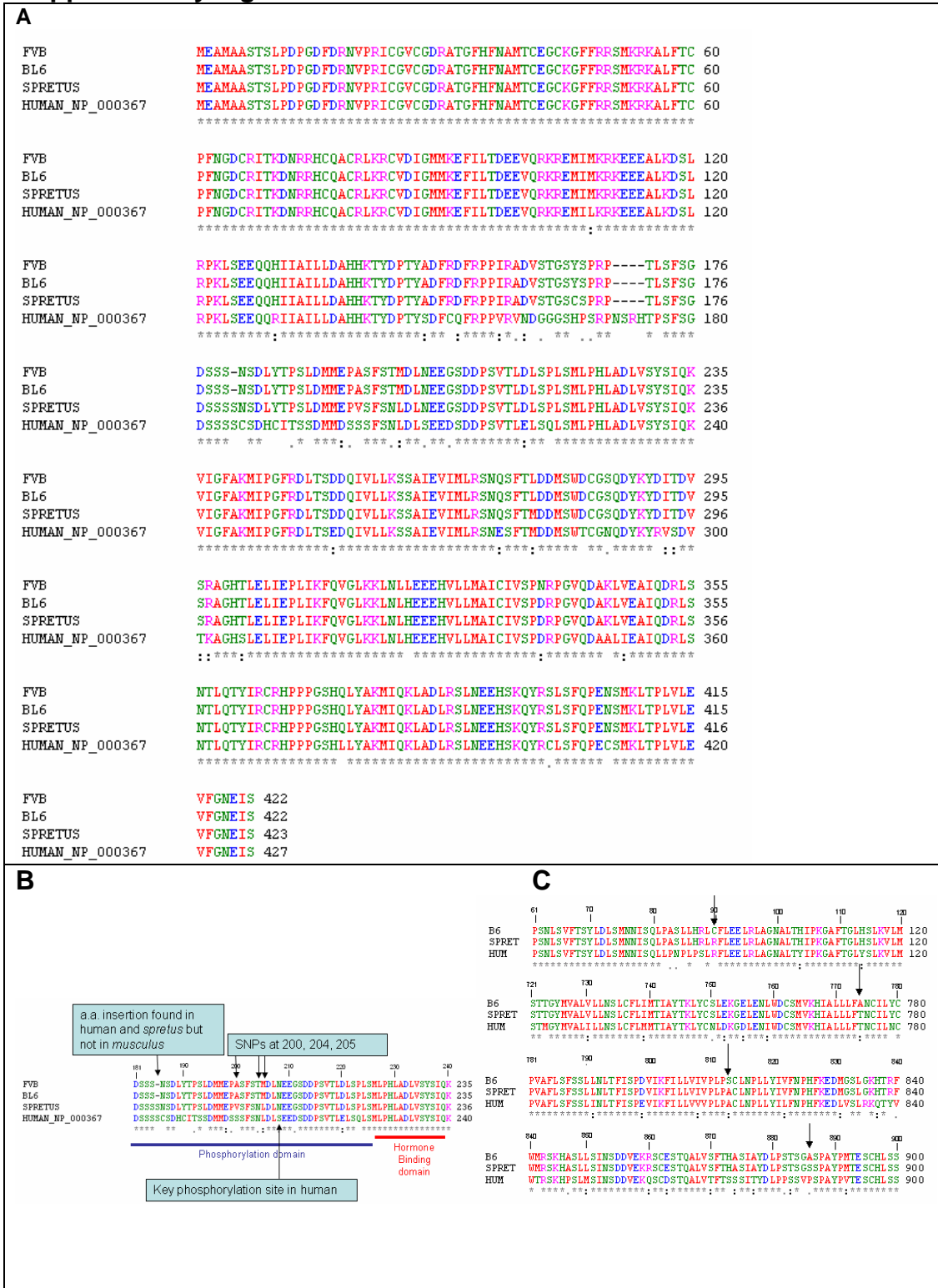
Cis-regulation of *Vdr* and *Lgr5* was verified by a cis-trans test. We performed allele-specific Taqman of SPRET/Ei (n = 4), FVB/N (n = 4), and F1 (n = 3) RNA. Allele-specific Taqman probes were designed by sequencing *Lgr5* and *Vdr* in SPRET/Ei and FVB/N. The first two columns show $\Delta\Delta\text{Ct}$ for the genomic DNA used as a control to adjust for unequal efficiency of the FAM and VIC probes. The next two columns show $\Delta\Delta\text{Ct}$ values for *Lgr5* and *Vdr* probes in F1 (also presented at right, smaller scale). The last four columns show $\Delta\Delta\text{Ct}$ values for *Lgr5* and *Vdr* probes in FVB/N and SPRET/Ei. Although the measured effect is modest, the difference from genomic DNA is significant ($p < 0.05$, both genes).

Supplementary Figure 6



Taqman validation of microarray expression measurements of *Lgr5* and *Vdr*. *Lgr5* and *Vdr* expression in parental FVB/N and SPRET/Ei strains as measured by Taqman was compared expression measured by Affymetrix microarray. *Lgr5* expression as measured by Taqman is highly correlated with expression measured by the microarray (correlation r-squared value 0.81, p-value 0.005). Expression of *Vdr* as measured by Taqman is highly correlated with expression measured by Affymetrix microarray (correlation r-squared 0.85, p-value 0.002).

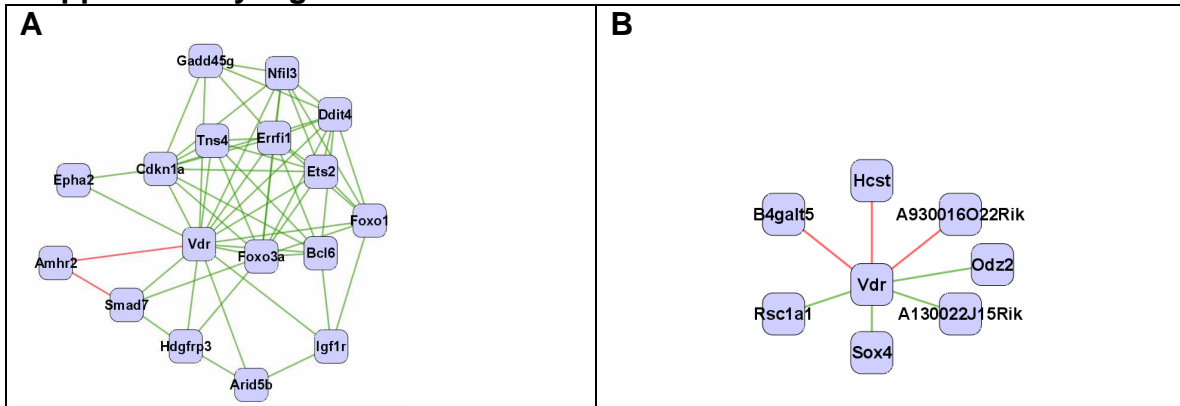
Supplementary Figure 7



Aligned protein sequences of FVB/N, C57/B6, SPRET/Ei, and human *Vdr*. We sequenced the coding exons of the *Vdr* in FVB/N and SPRET/Ei mice and aligned the imputed protein sequences against C57/BL6 and the human NP_000367 *Vdr* sequence (A). For the first 180 human amino acids (a.a.) there are no non-synonymous coding changes between mouse species in *Vdr*. There are

several loci that differ between human and mouse, and four inserted human a.a. not found in mouse. There are three protein-coding changes between FVB/N and SPRET/Ei in the second *Vdr* phosphorylation domain and an a.a. inserted in human and SPRET/Ei but not *Mus musculus* (B). S208 is known to be a key phosphorylation site in humans. There is also a SNP resulting in a protein change between Spretus and FVB in the hormone-binding domain at human a.a. 281.

Supplementary Figure 8



Distinct *Vdr* correlation networks for mice homozygous and heterozygous at Chr15, 101 Mb.

Genes correlated with *Vdr* in mice homozygous for FVB/N at Chr15:101 Mb (A) or heterozygous FVB/SPRET at that locus (B). Green lines indicate direct correlation; red lines indicate inverse correlation. R-squared values are 0.49 or higher ($r \geq 0.7$ or $r \leq -0.7$).

It has been shown that *Vdr* ablation sensitizes skin to chemical and UV models of tumorigenesis^{32,33}. Our results show that FVBBX mice with a spretus allele at Chr 15:101 Mb have lower levels of *Vdr*, which is associated with higher tumor susceptibility. We performed differential correlation analyses of *Vdr* to identify the individual co-expression networks for mice heterozygous at Chr 15:101 Mb (n=39) and mice homozygous at that allele (n = 32). There is not a significantly non-random sex distribution in these groups (chi-squared test). Using a r-squared cut-off of 0.49, *Vdr* is correlated with genes that affect *Wnt* signaling and tumor susceptibility in homozygous mice but not in heterozygous mice (Figure 2A, 2B). The strongest correlation in the homozygous *Vdr* network is between *Vdr* and the tumor suppressor *Cdkn1a* (*p21*). It is known that *Vdr* binds *p21* directly and this binding increases *p21* expression³⁴. *TGF β* inhibitory gene *Smad7*, which induces beta-catenin degradation³⁵, is one of several *Wnt* modifiers in the homozygous correlation network. *Vdr* is transactivated by *Smad3*³⁶, and *Smad7* disrupts the binding of *Vdr* with *Smad3*³⁷. The homozygous *Vdr*-correlated transcription factors *Foxo1* and *Foxo3a* compete with TCF for the opportunity to bind beta-catenin, which activates *Foxo* signaling. This activation inhibits cell cycle progression^{38,39}. Connections between *Vdr* and *Wnt* signaling have been identified by Cianferotti and co-workers who recently showed that the cooperative effects of *Wnt* signaling genes *Ctnnb1* and *Lef1* are abolished in keratinocytes derived from *Vdr* knockout mice⁴⁰. Other genes in this signature (*Igf1r*, *Ddit4*, *Bcl6*, *Tns4*, *Ets2*, *Hdgfrp3*, *Gadd45g*, and *Epha2*) have been linked directly to tumor susceptibility and proliferation.

Importantly, genes in the *Vdr*-homozygous network are absent in *Vdr*-heterozygous mice. The correlation network in *Vdr*-heterozygous mice is recapitulated at lower stringency in *Vdr*-homozygous mice but not vice-versa (data not shown), suggesting genetic differences may have far-reaching physiological consequences. We sequenced the coding exons of *Vdr* in SPRET/Ei and FVB/N and identified four polymorphisms between these species that result in amino acid changes (Supplementary Figure 7).

The same analysis was then performed for *Lgr5*, identifying the individual co-expression networks for mice heterozygous at Chr 10:118 Mb (n=31) and mice homozygous at that allele (n = 42). There is not a significantly non-random sex distribution in these groups (chi-squared test). Using a r-squared cut-off of 0.49, *Lgr5* is correlated with very similar networks of hair-follicle and epidermal genes in both the *Lgr5*-homozygous and *Lgr5*-heterozygous groups. The principle difference

between the networks is that *Lgr5* is more highly correlated with hair follicle keratins in the *Lgr5*-homozygous group. One possible explanation for this result is the overall much lower expression of hair follicle-related genes in SPRET/Ei tail RNA; hair follicle signaling may be attenuated in these animals, and animals receiving a SPRET/Ei allele have commensurately lower overall levels of hair follicle expression. This is compatible with the fact that these keratins have eQTL at the Chr 10:118 Mb. locus.

Supplementary Table 1

SNPs that are significantly frequent locations for *trans*-eQTL peaks in mouse skin.

P-values from chi-squared test. This lists all SNPs with significant p-values after 0.05 Bonferroni corrected of an alpha level 0.05 for 223 tests. Total *trans*-eQTL count was 1034.

SNP Location	<i>trans</i> -eQTL count	P-value
Chr. 2, 85 Mb.	63	$2.0 * 10^{-12}$
Chr. 15, 73 Mb.	50	$1.3 * 10^{-9}$
Chr. 1, 29 Mb.	47	$5.7 * 10^{-9}$
Chr. 1, 16 Mb.	43	$4.1 * 10^{-8}$
Chr. 9, 52 Mb.	41	$1.1 * 10^{-7}$
Chr. 1, 8 Mb.	29	$3.9 * 10^{-5}$
Chr. 7, 79 Mb.	27	$1.0 * 10^{-4}$

Supplementary Table 2

Details of the eQTL distribution

Highlighted p-values are chromosomes that have significantly more *trans*-eQTL than expected by chance after Bonferroni correction

Chr	# <i>cis</i> eQTL	# <i>trans</i> eQTL	# eQTL	# SNPs assayed	% eQTLs <i>Trans</i>	% of all <i>trans</i> eQTL	uncorrected p-val for over-representation
1	254	160	414	19	38.65%	15.47%	4.29E-13
2	346	133	479	20	27.77%	12.86%	7.60E-09
3	176	43	219	15	19.63%	4.16%	NS
4	220	49	269	12	18.22%	4.74%	NS
5	296	13	309	11	4.21%	1.26%	5.47E-07
6	187	91	278	15	32.73%	8.80%	0.002121
7	311	91	402	18	22.64%	8.80%	0.002121
8	190	37	227	10	16.30%	3.58%	0.07474
9	209	105	314	10	33.44%	10.15%	5.24E-05
10	130	34	164	7	20.73%	3.29%	0.03301
11	250	21	271	11	7.75%	2.03%	1.39E-04
12	166	17	183	13	9.29%	1.64%	1.13E-05
13	184	66	250	12	26.40%	6.38%	NS
14	142	22	164	13	13.41%	2.13%	2.42E-04
15	177	104	281	13	37.01%	10.06%	6.96E-05
16	99	10	109	6	9.17%	0.97%	3.80E-08
17	205	12	217	5	5.53%	1.16%	2.34E-07
18	76	20	96	8	20.83%	1.93%	7.74E-05
19	141	6	147	5	4.08%	0.58%	5.76E-10

Supplementary Table 3

Genes in the muscle gene expression sub-network (Figure 1 in manuscript)

The gene that bridges the muscle gene network and the hair follicle gene network is *Tpm1*, tropomyosin alpha.

Symbol	Title	Chr.	Mb.
1110002E22Rik	RIKEN cDNA 1110002E22 gene	3	138
1110028A07Rik	RIKEN cDNA 1110028A07 gene	14	54.5
2310002L09Rik	RIKEN cDNA 2310002L09 gene	4	73.4
2310016A09Rik	RIKEN cDNA 2310016A09 gene	15	31.5
2310033F14Rik	RIKEN cDNA 2310033F14 gene	3	89.5
2310039E09Rik	RIKEN cDNA 2310039E09 gene	4	48.7
2310046A06Rik	RIKEN cDNA 2310046A06 gene	9	76.9
2310079P10Rik	RIKEN cDNA 2310079P10 gene	1	40.8
4631423F02Rik	RIKEN cDNA 4631423F02 gene	1	93.2
8030451F13Rik	RIKEN cDNA 8030451F13 gene	10	87.9
A2bp1	Ataxin 2 binding protein 1	16	6.5
Acsf6	acyl-CoA synthetase long-chain family member 6	11	54.2
Acta1	actin, alpha 1, skeletal muscle	8	126.8
Actn2	Actinin alpha 2	13	12.3
Actn3	actinin alpha 3	19	4.9
Adssl1	adenylosuccinate synthetase like 1	12	113.1
Ak1	adenylate kinase 1	2	32.4
Akap6	A kinase (PRKA) anchor protein 6	12	54
Alpk3	alpha-kinase 3	7	80.9
Amot	angiominin	X	140.7
Ampd1	adenosine monophosphate deaminase 1 (isoform M)	3	103.2
Ankrd2	ankyrin repeat domain 2 (stretch responsive muscle)	19	42.1
Ankrd23	ankyrin repeat domain 23	1	36.5
Apobec2	apolipoprotein B editing complex 2	17	47.9
Art1	ADP-ribosyltransferase 1	7	102
Asb5	ankyrin repeat and SOCs box-containing protein 5	8	56
Asph	aspartate-beta-hydroxylase	4	9.4
Atp1a2	ATPase, Na ⁺ /K ⁺ transporting, alpha 2 polypeptide	1	174.1
Atp2a1	ATPase, Ca ⁺⁺ transporting, cardiac muscle, fast twitch 1	7	126.2
Bin1	bridging integrator 1	18	32.6
Cacna1s	calcium channel, voltage-dependent, L type, alpha 1S subunit	1	137.9
Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	5	15.4
Cacng1	calcium channel, voltage-dependent, gamma subunit 1	11	107.5
Cap2	CAP, adenylate cyclase-associated protein, 2 (yeast)	13	46.5
Casq1	calsequestrin 1	1	174
Cav3	caveolin 3	6	112.4
Cfl2	cofilin 2, muscle	12	55.8
Chrna1	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	2	73.4
Chrb1	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	11	69.6
Ckm	creatine kinase, muscle	7	18.6
Ckmt2	creatine kinase, mitochondrial 2	13	92.3
Cmya1	cardiomyopathy associated 1	9	119.9
Cmya5	cardiomyopathy associated 5	13	94.1

Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2		7	128
Cox7a1	cytochrome c oxidase, subunit VIIa 1		7	29.9
Cox8b	cytochrome c oxidase, subunit VIIIb		7	140.8
Cryab	crystallin, alpha B		9	50.5
Csrp3	cysteine and glycine-rich protein 3		7	48.7
Ddit4l	DNA-damage-inducible transcript 4-like		3	137.6
Des	desmin		1	75.2
Dhrs7c	dehydrogenase/reductase (SDR family) member 7C		11	67.6
Eef1a2	eukaryotic translation elongation factor 1 alpha 2		2	181.1
Eno3	Enolase 3, beta muscle		11	70.5
Fabp3	fatty acid binding protein 3, muscle and heart		4	129.8
Fgf13	fibroblast growth factor 13	X		55.4
Fhl1	four and a half LIM domains 1	X		53.1
Finc	filamin C, gamma (actin binding protein 280)		6	29.4
Gyg	glycogenin		3	20.3
Hfe2	hemochromatosis type 2 (juvenile) (human homolog)		3	96.6
Hrc	histidine rich calcium binding protein		7	45.2
Hspb2	heat shock protein 2		9	50.5
Hspb3	heat shock protein 3		13	114.8
Hspb6	heat shock protein, alpha-crystallin-related, B6		7	30.3
Hspb7	heat shock protein family, member 7 (cardiovascular)		4	140.7
Itgb1bp2	integrin beta 1 binding protein 2	X		97.7
Jph1	Junctophilin 1		1	17
Jph2	junctophilin 2		2	163
Kbtbd10	kelch repeat and BTB (POZ) domain containing 10		2	69.5
Kbtbd5	kelch repeat and BTB (POZ) domain containing 5		9	121.6
LOC380843	similar to RNA binding motif protein 24		13	46.4
LOC629147	similar to Cortixin-1		18	57.6
LOC671894	similar to myosin, heavy polypeptide 4, skeletal muscle		14	53.9
Ldb3	LIM domain binding 3		14	33.4
Lmcd1	LIM and cysteine-rich domains 1		6	112.2
Lmod2	leiomodulin 2 (cardiac)		6	24.6
Lrrn1	leucine rich repeat protein 1, neuronal		6	107.5
Mapk12	mitogen-activated protein kinase 12		15	89
Mb	myoglobin		15	76.8
Mef2c	Myocyte enhancer factor 2C		13	84.1
Myf6	myogenic factor 6		10	106.9
Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult		11	67
Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult		11	67
Myh3	myosin, heavy polypeptide 3, skeletal muscle, embryonic		11	66.9
Myh6	Myosin, heavy polypeptide 6, cardiac muscle, alpha		14	53.9
Myh8	myosin, heavy polypeptide 8, skeletal muscle, perinatal		11	67.1
Myl1	myosin, light polypeptide 1		1	66.9
Myl2	myosin, light polypeptide 2, regulatory, cardiac, slow		5	122.4
Myl3	myosin, light polypeptide 3		9	110.6
Mylpf	myosin light chain, phosphorylatable, fast skeletal muscle		7	127
Myom1	myomesin 1		17	70.9
Myot	myotilin		18	44.5
Myoz1	myozenin 1		14	19.4

Myoz2	myozenin 2		3	123
Mypn	myopalladin		10	62.5
Neb	nebulin		2	52
Nexn	Nexilin		3	152.2
Nrap	nebulin-related anchoring protein pre-B-cell leukemia transcription factor interacting protein 1		19	56.4
Pbxip1			3	89.5
Pde4dip	phosphodiesterase 4D interacting protein (myomegalin)		3	97.8
Pdlim3	PDZ and LIM domain 3		8	47.4
Pdlim5	PDZ and LIM domain 5		3	142.3
Pfkm	phosphofructokinase, muscle		15	97.9
Pgam2	phosphoglycerate mutase 2		11	5.7
Pitx2	paired-like homeodomain transcription factor 2		3	129.2
Pkia	protein kinase inhibitor, alpha		3	7.3
Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C		19	36.8
Prkcq	protein kinase C, theta		2	11.2
Pvalb	parvalbumin		15	78
Pygm	muscle glycogen phosphorylase		19	6.4
Rpl3l	ribosomal protein L3-like		17	24.5
Rragd	Ras-related GTP binding D		4	33.4
Rtn2	reticulum 2 (Z-band associated protein)		7	18.4
Ryr1	ryanodine receptor 1, skeletal muscle		7	28.8
Schip1	Schwannomin interacting protein 1		3	68.6
Sgca	sarcoglycan, alpha (dystrophin-associated glycoprotein)		11	94.8
Sgcb	sarcoglycan, gamma (dystrophin-associated glycoprotein)		14	60.2
Sh3bgr	SH3-binding domain glutamic acid-rich protein		16	96.3
Six1	sine oculis-related homeobox 1 homolog (Drosophila)		12	74
Slc25a4	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 4		8	47.7
Slc2a4	solute carrier family 2 (facilitated glucose transporter), member 4		11	69.8
Sln	sarcolipin		9	53.6
Smpx	small muscle protein, X-linked	X		153
Smtnl1	smoothelin-like 1		2	84.6
Smyd1	SET and MYND domain containing 1		6	71.1
Srl	sarcalumenin		16	4.4
Srpk3	serine/arginine-rich protein specific kinase 3	X		70
Stac3	SH3 and cysteine rich domain 3		10	126.9
Synpo2	synaptopodin 2		3	123.1
Synpo2l	Synaptopodin 2-like		14	19.5
Tcap	titin-cap		11	98.2
Tmem38a	transmembrane protein 38a		8	75.5
Tnnc1	troponin C, cardiac/slow skeletal		14	30
Tnnc2	troponin C2, fast		2	164.5
Tnni1	troponin I, skeletal, slow 1		1	137.6
Tnni2	troponin I, skeletal, fast 2		7	142.3
Tnnt1	troponin T1, skeletal, slow		7	4.1
Tnnt3	troponin T3, skeletal, fast		7	142.3
Tpm1	tropomyosin 1, alpha		9	66.8
Tpm2	tropomyosin 2, beta		4	43.5
Trdn	triadin		10	32.8
Trim54	tripartite motif-containing 54		5	31.4

Trim63	tripartite motif-containing 63	4	133.6
Ttn	Titin	2	76.7
Txlnb	taxilin beta	10	17.5
Uchl1	ubiquitin carboxy-terminal hydrolase L1	5	67
Vgll2	vestigial like 2 homolog (Drosophila)	10	51.7
Zmynd17	zinc finger, MYND domain containing 17	14	19.3

Supplementary Table 4

Genes in the Hair Follicle eQTL network (Figure 2 in manuscript)

Symbol	Title	Chr	Mb	Strongest QTL Locus	Raw QTL p-value	Permutation QTL p-value
Chac1	ChaC, cation transport regulator-like 1 (E. coli)	2	119	Chr 15, 84 Mb	7.88E-04	0.11
Crym	crystallin, mu	7	120	Chr. 10, 118 Mb	2.57E-04	0.06
Dlx3	distal-less homeobox 3	11	94.9	Chr. 10, 118 Mb	1.28E-03	0.18
Fbp1	fructose biphosphatase 1	13	62.9	Chr. 3, 19 Mb	9.42E-04	0.19
Gprc5d	G protein-coupled receptor, family C, group 5, member D	6	135.1	Chr. 3, 19 Mb	3.33E-04	0.08
Krt2-ps1	keratin complex 2, basic, pseudogene 1	15	101.3	Chr. 3, 19 Mb	3.75E-04	0.08
Krt25	keratin 25	11	99.1	Chr. 3, 19 Mb	8.29E-04	0.11
Krt26	keratin 26	11	99.1	Chr. 15, 84 Mb	3.71E-04	0.08
Krt27	keratin 27	11	99.2	Chr. 15, 84 Mb	7.75E-04	0.11
Krt28	keratin 28	11	99.2	Chr. 3, 19 Mb	3.26E-04	0.1
Krt31	keratin 31	11	99.9	Chr. 3, 19 Mb	7.93E-04	0.14
Krt32	keratin 32	11	99.9	Chr. 10, 118 Mb	5.43E-04	0.1
Krt33a	keratin 33A	11	99.8	Chr. 3, 19 Mb	9.76E-04	0.14
Krt33b	keratin 33B	11	99.8	Chr. 10, 118 Mb	8.84E-04	0.13
Krt34	keratin 34	11	99.9	Chr. 3, 19 Mb	8.89E-04	0.15
Krt35	keratin 35	11	99.9	Chr. 10, 118 Mb	4.26E-04	0.11
Krt39	keratin 39	11	99.9	Chr. 10, 118 Mb	7.00E-04	0.13
Krt71	keratin 71	15	101.6	Chr. 10, 118 Mb	2.38E-04	0.06
Krt72	keratin 72	15	101.6	Chr. 3, 19 Mb	8.33E-04	0.16
Krt73	keratin 73	15	101.6	Chr. 10, 118 Mb	1.09E-04	0.02
Krt75	keratin 75	15	101.4	Chr. 10, 118 Mb	1.68E-04	0.05
Krt81	keratin 81	15	101.3	Chr. 3, 19 Mb	7.13E-04	0.11
Krt85	keratin 85	15	101.3	Chr. 10, 118 Mb	1.91E-04	0.08
Krtap10-4	keratin associated protein 10-4	10	77.2	Chr. 10, 118 Mb	3.17E-04	0.06
Krtap12-1	keratin associated protein 12-1	10	77.2	Chr. 3, 19 Mb	4.47E-04	0.07
Krtap13-1	keratin associated protein 13-1	16	88.6	Chr. 3, 19 Mb	1.40E-03	0.16
Krtap14	keratin associated protein 14	16	88.7	Chr. 3, 19 Mb	1.05E-03	0.17
Krtap15	keratin associated protein 15	16	88.7	Chr. 3, 19 Mb	8.02E-04	0.14
Krtap16-1	keratin associated protein 16-1	16	88.8	Chr. 3, 19 Mb	1.40E-03	0.18
Krtap16-10	keratin associated protein 16-10	16	88.9	Chr. 10, 118 Mb	1.13E-03	0.17
Krtap16-5	keratin associated protein 16-5	16	88.8	Chr. 3, 26 Mb	1.07E-03	0.18
Krtap17-1	keratin associated protein 17-1	11	99.8	Chr. 3, 19 Mb	4.45E-04	0.08
Krtap2-4	keratin associated protein 2-4	11	99.4	Chr. 3, 26 Mb	8.14E-04	0.16
Krtap26-1	keratin associated protein 26-1	16	88.6	Chr. 3, 19 Mb	6.35E-04	0.08
Krtap4-7	keratin associated protein 4-7	11	99.5	Chr. 3, 19 Mb	4.13E-04	0.11
Krtap5-1	keratin associated protein 5-1	7	142.1	Chr. 10, 118 Mb	7.46E-04	0.13
Krtap5-2	keratin associated protein 5-2	7	142	Chr. 3, 19 Mb	1.29E-03	0.14
Krtap5-4	keratin associated protein 5-4	7	142.1	Chr. 3, 19 Mb	9.68E-04	0.12

Krtap5-5	Keratin associated protein 5-5	7	142	Chr. 3, 19 Mb	5.59E-04	0.1
Krtap6-1	keratin associated protein 6-1	16	88.9	Chr. 10, 118 Mb	6.48E-04	0.1
Krtap6-2	keratin associated protein 6-2	16	89.3	Chr. 10, 118 Mb	9.53E-04	0.16
Krtap8-1	keratin associated protein 8-1	16	89.4	Chr. 10, 118 Mb	1.30E-03	0.16
Krtap9-1	keratin associated protein 9-1	11	99.7	Chr. 10, 118 Mb	2.77E-04	0.05
Lap3	leucine aminopeptidase 3 leucine rich repeat containing G	5	45.8	Chr. 10, 118 Mb	2.75E-04	0.06
Lgr5	protein coupled receptor 5	10	114.9	Chr. 10, 118 Mb	2.88E-04	0.06
Lrrc15	leucine rich repeat containing 15	16	30.2	Chr. 15, 84 Mb	2.87E-04	0.09
Lrrc15	leucine rich repeat containing 15 lymphocyte antigen 6 complex, locus G6D	16	30.2	Chr. 15, 84 Mb	2.87E-04	0.09
Ly6g6d		17	34.7	Chr. 3, 19 Mb	1.82E-04	0.05
Lyg2	lysozyme, G-like 2	1	37.9	Chr 3, 19 Mb	2.26E-04	0.05
Msx2	homeo box, msh-like 2	13	53.5	Chr. 10, 118 Mb	5.58E-04	0.07
Padi1	peptidyl arginine deiminase, type I	4	140.1	Chr. 10, 118 Mb	9.61E-04	0.12
Padi3	peptidyl arginine deiminase, type III	4	140.1	Chr. 3, 19 Mb	4.66E-04	0.1
Pdzn3	PDZ domain containing RING finger 3	6	101.2	Chr. 10, 118 Mb	4.19E-04	0.08
Procr	protein C receptor, endothelial	2	155.4	Chr 15, 24 Mb	1.27E-03	0.17
Rab3ip	RAB3A interacting protein	10	116.3	Chr. 10, 118 Mb	1.42E-05	0.01
S100a3	S100 calcium binding protein A3 solute carrier family 39 (metal ion transporter), member 8	3	90.7	Chr. 10, 118 Mb	4.36E-04	0.12
Slc39a8	solute carrier family 40 (iron- regulated transporter), member 8	3	135.8	Chr. 10, 118 Mb	8.62E-04	0.16
Slc40a1	1	1	45.9	Chr. 3, 19 Mb	1.10E-03	0.12
Tchh	Trichohyalin	3	93.5	Chr. 3, 19 Mb	4.67E-04	0.1
Tchhl1	trichohyalin-like 1	3	93.6	Chr. 15, 84 Mb	6.65E-04	0.13
Vsig8	V-set and immunoglobulin domain containing 8	1	174.5	Chr. 3, 19 Mb	9.63E-04	0.14

Supplementary Table 5

Non-synonymous changes in *Lgr5* sequence between SPRET/Ei and FVB/N

We sequenced the coding exons of *Lgr5* in SPRET/Ei and FVB/N and identified four polymorphisms between these species that result in amino acid changes:

Lgr5 Amino Acid Location	FVB/N	Spretus	Human	Domain
90	C	R	R	Leucine-rich repeat 2
774	A	T	T	Trans-membrane 6
813	S	A	A	Trans-membrane 7
886	A	S	P	C-terminal tail

Supplementary Table 6

Genes in the Haematopoietic eQTL Network (Figure 3A in manuscript)

Symbol	Title	Chr	Mb	Strongest QTL Locus	Raw QTL p-value	Permutation QTL pval
Alas2	aminolevulinic acid synthase 2, erythroid	X	145.9	Chr. 7, 86 Mb	0.001	0.08
Bpgm	2,3-bisphosphoglycerate mutase	6	34.4	Chr. 14, 116 Mb	0.001	0.12
Hba-a1	hemoglobin alpha, adult chain 1	11	32.2	N.S.	N.S.	N.S.
Hbb-b1	hemoglobin, beta adult major chain	7	103.7	Chr 7, 63 Mb	0.002	0.242
Isg20	interferon-stimulated protein radical S-adenosyl methionine domain containing 2	7	78.8	Chr. 7, 86 Mb	0.0018	0.13
Rsad2	domain containing 2	12	27.0	Chr. 15, 101 Mb	0.0016	0.1
Sipar	RIKEN cDNA 2810453106 gene	5	143.8	Chr. 7, 86 Mb	0.0001	0.01
Slc25a37	solute carrier family 25, member 37	14	68.4	Chr. 7, 63 Mb	0.002	0.18
Snca	Synuclein, alpha	6	60.7	Chr. 7, 63 Mb	0.001	0.07
Spna1	spectrin alpha 1	1	176.0	N.S.	N.S.	N.S.

Supplementary Table 7

Genes in the Melanosomal Haematopoietic eQTL Network (Figure 3B in manuscript)

Symbol	Title	Chr	Mb.	Strongest QTL Locus	Raw QTL p-value	Permutation QTL p-value
Dct	dopachrome tautomerase	14	116.9	NA	NA	NA
Mcoln3	mucopolin 3	3	146.1	Chr. 7, 79 Mb	0.001	0.15
Mlana	melan-A	19	29.8	Chr. 13, 53 Mb	0.001	0.11
p	pink-eyed dilution	7	56.1	Chr. 13, 53 Mb	9.08E-05	0.01
Ptgds	prostaglandin D2 synthase (brain)	2	25.3	Chr 2, 48 Mb	NA	NA
Si	Silver	10	128.1	Chr 13, 53 Mb	0.003	0.31
Tyr	tyrosinase	7	87.3	Chr. 7, 79 Mb	6.70E-05	< 0.01
Tyrp1	tyrosinase-related protein 1	4	80.3	Chr. 13, 53 Mb	0.0014	0.2

Supplementary Table 8

Genes differentially expressed between low-susceptibility mice (zero papillomas at 20 weeks) and high-susceptibility mice (eight or more papillomas at 20 weeks). Genes listed first with gene symbol on a white background are higher in mice with eight or more papillomas; genes listed later on a green background are lower in that group (i.e. have inverse directionality with papilloma number).

Gene	Probe	Title	Chr.	Mb.	q-value
Arg1	1419549_at	arginase 1, liver	10	24.6	0.00
Atp6v1b2	1419883_s_at	ATPase, H+ transporting, lysosomal V1 subunit B2	8	72	0.00
2810047C21Rik	1453242_x_at	RIKEN cDNA 2810047C21 gene	7	8.3	0.00
Ndrp4	1436188_a_at	N-myc downstream regulated gene 4	8	98.6	0.00
Fert2	1421729_a_at	fer (fms/fps related) protein kinase, testis specific 2	17	63.6	0.00
Sprr2d	1420771_at	small proline-rich protein 2D	3	92.4	0.00
3200002M19Rik	1424327_at	RIKEN cDNA 3200002M19 gene	10	95.1	0.00
5930430L01Rik	1445558_at	RIKEN cDNA 5930430L01 gene	5	149.3	0.00
Trex2	1449367_at	three prime repair exonuclease 2	X	69.7	0.00
2810047C21Rik	1453241_a_at	RIKEN cDNA 2810047C21 gene	7	8.3	0.00
Cyp4f16	1430172_a_at	cytochrome P450, family 4, subfamily f, polypeptide 16	17	32.3	0.00

Pp11r	1449938_at	placental protein 11 related	15	97.5	1.74
Defb3	1421806_at	defensin beta 3	8	19.3	1.74
Atp6v0b	1416769_s_at	ATPase, H+ transporting, lysosomal V0 subunit B	4	117.4	1.74
Slc37a2	1452492_a_at	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	9	37	1.74
Rptn	1420431_at	repetin	3	93.5	1.74
E2f1	1431875_a_at	E2F transcription factor 1	2	154.3	1.74
Glo1	1424108_at	glyoxalase 1	2	35.2	1.74
Ell2	1450744_at	elongation factor RNA polymerase II 2	13	76.2	1.74
Sprr2k	1422425_at	small proline-rich protein 2K	3	92.5	1.74
Il1f5	1421370_a_at	interleukin 1 family, member 5 (delta)	2	24.1	1.74
Mal2	1427042_at	mal, T-cell differentiation protein 2	15	54.4	2.17
Shmt2	1426423_at	serine hydroxymethyl transferase 2 (mitochondrial)	10	126.9	2.17
Klk9	1431681_at	kallikrein 9	7	43.7	2.17
BC023179	1460381_at	cDNA sequence BC023179	7	6.9	2.17
Slc35b4	1416548_at	solute carrier family 35, member B4	6	34.1	2.17
Gsta4	1416368_at	glutathione S-transferase, alpha 4	9	78	2.17
Gjb6	1448397_at	gap junction membrane channel protein beta 6	14	56.1	2.17
Thop1	1448907_at	thimet oligopeptidase 1	10	80.5	2.17
Kctd4	1420537_at	potassium channel tetramerisation domain containing 4	14	74.7	2.17
Il1f6	1418609_at	interleukin 1 family, member 6	2	24	2.17
Gsdm2	1432141_x_at	gasdermin 2	11	98.5	2.17
Gsta1	1421041_s_at	glutathione S-transferase, alpha 1 (Ya)	9	78	2.17
Nphp1	1453686_x_at	nephronophthisis 1 (juvenile) homolog (human)	2	127.4	2.17
Asns	1433966_x_at	asparagine synthetase	1	?	2.17
Blmh	1452101_at	bleomycin hydrolase	11	76.8	2.17
Bad	1416582_a_at	Bcl-associated death promoter	19	7	3.08
Cdca8	1428481_s_at	cell division cycle associated 8	4	124.4	3.08
Mcm3	1426652_at	minichromosome maintenance deficient 3 (S. cerevisiae)	1	20.8	3.08
Serpib12	1429297_at	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 12	1	108.8	3.08
Arnt2	1434028_at	aryl hydrocarbon receptor nuclear translocator 2	7	84.1	3.08
Sprr2i	1422963_at	small proline-rich protein 2I	3	92.5	3.08
Il1f8	1425715_at	interleukin 1 family, member 8	2	24	3.08
Nphp1	1416919_a_at	nephronophthisis 1 (juvenile) homolog (human)	2	127.4	3.08
Cdc20	1439394_x_at	cell division cycle 20 homolog (S. cerevisiae)	4	117.9	3.08
Lce3a	1456001_at	similar to late cornified envelope protein	3	93	3.08
Tmprss11a	1455848_at	transmembrane protease, serine 11a	5	87.5	3.08
Wdr62	1424849_at	WD repeat domain 62	7	29.9	3.08
Cited4	1425400_a_at	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	4	120.2	3.08
Glrx	1416592_at	glutaredoxin	13	76.3	3.08
Rab25	1417738_at	RAB25, member RAS oncogene family	3	88.6	3.08
Pon2	1429019_s_at	paraoxonase 2	6	5.2	3.12
8030443D09Rik	1456186_at	RIKEN cDNA 8030443D09 gene	2	92.8	3.12
Tubb3	1415978_at	tubulin, beta 3	8	126.3	3.12
Cdca7	1428069_at	cell division cycle associated 7	2	72.3	3.12
Sdro	1456074_at	orphan short chain dehydrogenase/reductase	10	127.3	3.12

2310002A05Rik	1419317_x_at	RIKEN cDNA 2310002A05 gene	3	93	3.12
6330442E10Rik	1454632_at	RIKEN cDNA 6330442E10 gene	12	79.9	3.12
Otop3	1429036_at	otopetrin 3	11	115.2	3.12
Lrrc28	1430145_at	leucine rich repeat containing 28	7	67.5	3.12
Ttll1	1426427_at	tubulin tyrosine ligase-like 1	15	83.3	3.12
Dnase1l2	1450936_a_at	deoxyribonuclease 1-like 2	17	24.2	3.12
2310007F04Rik	1429641_x_at	RIKEN cDNA 2310007F04 gene solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	3	93	3.12
Slc25a5	1438360_x_at		X	33.2	3.12
Tdh	1449064_at	L-threonine dehydrogenase	2	111.8	3.12
6330442E10Rik	1457254_x_at	RIKEN cDNA 6330442E10 gene	12	79.9	3.12
Ptk6	1450271_at	PTK6 protein tyrosine kinase 6 SH3 domain binding glutamic acid-rich protein-like 3	2	181.1	3.12
Sh3bgrl3	1416528_at		4	133.4	3.12
1110058A15Rik	1449902_at	RIKEN cDNA 1110058A15 gene	3	92.8	3.12
Rpa2	1416433_at	replication protein A2	4	132	3.12
Tmem54	1417895_a_at	transmembrane protein 54 nephronophthisis 1 (juvenile) homolog (human)	4	128.6	3.12
Nphp1	1448523_at		2	127.4	3.52
2810047C21Rik	1431364_a_at	RIKEN cDNA 2810047C21 gene nudix (nucleoside diphosphate linked moiety X)-type motif 22	7	8.3	3.52
Nudt22	1460358_s_at		19	7.1	3.52
AI043046	1443594_at	expressed sequence AI043046 ankyrin repeat and SOCS box-containing protein 13	13	76.3	3.52
Asb13	1419401_at		13	3.6	3.52
Tmem141	1435258_at	transmembrane protein 141	2	25.4	3.52
Ptk6	1442923_at	PTK6 protein tyrosine kinase 6	2	181.1	3.52
Ak2	1448451_at	adenylate kinase 2	4	128.5	3.52
Atp13a4	1438707_at	ATPase type 13A4	16	29.3	3.52
Aox4	1419215_at	aldehyde oxidase 4	1	58.2	3.52
Sprr2h	1422240_s_at	small proline-rich protein 2H	3	92.5	3.52
Stfa3	1419709_at	stefin A3 eosinophil-associated, ribonuclease A family, member 5	16	36.4	3.52
Ear5	1450616_at		14	50.1	3.52
Mcm6	1416251_at	minichromosome maintenance deficient 6 (MIS5 homolog, <i>S. pombe</i>) (<i>S. cerevisiae</i>) sphingomyelin phosphodiesterase 3, neutral	1	130.2	3.52
Smpd3	1422779_at		8	109.1	3.52
Calm4	1450633_at	calmodulin 4	13	3.8	3.52
Ndufa4	1424085_at	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	6	11.9	3.97
Ect2	1419513_a_at	ect2 oncogene	3	27.3	3.97
Atp6v0b	1437013_x_at	ATPase, H+ transporting, lysosomal V0 subunit B mitochondrial trans-2-enoyl-CoA reductase	4	117.4	3.97
Mecr	1417097_at		4	131.1	3.97
Ndufc1	1448284_a_at	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	3	51.5	3.97
Krt78	1438849_at	Keratin 78 bactericidal/permeability-increasing protein-like 2	15	101.8	3.97
Bpil2	1437232_at		10	85.4	3.97
Lypd3	1417942_at	Ly6/Plaur domain containing 3 solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	7	24.3	3.97
Slc25a5	1438545_at		5	97.5	3.97
Slc5a9	1439494_at	solute carrier family 5 (sodium/glucose cotransporter), member 9	4	111.4	3.97
Sult2b1	1417335_at	sulfotransferase family, cytosolic, 2B, member 1	7	45.6	3.97

Scd2	1415823_at	stearoyl-Coenzyme A desaturase 2	19	44.3	3.97
Pon2	1450686_at	paraoxonase 2	6	5.2	3.97
Clsfn	1456280_at	claspin homolog (<i>Xenopus laevis</i>)	4	126.1	4.45
Mtmr6	1425486_s_at	myotubularin related protein 6	14	59.2	4.45
Galnt3	1417588_at	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	2	65.9	4.45
Ppp1r3d	1452922_at	protein phosphatase 1, regulatory subunit 3D	2	178.3	4.45
Aprt	1423801_a_at	adenine phosphoribosyl transferase	8	125.5	4.45
Asns	1451095_at	asparagine synthetase	6	7.6	4.45
Ccdc22	1455805_x_at	coiled-coil domain containing 22	2	?	4.45
Gna15	1421302_a_at	guanine nucleotide binding protein, alpha 15	10	80.9	4.45
Cklf	1425769_x_at	chemokine-like factor	8	107.1	4.45
Prim1	1418369_at	DNA primase, p49 subunit	10	127.4	4.45
Ptk9	1420874_at	protein tyrosine kinase 9	15	94.4	4.45
Nek2	1437580_s_at	NIMA (never in mitosis gene a)-related expressed kinase 2	1	193.5	4.45
Tpd52	1419494_a_at	tumor protein D52	3	8.9	4.45
Glo1	1451240_a_at	glyoxalase 1	2	35.2	4.45
Pp11r	1449937_at	placental protein 11 related	15	97.5	4.45
Serpnb3a	1437517_x_at	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 3A	1	108.9	4.45
RP23-219P13.3	1455973_at	hypothetical protein LOC626870	11	9	4.45
2810433K01Rik	1450496_a_at	RIKEN cDNA 2810433K01 gene	18	74.3	4.45
Fdft1	1438322_x_at	farnesyl diphosphate farnesyl transferase 1	14	17.3	4.45
Sprr1b	1422672_at	small proline-rich protein 1B	3	92.5	4.45
Krt6b	1422588_at	keratin 6B	15	101.5	4.45
Susd5	1438636_s_at	sushi domain containing 5	9	113.9	4.45
Rbp2	1422846_at	retinol binding protein 2, cellular exportin, tRNA (nuclear export receptor for tRNAs)	9	98.3	4.45
Xpot	1441682_s_at		10	121	4.45
Aurkb	1424128_x_at	aurora kinase B	11	68.9	4.45
Cdkn3	1430574_at	cyclin-dependent kinase inhibitor 3	14	45.7	4.45
Wfdc5	1425418_at	WAP four-disulfide core domain 5	2	163.9	4.45
Kns2	1417005_at	kinesin 2	12	112.2	4.45
2010315L10Rik	1453430_at	RIKEN cDNA 2010315L10 gene	8	74.3	4.45
Uchl3	1449855_s_at	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	14	100.5	4.45
Pla2g4e	1429862_at	phospholipase A2, group IVE	2	119.9	5.89
Slc25a5	1438922_x_at	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	X	33.2	5.89
Qpct	1426622_a_at	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	17	79	5.89
1500031L02Rik	1417840_at	RIKEN cDNA 1500031L02 gene	16	32	5.89
Ndrg4	1426615_s_at	N-myc downstream regulated gene 4	8	98.6	5.89
Ppil5	1452458_s_at	peptidylprolyl isomerase (cyclophilin) like 5	12	70.1	5.89
Cdc20	1416664_at	cell division cycle 20 homolog (<i>S. cerevisiae</i>)	4	117.9	5.89
Rnf11	1442048_at	ring finger protein 11	4	108.9	5.89
Nkpd1	1430087_at	NTPase, KAP family P-loop domain containing 1	7	18.7	5.89
1456672_at	1456672_at	CDNA, clone:Y1G0143G21, strand:unspecified	17	?	5.89
3000002C10Rik	1431997_at	RIKEN cDNA 3000002C10 gene	9	109.7	5.89

Tgm5	1430142_at	transglutaminase 5	2	120.7	5.89
Ada	1417976_at	adenosine deaminase	2	163.4	5.89
St3gal6	1447841_x_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	16	58.4	5.89
Mcm3	1426653_at	minichromosome maintenance deficient 3 (S. cerevisiae)	1	20.8	5.89
2510005D08Rik	1449072_a_at	RIKEN cDNA 2510005D08 gene	14	56.5	5.89
4833423E24Rik	1439528_at	RIKEN cDNA 4833423E24 gene	2	85.3	5.89
Sass6	1448016_at	spindle assembly 6 homolog (C. elegans)	3	116.6	5.89
Degs2	1424549_at	degenerative spermatocyte homolog 2 (Drosophila), lipid desaturase	12	109.1	5.89
Elovl1	1425676_a_at	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	4	117.9	5.89
Camk2n2	1429204_at	calcium/calmodulin-dependent protein kinase II inhibitor 2	16	20.5	5.89
Pla2g2f	1421325_at	phospholipase A2, group IIF	4	138	5.89
Rabep2	1425602_a_at	rabaptin, RAB GTPase binding effector protein 2	7	126.2	5.89
Nlk	1435970_at	nemo like kinase	2	87	5.89
Higd1a	1416480_a_at	HIG1 domain family, member 1A	9	121.7	5.89
Nsg2	1416107_at	neuron specific gene family member 2	11	31.9	5.89
Nup43	1432187_at	nucleoporin 43	10	7.4	5.89
Mrpl28	1456313_x_at	mitochondrial ribosomal protein L28	17	25.9	5.89
Cnfn	1429540_at	cornifelin	7	25.1	5.89
Igk-V21-12	1425738_at	immunoglobulin kappa chain variable 21 (V21)-12	6	70.5	5.89
Thtpa	1433436_s_at	thiamine triphosphatase	14	54.1	5.89
1436092_at	1436092_at	Transcribed locus, moderately similar to XP_574723.1 PREDICTED: similar to LRRGT00097 [Rattus norvegicus]	15	75.6	5.89
Tnpo3	1453124_at	transportin 3	6	29.5	5.89
E430028B21Rik	1443869_at	RIKEN cDNA E430028B21 gene	14	25.5	5.89
Srxn1	1426875_s_at	sulfiredoxin 1 homolog (S. cerevisiae)	2	151.8	5.89
Mlkl	1429570_at	mixed lineage kinase domain-like	8	114.2	5.89
2610036D13Rik	1427080_at	RIKEN cDNA 2610036D13 gene	2	157.7	5.89
Etv6	1423401_at	ets variant gene 6 (TEL oncogene)	6	134	5.89
S100a8	1419394_s_at	S100 calcium binding protein A8 (calgranulin A)	3	90.8	5.89
Csta	1435760_at	cystatin A	18	42.3	5.89
5730494M16Rik	1459875_x_at	RIKEN cDNA 5730494M16 gene	18	25.3	5.89
Rhod	1419061_at	ras homolog gene family, member D	19	4.4	5.89
Scd2	1415822_at	stearoyl-Coenzyme A desaturase 2	19	44.3	5.89
Zcchc17	1452084_at	zinc finger, CCHC domain containing 17	4	129.8	5.89
Ccdc5	1424955_at	coiled-coil domain containing 5	18	78	5.89
Lig3	1423419_at	ligase III, DNA, ATP-dependent	11	82.6	5.89
Tardbp	1423723_s_at	TAR DNA binding protein	4	147.5	5.89
Krt1	1422481_at	keratin 1	15	101.7	5.89
Slc28a3	1419570_at	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	13	58.6	5.89
Cks1b	1416698_a_at	CDC28 protein kinase 1b	3	89.5	5.89
Lce1f	1420550_at	RIKEN cDNA 1110055J05 gene	3	92.8	6.96
Mcm5	1436808_x_at	minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	8	78	6.96
Aars	1423685_at	alanyl-tRNA synthetase	8	113.9	6.96
Slc5a1	1455431_at	solute carrier family 5 (sodium/glucose cotransporter), member 1	5	33.5	6.96
Rab32	1416527_at	RAB32, member RAS oncogene family	10	10.2	6.96

Slc25a5	1438546_x_at	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	5	97.5	6.96
Ckmt1	1432418_a_at	creatine kinase, mitochondrial 1, ubiquitous	2	121.1	6.96
Kifc1	1449877_s_at	kinesin family member C1	17	26.6	6.96
Kif20a	1449207_a_at	kinesin family member 20A	18	34.7	6.96
Brrn1	1423920_at	barren homolog (Drosophila)	2	126.8	6.96
Sh3kbp1	1431592_a_at	SH3-domain kinase binding protein 1	X	155.3	6.96
Tuba4	1417374_at	tubulin, alpha 4	1	75.1	6.96
Nthl1	1419433_at	nth (endonuclease III)-like 1 (E.coli)	17	24.4	6.96
Cdca1	1430811_a_at	cell division cycle associated 1	1	171.3	6.96
1500026D16Rik	1435733_x_at	RIKEN cDNA 1500026D16 gene	19	5.6	6.96
Krt16	1448932_at	keratin 16	11	100.1	6.96
Rab11a	1449256_a_at	RAB11a, member RAS oncogene family	9	64.5	6.96
2610528J11Rik	1450947_at	RIKEN cDNA 2610528J11 gene	4	118	6.96
Tgm1	1451416_a_at	transglutaminase 1, K polypeptide minichromosome maintenance deficient 5, cell division cycle 46 (S. cerevisiae)	14	54.7	6.96
Mcm5	1415945_at	microtubule associated serine/threonine kinase-like	8	78	6.96
Mastl	1423525_at	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	2	22.9	6.96
Bub1	1424046_at	RIKEN cDNA 9630033F20 gene	2	127.5	7.41
9630033F20Rik	1447934_at	budding uninhibited by benzimidazoles 1 homolog, beta (S. cerevisiae)	6	127.1	7.41
Bub1b	1416961_at	RIKEN cDNA 2610510J17 gene	2	118.3	7.41
2610510J17Rik	1427105_at	septin 8	8	119.8	7.41
Sept8	1426802_at	RIKEN cDNA 5730494M16 gene	11	53.4	7.41
5730494M16Rik	1428189_at	amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 12 (human)	18	25.3	7.41
Als2cr12	1439758_at	stearoyl-Coenzyme A desaturase 2	1	58.6	7.41
Scd2	1415824_at	PDZK1 interacting protein 1	19	44.3	7.41
Pdzk1ip1	1455477_s_at	regulator of G-protein signaling 19	4	114.6	7.41
Rgs19	1434940_x_at	keratin 6A	2	181.6	7.41
Krt6a	1427700_x_at	PYD and CARD domain containing	15	101.5	7.41
Pycard	1417346_at	stefin A3	7	127.8	7.41
Stfa3	1435761_at	interleukin 1 family, member 9	16	36.2	8.51
Il1f9	1425958_at	WAP four-disulfide core domain 12	2	24	8.51
Wfdc12	1449191_at	NHS-like 1	2	163.9	8.51
Nhsl1	1438904_at	argininosuccinate lyase	10	18.2	8.51
Asl	1448350_at	hematological and neurological expressed sequence 1	5	130.3	8.51
Hn1	1448180_a_at	RIKEN cDNA 2410018C20 gene	11	115.3	8.51
2410018C20Rik	1417146_at	split hand/foot malformation (ectrodactyly) type 1	8	87.1	8.51
Shfm1	1418575_at	Widely-interspaced zinc finger motifs 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833418G05	6	6.5	8.51
Wiz	1434280_at	product:unclassifiable, full insert sequence	6	?	8.51
1458519_at	1458519_at	PDZK1 interacting protein 1	13	35.6	8.51
Pdzk1ip1	1417689_a_at	polymerase (DNA-directed), delta 3, accessory subunit	4	114.6	8.51
Pold3	1443733_x_at	cDNA sequence BC038331	7	100	8.51
BC038331	1458295_at	RAN GTPase activating protein 1	3	88.4	8.51
Rangap1	1451092_a_at	geminin	15	81.5	8.51
Gmnn	1417506_at		13	24.8	8.51

Pttg1	1438390_s_at	pituitary tumor-transforming 1	11	43.3	8.51
4921525H12Rik	1440249_at	RIKEN cDNA 4921525H12 gene	3	108.9	8.51
Dsc1	1421460_at	desmocollin 1	18	20.2	8.51
Maf	1456060_at	avian musculoaponeurotic fibrosarcoma (v-maf) AS42 oncogene homolog ER degradation enhancer, mannosidase alpha-like 1	8	118.6	8.51
Edem1	1424065_at	similar to aplysia ras-related homolog A2	6	108.8	8.51
LOC433749	1450632_at	similar to aplysia ras-related homolog A2	4	117.2	8.51
1190003J15Rik	1431786_s_at	RIKEN cDNA 1190003J15 gene	7	140.7	8.51
Krt6a	1422783_a_at	keratin 6A	15	101.5	8.51
Dars2	1433838_at	aspartyl-tRNA synthetase 2 (mitochondrial)	1	162.9	8.51
2310042E22Rik	1423494_at	RIKEN cDNA 2310042E22 gene	16	20.8	8.51
9930013L23Rik	1429987_at	RIKEN cDNA 9930013L23 gene	7	83.8	9.15
Coro1c	1449660_s_at	coronin, actin binding protein 1C	5	114.1	9.15
1110051B16Rik	1445710_x_at	RIKEN cDNA 1110051B16 gene	14	25.1	9.15
Paqr4	1423101_at	progesterin and adipoQ receptor family member IV	17	23.5	9.15
Them5	1431211_s_at	thioesterase superfamily member 5	3	94.4	9.15
2810405K02Rik	1423266_at	RIKEN cDNA 2810405K02 gene	4	153.7	9.15
BC057079	1435209_at	cDNA sequence BC057079	4	87.8	9.15
Alox8	1425376_at	arachidonate 8-lipoxygenase	11	69	9.15
Tfb1m	1449749_s_at	transcription factor B1, mitochondrial	17	3.5	9.15
Vps24	1428165_at	vacuolar protein sorting 24 (yeast)	6	71.5	9.15
Dynl1	1448682_at	dynein light chain LC8-type 1	5	115.6	9.15
Melk	1416558_at	maternal embryonic leucine zipper kinase	4	44.3	9.15
Ptk9	1420873_at	protein tyrosine kinase 9	15	94.4	9.15
1700123O20Rik	1416917_at	RIKEN cDNA 1700123O20 gene	14	53.6	9.15
Gjb2	1423271_at	gap junction membrane channel protein beta 2	14	56.1	9.15
Mettl1	1439155_at	methyltransferase-like 1	10	126.4	9.15
Bace2	1416673_at	beta-site APP-cleaving enzyme 2	16	97.5	9.15
Phgdh	1426658_x_at	3-phosphoglycerate dehydrogenase	3	65.7	9.15
Hmgb2	1437313_x_at	high mobility group box 2 branched chain ketoacid dehydrogenase	4	145.9	9.15
Bckdk	1460644_at	kinase	7	127.7	9.15
Ccnb2	1450920_at	cyclin B2	9	70.2	9.15
Cdca8	1436847_s_at	cell division cycle associated 8	4	124.4	9.15
Ck1f	1451374_x_at	chemokine-like factor	8	107.1	9.15
Aebp2	1437743_at	AE binding protein 2	6	140.6	9.15
Syce2	1429270_a_at	synaptonemal complex central element protein 2	8	87.8	9.15
Nhs1	1426934_at	NHS-like 1	10	18.2	0.00
Mt1	1451612_at	metallothionein 1	8	97.1	0.00
Pde4b	1422474_at	phosphodiesterase 4B, cAMP specific	4	101.8	0.00
Als2cr19	1445377_at	Amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 19 (human)	1	61.7	2.17
Prickle2	1428808_at	prickle-like 2 (Drosophila)	6	92.3	2.17
AW214353	1454923_at	expressed sequence AW214353	6	?	2.17
LOC669490	1457273_at	similar to odd Oz/ten-m homolog 2	11	35.9	2.17
Vdr	1418176_at	vitamin D receptor	15	97.7	3.34
Bcl6	1421818_at	B-cell leukemia/lymphoma 6	16	23.9	5.89
Msl211	1429109_at	male-specific lethal 2-like 1 (Drosophila)	9	101	5.89
Dopey1	1435295_at	dopey family member 1	9	86.4	5.89

Mgat5	1428644_at	mannoside acetylglucosaminyltransferase 5	1	129.3	5.89
Npas2	1421037_at	neuronal PAS domain protein 2	1	39.1	6.96
Pdlim5	1442710_at	PDZ and LIM domain 5	3	142.3	6.96
Tera	1448126_at	teratocarcinoma expressed, serine rich	14	118.4	6.96
Pim3	1437100_x_at	proviral integration site 3	15	88.7	6.96
Hdac11	1454803_a_at	histone deacetylase 11	6	91.1	6.96
Sf1	1423750_a_at	Splicing factor 1	19	6.4	7.41
BC035295	1434532_at	cDNA sequence BC035295	15	100.3	7.41
Csnk1g3	1429383_at	casein kinase 1, gamma 3	18	54	7.41
Pdik11	1437175_at	PDLIM1 interacting kinase 1 like	4	133.5	7.41
Tbc1d8	1416996_at	TBC1 domain family, member 8	1	39.3	7.41
Ahr	1422631_at	aryl-hydrocarbon receptor	12	36.1	7.41
Acvr2a	1451004_at	activin receptor IIA	2	48.6	7.41
Btbd7	1432910_at	BTB (POZ) domain containing 7	2	?	7.41
Clk4	1422886_a_at	CDC like kinase 4	11	51.1	7.41
Ubr1	1458033_at	Ubiquitin protein ligase E3 component n-recognin 1	2	120.6	7.41
Cuedc1	1451447_at	CUE domain containing 1	11	88	7.41
Gatad2b	1437474_at	GATA zinc finger domain containing 2B	3	90.4	7.41
N28178	1441610_at	expressed sequence N28178	4	43	8.51
Api5	1443112_at	apoptosis inhibitor 5	2	94.2	8.51
Grasp	1441894_s_at	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	15	101.1	8.51
Amid	1431143_x_at	apoptosis-inducing factor (AIF)-like mitochondrion-associated inducer of death	10	61.1	8.51
Tgfbr3	1447314_at	Transforming growth factor, beta receptor III	5	107.4	8.51
Hdgfrp3	1435977_at	hepatoma-derived growth factor, related protein 3	7	81.8	8.51
Foxp1	1421142_s_at	forkhead box P1	6	98.9	8.51
Myo9a	1444541_at	Myosin IXa	9	59.6	8.51
Syde2	1437424_at	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	3	146	8.51
Mll3	1434179_at	myeloid/lymphoid or mixed-lineage leukemia 3	5	24.8	8.51
Odz2	1420718_at	odd Oz/ten-m homolog 2 (Drosophila)	11	35.9	8.51
Prkx	1424286_at	protein kinase, X-linked	X	74	8.51
AA536808	1455495_at	Expressed sequence AA536808	1	158.5	8.51
Ptpn21	1419054_a_at	protein tyrosine phosphatase, non-receptor type 21	12	99.1	8.51
Slc25a36	1419657_a_at	solute carrier family 25, member 36	9	96.9	8.51
BC030863	1434221_at	cDNA sequence BC030863	6	120.9	8.51
Trim2	1417027_at	tripartite motif protein 2	3	84.2	8.51
Apc	1435543_at	adenomatosis polyposis coli	18	34.4	8.51
1459202_at	1459202_at	---	6	120.7	8.51
Csad	1427981_a_at	cysteine sulfinic acid decarboxylase thyroid hormone receptor associated protein 3	15	102	8.51
Thrap3	1460545_at	protein 3	7	63.4	9.15
Jmjd2b	1440368_at	Jumonji domain containing 2B	17	56	9.15
Marcks1	1435627_x_at	MARCKS-like 1	4	129	9.15
Trim2	1459860_x_at	tripartite motif protein 2	7	?	9.15
9630054F20Rik	1455862_at	RIKEN cDNA 9630054F20 gene	11	32.4	9.15
Sfrs7	1436871_at	splicing factor, arginine/serine-rich 7	17	80.1	9.15
5430405G24Rik	1424666_at	RIKEN cDNA 5430405G24 gene	11	102.3	9.15

Ddef2	1436181_at	development and differentiation enhancing factor 2	12	21.5	9.15
Vdr	1418175_at	vitamin D receptor	15	97.7	9.15
9030420J04Rik	1457682_at	RIKEN cDNA 9030420J04 gene	9	9	9.15
Usp11	1426539_at	ubiquitin specific peptidase 11 mitogen activated protein kinase binding protein 1	X	19.9	9.15
Mapkbp1	1423403_at		2	119.7	9.15
9030611O19Rik	1418879_at	RIKEN cDNA 9030611O19 gene	12	31.7	9.15
Trim2	1417028_a_at	tripartite motif protein 2	3	84.2	9.15
ErbB2ip	1439079_a_at	ErbB2 interacting protein nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	13	104.9	9.15
Nfkbia	1449731_s_at	5-hydroxytryptamine (serotonin) receptor 1D	12	56.4	9.15
Htr1d	1440166_x_at		4	135.7	9.15
Arhgap17	1459667_at	Rho GTPase activating protein 17 LON peptidase N-terminal domain and ring finger 1	7	123.1	9.15
Lonrf1	1455665_at		8	37.7	9.15
Foxp1	1435222_at	forkhead box P1	6	98.9	9.15
Nisch	1452156_a_at	nischarin	14	30	9.15
2810455D13Rik	1435947_at	RIKEN cDNA 2810455D13 gene DEAH (Asp-Glu-Ala-His) box polypeptide 36	19	23.8	9.15
Dhx36	1424397_at		3	62.6	9.15
C130068B02Rik	1440317_at	RIKEN cDNA C130068B02 gene ATP-binding cassette, sub-family A (ABC1), member 5	17	29.9	9.15
Abca5	1459391_at		11	110.1	9.15
2010010M04Rik	1436631_at	RIKEN cDNA 2010010M04 gene	18	35.3	9.15
2310058N22Rik	1429215_at	RIKEN cDNA 2310058N22 gene secretoglobin, family 1A, member 1 (uterglobin)	12	116.8	9.15
Scgb1a1	1452543_a_at		19	9.2	9.15
1436248_at	1436248_at	Adult male spinal cord cDNA, RIKEN full-length enriched library, clone:A330033L11 product:unclassifiable, full insert sequence Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430530F17 product:unclassifiable, full insert sequence	1	159	9.15
1442743_at	1442743_at		9	65.6	9.15
1435872_at	1435872_at	Transcribed locus	6	29.2	9.15
Tbc1d17	1423659_a_at	TBC1 domain family, member 17	7	44.7	9.15
3732413I11Rik	1452769_at	RIKEN cDNA 3732413I11 gene	11	44.4	9.15
Mbtd1	1448641_at	mbt domain containing 1	11	93.7	9.15
Pcbp2	1435881_at	poly(rC) binding protein 2 solute carrier organic anion transporter family, member 4a1	15	102.3	9.15
Slco4a1	1455803_at		2	180.4	9.15
A430102J17Rik	1438895_at	RIKEN cDNA A430102J17 gene	18	7.9	9.15
1439631_at	1439631_at	---	4	108	9.15
Ly6e	1439773_at	lymphocyte antigen 6 complex, locus E Calcium/calmodulin-dependent serine protein kinase (MAGUK family)	15	74.8	9.15
Cask	1445152_at		X	12.9	9.15
Usp46	1436518_at	Ubiquitin specific peptidase 46 solute carrier family 36 (proton/amino acid symporter), member 2	5	74.3	9.15
Slc36a2	1436521_at		11	55	9.15
Prr3	1424145_at	proline-rich polypeptide 3	17	35.6	9.15
Ihpk2	1435319_at	inositol hexaphosphate kinase 2	9	108.7	9.15
Ncor1	1423202_a_at	nuclear receptor co-repressor 1	11	62.1	9.15
Top3b	1438387_x_at	topoisomerase (DNA) III beta	16	16.8	9.15
Yaf2	1429839_a_at	YY1 associated factor 2	15	93.1	9.15
2310032F03Rik	1453568_at	RIKEN cDNA 2310032F03 gene	2	59.3	9.15
Prkci	1417410_s_at	protein kinase C, iota	3	31.2	9.15

Cblb	1458469_at	Casitas B-lineage lymphoma b	16	52	9.15
1700019H03Rik	1432023_a_at	RIKEN cDNA 1700019H03 gene	2	180.7	9.15
Pex19	1442815_at	Peroxisome biogenesis factor 19	9	?	9.15
1443862_at	1443862_at	---	11	93.7	9.15
Hsf1	1424622_at	heat shock factor 1 ADP-ribosylation factor-like 6 interacting protein 5	15	76.3	9.15
Arl6ip5	1440360_at		6	97.2	9.15
Otx1	1437601_at	orthodenticle homolog 1 (Drosophila)	11	21.9	9.15
Pak3	1417923_at	p21 (CDKN1A)-activated kinase 3	X	138.9	9.15

Supplementary Table 9

Genes in the Papilloma Susceptibility Network (Figure 4 in manuscript)

Symbol	Title	Chr.	Mb	Strongest QTL	Raw P value	Corrected p-value
Alox8	arachidonate 8-lipoxygenase	11	69	Chr. 15, 101 Mb	0.0004	0.03
Aox4	aldehyde oxidase 4	1	58	Chr. 15, 101 Mb	0.003	0.08
Defb3	defensin beta 3 eosinophil-associated,	8	19	Chr. 15, 101 Mb	0.003	0.4
Ear5	ribonuclease A family, member 5 GRP1 (general receptor for phosphoinositides 1)-associated	14	50	Chr. 15, 101 Mb	0.002	0.11
Grasp	scaffold protein interleukin 1 family, member 5	15	101	Chr. 15, 101 Mb	3.36E-09	< 0.01
Il1f5	(delta)	2	24	Chr. 15, 101 Mb	0.001	0.08
Il1f6	interleukin 1 family, member 6	2	24	Chr. 15, 101 Mb	0.0004	0.01
Il1f8	interleukin 1 family, member 8	2	24	Chr. 1, 8 Mb	0.005	0.32
Il1f9	interleukin 1 family, member 9	2	24	Chr. 8, 20 Mb	0.002	0.19
Kifc1	Kinesin family member C1	17	34	Chr 17, 22 Mb	4.73E-09	< 0.01
Krt6b	keratin 6B	15	102	NA	NA	NA
Krt78	keratin 78	15	102	Chr. 15, 101 Mb	1.05E-05	< 0.01
Ly6e	lymphocyte antigen 6 complex, locus E NTPase, KAP family P-loop domain containing 1	15	75	Chr. 15, 73 Mb	1.28E-07	< 0.01
Nkpd1		7	19	Chr. 15, 101 Mb	0.0002	0.01
Pcbp2	poly(rC) binding protein 2 phosphodiesterase 4B, cAMP specific	15	102	Chr. 15, 101 Mb	1.97E-10	< 0.01
Pde4b		4	102	Chr. 15, 101 Mb	2.00E-03	0.2
Pdzk1ip1	PDZK1 interacting protein 1	4	115	Chr. 15, 101 Mb	0.0017	0.17
Pla2g2f	phospholipase A2, group IIF	4	138	Chr. 15, 84 Mb	0.0008	0.1
Pp11r	placental protein 11 related rabaptin, RAB GTPase binding effector protein 2	15	98	E15.101.379_10	0.002	0.16
Rabep2		7	126	Chr. 15, 101 Mb	0.001	0.13
Rptn	repetin S100 calcium binding protein A8 (calgranulin A)	3	94	NA	NA	NA
S100a8		3	91	Chr. 6, 147 Mb	0.001	0.18
Scd2	stearoyl-Coenzyme A desaturase 2 solute carrier family 37 (glycerol- 3-phosphate transporter), member 2	19	44	Chr. 15, 101 Mb	0.0006	0.04
Slc37a2	solute carrier family 5 (sodium/glucose cotransporter), member 9	9	37	Chr. 15, 101 Mb	4.76E-05	< 0.01
Slc5a9		4	111	Chr. 15, 101 Mb	0.0004	0.07
Sprr2d	small proline-rich protein 2D	3	92	Chr 18, 69 Mb	0.004	0.37
Sprr2i	small proline-rich protein 2I	3	93	NA	NA	NA
Tbc1d17	TBC1 domain family, member 17	7	45	Chr 17, 22 Mb	3.98E-05	< 0.01
Thop1	thimet oligopeptidase 1	10	81	Chr. 15, 101 Mb	0.001	0.12
Tmprss1	transmembrane protease, serine	5	88	NA	NA	NA

1a	11a					
Tuba4	tubulin, alpha 4	1	75	Chr. 15, 101 Mb	0.0004	0.05
Vdr	vitamin D receptor	15	98	Chr. 15, 101 Mb	1.66E-06	0.01

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