Supplemental Methods and Data

Increased Proliferative Cells in the Medullary Thick Ascending Limb of the Loop of Henle in the Dahl Salt-Sensitive Rat

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Detailed Methods

Animals. The consomic strain SS.13^{BN} was developed from selective breeding of the salt-resistant Brown Norway rat (BN/MCWi; BN) and the Dahl salt-sensitive rat of the MCW colony (SS/JrHsdMcwi; SS) (Cowley 2001). BN chromosome 13 has been substituted into the SS genome in the SS.13^{BN} rat. Male, inbred SS and SS.13^{BN} rats, including breeder pairs and experimental rats, were maintained on the AIN-76A diet containing 0.4% NaCl (Dyets) and had free access to water. Rats were studied at 6 weeks of age while maintained on 0.4% salt diet or at 7 weeks of age after one week of 8% salt diet (Lu 2010). All animal protocols were approved by the Institutional Animal Care and Use Committee of MCW.

Isolation of medullary thick ascending limbs (mTAL). mTALs were isolated using a bulk dissection method as described previously (Trinh-Trang-Tan 1986, Ito 1999) except two sieves rather than one were used. Briefly, the kidneys were flushed with 10ml of cold saline followed by 10ml of HEPES buffered HBSS containing 200 U/ml of type II collagenase (Worthington Biochemical, NJ). The kidneys were collected and cut into thin slices transversely along the cortical-medullary axis. The inner stripe of the outer medulla was isolated and incubated with the collagenase solution at 37ºC for 45minutes with intermittent pipetting. At every 5 min, the digested tissue was pipetted out and passed through a 100μm and 70 μm sieve, and mTAL segments collected on the 70μm sieve by 1% BSA HBSS HEPES solution.

Tamm-Horshfall protein staining. Samples of isolated mTALs were put on poly-L lysine treated coverslips and stained with antibody against Tamm-Horshfall protein after fixation in cold 20% methanol and permeabilization (sc-19554 1:100 diluted in 2%BSA of TBS-0.1% TX for 1h at RT). Goat pAb to Fluorocein TR 2nd antibody (Abcam ab6654-100, 1:100) was then incubated at room temperature for 45 min. The fluorescent images and bright field images were acquired with a Nikon E600 upright microscope.

RNA extraction. RNA was extracted from isolated mTALs using TRIzol reagent. The quality and quantity of the extracted RNA were determined by Agilent BioAnalyzer 2100 and spectrophotometry.

Real-time PCR. Real-time PCR analysis of selected mRNAs was performed using the SYBR Green chemistry. 18S rRNA was used as the normalizer. Primer sequences used were shown in **Supplemental Table S1**.

Affymetrix Expression Array analysis. Affymetrix Rat Expression Array 230 2.0 was hybridized following the manufacturer's protocols. A total of 16 arrays were used to analyze two rat strains and two salt conditions (0.4% and 7 days of 8%) with four individual samples in each experimental group. Signal intensities were normalized by Robust Multi-array Average Expression Measure (RMA). Differentially expressed genes were identified by Rank Product methods with a threshold of Log_2(expression intensity ratio) > 0.5 or < -0.5 and a false discovery rate < 5%. Ingenuity Pathway Analysis was used for pathway analysis.

Chromosomal Representation Index. Representation index was calculated as $(n_{chr}/n)/(N_{chr}/N)$ as we described previously (Liang 2008), where n_{chr} is the number of differentially expressed probe sets located on a chromosome, n is the total number of differentially expressed probe sets with known chromosomal locations, N_{chr} is the number of probe sets in the entire array located on a chromosome, and N is the total number of probe sets on the array with known chromosomal locations.

Bayesian Analysis. A pathway-based analysis was performed using a modified version of the Bayesian model proposed by Stingo *et al.* (2011). The proposed Bayesian method integrates pathway information, retrieved from public databases, with the experimental data with the goal of identifying pathways and genes related to a binary phenotype. We used the Kyoto Encyclopedia of Genes and Genomes (KEGG) to retrieve the following information:

- **S**, a K × p matrix indicating memberships of genes to pathways, with element $s_{kj} = 1$ if gene j belongs to pathway k, and $s_{kj} = 0$ otherwise.

- **R**, a p × p matrix describing relationships between genes, with $r_{ij} = 1$ if genes i and j have a direct link in the gene-gene network, and $r_{ij} = 0$ otherwise.

The goal of the analysis is to study the association between the response variable and the pathways. Following the method of Stingo et al (2011), scores as measures of "pathway expression" summarizing the group behavior of included genes within pathways are defined as the first principal components from a Principal component analysis (PCA) on selected subsets of genes from each pathway. Relevant groups and important genes are then identified by introducing two binary vector indicators, a K × 1 vector θ for the inclusion of the groups ($\theta_k = 1$ if pathway k is included and $\theta_k = 0$ otherwise) and a p × 1 vector γ for the inclusion of genes, i.e. $\gamma_j = 1$ if gene j is selected for at least one pathway score, and $\gamma_j = 0$ otherwise. Although the response Y is binary, we can relate a latent variable Z to the selected pathways and genes via a linear regression model

$$Z_i = \alpha + \sum_{k=1}^{K_\theta} \mathrm{T}_{ik(\gamma)}\, \beta_{k(\gamma)} + \varepsilon_i , \qquad \varepsilon_i \sim N(0,1).$$

Here $K_\theta = \sum_{k=1}^{K} \theta_k$ is the number of selected pathways and where $\mathrm{T}_{ik(\gamma)}$ corresponds to the first principal component generated based on the expression levels. Z_i is a latent variable corresponding to the unobserved propensities of subject i to belong to one class ($Y_i = 1$). When $Y_i = 1$ the latent variable Z_i is constrained to be positive ($Z_i > 0$) while $Z_i < 0$ if $Y_i = 0$. The error variance is fixed to $\sigma^2 = 1$ since it is evident that multiplying α and β by a constant c and σ^2 by the same constant leaves the model unchanged.

In the Bayesian approach to inference probability distributions (called "priors") are specified for the unknown quantities of the model. We define a standard conjugate Normal prior for the intercept parameter α. For the model parameter θ we use a product of Bernoulli distributions with parameter ψ that determines the proportion of pathways expected a priori in the model. We use the latent vector θ to specify a scale mixture of a normal density and a point mass at zero for the prior on each β_k:

$$\beta_k \mid \theta_k \sim \theta_k \, N(\beta_0, h) + (1 - \theta_k)\, \delta_0(\beta_k), \quad k = 1, \ldots, K,$$

where $\delta_0(\beta_k)$ is a Dirac delta function.

For the gene selection parameter γ we use a network prior that takes into account the biological relationships between genes within and across pathways, which are captured by the matrix R. A Markov Random Field (MRF) distribution

$$p(\gamma) \propto \exp(\mu \, 1_p \gamma + \eta \, \gamma' R \, \gamma)$$

defines a network prior over the binary vector γ taking into account the network structure defined by the matrix R. The parameter μ controls the sparsity of the model, while η regulates the smoothness of the distribution of γ over the graph by controlling the prior probability of selecting a gene based on how many of its neighbors are selected. In particular, higher values of η encourage the selection of genes with neighbors already selected into the model.

Constraints need to be imposed to ensure both interpretability and identifiability of the model. We essentially want to avoid the following:

1. empty pathways, that is, selecting a pathway but none of its member genes;
2. orphan genes, that is, selecting a gene but none of the pathways that contain it;
3. selection of identical subsets of genes by different pathways, a situation that generates identical values $T_{ik(\gamma)}$, for pathway k, and $T_{ik'(\gamma)}$, for pathway k', to be included in the model.

These constraints imply that some combinations of θ and γ values are not allowed.

Having chosen the prior distributions, a Bayesian approach proceeds by updating knowledge on the model parameters with the information from the data via the calculation of the so-called “posterior” distribution. Here we are interested in the parameters θ and γ, representing the selection of genes and pathways related to the binary response variable. Stingo et al (2011) use a Monte Carlo Markov chain (MCMC) algorithm that can be seen as a stochastic search that explores the posterior space in an effective way, quickly finding the most probable configurations of genes and pathways, that is, those with high marginal probabilities, while spending less time in regions with low posterior probability. The MCMC procedure results in a list of visited models with included pathways indexed by θ and selected genes indexed by γ, and their corresponding relative posterior probabilities. Pathway selection can be based on the marginal posterior probabilities $p(\theta_k | \mathrm{T}, Y)$. Given a subset of selected pathways, P, the relevant genes from these pathways are identified based on the marginal posterior probability conditional on at least one pathway the gene belongs to being represented in the model, $p(\gamma_j | \mathrm{T}, Y, I\{\sum_{k \in P} \theta_k s_{kj} > 0\})$.

Defining boundaries of congenic segments using single nucleotide polymorphism (SNP) chips. We previously identified four congenic regions on rat chromosome 13 that had significant effects on hypertension, designated congenic lines 1, 5, 9, and 26 (Moreno 2007). We obtained precise boundaries of lines 5, 9, and 26 using the RATDIVm520813 SNP array. The SNP array was hybridized according to the manufacturer's instructions for the Affymetrix Genome-Wide Human SNP Nsp/Sty 6.0 array. Data were analyzed with the Affymetrix Power Tools apt-1.12.0 using Brlmm-p algorithm without model-file.

Immunofluorescence analysis of cell proliferation. Flushed Kidneys were fixed in 10% formalin, paraffin embedded, and sectioned for immunofluorescence analysis. Proliferating cells were identified by positive staining of Ki-67 (Abcam ab16667,1:250, 1hr incubation at room temperature, 45 min incubation with 2nd antibody of Alexa Fluor 488 goat anti—rabbit IgG ,life technologies, A11034, 1:250). Cells in the G2/M phase were identified by positive staining of histone H3 phosphorylated at Ser10 (p-H3 or H3-P) (Abcam ab 5176,1:250, 1 hr at room temperature, 45 min incubation with 2nd antibody of Texas Red anti-rabbit IgG(H+L) ,Vector Laboratories, T1-1000, 1:250). Cell nucleus was visualized by DAPI staining. Ten fields were randomly selected from each kidney. mTALs were identified by morphology. The numbers of all cells (cell nuclei), Ki-67 positive cells, and H3-P positive cells within mTALs were manually counted. The investigator analyzing the images was blinded to the treatment conditions of the rats. The same staining condition was also used in cultured human Hela cells after fixation by cold 20% methanol and permeabilization by 0.1% triton-100.

References for Supplemental Materials

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7. Trinh-Trang-Tan MM, Bouby N, Coutaud C, Bankir L. Quick isolation of rat medullary thick ascending limbs. Enzymatic and metabolic characterization. *Pflugers Arch*. 1986; 407:228-234.

Supplemental Table S1. Primer sequences used in real-time PCR.

Gene	forward primer	reverse primer
Col1a1	TGGATGGCTGCACGAGTCACAC	ATGGGCAGGCGGGAGGTCTT
IL1b	GGCTGACAGACCCCAAAAGAT	GTCGAGATGCTGCTGTGAGATT
IL33	GTTTTGTTTTGGAGAATGGATGTT	GTGCAGGAAAGGAAGACTCGTAG
Fam 129	CGCTTCAGATTCCCTCACG	CGATGGCCACTGCTGTTCT
Cdc73	ATGCTTGCTGATGTTGATGCTT	CGCATCCTGTTTATGTCcG
Cdc2	CCCCGGTTGACATCTGGAG	CTGAGTCGCCGTGGAAAAG
Cenpf	AGGAGAGCCTGTGTGCATGTG	TGGTACGCACAGGTTAcG
E2f8	GGGTGGGCGGGTTCATTT	GTTTGAGCAGGTGCTGtG
Cxcl13	CTCCACCTCCAGGCAGAATG	TCCCAGGGCGTATAACTTGAAT
Ccr5	CTATGCCTTTGTTGGGGAGAA	GTGGACCGGGTATAGACTGAGC
Matn	CCTGGAGAACAGAGTCATCTAAGGA	TGCTAAAGTAGCACAGCCAGACTAA
Aqp1	AGTGCTGATCTATGACTTCATCCTG	ATCCAGGTCATACTCCTCCACTTG
Ut-b	ACCTACAAAACAAGAAAAGGGTGGT	GAGAGCTGTTCCAAGTGAAGAAAAG
Pv-1	GTCCAGCCTCTCTCTTAAAGGTTTC	AACCTGCAGACTCTAGAAAGGGTTC
Nkcc2	ACGTCGGGGAGTTCAATCAGA	TCAACCCTCCATCATCAAATAACC
Aqp2	GCCACCTCCTTGGGATCTATT	AAGACCCAGTGATCATCAAACTTG
Plekha6	TGTTCTCAGGGTCAGGAGCA	TCACTTTCCAGGGGCAGATG
Slc45a3	GTGGGGCTTGTTGAACCCTA	GATGAGCTCACTGGCTCTGG
Dars2	TATGGCCAAGTCACGAAGCTC	GCCGTCCTTCAGTTCCTGTA
Elk4	AGGATATTGCCGGTCAGGGA	CTCACACAGCCTGGAAGGAA
Golt1a	TTGGAAACCTGCTGTTCCTG	ATTGAGCTGGAGGAGCCTTG

Supplemental Table S2. ESTs differentially expressed in mTALs between SS and SS.13^{BN} rats on 0.4% or 8% NaCl diets. Log2R, log2(SS/SS.13^{BN} ratio); LS, 0.4% NaCl diet; HS, 8% NaCl diet for 7 days; RP-FDR, rank product – false discovery rate.

A. 0.4% NaCl diet

ProbeSet ID	Gene Symbol	UniGene ID	Alignments	Congenic line	Log2R LS	RP-FDR LS	Gene Title
1371194_at	Tnfaip6	Rn.195358	---		0.79	0.004	tumor necrosis factor alpha induced protein 6
1371731_at	RGD1566215	Rn.216502	---		0.86	0.002	Similar to Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP)
1373908_at	---	---	---		1.52	0.000	---
1378713_at	---	Rn.211170	---		-0.88	0.003	---
1379259_at	---	Rn.146603	---		-1.39	0.000	---
1382329_at	---	---	---		0.81	0.029	---
1383682_at	---	Rn.147429	---		-0.65	0.048	---
1386921_at	Cpe	Rn.7149	---		0.67	0.013	carboxypeptidase E
1387158_at	Mep1b	Rn.3520	---		-0.68	0.019	meprin 1 beta
1389500_at	---	Rn.216504	---		0.69	0.011	---
1390722_at	---	---	---		2.64	0.000	---
1391072_at	Fcer2	Rn.10326	---		0.76	0.010	Fc fragment of IgE, low affinity II, receptor for

							(CD23)
1395863_at	Nr2f2	Rn.17815	chr1:125284519-125293221 (+) // 77.25 // q31		-0.63	0.045	Nuclear receptor subfamily 2, group F, member 2
1381402_at	---	Rn.33502	chr1:125318857-125319254 (+) // 70.07 // q31		-0.58	0.048	---
1387219_at	Adm	Rn.10232	chr1:168380254-168382426 (+) // 95.33 // q33		0.97	0.003	adrenomedullin
1390707_at	Rgs10	Rn.23957	chr1:187622487-187622918 (-) // 99.77 // q36		0.66	0.025	regulator of G-protein signaling 10
1390026_at	Bag3	Rn.46304	chr1:187803867-187804835 (+) // 99.69 // q36		0.73	0.010	Bcl2-associated athanogene 3
1390801_at	RGD1359349	Rn.23870	chr1:228102009-228102637 (+) // 72.48 // q51		0.81	0.003	similar to hypothetical protein MGC34760
1380063_at	Ch25h	Rn.155971	chr1:238457016-238457640 (-) // 99.68 // q52		0.79	0.005	cholesterol 25-hydroxylase
1389424_at	LOC365157	---	chr1:56497900-56498510 (+) // 99.67 // q12		-0.68	0.019	similar to ribosomal protein L22 proprotein
1373759_at	---	Rn.32994	chr1:78666419-78666858 (-) // 98.21 // q21		1.27	0.003	---

1370862_at	Apoe	Rn.32351	chr1:79003632-79005597 (-) // 94.03 // q21		0.61	0.040	apolipoprotein E
1370174_at	Ppp1r15a	Rn.2232	chr1:95994024-95996671 (-) // 98.79 // q22		0.87	0.011	protein phosphatase 1, regulatory (inhibitor) subunit 15A
1398243_at	Csrp3	Rn.11345	chr1:98601680-98611747 (-) // 96.77 // q22		0.62	0.040	cysteine and glycine-rich protein 3
1367913_at	Cygb	Rn.105938	chr10:106759676-106769559 (-) // 86.6 // q32.3		0.63	0.040	cytoglobin
1377092_at	---	Rn.153630	chr10:107957147-107957566 (-) // 96.32 // q32.3		0.66	0.047	---
1387946_at	Lgals3bp	Rn.3251	chr10:108388180-108397523 (-) // 99.81 // q32.3		0.57	0.049	lectin, galactoside-binding, soluble, 3 binding protein
1372590_at	---	Rn.53880	chr10:108452555-108453216 (+) // 100.0 // q32.3		0.67	0.029	---
1371785_at	Tnfrsf12a	Rn.105040	chr10:12940331-12940788 (-) // 96.21 // q12		0.72	0.011	tumor necrosis factor receptor superfamily, member 12a
1387965_at	Havcr1	Rn.11154	chr10:31834518-31858017 (+) // 97.99 // q21		0.70	0.014	hepatitis A virus cellular receptor 1
1382805	LOC3605	Rn.106	chr10:63893		-	0.007	similar to

_at	70	278	773-63894421 (+) // 100.0 // q25		0.66		myosin XVIIIa
1370832_at	Ccl4	Rn.37880	chr10:71759428-71761403 (+) // 99.87 // q26		0.64	0.030	chemokine (C-C motif) ligand 4
1370864_at	Col1a1	Rn.2953	chr10:83622548-83639368 (+) // 98.17 // q31		0.77	0.011	collagen, type I, alpha 1
1388116_at	Col1a1	Rn.2953	chr10:83622548-83639368 (+) // 98.17 // q31		0.72	0.014	collagen, type I, alpha 1
1374679_at	Higd1b	Rn.38891	chr10:92010249-92011724 (+) // 94.65 // q32.1		0.58	0.049	HIG1 hypoxia inducible domain family, member 1B
1377390_at	Bace2	Rn.38581	chr11:37427898-37428364 (+) // 98.94 // q12		0.62	0.031	beta-site APP-cleaving enzyme 2
1368826_at	Comt	Rn.220	chr11:84576766-84581706 (+) // 86.88 // q23		0.81	0.010	catechol-O-methyltransferase
1374104_at	Cldn5	Rn.17420	chr11_random:1224086-1224641 (-) // 99.82 //		0.63	0.030	claudin 5
1395153_at	Cldn15	Rn.202600	chr12:20844848-20845311 (+) // 51.17 // q12		0.74	0.009	claudin 15
1367577_at	Hspb1	Rn.3841	chr12:21911200-21912765 (-)		0.92	0.006	heat shock protein 1

			// 93.62 // q12				
1372935_at	Tmem119	Rn.155038	chr12:43869671-43870067 (+) // 95.19 // q16		0.63	0.040	transmembrane protein 119
1393179_at	---	Rn.203900	chr12:7957931-7958631 (+) // 98.3 // p11		-0.64	0.037	---
1369268_at	Atf3	Rn.9664	chr13:107191621-107223850 (-) // 99.58 // q27		1.21	0.004	activating transcription factor 3
1379286_at	Rnf152	Rn.169056	chr13:11309459-11310197 (-) // 100.0 // p13		0.88	0.002	ring finger protein 152
1376731_at	---	Rn.201834	chr13:11667148-11668111 (-) // 67.4 // p13		-0.67	0.020	---
1391552_at	---	Rn.25189	chr13:30916626-30917344 (+) // 97.42 // q11		-0.93	0.003	---
1391757_at	---	Rn.25328	chr13:32435090-32435651 (-) // 97.91 // q11		-0.66	0.032	---
1388219_at	Htr5b	Rn.202942	chr13:33545127-33558050 (-) // 88.44 // q11	congenic Line 5	1.57	0.000	5-hydroxytryptamine (serotonin) receptor 5B
1371099_at	---	Rn.107069	chr13:43785844-43805288 (+) // 64.51 // q13	congenic Line 5	-0.63	0.043	---
1378831	---	Rn.207	chr13:44448	cong	-	0.005	---

_at		934	493-44448945 (-) // 92.46 // q13	enic Line 5	0.82		
1397746_at	---	Rn.212168	chr13:45195611-45195996 (+) // 72.51 // q13	congenic Line 5	-0.68	0.018	---
1391601_at	Lrrn2	Rn.11847	chr13:45837783-45838309 (+) // 100.0 // q13	congenic Line 9	-0.84	0.004	leucine rich repeat neuronal 2
1391143_at	---	Rn.208076	chr13:46200201-46200743 (+) // 80.51 // q13	congenic Line 9	1.10	0.001	---
1398516_at	Golt1a	Rn.13207	chr13:46224432-46237119 (+) // 100.0 // q13	congenic Line 9	1.20	0.001	golgi transport 1 homolog A (S. cerevisiae)
1386994_at	Btg2	Rn.27923	chr13:47026963-47030745 (-) // 99.88 // q13	congenic Line 9	0.77	0.041	B-cell translocation gene 2, anti-proliferative
1381796_at	---	Rn.205091	chr13:47509958-47510284 (+) // 48.24 // q13	congenic Line 9	-0.82	0.004	---
1382152_at	Kdm5b	Rn.22866	chr13:47575639-47576287 (+) // 99.23 // q13	congenic Line 9	-0.65	0.033	lysine (K)-specific demethylase 5B
1374123_at	---	Rn.25048	chr13:47945366-47946010 (-) // 100.0 // q13	congenic Line 9	1.90	0.000	---
1389619_at	---	Rn.161322	chr13:48378300-	congenic	-0.6	0.030	---

			48378952 (-) // 81.9 // q13	Line 9	4		
1377301_at	---	Rn.161322	chr13:48378890-48379420 (-) // 83.74 // q13	congenic Line 9	-0.88	0.004	---
1379398_at	---	Rn.17272	chr13:52526134-52526731 (+) // 52.37 // q13		-0.89	0.003	---
1393159_at	---	Rn.204157	chr13:57581389-57582128 (-) // 95.81 // q21		-0.81	0.006	---
1386594_at	---	Rn.204157	chr13:57582015-57582424 (-) // 97.56 // q21		-0.99	0.003	---
1382368_at	Trove2	Rn.146598	chr13:57584586-57585024 (-) // 65.13 // q21		-0.65	0.042	TROVE domain family, member 2
1398540_at	Rgs1	Rn.14787	chr13:58121195-58121856 (-) // 99.1 // q21		0.65	0.029	regulator of G-protein signaling 1
1387566_at	Pla2g4a	Rn.10162	chr13:64135723-64280803 (-) // 97.69 // q21		-0.63	0.045	phospholipase A2, group IVA (cytosolic, calcium-dependent)
1368527_at	Ptgs2	Rn.44369	chr13:64427165-64435400 (+) // 95.46 // q21		0.54	0.045	prostaglandin-endoperoxide synthase 2
1379340_at	Lamc2	Rn.9278	chr13:68151073-68152288 (-) // 89.33 // q21	congenic Line 26	0.61	0.039	laminin, gamma 2

1379889_at	Lamc2	Rn.9278	chr13:68155279-68159154 (-) // 97.59 // q21	congenic Line 26	0.58	0.043	laminin, gamma 2
1396877_at	---	Rn.204402	chr13:68362089-68362554 (-) // 50.31 // q21	congenic Line 26	2.00	0.000	---
1373777_at	---	Rn.1141	chr13:68812523-68812911 (+) // 91.29 // q21	congenic Line 26	0.66	0.020	---
1389775_at	---	---	chr13:70179712-70180139 (-) // 95.29 // q21	congenic Line 26	0.82	0.003	---
1377899_at	RGD1304982	Rn.198952	chr13:72755982-72756590 (+) // 20.13 // q22	congenic Line 26	0.70	0.024	similar to RIKEN cDNA 2810025M15
1377675_at	LOC100302372	---	chr13:75494982-75495823 (+) // 82.16 // q22	congenic Line 26	-0.69	0.025	hypothetical protein LOC100302372
1398475_at	Dars2	Rn.137838	chr13:76602121-76602835 (-) // 53.78 // q22	congenic Line 26	-0.64	0.030	aspartyl-tRNA synthetase 2 (mitochondrial)
1395471_at	---	Rn.34102	chr13:76743684-76744061 (+) // 95.69 // q22	congenic Line 26	0.69	0.011	---
1374462_at	Kifap3	Rn.163223	chr13:79672432-79673772 (+) // 99.85 // q22		-0.61	0.046	kinesin-associated protein 3
1374320	F5	Rn.829	chr13:79992		-	0.000	coagulation

_at		10	843-79997293 (+) // 97.52 // q22		1.57		factor V (proaccelerin, labile factor)
1373947_at	Dpt	Rn.8396	chr13:80574810-80590528 (+) // 99.6 // q23		-0.64	0.031	dermatopontin
1377807_a_at	Iqwd1	Rn.3917	chr13:81082255-81082601 (+) // 94.79 // q23		-0.68	0.031	IQ motif and WD repeats 1
1390852_x_at	Iqwd1	Rn.3917	chr13:81082255-81082601 (+) // 94.79 // q23		-0.68	0.035	IQ motif and WD repeats 1
1375428_at	Creg1	Rn.8051	chr13:81491321-81502708 (+) // 98.73 // q23		-1.51	0.000	cellular repressor of E1A-stimulated genes 1
1370995_at	Pou2f1	Rn.46306	chr13:81607332-81646888 (-) // 99.4 // q23		-1.32	0.000	POU domain, class 2, transcription factor 1
1373523_at	Fcgr3a	Rn.23977	chr13:86873777-86877669 (+) // 99.75 // q24		0.81	0.003	Fc fragment of IgG, low affinity IIIa, receptor
1393730_at	---	Rn.150301	chr13:87151340-87151783 (+) // 59.14 // q24		0.74	0.009	---
1393551_at	---	Rn.131538	chr13:87345603-87346258 (+) // 100.0 // q24		0.66	0.037	---
1391561_at	---	Rn.28553	chr13:93976176-93977036 (-)		-1.35	0.000	---

			// 95.41 // q26				
1398390_at	Cxcl13	Rn.6917	chr14:15126331-15126759 (-) // 95.32 // p22		1.18	0.000	chemokine (C-X-C motif) ligand 13
1379365_at	Cxcl11	Rn.13664	chr14:17252699-17253487 (+) // 100.0 // p22		0.93	0.002	chemokine (C-X-C motif) ligand 11
1368760_at	Cxcl2	Rn.10230	chr14:18677128-18679175 (-) // 93.82 // p22		0.83	0.003	chemokine (C-X-C motif) ligand 2
1387316_at	Cxcl1	Rn.10907	chr14:18690338-18692118 (-) // 91.01 // p22		1.47	0.002	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)
1383163_at	Igj	Rn.17804	chr14:21126209-21126678 (+) // 80.98 // p22		0.58	0.040	immunoglobulin joining chain
1367816_at	Hopx	Rn.2989	chr14:33369052-33377951 (+) // 97.64 // p11		0.64	0.035	HOP homeobox
1368168_at	Slc34a2	Rn.16933	chr14:62659554-62671676 (-) // 95.65 // q11		0.81	0.003	solute carrier family 34 (sodium phosphate), member 2
1386865_at	Sparcl1	Rn.3091	chr14:6766346-6797580 (+) // 97.57 // p22		-0.67	0.030	SPARC-like 1 (hevin)
1379903_at	---	Rn.98831	chr14:79415489-79416111 (-)		0.73	0.005	---

			// 99.68 // q21				
1372301_at	Aebp1	Rn.37157	chr14:86533927-86535668 (+) // 91.65 // q21		0.65	0.031	AE binding protein 1
1383772_at	---	Rn.165369	chr15:39850675-39851364 (+) // 83.33 // p12		-0.62	0.028	---
1378140_at	Arl11	Rn.23090	chr15:40460318-40460922 (+) // 99.5 // p12		0.62	0.041	ADP-ribosylation factor-like 11
1391462_at	Ebpl	Rn.99955	chr15:40484463-40485990 (-) // 91.4 // p12		0.64	0.025	emopamil binding protein-like
1382458_at	---	Rn.169353	chr15:40759937-40760437 (+) // 65.7 // p12		-0.68	0.026	---
1392791_at	---	Rn.203676	chr15:50481649-50482555 (+) // 96.8 // p11		0.73	0.013	---
1384509_s_at	Pcdh17	Rn.198988	chr15:66481665-66482028 (+) // 85.08 // q12		-0.87	0.003	protocadherin 17
1393454_at	Pcdh17	Rn.198988	chr15:66481665-66482028 (+) // 85.08 // q12		-0.66	0.031	protocadherin 17
1375726_at	Lmo7	Rn.98417	chr15:85920179-85928553 (+) // 99.71 // q21 ///		-0.71	0.025	LIM domain 7

			chr20:1274370-1275048 (-) // 96.91 // p12				
1372809_at	LOC290595	Rn.103148	chr16:13308803-13316409 (-) // 95.97 // p14		1.02	0.002	hypothetical gene supported by AF152002
1392054_at	Pbrm1	Rn.19314	chr16:6547196-6547698 (+) // 86.02 // p16		-0.75	0.031	polybromo 1
1383266_at	Sfrp1	Rn.163333	chr16:73030854-73031909 (-) // 93.34 // q12.5		0.60	0.041	secreted frizzled-related protein 1
1385025_a_at	Gpr137b	Rn.60453	chr17:67000798-67004339 (+) // 99.81 // q12.1		0.83	0.002	G protein-coupled receptor 137B
1393148_at	Gpr137b	Rn.60453	chr17:67000855-67006473 (+) // 99.84 // q12.1		0.74	0.004	G protein-coupled receptor 137B
1384747_at	Gpr137b	Rn.60453	chr17:67006941-67007441 (+) // 99.4 // q12.1		0.91	0.002	G protein-coupled receptor 137B
1380418_at	---	Rn.209714	chr17:86152733-86152909 (-) // 41.87 // q12.3		-0.96	0.003	---
1379423_at	Rsu1	Rn.11453	chr17:87345488-87345935 (+) // 96.1 // q12.3		-0.95	0.002	Ras suppressor protein 1
1392953_at	Ptpla	Rn.38334	chr17:88239566-88243637 (-)		1.10	0.001	protein tyrosine phosphatase-like (proline

			// 92.97 // q12.3				instead of catalytic arginine), member a
1383696_at	Ptpla	Rn.38334	chr17:88253097-88253571 (-) // 100.0 // q12.3		1.03	0.002	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
1368810_a_at	Mbp	Rn.63285	chr18:79025625-79057329 (+) // 99.95 // q12.3		-0.55	0.032	myelin basic protein
1370080_at	Hmox1	Rn.3160	chr19:13963136-13969960 (+) // 99.94 // p11		0.96	0.003	heme oxygenase (decycling) 1
1388722_at	Dnajb1	Rn.128947	chr19:26213753-26214684 (-) // 90.47 // q11		0.64	0.046	DnaJ (Hsp40) homolog, subfamily B, member 1
1383302_at	Dnajb1	Rn.128947	chr19:26214668-26215653 (-) // 97.57 // q11		0.75	0.025	DnaJ (Hsp40) homolog, subfamily B, member 1
1392566_at	---	Rn.203180	chr19:45857968-45858621 (+) // 95.18 // q12		0.62	0.026	---
1387280_a_at	Slc7a5	Rn.32261	chr19:52120725-52149332 (-) // 99.77 // q12		0.63	0.030	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5
1368420_at	Cp	Rn.32777	chr2:105086277-105135381 (+) // 98.85 //		0.61	0.041	ceruloplasmin

			q24				
1384824_at	Pcdh18	Rn.61115	chr2:138615285-138615985 (-) // 98.72 // q26		-0.62	0.036	protocadherin 18
1390656_at	---	Rn.161410	chr2:153117890-153118435 (+) // 99.82 // q31		-0.60	0.045	---
1387349_at	Shox2	Rn.11258	chr2:156881043-156889657 (-) // 97.27 // q31		0.65	0.030	short stature homeobox 2
1383008_at	Smc4	Rn.163695	chr2:158998991-159001274 (+) // 100.0 // q31		-0.72	0.023	structural maintenance of chromosomes 4
1367846_at	S100a4	Rn.504	chr2:182885069-182887483 (+) // 99.83 // q34		0.76	0.005	S100 calcium-binding protein A4
1396194_at	---	Rn.54305	chr2:191086479-191086904 (+) // 72.62 // q34		-0.62	0.039	---
1371924_at	Olfml3	Rn.106761	chr2:198958478-198959336 (-) // 93.3 // q34		0.60	0.048	olfactomedin-like 3
1382193_at	Cisd2	Rn.24858	chr2:232903676-232904157 (-) // 96.18 // q43		-0.72	0.014	CDGSH iron sulfur domain 2
1383291_at	C7 /// Tubb2c	Rn.33787	chr2:54146300-54147392 (-) // 99.82 // q16		0.61	0.035	complement component 7 /// tubulin, beta 2c

1391587_at	---	Rn.16809	chr2:77392335-77392908 (+) // 52.53 // q22		-1.36	0.000	---
1373990_at	LOC361914 /// Slc7a12	Rn.34357	chr2:88620186-88620706 (-) // 54.53 // q23 /// chr2:88429242-88429760 (-) // 53.77 // q23		-0.69	0.033	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 12 /// solute carrier family 7 (cationic amino acid transporter, y+ system), member 12
1372426_at	Adamtsl4	Rn.62115	chr2_random:2876879-2877369 (+) // 94.23 //		0.63	0.039	ADAMTS-like 4
1386903_at	S100b	Rn.8937	chr20:12791436-12824508 (-) // 99.46 // p12		0.61	0.041	S100 calcium binding protein B
1370157_at	Pln	Rn.9740	chr20:32000370-32008915 (+) // 95.3 // q11		0.63	0.030	phospholamban
1370186_at	Psmb9	Rn.13686	chr20:4801219-4806608 (+) // 93.3 // p12		0.65	0.024	proteasome (prosome, macropain) subunit, beta type 9 (large multifunctional peptidase 2)
1396184_at	---	Rn.171910	chr20:6216552-6216994 (-) // 96.08 // p12		-0.63	0.028	---
1392547_at	MGC105649	Rn.106101	chr3:109610058-109613034 (+) // 99.57 //		0.58	0.048	hypothetical LOC302884

			q35				
1387011_at	Lcn2	Rn.11303	chr3:11511397-11514747 (-) // 100.0 // p11		0.91	0.003	lipocalin 2
1376513_a_at	---	Rn.125774	chr3:115976134-116033752 (-) // 96.8 // q36		0.59	0.041	---
1372729_at	Procr	Rn.144312	chr3:146272738-146273764 (+) // 64.84 // q42		0.59	0.045	protein C receptor, endothelial
1392969_at	---	Rn.12238	chr3:154485187-154485651 (+) // 94.89 // q42		-0.54	0.004	---
1372264_at	Pck1	Rn.104376	chr3:164017885-164018347 (+) // 74.9 // q42		-0.53	0.000	phosphoenolpyruvate carboxykinase 1 (soluble)
1379058_at	---	Rn.5854	chr3:17130284-17130625 (+) // 88.31 // q11		-0.72	0.030	---
1387382_at	Hnmt	Rn.13145	chr3:2057594-2090011 (-) // 94.09 // p13		-0.82	0.006	histamine N-methyltransferase
1381575_at	Neb	Rn.134031	chr3:33634432-33634813 (-) // 100.0 // q12		-0.60	0.033	nebulin
1390672_at	Rprm	Rn.45197	chr3:35590161-35590683 (-) // 100.0 // q12		0.65	0.036	reprimo, TP53 dependent G2 arrest mediator candidate
1372254	Serping1	Rn.100	chr3:679687		0.6	0.040	serine (or

_at		285	95-67973561 (-) // 98.56 // q24		3		cysteine) peptidase inhibitor, clade G, member 1
1387378_at	Fcnb	Rn.48281	chr3:7010934-7019366 (-) // 99.58 // p12		0.76	0.007	ficolin B
1369008_a_at	Olfm1	Rn.11005	chr3:7170420-7195345 (+) // 94.93 // p12		0.73	0.009	olfactomedin 1
1394153_at	---	Rn.16559	chr4:120619809-120620211 (-) // 98.05 // q34		-0.73	0.030	---
1367794_at	A2m	Rn.109457	chr4:158103688-158153693 (+) // 98.55 // q42		0.69	0.026	alpha-2-macroglobulin
1382153_at	Clecsf6	Rn.24032	chr4:159707345-159710266 (+) // 94.64 // q42		0.66	0.031	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 6
1379205_at	---	Rn.148149	chr4:160710031-160710327 (+) // 93.91 // q42		0.64	0.022	---
1373931_at	RGD1304952	Rn.13411	chr4:161123258-161123926 (+) // 84.73 // q42		0.61	0.039	similar to RIKEN cDNA C530028O21 gene
1396811_at	---	---	chr4:163919402-163919750 (+) // 43.96 // q42		-0.67	0.031	---
1398253_at	Kap	Rn.11143	chr4:170652192-		-0.5	0.008	kidney androgen regulated

			170655239 (-) // 90.17 // q43		8		protein
1377340_at	Tfpi2	Rn.15776	chr4:28806687-28807196 (-) // 100.0 // q13		1.16	0.002	tissue factor pathway inhibitor 2
1375724_at	RGD1563612	Rn.204577	chr4:33657189-33657917 (+) // 98.51 // q21		0.98	0.003	similar to testhymin
1369191_at	Il6	Rn.9873	chr4:456798-461376 (-) // 90.73 // q11		1.11	0.002	interleukin 6
1371691_at	Rarres2	Rn.28532	chr4:76659506-76662510 (-) // 99.59 // q24		0.73	0.010	retinoic acid receptor responder (tazarotene induced) 2
1368187_at	Gpnmb	Rn.13778	chr4:77161351-77182624 (+) // 96.6 // q24		0.73	0.009	glycoprotein (transmembrane) nmb
1378754_at	---	Rn.16196	chr4:81616963-81617451 (+) // 98.16 // q24		0.65	0.036	---
1392894_at	Fgl2	Rn.64635	chr4:9176326-9177000 (-) // 95.73 // q11		0.62	0.050	fibrinogen-like 2
1383516_at	Fgl2	Rn.64635	chr4:9177027-9177778 (-) // 100.0 // q11		0.62	0.040	fibrinogen-like 2
1368607_at	Cyp4a8	Rn.10034	chr5:135547363-135578186 (-) // 98.88 // q36		-0.75	0.003	cytochrome P450, family 4, subfamily a, polypeptide 8
1384649_at	---	---	chr5:136275574-		0.61	0.040	---

			136276063 (-) // 42.74 // q36				
1368471_at	Guca2a	Rn.11388	chr5:140227305-140229145 (+) // 97.88 // q36		1.03	0.003	guanylate cyclase activator 2a (guanylin)
1387253_at	Guca2b	Rn.97593	chr5:140237183-140239236 (-) // 80.12 // q36		0.79	0.005	guanylate cyclase activator 2B
1370561_at	A3galt2	Rn.37737	chr5:147981008-147994141 (+) // 99.74 // q36		0.59	0.041	alpha 1,3-galactosyltransferase 2
1368006_at	Laptm5	Rn.24799	chr5:149775671-149797167 (+) // 94.28 // q36		0.88	0.002	lysosomal multispanning membrane protein 5
1380579_at	Matn1	Rn.15159	chr5:149812569-149815428 (+) // 95.39 // q36		-3.91	0.000	matrilin 1, cartilage matrix protein
1374806_at	Sfn	Rn.145079	chr5:151479869-151480392 (+) // 89.34 // q36 /// chr13:107508826-107509347 (+) // 87.13 // q27 /// chr6:23095417-23095966 (-) // 84.38 // q13		0.73	0.016	stratifin
1392265_s_at	Mmp23	Rn.22562	chr5:172486915-172487324		0.64	0.027	matrix metallopeptidase 23

			(-) // 99.27 // q36				
1382351_at	Gem	Rn.40436	chr5:26007476-26008270 (+) // 91.81 // q13		0.60	0.032	GTP binding protein (gene overexpressed in skeletal muscle)
1384770_at	---	Rn.147581	chr5:28896913-28897334 (-) // 100.0 // q13		-0.65	0.025	---
1384831_at	Slc7a13	Rn.22708	chr5:34437702-34438124 (+) // 50.94 // q13		-0.83	0.018	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13
1394490_at	Abca1	Rn.148916	chr5:70491315-70492240 (-) // 99.25 // q24		-0.67	0.039	ATP-binding cassette, sub-family A (ABC1), member 1
1395148_at	RGD1561090	Rn.99077	chr5:94069398-94069864 (+) // 85.23 // q31		-0.73	0.011	Similar to protein tyrosine phosphatase, receptor type, D
1375653_at	---	Rn.203993	chr6:113348113-113348784 (+) // 84.91 // q31		0.71	0.011	---
1382319_at	Gpr68	Rn.16653	chr6:125134282-125134697 (-) // 95.83 // q32		0.67	0.026	G protein-coupled receptor 68
1376845_at	isg12(b)	Rn.22509	chr6:127733539-127735008 (-) // 100.0 // q32		0.70	0.015	putative ISG12(b) protein
1372256_at	Crip	Rn.8405	chr6:138159129-138160959		0.57	0.045	cysteine-rich intestinal protein

			(+) // 99.77 // q32				
1379636_at	Fam82a	Rn.25365	chr6:2507279-2514576 (+) // 99.45 // q11		-0.63	0.041	family with sequence similarity 82, member A
1368440_at	Slc3a1	Rn.11196	chr6:8385159-8419461 (+) // 97.98 // q12		-0.60	0.033	solute carrier family 3, member 1
1374070_at	Gpx2	Rn.3503	chr6:99372417-99376230 (-) // 100.0 // q24		0.60	0.044	glutathione peroxidase 2
1381533_at	Rnd1	Rn.198250	chr7:137418519-137418908 (-) // 100.0 // q36		0.99	0.003	Rho family GTPase 1
1387625_at	Igfbp6	Rn.6431	chr7:140885387-140890032 (+) // 90.0 // q36		0.59	0.048	insulin-like growth factor binding protein 6
1368337_at	Glycam1	Rn.10939	chr7:142455641-142457903 (-) // 96.69 // q36		1.41	0.000	glycosylation dependent cell adhesion molecule 1
1388924_at	Angptl4	Rn.119611	chr7:16261620-16262022 (-) // 89.33 // q12		0.76	0.026	angiopoietin-like 4
1389018_at	---	---	chr7:67493450-67494305 (+) // 97.39 // q22		0.59	0.037	---
1368308_at	Myc	Rn.12072	chr7:98953306-98958042 (+) // 96.29 // q33		0.67	0.046	myelocytomatosis oncogene
1375777	---	Rn.202	chr8:343471		-	0.003	---

_at		475	74-34347793 (+) // 78.73 // q21		1.01		
1376198_at	Asam	Rn.163013	chr8:43766786-43767276 (+) // 95.87 // q22		0.61	0.030	adipocyte-specific adhesion molecule
1381811_at	---	Rn.92548	chr8:47077615-47077945 (+) // 99.1 // q22		0.64	0.041	---
1374013_at	C1qtnf5	Rn.99884	chr8:47090809-47091433 (+) // 100.0 // q22		0.64	0.035	C1q and tumor necrosis factor related protein 5
1397225_at	---	Rn.170224	chr8:51926554-51927008 (-) // 70.11 // q23		0.85	0.024	---
1380306_at	---	Rn.54177	chr8:51928782-51929247 (-) // 85.07 // q23		1.03	0.009	---
1392613_at	---	Rn.166664	chr8:51929265-51930063 (-) // 90.78 // q23		1.09	0.010	---
1390127_at	Dixdc1	Rn.8331	chr8:54018178-54019623 (-) // 71.0 // q23		-0.66	0.034	DIX domain containing 1
1373839_at	Nope	Rn.164673	chr8:69383115-69383839 (+) // 99.86 // q24		0.79	0.006	neighbor of Punc E11
1379397_at	Rora	Rn.43530	chr8:73814004-73817765		-0.63	0.033	RAR-related orphan receptor alpha

			(+) // 100.0 // q24				
1370688_at	Gclc	Rn.8365	chr8:82724456-82762006 (+) // 99.95 // q31		-0.73	0.021	glutamate-cysteine ligase, catalytic subunit
1379747_at	Prss35	Rn.161916	chr8:92024143-92024661 (-) // 97.35 // q31		-1.26	0.000	Protease, serine, 35
1381768_at	Mthfs	Rn.2215	chr8:94105901-94106254 (+) // 99.43 // q31		1.05	0.001	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
1392719_at	Mthfs	Rn.2215	chr8:94107662-94108310 (+) // 67.44 // q31		0.76	0.003	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
1392702_at	---	---	chr9:112684763-112685036 (+) // 35.36 // q38		0.63	0.044	---
1368236_at	Mep1a	Rn.16265	chr9:13170761-13201094 (+) // 99.39 // q12		-0.55	0.042	meprin 1 alpha
1393705_at	---	Rn.33933	chr9:13889268-13889744 (+) // 96.53 // q12		-3.19	0.000	---
1370959_at	Col3a1	Rn.3247	chr9:44307338-44317829 (+) // 98.4 // q22		0.60	0.048	collagen, type III, alpha 1

1382452_at	Sdpr	Rn.203035	chr9:47373043-47373555 (-) // 81.9 // q22		-0.66	0.033	serum deprivation response
1391152_at	LOC367381 /// LOC680281 /// LOC685769 /// LOC690576 /// LOC691414 /// RGD1563862	Rn.78670	chr9:5795046-5795580 (+) // 79.3 // q11 /// chr9:5676794-5677328 (+) // 75.27 // q11 /// chr9:5756336-5756870 (+) // 75.27 // q11 /// chr9:5531827-5532361 (+) // 75.09 // q11 /// chr9:5566056-5566590 (+) // 74.54 // q11 /// chr9:5718964-5719498 (+) // 74.		0.56	0.049	similar to RIKEN cDNA 4930555G01 /// similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large protein P-dlg) /// similar to Discs large homolog 5 (Placenta and prostate DLG) (Discs large protein P-dlg) /// similar to Discs large homolog 5
1367600_at	Des	Rn.39196	chr9:74637666-74645499 (+) // 98.92 // q33		0.58	0.048	desmin
1367712_at	Timp1	Rn.25754	chrX:12542480-12547161 (-) // 99.88 // q12		0.85	0.003	TIMP metallopeptidase inhibitor 1
1391476_at	---	Rn.44028	chrX:138964585-138965630 (+) // 98.31 // q36		-0.81	0.006	---
1368372_at	Sts	Rn.6312	chrX:63915802-63923833 (+) // 99.15 //		0.62	0.028	steroid sulfatase

			q22				

B. 8% NaCl diet for 7 days

ProbeSet ID	Gene Symbol	UniGene ID	Alignments	Congenic line	Log2R HS	RP-FDR HS	Gene Title
1367948_a_at	Kdr	Rn.88869	---		-0.54	0.045	kinase insert domain protein receptor
1373401_at	Tnc	Rn.12723	---		0.77	0.008	Tenascin C
1373908_at	---	---	---		1.45	0.000	---
1373921_at	Echdc3	Rn.202613	---		-0.51	0.048	enoyl Coenzyme A hydratase domain containing 3
1379259_at	---	Rn.146603	---		-2.19	0.000	---
1383665_at	Lpin2	Rn.203839	---		-0.58	0.029	lipin 2
1384231_at	LOC687121	---	---		0.77	0.009	similar to Shc SH2-domain binding protein 1
1387158_at	Mep1b	Rn.3520	---		-0.99	0.001	meprin 1 beta
1389858_at	Tk1	Rn.217952	---		0.57	0.045	thymidine kinase 1, soluble
1390722_at	---	---	---		1.86	0.000	---
1396417_at	---	Rn.153725	---		-0.53	0.038	---
1397577_at	---	---	---		-0.57	0.029	---
1371245_a_at	LOC689064	---	chr1:161578125-		1.03	0.004	beta-globin

			161579489 (-) // 93.18 // q32				
1367553_x_at	Hbb	Rn.202945	chr1:161584855-161620196 (-) // 90.7 // q32 /// chr1:161578238-161579551 (-) // 77.18 // q32		0.71	0.018	hemoglobin, beta
1373336_at	Gprc5b	Rn.47330	chr1:177206414-177206826 (-) // 88.89 // q35		-0.69	0.004	G protein-coupled receptor, family C, group 5, member B
1370436_at	Acsm2	Rn.14875	chr1:177830612-177869061 (+) // 96.46 // q35		-0.97	0.002	acyl-CoA synthetase medium-chain family member 2
1370746_at	Prkacb	Rn.202491	chr1:186619404-186620435 (+) // 90.82 // q36 /// chr2:244949302-245035266 (-) // 99.91 // q44		0.63	0.045	protein kinase, cAMP dependent, catalytic, beta
1389566_at	Ccnb2	Rn.6743	chr1:20585333-20586031 (-) // 96.67 // p12 /// chr8:74892113-74896194 (-) // 96.81 // q24		0.56	0.050	cyclin B2
1395634_at	---	Rn.168253	chr1:207360231-207360634		-0.71	0.012	---

			(+) // 52.57 // q42				
1396039_at	Slc22a12	Rn.137035	chr1:209320805-209321109 (-) // 50.86 // q43		-0.57	0.041	solute carrier family 22 (organic anion/urate transporter), member 12
1388172_at	Slc22a25	Rn.31066	chr1:211122125-211204306 (-) // 82.9 // q43		-0.63	0.033	solute carrier family 22, member 25
1378193_at	Ms4a7	Rn.44037	chr1:213828861-213835028 (-) // 99.08 // q43		0.59	0.049	membrane-spanning 4-domains, subfamily A, member 7
1369427_at	Mpeg1	Rn.162497	chr1:215387911-215390172 (+) // 99.55 // q43		0.80	0.009	macrophage expressed gene 1
1371970_at	Fam111a	Rn.112856	chr1:215596336-215597225 (+) // 99.89 // q43		0.53	0.049	family with sequence similarity 111, member A
1389581_at	Il33	Rn.106849	chr1:233681966-233684615 (+) // 100.0 // q52		0.71	0.015	interleukin 33
1373970_at	Il33	Rn.106849	chr1:233684782-233685804 (+) // 98.17 // q52		0.66	0.023	interleukin 33
1380775_at	Kif20b	Rn.208134	chr1:238943389-238947659 (+) // 92.21 // q52		0.59	0.036	kinesin family member 20B
1385619_at	Kif11	Rn.58850	chr1:241717842-241721610		0.58	0.036	kinesin family member 11

			(+) // 100.0 // q53				
1390891_at	Kif11	Rn.58850	chr1:241722204-241722847 (+) // 78.07 // q53		0.55	0.041	kinesin family member 11
1375475_at	---	Rn.208145	chr1:259756929-259757430 (+) // 95.19 // q55		0.60	0.020	---
1391518_at	LOC689399	Rn.51	chr1:28272669-28273208 (+) // 59.96 // p11 /// chrX:76343579-76344119 (+) // 89.94 // q22		0.57	0.039	hypothetical protein LOC689399
1374726_at	Fndc1	Rn.20633	chr1:41583322-41584011 (+) // 91.51 // q11		0.66	0.018	fibronectin type III domain containing 1
1387303_at	Slc22a2	Rn.10555	chr1:42395673-42442837 (-) // 97.9 // q11		-0.78	0.004	solute carrier family 22 (organic cation transporter), member 2
1388036_a_at	Mllt4	Rn.58	chr1:48827686-48903967 (+) // 68.36 // q12		0.67	0.015	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4
1370493_a_at	Lilrb3l /// LOC683446 /// LOC690948 ///	Rn.198480	chr1:63677485-63735563 (+) // 99.24 // q12 ///		0.80	0.008	leukocyte immunoglobulin-like receptor, subfamily B (with TM and

	LOC690955 /// RGD1562625		chr1:63770467-63777226 (+) // 94.2 // q12				ITIM domains), member 3-like /// similar to paired-Ig-like receptor A11 /// similar to paired-Ig-like receptor A11 /// similar to paired-Ig-like receptor B /// similar to killer activatory r
1397657_at	---	---	chr1:67664344-67664648 (+) // 18.41 // q12		-0.54	0.038	---
1372306_at	Ethe1	Rn.14691	chr1:79875662-79890680 (+) // 100.0 // q21		0.55	0.047	ethylmalonic encephalopathy 1
1380557_at	Bckdha	Rn.49145	chr1:80865713-80866687 (-) // 66.13 // q21		-0.65	0.014	branched chain ketoacid dehydrogenase E1, alpha polypeptide
1390847_at	Tmem86a	Rn.23056	chr1:97604476-97607566 (+) // 99.79 // q22		-0.54	0.040	transmembrane protein 86A
1377410_at	E2f8	Rn.15287	chr1:98640380-98640837 (-) // 80.57 // q22		0.64	0.016	E2F transcription factor 8
1370239_at	Hba-a2 /// LOC360504	Rn.107334	chr10:15584358-15585213 (-) // 91.28 // q12 /// chr10:15554907-15571771 (-) // 91.45 //		0.89	0.009	hemoglobin alpha, adult chain 2 /// hemoglobin alpha 2 chain

			q12				
1370240_x_at	Hba-a2 /// LOC360504	Rn.107334	chr10:15584358-15585213 (-) // 91.28 // q12 /// chr10:15554907-15571771 (-) // 91.45 // q12		0.84	0.010	hemoglobin alpha, adult chain 2 /// hemoglobin alpha 2 chain
1385190_at	---	Rn.66394	chr10:18453301-18453731 (-) // 99.77 // q12		0.79	0.009	---
1387600_at	Gabrp	Rn.21401	chr10:18454554-18474566 (-) // 87.86 // q12		0.85	0.005	gamma-aminobutyric acid (GABA-A) receptor, pi
1370461_at	Hmmr	Rn.92304	chr10:25732539-25762825 (-) // 85.03 // q12		0.69	0.013	hyaluronan mediated motility receptor (RHAMM)
1391516_at	LOC303140	---	chr10:39408312-39408866 (-) // 85.23 // q22		-0.51	0.043	up-regulator of carnitine transporter, OCTN2
1368260_at	Aurkb	Rn.10865	chr10:55798709-55804363 (+) // 73.53 // q24		0.58	0.035	aurora kinase B
1370864_at	Col1a1	Rn.2953	chr10:83622548-83639368 (+) // 98.17 // q31		0.73	0.013	collagen, type I, alpha 1
1388116_at	Col1a1	Rn.2953	chr10:83622548-83639368 (+) // 98.17 // q31		0.84	0.009	collagen, type I, alpha 1

1372186_a_at	Top2a	Rn.90996	chr10:87770881-87771650 (-) // 100.0 // q31		0.69	0.009	topoisomerase (DNA) II alpha
1372153_at	Krt15	Rn.153568	chr10:89071914-89073533 (-) // 98.02 // q32.1		0.71	0.018	keratin 15
1381233_at	---	Rn.21708	chr10:97297929-97298374 (-) // 100.0 // q32.1		-0.82	0.004	---
1368223_at	Adamts1	Rn.7897	chr11:25433792-25443150 (-) // 95.74 // q11		0.88	0.005	ADAM metallopeptidase with thrombospondin type 1 motif, 1
1374251_at	---	Rn.146492	chr11:35596790-35597418 (+) // 99.68 // q11		-0.64	0.020	---
1373628_at	---	Rn.1026	chr11:43736425-43737048 (+) // 89.21 // q12		0.60	0.034	---
1370161_at	Ccdc80	Rn.2193	chr11:57223053-57257257 (-) // 95.08 // q21		0.61	0.039	coiled-coil domain containing 80
1398514_at	Hgd	Rn.24631	chr11:64876270-64876614 (-) // 94.77 // q21		-0.59	0.049	homogentisate 1, 2-dioxygenase
1370926_at	Muc4	Rn.24930	chr11:69830275-69858170 (-) // 94.62 // q22		0.63	0.018	mucin 4, cell surface associated
1397326	---	Rn.208	chr11:84680		-	0.038	---

_at		647	821-84681238 (+) // 54.34 // q23		0.54		
1397370_at	---	Rn.204907	chr12:19724858-19725627 (-) // 40.08 // q12		-0.57	0.020	---
1368188_at	Hpd	Rn.3664	chr12:34548319-34558384 (+) // 89.65 // q16		-0.62	0.016	4-hydroxyphenylpyruvate dioxygenase
1369491_at	Dao	Rn.81058	chr12:43627592-43648332 (-) // 98.06 // q16		-0.90	0.004	D-amino-acid oxidase
1382493_at	Cenpf	Rn.41236	chr13:105920538-105920931 (-) // 95.62 // q27		0.61	0.020	---
1397730_at	RGD1307235	Rn.38292	chr13:11849937-11863618 (+) // 100.0 // p13		-0.53	0.049	similar to RIKEN cDNA 2310035C23
1367728_at	Tsn	Rn.156195	chr13:30917405-30928093 (-) // 96.66 // q11		0.72	0.008	translin
1388219_at	Htr5b	Rn.202942	chr13:33545127-33558050 (-) // 88.44 // q11	congenic Line 5	0.63	0.013	5-hydroxytryptamine (serotonin) receptor 5B
1395886_at	Actr3	Rn.103326	chr13:37881320-37904643 (-) // 99.79 // q11	congenic Line 5	0.69	0.013	ARP3 actin-related protein 3 homolog (yeast)
1383111_at	---	Rn.220664	chr13:40545750-	congenic	-0.6	0.020	---

			40546434 (-) // 81.78 // q12	Line 5	2		
1373661_a_at	Cxcr4	Rn.44431	chr13:41308284-41308707 (-) // 94.09 // q12	congenic Line 5	0.58	0.035	chemokine (C-X-C motif) receptor 4
1389244_x_at	Cxcr4	Rn.44431	chr13:41308284-41308707 (-) // 94.09 // q12	congenic Line 5	0.57	0.035	chemokine (C-X-C motif) receptor 4
1370097_a_at	Cxcr4	Rn.44431	chr13:41308548-41312156 (-) // 95.81 // q12	congenic Line 5	0.68	0.012	chemokine (C-X-C motif) receptor 4
1389113_at	Slc45a3	Rn.9239	chr13:44860762-44861168 (+) // 95.08 // q13	congenic Line 5	-0.90	0.001	solute carrier family 45, member 3
1391613_at	Elk4	Rn.204345	chr13:44911374-44911848 (+) // 52.34 // q13	congenic Line 5	-0.60	0.021	ELK4, member of ETS oncogene family
1382230_at	Klhdc8a	Rn.44339	chr13:45194599-45195439 (+) // 97.11 // q13	congenic Line 5	-0.55	0.031	kelch domain containing 8A
1397746_at	---	Rn.212168	chr13:45195611-45195996 (+) // 72.51 // q13	congenic Line 5	-0.69	0.004	---
1391601_at	Lrrn2	Rn.11847	chr13:45837783-45838309 (+) // 100.0 // q13	congenic Line 9	-0.52	0.047	leucine rich repeat neuronal 2
1390271_at	Plekha6	Rn.21422	chr13:46210058-46210710	congenic Line	-2.06	0.000	pleckstrin homology domain

			(+) // 96.41 // q13	9			containing, family A member 6
1398516_at	Golt1a	Rn.13207	chr13:46224432-46237119 (+) // 100.0 // q13	congenic Line 9	1.16	0.000	golgi transport 1 homolog A (S. cerevisiae)
1378008_at	---	Rn.204209	chr13:47449221-47449993 (+) // 86.62 // q13	congenic Line 9	-0.57	0.022	---
1374123_at	---	Rn.25048	chr13:47945366-47946010 (-) // 100.0 // q13	congenic Line 9	0.94	0.001	---
1389619_at	---	Rn.161322	chr13:48378300-48378952 (-) // 81.9 // q13	congenic Line 9	-0.81	0.001	---
1379346_at	Cdc73	Rn.162332	chr13:57441291-57442992 (-) // 98.15 // q21		-1.10	0.000	cell division cycle 73, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)
1398540_at	Rgs1	Rn.14787	chr13:58121195-58121856 (-) // 99.1 // q21		0.57	0.013	regulator of G-protein signaling 1
1387566_at	Pla2g4a	Rn.10162	chr13:64135723-64280803 (-) // 97.69 // q21		-0.60	0.016	phospholipase A2, group IVA (cytosolic, calcium-dependent)
1387454_at	Fam129a	Rn.211984	chr13:66467072-66620158 (+) // 98.56 // q21	congenic Line 26	0.93	0.001	family with sequence similarity 129, member A
1379889_at	Lamc2	Rn.9278	chr13:68155279-	congenic	1.27	0.000	laminin, gamma 2

			68159154 (-) // 97.59 // q21	Line 26			
1396877_at	---	Rn.204402	chr13:68362089-68362554 (-) // 50.31 // q21	congenic Line 26	1.84	0.000	---
1374174_at	---	Rn.114503	chr13:70171114-70171528 (+) // 58.62 // q21	congenic Line 26	-0.53	0.036	---
1389775_at	---	---	chr13:70179712-70180139 (-) // 95.29 // q21	congenic Line 26	0.75	0.008	---
1388963_at	Astn1	Rn.28132	chr13:73966983-73967532 (+) // 100.0 // q22	congenic Line 26	-0.72	0.004	astrotactin 1
1377675_at	LOC100302372	---	chr13:75494982-75495823 (+) // 82.16 // q22	congenic Line 26	-0.72	0.004	hypothetical protein LOC100302372
1398475_at	Dars2	Rn.137838	chr13:76602121-76602835 (-) // 53.78 // q22	congenic Line 26	-0.71	0.004	aspartyl-tRNA synthetase 2 (mitochondrial)
1395471_at	---	Rn.34102	chr13:76743684-76744061 (+) // 95.69 // q22	congenic Line 26	0.64	0.012	---
1394574_at	---	Rn.210473	chr13:76829595-76829997 (-) // 94.58 // q22	congenic Line 26	-1.09	0.000	---
1382031_at	---	Rn.2564	chr13:78543793-78544624 (-)	congenic Line	-0.84	0.003	---

			// 42.16 // q22	26			
1392278_at	---	Rn.211531	chr13:79665934-79666319 (+) // 68.58 // q22		0.90	0.001	---
1374320_at	F5	Rn.82910	chr13:79992843-79997293 (+) // 97.52 // q22		-1.53	0.000	coagulation factor V (proaccelerin, labile factor)
1373947_at	Dpt	Rn.8396	chr13:80574810-80590528 (+) // 99.6 // q23		-1.46	0.000	dermatopontin
1381588_at	Sft2d2	Rn.8424	chr13:80926906-80927283 (-) // 99.47 // q23		0.57	0.044	SFT2 domain containing 2
1392947_at	---	Rn.6374	chr13:83835340-83836041 (-) // 96.82 // q24		0.68	0.011	---
1386911_at	Atp1a2	Rn.1042	chr13:88258984-88283918 (-) // 97.5 // q24		0.69	0.012	ATPase, Na+/K+ transporting, alpha 2 polypeptide
1398390_at	Cxcl13	Rn.6917	chr14:15126331-15126759 (-) // 95.32 // p22		0.81	0.009	chemokine (C-X-C motif) ligand 13
1368760_at	Cxcl2	Rn.10230	chr14:18677128-18679175 (-) // 93.82 // p22		0.70	0.009	chemokine (C-X-C motif) ligand 2
1387314_at	Sult1b1	Rn.1183	chr14:22019200-22031908 (+) // 95.26 //		-0.70	0.012	sulfotransferase family, cytosolic, 1B, member 1

			p21				
1382954_at	---	Rn.131875	chr14:38340370-38340833 (+) // 94.4 // p11		-1.36	0.000	---
1368168_at	Slc34a2	Rn.16933	chr14:62659554-62671676 (-) // 95.65 // q11		0.79	0.009	solute carrier family 34 (sodium phosphate), member 2
1379903_at	---	Rn.98831	chr14:79415489-79416111 (-) // 99.68 // q21		0.71	0.012	---
1384043_at	---	Rn.173529	chr14:79416114-79416960 (-) // 91.81 // q21		0.58	0.040	---
1396742_at	Ipo5	Rn.79893	chr15:106001263-106003232 (+) // 94.3 // q24		0.59	0.046	importin 5
1379739_at	---	Rn.25345	chr15:12068174-12068719 (-) // 95.78 // p16		-0.57	0.022	---
1372685_at	Cdkn3	Rn.107220	chr15:22624369-22628748 (+) // 100.0 // p14		0.64	0.019	cyclin-dependent kinase inhibitor 3
1380883_at	---	Rn.14588	chr15:36851030-36851547 (+) // 98.84 // p12		-0.57	0.021	---
1372979_at	---	Rn.9334	chr15:3866283-3866864 (+) // 96.83 // p16		-0.57	0.028	---
1397341	Pbk	Rn.137	chr15:45237		0.5	0.034	PDZ binding

_at		333	699-45238098 (+) // 100.0 // p12		6		kinase
1372809_at	LOC290595	Rn.103148	chr16:13308803-13316409 (-) // 95.97 // p14		0.80	0.008	hypothetical gene supported by AF152002
1376829_at	---	Rn.39005	chr16:67694032-67694522 (+) // 92.45 // q12.3		-0.75	0.004	---
1397547_at	Ikbkb	Rn.19222	chr16:73861758-73862249 (+) // 8.63 // q12.5		-0.59	0.016	Inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
1371913_at	Tgfbi	Rn.1046	chr17:13904881-13905464 (-) // 99.66 // p14		0.73	0.015	transforming growth factor, beta induced
1389678_at	---	Rn.38259	chr17:14076943-14077620 (-) // 97.49 // p14		-0.79	0.003	---
1368680_a_at	Slc34a1	Rn.92022	chr17:15262928-15268863 (-) // 89.81 // p14		-0.77	0.006	solute carrier family 34 (sodium phosphate), member 1
1385856_at	Riok1	Rn.132553	chr17:32994646-32995672 (-) // 91.93 // p12		0.82	0.007	RIO kinase 1 (yeast)
1380346_at	Serpinb1a	Rn.103402	chr17:37951976-37954921 (+) // 100.0 // p12		0.88	0.004	serine (or cysteine) proteinase inhibitor, clade B, member 1a
1377034	Serpinb1a	Rn.103	chr17:37958		0.7	0.009	serine (or

_at		402	777-37959288 (+) // 100.0 // p12		8		cysteine) proteinase inhibitor, clade B, member 1a
1378236_at	Lrrc16a	Rn.40387	chr17:48180102-48188855 (+) // 99.6 // p11		0.60	0.034	leucine rich repeat containing 16A
1383486_at	---	Rn.35842	chr17:57240189-57240871 (-) // 97.14 // q12.1		0.70	0.013	---
1385025_a_at	Gpr137b	Rn.60453	chr17:67000798-67004339 (+) // 99.81 // q12.1		0.77	0.009	G protein-coupled receptor 137B
1393148_at	Gpr137b	Rn.60453	chr17:67000855-67006473 (+) // 99.84 // q12.1		0.65	0.015	G protein-coupled receptor 137B
1378097_at	---	Rn.21452	chr17:67016111-67016772 (+) // 91.72 // q12.1		-0.66	0.009	---
1368077_at	Fbp1	Rn.33703	chr17:7795814-7818041 (+) // 86.78 // p14		-0.81	0.004	fructose-1,6-biphosphatase 1
1380670_at	---	Rn.207220	chr17:82995739-82996341 (+) // 97.73 // q12.3		-0.55	0.035	---
1383380_at	Rpp38	Rn.2690	chr17:86036507-86036982 (+) // 95.19 // q12.3		0.58	0.047	ribonuclease P/MRP 38 subunit (human)
1391256_at	---	Rn.91712	chr17:86038215-86038649		0.88	0.004	---

			(+) // 52.43 // q12.3				
1380418_at	---	Rn.209714	chr17:86152733-86152909 (-) // 41.87 // q12.3		1.29	0.000	---
1379423_at	Rsu1	Rn.11453	chr17:87345488-87345935 (+) // 96.1 // q12.3		-1.89	0.000	Ras suppressor protein 1
1392953_at	Ptpla	Rn.38334	chr17:88239566-88243637 (-) // 92.97 // q12.3		0.59	0.025	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
1383696_at	Ptpla	Rn.38334	chr17:88253097-88253571 (-) // 100.0 // q12.3		0.57	0.034	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member a
1368172_a_at	Lox	Rn.11372	chr18:47893877-47906673 (-) // 99.45 // q11		0.63	0.015	lysyl oxidase
1391693_at	Atp8b1	Rn.6957	chr18:60749041-60756769 (-) // 97.39 // q12.1		0.65	0.020	ATPase, Class I, type 8B, member 1
1391317_at	RGD1310784	Rn.106906	chr18:70988483-70989335 (-) // 93.9 // q12.2		0.67	0.012	similar to RIKEN cDNA 2810433K01
1369254_a_at	Ptger1	Rn.11423	chr19:26160457-26163156 (-) // 88.13 // q11		-0.53	0.037	prostaglandin E receptor 1 (subtype EP1)

1374167_at	rCG_51406	Rn.220423	chr19:35732521-35733120 (+) // 100.0 // q12		-0.57	0.025	neuritin 1-like
1387157_at	Pmfbp1	Rn.51502	chr19:39362519-39411269 (+) // 96.77 // q12		0.68	0.019	polyamine modulated factor 1 binding protein 1
1378898_at	---	Rn.208048	chr19:40900622-40901049 (+) // 46.85 // q12		-0.71	0.004	---
1394079_at	Tbl1xr1	Rn.140831	chr2:107683655-107684388 (+) // 89.51 // q24		0.61	0.043	transducin (beta)-like 1 X-linked receptor 1
1383747_at	Ect2	Rn.168292	chr2:112969263-112969828 (-) // 96.23 // q24		0.58	0.030	epithelial cell transforming sequence 2 oncogene
1379582_a_at	Ccna2	Rn.13094	chr2:123062863-123063335 (-) // 99.79 // q25		0.79	0.005	cyclin A2
1373911_at	Postn	Rn.30516	chr2:143567577-143568339 (+) // 100.0 // q26		0.84	0.009	periostin, osteoblast specific factor
1371173_a_at	Cast	Rn.17481	chr2:1497325-1558604 (-) // 99.5 // q11		0.62	0.038	calpastatin
1383008_at	Smc4	Rn.163695	chr2:158998991-159001274 (+) // 100.0 // q31		0.69	0.012	structural maintenance of chromosomes 4
1375335_at	Hsp90ab1	Rn.98667	chr2:170299391-		0.60	0.046	heat shock protein 90kDa

			170308287 (+) // 85.61 // q32 /// chr2:174024305-174026774 (+) // 84.27 // q33 /// chr3:36633862-36636364 (+) // 92.61 // q12 /// chr9:11033454-11039001 (+) // 95.65 // q12 /// chr19:34281728-34284213 (+) // 84.23 // q11 /// chr1:106346670-				alpha (cytosolic), class B member 1
1395126_at	Fcrls	Rn.76819	chr2:179283588-179284079 (-) // 97.97 // q34		0.76	0.011	Fc receptor-like S, scavenger receptor
1390878_at	LOC681309	Rn.198600	chr2:181393216-181395130 (+) // 100.0 // q34		0.61	0.045	similar to Thrombospondin-3 precursor
1369502_a_at	Amy1a /// Amy2	Rn.67070	chr2:209469273-209518455 (-) // 99.81 // q41 /// chr2:209325427-209447436 (-) // 96.76 // q41 /// chr2:209291		-0.55	0.034	amylase, alpha 1A (salivary) /// amylase 2, pancreatic

			708-209482095 (-) // 75.98 // q41 /// chr2:209293259-209478431 (-) // 61.37 // q41				
1373351_at	Ank2	Rn.133131	chr2:224180616-224181006 (-) // 88.56 // q42		-0.53	0.049	ankyrin 2, neuronal
1368205_at	Cfi	Rn.7424	chr2:227281540-227325106 (+) // 76.28 // q43		0.74	0.015	complement factor I
1391417_at	Bhmt2	Rn.8494	chr2:23958044-23976415 (-) // 96.24 // q12		-0.99	0.002	betaine-homocysteine methyltransferase 2
1370936_at	Dmgdh	Rn.3646	chr2:23976594-24052768 (+) // 99.29 // q12		-0.70	0.008	dimethylglycine dehydrogenase
1376914_at	Depdc1	Rn.27037	chr2:257796817-257797372 (+) // 84.35 // q45		0.55	0.049	DEP domain containing 1
1370345_at	Ccnb1	Rn.9232	chr2:31573578-31581754 (-) // 88.03 // q12		0.67	0.021	cyclin B1
1376944_at	---	Rn.205026	chr2:59688547-59689210 (+) // 100.0 // q16		-0.90	0.001	---
1368659_at	Agxt2	Rn.1874	chr2:59713350-		-0.6	0.043	alanine-glyoxylate

			59755149 (+) // 80.21 // q16		0		aminotransferase 2
1391587_at	---	Rn.16809	chr2:77392335-77392908 (+) // 52.53 // q22		-0.62	0.012	---
1373990_at	LOC361914 /// Slc7a12	Rn.34357	chr2:88620186-88620706 (-) // 54.53 // q23 /// chr2:88429242-88429760 (-) // 53.77 // q23		-0.88	0.002	similar to solute carrier family 7 (cationic amino acid transporter, y+ system), member 12 /// solute carrier family 7 (cationic amino acid transporter, y+ system), member 12
1380340_at	---	Rn.63789	chr2_random:3132330-3132781 (-) // 96.15 //		-0.82	0.003	---
1380972_at	---	---	chr2_random:3463968-3464468 (+) // 84.2 //		-0.55	0.030	---
1367776_at	Cdc2	Rn.6934	chr20:20018043-20044033 (+) // 100.0 // p11		0.64	0.018	cell division cycle 2, G1 to S and G2 to M
1387218_at	Tff3	Rn.87477	chr20:9469887-9474604 (-) // 99.54 // p12		-0.79	0.006	trefoil factor 3, intestinal
1383578_at	Rad51	Rn.20474	chr3:105649900-105650400 (+) // 90.52 // q35		0.66	0.021	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
1392732_at	Nusap1	Rn.106933	chr3:106134434-106164609 (+) // 95.35 //		0.55	0.045	nucleolar and spindle associated protein 1

			q35				
1384280_at	Nusap1	Rn.106933	chr3:106164591-106164957 (+) // 94.82 // q35		0.55	0.045	nucleolar and spindle associated protein 1
1398256_at	Il1b	Rn.9869	chr3:116964426-116970887 (-) // 96.03 // q36		0.70	0.009	interleukin 1 beta
1390743_at	---	Rn.60798	chr3:148264702-148264983 (-) // 51.23 // q42		-0.51	0.043	---
1392969_at	---	Rn.12238	chr3:154485187-154485651 (+) // 94.89 // q42		-0.75	0.006	---
1372264_at	Pck1	Rn.104376	chr3:164017885-164018347 (+) // 74.9 // q42		-1.11	0.001	phosphoenolpyruvate carboxykinase 1 (soluble)
1379058_at	---	Rn.5854	chr3:17130284-17130625 (+) // 88.31 // q11		0.53	0.026	---
1387382_at	Hnmt	Rn.13145	chr3:2057594-2090011 (-) // 94.09 // p13		-1.29	0.000	histamine N-methyltransferase
1381575_at	Neb	Rn.134031	chr3:33634432-33634813 (-) // 100.0 // q12		-0.89	0.001	nebulin
1374630_at	Clic3	Rn.25003	chr3:3623981-3725117 (+) // 96.43 // p13		-0.58	0.044	chloride intracellular channel 3
1376945_at	---	Rn.47139	chr3:47981103-		-0.5	0.046	---

			47981762 (+) // 93.81 // q21		1		
1367952_at	Lrp2	Rn.26430	chr3:51563760-51724478 (-) // 99.77 // q21		-0.67	0.015	low density lipoprotein-related protein 2
1387378_at	Fcnb	Rn.48281	chr3:7010934-7019366 (-) // 99.58 // p12		0.60	0.050	ficolin B
1395173_at	Caprin1	Rn.22572	chr3:89069911-89073766 (-) // 98.0 // q32		0.87	0.003	cell cycle associated protein 1
1394419_at	Arhgap11a	Rn.51673	chr3:99676955-99677766 (-) // 100.0 // q34		0.61	0.022	Rho GTPase activating protein 11A
1378365_at	---	Rn.154314	chr4:117516422-117516800 (+) // 100.0 // q34		-0.96	0.001	---
1388176_at	Cml5	Rn.205673	chr4:119981268-119981789 (-) // 97.74 // q34		-0.56	0.029	camello-like 5
1368249_at	Klf15	Rn.22556	chr4:124714394-124726985 (+) // 98.95 // q34		-0.91	0.001	Kruppel-like factor 15
1381396_s_at	Klf15	Rn.22556	chr4:124719208-124726016 (+) // 51.46 // q34		-0.66	0.009	Kruppel-like factor 15
1373823_at	Cks2	Rn.6116	chr4:146600456-146601035 (+) // 92.8 // q41 ///		0.62	0.035	CDC28 protein kinase regulatory subunit 2

			chr17:19423498-19429420 (-) // 98.49 // p14 /// chr3:104267742-104268325 (-) // 91.46 // q35				
1379135_at	Ttll3	Rn.198684	chr4:149282067-149282413 (+) // 69.23 // q42		-0.59	0.020	tubulin tyrosine ligase-like family, member 3
1387295_at	Slc6a12	Rn.11352	chr4:157781177-157800190 (+) // 94.47 // q42		-0.68	0.011	solute carrier family 6 (neurotransmitter transporter, betaine/GABA), member 12
1367794_at	A2m	Rn.109457	chr4:158103688-158153693 (+) // 98.55 // q42		1.36	0.000	alpha-2-macroglobulin
1374449_at	Cdca3	Rn.129078	chr4:160955417-160956856 (+) // 94.21 // q42 /// chr9:43464499-43465083 (+) // 66.44 // q22		0.64	0.016	cell division cycle associated 3
1368683_at	Olr1	Rn.87449	chr4:166747226-166769340 (-) // 64.04 // q42		0.60	0.035	oxidized low density lipoprotein (lectin-like) receptor 1
1388282_s_at	Klra5 /// Ly49s7	Rn.37467	chr4:168698329-168716439 (-) // 99.38 // q42 ///		0.91	0.004	killer cell lectin-like receptor, subfamily A, member 5 /// Ly49 stimulatory

			chr4:168640016-168670204 (-) // 98.89 // q42				receptor 7
1398253_at	Kap	Rn.11143	chr4:170652192-170655239 (-) // 90.17 // q43		-0.89	0.003	kidney androgen regulated protein
1375704_at	Atf7ip	Rn.98469	chr4:173566919-173570093 (+) // 100.0 // q43		0.58	0.034	activating transcription factor 7 interacting protein
1395687_at	Atf7ip	Rn.98469	chr4:173571332-173576643 (+) // 95.32 // q43		0.64	0.018	activating transcription factor 7 interacting protein
1387567_at	Slco1a1	---	chr4:179431195-179829799 (-) // 92.28 // q44		-0.91	0.002	solute carrier organic anion transporter family, member 1a1
1368498_a_at	Slc21a4	Rn.202967	chr4:179552663-179592111 (-) // 95.75 // q44		-0.81	0.004	kidney specific organic anion transporter
1369401_at	Slco1a6	---	chr4:179688188-179723995 (-) // 100.0 // q44		-0.96	0.002	solute carrier organic anion transporter family, member 1a6
1387287_a_at	Abcc9	Rn.10528	chr4:180168420-180582914 (-) // 66.98 // q44		0.71	0.012	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
1370869_at	Bcat1	Rn.8273	chr4:182641519-182725922 (-) // 85.23 // q44		0.52	0.049	branched chain aminotransferase 1, cytosolic
1387487	Calcr	Rn.100	chr4:284862		0.7	0.009	calcitonin

_a_at		62	13-28561065 (-) // 98.23 // q13		5		receptor
1370155_at	Col1a2	Rn.107239	chr4:29393644-29429088 (+) // 97.96 // q13		0.59	0.034	collagen, type I, alpha 2
1387854_at	Col1a2	Rn.107239	chr4:29393644-29429088 (+) // 97.96 // q13		0.61	0.034	collagen, type I, alpha 2
1369218_at	Met	Rn.10617	chr4:43134182-43211357 (+) // 99.9 // q21		0.64	0.035	met proto-oncogene
1384960_at	Cftr	Rn.124539	chr4:44041161-44041873 (+) // 97.05 // q21		-0.67	0.010	cystic fibrosis transmembrane conductance regulator homolog
1369191_at	Il6	Rn.9873	chr4:456798-461376 (-) // 90.73 // q11		0.58	0.025	interleukin 6
1391625_at	Wasl	---	chr4:51063714-51067525 (-) // 70.18 // q22		0.59	0.035	Wiskott-Aldrich syndrome-like
1368187_at	Gpnmb	Rn.13778	chr4:77161351-77182624 (+) // 96.6 // q24		0.64	0.049	glycoprotein (transmembrane) nmb
1388778_at	---	Rn.17629	chr4:87392455-87393064 (+) // 99.34 // q24		-0.61	0.019	---
1376685_at	---	Rn.40821	chr5:101680817-101681630 (-) // 84.0 //		0.83	0.005	---

			q31				
1373538_at	Usp1	Rn.155728	chr5:119368425-119371527 (+) // 97.99 // q33		0.60	0.049	ubiquitin specific peptidase 1
1371824_at	Ak3l1	Rn.1086	chr5:122122204-122122785 (+) // 100.0 // q33		-0.66	0.023	adenylate kinase 3-like 1
1368607_at	Cyp4a8	Rn.10034	chr5:135547363-135578186 (-) // 98.88 // q36		-0.86	0.003	cytochrome P450, family 4, subfamily a, polypeptide 8
1394844_s_at	Cyp4a2 /// Cyp4a3	Rn.33492	chr5:135876135-135876559 (-) // 94.81 // q36		-1.14	0.000	cytochrome P450, family 4, subfamily a, polypeptide 2 /// cytochrome P450, family 4, subfamily a, polypeptide 3
1368006_at	Laptm5	Rn.24799	chr5:149775671-149797167 (+) // 94.28 // q36		0.80	0.009	lysosomal multispanning membrane protein 5
1380579_at	Matn1	Rn.15159	chr5:149812569-149815428 (+) // 95.39 // q36		-3.58	0.000	matrilin 1, cartilage matrix protein
1392607_at	---	Rn.22747	chr5:150809645-150810008 (-) // 91.18 // q36		-0.58	0.024	---
1387804_at	Trim63	Rn.40636	chr5:153059572-153073942 (+) // 88.38 // q36		-0.61	0.029	tripartite motif-containing 63
1368121_at	Akr7a3	Rn.6043	chr5:158139987-		-0.7	0.004	aldo-keto reductase family

			158147516 (+) // 98.66 // q36		8		7, member A3 (aflatoxin aldehyde reductase)
1373282_at	LOC691431	Rn.8763	chr5:166836558-166838641 (-) // 97.58 // q36		-0.58	0.020	similar to mitochondrial carrier protein MGC4399
1374259_at	---	Rn.147583	chr5:17211606-17212202 (-) // 99.5 // q12		-0.54	0.037	---
1388484_at	Ube2c	Rn.3102	chr5:19334583-19335249 (+) // 84.35 // q12 /// chr12:13093644-13094371 (+) // 90.61 // q11 /// chr3:155800391-155802751 (+) // 95.24 // q42		0.58	0.045	ubiquitin-conjugating enzyme E2C
1378315_at	---	Rn.147582	chr5:21948815-21949253 (-) // 40.41 // q13		-0.55	0.040	---
1384770_at	---	Rn.147581	chr5:28896913-28897334 (-) // 100.0 // q13		-0.81	0.002	---
1384831_at	Slc7a13	Rn.22708	chr5:34437702-34438124 (+) // 50.94 // q13		-1.28	0.000	solute carrier family 7, (cationic amino acid transporter, y+ system) member 13
1393945_at	---	Rn.147572	chr5:40706887-		0.64	0.031	---

			40707255 (-) // 95.32 // q21				
1389756_at	Melk	Rn.28232	chr5:60847703-60848245 (+) // 99.82 // q22		0.62	0.018	maternal embryonic leucine zipper kinase
1389548_at	Adhfe1	Rn.17173	chr5:9276933-9290608 (-) // 74.69 // q11		-0.55	0.036	alcohol dehydrogenase, iron containing, 1
1375653_at	---	Rn.203993	chr6:113348113-113348784 (+) // 84.91 // q31		1.30	0.000	---
1387423_at	Lhcgr	Rn.11216	chr6:12610848-12651587 (-) // 65.88 // q12		-0.60	0.020	luteinizing hormone/choriogonadotropin receptor
1368224_at	Serpina3n	Rn.202939	chr6:128461774-128469320 (+) // 99.76 // q32		0.56	0.031	serine (or cysteine) peptidase inhibitor, clade A, member 3N
1379294_at	---	Rn.13051	chr6:21637129-21637599 (-) // 95.92 // q13		-0.75	0.004	---
1391442_at	Ehd3	Rn.7771	chr6:21638134-21638721 (-) // 79.88 // q13		-0.60	0.021	EH-domain containing 3
1392730_at	---	Rn.204638	chr6:24097935-24098520 (-) // 96.06 // q13		0.77	0.012	---
1393848_at	Rrm2	Rn.144946	chr6:42357756-42358068 (+) // 99.36 //		1.10	0.000	ribonucleotide reductase M2

			q16 /// chr6:42355082-42355497 (+) // 99.36 // q16 /// chr19:25563985-25564297 (-) // 99.36 // q11				
1389408_at	Rrm2	Rn.144946	chr6:42358769-42359312 (+) // 75.98 // q16 /// chr6:42356188-42356731 (+) // 73.84 // q16 /// chr19:25562741-25563284 (-) // 73.67 // q11 /// chr19:25560608-25561151 (-) // 73.84 // q11		0.71	0.008	ribonucleotide reductase M2
1396114_at	---	Rn.211596	chr6:79928608-79929218 (-) // 89.58 // q23		0.66	0.018	---
1395338_at	Lrpprc	Rn.92051	chr6:8151162-8156660 (-) // 89.88 // q12		0.80	0.009	leucine-rich PPR-motif containing
1397205_at	Dhrs7	Rn.119024	chr6:95005646-95006263 (-) // 85.26 // q24		-1.00	0.001	dehydrogenase/reductase (SDR family) member 7
1387402	Myh9	Rn.113	chr7:115681		0.6	0.042	myosin, heavy

_at		85	460-115760836 (-) // 99.19 // q34		2		chain 9, non-muscle
1367937_at	Miox	Rn.19959	chr7:127632434-127634935 (+) // 94.04 // q34		-0.81	0.005	myo-inositol oxygenase
1368467_at	Cyp4f1	Rn.5722	chr7:13589661-13600729 (-) // 98.89 // q11		-0.75	0.006	cytochrome P450, family 4, subfamily f, polypeptide 1
1376084_a_at	Espl1	Rn.135286	chr7:141072935-141074383 (+) // 98.54 // q36		0.63	0.019	extra spindle poles like 1 (S. cerevisiae)
1381482_at	---	Rn.166635	chr7:142102412-142102796 (+) // 60.75 // q36		0.73	0.008	---
1368337_at	Glycam1	Rn.10939	chr7:142455641-142457903 (-) // 96.69 // q36		0.61	0.050	glycosylation dependent cell adhesion molecule 1
1369203_at	Wif1	Rn.74256	chr7:60330516-60400696 (+) // 98.72 // q22		-0.66	0.012	Wnt inhibitory factor 1
1397704_at	LOC691979	Rn.145486	chr7:68106108-68106720 (-) // 39.21 // q22 /// chr15:45238650-45239262 (-) // 43.33 // p12 /// chr15:55996223-		0.55	0.044	similar to N-acetyltransferase ESCO2 (Establishment of cohesion 1 homolog 2) (ECO1 homolog 2)

			55996835 (-) // 39.21 // q11				
1384063_at	Cthrc1	Rn.9468	chr7:74637755-74640321 (+) // 94.1 // q22		0.79	0.008	collagen triple helix repeat containing 1
1376105_at	Col14a1	Rn.99441	chr7:92032161-92032967 (+) // 99.88 // q32		0.73	0.018	collagen, type XIV, alpha 1
1374775_at	Mki67	Rn.73551	chr7:92485651-92486249 (+) // 93.9 // q32 /// chrX:93998874-93999473 (+) // 93.58 // q31 /// chr18:39143050-39150353 (+) // 93.26 // q11 /// chr1:195310031-195313257 (-) // 96.47 // q41 /// chr2:130883075-130883673 (-) // 92.94 // q26 /// chr17:96790831-9		0.55	0.049	antigen identified by monoclonal antibody Ki-67
1384183_at	---	Rn.39381	chr8:125480208-125480639 (+) // 87.05 // q32		-0.62	0.032	---
1387742	Ccr2	Rn.211	chr8:128892		0.7	0.012	chemokine (C-C

_at		983	783-128893905 (+) // 99.91 // q32		9		motif) receptor 2
1369290_at	Ccr5	Rn.10736	chr8:128907156-128911211 (+) // 96.84 // q32		0.70	0.017	chemokine (C-C motif) receptor 5
1373026_at	Spc24	Rn.162984	chr8:20854253-20859032 (-) // 98.28 // q13		0.57	0.039	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)
1387703_a_at	Usp2	Rn.203590	chr8:47052084-47076289 (+) // 97.9 // q22		-0.60	0.016	ubiquitin specific peptidase 2
1375549_at	---	Rn.168987	chr8:47076382-47077631 (+) // 98.26 // q22		-0.69	0.006	---
1381811_at	---	Rn.92548	chr8:47077615-47077945 (+) // 99.1 // q22		-0.80	0.003	---
1367570_at	Tagln	Rn.34397	chr8:48901875-48907693 (-) // 92.93 // q22		0.64	0.018	transgelin
1397225_at	---	Rn.170224	chr8:51926554-51927008 (-) // 70.11 // q23		-0.85	0.006	---
1380306_at	---	Rn.54177	chr8:51928782-51929247 (-) // 85.07 // q23		-0.75	0.004	---
1392613	---	Rn.166	chr8:519292		-	0.005	---

_at		664	65-51930063 (-) // 90.78 // q23		0.83		
1391063_at	Kif23	Rn.63734	chr8:66050159-66050549 (-) // 100.0 // q24		0.57	0.044	kinesin family member 23
1388340_at	Ns5atp9	Rn.7233	chr8:70159233-70172540 (+) // 91.76 // q24		0.64	0.021	NS5A (hepatitis C virus) transactivated protein 9
1370955_at	Adam10	Rn.42924	chr8:75288633-75291137 (+) // 40.88 // q24 /// chr8:75202774-75233710 (-) // 58.33 // q24		0.98	0.001	ADAM metallopeptidase domain 10
1372523_at	Gclc	Rn.8365	chr8:82762176-82762995 (+) // 100.0 // q31		-0.65	0.020	glutamate-cysteine ligase, catalytic subunit
1368180_s_at	Gsta2 /// LOC494499	Rn.40574	chr8:83299323-83310573 (-) // 85.77 // q31		-0.73	0.006	glutathione S-transferase A2 /// LOC494499 protein
1379448_at	Ttk	Rn.107533	chr8:88942279-88944612 (+) // 75.4 // q31		0.71	0.009	Ttk protein kinase
1394940_at	Fam46a	Rn.788	chr8:90503236-90505323 (-) // 98.69 // q31		1.59	0.000	family with sequence similarity 46, member A
1392685_at	Ube2cbp	Rn.205206	chr8:91537317-		-0.5	0.034	ubiquitin-conjugating

			91537978 (-) // 99.39 // q31		4		enzyme E2C binding protein
1379747_at	Prss35	Rn.161916	chr8:92024143-92024661 (-) // 97.35 // q31		-2.85	0.000	Protease, serine, 35
1392727_at	RGD1307365	Rn.55758	chr8:92448321-92448938 (-) // 80.1 // q31		-0.53	0.046	similar to KIAA1009 protein
1384370_at	Mthfs	Rn.2215	chr8:94058362-94062777 (+) // 91.68 // q31		0.70	0.009	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
1381768_at	Mthfs	Rn.2215	chr8:94105901-94106254 (+) // 99.43 // q31		1.09	0.000	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
1392719_at	Mthfs	Rn.2215	chr8:94107662-94108310 (+) // 67.44 // q31		0.79	0.005	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)
1380508_at	---	Rn.64342	chr8:95003665-95004012 (-) // 83.82 // q31		0.67	0.013	---
1387672_at	Gnmt	Rn.11142	chr9:10127076-10130446 (+) // 97.95 // q12		-0.59	0.020	glycine N-methyltransferase
1391378_at	---	Rn.211524	chr9:110446091-110446436		-0.65	0.029	---

			(+) // 39.39 // q38				
1392702_at	---	---	chr9:112684763-112685036 (+) // 35.36 // q38		0.62	0.018	---
1368236_at	Mep1a	Rn.16265	chr9:13170761-13201094 (+) // 99.39 // q12		-1.04	0.000	meprin 1 alpha
1385889_at	RGD1565095	Rn.3412	chr9:36363488-36364345 (+) // 14.21 // q21		0.59	0.045	Similar to hypothetical protein MGC52110
1383439_at	Npas2	Rn.8285	chr9:38433982-38434350 (+) // 95.09 // q21		-0.58	0.030	neuronal PAS domain protein 2
1396055_at	Col6a3	Rn.219672	chr9:89975177-89978276 (-) // 99.63 // q35		0.60	0.045	procollagen, type VI, alpha 3
1368984_at	Sept2	Rn.98570	chr9:92768693-92787764 (+) // 96.62 // q36 /// chr15:49005566-49007307 (+) // 90.21 // p11		0.61	0.044	septin 2
1375422_at	---	---	chrUn:433789-434708 (-) // 69.37 // /// chrUn:427660-428579 (-) // 69.47 // /// chrUn:482997-483915 (-) // 69.16 // ///		-1.22	0.000	---

			chrUn:23399826-23400740 (-) // 68.95 //				
1367712_at	Timp1	Rn.25754	chrX:12542480-12547161 (-) // 99.88 // q12		0.74	0.013	TIMP metallopeptidase inhibitor 1
1368627_at	Rgn	Rn.10006	chrX:13037172-13052846 (-) // 99.44 // q12		-0.94	0.001	regucalcin (senescence marker protein-30)
1384283_at	Asb9	Rn.22749	chrX:50712265-50720903 (-) // 95.32 // q21		-0.72	0.004	ankyrin repeat and SOCS box-containing 9
1387013_at	Tmem27	Rn.32298	chrX:51118662-51149768 (-) // 99.75 // q21		-0.78	0.005	transmembrane protein 27
1370728_at	Il13ra1	Rn.81210	chrX:8760956-8820529 (-) // 99.63 // q12 /// chr11:73147625-73148964 (-) // 99.7 // q22		0.61	0.039	interleukin 13 receptor, alpha 1

Supplemental Table S3. Boundaries of SS.13^{BN}-derived congenic lines newly defined by single nucleotide polymorphism (SNP) array. Flanking markers at each end of a congenic region are shown. Each SNP name contains rat genome version, chromosome number (chr. 13), and base pair location on chr. 13. The number of SNPs analyzed within each congenic region is also shown. The development and characterization of the congenic lines were described previously (Moreno 2007). See Supplemental Methods for details on the SNP array analysis.

SS.13^{BN}-derived congenic line	P-end SNP names	q-end SNP names	number of SNPs
Line 5	Rn34_13032726371-Rn34_13032797309	Rn34_13045299284-Rn34_13045797163	5443
Line 9	Rn34_13045299284-Rn34_13045797163	Rn34_13048606818-Rn34_13048990782	846
Line 26	Rn34_13066163425-Rn34_13066167690	Rn34_13079111404-Rn34_13079126162	4375

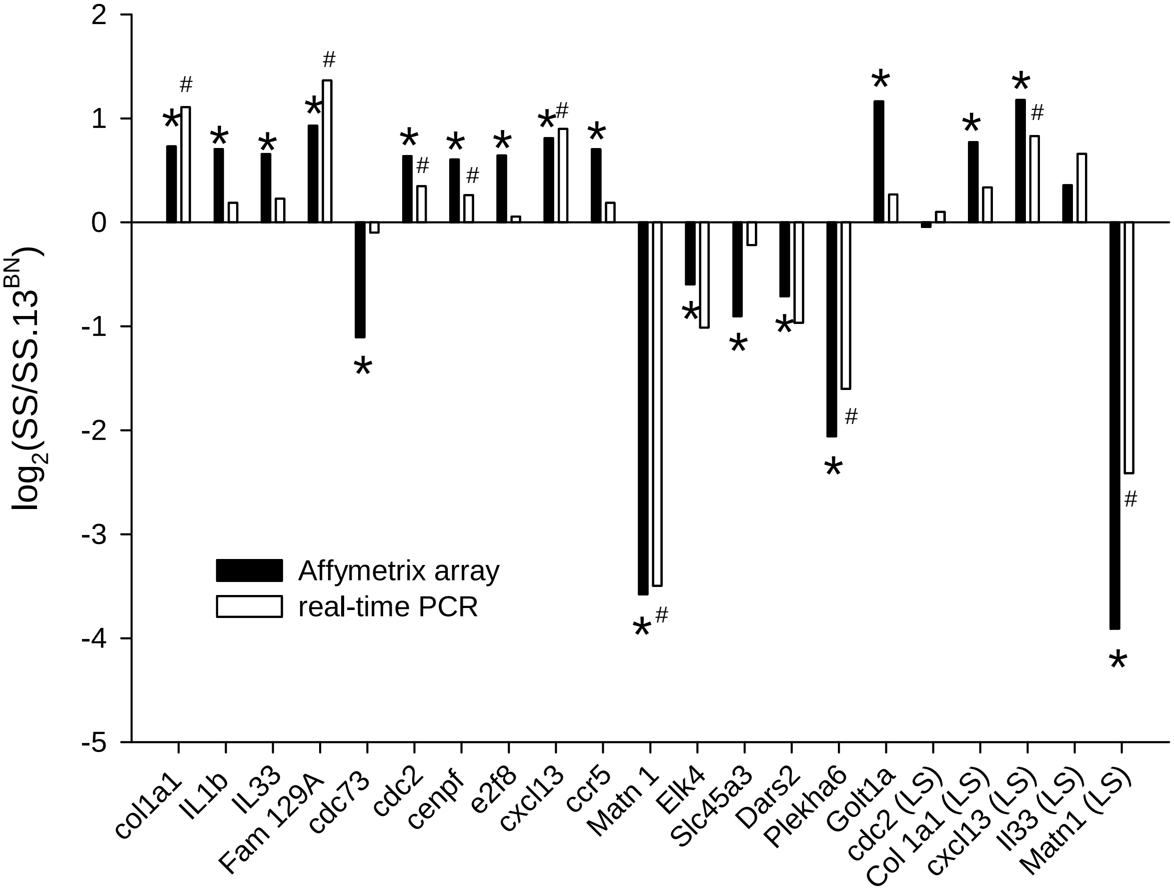
Supplemental Table S4. Top 10 canonical pathways identified by Ingenuity Pathway Analysis as highly represented in genes differentially expressed in mTALs between SS and SS.13^{BN} rats on each salt diet. Cxcr4, F5, Fcgr3a, Pla2g4a, and Ptgs2 are located on rat chr. 13.

Ingenuity Canonical Pathways	Molecules
0.4% salt	
Atherosclerosis Signaling	COL1A1,PLA2G4A,IL6,COL3A1,TNFRSF12A
IL-6 Signaling	COL1A1,IL6,TNFAIP6,A2M,HSPB1
Hepatic Fibrosis / Hepatic Stellate Cell Activation	COL1A1,CXCL3,TIMP1,IL6,A2M,COL3A1
Pathogenesis of Multiple Sclerosis	CCL4,CXCL11
IL-17 Signaling	TIMP1,PTGS2,IL6,CXCL11
LXR/RXR Activation	APOE,IL6,ABCA1
Arachidonic Acid Metabolism	PLA2G4A,CYP4A22,GPX2,PTGS2
Acute Phase Response Signaling	HMOX1,SERPING1,CP,IL6,A2M
Dendritic Cell Maturation	COL1A1,IL6,FCGR3A,COL3A1
Coagulation System	F5,A2M
8% salt for 7 days	
Hepatic Fibrosis / Hepatic Stellate Cell Activation	MET,COL1A2,COL1A1,CXCL3,CCR5,TIMP1,KDR,MYH9,IL1B,IL6,A2M
Mitotic Roles of Polo-Like Kinase	KIF23,null,ESPL1,HSP90AB1,CCNB2,CDK1,KIF11
Atherosclerosis Signaling	COL1A2,COL1A1,PLA2G4A,CXCR4,IL1B,IL6,CCR2
Cell Cycle: G2/M DNA Damage Checkpoint Regulation	null,TOP2A,CCNB2,CDK1
ATM Signaling	RAD51,null,CCNB2,CDK1
Sonic Hedgehog Signaling	PRKACB,null,CDK1
IL-6 Signaling	COL1A1,IKBKB,IL1B,IL6,A2M
IL-10 Signaling	IKBKB,CCR5,IL1B,IL6
Tyrosine Metabolism	HPD,BCKDHA,HGD,ADHFE1
Pentose and Glucuronate Interconversions	MIOX,AKR7A3,BCKDHA

Supplemental Table S5. Top KEGG pathways (posterior probability > 0.5) and top genes given pathways identified by the Bayesian model analysis of data from rats fed the 0.4% NaCl diet. The pathways and genes were identified as being best able to discriminate SS and SS.13^{BN} rats fed the 0.4% NaCl diet. See Methods for detail.

Pathway id	**Pathway name**	**Posterior Probability**	**Top 10 genes with posterior probability > 0.5 and in order of ranking**
hmr04010	MAPK signaling pathway	0.9988	Hras, Nras, Mapk3, Mapk1, Kras, Egfr, Pdgfra, Prkcb, Prkca, Mapk13
hmr04144	Endocytosis	0.9735	Igf1r, Hras, Egfr, Met, Pdgfra, Kdr, Src, Cblb, Flt1, Kit
hmr05200	Pathways in cancer	0.8224	Pik3r2, Pik3ca, Pik3r3, Hras, Pik3r1, Pik3cd, Igf1r, Egfr, Nras, Mapk3
hmr04080	Neuroactive ligand-receptor interaction	0.8137	Grm2, Gabbr1
hmr04062	Chemokine signaling pathway	0.6660	Gnai1, Pik3r3, Pik3r2, Pik3r1, Gnai2, Pik3ca, Gnai3, Pik3cd, Pik3cb, Mapk3
hmr04141	Protein processing in endoplasmic reticulum	0.6387	Mapk9, Mapk10
hmr04060	Cytokine-cytokine receptor interaction	0.6089	Egfr, Met, Pdgfra, Kdr, Flt1, Kit, Csf1r, Flt4, Il2rb, Figf
hmr04910	Insulin signaling pathway	0.5984	Pik3r1, Pik3r2, Pik3ca, Pik3r3, Pik3cd, Hras, Mapk1, Nras, Mapk3, Kras
hmr03013	RNA transport	0.5489	(none)

Supplemental Figure S1. Verification of Affymetrix Expression Array results by real-time PCR. Data were from rats fed the 8% salt diet except the ones labeled "LS". LS, 0.4% NaCl diet. N=4 for Affymetrix Array, n=10-12 for real-time PCR, *, significant differential expression between SS and SS.13^{BN} according to the array (see Methods for criteria), #, P<0.05 according to real-time PCR.



Supplemental Figure S2. Validation of the H3-P antibody staining procedure in cultured Hela cells. Hela cells were stained with DAPI (for nucleus staining) and the H3-P antibody used to stain kidney tissues. See Methods for details.