

Table S5. eQTLs that were detected in common to all tissues by the SBR model (FDR <5%). The results from the Bayesian modeling are from the best model visited (see Materials and Methods). For the probe sets, we determined which eQTLs were regulated in *cis* or *trans* by defining *cis*-eQTLs as those with a peak of linkage within 10 Mbp of the physical location of the probe set. We also report the R^2 for the best SBR model visited within each tissue. For comparison with the single tissue SBR model, we report the results from the QTL Reaper, SSM, SBMR and Hotelling's T^2 -test analyses using the same FDR cut-off of 5%, and use "Y" or "N" to indicate whether the shared eQTL was commonly detected or missed, respectively.

Probe identifier	Gene symbol	Gene name	Transcript chromosome	Transcript physical position (Mb)	Genetic marker at peak of linkage	Marker chromosome	Marker physical position (Mb)	<i>cis/trans</i>	Marker/transcript distance (Mb)	R^2 for the best model				SSM (FDR < 5%)	eQTL Reaper (FDR < 5%)	SBMR (FDR < 5%)	Hotelling's T^2 test (FDR < 5%)
										FAT	KIDNEY	ADRENAL	HEART				
1376249_at	<i>Fuca2</i>	plasma alpha-L-fucosidase precursor	1	8.30	<i>D1Ra1327</i>	1	8.21	<i>cis</i>	0.09	73%	86%	88%	89%	Y	Y	Y	Y
1389650_at	--	--	1	135.87	<i>D1Ra142</i>	1	135.50	<i>cis</i>	0.37	83%	81%	63%	88%	Y	Y	Y	Y
1376780_at	<i>RGD1310022</i>	similar to RIKEN cDNA 2610204K14	1	137.98	<i>D1Cebr103s1</i>	1	135.50	<i>cis</i>	2.49	91%	94%	74%	94%	N	N	Y	Y
1370334_at	<i>Plekhh1</i>	pleckstrin homology domain containing, family B (evectins) member 1	1	158.09	<i>D1Ra147</i>	1	158.59	<i>cis</i>	0.50	54%	57%	50%	66%	N	N	N	Y
1374907_at	--	--	1	158.32	<i>D1Ra147</i>	1	158.59	<i>cis</i>	0.27	90%	88%	55%	52%	N	N	Y	Y
1375664_at	--	--	1	182.05	<i>Sonn1g</i>	1	175.73	<i>cis</i>	6.33	87%	94%	96%	93%	Y	Y	Y	Y
1372846_at	<i>Cybas3</i>	cytochrome b, ascorbate dependent 3	1	213.07	<i>D1Ra1293</i>	1	213.04	<i>cis</i>	0.03	69%	78%	96%	75%	Y	Y	Y	Y
1374960_at	<i>RGD1564887_predicted</i>	similar to R13011E15Rik protein (predicted)	1	251.07	<i>D1Ra181</i>	1	250.38	<i>cis</i>	0.69	94%	67%	65%	57%	Y	N	Y	Y
1370114_a_at	<i>LOC497750</i>	phosphatidylinositol 3-kinase	2	32.61	<i>D2Ra194</i>	2	31.10	<i>cis</i>	1.50	94%	65%	57%	64%	N	N	N	Y
1371776_at	<i>Pik3r1</i>	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide 1	2	32.61	<i>D2Ra194</i>	2	31.10	<i>cis</i>	1.51	94%	94%	94%	92%	N	N	Y	Y
1373389_at	<i>Aca09</i>	acyl-CoA dehydrogenase 9	2	122.57	<i>D2Mit7</i>	2	114.72	<i>cis</i>	7.86	82%	73%	85%	81%	Y	Y	Y	N
1374006_at	<i>Kat3</i>	kynurenine aminotransferase III	2	240.85	<i>D2Ra166</i>	2	241.76	<i>cis</i>	0.91	77%	78%	71%	89%	Y	Y	Y	Y
1388912_at	<i>Rexo4</i>	XPMC2 prevents mitotic catastrophe 2 homolog	3	5.85	<i>D3Cebr204s4</i>	3	5.00	<i>cis</i>	0.85	90%	92%	88%	86%	Y	Y	Y	Y
1389816_at	<i>Endog</i>	endonuclease G	3	9.19	<i>D3Cebr204s4</i>	3	5.00	<i>cis</i>	4.19	78%	92%	60%	92%	Y	Y	Y	Y
1373537_at	--	--	3	10.09	<i>D3Cebr26s1</i>	3	10.21	<i>cis</i>	0.12	75%	83%	53%	61%	N	N	Y	Y
1375687_at	<i>Rab14</i>	Ras-related protein Rab-14	3	14.24	<i>D3Ra153</i>	3	13.01	<i>cis</i>	1.23	85%	79%	81%	84%	Y	Y	Y	Y
1376796_at	<i>Rab14</i>	Ras-related protein Rab-14	3	14.24	<i>D3Ra153</i>	3	13.01	<i>cis</i>	1.24	79%	71%	99%	84%	Y	N	Y	Y
1385314_at	<i>Rab14</i>	Ras-related protein Rab-14	3	14.24	<i>D3Ra153</i>	3	13.01	<i>cis</i>	1.24	89%	81%	91%	95%	Y	Y	Y	Y
1375676_at	--	--	3	95.34	<i>D3Ra166</i>	3	101.26	<i>cis</i>	5.92	89%	86%	88%	77%	Y	Y	Y	Y
1374921_at	<i>Rtel1</i>	Rtel1 protein	3	170.50	<i>Ecn3</i>	3	166.49	<i>cis</i>	4.00	95%	91%	90%	82%	Y	Y	Y	Y
1367689_a_at	<i>Cd36</i>	Cd36 antigen	4	13.51	<i>Cd36</i>	4	13.51	<i>cis</i>	0.00	76%	81%	70%	71%	Y	Y	Y	Y
1386901_at	<i>Cd36</i>	Cd36 antigen	4	13.51	<i>Cd36</i>	4	13.51	<i>cis</i>	0.00	97%	88%	93%	88%	Y	Y	Y	Y
1375724_at	<i>Glcet1</i>	glucocorticoid induced transcript 1	4	33.66	<i>D4Utr3</i>	4	34.41	<i>cis</i>	0.75	76%	63%	71%	78%	N	Y	Y	Y
1370906_at	<i>Riscat</i>	all-trans-retinol 13,14-reductase precursor	4	106.10	<i>D4Ra135</i>	4	91.58	<i>trans</i>	14.52	62%	85%	84%	98%	Y	Y	Y	Y
1371996_at	--	--	4	117.56	<i>D4Ra149</i>	4	119.52	<i>cis</i>	1.97	64%	68%	74%	77%	Y	N	Y	Y
1369415_at	<i>Bhlhb2</i>	basic helix-loop-helix family, member e40	4	144.14	<i>D4Ra1240</i>	4	148.25	<i>cis</i>	4.11	50%	73%	64%	73%	N	N	Y	Y
1390284_at	<i>Ccdc77</i>	coiled-coil domain containing 77	4	156.71	<i>D4Utr4</i>	4	160.25	<i>cis</i>	3.54	78%	67%	74%	54%	N	N	Y	Y
1373440_at	--	--	5	49.10	<i>D5Ra16</i>	5	52.53	<i>cis</i>	3.44	63%	70%	74%	65%	Y	Y	Y	Y
1374527_at	<i>Echdc2</i>	enoyl Coenzyme A hydratase domain containing 2	5	129.28	<i>D5Ra179</i>	5	156.50	<i>trans</i>	27.22	68%	63%	69%	62%	N	N	Y	Y
1371960_at	--	--	5	151.06	<i>D5Ra138</i>	5	149.77	<i>cis</i>	1.30	94%	66%	92%	96%	N	N	Y	Y
1372475_at	<i>Pink1</i>	PTEN induced putative kinase 1	5	157.09	<i>D6Mit3</i>	8	45.30	<i>trans</i>	--	85%	91%	88%	97%	N	N	N	N
1392720_at	--	--	7	13.11	<i>D7Mit17</i>	7	13.08	<i>cis</i>	0.04	80%	76%	68%	61%	Y	N	Y	Y
1382778_at	<i>Dusp6</i>	dual specificity phosphatase 6	7	36.90	<i>D7Utr1</i>	7	23.79	<i>trans</i>	13.10	92%	52%	54%	94%	N	N	Y	Y
1384717_at	<i>Ddef1_predicted</i>	130 kDa ARF1 GTPase-activating protein	7	101.49	<i>D7Ra177</i>	7	100.29	<i>cis</i>	1.19	94%	93%	88%	85%	Y	Y	Y	N
1386941_at	<i>Plec1</i>	plectin 1	7	114.22	<i>D7Cebr77s1</i>	7	114.49	<i>cis</i>	0.27	60%	53%	59%	55%	N	N	Y	Y
1376091_at	<i>Adsl</i>	adenylosuccinate lyase	7	119.24	<i>D7Ra1129</i>	7	119.20	<i>cis</i>	0.04	52%	63%	54%	78%	N	N	Y	Y
1372805_at	--	--	8	11.15	<i>D8Utr3</i>	8	8.94	<i>cis</i>	2.21	58%	72%	73%	74%	Y	N	Y	Y
1380286_x_at	<i>RGD1311723</i>	similar to KIAA1731 protein	8	12.11	<i>D8Utr3</i>	8	8.94	<i>cis</i>	3.17	82%	87%	80%	75%	Y	Y	Y	Y
1398460_at	<i>RGD1311723_predicted</i>	similar to KIAA1731 protein (predicted)	8	12.12	<i>D8Ra156</i>	8	8.30	<i>cis</i>	3.82	95%	77%	76%	72%	Y	Y	Y	Y
1377501_at	<i>Zfp75</i>	zinc finger protein 75	8	18.08	<i>D8Ra168</i>	8	19.46	<i>cis</i>	1.38	79%	66%	64%	72%	Y	N	Y	Y
1388366_at	<i>Mprl4</i>	mitochondrial ribosomal protein L4	8	20.03	<i>D8Ra168</i>	8	19.46	<i>cis</i>	0.57	94%	97%	96%	90%	Y	Y	Y	Y
1387366_at	<i>Ilf3</i>	Interleukin enhancer-binding factor 3	8	20.50	<i>D8Ra168</i>	8	19.46	<i>cis</i>	1.03	93%	96%	96%	97%	Y	Y	Y	Y
1374583_at	<i>Dcps</i>	decapping enzyme, scavenger	8	34.90	<i>Es6</i>	8	32.40	<i>cis</i>	2.50	97%	97%	98%	98%	Y	Y	Y	N
1374485_at	--	--	8	45.98	<i>Grik4</i>	8	45.77	<i>cis</i>	0.21	45%	52%	72%	48%	N	N	Y	Y
1371442_at	<i>Hyou1</i>	hypoxia up-regulated protein 1 precursor	8	47.35	<i>D8Cebr81s4</i>	8	40.26	<i>cis</i>	7.09	64%	74%	95%	90%	N	Y	Y	Y
1377452_at	<i>Clec3b</i>	C-type lectin domain family 3, member B	8	127.91	<i>D8Cebr16s5</i>	8	124.95	<i>cis</i>	2.96	88%	83%	53%	83%	N	N	Y	Y
1387376_at	<i>Aox1</i>	aldehyde oxidase	9	56.73	<i>D9Ra193</i>	9	59.61	<i>cis</i>	2.88	79%	91%	60%	72%	Y	N	Y	Y
1370176_at	<i>Trak2</i>	trafficking kinesin-binding protein 2	9	57.48	<i>D9Ra119</i>	9	59.61	<i>cis</i>	2.13	85%	57%	74%	94%	N	N	Y	Y
1374196_at	<i>Lancl1</i>	lanC-like protein 1	9	65.81	<i>Cryga</i>	9	65.28	<i>cis</i>	0.54	83%	97%	71%	95%	Y	Y	Y	Y
1389334_at	<i>Ndufa10</i>	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 1	9	91.66	<i>D9Ra15</i>	9	85.37	<i>cis</i>	6.29	95%	49%	51%	50%	N	N	Y	Y
1370705_at	<i>Zfp597</i>	zinc finger protein HIT-4	10	11.92	<i>D10Utr3</i>	10	9.09	<i>cis</i>	2.83	62%	85%	96%	59%	Y	N	Y	Y
1398910_at	<i>Stub1</i>	STIP1 homology and U-box containing protein 1	10	15.10	<i>D10Mit6</i>	10	14.72	<i>cis</i>	0.38	55%	59%	45%	65%	N	N	Y	Y
1375519_at	<i>LOC287167</i>	globin, alpha	10	15.56	<i>D10Mit6</i>	10	14.72	<i>cis</i>	0.84	88%	51%	60%	81%	N	N	Y	Y
1373417_at	<i>Piscr3</i>	phospholipid scramblase 3	10	56.69	<i>D10Wox13</i>	10	55.87	<i>cis</i>	0.82	79%	68%	73%	63%	Y	N	Y	Y
1370930_at	--	--	10	57.62	<i>D10Wox13</i>	10	55.87	<i>cis</i>	1.76	78%	79%	75%	70%	Y	Y	Y	Y
1374888_at	<i>Ccdc49</i>	coiled-coil domain containing 49 (predicted)	10	86.49	<i>D10Ra145</i>	10	84.92	<i>cis</i>	1.57	93%	81%	66%	80%	Y	Y	Y	N
1379896_at	<i>Ddx42</i>	ATP-dependent RNA helicase DDX42	10	95.63	<i>D10Utr2</i>	10	96.24	<i>cis</i>	0.62	69%	79%	75%	66%	Y	Y	Y	Y
1389935_at	<i>RGD1309310_predicted</i>	similar to mKIAA0195 protein	10	105.90	<i>D10Cebr39s1</i>	10	76.77	<i>trans</i>	29.13	51%	67%	83%	81%	N	N	Y	Y
1390364_at	--	--	11	32.73	<i>D11Mit2</i>	11	30.89	<i>cis</i>	1.84	85%	70%	66%	75%	Y	Y	Y	Y
1372438_at	<i>Nil2</i>	nitrilase family, member 2	11	44.29	<i>D11Ra17</i>	11	46.56	<i>cis</i>	2.26	67%	70%	63%	93%	Y	Y	Y	Y
1376840_at	--	--	12	9.67	<i>D12Cebr97s9</i>	12	5.40	<i>cis</i>	4.27	75%	93%	84%	86%	Y	Y	Y	Y
1377244_at	<i>Zfp95</i>	zinc finger with KRAB and SCAN domains 5	12	9.70	<i>D12Cebr97s9</i>	12	5.40	<i>cis</i>	4.30	76%	68%	47%	80%	N	N	Y	Y
1376550_at	--	--	12	13.17	<i>D12Mit5</i>	12	12.80	<i>cis</i>	0.37	93%	73%	61%	65%	Y	Y	Y	Y
1371905_at	<i>MGC94190</i>	similar to 0610007L01Rik protein	12	27.48	<i>D12Mit7</i>	12	17.76	<i>cis</i>	9.72	79%	84%	80%	72%	Y	Y	Y	Y
1373682_at	<i>DDX51</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	12	46.16	<i>D12Ra120</i>	12	44.12	<i>cis</i>	2.04	63%	79%	58%	72%	Y	Y	Y	Y
1370815_at	<i>Nefh</i>	Neurofilament heavy polypeptide	14	85.60	<i>D14Utr1</i>	14	77.70	<i>cis</i>	7.89	72%	73%	54%	73%	N	N	Y	Y
1388654_at	<i>RGD:1309297</i>	mitochondrial ribosomal protein L52 (predicted)	15	32.49	<i>D15Ra16</i>	15	32.65	<i>cis</i>	0.16	97%	92%	99%	96%	Y	Y	Y	Y
1390435_at	<i>RGD1307583_predicted</i>	LOC361111 (predicted)	16	6.56	<i>D16Mit2</i>	16	4.30	<i>cis</i>	2.25	72%	56%	64%	72%	Y	Y	Y	Y
1376732_at	<i>Cair3</i>	calreticulin 3	16	17.83	<i>D16Utr1</i>	16	16.19	<i>cis</i>	1.63	66%	59%	79%	89%	Y	Y	Y	Y
1388908_at	<i>Ap1m1</i>	adaptor-related protein complex 1, mu 1 subunit	16	18.03	<i>D16Utr1</i>	16	16.19	<i>cis</i>	1.83	92%	84%	92%	93%	Y	Y	Y	Y
1389793_at	--	--	16	20.00	<i>D16Utr1</i>	16	16.19	<i>cis</i>	3.81	89%	77%	83%	78%	Y	Y	Y	Y
1389722_at	--	--	16	62.67	<i>D16Ra160</i>	16	64.08	<i>cis</i>	1.41	75%	55%	89%	62%	N	N	Y	Y
1375315_at	<i>Ai316807</i>	expressed sequence AI316807	16	74.19	<i>D16Ra134</i>	16	72.65	<i>cis</i>	1.53	62%	70%	79%	77%	N	N	Y	N
1388903_a_at	<i>Hbid2</i>	Iron-sulfur cluster assembly 1 homolog, mitochondrial precursor	17	10.62	<i>D17Uic2</i>	17	14.57	<i>cis</i>	3.75	70%	65%	59%	85%	N	N	Y	N
1383293_at	<i>Ogn_predicted</i>	osteo glycin	17	20.98													