

Supplement – Gene Expression and Genetic Variation in Human Atria

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Supplemental Methods and Results

False Discovery Rate Estimated by Permutation Test

We employed an empirical false discovery rate (FDR) to account multiple testing and the linkage disequilibrium between SNPs and co-expression between genes.² At each permutation, the sample labels of gene expression were randomized, and then we tested their association with genetic variations. FDR was estimated as the ratio of average number of associations from the permuted samples to the actual number of associations in the real data.² A total of 1,000 permutations were performed to obtain stable FDR estimation, and the significance was claimed for the association with an FDR less than 5%. FDR was estimated separately for *cis*-eQTLs and *trans*-eQTLs. The association analysis was performed using linear regression function from GNU Scientific Library (<http://www.gnu.org/software/gsl/>) and validated using R software package (www.r-project.org/).

qPCR Confirmation

For DNA extraction, the tissues were digested in 200ul DirectPCR solution (VIAGEN Biotech Inc, Los Angeles, CA) containing about 80 ug of Proteinase K followed by phenol:chloroform:isoamyl alcohol extraction and ethanol precipitation. The region containing rs3740293 was amplified by standard PCR reaction. The band of the appropriate size was excised, the gel was extracted and then sequenced by Sanger sequencing.

For RNA extraction, the tissues were homogenized in 1 ml of TRIZOL[®] Reagent (Life Technologies, Carlsbad, CA) after addition of chloroform. The centrifugation aqueous phase was then collected, and mixed with an equal amount of 100% ethanol and purified on the RNeasy column according manufacturer's instructions. The reverse transcription reaction was

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performed using iScript kit (Bio-Rad Laboratories, Hercules, CA) according to manufacturer's instructions. We then performed qPCR using iTaq SYBR-green reagent (Bio-Rad) on CFX384 Real-Time System. Conditions for qPCR were 50°C for 2 min, 95°C for 10 min, 95°C for 15 sec, 60°C for 1 min (last two steps was repeated for 40 times). Cq values were exported and relative expression was calculated. Each experiment was replicated with three different pairs of primers for *MYOZ1* and two different pairs of primers for *SYNPO2L*. The primer sequences are listed in **Supplemental Table 6**.

Differential Gene Expression for Heart Failure and AF

We also compared the differential gene expression in participants with and without heart failure separately in LA and RA tissues. Three genes were differentially expressed in LA (**Supplemental Table 7a**), and 16 genes were differentially expressed in RA (**Supplemental Table 7b**). However, none of the differentially expressed genes were shared between LA and RA tissues. We also compared the differential gene expression in participants with and without AF. The analysis of differential expression did not identify any significant gene in LA. Only two genes, *PPM1H* ($P=1.6 \times 10^{-6}$) and *DEXI* ($P=2.5 \times 10^{-6}$) were found to be under-expressed in RA in the participants with AF, and no genes were over-expressed. The lack of significant genes might be attributable to the small number of samples had history of AF or without HF, which might result in the lack of power to identify differentially expressed genes consistently (**Supplemental Table 8**).

We then performed additional analysis by limiting samples with history of AF. As shown in the **Supplemental Table 9**, the most significant differentially expressed gene was *IL10* ($P=3.0 \times 10^{-4}$),

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which did not reach the Bonferroni P-value cutoff ($P=4.2 \times 10^{-6}$), probably due to that only 9 out of 64 samples had history of AF.

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Table 1a. Over-expressed transcripts in left atrial tissues (LA)

ID	Gene Symbol	Left Atrium		Right Atrium		P value of two-sided t-test
		Average Expression [§]	SD	Average Expression [§]	SD	
201272_at	<i>AKR1B1</i>	9.81	0.37	9.29	0.26	6.0x10 ⁻¹³
210372_s_at	<i>TPD52L1</i>	6.21	0.37	5.65	0.33	7.6x10 ⁻¹³
204776_at	<i>THBS4</i>	8.73	0.69	7.72	0.67	9.4x10 ⁻¹²
207558_s_at	<i>PITX2</i>	4.00	0.30	3.62	0.20	1.7x10 ⁻¹¹
219719_at	<i>HIGD1B</i>	7.44	0.24	7.10	0.25	2.6x10 ⁻¹⁰
203786_s_at	<i>TPD52L1</i>	8.57	0.39	8.08	0.32	2.6x10 ⁻¹⁰
208335_s_at	<i>DARC</i>	7.61	0.46	7.01	0.44	5.0x10 ⁻¹⁰
203700_s_at	<i>DIO2</i>	5.66	0.21	5.39	0.19	5.3x10 ⁻¹⁰
209047_at	<i>AQP1</i>	9.29	0.28	8.92	0.29	1.2x10 ⁻⁹
206768_at	<i>RPL3L</i>	8.05	0.29	7.67	0.31	2.2x10 ⁻⁹
204174_at	<i>ALOX5AP</i>	7.28	0.30	6.92	0.28	7.1x10 ⁻⁹
219728_at	<i>MYOT</i>	7.43	1.14	6.36	0.57	3.9x10 ⁻⁸
210299_s_at	<i>FHL1</i>	8.62	0.44	8.16	0.38	7.6x10 ⁻⁸
218856_at	<i>TNFRSF21</i>	7.25	0.30	6.88	0.34	7.6x10 ⁻⁸
204606_at	<i>CCL21</i>	7.24	0.33	6.91	0.24	1.1x10 ⁻⁷
214505_s_at	<i>FHL1</i>	10.30	0.47	9.77	0.48	1.5x10 ⁻⁷
206637_at	<i>P2RY14</i>	4.35	0.52	3.89	0.24	1.6x10 ⁻⁷
218412_s_at	<i>GTF2IRD1</i>	6.89	0.18	6.71	0.15	3.0x10 ⁻⁷
217014_s_at	<i>AZGP1</i>	7.14	0.32	6.82	0.28	3.1x10 ⁻⁷
217848_s_at	<i>PPA1</i>	9.54	0.31	9.21	0.30	4.4x10 ⁻⁷
212793_at	<i>DAAM2</i>	6.66	0.19	6.46	0.20	6.5x10 ⁻⁷
204482_at	<i>CLDN5</i>	7.13	0.25	6.86	0.27	6.9x10 ⁻⁷

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201539_s_at	<i>FHL1</i>	8.93	0.56	8.35	0.57	8.2X10 ⁻⁷
218966_at	<i>MYO5C</i>	7.39	0.29	7.14	0.20	1.1X10 ⁻⁶
215177_s_at	<i>ITGA6</i>	7.53	0.25	7.28	0.25	1.2X10 ⁻⁶
209309_at	<i>AZGP1</i>	5.11	0.49	4.67	0.38	1.3X10 ⁻⁶
203548_s_at	<i>LPL</i>	9.51	0.72	8.75	0.80	1.3X10 ⁻⁶
203549_s_at	<i>LPL</i>	10.41	0.65	9.73	0.70	1.6X10 ⁻⁶
205226_at	<i>PDGFRL</i>	6.21	0.46	5.75	0.46	1.8X10 ⁻⁶
211113_s_at	<i>ABCG1</i>	6.37	0.17	6.20	0.16	2.4X10 ⁻⁶
206227_at	<i>CILP</i>	7.87	0.41	7.49	0.39	3.1X10 ⁻⁶
205257_s_at	<i>AMPH</i>	6.61	0.33	6.31	0.29	3.7X10 ⁻⁶
209924_at	<i>CCL18</i>	7.29	0.69	6.70	0.54	3.9X10 ⁻⁶

⁵Average expression represents the mean expression of the transcript across all studied samples. It was calculated by summarizing signals from all the probes on the Affymetrix GeneChip Human Genome U133A Array that targeted the transcript using RMA algorithm.³ The signal intensity from the probes was further log2 transformed. Higher values indicate higher expression for the same transcript.

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Supplemental Table 1. Over-expressed transcripts in right atrial tissues (RA)

Gene ID	Gene Symbol	Left Atrium		Right Atrium		P value of two-sided t-test
		Average Expression	SD	Average Expression	SD	
207069_s_at	<i>SMAD6</i>	7.12	0.33	7.77	0.32	2.3x10 ⁻¹⁷
220491_at	<i>HAMP</i>	7.68	0.77	9.35	0.91	4.0x10 ⁻¹⁷
204790_at	<i>SMAD7</i>	7.44	0.43	8.17	0.39	6.3X10 ⁻¹⁵
204811_s_at	<i>CACNA2D2</i>	7.18	0.34	7.79	0.39	1.0X10 ⁻¹³
219873_at	<i>COLEC11</i>	7.57	0.41	8.20	0.34	1.8X10 ⁻¹³
202912_at	<i>ADM</i>	8.42	0.49	9.15	0.42	1.2X10 ⁻¹²
211959_at	<i>IGFBP5</i>	10.49	0.42	11.13	0.41	3.1X10 ⁻¹²
213094_at	<i>GPR126</i>	4.84	0.34	5.43	0.42	3.5X10 ⁻¹²
208292_at	<i>BMP10</i>	6.81	0.80	8.21	1.01	4.3X10 ⁻¹²
203146_s_at	<i>GABBR1</i>	7.68	0.14	7.90	0.14	5.0X10 ⁻¹²
201565_s_at	<i>ID2</i>	7.64	0.46	8.30	0.42	9.3X10 ⁻¹²
205554_s_at	<i>DNASE1L3</i>	6.45	0.29	6.91	0.36	1.5X10 ⁻¹⁰
201809_s_at	<i>ENG</i>	9.13	0.40	9.64	0.33	2.0X10 ⁻¹⁰
206050_s_at	<i>RNH1</i>	8.69	0.21	8.99	0.23	7.5X10 ⁻¹⁰
211958_at	<i>IGFBP5</i>	7.56	0.32	8.04	0.40	1.5X10 ⁻⁹
205374_at	<i>SLN</i>	10.30	0.71	11.09	0.53	3.9X10 ⁻⁹
221933_at	<i>NLGN4X</i>	4.00	0.20	4.35	0.33	4.2X10 ⁻⁹
207016_s_at	<i>ALDH1A2</i>	7.79	0.35	8.23	0.36	5.4X10 ⁻⁹
203637_s_at	<i>MID1</i>	6.64	0.32	7.02	0.29	7.3X10 ⁻⁹
204099_at	<i>SMARCD3</i>	8.16	0.30	8.55	0.32	7.4X10 ⁻⁹
209291_at	<i>ID4</i>	6.44	0.51	7.08	0.53	7.7X10 ⁻⁹
202949_s_at	<i>FHL2</i>	9.28	0.70	10.05	0.54	8.1X10 ⁻⁹

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201042_at	<i>TGM2</i>	8.87	0.23	9.16	0.25	1.3X10 ⁻⁸
1007_s_at	<i>DDR1</i>	7.75	0.15	7.98	0.22	1.6X10 ⁻⁸
213135_at	<i>TIAM1</i>	5.32	0.35	5.74	0.36	1.8X10 ⁻⁸
201313_at	<i>ENO2</i>	6.45	0.26	6.79	0.30	1.8X10 ⁻⁸
210036_s_at	<i>KCNH2</i>	8.44	0.26	8.73	0.22	2.1X10 ⁻⁸
210095_s_at	<i>IGFBP3</i>	8.86	0.52	9.46	0.48	2.3X10 ⁻⁸
222020_s_at	<i>NTM</i>	4.94	0.19	5.24	0.30	2.9X10 ⁻⁸
213974_at	<i>ADAMTSL3</i>	6.41	0.34	6.82	0.37	4.9X10 ⁻⁸
204931_at	<i>TCF21</i>	5.95	0.31	6.34	0.37	5.4X10 ⁻⁸
212775_at	<i>OBSL1</i>	6.52	0.34	6.93	0.37	5.7X10 ⁻⁸
209292_at	<i>ID4</i>	4.28	0.38	4.77	0.47	8.1X10 ⁻⁸
209409_at	<i>GRB10</i>	8.25	0.35	8.60	0.27	8.1X10 ⁻⁸
203813_s_at	<i>SLIT3</i>	7.37	0.35	7.74	0.30	1.1X10 ⁻⁷
203636_at	<i>MID1</i>	6.96	0.23	7.23	0.25	1.1X10 ⁻⁷
203619_s_at	<i>FAIM2</i>	6.06	0.34	6.47	0.39	1.2X10 ⁻⁷
203886_s_at	<i>FBLN2</i>	7.89	0.35	8.25	0.31	1.6X10 ⁻⁷
207220_at	<i>ART4</i>	6.00	0.19	6.19	0.17	1.6X10 ⁻⁷
219985_at	<i>HS3ST3A1</i>	3.99	0.16	4.21	0.24	2.2X10 ⁻⁷
212922_s_at	<i>SMYD2</i>	7.97	0.66	8.63	0.54	2.2X10 ⁻⁷
203088_at	<i>FBLN5</i>	9.18	0.27	9.48	0.29	2.5X10 ⁻⁷
214928_at	<i>OBSL1</i>	7.28	0.26	7.61	0.35	2.5X10 ⁻⁷
201952_at	<i>ALCAM</i>	6.61	0.32	7.04	0.46	3.0X10 ⁻⁷
205990_s_at	<i>WNT5A</i>	4.87	0.14	5.05	0.19	3.3X10 ⁻⁷
205792_at	<i>WISP2</i>	7.19	0.41	7.63	0.41	3.6X10 ⁻⁷
209167_at	<i>GPM6B</i>	6.79	0.42	7.26	0.46	4.1X10 ⁻⁷
215813_s_at	<i>PTGS1</i>	6.47	0.30	6.77	0.29	5.2X10 ⁻⁷

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209469_at	<i>GPM6A</i>	4.19	0.13	4.34	0.16	5.3X10 ⁻⁷
205127_at	<i>PTGS1</i>	6.16	0.21	6.38	0.21	5.3X10 ⁻⁷
205984_at	<i>CRHBP</i>	5.92	0.23	6.20	0.29	5.7X10 ⁻⁷
206898_at	<i>CDH19</i>	7.49	0.45	7.95	0.46	6.5X10 ⁻⁷
212143_s_at	<i>IGFBP3</i>	8.33	0.49	8.85	0.52	6.7X10 ⁻⁷
59375_at	<i>MYO15B</i>	6.56	0.15	6.72	0.17	7.4X10 ⁻⁷
209170_s_at	<i>GPM6B</i>	5.86	0.34	6.27	0.45	7.7X10 ⁻⁷
203425_s_at	<i>IGFBP5</i>	6.52	0.26	6.80	0.29	7.7X10 ⁻⁷
206464_at	<i>BMX</i>	6.32	0.31	6.62	0.26	8.5X10 ⁻⁷
218162_at	<i>OLFML3</i>	8.00	0.28	8.27	0.24	1.0X10 ⁻⁶
200696_s_at	<i>GSN</i>	11.60	0.23	11.84	0.24	1.0X10 ⁻⁶
201005_at	<i>CD9</i>	9.07	0.35	9.39	0.29	1.2X10 ⁻⁶
207480_s_at	<i>MEIS2</i>	5.66	0.30	6.00	0.36	1.3X10 ⁻⁶
205934_at	<i>PLCL1</i>	5.63	0.38	5.99	0.34	1.4X10 ⁻⁶
207695_s_at	<i>IGSF1</i>	5.28	0.32	5.62	0.36	1.4X10 ⁻⁶
206070_s_at	<i>EPHA3</i>	5.03	0.32	5.36	0.35	1.5X10 ⁻⁶
213058_at	<i>TTC28</i>	6.56	0.16	6.72	0.15	1.6X10 ⁻⁶
213800_at	<i>CFH</i>	8.42	0.55	8.96	0.53	1.8X10 ⁻⁶
211276_at	<i>TCEAL2</i>	4.82	0.48	5.42	0.70	2.0X10 ⁻⁶
216836_s_at	<i>ERBB2</i>	8.06	0.23	8.30	0.27	2.3X10 ⁻⁶
204451_at	<i>FZD1</i>	6.78	0.26	7.04	0.28	2.3X10 ⁻⁶
205200_at	<i>CLEC3B</i>	8.29	0.62	8.83	0.47	2.4X10 ⁻⁶
206481_s_at	<i>LDB2</i>	8.10	0.36	8.41	0.28	2.5X10 ⁻⁶
205594_at	<i>ZNF652</i>	3.71	0.14	3.87	0.18	2.8X10 ⁻⁶
220415_at	<i>TNNI3K</i>	8.16	0.67	8.71	0.41	2.9X10 ⁻⁶
204345_at	<i>COL16A1</i>	6.22	0.24	6.48	0.29	2.9X10 ⁻⁶

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207826_s_at	<i>ID3</i>	7.23	0.33	7.52	0.28	3.3×10^{-6}
204396_s_at	<i>GRK5</i>	7.27	0.33	7.58	0.33	3.3×10^{-6}

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Supplemental Table 2. Comparison with top 20 differentially expressed genes reported in the previous study by Hsu, et al.¹ Nine of eleven genes available in the current study replicated ($P \leq 0.05$).

Gene ID	Hsu, et al. ¹		Current Study		Consistency*
	<i>P</i> value	Over Expressed Atrium	<i>P</i> value	Over Expressed Atrium	
<i>HAMP</i>	1.6×10^{-111}	Right	4.0×10^{-17}	Right	√
<i>BMP10</i>	1.4×10^{-96}	Right	4.3×10^{-12}	Right	√
<i>PITX2</i>	8.7×10^{-72}	Left	1.7×10^{-11}	Left	√
<i>C2orf14</i>	1.2×10^{-48}	Right			
<i>C19orf33</i>	2.7×10^{-39}	Left			
<i>LOC100144602</i>	1.3×10^{-33}	Left			
<i>MYL2</i>	5.1×10^{-33}	Left	2.8×10^{-3}	Left	√
<i>BDKRB1</i>	1.1×10^{-31}	Left			
<i>SALL1</i>	6.5×10^{-31}	Right	2.3×10^{-1}	Right	×
<i>DNASE1L3</i>	8.3×10^{-31}	Right	1.5×10^{-10}	Right	√
<i>KRT7</i>	1.5×10^{-30}	Left	1.3×10^{-1}	Left	×
<i>FAM84A</i>	5.7×10^{-30}	Right			
<i>IRX3</i>	3.8×10^{-29}	Right			
<i>THBS4</i>	2.6×10^{-27}	Left	9.4×10^{-12}	Left	√
<i>ANKRD30BL</i>	2.0×10^{-26}	Left			
<i>SYT4</i>	2.1×10^{-26}	Left			
<i>ALOX15</i>	2.1×10^{-26}	Left			
<i>CLDN18</i>	5.2×10^{-26}	Left	5.1×10^{-5}	Left	√
<i>RBP4</i>	1.1×10^{-24}	Left	6.6×10^{-3}	Left	√
<i>HCN4</i>	1.3×10^{-24}	Right	2.4×10^{-2}	Right	√

*Indication of consistency: √ - The gene was also significant in the current study ($P \leq 0.05$); × - The gene was not significant in the current study ($P > 0.05$)

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Supplemental Table 3a. Top cis-associations in LA

Gene ID	Gene	SNP_ID	Chr	Position	Estimate	SD	P value	Reported*
210910_s_at	<i>POMZP3</i>	rs2110465	chr7	76,137,284	0.55	0.06	2.2x10 ⁻¹³	✓
217753_s_at	<i>RPS26</i>	rs11171739	chr12	56,470,625	0.59	0.06	5.5x10 ⁻¹³	✓
201141_at	<i>GPNMB</i>	rs6952947	chr7	23,121,042	-0.40	0.05	2.8x10 ⁻¹¹	✓
201141_at	<i>GPNMB</i>	rs1728292	chr7	23,263,474	-0.39	0.05	1.9x10 ⁻¹⁰	✓
201141_at	<i>GPNMB</i>	rs1468592	chr7	23,140,647	-0.38	0.05	3.9x10 ⁻¹⁰	✓
201141_at	<i>GPNMB</i>	rs6461693	chr7	23,160,133	-0.38	0.05	3.9x10 ⁻¹⁰	✓
210305_at	<i>PDE4DIP</i>	rs12124527	chr1	144,896,319	-0.48	0.06	5.8x10 ⁻¹⁰	
205197_s_at	<i>ATP7A</i>	rs2092621	chrX	77,340,216	0.21	0.03	6.8x10 ⁻¹⁰	
201141_at	<i>GPNMB</i>	rs7341483	chr7	23,127,657	-0.39	0.05	6.9x10 ⁻¹⁰	✓
201141_at	<i>GPNMB</i>	rs10255155	chr7	23,402,147	-0.37	0.05	7.1x10 ⁻¹⁰	✓
217753_s_at	<i>RPS26</i>	rs7312770	chr12	56,467,587	0.52	0.07	8.9x10 ⁻¹⁰	✓
205048_s_at	<i>PSPH</i>	rs11238381	chr7	55,891,901	1.24	0.17	9.7x10 ⁻¹⁰	
205197_s_at	<i>ATP7A</i>	rs320992	chrX	77,532,103	0.21	0.03	1.0x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs5913634	chrX	77,325,118	0.21	0.03	1.0x10 ⁻⁹	
201141_at	<i>GPNMB</i>	rs1624451	chr7	23,262,435	-0.39	0.05	1.2x10 ⁻⁹	✓
201141_at	<i>GPNMB</i>	rs1881201	chr7	23,194,013	-0.39	0.05	1.3x10 ⁻⁹	✓
201141_at	<i>GPNMB</i>	rs156425	chr7	23,309,119	-0.37	0.05	1.3x10 ⁻⁹	✓
205197_s_at	<i>ATP7A</i>	rs17139585	chrX	77,360,724	0.21	0.03	1.4x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs5913664	chrX	77,512,840	0.21	0.03	1.4x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs4826248	chrX	77,372,275	0.21	0.03	1.4x10 ⁻⁹	
219629_at	<i>FAM118A</i>	rs1569413	chr22	45,756,081	0.40	0.05	1.4x10 ⁻⁹	✓
219629_at	<i>FAM118A</i>	rs3827393	chr22	45,736,153	0.40	0.05	1.4x10 ⁻⁹	✓
219629_at	<i>FAM118A</i>	rs6006992	chr22	45,742,760	0.40	0.05	1.4x10 ⁻⁹	✓
219629_at	<i>FAM118A</i>	rs5765272	chr22	45,747,901	0.40	0.05	1.4x10 ⁻⁹	✓
219629_at	<i>FAM118A</i>	rs5765327	chr22	45,800,926	0.40	0.05	1.4x10 ⁻⁹	✓
201141_at	<i>GPNMB</i>	rs433395	chr7	23,401,955	-0.35	0.05	1.6x10 ⁻⁹	✓
205197_s_at	<i>ATP7A</i>	rs17139617	chrX	77,274,859	0.21	0.03	1.8x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs17139569	chrX	77,422,268	0.21	0.03	1.8x10 ⁻⁹	
219629_at	<i>FAM118A</i>	rs136610	chr22	45,794,212	0.40	0.05	1.8x10 ⁻⁹	
209316_s_at	<i>HBS1L</i>	rs4896128	chr6	135,349,756	-0.36	0.05	2.1x10 ⁻⁹	✓
209316_s_at	<i>HBS1L</i>	rs6923512	chr6	135,335,268	-0.36	0.05	2.1x10 ⁻⁹	✓
209316_s_at	<i>HBS1L</i>	rs4289677	chr6	135,275,485	-0.36	0.05	2.1x10 ⁻⁹	✓
209316_s_at	<i>HBS1L</i>	rs4896118	chr6	135,276,065	-0.36	0.05	2.1x10 ⁻⁹	✓
217753_s_at	<i>RPS26</i>	rs705698	chr12	56,384,687	0.52	0.07	2.4x10 ⁻⁹	✓
206029_at	<i>ANKRD1</i>	rs4933620	chr10	92,659,865	1.10	0.15	2.5x10 ⁻⁹	
209480_at	<i>HLA-DQB1</i>	rs9272346	chr6	32,604,372	0.39	0.05	3.0x10 ⁻⁹	✓
206029_at	<i>ANKRD1</i>	rs7089533	chr10	92,605,364	1.12	0.16	3.0x10 ⁻⁹	
201141_at	<i>GPNMB</i>	rs199355	chr7	23,296,533	-0.43	0.06	3.2x10 ⁻⁹	✓
205197_s_at	<i>ATP7A</i>	rs5959985	chrX	77,502,906	0.21	0.03	3.5x10 ⁻⁹	
209788_s_at	<i>ERAP1</i>	rs17401719	chr5	96,089,046	-0.21	0.03	3.8x10 ⁻⁹	✓
209788_s_at	<i>ERAP1</i>	rs10037212	chr5	96,084,776	-0.21	0.03	3.8x10 ⁻⁹	
209788_s_at	<i>ERAP1</i>	rs1862609	chr5	96,086,690	-0.21	0.03	3.8x10 ⁻⁹	

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219509_at	<i>MYOZ1</i>	rs3740293	chr10	75,406,141	0.73	0.10	4.0x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs5912576	chrX	77,513,603	0.21	0.03	4.9x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs320988	chrX	77,534,962	0.21	0.03	5.0x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs2073178	chrX	77,381,014	0.21	0.03	5.0x10 ⁻⁹	
201141_at	<i>GPNMB</i>	rs156429	chr7	23,306,020	-0.37	0.05	5.9x10 ⁻⁹	√
205197_s_at	<i>ATP7A</i>	rs320990	chrX	77,533,502	0.20	0.03	5.9x10 ⁻⁹	
213831_at	<i>HLA-DQA1</i>	rs9272346	chr6	32,604,372	0.80	0.11	5.9x10 ⁻⁹	√
218505_at	<i>WDR59</i>	rs8043624	chr16	74,967,819	0.40	0.06	6.2x10 ⁻⁹	
218505_at	<i>WDR59</i>	rs9937106	chr16	74,966,742	0.40	0.06	6.2x10 ⁻⁹	
210790_s_at	<i>SAR1A</i>	rs1046747	chr10	71,910,630	0.31	0.04	6.4x10 ⁻⁹	
201141_at	<i>GPNMB</i>	rs5850	chr7	23,314,547	-0.36	0.05	6.5x10 ⁻⁹	√
205176_s_at	<i>ITGB3BP</i>	rs855325	chr1	64,064,780	0.30	0.04	6.9x10 ⁻⁹	√
205176_s_at	<i>ITGB3BP</i>	rs10789138	chr1	63,859,046	0.30	0.04	6.9x10 ⁻⁹	
219629_at	<i>FAM118A</i>	rs104664	chr22	45,711,854	0.42	0.06	7.1x10 ⁻⁹	√
203411_s_at	<i>LMNA</i>	rs16837622	chr1	156,695,504	-0.55	0.08	7.6x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs3922593	chrX	77,468,792	0.21	0.03	7.7x10 ⁻⁹	
211200_s_at	<i>EFCAB2</i>	rs11580510	chr1	245,205,876	0.28	0.04	8.1x10 ⁻⁹	√
205176_s_at	<i>ITGB3BP</i>	rs855316	chr1	64,069,495	0.30	0.04	8.2x10 ⁻⁹	√
205197_s_at	<i>ATP7A</i>	rs7881148	chrX	77,455,168	0.20	0.03	8.8x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs167674	chrX	77,535,996	0.20	0.03	8.8x10 ⁻⁹	
205197_s_at	<i>ATP7A</i>	rs321074	chrX	77,541,469	0.20	0.03	8.8x10 ⁻⁹	
217753_s_at	<i>RPS26</i>	rs705702	chr12	56,390,636	0.50	0.07	8.9x10 ⁻⁹	√
205197_s_at	<i>ATP7A</i>	rs10991	chrX	77,385,748	0.21	0.03	1.2x10 ⁻⁸	
205197_s_at	<i>ATP7A</i>	rs1600069	chrX	77,708,727	0.20	0.03	1.6x10 ⁻⁸	
201141_at	<i>GPNMB</i>	rs200717	chr7	23,392,271	-0.35	0.05	1.7x10 ⁻⁸	√
201141_at	<i>GPNMB</i>	rs870476	chr7	23,193,271	-0.42	0.06	1.8x10 ⁻⁸	√
218496_at	<i>RNASEH1</i>	rs17463250	chr2	3,924,349	-0.38	0.06	2.0x10 ⁻⁸	
220182_at	<i>SLC25A23</i>	rs173229	chr19	6,452,305	-0.23	0.03	2.1x10 ⁻⁸	
218747_s_at	<i>TAPBPL</i>	rs2243977	chr12	6,569,983	0.26	0.04	2.1x10 ⁻⁸	√
201577_at	<i>NME1</i>	rs16949649	chr17	49,230,308	0.28	0.04	2.3x10 ⁻⁸	√
218747_s_at	<i>TAPBPL</i>	rs2244083	chr12	6,570,539	0.25	0.04	2.4x10 ⁻⁸	√
201141_at	<i>GPNMB</i>	rs4140959	chr7	23,170,776	-0.37	0.06	2.4x10 ⁻⁸	√
209480_at	<i>HLA-DQB1</i>	rs9272723	chr6	32,609,427	0.34	0.05	3.4x10 ⁻⁸	
207974_s_at	<i>SKP1</i>	rs1109309	chr5	133,079,344	0.23	0.04	3.5x10 ⁻⁸	
210790_s_at	<i>SAR1A</i>	rs6480442	chr10	71,900,246	0.32	0.05	4.4x10 ⁻⁸	
201141_at	<i>GPNMB</i>	rs6956974	chr7	23,252,318	-0.38	0.06	4.6x10 ⁻⁸	√
201141_at	<i>GPNMB</i>	rs6961109	chr7	23,252,413	-0.38	0.06	4.6x10 ⁻⁸	√
205197_s_at	<i>ATP7A</i>	rs2227291	chrX	77,268,502	0.21	0.03	4.7x10 ⁻⁸	
203815_at	<i>GSTT1</i>	rs4822458	chr22	24,265,659	0.68	0.11	4.9x10 ⁻⁸	√
219269_at	<i>HMBOX1</i>	rs2279442	chr8	28,913,888	-0.26	0.04	5.6x10 ⁻⁸	
213160_at	<i>DOCK2</i>	rs4867947	chr5	169,629,403	0.36	0.06	6.0x10 ⁻⁸	
201141_at	<i>GPNMB</i>	rs7805206	chr7	23,160,210	-0.36	0.06	6.5x10 ⁻⁸	√
205197_s_at	<i>ATP7A</i>	rs5959980	chrX	77,454,133	0.18	0.03	7.2x10 ⁻⁸	
218948_at	<i>QRSL1</i>	rs11153019	chr6	107,090,614	-0.21	0.03	8.2x10 ⁻⁸	√
205176_s_at	<i>ITGB3BP</i>	rs17391823	chr1	63,986,865	0.35	0.06	8.6x10 ⁻⁸	√

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205197_s_at	<i>ATP7A</i>	rs5913656	chrX	77,471,090	0.18	0.03	9.3x10 ⁻⁸	
209316_s_at	<i>HBS1L</i>	rs6569982	chr6	135,256,495	-0.33	0.05	1.1x10 ⁻⁷	
208641_s_at	<i>RAC1</i>	rs2689420	chr7	6,410,321	0.30	0.05	1.1x10 ⁻⁷	
203374_s_at	<i>TPP2</i>	rs1887355	chr13	103,235,169	0.21	0.03	1.1x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs2549794	chr5	96,244,549	0.27	0.04	1.2x10 ⁻⁷	√
219759_at	<i>ERAP2</i>	rs27307	chr5	96,338,505	0.27	0.04	1.2x10 ⁻⁷	√
218327_s_at	<i>SNAP29</i>	rs5751939	chr22	21,139,242	0.29	0.05	1.2x10 ⁻⁷	√
208727_s_at	<i>CDC42</i>	rs7412010	chr1	22,436,446	0.77	0.13	1.2x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs27712	chr5	96,364,063	0.28	0.05	1.2x10 ⁻⁷	√
218496_at	<i>RNASEH1</i>	rs985858	chr2	3,921,722	-0.35	0.06	1.3x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs321014	chrX	77,620,061	0.18	0.03	1.3x10 ⁻⁷	
212494_at	<i>TENC1</i>	rs6580907	chr12	53,169,676	-0.40	0.06	1.4x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs27300	chr5	96,363,407	0.27	0.04	1.4x10 ⁻⁷	√
201141_at	<i>GPNMB</i>	rs7796541	chr7	23,389,073	-0.37	0.06	1.6x10 ⁻⁷	√
205439_at	<i>GSTT2</i>	rs17004049	chr22	24,241,594	0.41	0.07	1.7x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs320999	chrX	77,576,690	0.18	0.03	1.8x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs7736466	chr5	96,289,711	0.26	0.04	1.8x10 ⁻⁷	√
205197_s_at	<i>ATP7A</i>	rs5913717	chrX	77,700,678	0.18	0.03	1.9x10 ⁻⁷	
218948_at	<i>QRSL1</i>	rs1026619	chr6	107,114,361	-0.22	0.04	1.9x10 ⁻⁷	√
205176_s_at	<i>ITGB3BP</i>	rs217483	chr1	64,017,830	0.29	0.05	2.0x10 ⁻⁷	
208727_s_at	<i>CDC42</i>	rs2268177	chr1	22,415,410	0.75	0.12	2.1x10 ⁻⁷	
211200_s_at	<i>EFCAB2</i>	rs10927361	chr1	245,140,654	0.27	0.04	2.2x10 ⁻⁷	√
209788_s_at	<i>ERAP1</i>	rs731827	chr5	96,087,015	-0.23	0.04	2.3x10 ⁻⁷	√
205185_at	<i>SPINK5</i>	rs1862446	chr5	147,480,556	0.24	0.04	2.3x10 ⁻⁷	
205185_at	<i>SPINK5</i>	rs1862439	chr5	147,494,931	0.24	0.04	2.3x10 ⁻⁷	
202070_s_at	<i>IDH3A</i>	rs8035724	chr15	78,470,542	0.27	0.05	2.4x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs3909451	chr5	96,295,121	0.27	0.04	2.5x10 ⁻⁷	√
213831_at	<i>HLA-DQA1</i>	rs9272723	chr6	32,609,427	0.67	0.11	2.6x10 ⁻⁷	√
205197_s_at	<i>ATP7A</i>	rs321028	chrX	77,587,600	0.17	0.03	2.8x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs320986	chrX	77,690,251	0.17	0.03	2.8x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs321034	chrX	77,635,122	0.17	0.03	2.8x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs9127	chr5	96,372,165	0.27	0.04	2.9x10 ⁻⁷	
218347_at	<i>TYW1</i>	rs3845174	chr7	66,533,678	0.16	0.03	2.9x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs5751770	chr22	24,252,842	-0.61	0.10	3.0x10 ⁻⁷	√
205197_s_at	<i>ATP7A</i>	rs321090	chrX	77,559,987	0.18	0.03	3.2x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs1129067	chr22	24,228,125	-0.75	0.13	3.3x10 ⁻⁷	√
219759_at	<i>ERAP2</i>	rs27993	chr5	96,355,603	0.28	0.05	3.4x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs1002286	chr22	24,257,337	0.65	0.11	3.5x10 ⁻⁷	√
202070_s_at	<i>IDH3A</i>	rs3816253	chr15	78,458,485	0.27	0.05	3.5x10 ⁻⁷	
202070_s_at	<i>IDH3A</i>	rs12910386	chr15	78,472,644	0.27	0.05	3.5x10 ⁻⁷	
203411_s_at	<i>LMNA</i>	rs3795737	chr1	156,697,056	-0.47	0.08	3.6x10 ⁻⁷	
209316_s_at	<i>HBS1L</i>	rs728030	chr6	135,246,294	-0.33	0.06	3.6x10 ⁻⁷	
211200_s_at	<i>EFCAB2</i>	rs6699566	chr1	245,136,331	0.23	0.04	3.7x10 ⁻⁷	√
208982_at	<i>PECAM1</i>	rs1122800	chr17	62,391,365	-0.42	0.07	3.7x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs5913659	chrX	77,506,965	0.18	0.03	4.1x10 ⁻⁷	

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203815_at	<i>GSTT1</i>	rs2154594	chr22	24,254,055	-0.62	0.11	4.3x10 ⁻⁷	✓
203815_at	<i>GSTT1</i>	rs140245	chr22	24,329,711	0.68	0.12	4.4x10 ⁻⁷	✓
208982_at	<i>PECAM1</i>	rs9902260	chr17	62,399,872	-0.42	0.07	4.6x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs2000468	chr22	24,241,611	0.63	0.11	4.8x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs5913725	chrX	77,716,546	0.17	0.03	4.8x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs1974871	chr5	96,226,535	0.24	0.04	5.0x10 ⁻⁷	✓
212921_at	<i>SMYD2</i>	rs320413	chr1	213,605,355	0.42	0.07	6.0x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs2186366	chr22	24,254,113	-0.63	0.11	6.0x10 ⁻⁷	✓
219759_at	<i>ERAP2</i>	rs2548533	chr5	96,238,401	0.24	0.04	6.1x10 ⁻⁷	✓
219759_at	<i>ERAP2</i>	rs2549797	chr5	96,245,518	0.24	0.04	6.1x10 ⁻⁷	✓
219759_at	<i>ERAP2</i>	rs2910787	chr5	96,274,223	0.24	0.04	6.1x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs1547247	chr6	135,390,836	-0.35	0.06	6.4x10 ⁻⁷	
207344_at	<i>AKAP3</i>	rs10849105	chr12	4,719,675	0.79	0.14	6.4x10 ⁻⁷	
203096_s_at	<i>RAPGEF2</i>	rs11732785	chr4	160,312,930	0.31	0.05	6.4x10 ⁻⁷	
209316_s_at	<i>HBS1L</i>	rs4472368	chr6	135,274,232	-0.29	0.05	6.7x10 ⁻⁷	✓
209314_s_at	<i>HBS1L</i>	rs4896128	chr6	135,349,756	-0.23	0.04	6.7x10 ⁻⁷	✓
209314_s_at	<i>HBS1L</i>	rs6923512	chr6	135,335,268	-0.23	0.04	6.7x10 ⁻⁷	✓
209314_s_at	<i>HBS1L</i>	rs4289677	chr6	135,275,485	-0.23	0.04	6.7x10 ⁻⁷	✓
209314_s_at	<i>HBS1L</i>	rs4896118	chr6	135,276,065	-0.23	0.04	6.7x10 ⁻⁷	✓
207344_at	<i>AKAP3</i>	rs1990316	chr12	4,733,056	0.76	0.13	6.9x10 ⁻⁷	
208895_s_at	<i>DDX18</i>	rs13427023	chr2	117,719,892	-0.92	0.16	7.1x10 ⁻⁷	
201922_at	<i>NSA2</i>	rs16872345	chr5	74,149,478	0.39	0.07	7.1x10 ⁻⁷	
212494_at	<i>TENC1</i>	rs4564385	chr12	53,133,012	-0.30	0.05	7.3x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs27290	chr5	96,350,088	0.24	0.04	7.6x10 ⁻⁷	✓
203815_at	<i>GSTT1</i>	rs5760106	chr22	24,250,645	-0.61	0.11	8.4x10 ⁻⁷	✓
209788_s_at	<i>ERAP1</i>	rs7705827	chr5	96,082,433	-0.21	0.04	8.4x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs2284753	chrX	77,371,470	0.17	0.03	8.5x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs321013	chrX	77,621,340	0.17	0.03	9.5x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs321033	chrX	77,634,947	0.17	0.03	9.5x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs599931	chrX	77,660,137	0.17	0.03	9.5x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs320985	chrX	77,688,471	0.17	0.03	9.5x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs5913716	chrX	77,700,395	0.17	0.03	9.5x10 ⁻⁷	
212921_at	<i>SMYD2</i>	rs320448	chr1	213,618,740	0.42	0.08	9.7x10 ⁻⁷	
212921_at	<i>SMYD2</i>	rs320447	chr1	213,619,065	0.42	0.08	9.7x10 ⁻⁷	
212921_at	<i>SMYD2</i>	rs320441	chr1	213,625,934	0.42	0.08	9.7x10 ⁻⁷	
205197_s_at	<i>ATP7A</i>	rs321032	chrX	77,634,925	0.17	0.03	9.8x10 ⁻⁷	
219027_s_at	<i>MYO9A</i>	rs7182776	chr15	72,462,831	0.16	0.03	1.0x10 ⁻⁶	
219759_at	<i>ERAP2</i>	rs2278019	chr5	96,225,252	0.27	0.05	1.0x10 ⁻⁶	✓
203815_at	<i>GSTT1</i>	rs17004811	chr22	24,404,830	-0.70	0.13	1.0x10 ⁻⁶	✓
221808_at	<i>RAB9A</i>	rs11095593	chrX	12,952,580	0.19	0.03	1.0x10 ⁻⁶	
201577_at	<i>NME1</i>	rs2318782	chr17	49,227,606	0.27	0.05	1.0x10 ⁻⁶	✓
219509_at	<i>MYOZ1</i>	rs9664184	chr10	75,409,967	0.59	0.11	1.1x10 ⁻⁶	✓
205185_at	<i>SPINK5</i>	rs1423007	chr5	147,442,868	0.23	0.04	1.1x10 ⁻⁶	
205185_at	<i>SPINK5</i>	rs1423001	chr5	147,449,855	0.23	0.04	1.1x10 ⁻⁶	
219759_at	<i>ERAP2</i>	rs1056893	chr5	96,245,439	0.24	0.04	1.1x10 ⁻⁶	✓

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205197_s_at	<i>ATP7A</i>	rs5913723	chrX	77,710,039	0.17	0.03	1.1x10 ⁻⁶	
205197_s_at	<i>ATP7A</i>	rs17313128	chrX	77,748,728	0.17	0.03	1.1x10 ⁻⁶	
219759_at	<i>ERAP2</i>	rs27397	chr5	96,340,616	0.25	0.05	1.1x10 ⁻⁶	√
205185_at	<i>SPINK5</i>	rs9325064	chr5	147,448,360	0.24	0.04	1.2x10 ⁻⁶	
203815_at	<i>GSTT1</i>	rs113413	chr22	24,292,264	-0.78	0.14	1.2x10 ⁻⁶	√
205197_s_at	<i>ATP7A</i>	rs5913740	chrX	77,732,760	0.17	0.03	1.3x10 ⁻⁶	
205197_s_at	<i>ATP7A</i>	rs5913718	chrX	77,700,773	0.17	0.03	1.3x10 ⁻⁶	
205197_s_at	<i>ATP7A</i>	rs417862	chrX	77,628,865	0.17	0.03	1.3x10 ⁻⁶	
209316_s_at	<i>HBS1L</i>	rs4440481	chr6	135,276,696	-0.29	0.05	1.3x10 ⁻⁶	√
219269_at	<i>HMBOX1</i>	rs10503836	chr8	28,885,470	0.24	0.04	1.3x10 ⁻⁶	

*√ represents that the eQTL has already been reported in other tissues from eQTL Browser

(<http://eqtl.uchicago.edu/Home.html>)

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Supplemental Table 3b. Top cis-associations in RA

Gene ID	Gene	SNP ID	Chr	Position	Estimate	Std. Error	P value	Reported*
217753_s_at	<i>RPS26</i>	rs11171739	chr12	56,470,625	0.64	0.06	3.4x10 ⁻¹⁴	✓
219629_at	<i>FAM118A</i>	rs3827393	chr22	45,736,153	0.54	0.05	2.2x10 ⁻¹³	✓
219629_at	<i>FAM118A</i>	rs6006992	chr22	45,742,760	0.54	0.05	2.2x10 ⁻¹³	✓
219629_at	<i>FAM118A</i>	rs5765272	chr22	45,747,901	0.54	0.05	2.2x10 ⁻¹³	✓
219629_at	<i>FAM118A</i>	rs1569413	chr22	45,756,081	0.54	0.05	2.2x10 ⁻¹³	✓
219629_at	<i>FAM118A</i>	rs5765327	chr22	45,800,926	0.54	0.05	2.2x10 ⁻¹³	✓
203815_at	<i>GSTT1</i>	rs4822458	chr22	24,265,659	0.99	0.10	2.4x10 ⁻¹³	✓
219629_at	<i>FAM118A</i>	rs136610	chr22	45,794,212	0.54	0.06	4.7x10 ⁻¹³	
209316_s_at	<i>HBS1L</i>	rs6923512	chr6	135,335,268	-0.45	0.05	4.8x10 ⁻¹³	✓
209316_s_at	<i>HBS1L</i>	rs4896128	chr6	135,349,756	-0.45	0.05	4.8x10 ⁻¹³	✓
209316_s_at	<i>HBS1L</i>	rs4289677	chr6	135,275,485	-0.45	0.05	4.8x10 ⁻¹³	✓
209316_s_at	<i>HBS1L</i>	rs4896118	chr6	135,276,065	-0.45	0.05	4.8x10 ⁻¹³	✓
213831_at	<i>HLA-DQA1</i>	rs9272346	chr6	32,604,372	0.89	0.10	4.5x10 ⁻¹²	✓
203815_at	<i>GSTT1</i>	rs1002286	chr22	24,257,337	0.97	0.11	5.4x10 ⁻¹²	✓
218747_s_at	<i>TAPBPL</i>	rs2244083	chr12	6,570,539	0.33	0.04	1.1x10 ⁻¹¹	✓
209316_s_at	<i>HBS1L</i>	rs6569982	chr6	135,256,495	-0.44	0.05	2.0x10 ⁻¹¹	
203815_at	<i>GSTT1</i>	rs140245	chr22	24,329,711	0.96	0.11	3.1x10 ⁻¹¹	✓
219759_at	<i>ERAP2</i>	rs2549794	chr5	96,244,549	0.36	0.04	3.1x10 ⁻¹¹	✓
219759_at	<i>ERAP2</i>	rs27307	chr5	96,338,505	0.36	0.04	3.1x10 ⁻¹¹	✓
208727_s_at	<i>CDC42</i>	rs2268177	chr1	22,415,410	0.69	0.08	4.8x10 ⁻¹¹	
219759_at	<i>ERAP2</i>	rs3909451	chr5	96,295,121	0.37	0.04	4.9x10 ⁻¹¹	✓
203815_at	<i>GSTT1</i>	rs113413	chr22	24,292,264	-1.05	0.12	5.2x10 ⁻¹¹	✓
219759_at	<i>ERAP2</i>	rs27712	chr5	96,364,063	0.37	0.04	7.9x10 ⁻¹¹	✓
218747_s_at	<i>TAPBPL</i>	rs2243977	chr12	6,569,983	0.33	0.04	1.0x10 ⁻¹⁰	✓
218746_at	<i>TAPBPL</i>	rs2243977	chr12	6,569,983	0.31	0.04	1.1x10 ⁻¹⁰	✓
218746_at	<i>TAPBPL</i>	rs2244083	chr12	6,570,539	0.30	0.04	1.5x10 ⁻¹⁰	✓
203815_at	<i>GSTT1</i>	rs5760176	chr22	24,402,321	0.97	0.12	2.3x10 ⁻¹⁰	✓
203290_at	<i>HLA-DQA1</i>	rs502771	chr6	32,578,970	0.56	0.07	2.6x10 ⁻¹⁰	✓
206029_at	<i>ANKRD1</i>	rs1892110	chr10	92,457,246	0.80	0.10	3.4x10 ⁻¹⁰	
203815_at	<i>GSTT1</i>	rs2000468	chr22	24,241,611	0.93	0.12	3.5x10 ⁻¹⁰	
206918_s_at	<i>CPNE1</i>	rs6060625	chr20	34,414,318	-0.37	0.05	5.7x10 ⁻¹⁰	✓
206918_s_at	<i>CPNE1</i>	rs6060578	chr20	34,305,445	-0.37	0.05	5.7x10 ⁻¹⁰	✓
213831_at	<i>HLA-DQA1</i>	rs9272723	chr6	32,609,427	0.79	0.10	5.9x10 ⁻¹⁰	✓
218747_s_at	<i>TAPBPL</i>	rs1043262	chr12	6,639,088	0.31	0.04	7.0x10 ⁻¹⁰	✓
219759_at	<i>ERAP2</i>	rs27290	chr5	96,350,088	0.37	0.05	9.0x10 ⁻¹⁰	✓
218747_s_at	<i>TAPBPL</i>	rs758739	chr12	6,626,369	0.32	0.04	9.1x10 ⁻¹⁰	✓
201445_at	<i>CNN3</i>	rs859062	chr1	95,361,793	-0.54	0.07	1.1x10 ⁻⁹	
219759_at	<i>ERAP2</i>	rs1974871	chr5	96,226,535	0.32	0.04	1.1x10 ⁻⁹	✓
219629_at	<i>FAM118A</i>	rs104664	chr22	45,711,854	0.48	0.06	1.5x10 ⁻⁹	✓
218747_s_at	<i>TAPBPL</i>	rs2079867	chr12	6,622,111	0.31	0.04	1.7x10 ⁻⁹	✓
201445_at	<i>CNN3</i>	rs859064	chr1	95,352,701	-0.51	0.07	1.7x10 ⁻⁹	
209316_s_at	<i>HBS1L</i>	rs4472368	chr6	135,274,232	-0.38	0.05	1.9x10 ⁻⁹	✓

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219759_at	<i>ERAP2</i>	rs27711	chr5	96,345,739	0.36	0.05	1.9x10 ⁻⁹	✓
219759_at	<i>ERAP2</i>	rs27300	chr5	96,363,407	0.34	0.05	1.9x10 ⁻⁹	✓
218795_at	<i>ACP6</i>	rs2275552	chr1	147,131,945	-0.22	0.03	2.0x10 ⁻⁹	✓
209480_at	<i>HLA-DQB1</i>	rs9272346	chr6	32,604,372	0.38	0.05	2.2x10 ⁻⁹	✓
219759_at	<i>ERAP2</i>	rs27993	chr5	96,355,603	0.35	0.05	2.4x10 ⁻⁹	
210910_s_at	<i>POMZP3</i>	rs2110465	chr7	76,137,284	0.51	0.07	3.0x10 ⁻⁹	✓
217753_s_at	<i>RPS26</i>	rs7312770	chr12	56,467,587	0.57	0.08	3.0x10 ⁻⁹	✓
206029_at	<i>ANKRD1</i>	rs12259754	chr10	92,472,510	0.81	0.11	3.1x10 ⁻⁹	
206029_at	<i>ANKRD1</i>	rs11186286	chr10	92,477,076	0.81	0.11	3.1x10 ⁻⁹	
201123_s_at	<i>EIF5A</i>	rs4796398	chr17	7,208,197	1.16	0.16	3.2x10 ⁻⁹	✓
217753_s_at	<i>RPS26</i>	rs705698	chr12	56,384,687	0.57	0.08	3.5x10 ⁻⁹	✓
217753_s_at	<i>RPS26</i>	rs705702	chr12	56,390,636	0.57	0.08	3.5x10 ⁻⁹	✓
218795_at	<i>ACP6</i>	rs6674938	chr1	147,131,465	-0.22	0.03	4.3x10 ⁻⁹	✓
209316_s_at	<i>HBS1L</i>	rs4646871	chr6	135,265,617	-0.40	0.05	4.4x10 ⁻⁹	✓
206029_at	<i>ANKRD1</i>	rs7913197	chr10	92,451,763	0.85	0.12	4.7x10 ⁻⁹	
203815_at	<i>GSTT1</i>	rs5760106	chr22	24,250,645	-0.81	0.11	4.8x10 ⁻⁹	✓
201445_at	<i>CNN3</i>	rs859058	chr1	95,367,649	-0.53	0.07	5.0x10 ⁻⁹	
203815_at	<i>GSTT1</i>	rs5751770	chr22	24,252,842	-0.80	0.11	5.3x10 ⁻⁹	✓
218948_at	<i>QRSL1</i>	rs11153019	chr6	107,090,614	-0.26	0.04	5.3x10 ⁻⁹	✓
203290_at	<i>HLA-DQA1</i>	rs9272535	chr6	32,606,756	0.57	0.08	5.3x10 ⁻⁹	✓
203290_at	<i>HLA-DQA1</i>	rs9272219	chr6	32,602,269	0.57	0.08	5.3x10 ⁻⁹	✓
209316_s_at	<i>HBS1L</i>	rs4440481	chr6	135,276,696	-0.39	0.06	5.6x10 ⁻⁹	✓
206918_s_at	<i>CPNE1</i>	rs6120998	chr20	34,187,313	-0.36	0.05	6.5x10 ⁻⁹	✓
203628_at	<i>IGF1R</i>	rs2229765	chr15	99,478,225	0.60	0.09	6.5x10 ⁻⁹	
206029_at	<i>ANKRD1</i>	rs12783703	chr10	92,560,413	0.72	0.10	7.0x10 ⁻⁹	
206029_at	<i>ANKRD1</i>	rs12766851	chr10	92,562,831	0.72	0.10	7.0x10 ⁻⁹	
206918_s_at	<i>CPNE1</i>	rs1970357	chr20	34,339,200	-0.35	0.05	7.6x10 ⁻⁹	✓
202070_s_at	<i>IDH3A</i>	rs8035724	chr15	78,470,542	0.30	0.04	7.7x10 ⁻⁹	
218948_at	<i>QRSL1</i>	rs1026619	chr6	107,114,361	-0.27	0.04	8.3x10 ⁻⁹	✓
219759_at	<i>ERAP2</i>	rs10434709	chr5	96,225,774	0.34	0.05	1.0x10 ⁻⁸	✓
219509_at	<i>MYOZ1</i>	rs3740293	chr10	75,406,141	0.79	0.12	1.1x10 ⁻⁸	
207040_s_at	<i>ST13</i>	rs5996064	chr22	42,172,080	-0.29	0.04	1.1x10 ⁻⁸	
208727_s_at	<i>CDC42</i>	rs7412010	chr1	22,436,446	0.75	0.11	1.1x10 ⁻⁸	
206918_s_at	<i>CPNE1</i>	rs7271036	chr20	34,467,215	-0.36	0.05	1.5x10 ⁻⁸	✓
209316_s_at	<i>HBS1L</i>	rs728030	chr6	135,246,294	-0.41	0.06	1.6x10 ⁻⁸	
209314_s_at	<i>HBS1L</i>	rs4646871	chr6	135,265,617	-0.27	0.04	1.7x10 ⁻⁸	✓
202070_s_at	<i>IDH3A</i>	rs3816253	chr15	78,458,485	0.29	0.04	1.7x10 ⁻⁸	
219759_at	<i>ERAP2</i>	rs2278019	chr5	96,225,252	0.38	0.06	1.8x10 ⁻⁸	✓
209314_s_at	<i>HBS1L</i>	rs6923512	chr6	135,335,268	-0.26	0.04	1.9x10 ⁻⁸	✓
209314_s_at	<i>HBS1L</i>	rs4896128	chr6	135,349,756	-0.26	0.04	1.9x10 ⁻⁸	✓
209314_s_at	<i>HBS1L</i>	rs4289677	chr6	135,275,485	-0.26	0.04	1.9x10 ⁻⁸	✓
209314_s_at	<i>HBS1L</i>	rs4896118	chr6	135,276,065	-0.26	0.04	1.9x10 ⁻⁸	✓
202070_s_at	<i>IDH3A</i>	rs12910386	chr15	78,472,644	0.29	0.04	1.9x10 ⁻⁸	
219759_at	<i>ERAP2</i>	rs11135482	chr5	96,221,426	0.30	0.05	1.9x10 ⁻⁸	
203815_at	<i>GSTT1</i>	rs5751761	chr22	24,243,736	0.98	0.14	2.2x10 ⁻⁸	✓

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218747_s_at	<i>TAPBPL</i>	rs2079868	chr12	6,622,346	0.30	0.05	2.5x10 ⁻⁸	✓
218055_s_at	<i>WDR41</i>	rs335628	chr5	76,729,538	-0.32	0.05	2.6x10 ⁻⁸	✓
203290_at	<i>HLA-DQA1</i>	rs502055	chr6	32,579,003	0.48	0.07	2.7x10 ⁻⁸	
205048_s_at	<i>PSPH</i>	rs11238381	chr7	55,891,901	1.01	0.15	2.7x10 ⁻⁸	
210305_at	<i>PDE4DIP</i>	rs12124527	chr1	144,896,319	-0.52	0.08	2.8x10 ⁻⁸	
204194_at	<i>BACH1</i>	rs2832175	chr21	30,475,606	0.16	0.02	2.8x10 ⁻⁸	
203290_at	<i>HLA-DQA1</i>	rs615672	chr6	32,574,171	0.52	0.08	2.8x10 ⁻⁸	✓
219759_at	<i>ERAP2</i>	rs7736466	chr5	96,289,711	0.32	0.05	3.3x10 ⁻⁸	✓
219759_at	<i>ERAP2</i>	rs2910787	chr5	96,274,223	0.31	0.05	3.4x10 ⁻⁸	✓
209480_at	<i>HLA-DQB1</i>	rs9272723	chr6	32,609,427	0.33	0.05	3.4x10 ⁻⁸	
203815_at	<i>GSTT1</i>	rs2186366	chr22	24,254,113	-0.81	0.12	3.8x10 ⁻⁸	✓
205048_s_at	<i>PSPH</i>	rs11238377	chr7	55,776,532	1.26	0.19	4.0x10 ⁻⁸	
208982_at	<i>PECAM1</i>	rs9902260	chr17	62,399,872	-0.39	0.06	4.5x10 ⁻⁸	
203815_at	<i>GSTT1</i>	rs2154594	chr22	24,254,055	-0.78	0.12	5.1x10 ⁻⁸	✓
221562_s_at	<i>SIRT3</i>	rs4980329	chr11	232,598	0.23	0.04	5.7x10 ⁻⁸	
219759_at	<i>ERAP2</i>	rs13167902	chr5	96,222,020	0.31	0.05	6.0x10 ⁻⁸	✓
219759_at	<i>ERAP2</i>	rs2548533	chr5	96,238,401	0.31	0.05	6.0x10 ⁻⁸	✓
219759_at	<i>ERAP2</i>	rs2549797	chr5	96,245,518	0.31	0.05	6.0x10 ⁻⁸	✓
209314_s_at	<i>HBS1L</i>	rs6569982	chr6	135,256,495	-0.27	0.04	6.0x10 ⁻⁸	
204125_at	<i>NDUFAF1</i>	rs1899	chr15	41,689,232	-0.28	0.04	6.5x10 ⁻⁸	
320_at	<i>PEX6</i>	rs2274517	chr6	42,932,715	0.18	0.03	6.9x10 ⁻⁸	✓
218747_s_at	<i>TAPBPL</i>	rs2534717	chr12	6,573,749	0.31	0.05	7.0x10 ⁻⁸	✓
218948_at	<i>QRSL1</i>	rs7750365	chr6	107,089,289	-0.30	0.05	7.3x10 ⁻⁸	✓
204194_at	<i>BACH1</i>	rs1888439	chr21	30,454,457	0.16	0.03	7.3x10 ⁻⁸	
34764_at	<i>LARS2</i>	rs3774692	chr3	45,507,305	-0.21	0.03	7.8x10 ⁻⁸	✓
218948_at	<i>QRSL1</i>	rs3121434	chr6	107,128,371	-0.28	0.04	8.1x10 ⁻⁸	✓
209314_s_at	<i>HBS1L</i>	rs4472368	chr6	135,274,232	-0.24	0.04	9.1x10 ⁻⁸	✓
208982_at	<i>PECAM1</i>	rs1122800	chr17	62,391,365	-0.39	0.06	9.6x10 ⁻⁸	
208907_s_at	<i>MRPS18B</i>	rs1737060	chr6	29,732,969	-0.29	0.05	1.1x10 ⁻⁷	
218505_at	<i>WDR59</i>	rs8043624	chr16	74,967,819	0.40	0.06	1.1x10 ⁻⁷	
206918_s_at	<i>CPNE1</i>	rs11907811	chr20	34,428,078	-0.35	0.06	1.2x10 ⁻⁷	✓
218106_s_at	<i>MRPS10</i>	rs2180174	chr6	42,167,970	-0.26	0.04	1.3x10 ⁻⁷	✓
204245_s_at	<i>RPP14</i>	rs2363686	chr3	58,253,885	-0.24	0.04	1.3x10 ⁻⁷	
204245_s_at	<i>RPP14</i>	rs4681823	chr3	58,199,630	-0.23	0.04	1.3x10 ⁻⁷	
204245_s_at	<i>RPP14</i>	rs4681824	chr3	58,199,669	-0.23	0.04	1.3x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs1056893	chr5	96,245,439	0.31	0.05	1.3x10 ⁻⁷	✓
210790_s_at	<i>SAR1A</i>	rs6480442	chr10	71,900,246	0.32	0.05	1.4x10 ⁻⁷	
204245_s_at	<i>RPP14</i>	rs3773010	chr3	58,269,751	-0.23	0.04	1.4x10 ⁻⁷	
219629_at	<i>FAM118A</i>	rs136611	chr22	45,794,283	0.44	0.07	1.4x10 ⁻⁷	✓
218106_s_at	<i>MRPS10</i>	rs6912658	chr6	42,167,161	-0.25	0.04	1.5x10 ⁻⁷	✓
202070_s_at	<i>IDH3A</i>	rs9920103	chr15	78,435,527	0.27	0.05	1.7x10 ⁻⁷	
204125_at	<i>NDUFAF1</i>	rs7164211	chr15	41,705,041	-0.26	0.04	1.8x10 ⁻⁷	
204125_at	<i>NDUFAF1</i>	rs316611	chr15	41,751,678	-0.26	0.04	1.8x10 ⁻⁷	
204125_at	<i>NDUFAF1</i>	rs11854632	chr15	41,682,094	-0.26	0.04	1.8x10 ⁻⁷	
211200_s_at	<i>EFCAB2</i>	rs6699566	chr1	245,136,331	0.20	0.03	1.9x10 ⁻⁷	✓

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202070_s_at	<i>IDH3A</i>	rs11855354	chr15	78,443,631	0.27	0.05	2.0x10 ⁻⁷	
209316_s_at	<i>HBS1L</i>	rs12526055	chr6	135,325,918	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs1014021	chr6	135,334,600	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs12661423	chr6	135,349,570	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs7750300	chr6	135,350,950	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs1590975	chr6	135,352,088	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs7741515	chr6	135,374,368	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs2150681	chr6	135,375,232	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs11754265	chr6	135,356,216	-0.34	0.06	2.0x10 ⁻⁷	✓
209316_s_at	<i>HBS1L</i>	rs6923765	chr6	135,335,176	-0.34	0.06	2.0x10 ⁻⁷	✓
210790_s_at	<i>SAR1A</i>	rs1046747	chr10	71,910,630	0.29	0.05	2.1x10 ⁻⁷	
218505_at	<i>WDR59</i>	rs9937106	chr16	74,966,742	0.39	0.06	2.3x10 ⁻⁷	
202378_s_at	<i>LEPROT</i>	rs9436748	chr1	65,911,672	-0.38	0.06	2.5x10 ⁻⁷	
203674_at	<i>HELZ</i>	rs2642066	chr17	65,639,014	-0.30	0.05	2.5x10 ⁻⁷	
201445_at	<i>CNN3</i>	rs698969	chr1	95,353,163	-0.46	0.08	2.7x10 ⁻⁷	
204194_at	<i>BACH1</i>	rs2255055	chr21	30,537,045	-0.16	0.03	2.7x10 ⁻⁷	
208666_s_at	<i>ST13</i>	rs5996064	chr22	42,172,080	-0.40	0.07	2.7x10 ⁻⁷	
204194_at	<i>BACH1</i>	rs2832198	chr21	30,498,240	0.16	0.03	2.7x10 ⁻⁷	
202378_s_at	<i>LEPROT</i>	rs7513047	chr1	65,950,340	-0.36	0.06	3.0x10 ⁻⁷	
207344_at	<i>AKAP3</i>	rs7315434	chr12	4,563,810	0.87	0.14	3.0x10 ⁻⁷	
209316_s_at	<i>HBS1L</i>	rs6569976	chr6	135,224,753	-0.36	0.06	3.1x10 ⁻⁷	
209314_s_at	<i>HBS1L</i>	rs4440481	chr6	135,276,696	-0.24	0.04	3.3x10 ⁻⁷	✓
204083_s_at	<i>TPM2</i>	rs7389781	chr9	35,573,942	-0.27	0.05	3.3x10 ⁻⁷	
202203_s_at	<i>AMFR</i>	rs2432540	chr16	56,419,628	-0.40	0.07	3.4x10 ⁻⁷	✓
218795_at	<i>ACP6</i>	rs583583	chr1	147,083,114	-0.19	0.03	3.4x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs17004811	chr22	24,404,830	-0.81	0.14	3.5x10 ⁻⁷	✓
34764_at	<i>LARS2</i>	rs267257	chr3	45,600,868	0.18	0.03	3.6x10 ⁻⁷	✓
218948_at	<i>QRSL1</i>	rs13218960	chr6	106,983,465	-0.27	0.05	3.7x10 ⁻⁷	✓
218948_at	<i>QRSL1</i>	rs13202942	chr6	106,983,546	-0.27	0.05	3.7x10 ⁻⁷	✓
206029_at	<i>ANKRD1</i>	rs11596991	chr10	92,598,458	1.07	0.18	3.8x10 ⁻⁷	
202259_s_at	<i>N4BP2L2</i>	rs499966	chr13	32,998,610	0.28	0.05	4.0x10 ⁻⁷	
206029_at	<i>ANKRD1</i>	rs11597471	chr10	92,598,767	0.59	0.10	4.0x10 ⁻⁷	
206029_at	<i>ANKRD1</i>	rs11599902	chr10	92,598,823	0.59	0.10	4.0x10 ⁻⁷	
205048_s_at	<i>PSPH</i>	rs7809922	chr7	55,823,581	1.23	0.21	4.2x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs18059	chr5	96,352,068	0.33	0.06	4.3x10 ⁻⁷	✓
34764_at	<i>LARS2</i>	rs1877960	chr3	45,496,144	-0.18	0.03	4.8x10 ⁻⁷	✓
219759_at	<i>ERAP2</i>	rs9127	chr5	96,372,165	0.33	0.06	5.0x10 ⁻⁷	
209316_s_at	<i>HBS1L</i>	rs9321481	chr6	135,352,648	-0.33	0.06	5.0x10 ⁻⁷	✓
206918_s_at	<i>CPNE1</i>	rs2425071	chr20	34,292,961	-0.30	0.05	5.1x10 ⁻⁷	✓
320_at	<i>PEX6</i>	rs9986447	chr6	42,942,779	0.18	0.03	5.2x10 ⁻⁷	✓
218106_s_at	<i>MRPS10</i>	rs9369346	chr6	42,159,132	-0.24	0.04	5.2x10 ⁻⁷	✓
218106_s_at	<i>MRPS10</i>	rs2180172	chr6	42,168,542	-0.24	0.04	5.2x10 ⁻⁷	✓
202378_s_at	<i>LEPROT</i>	rs7524834	chr1	65,950,230	-0.34	0.06	5.3x10 ⁻⁷	
218948_at	<i>QRSL1</i>	rs9480682	chr6	106,983,406	-0.27	0.05	5.5x10 ⁻⁷	
206029_at	<i>ANKRD1</i>	rs11186320	chr10	92,576,448	0.60	0.10	5.6x10 ⁻⁷	

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201123_s_at	<i>EIF5A</i>	rs3809824	chr17	7,238,128	0.99	0.17	5.7x10 ⁻⁷	
218055_s_at	<i>WDR41</i>	rs163017	chr5	76,711,667	-0.35	0.06	5.9x10 ⁻⁷	
206029_at	<i>ANKRD1</i>	rs4933620	chr10	92,659,865	0.83	0.15	6.4x10 ⁻⁷	
202378_s_at	<i>LEPROT</i>	rs17412723	chr1	65,952,741	-0.37	0.06	6.5x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs27397	chr5	96,340,616	0.31	0.05	6.7x10 ⁻⁷	v
201922_at	<i>NSA2</i>	rs16872235	chr5	74,037,386	0.39	0.07	6.7x10 ⁻⁷	
214823_at	<i>ZNF204P</i>	rs1555040	chr6	27,314,071	0.28	0.05	7.2x10 ⁻⁷	
217623_at	<i>MYLK3</i>	rs4966616	chr16	46,705,576	0.50	0.09	7.2x10 ⁻⁷	
209316_s_at	<i>HBS1L</i>	rs1547247	chr6	135,390,836	-0.38	0.07	7.4x10 ⁻⁷	
203815_at	<i>GSTT1</i>	rs1006771	chr22	24,314,006	-0.73	0.13	7.4x10 ⁻⁷	v
212183_at	<i>NUDT4</i>	rs12422642	chr12	93,924,410	-0.30	0.05	7.4x10 ⁻⁷	
205988_at	<i>CD84</i>	rs3795326	chr1	160,466,356	-0.23	0.04	7.5x10 ⁻⁷	
209314_s_at	<i>HBS1L</i>	rs728030	chr6	135,246,294	-0.25	0.04	7.8x10 ⁻⁷	
205988_at	<i>CD84</i>	rs11265412	chr1	160,453,309	-0.23	0.04	8.6x10 ⁻⁷	
201922_at	<i>NSA2</i>	rs10515194	chr5	74,059,851	0.34	0.06	8.7x10 ⁻⁷	
213812_s_at	<i>CAMKK2</i>	rs11065478	chr12	121,637,133	0.35	0.06	8.8x10 ⁻⁷	v
206505_at	<i>UGT2B4</i>	rs11736579	chr4	70,401,931	-0.41	0.07	8.9x10 ⁻⁷	
219509_at	<i>MYOZ1</i>	rs12570126	chr10	75,416,789	0.67	0.12	8.9x10 ⁻⁷	v
219932_at	<i>SLC27A6</i>	rs11241981	chr5	128,287,181	0.42	0.08	9.0x10 ⁻⁷	
202259_s_at	<i>N4BP2L2</i>	rs12427832	chr13	33,219,033	0.25	0.04	9.1x10 ⁻⁷	
219759_at	<i>ERAP2</i>	rs11135484	chr5	96,221,889	0.31	0.05	9.1x10 ⁻⁷	
65588_at	<i>LOC388796</i>	rs3752278	chr20	37,050,817	0.23	0.04	9.3x10 ⁻⁷	
65588_at	<i>LOC388796</i>	rs3752280	chr20	37,051,007	0.23	0.04	9.3x10 ⁻⁷	
65588_at	<i>LOC388796</i>	rs788350	chr20	37,064,636	0.23	0.04	9.3x10 ⁻⁷	
204245_s_at	<i>RPP14</i>	rs2138240	chr3	58,256,425	-0.26	0.05	9.4x10 ⁻⁷	
211064_at	<i>ZNF493</i>	rs2968084	chr19	21,615,899	-0.09	0.02	9.5x10 ⁻⁷	v
218948_at	<i>QRSL1</i>	rs9486383	chr6	106,983,359	-0.28	0.05	9.6x10 ⁻⁷	v
218948_at	<i>QRSL1</i>	rs9320173	chr6	106,984,669	-0.28	0.05	9.6x10 ⁻⁷	v
218948_at	<i>QRSL1</i>	rs9320174	chr6	106,985,408	-0.28	0.05	9.6x10 ⁻⁷	v
202399_s_at	<i>AP3S2</i>	rs11638138	chr15	90,428,755	0.14	0.02	9.6x10 ⁻⁷	v
206029_at	<i>ANKRD1</i>	rs11817364	chr10	92,498,026	0.71	0.13	9.7x10 ⁻⁷	
218698_at	<i>APIP</i>	rs7111607	chr11	34,924,891	-0.19	0.03	1.0x10 ⁻⁶	v
217623_at	<i>MYLK3</i>	rs7186662	chr16	46,640,695	0.49	0.09	1.0x10 ⁻⁶	
202378_s_at	<i>LEPROT</i>	rs11587159	chr1	65,987,205	-0.40	0.07	1.1x10 ⁻⁶	
207728_at	<i>ATF7IP</i>	rs4763346	chr12	13,604,672	0.15	0.03	1.1x10 ⁻⁶	
214012_at	<i>ERAP1</i>	rs17401719	chr5	96,089,046	0.26	0.05	1.1x10 ⁻⁶	v
214012_at	<i>ERAP1</i>	rs10037212	chr5	96,084,776	0.26	0.05	1.1x10 ⁻⁶	
214012_at	<i>ERAP1</i>	rs1862609	chr5	96,086,690	0.26	0.05	1.1x10 ⁻⁶	
206029_at	<i>ANKRD1</i>	rs10881844	chr10	92,648,024	0.58	0.10	1.1x10 ⁻⁶	
210001_s_at	<i>SOCS1</i>	rs243325	chr16	11,354,497	0.19	0.03	1.2x10 ⁻⁶	
218698_at	<i>APIP</i>	rs1326942	chr11	34,916,785	-0.18	0.03	1.2x10 ⁻⁶	v
214012_at	<i>ERAP1</i>	rs731827	chr5	96,087,015	0.29	0.05	1.2x10 ⁻⁶	v
211200_s_at	<i>EFCAB2</i>	rs2050632	chr1	245,159,567	0.19	0.04	1.3x10 ⁻⁶	v
211200_s_at	<i>EFCAB2</i>	rs522595	chr1	245,159,739	0.19	0.04	1.3x10 ⁻⁶	v
211200_s_at	<i>EFCAB2</i>	rs644341	chr1	245,159,822	0.19	0.04	1.3x10 ⁻⁶	v

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211200_s_at	<i>EFCAB2</i>	rs626070	chr1	245,167,331	0.19	0.04	1.3x10 ⁻⁶	✓
221562_s_at	<i>SIRT3</i>	rs12363280	chr11	231,980	0.22	0.04	1.3x10 ⁻⁶	
34764_at	<i>LARS2</i>	rs12638088	chr3	45,537,973	-0.19	0.03	1.3x10 ⁻⁶	✓
34764_at	<i>LARS2</i>	rs3821895	chr3	45,587,983	-0.19	0.03	1.3x10 ⁻⁶	✓
206918_s_at	<i>CPNE1</i>	rs2425132	chr20	34,338,390	-0.32	0.06	1.4x10 ⁻⁶	✓
202070_s_at	<i>IDH3A</i>	rs12903696	chr15	78,439,018	0.25	0.05	1.4x10 ⁻⁶	
202070_s_at	<i>IDH3A</i>	rs8032618	chr15	78,452,003	0.25	0.05	1.4x10 ⁻⁶	
206918_s_at	<i>CPNE1</i>	rs6060692	chr20	34,517,925	-0.28	0.05	1.5x10 ⁻⁶	✓
218746_at	<i>TAPBPL</i>	rs2534717	chr12	6,573,749	0.26	0.05	1.5x10 ⁻⁶	✓
202554_s_at	<i>GSTM3</i>	rs1887547	chr1	110,295,772	-0.27	0.05	1.5x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs12526055	chr6	135,325,918	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs1014021	chr6	135,334,600	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs12661423	chr6	135,349,570	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs7750300	chr6	135,350,950	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs1590975	chr6	135,352,088	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs7741515	chr6	135,374,368	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs2150681	chr6	135,375,232	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs6923765	chr6	135,335,176	-0.22	0.04	1.6x10 ⁻⁶	✓
209314_s_at	<i>HBS1L</i>	rs11754265	chr6	135,356,216	-0.22	0.04	1.6x10 ⁻⁶	✓
218746_at	<i>TAPBPL</i>	rs2079867	chr12	6,622,111	0.25	0.05	1.6x10 ⁻⁶	✓
203628_at	<i>IGF1R</i>	rs7162314	chr15	99,489,916	0.64	0.12	1.6x10 ⁻⁶	
217623_at	<i>MYLK3</i>	rs40355	chr16	46,792,881	0.49	0.09	1.6x10 ⁻⁶	
203815_at	<i>GSTT1</i>	rs2000467	chr22	24,241,533	-0.73	0.13	1.6x10 ⁻⁶	✓
206029_at	<i>ANKRD1</i>	rs7089533	chr10	92,605,364	0.81	0.15	1.7x10 ⁻⁶	
218795_at	<i>ACP6</i>	rs12037951	chr1	147,102,854	-0.20	0.04	1.7x10 ⁻⁶	✓
212447_at	<i>KBTBD2</i>	rs17335094	chr7	32,017,493	0.13	0.02	1.8x10 ⁻⁶	
218698_at	<i>APIP</i>	rs3763934	chr11	34,937,076	-0.18	0.03	1.9x10 ⁻⁶	✓
212761_at	<i>TCF7L2</i>	rs1421050	chr10	113,754,544	-0.29	0.05	1.9x10 ⁻⁶	
217254_s_at	<i>EPO</i>	rs11977827	chr7	99,526,316	0.27	0.05	2.0x10 ⁻⁶	
221562_s_at	<i>SIRT3</i>	rs7946716	chr11	224,676	0.22	0.04	2.0x10 ⁻⁶	
211200_s_at	<i>EFCAB2</i>	rs10927369	chr1	245,179,960	0.20	0.04	2.1x10 ⁻⁶	✓
218698_at	<i>APIP</i>	rs2915223	chr11	34,914,137	-0.17	0.03	2.1x10 ⁻⁶	✓
211276_at	<i>TCEAL2</i>	rs4898338	chrX	101,413,853	-0.66	0.12	2.1x10 ⁻⁶	
34764_at	<i>LARS2</i>	rs2276860	chr3	45,559,621	-0.20	0.04	2.2x10 ⁻⁶	✓
220061_at	<i>ACSM5</i>	rs12103211	chr16	20,435,262	0.40	0.07	2.2x10 ⁻⁶	
201283_s_at	<i>TRAK1</i>	rs734898	chr3	42,263,535	0.26	0.05	2.3x10 ⁻⁶	
209314_s_at	<i>HBS1L</i>	rs9321481	chr6	135,352,648	-0.22	0.04	2.4x10 ⁻⁶	✓

*✓ represents that the eQTL has already been reported in other tissues from eQTL Browser

(<http://eqtl.uchicago.edu/Home.html>)

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Supplemental Table 4. Differentially expressed transcripts between LA and RA identified from samples from heart transplantation (total 70 transcripts), comparing to 109 differentially expressed transcripts identified from all samples.

ID	Gene Symbol	Left Atrium		Right Atrium		P value Left atrium vs. Right Atrium
		Average Expression	SD	Average Expression	SD	
220491_at	<i>HAMP</i>	7.65	9.28	0.71	0.90	7.9x10 ⁻¹⁶
207069_s_at	<i>SMAD6</i>	7.12	7.75	0.33	0.32	4.3x10 ⁻¹⁵
204790_at	<i>SMAD7</i>	7.46	8.17	0.43	0.39	4.4x10 ⁻¹³
204811_s_at	<i>CACNA2D2</i>	7.19	7.77	0.33	0.39	9.3x10 ⁻¹²
219873_at	<i>COLEC11</i>	7.58	8.19	0.41	0.35	1.1x10 ⁻¹¹
211959_at	<i>IGFBP5</i>	10.50	11.13	0.39	0.42	2.5x10 ⁻¹¹
201272_at	<i>AKR1B1</i>	9.79	9.29	0.37	0.27	3.4x10 ⁻¹¹
203146_s_at	<i>GABBR1</i>	7.70	7.90	0.13	0.14	5.2x10 ⁻¹¹
204776_at	<i>THBS4</i>	8.78	7.74	0.68	0.68	5.8x10 ⁻¹¹
208292_at	<i>BMP10</i>	6.79	8.13	0.73	1.00	6.0x10 ⁻¹¹
210372_s_at	<i>TPD52L1</i>	6.20	5.65	0.37	0.34	7.1x10 ⁻¹¹
202912_at	<i>ADM</i>	8.45	9.15	0.50	0.44	9.8x10 ⁻¹¹
201565_s_at	<i>ID2</i>	7.64	8.28	0.45	0.41	1.3x10 ⁻¹⁰
213094_at	<i>GPR126</i>	4.86	5.42	0.35	0.41	1.9x10 ⁻¹⁰
205554_s_at	<i>DNASE1L3</i>	6.44	6.92	0.29	0.37	2.9x10 ⁻¹⁰
207558_s_at	<i>PITX2</i>	4.01	3.63	0.31	0.20	7.2x10 ⁻¹⁰
203700_s_at	<i>DIO2</i>	5.67	5.39	0.20	0.20	1.0x10 ⁻⁹
219719_at	<i>HIGD1B</i>	7.43	7.10	0.25	0.24	1.6x10 ⁻⁹
203786_s_at	<i>TPD52L1</i>	8.57	8.09	0.38	0.33	3.6x10 ⁻⁹
206050_s_at	<i>RNH1</i>	8.69	8.98	0.20	0.23	3.9x10 ⁻⁹
208335_s_at	<i>DARC</i>	7.63	7.04	0.45	0.44	6.9x10 ⁻⁹
211958_at	<i>IGFBP5</i>	7.56	8.03	0.31	0.41	1.2x10 ⁻⁸
205374_at	<i>SLN</i>	10.25	11.05	0.71	0.53	1.5x10 ⁻⁸
209047_at	<i>AQP1</i>	9.30	8.93	0.28	0.30	1.5x10 ⁻⁸
201809_s_at	<i>ENG</i>	9.14	9.62	0.41	0.33	1.6x10 ⁻⁸
210036_s_at	<i>KCNH2</i>	8.42	8.71	0.25	0.21	2.4x10 ⁻⁸
206768_at	<i>RPL3L</i>	8.05	7.67	0.30	0.31	3.1x10 ⁻⁸
201042_at	<i>TGM2</i>	8.85	9.13	0.22	0.24	5.0x10 ⁻⁸
204174_at	<i>ALOX5AP</i>	7.26	6.91	0.31	0.28	6.9x10 ⁻⁸
221933_at	<i>NLGN4X</i>	4.00	4.34	0.20	0.34	1.2x10 ⁻⁷
203637_s_at	<i>MID1</i>	6.68	7.02	0.30	0.28	1.2x10 ⁻⁷
209291_at	<i>ID4</i>	6.46	7.05	0.52	0.51	1.7x10 ⁻⁷
204099_at	<i>SMARCD3</i>	8.17	8.53	0.29	0.33	1.8x10 ⁻⁷
201313_at	<i>ENO2</i>	6.47	6.80	0.27	0.30	1.9x10 ⁻⁷
219985_at	<i>HS3ST3A1</i>	3.97	4.21	0.15	0.24	2.0x10 ⁻⁷
210095_s_at	<i>IGFBP3</i>	8.87	9.45	0.53	0.48	2.8x10 ⁻⁷
218856_at	<i>TNFRSF21</i>	7.27	6.91	0.29	0.34	2.9x10 ⁻⁷
1007_s_at	<i>DDR1</i>	7.76	7.98	0.16	0.22	3.0x10 ⁻⁷

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213135_at	<i>TIAM1</i>	5.33	5.73	0.35	0.36	3.1x10 ⁻⁷
202949_s_at	<i>FHL2</i>	9.33	10.04	0.70	0.54	3.3x10 ⁻⁷
213974_at	<i>ADAMTSL3</i>	6.42	6.82	0.35	0.36	3.9x10 ⁻⁷
207016_s_at	<i>ALDH1A2</i>	7.83	8.23	0.34	0.37	4.0x10 ⁻⁷
222020_s_at	<i>NTM</i>	4.94	5.23	0.19	0.31	4.6x10 ⁻⁷
219728_at	<i>MYOT</i>	7.43	6.39	1.16	0.58	6.4x10 ⁻⁷
212775_at	<i>OBSL1</i>	6.53	6.91	0.33	0.37	7.1x10 ⁻⁷
203619_s_at	<i>FAIM2</i>	6.05	6.43	0.32	0.38	7.1x10 ⁻⁷
204345_at	<i>COL16A1</i>	6.21	6.49	0.21	0.28	7.6x10 ⁻⁷
204606_at	<i>CCL21</i>	7.24	6.92	0.33	0.24	7.8x10 ⁻⁷
209409_at	<i>GRB10</i>	8.26	8.61	0.35	0.26	8.0x10 ⁻⁷
209292_at	<i>ID4</i>	4.28	4.73	0.36	0.46	8.3x10 ⁻⁷
205990_s_at	<i>WNT5A</i>	4.86	5.04	0.13	0.19	9.7x10 ⁻⁷
210299_s_at	<i>FHL1</i>	8.63	8.18	0.45	0.39	1.4x10 ⁻⁶
203549_s_at	<i>LPL</i>	10.46	9.79	0.57	0.69	1.4x10 ⁻⁶
203636_at	<i>MID1</i>	6.99	7.24	0.22	0.25	1.5x10 ⁻⁶
201952_at	<i>ALCAM</i>	6.60	7.04	0.34	0.48	1.5x10 ⁻⁶
209469_at	<i>GPM6A</i>	4.19	4.35	0.14	0.16	1.5x10 ⁻⁶
206403_at	<i>ZNF536</i>	5.46	5.66	0.16	0.20	1.7x10 ⁻⁶
205984_at	<i>CRHBP</i>	5.92	6.20	0.23	0.30	1.7x10 ⁻⁶
214505_s_at	<i>FHL1</i>	10.30	9.78	0.49	0.50	1.7x10 ⁻⁶
217848_s_at	<i>PPA1</i>	9.54	9.21	0.31	0.31	1.7x10 ⁻⁶
205127_at	<i>PTGS1</i>	6.15	6.38	0.21	0.21	2.2x10 ⁻⁶
214533_at	<i>CMA1</i>	6.08	5.90	0.16	0.17	2.2x10 ⁻⁶
204931_at	<i>TCF21</i>	5.98	6.33	0.31	0.38	2.3x10 ⁻⁶
203886_s_at	<i>FBLN2</i>	7.91	8.24	0.35	0.31	2.5x10 ⁻⁶
206637_at	<i>P2RY14</i>	4.35	3.91	0.53	0.24	2.8x10 ⁻⁶
203813_s_at	<i>SLIT3</i>	7.41	7.74	0.34	0.31	3.1x10 ⁻⁶
209706_at	<i>NKX3-1</i>	5.54	5.71	0.15	0.18	3.1x10 ⁻⁶
203425_s_at	<i>IGFBP5</i>	6.52	6.80	0.25	0.29	3.4x10 ⁻⁶
203088_at	<i>FBLN5</i>	9.20	9.48	0.26	0.29	3.7x10 ⁻⁶
203548_s_at	<i>LPL</i>	9.55	8.81	0.67	0.80	3.7x10 ⁻⁶

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Supplemental Table 5. Top 10 differentially expressed genes between LA and RA in samples from healthy donors. None of them reached the Bonferroni p-value cutoff ($P < 4.2 \times 10^{-6}$).

ID	Gene Symbol	Left Atrium		Right Atrium		P value Left atrium vs. Right Atrium
		Average Expression	SD	Average Expression	SD	
202357_s_at	<i>CFB</i>	6.29	0.12	6.75	0.09	1.1×10^{-4}
202315_s_at	<i>BCR</i>	6.50	0.05	6.76	0.05	1.3×10^{-4}
201951_at	<i>ALCAM</i>	4.06	0.12	4.38	0.05	5.7×10^{-4}
215783_s_at	<i>ALPL</i>	5.27	0.15	5.68	0.06	5.8×10^{-4}
210511_s_at	<i>INHBA</i>	5.85	0.17	6.47	0.16	6.4×10^{-4}
202611_s_at	<i>MED14</i>	3.94	0.07	4.13	0.04	8.6×10^{-4}
202806_at	<i>DBN1</i>	5.78	0.11	6.06	0.03	1.0×10^{-3}
209169_at	<i>GPM6B</i>	4.70	0.09	4.96	0.08	1.3×10^{-3}
201158_at	<i>NMT1</i>	6.63	0.11	6.94	0.09	1.5×10^{-3}
221933_at	<i>NLGN4X</i>	3.96	0.19	4.48	0.15	1.5×10^{-3}

Supplemental Table 6. qPCR primer pairs for validation

MYOZ1-forward-1	CTTCCCAAATATAAGTCCTTCAACAG
MYOZ1-reverse-1	GGAGAGGTTTTGGTTGTAGAGG
MYOZ1-forward-2	CAGATGAGGGTGGAGAAGTTT
MYOZ1-reverse-2	GCTCTTGCTGTATGAGAATCCC
MYOZ1-forward-3	designed and validated by BioRad
MYOZ1-reverse-3	designed and validated by BioRad
SYNPO2L-forward-1	GAGACCTTTGAGCCCATCAG
SYNPO2L-reverse-1	CTTGGCCTCTTTTATGCTCTTC
SYNPO2L-forward-2	AGCAGAGGAAACCGTTACAG
SYNPO2L-reverse-2	GAGAGGTTGGTGCAAGAGAC
TBP-forward	GAATATAATCCCAAGCGTTTG
TBP-reverse	ACTTCACATCACAGCTCCCC
HPRT-forward	ATCAGACTGAAGAGCTATTGTAATGACCA
HPRT-reverse	TGGCTTATATCCAACACTTCGTG

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Table 7a. Genes differentially expressed in heart failure cases vs. referents in LA

Gene ID	Gene Symbol	Cases		Referents		P value Heart failure cases vs. referents
		Average Expression	SD	Average Expression	SD	
204208_at	<i>RNGTT</i>	4.15	0.10	4.05	0.02	1.2x10 ⁻⁷
201426_s_at	<i>VIM</i>	11.41	0.29	11.11	0.07	1.2x10 ⁻⁶
218595_s_at	<i>HEATR1</i>	6.82	0.11	6.97	0.04	1.7x10 ⁻⁶

Table 7b. Genes differentially expressed in heart failure cases vs. referents in RA

Gene ID	Gene Symbol	Cases		Referents		P value Heart failure cases vs. referents
		Average Expression	SD	Average Expression	SD	
201416_at	<i>SOX4</i>	5.59	0.17	5.35	0.01	1.5x10 ⁻¹²
203241_at	<i>UVRAG</i>	6.32	0.13	6.11	0.02	1.2x10 ⁻⁹
222043_at	<i>CLU</i>	7.01	0.48	6.49	0.05	8.0x10 ⁻⁹
211340_s_at	<i>MCAM</i>	8.69	0.20	8.40	0.04	1.3x10 ⁻⁸
219495_s_at	<i>ZNF180</i>	4.66	0.15	4.52	0.02	1.4x10 ⁻⁷
201540_at	<i>FHL1</i>	11.41	0.23	11.16	0.04	2.2x10 ⁻⁷
202806_at	<i>DBN1</i>	5.87	0.14	6.06	0.03	2.3x10 ⁻⁷
209596_at	<i>MXRA5</i>	8.22	0.58	7.61	0.09	3.4x10 ⁻⁷
218856_at	<i>TNFRSF21</i>	6.91	0.34	6.57	0.05	3.5x10 ⁻⁷
217234_s_at	<i>EZR</i>	6.28	0.42	6.72	0.07	4.0x10 ⁻⁷
213735_s_at	<i>COX5B</i>	11.34	0.16	11.53	0.03	4.4x10 ⁻⁷
215235_at	<i>SPTAN1</i>	9.10	0.22	8.86	0.04	8.6x10 ⁻⁷
202780_at	<i>OXCT1</i>	8.87	0.26	8.61	0.04	9.4x10 ⁻⁷
209024_s_at	<i>SYNCRIP</i>	6.22	0.37	6.52	0.03	1.8x10 ⁻⁶
201621_at	<i>NBL1</i>	7.93	0.26	7.67	0.05	1.9x10 ⁻⁶
213180_s_at	<i>GOSR2</i>	6.38	0.18	6.53	0.02	3.6x10 ⁻⁶

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Supplemental Table 8. Differentially expressed genes ($P < 4.2 \times 10^{-6}$) in patients with history of AF cases in RA by the leave-one-out cross validation. The two significant genes from the whole dataset, *DEXI* and *PPM1H*, were just picked up by 2 out of 9 permutations, suggesting that the lack of significant genes is likely attributable to the small sample size.

ID	Gene Symbol	Number of permutations ⁺ (total n=9)
203733_at	<i>DEXI</i>	2
212686_at	<i>PPM1H</i>	2
201690_s_at	<i>TPD52</i>	1
202591_s_at	<i>SSBP1</i>	1
205530_at	<i>ETFDH</i>	1
208782_at	<i>FSTL1</i>	1
209899_s_at	<i>PUF60</i>	1
217678_at	<i>SLC7A11</i>	1
219059_s_at	<i>LYVE1</i>	1
33494_at	<i>ETFDH</i>	1

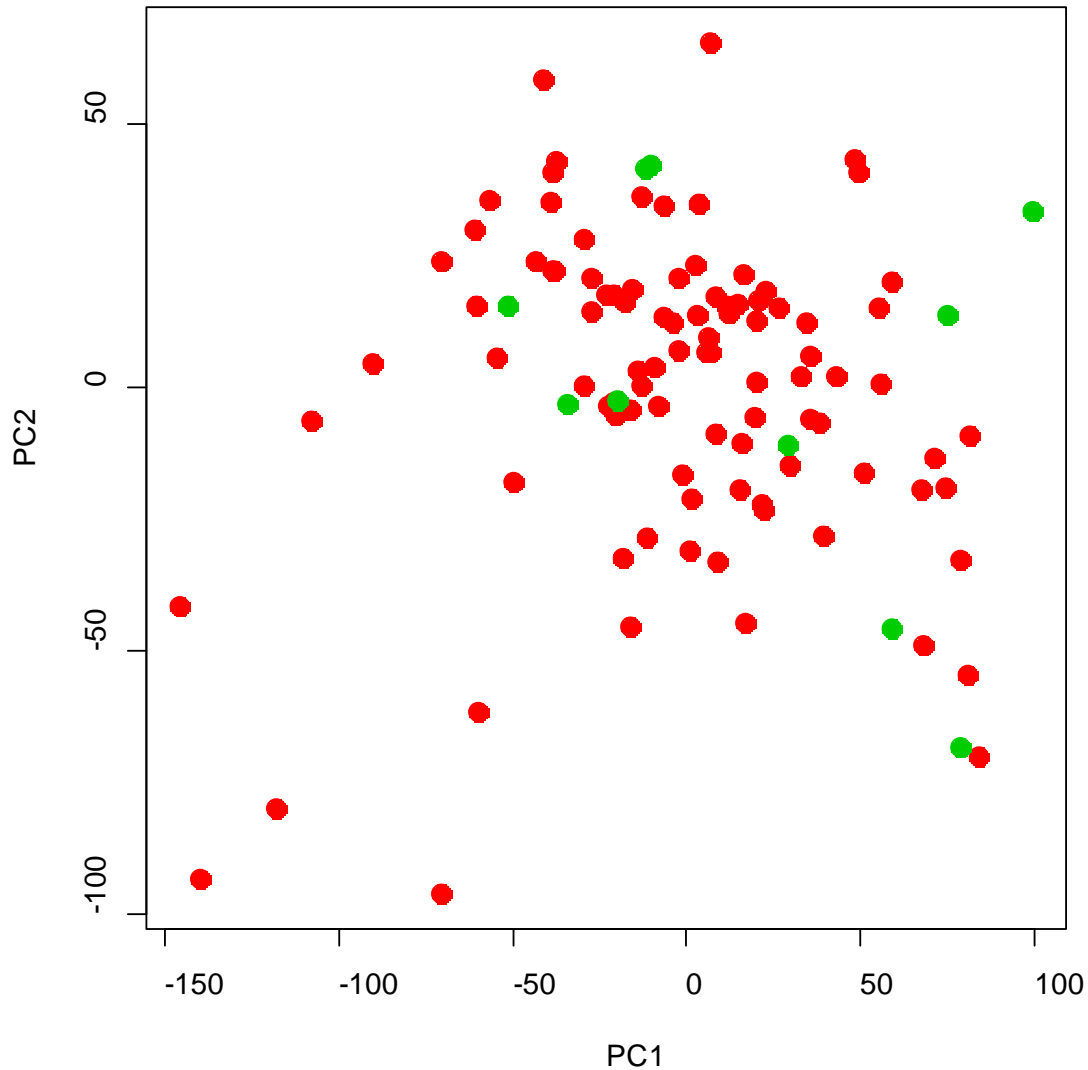
⁺It indicates that the number of permutations when the gene was considered as differential expressed.

Supplemental Table 9. Top 10 differentially expressed genes between LA and RA in samples with history of AF. None of them reached the Bonferroni p-value cutoff ($P < 4.2 \times 10^{-6}$).

ID	Gene Symbol	Left Atrium		Right Atrium		P value Left atrium vs. Right Atrium
		Average Expression	SD	Average Expression	SD	
207433_at	<i>IL10</i>	4.42	0.08	4.64	0.11	3.0×10^{-4}
209047_at	<i>AQP1</i>	9.26	0.21	8.85	0.17	4.1×10^{-4}
205431_s_at	<i>BMP5</i>	6.35	0.17	6.03	0.14	5.0×10^{-4}
203700_s_at	<i>DIO2</i>	5.71	0.19	5.38	0.12	6.9×10^{-4}
207228_at	<i>PRKACG</i>	6.24	0.12	6.04	0.10	1.2×10^{-3}
214081_at	<i>PLXDC1</i>	6.40	0.07	6.17	0.14	1.2×10^{-3}
211594_s_at	<i>MRPL9</i>	6.82	0.12	6.64	0.07	1.7×10^{-3}
207069_s_at	<i>SMAD6</i>	7.18	0.34	7.79	0.36	1.9×10^{-3}
201527_at	<i>ATP6V1F</i>	9.39	0.15	9.14	0.13	2.0×10^{-3}
211113_s_at	<i>ABCG1</i>	6.44	0.16	6.17	0.16	2.8×10^{-3}

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Supplemental Figure 1. Principle component analysis of transcriptional profiles. Each point represents one sample, mapping to the first two principle components (PCs). Red points represent samples from heart transplantation surgery, whereas green points represent samples from healthy donors. No significant distinction could be found between two groups.



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