

Genes Differentially Regulated by 2-Fold or higher in Male WT vs. Female WT Comparison:

Probe Set ID	Femal e		Male		Male		Male		p-value	p-value	p-value	p-value	Gene	Description	GB	Entrez Id	Cytoband
	Cd82-/-	Cd82+/+	Cd82-/-	Cd82+/+	Cd82-/-	Cd82+/+	Cd82-/-	Cd82+/+									
	signal	signal	signal	signal	Ratio	Ratio	Ratio	Ratio	Female Cd82+/+ vs Female Cd82-/-	Male Cd82+/+ vs Male Cd82-/-	Female Cd82+/+ vs Male Cd82-/-	Male Cd82+/+ vs Female Cd82-/-					
1457666_s_at	3	1	1	3269	2884.4	2.2985	0.0004	0.5564	2E-13	0.1337	7E-11	0.287	Ifi202b	interferon activated gene 202B	AV229143	26388	1 H3
1421551_s_at	5	4	3	3224	845.2	1.2393	0.0008	0.5317	9E-09	0.6723	3E-10	0.1814	Ifi202b	interferon activated gene 202B	NM_011940	26388	1 H3
1426438_at	3	4	1928	2573	597.91	0.7865	0.7493	569.62	8E-09	0.6772	0.0719	5E-08	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	AA210261	26900	Y A1
1452077_at	5	3	1228	1653	488.7	1.4532	0.7426	249.73	1E-07	0.5858	0.0983	5E-07	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	AA210261	26900	Y A1
1417210_at	5	3	1083	1072	399.38	2.0054	1.011	201.34	1E-06	0.4049	0.731	2E-06	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural ger	NM_012011	26908	Y A1
1424903_at	6	3	325	369	137.76	2.2151	0.8804	54.752	4E-07	0.3192	0.0775	5E-05	Jarid1d	jumonji, AT rich interactive domain 1D (Rbp2 like)	AF127244	20592	Y A1
1426439_at	16	8	670	1098	132.79	1.942	0.6099	41.709	4E-06	0.2205	0.0265	7E-09	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	AA210261	26900	Y A1
1426598_at	10	4	243	304	79.421	2.5006	0.7998	25.401	5E-06	0.2296	0.0331	7E-05	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chrom	BB742957	22290	Y A1
1419728_at	5	5	7	231	49.786	1.1236	0.0302	1.3402	3E-05	0.8662	3E-06	0.6036	Cxcl5	chemokine (C-X-C motif) ligand 5	NM_009141	20311	5 E1
1442140_at	46	43	92	1855	42.915	1.0673	0.0495	1.9918	2E-05	0.9125	2E-10	0.0676	Tnn	tenascin N	AI591634	329278	1 H2.1
1419332_at	4	5	7	130	26.448	0.8547	0.0558	1.7274	2E-05	0.7995	0.0001	0.3935	Egfl6	EGF-like-domain, multiple 6	NM_019397	54156	X F5
1433716_x_at	13	6	11	112	17.795	1.9893	0.0998	0.8927	4E-06	0.1654	0.0001	0.821	Gfra2	glial cell line derived neurotrophic factor family receptor alpha 2	BB284482	14586	14 D3-E1
1422247_a_at	9	16	207	238	15.263	0.5647	0.8689	23.486	2E-08	0.3835	0.0376	0.0002	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chrom	NM_009484	22290	Y A1
1456935_at	9	7	7	102	14.961	1.2626	0.0649	0.7695	0.0004	0.7065	0.0001	0.6402	Al606473	expressed sequence Al606473	Al606473		99686
1457945_at	21	25	365	350	13.876	0.8164	1.0408	17.689	3E-08	0.4352	0.596	4E-08			BM121819		
1427300_at	68	38	37	514	13.542	1.7899	0.0729	0.5517	2E-07	0.0573	4E-08	0.0362	Lhx8	LIM homeobox protein 8	D49658	16875	3 H3-H4
1438946_at	8	14	14	174	12.6	0.599	0.0827	1.7401	0.0007	0.5226	4E-05	0.4096	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	BB221015	18595	5 C3.3
1460248_at	39	39	51	488	12.469	1.0055	0.1045	1.2958	2E-08	0.9806	5E-10	0.1899	Cpxm2	carboxypeptidase X 2 (M14 family)	AF017639	55987	7 F4
1421917_at	69	112	121	1293	11.587	0.6186	0.0936	1.7527	7E-10	0.0164	6E-10	0.0057	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	AW537708	18595	5 C3.3
1449340_at	47	36	31	334	9.3726	1.3274	0.0919	0.6491	4E-07	0.1462	1E-05	0.1765	Sostdc1	sclerostin domain containing 1	BC021458	66042	12 B2
1431418_at	5	11	87	101	9.2042	0.4853	0.8652	16.409	0.0007	0.2768	0.2967	6E-05	C030026M15Rik	RIKEN cDNA C030026M15 gene	AK021104	77378	
1421058_at	13	22	11	184	8.3896	0.5882	0.0609	0.8692	2E-07	0.2169	6E-06	0.7693	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	NM_009626	11529	3 G3
1435227_at	69	37	58	251	6.8632	1.8781	0.2324	0.8493	9E-05	0.0598	2E-09	0.0938	Bcl11b	B-cell leukemia/lymphoma 11B	BM117007	58208	12 F1
1426278_at	191	200	115	1337	6.6789	0.9537	0.0864	0.6048	9E-10	0.5953	2E-08	0.0097	Ifi27	interferon, alpha-inducible protein 27	AY090098	76933	12 E
1416855_at	305	199	219	1310	6.5691	1.5289	0.167	0.7176	7E-07	0.1131	7E-06	0.2465	Gas1	growth arrest specific 1	BB550400	14451	13 B3-C2
1451567_a_at	116	182	82	1184	6.507	0.6393	0.0689	0.7011	3E-07	0.0131	3E-10	0.0121	Ifi203	interferon activated gene 203	BC008167	15950	1 H3
1457429_s_at	42	26	29	155	6.0147	1.6334	0.184	0.6775	0.0003	0.217	0.0001	0.265	Gm106	gene model 106, (NCBI)	BB549174	226866	1 A3
1419000_at	20	18	30	109	5.9328	1.0882	0.2748	1.4983	1E-07	0.8285	7E-07	0.2699	Cpxm2	carboxypeptidase X 2 (M14 family)	AF017639	55987	7 F4
1417411_at	34	18	22	104	5.8382	1.8986	0.2074	0.6377	0.0031	0.2562	0.0002	0.2682	Nap115	nucleosome assembly protein 1-like 5	NM_021432	58243	6 C1
1417986_at	47	17	25	100	5.8276	2.7173	0.2519	0.5402	0.0003	0.0416	1E-05	0.0799	Nrarp	Notch-regulated ankyrin repeat protein	BI696369	67122	2 A3
1429947_a_at	81	70	29	390	5.6017	1.163	0.0736	0.3547	6E-05	0.5703	7E-05	0.0295	Zbp1	Z-DNA binding protein 1	AK008179	58203	2 H3
1434848_at	38	34	31	177	5.2204	1.133	0.1745	0.8042	1E-05	0.562	1E-08	0.1186			BB259283		
1442153_at	35	33	170	170	5.1022	1.0521	1.0023	4.8606	0.0002	0.8651	0.976	5E-08			BB206087		
1448291_at	56	102	86	519	5.1011	0.5539	0.1666	1.5346	7E-07	0.0368	2E-09	0.0588	Mmp9	matrix metalloproteinase 9	NM_013599	17395	2 H1-H2
1450110_at	85	82	75	414	5.0212	1.0367	0.1812	0.8777	5E-09	0.6413	3E-06	0.4949	Adh7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide	NM_009626	11529	3 G3
1451648_a_at	99	81	69	403	4.9514	1.2205	0.1711	0.6943	4E-06	0.3157	1E-09	0.0114	Folr2	folate receptor 2 (fetal)	BC022108	14276	7 E3
1421916_at	49	66	58	317	4.8337	0.7408	0.1817	1.1857	7E-08	0.0852	4E-09	0.2559	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	AW537708	18595	5 C3.3
1422317_a_at	919	2017	1707	9559	4.7388	0.4555	0.1786	1.8586	4E-09	4E-05	6E-14	1E-05	Il1rl1	interleukin 1 receptor-like 1	NM_010743	17082	1 B
1439549_at	88	42	62	198	4.7166	2.1108	0.3152	0.7044	5E-05	0.015	2E-06	0.0562	Prrg3	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	BB164509	208748	X A7.3
1416371_at	217	162	162	750	4.6418	1.3449	0.2165	0.7473	2E-07	0.1078	4E-09	0.0619	Apod	apolipoprotein D	NM_007470	11815	16 B2
1424807_at	372	285	342	1304	4.5776	1.3064	0.2624	0.9193	4E-10	0.0056	1E-07	0.4664	Lama4	laminin, alpha 4	BB053010	16775	10 B1
1418536_at	54	44	27	197	4.4362	1.2083	0.1381	0.5072	1E-05	0.365	1E-04	0.0658	H2-Q7	histocompatibility 2, Q region locus 7	M29881	15018	17 B1
1460661_at	76	118	111	521	4.4361	0.6479	0.2128	1.4569	5E-08	0.0876	2E-09	0.0921	S1pr3	sphingosine-1-phosphate receptor 3	NM_010101	13610	13 B1
1430310_at	8	34	23	148	4.381	0.2372	0.1572	2.9034	0.0009	0.0321	2E-05	0.0571	Tspan11	tetraspanin 11	BB535262	68498	6 F3
1460250_at	11	37	15	160	4.3074	0.2959	0.093	1.3539	0.0001	0.0161	0.0006	0.6103	Sostdc1	sclerostin domain containing 1	BC021458	66042	12 B2
1438055_at	66	37	60	157	4.2501	1.7802	0.3853	0.9198	4E-06	0.0107	2E-07	0.5017	Rarres1	retinoic acid receptor responder (tazarotene induced) 1	BB035017	109222	3 E1
1450339_a_at	70	55	65	233	4.2469	1.2698	0.2797	0.9354	5E-06	0.1744	3E-07	0.5793	Bcl11b	B-cell leukemia/lymphoma 11B	NM_021399	58208	12 F1
1416298_at	110	144	147	604	4.1799	0.76	0.243	1.3368	4E-09	0.1135	4E-06	0.1845	Mmp9	matrix metalloproteinase 9	NM_013599	17395	2 H1-H2
1418796_at	52	37	36	154	4.1217	1.3931	0.2362	0.6989	0.0031	0.3783	0.0029	0.3586	Clec11a	C-type lectin domain family 11, member a	NM_009131	20256	7 B3-B5
1448494_at	223	179	191	733	4.1038	1.2465	0.2606	0.8581	3E-08	0.1107	2E-08	0.2344	Gas1	growth arrest specific 1	BB550400	14451	13 B3-C2
1417985_at	90	58	74	229	3.9726	1.5559	0.3242	0.8278	6E-09	0.0037	2E-09	0.0927	Nrarp	Notch-regulated ankyrin repeat protein	BI696369	67122	2 A3
1448601_s_at	202	144	151	573	3.9704	1.3968	0.2639	0.75	5E-08	0.024	2E-08	0.0335	Msx1	homeobox, msh-like 1	BC016426	17701	5 B3
1427746_x_at	324	340	218	1347	3.964	0.9531	0.1618	0.673	9E-06	0.691	1E-07	0.0031	H2-K1	histocompatibility 2, K1, K region	S70184	14972	17 B1
1452966_at	37	27	29	108	3.9524	1.3622	0.2725	0.7907	1E-05	0.0719	2E-05	0.1914	Bcl11b	B-cell leukemia/lymphoma 11B	AK020296	58208	12 F1
1435264_at	148	150	136	593	3.9511	0.9882	0.2289	0.9153	3E-08	0.9014	7E-12	0.1734	Emilin2	elastin microfibril interfacar 2	BB811788	246707	17 E1.3

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82-/-	Femal e Cd82+/-	Male Cd82-/-	Male Cd82+/-	Male Cd82+/-	Male Cd82+/-	Male Cd82+/-	p-value Male Cd82+/-	p-value Female Cd82+/-	p-value Male Cd82+/-	p-value Female Cd82+/-	Gene	Description	GB	Entrez Id	Cytoband
	averag e signal	averag e signal	averag e signal	averag e signal	+ Ratio	+ Ratio	+ Ratio	+ vs Female Cd82+/-	+ vs Female Cd82+/-	+ vs Male Cd82+/-	+ vs Male Cd82+/-					
1418317_at	50	41	40	162	3.9443	1.2042	0.2472	0.8098	5E-05	0.3918	2E-07	0.1457	Lhx2	LIM homeobox protein 2	NM_010710	16870 2 B
1419209_at	50	67	51	264	3.916	0.7416	0.1944	1.0266	2E-07	0.0022	1E-07	0.8072	Cxcl1	chemokine (C-X-C motif) ligand 1	NM_008176	14825 5 E-F
1448789_at	251	441	412	1713	3.8836	0.5686	0.2406	1.6434	2E-08	0.0008	6E-10	0.0005	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	AF253409	56847 7 C
1448326_a_at	407	934	606	3602	3.8573	0.4354	0.1683	1.4906	3E-06	7E-05	3E-07	0.0184	Crabp1	cellular retinoic acid binding protein I	NM_013496	12903 9 A5.3
1437056_x_at	885	931	924	3543	3.8059	0.951	0.2607	1.0434	2E-08	0.6206	5E-10	0.6207	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	BB558800	78892 8 E1
1441743_at	194	99	116	374	3.7872	1.9664	0.3091	0.5953	9E-07	0.0034	2E-07	0.0063	Pax3	paired box gene 3	BB759978	18505 1 C4
1450506_at	306	251	222	944	3.76	1.2193	0.2354	0.7259	4E-08	0.0946	2E-09	0.0079	Lmo7	LIM domain only 7	BM231903	380928 14 E2.3
1436094_at	100	49	47	184	3.759	2.0307	0.2565	0.4748	0.0001	0.009	0.0004	0.0189	Vgf	VEGF nerve growth factor inducible	BF458396	381677 5 G2
1460458_at	195	238	248	891	3.7455	0.8207	0.2783	1.2702	2E-07	0.173	1E-12	0.0243	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	AK019034	78892 8 E1
1424923_at	222	239	281	896	3.7442	0.929	0.3133	1.2629	1E-06	0.6539	5E-06	0.1848	Serpina3g	serine (or cysteine) peptidase inhibitor, clade A, member 3G	BC002065	20715 12 E
1437173_at	271	399	413	1480	3.7082	0.6793	0.2793	1.5246	2E-09	0.0023	5E-10	0.0006	S1pr3	sphingosine-1-phosphate receptor 3	BB532532	13610 13 B1
1444821_s_at	237	304	357	1119	3.6799	0.7805	0.3194	1.5058	1E-05	0.0697	1E-05	0.0054	Aspn	aspirin	NM_025711	66695 13 B1
1456335_at	51	44	47	161	3.6654	1.1654	0.2916	0.9172	2E-06	0.4103	2E-06	0.6206	Gm106	gene model 106, (NCBI)	BB258317	226866 1 A3
1427395_a_at	63	189	146	681	3.6063	0.3356	0.2142	2.3018	6E-06	0.0105	1E-05	0.0346	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	BC026667	56847 7 C
1416203_at	253	485	351	1738	3.58	0.5214	0.2019	1.3866	8E-10	8E-05	6E-09	0.018	Aqp1	aquaporin 1	NM_007472	11826 6 B3
1419015_at	753	754	889	2693	3.5712	0.9981	0.3301	1.1811	2E-08	0.9865	2E-08	0.136	Wispl2	WNT1 inducible signaling pathway protein 2	NM_016873	22403 2 H3
1418133_at	78	73	96	260	3.5434	1.0687	0.3683	1.2211	6E-07	0.5921	3E-07	0.0747	Bcl3	B-cell leukemia/lymphoma 3	NM_033601	12051 7 A3
1418842_at	86	40	48	141	3.5351	2.1676	0.3412	0.5564	0.0003	0.0058	4E-05	0.0032	Hcls1	hematopoietic cell specific Lyn substrate 1	NM_008225	15163 16 B
1434758_at	364	434	453	1525	3.5169	0.8405	0.2968	1.2418	2E-10	0.0038	3E-11	0.0005	Crispld2	cysteine-rich secretory protein LCCL domain containing 2	BB745401	78892 8 E1
1449939_s_at	460	630	495	2213	3.5135	0.7298	0.2239	1.0779	5E-09	0.0005	3E-09	0.3601	Dlk1	delta-like 1 homolog (Drosophila)	NM_010052	13386 12 E-F1
1417642_at	88	176	147	614	3.4847	0.4998	0.2389	1.6654	7E-09	0.0006	2E-08	0.0051	Aldh1a3	aldehyde dehydrogenase family 1, subfamily A3	AF253409	56847 7 C
1438658_a_at	849	1215	1197	4201	3.457	0.6989	0.2849	1.4092	3E-10	0.0026	5E-10	0.0027	S1pr3	sphingosine-1-phosphate receptor 3	AV238324	13610 13 B1
1419042_at	149	172	67	591	3.4332	0.8676	0.1141	0.4514	7E-05	0.492	3E-08	0.0007	Iigp1	interferon inducible GTPase 1	BM239828	60440 18 D3
1425145_at	603	1120	954	3845	3.4316	0.538	0.2482	1.5834	6E-08	0.0003	4E-11	0.0003	Il1rl1	interleukin 1 receptor-like 1	D13695	17082 1 B
1435477_s_at	72	59	40	204	3.4219	1.2117	0.1953	0.5515	3E-06	0.2747	1E-07	0.004	Fcgr2b	Fc receptor, IgG, low affinity IIb	BM224327	14130 1 H3
1448775_at	117	197	95	671	3.3985	0.5907	0.1412	0.8126	2E-05	0.0093	2E-08	0.1307	Ifi203	interferon activated gene 203	NM_008328	15950 1 H3
1455844_at	53	34	29	114	3.3639	1.557	0.2545	0.55	0.0079	0.2679	0.0029	0.1326	Cables1	Cdk5 and Abl enzyme substrate 1	BI079333	63955 18 A2
1427054_s_at	47	50	45	165	3.3199	0.9407	0.2734	0.9648	2E-06	0.7379	2E-09	0.8008	Abi3bp	ABI gene family, member 3 (NESH) binding protein	BC026627	320712 16 C.1
1418666_at	521	546	474	1811	3.3189	0.9549	0.2617	0.9095	7E-07	0.6636	7E-08	0.3617	Ptx3	pentraxin related gene	NM_008987	19288 3 E1
1418204_s_at	72	50	20	164	3.3025	1.4443	0.1209	0.2765	3E-07	0.0065	1E-06	0.0001	Aif1	allograft inflammatory factor 1	NM_019467	11629 17 B1
1417633_at	163	58	134	192	3.295	2.7982	0.6991	0.8232	4E-05	0.0036	0.0051	0.3867	Sod3	superoxide dismutase 3, extracellular	NM_011435	20657 5 C1
1436124_at	47	43	47	139	3.2514	1.0974	0.3413	1.0114	4E-05	0.6459	1E-05	0.9481	Pcyt1b	phosphate cytidylyltransferase 1, choline, beta isoform	BE996519	236899 X C3
1424808_at	83	82	81	265	3.2474	1.0196	0.3045	0.9697	1E-06	0.9198	1E-06	0.8692	Lama4	laminin, alpha 4	BB053010	16775 10 B1
1448475_at	475	371	360	1199	3.2285	1.2801	0.3	0.7565	4E-08	0.0527	7E-08	0.0379	Olfml3	olfactomedin-like 3	NM_133859	99543 3 F2.2
1420389_at	274	134	125	431	3.2168	2.0476	0.2901	0.4558	5E-08	0.0005	1E-06	0.0006	Pax3	paired box gene 3	NM_008781	18505 1 C4
1431008_at	57	64	25	205	3.2034	0.8964	0.1237	0.4421	5E-05	0.7074	0.0015	0.1531	O610037M15Rik	RIKEN cDNA O610037M15 gene	BG916808	68395
1424948_x_at	329	372	192	1180	3.1734	0.8849	0.1623	0.5821	1E-05	0.2787	3E-08	0.0002	H2-K1	histocompatibility 2, K1, K region	L23495	14972 17 B1
1418156_at	45	36	32	114	3.1711	1.264	0.2819	0.7073	0.0002	0.4533	0.0006	0.3161	Kcne4	potassium voltage-gated channel, Isk-related subfamily, gene 4	NM_021342	57814 1 C4
1457664_x_at	90	39	42	123	3.1574	2.3059	0.3411	0.467	0.0061	0.0339	0.0042	0.0303	C2	complement component 2 (within H-2S)	AV227574	12263 17 B1
1430335_a_at	244	132	139	415	3.1491	1.8483	0.3361	0.5727	1E-07	0.0044	3E-06	0.0095	Pax3	paired box gene 3	AK012493	18505 1 C4
1451944_a_at	34	38	54	119	3.1359	0.9021	0.4561	1.5853	3E-05	0.7972	0.0005	0.2289	Tnfrsf11	tumor necrosis factor (ligand) superfamily, member 11	AB032771	21943 14 D3
1460667_at	37	65	53	201	3.1091	0.5781	0.264	1.4199	9E-06	0.0906	0.0001	0.3048	U90926	cDNA sequence U90926	NM_020562	57425 5 E2
1421996_at	149	73	91	224	3.0778	2.0384	0.4044	0.6107	0.0002	0.0076	2E-05	0.0074	Tcfap2a	transcription factor AP-2, alpha	NM_011547	21418 13 A5-B1
1441165_s_at	105	47	71	142	3.0522	2.2607	0.4985	0.6731	1E-06	0.0093	4E-05	0.1128	C12n2	calyntenin 2	AI448973	6408
1419043_a_at	446	592	200	1804	3.0485	0.753	0.1107	0.4481	8E-05	0.1429	4E-09	0.0001	Iigp1	interferon inducible GTPase 1	BM239828	60440 18 D3
1450696_at	99	84	42	255	3.0383	1.1814	0.1634	0.4202	2E-06	0.2179	8E-06	0.0032	Psmb9	proteasome (prosome, macropain) subunit, beta type 9 (large n	NM_013585	16912 17 B1
1457035_at	102	91	51	276	3.031	1.1185	0.1858	0.5035	1E-05	0.4955	4E-06	0.0077	Al607873	expressed sequence Al607873	AI607873	226691 1 H3
1421855_at	48	35	26	105	3.0206	1.3817	0.2493	0.5451	0.0014	0.3126	8E-06	0.0254	Fgl2	fibrinogen-like protein 2	BF136544	14190 5 A3
1422013_at	41	44	12	132	2.9946	0.924	0.0918	0.2974	8E-07	0.585	0.0002	0.0196	Clec4a2	C-type lectin domain family 4, member a2	NM_011999	26888 6 F3
1429310_at	309	292	274	875	2.9931	1.0576	0.313	0.8857	1E-07	0.5284	1E-06	0.3318	Flrt3	fibronectin leucine rich transmembrane protein 3	BE945486	71436 2 F3
1426937_at	88	109	121	323	2.9697	0.8135	0.3751	1.3694	1E-07	0.0067	1E-06	0.004	G33040615Rik	RIKEN cDNA G33040615 gene	AK018128	70717 5 G3
1416321_s_at	187	65	68	193	2.9593	2.8699	0.354	0.365	6E-06	0.0003	0.0101	0.0175	Prepl	proline arginine-rich end leucine-rich repeat	NM_054077	116847 1 E4
1449945_at	96	103	89	305	2.9487	0.9289	0.2909	0.9235	6E-07	0.3388	2E-08	0.239	Ppargc1b	peroxisome proliferative activated receptor, gamma, coactivator	NM_133249	170826 18 E1
1446682_at	145	83	117	244	2.9431	1.7488	0.4784	0.8051	4E-05	0.071	0.0237	0.5466			BB660139	
1453571_at	30	40	83	118	2.9381	0.738	0.699	2.7829	0.0003	0.4523	0.0451	0.0133	Depdc6	DEP domain containing 6	BB324973	97998 15 D1
1450430_at	143	117	73	342	2.911	1.2195	0.2143	0.5115	1E-10	0.044	3E-07	0.001	Mrc1	mannose receptor, C type 1	NM_008625	17533 2 A2

Table S1 - M vs F (WT)

Probe Set ID	Female Cd82- /-	Female Cd82 +/+	Male Cd82- /	Male Cd82+ /	Male Cd82+/ /	Female Cd82-/ /	Male Cd82-/ /	p-value Male Cd82+/ + vs Female Cd82-/ +	p-value Female Cd82+/ + vs Female Cd82-/ -	p-value Male Cd82+/ + vs Male Cd82-/ -	p-value M/F Cd82-/ - vs Cd82-/ -	Gene	Description	GB	Entrez Id	Cytoband	
	averag ge signal	averag ge signal	averag ge signal	averag ge signal	FMale Cd82+/ + Ratio	Female Cd82+/ + Ratio	/ Male Cd82+/ + Ratio	Female Cd82-/ Ratio	Female Cd82-/ -	Male Cd82-/ -	Female Cd82-/ -						
1418872_at	201	202	206	587	2.9075	0.9959	0.3514	1.0258	3E-07	0.9523	4E-07	0.7626	Abcb1b	ATP-binding cassette, sub-family B (MDR/TAP), member 1B	NM_011075	18669	5 A2-A3
1419604_at	48	78	25	227	2.9013	0.6067	0.1085	0.5186	0.001	0.0501	3E-06	0.0179	Zbp1	Z-DNA binding protein 1	NM_021394	58203	2 H3
1423260_at	314	221	253	639	2.8945	1.4235	0.3961	0.8054	7E-06	0.0125	4E-06	0.0609	Id4	inhibitor of DNA binding 4	BB121406	15904	13 B
1417381_at	1288	988	528	2825	2.8591	1.3036	0.1869	0.4098	8E-11	2E-05	7E-10	3E-07	C1qa	complement component 1, q subcomponent, alpha polypeptide	NM_007572	12259	4 D3
1435990_at	44	64	90	183	2.8424	0.6762	0.4917	2.0671	8E-06	0.2948	4E-05	0.0453	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with thr	BG073461	216725	11 B1.3
1421001_a_at	36	36	41	103	2.8322	0.9984	0.3967	1.1253	0.0019	0.995	3E-07	0.2504	Car6	carbonic anhydrase 6	NM_009802	12353	4 E2
1416652_at	340	476	530	1347	2.8294	0.7144	0.3938	1.5594	1E-06	0.0004	1E-05	0.0015	Aspn	asporin	NM_025711	66695	13 B1
1416715_at	462	495	544	1398	2.8257	0.9345	0.3893	1.1773	1E-07	0.2299	4E-07	0.0403	Gjb3	gap junction protein, beta 3	NM_008126	14620	4 D2.2
1422979_at	46	64	59	180	2.8203	0.7201	0.3283	1.2859	1E-05	0.1564	1E-06	0.2221	Suv39h2	suppressor of variegation 3-9 homolog 2 (Drosophila)	NM_022724	64707	2 2.5 cM
1439902_at	78	56	41	159	2.8191	1.3889	0.2572	0.5221	2E-05	0.0781	4E-07	0.0014	C5ar1	complement component 5a receptor 1	BB552085	12273	7 A2
1424443_at	122	78	46	219	2.8167	1.57	0.2088	0.3747	6E-07	0.0007	1E-05	0.0006	Tm6sf1	transmembrane 6 superfamily member 1	AV378394	107769	7 D1
1443229_at	13	37	12	104	2.8104	0.3507	0.1157	0.9277	0.0015	0.0272	5E-05	0.8659	Atad2	ATPase family, AAA domain containing 2	AV319821	70472	15 D2
1449175_at	81	56	39	158	2.8015	1.4423	0.2445	0.475	2E-05	0.0487	4E-05	0.0071	Gpr65	G-protein coupled receptor 65	NM_008152	14744	12 E
1425894_at	77	90	88	251	2.7939	0.8547	0.3492	1.1416	8E-06	0.4679	3E-05	0.5515	Mrgprf	MAS-related GPR, member F	BC019711	211577	7 F5
1420380_at	806	939	919	2622	2.7917	0.8577	0.3504	1.1406	1E-08	0.0438	3E-09	0.0728	Ccl2	chemokine (C-C motif) ligand 2	AF065933	20296	11 C-E1
1416051_at	92	62	68	172	2.7877	1.4885	0.3967	1.7411	0.0005	0.2121	0.0001	0.2681	C2	complement component 2 (within H-2S)	NM_013484	12263	7 B1
1434667_at	84	84	92	232	2.7756	1.0071	0.3958	1.0908	8E-05	0.9678	7E-05	0.5991	Col8a2	collagen, type VIII, alpha 2	BG229308	329941	4 D2.2
1424041_s_at	116	57	83	156	2.7525	2.0323	0.5283	0.7155	4E-06	5E-05	7E-05	0.0048	C1s	complement component 1, s subcomponent	BC022123	50908	6 F2
1424067_at	138	63	79	174	2.752	2.1772	0.4532	0.5729	7E-05	0.0014	0.0004	0.0086	Icam1	intercellular adhesion molecule 1	BC008626	15894	9 A3
1419132_at	106	76	83	210	2.7498	1.3918	0.3946	0.7796	8E-06	0.0515	1E-08	0.0366	Tlr2	toll-like receptor 2	NM_011905	24088	3 E3
1455396_at	56	63	80	173	2.7487	0.8962	0.4639	1.4228	5E-06	0.557	9E-06	0.055	Atp8b1	ATPase, class I, type 8B, member 1	BF451402	54670	18 E1
1434903_s_at	154	182	172	499	2.7456	0.8501	0.3451	1.1148	2E-08	0.0408	6E-10	0.0913	Il1rl2	interleukin 1 receptor-like 2	BG073776	107527	1 B
1439831_at	70	106	34	289	2.7219	0.6583	0.1191	0.4922	5E-05	0.0101	6E-07	0.0034			AW111920		
1424131_at	1471	3923	3119	10666	2.7187	0.3749	0.2924	2.1206	2E-11	1E-09	1E-07	1E-05	Col6a3	collagen, type VI, alpha 3	AF064749	12835	1 D
1420671_x_at	37	44	23	119	2.6846	0.8253	0.192	0.6246	1E-06	0.3268	3E-05	0.1164	Ms4a4c	membrane-spanning 4-domains, subfamily A, member 4C	NM_029499	64380	19 A
1459816_x_at	103	44	63	116	2.6752	2.3703	0.5417	0.6114	0.0017	0.0869	0.0991	0.3372	Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	BB060663	59001	4 C1
1425336_x_at	2752	3236	1785	8648	2.6725	0.8506	0.2064	0.6486	6E-06	0.173	6E-09	0.0008	H2-K1	histocompatibility 2, K1, K region	BC011306	14972	17 B1
1422962_a_at	351	473	216	1262	2.6681	0.7413	0.1714	0.617	2E-05	0.043	1E-09	0.0003	Psmb8	proteasome (prosome, macropain) subunit, beta type 8 (large n	NM_010724	16913	17 B1
1425407_s_at	43	45	31	121	2.6662	0.9407	0.2524	0.7154	0.0003	0.7207	6E-05	0.1335	Clec4a2	C-type lectin domain family 4, member a2	BC006623	26888	6 F3
1458453_at	60	62	46	166	2.6581	0.9577	0.2787	0.7736	4E-05	0.8574	0.0013	0.4646	Lmo7	LIM domain only 7	AW553387	380928	14 E2.3
1430485_at	58	81	84	214	2.6478	0.7181	0.391	1.4416	9E-07	0.0217	0.0004	0.0933	Trpc2	transient receptor potential cation channel, subfamily C, membe	AW324327	22064	7 F1
1452296_at	524	401	496	1059	2.6419	1.3074	0.4682	0.946	5E-08	0.0505	2E-06	0.6568	Slit3	slit homolog 3 (Drosophila)	BM570006	20564	
1425094_a_at	80	63	61	166	2.6415	1.277	0.3681	0.7614	6E-08	0.0184	0.0001	0.1452	Lhx6	LIM homeobox protein 6	AB031040	16874	2 B
1420464_s_at	50	39	36	104	2.6378	1.2764	0.345	0.713	0.0007	0.2696	5E-05	0.0794	Pira6	paired-Ig-like receptor A6	NM_011093	18729	7 A1
1419598_at	361	320	155	842	2.6348	1.1306	0.1846	0.4302	1E-05	0.26	4E-06	0.0009	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	NM_026835	68774	19 A
1452244_at	177	187	217	493	2.6324	0.9452	0.4391	1.2227	7E-06	0.5952	3E-05	0.1041	633040615Rik	RIKEN cDNA 633040615 gene	AK018128	70717	5 G3
1420798_s_at	88	55	55	145	2.6285	1.5867	0.3764	0.6235	0.0005	0.016	0.0001	0.0057	Pcdha1	protocadherin alpha 1	NM_054072	116731	
1438511_a_at	173	95	139	248	2.6066	1.8197	0.5595	0.8014	9E-06	0.0003	0.0008	0.095	1190002H23Rik	RIKEN cDNA 1190002H23 gene	BB408123	66214	14 D3
1424339_at	70	87	72	226	2.6053	0.8049	0.3179	1.0289	3E-05	0.2265	6E-06	0.869	Oasl1	2'-5' oligoadenylate synthetase-like 1	AB067533	231655	5 F
1416625_at	169	117	127	305	2.6034	1.4394	0.4161	0.7526	5E-07	0.0096	6E-06	0.0477	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	NM_009776	12258	2 D
1448755_at	60	93	67	243	2.6005	0.6435	0.277	1.1195	7E-06	0.0032	2E-05	0.5182	Col15a1	collagen, type XV, alpha 1	AF011450	12819	4 B1-B3
1443219_at	166	259	201	671	2.5963	0.6438	0.2987	1.2046	2E-07	0.0005	6E-06	0.2301			BM232535		
1424010_at	137	211	173	547	2.594	0.6515	0.3158	1.2575	1E-05	0.0029	5E-07	0.0392	Mfap4	microfibrillar-associated protein 4	BC022666	76293	11 B2
1448201_at	111	68	85	176	2.5922	1.6287	0.4814	0.7662	0.0001	0.0562	8E-05	0.1861	Sfrp2	secreted frizzled-related protein 2	NM_009144	20319	3 E2
1450928_at	496	370	377	951	2.5726	1.342	0.3963	0.7596	1E-06	0.006	4E-07	0.0067	Id4	inhibitor of DNA binding 4	BB121406	15904	13 B
1460437_at	101	58	31	150	2.5682	1.7215	0.2052	0.3061	5E-07	0.0003	0.0001	0.0014	Cyth4	cytohesin 4	AK010908	72318	15 E1
1417595_at	56	143	92	366	2.555	0.3911	0.2522	1.6475	3E-05	0.0005	0.0001	0.0758	Meox1	mesenchyme homeobox 1	NM_010791	17285	11 D
1458669_at	80	101	77	258	2.5547	0.7945	0.2975	0.9566	6E-06	0.3088	9E-07	0.833			BG862223		
1445574_at	49	46	42	118	2.542	1.0559	0.3533	0.8505	0.0002	0.7235	8E-05	0.3332			BG067678		
1433795_at	240	287	287	730	2.5418	0.8343	0.3926	1.1962	4E-08	0.0393	8E-10	0.0174	Tgfb3	transforming growth factor, beta receptor III	BM122301	21814	5 E5
1442338_at	25	53	30	135	2.5407	0.4647	0.2244	1.227	0.0002	0.1411	6E-05	0.6689			BB740904		
1433885_at	206	111	116	281	2.5388	1.8567	0.411	0.562	8E-05	0.0019	3E-06	0.0002	Iqgap2	IQ motif containing GTPase activating protein 2	BM240173	544963	13 D1
1456258_at	293	168	214	426	2.5352	1.7425	0.5014	0.7295	1E-07	2E-06	7E-08	4E-06	Emx2	empty spiracles homolog 2 (Drosophila)	BG072869	13797	19 D3
1451683_x_at	1018	1132	651	2865	2.5312	0.8993	0.2273	0.6398	6E-05	0.3739	1E-07	0.0007	H2-K1	histocompatibility 2, K1, K region	M34962	14972	17 B1
1426112_a_at	328	216	132	545	2.5278	1.523	0.2417	0.4012	5E-08	0.0048	2E-08	2E-05	Cd72	CD72 antigen	BC003824	12517	4 B1
1429229_s_at	40	40	52	102	2.5266	0.9838	0.5153	1.3235	0.0023	0.9647	0.001	0.3631	4930534B04Rik	RIKEN cDNA 4930534B04 gene	BE980134	75216	12 E

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82-/-	Femal e Cd82+/-	Male Cd82-/-	Male Cd82+/-	Male Cd82+/-	Male Cd82+/-	Male Cd82+/-	p-value Male Cd82+/-	p-value Female Cd82+/-	p-value Male Cd82+/-	p-value Female Cd82+/-	Gene	Description	GB	Entrez Id	Cytoband
	averag e signal	averag e signal	averag e signal	averag e signal	FMale Cd82+/-	Female Cd82+/-	/ Male Cd82+/-	Female Cd82+/-	+ vs Female Cd82+/-	+ vs Female Cd82+/-	+ vs Male Cd82+/-					
1434789_at	85	124	103	314	2.5237	0.6829	0.3284	1.2135	8E-07	0.0143	5E-08	0.1337	Depdc1b	DEP domain containing 1B	BB136172	218581 13 D2.1
1435827_at	75	94	89	236	2.5231	0.8061	0.3775	1.1815	0.0001	0.2736	1E-05	0.3254	4933404O12Rik	RIKEN cDNA 4933404O12 gene	BB501711	66752
1450905_at	101	68	62	171	2.5161	1.478	0.3626	0.6173	1E-05	0.0221	1E-05	0.0102	Plxnc1	plexin C1	BB476707	54712 10 C3
1425620_at	55	51	47	127	2.5114	1.0758	0.3675	0.858	0.0001	0.6235	8E-07	0.1453	Tgfb3	transforming growth factor, beta receptor III	AF039601	21814 5 E5
1417127_at	56	56	68	140	2.5076	1.0011	0.4859	1.2171	3E-05	0.9952	0.0001	0.2648	Msx1	homeobox, msh-like 1	BC016426	17701 5 B3
1449528_at	142	169	193	424	2.5055	0.8376	0.4547	1.36	1E-06	0.0519	2E-06	0.0031	Figf	c-fos induced growth factor	NM_010216	14205 X F5
1438160_x_at	91	71	73	177	2.4949	1.2804	0.4116	0.802	6E-06	0.0524	3E-05	0.1267	Slco4a1	solute carrier organic anion transporter family, member 4a1	AV348121	108115 2 H4
1450924_at	106	140	115	350	2.4912	0.756	0.3298	1.0867	2E-07	0.0456	3E-07	0.5348	Hdgfr3	hepatoma-derived growth factor, related protein 3	BB291880	29877 7 D3
1451905_a_at	44	42	17	105	2.4912	1.0367	0.1599	0.3843	0.0003	0.8724	5E-05	0.0102	Mx1	myxovirus (influenza virus) resistance 1	M21039	17857 16 71.2 cM
1459894_at	138	85	62	211	2.483	1.6183	0.2918	0.4477	4E-05	0.005	7E-06	0.0003	Iqgap2	IQ motif containing GTPase activating protein 2	BE631962	544963 13 D1
1434194_at	153	129	128	319	2.4727	1.1857	0.4006	0.8355	1E-05	0.1739	5E-07	0.0869	Mtap2	microtubule-associated protein 2	AV337593	17756 1 C3
1435343_at	154	148	97	365	2.4695	1.0413	0.2658	0.6305	3E-07	0.5776	2E-07	0.0016	Dock10	dedicator of cytokinesis 10	BF715043	210293 1 C4
1426947_x_at	1141	1604	1566	3939	2.4566	0.7113	0.3975	1.373	1E-08	0.0013	2E-09	0.0011	Col6a2	collagen, type VI, alpha 2	BI455189	12834 10 41.1 cM
1424270_at	123	99	78	242	2.4517	1.2496	0.3235	0.6347	1E-05	0.2257	2E-06	0.0225	Dclk1	doublecortin-like kinase 1	AW105916	13175 3 D
1435022_at	135	120	116	295	2.4509	1.1193	0.3947	0.8643	6E-07	0.3936	2E-06	0.3018	Alx1	ALX homeobox 1	BB366930	216285 10 D1
1456288_at	26	45	15	111	2.4477	0.5843	0.1362	0.5705	0.0002	0.2522	3E-06	0.2195	Slnf5	schlafen 5	BB134615	327978 11 C
1451866_a_at	37	56	44	136	2.4413	0.664	0.324	1.1912	0.0002	0.0535	3E-05	0.3711	Hgf	hepatocyte growth factor	AF042856	15234 5 4.0 cM
1435014_at	70	80	67	194	2.4392	0.8837	0.3432	0.9473	0.0001	0.2857	7E-06	0.608	Rab39b	RAB39B, member RAS oncogene family	AV162168	67790 X A7.3
1424341_s_at	57	42	42	103	2.4339	1.3434	0.4054	0.7344	3E-05	0.0479	9E-05	0.0706	Pcdha6	protocadherin alpha 6	AW146252	12937 18 B2-B3
1453102_at	226	208	199	506	2.4258	1.0841	0.3928	0.8789	8E-07	0.3782	8E-09	0.0848	Fln3	fibronectin leucine rich transmembrane protein 3	BE945486	71436 2 F3
1418061_at	2056	2375	2572	5747	2.4195	0.8655	0.4475	1.251	8E-10	0.0053	2E-10	0.0001	Ltbp2	latent transforming growth factor beta binding protein 2	NM_013589	16997 12 D
1419589_at	94	81	74	195	2.416	1.165	0.3822	0.7927	7E-05	0.0624	3E-05	0.038	Cd93	CD93 antigen	BB039247	17064 2 G3
1456046_at	113	98	97	237	2.4101	1.1543	0.4088	0.8536	9E-07	0.1868	2E-05	0.2569	Cd93	CD93 antigen	AV319144	17064 2 G3
1448562_at	54	61	49	147	2.4097	0.8831	0.3319	0.9057	2E-05	0.2271	4E-06	0.4119	Upp1	uridine phosphorylase 1	NM_009477	22271 39815.458
1421995_at	67	54	67	131	2.4047	1.243	0.5154	0.997	0.001	0.4337	5E-05	0.9882	Tcfap2a	transcription factor AP-2, alpha	NM_011547	21418 13 A5-B1
1434932_at	46	46	54	111	2.3995	0.9871	0.4906	1.1925	2E-05	0.9624	2E-05	0.4806	Adarb1	adenosine deaminase, RNA-specific, B1	BI734168	110532 10 41.4 cM
1433551_at	76	53	37	127	2.3972	1.4272	0.2942	0.4942	0.0002	0.0422	2E-05	0.0017	AI427515	expressed sequence AI427515	AV173683	270097 8 E1
1423327_at	142	185	254	443	2.3947	0.7683	0.5723	1.7839	2E-07	0.0363	0.0002	0.0008	Rpl39l	ribosomal protein L39-like	AK005645	68172 16 A1
1419599_s_at	410	346	180	828	2.3928	1.1849	0.218	0.4402	3E-07	0.0405	2E-06	0.0005	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	NM_026835	68774 19 A
1426048_s_at	129	96	93	230	2.3884	1.3346	0.4042	0.7233	3E-07	0.0395	3E-06	0.0359	Hrc	histidine rich calcium binding protein	BC021623	15464 7 B4
1421075_s_at	56	51	62	121	2.3877	1.1107	0.5124	1.1014	0.0002	0.3239	0.0004	0.3388	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	NM_007825	13123 3 A1
1448891_at	392	265	145	633	2.3849	1.4754	0.229	0.3702	1E-07	0.0008	2E-08	2E-06	Fcrls	Fc receptor-like S, scavenger receptor	BC016551	80891 3 F1
1419083_at	104	101	105	241	2.3844	1.025	0.4355	1.0132	9E-06	0.8083	4E-07	0.8633	Tnfsf11	tumor necrosis factor (ligand) superfamily, member 11	NM_011613	21943 14 D3
1449265_at	73	56	48	133	2.384	1.3111	0.361	0.6565	2E-05	0.0248	3E-05	0.0117	Casp1	caspase 1	BC008152	12362 9 A1
1431087_at	146	222	169	530	2.3814	0.6557	0.3182	1.1557	7E-06	0.0012	5E-08	0.0869	Spc24	SPC24, NDC80 kinetochore complex component, homolog (S)	BF577722	67629 9 A3
1426505_at	90	64	45	153	2.3784	1.3969	0.2952	0.5026	3E-05	0.0441	1E-07	0.0002	Evi2a	ecotropic viral integration site 2a	AI122415	14017 11 B5
1450534_x_at	52	58	32	138	2.3782	0.8994	0.2284	0.6038	7E-06	0.5828	0.0002	0.1239	H2-K1	histocompatibility 2, K1, K region	M58156	14972 17 B1
1443161_at	145	171	191	407	2.3746	0.8467	0.4684	1.3136	4E-07	0.3313	3E-05	0.1407	Figf	c-fos induced growth factor	BM240648	
1438953_at	72	80	80	189	2.3679	0.899	0.4219	1.1112	2E-05	0.4854	5E-06	0.4484	Rbp1	retinol binding protein 1, cellular	BB359521	14205 X F5
1448754_at	779	997	1261	2356	2.3633	0.7817	0.5355	1.619	1E-08	0.0051	4E-07	4E-05	Parp14	poly (ADP-ribose) polymerase family, member 14	NM_011254	19659 9 E3.3
1432548_at	33	47	14	111	2.3603	0.6962	0.1221	0.4141	0.0021	0.3687	0.0003	0.1023	Eif2a	eukaryotic translation initiation factor 2a	AK005563	547253 16 B3
1434452_x_at	423	354	327	835	2.3589	1.1953	0.3912	0.7721	3E-07	0.1084	4E-08	0.0202	Adamts2	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motifs	BG797460	229317 3 D
1457058_at	172	245	254	579	2.3579	0.7003	0.4384	1.476	3E-06	0.0059	2E-07	0.0007	AI646023	expressed sequence AI646023	BM125019	216725 11 B1.3
1456878_at	114	61	84	143	2.3546	1.8822	0.5893	0.7372	8E-05	0.0054	2E-05	0.0395	Nlrp3	NLR family, pyrin domain containing 3	BE910952	192734 10 C1
1425412_at	75	55	60	130	2.3509	1.3495	0.461	0.8031	0.0003	0.0721	2E-05	0.0538	Csf1r	colony stimulating factor 1 receptor	AF486632	216799 11 B1.3
1419872_at	1353	919	524	2160	2.35	1.4721	0.2426	0.3873	9E-10	4E-06	2E-08	1E-06	Matn2	matrilin 2	AI323359	12978 18 D
1455978_a_at	151	150	123	354	2.349	1.0004	0.3477	0.8164	9E-07	0.9981	1E-07	0.2543	Fabp4	fatty acid binding protein 4, adipocyte	BB338441	17181 15 B3.3
1451263_a_at	126	114	123	267	2.3431	1.1029	0.4591	0.9753	6E-05	0.4881	2E-05	0.8346	Anxa8	annexin A8	BC002148	11770 3 A1
1435144_at	203	151	110	353	2.3408	1.3432	0.311	0.542	1E-06	0.0106	2E-05	0.0031	Anxa8	annexin A8	BM243379	
1425789_s_at	562	509	524	1190	2.3378	1.1037	0.44	0.9321	8E-07	0.4563	8E-06	0.6184	Esco2	establishment of cohesion 1 homolog 2 (S. cerevisiae)	BC013271	11752 14 B
1428304_at	73	130	88	303	2.3343	0.5646	0.2905	1.2011	1E-06	0.0058	2E-09	0.2231	Wnt4	wingless-related MMTV integration site 4	AK010391	71988 14 D1
1450782_at	173	116	113	271	2.3325	1.4915	0.4177	0.6533	2E-06	0.0348	7E-06	0.0253	11Rik	RIKEN cDNA 9030425E11 gene	NM_009523	22417 4 D3
1448251_at	241	343	291	800	2.3323	0.7024	0.3635	1.0688	3E-07	0.0004	1E-07	0.0399	Anxa8	annexin A8	BG072972	71566 9 A5.1
1417732_at	778	681	738	1588	2.3321	1.1429	0.4645	0.9478	2E-08	0.1786	2E-06	0.6229	Csf1r	colony stimulating factor 1 receptor	NM_013473	11752 14 B
1419873_s_at	552	339	279	789	2.329	1.631	0.3538	0.5052	2E-08	2E-07	1E-06	4E-05	Shmt1	serine hydroxymethyltransferase 1 (soluble)	AI323359	12978 18 D
1422198_a_at	32	101	59	234	2.3244	0.318	0.2538	1.855	0.0003	0.0029	0.0027	0.1623			NM_009171	20425 11 B2

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82- /-	Femal e Cd82 +/-	Male Cd82- /-	Male Cd82+ /+	Male Cd82+/- /+	Female Cd82-/- /-	Female Cd82+/- /+	Male Cd82-/- /-	Male Cd82+/- /+	p-value Male Cd82+/- /+ vs Female Cd82+/- /+	p-value Female Cd82+/- /+ vs Female Cd82-/- /-	p-value Male Cd82+/- /+ vs Male Cd82-/- /-	p-value MFemale e Cd82-/- /- vs Female Cd82-/- /-	Gene	Description	GB	Entrez Id	Cytoband
	signal	signal	signal	signal	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio					
1434639_at	115	104	117	241	2.3201	1.1111	0.4834	1.0095	9E-06	0.4035	6E-06	0.9316	Klhl29	kelch-like 29 (Drosophila)	BI988550	208439	12 A.1.1	
1424630_a_at	36	56	47	130	2.3199	0.6487	0.3615	1.2927	8E-05	0.0064	0.0002	0.1786	Brca1	breast cancer 1	U31625	12189	11 D	
1421074_at	99	100	108	233	2.3175	0.9877	0.4642	1.0892	0.0004	0.9422	7E-05	0.5297	Cyp7b1	cytochrome P450, family 7, subfamily b, polypeptide 1	NM_007825	13123	3 A1	
1424613_at	214	168	188	388	2.3161	1.2756	0.483	0.877	8E-08	0.0442	4E-06	0.2757	Gprc5b	G protein-coupled receptor, family C, group 5, member B	BC020004	64297	7 F3	
1426352_s_at	71	67	68	155	2.3122	1.0634	0.4406	0.9581	4E-05	0.6404	1E-07	0.6192	Tial1	Tia1 cytotoxic granule-associated RNA binding protein-like 1	BF731381	21843	7 F4	
1455720_at	50	55	55	126	2.3053	0.9203	0.4323	1.083	0.0003	0.7201	0.0018	0.759	Adamts2	a disintegrin-like and metalloproteinase (reprolysin type) with thrombospondin type 1 motifs	BB477652	216725	11 B1.3	
1422413_at	69	49	67	113	2.3044	1.4109	0.5943	0.9706	0.0015	0.1651	0.002	0.8663	Cramp11	Crmp, cramped-like (Drosophila)	NM_020608	57354	17 A3.3	
1451353_at	128	95	67	218	2.3042	1.3499	0.3081	0.5259	1E-05	0.0312	1E-05	0.0025	Tm6sf1	transmembrane 6 superfamily member 1	AV378394	107769	7 D1	
1425015_at	148	168	159	386	2.2964	0.879	0.4116	1.0753	2E-05	0.3665	2E-07	0.5205	Ephb2	Eph receptor B2	AV221401	13844	4 D-E	
1417821_at	377	627	527	1438	2.2951	0.6008	0.3665	1.3999	9E-07	1E-04	3E-09	0.0002	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	NM_033075	110956	17 B1	
1418930_at	122	183	111	418	2.2895	0.6699	0.2665	0.9109	5E-06	0.0074	3E-07	0.4914	Cxcl10	chemokine (C-X-C motif) ligand 10	NM_021274	15945	5 E2	
1416985_at	465	428	309	980	2.2881	1.0863	0.3157	0.665	2E-07	0.1127	6E-09	3E-05	Sirpa	signal-regulatory protein alpha	AB018194	19261	2 F3	
1460069_at	89	97	86	221	2.2793	0.9194	0.3882	0.9623	0.0049	0.5981	0.0012	0.8084	Smc6	structural maintenance of chromosomes 6	BB056038	67241	12 A2	
1423259_at	1273	1005	976	2290	2.2791	1.2668	0.4263	0.767	1E-06	0.0065	2E-06	0.0116	Id4	inhibitor of DNA binding 4	BB121406	15904	13 B	
1450414_at	356	215	249	490	2.2775	1.6532	0.5077	0.6994	9E-06	0.0007	1E-06	0.0008	Pdgfrb	platelet derived growth factor, B polypeptide	BC023427	18591	15 E	
1418250_at	80	68	69	153	2.2685	1.1792	0.4485	0.8627	9E-05	0.2874	0.0002	0.3702	Arl4d	ADP-ribosylation factor-like 4D	NM_025404	80981	11 D	
1418003_at	124	83	118	189	2.2644	1.4905	0.6233	0.9469	1E-05	0.0051	0.0002	0.588	1190002H23Rik	RIKEN cDNA 1190002H23 gene	NM_025427	66214	14 D3	
1439774_at	806	753	775	1703	2.2622	1.0704	0.455	0.9616	6E-08	0.2411	1E-08	0.4554	Prrx1	paired related homeobox 1	BB051738	18933	1 H2.1	
1449195_s_at	176	147	104	333	2.2608	1.1901	0.3132	0.5949	1E-06	0.0561	1E-05	0.0059	Cxcl16	chemokine (C-X-C motif) ligand 16	BC019961	66102	11 B4	
1451306_at	124	158	130	356	2.2604	0.7888	0.3659	1.0486	4E-07	0.0421	7E-08	0.6496	Cdca71	cell division cycle associated 7 like	BC006933	217946	12 F2	
1426604_at	59	52	29	117	2.2526	1.1454	0.2506	0.4927	0.0002	0.327	0.0002	0.0128	Rnasel	ribonuclease L (2', 5'-oligoadenylate synthetase-dependent)	BF714880	24014	1 G2	
1428767_at	197	186	154	417	2.2418	1.0581	0.3699	0.7838	1E-05	0.5874	4E-08	0.0103	Gsdmd	gasdermin D	AK007710	69146	15 D3-E1	
1425065_at	115	169	73	378	2.2411	0.6796	0.1933	0.6374	5E-05	0.0551	4E-09	0.0134	Oas2	2'-5' oligoadenylate synthetase 2	AB067535	246728	5 F	
1437324_x_at	141	76	125	171	2.24	1.8559	0.7322	0.8837	0.0036	0.0121	0.0171	0.217	Fmod	fibromodulin	BB504826	14264	1 E4	
1447927_at	75	88	32	197	2.2373	0.851	0.1643	0.4318	0.0006	0.402	7E-09	9E-05	Mpa2l	macrophage activation 2 like	BG092512	100702	5 E5	
1437726_x_at	838	641	387	1432	2.2347	1.3073	0.2699	0.4613	4E-07	0.0007	2E-06	0.0002	C1qb	complement component 1, q subcomponent, beta polypeptide	BB111335	12260	4 D3	
1434470_at	207	118	138	264	2.2328	1.7511	0.5204	0.6636	1E-04	0.003	0.0074	0.0729	Syt13	synaptotagmin XIII	BB244585	80976	2 E1	
1451348_at	53	55	75	122	2.232	0.9788	0.6126	1.3968	5E-05	0.9006	0.0091	0.1082	Depdc6	DEP domain containing 6	BC004774	97998	15 D1	
1438676_at	52	75	33	168	2.2306	0.6912	0.1985	0.6406	0.0003	0.009	2E-07	0.0018	Mpa2l	macrophage activation 2 like	BM241485	100702	5 E5	
1422190_at	111	99	59	222	2.23	1.1128	0.2679	0.5368	4E-05	0.4072	2E-05	0.0056	C5ar1	complement component 5a receptor 1	NM_007577	12273	7 A2	
1426324_at	352	470	251	1048	2.229	0.7483	0.2396	0.7139	4E-06	0.0212	5E-11	0.0013	H2-K1	histocompatibility 2, K1, K region	M33151	14972	17 B1	
1437716_x_at	1397	2188	1580	4876	2.2288	0.6387	0.324	1.1306	8E-06	5E-05	1E-08	0.0064	Kif22	kinesin family member 22	BB251322	110033	7 F3	
1455899_x_at	239	215	239	480	2.2266	1.1111	0.4985	0.9988	0.0001	0.5139	0.0001	0.9937	Socs3	suppressor of cytokine signaling 3	BB241535	12702	11 E2	
1418271_at	158	144	135	321	2.2246	1.0954	0.4206	0.8542	1E-06	0.2114	8E-08	0.0293	Bhlhb5	basic helix-loop-helix domain containing, class B5	NM_021560	59058		
1416326_at	487	569	684	1260	2.2146	0.8553	0.543	1.4059	4E-07	0.0385	0.0001	0.0071	Crip1	cysteine-rich protein 1 (intestinal)	NM_007763	12925	12 F1	
1451939_a_at	140	165	153	366	2.2125	0.8445	0.417	1.0925	8E-05	0.1995	4E-07	0.301	Srxp	sushi-repeat-containing protein	AB028050	51795	X A1.2	
1451904_a_at	72	81	72	178	2.2101	0.8918	0.4065	1.0074	0.0002	0.2042	0.0002	0.9573	Adam33	a disintegrin and metalloproteinase domain 33	AB059633	110751	2 F1	
1436425_at	142	95	99	210	2.2091	1.4953	0.47	0.6944	0.0015	0.0072	0.0008	0.0066	Kank4	KN motif and ankyrin repeat domains 4	BB486252	242553	4 C6	
1456077_x_at	56	93	73	205	2.2088	0.6074	0.3563	1.2958	7E-05	0.0094	2E-06	0.093	Cdc25c	cell division cycle 25 homolog C (S. pombe)	BB209183	12532	18 B1	
1420097_at	98	138	197	305	2.2082	0.7074	0.645	2.0134	0.0024	0.0921	0.0729	0.0085	D13Erd787e	DNA segment, Chr 13, ERATO Doi 787, expressed	AU020421	52680	13 29.0 cM	
1423975_s_at	518	540	741	1190	2.205	0.9597	0.6225	1.4304	2E-09	0.149	0.0091	0.0339	Numa1	nuclear mitotic apparatus protein 1	BC006631	101706	7 E3	
1435193_at	109	168	88	370	2.2027	0.6477	0.2375	0.8077	0.0002	0.0185	2E-08	0.0902	A230050P20Rik	RIKEN cDNA A230050P20 gene	BB085904	319278	9 A3	
1415983_at	750	535	390	1178	2.202	1.4024	0.3308	0.5194	4E-07	0.0003	7E-07	7E-05	Lcp1	lymphocyte cytosolic protein 1	NM_008879	18826	14 D3	
1425548_a_at	152	150	89	330	2.1989	1.0126	0.2702	0.5868	3E-07	0.9106	5E-08	0.0015	Lst1	leukocyte specific transcript 1	U72644	16988	17 B1	
1424754_at	1220	1110	728	2441	2.1988	1.0993	0.2981	0.5963	7E-09	0.0567	2E-07	0.0003	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	BC024402	109225	19 A	
1451655_at	82	110	52	241	2.1981	0.7468	0.2161	0.636	0.0007	0.1168	7E-07	0.0132	Sfn8	schlafen 8	BC024709	276950	11 C	
1438441_at	133	96	87	210	2.1973	1.3946	0.4128	0.6505	0.0001	0.0307	7E-07	0.0007	Id4	inhibitor of DNA binding 4	AI323288	15904	13 B	
1442471_at	80	109	108	240	2.1968	0.7293	0.45	1.3554	4E-07	0.0248	3E-06	0.0351			BG060522			
1456212_x_at	311	221	252	485	2.1936	1.4077	0.5192	0.8091	5E-05	0.0063	2E-05	0.0175	Socs3	suppressor of cytokine signaling 3	BB831725	12702	11 E2	
1438027_at	76	64	34	140	2.1867	1.1849	0.2444	0.4511	0.0035	0.3603	1E-07	2E-07			BB668084			
1435670_at	120	84	92	185	2.1859	1.416	0.4964	0.7663	2E-05	0.1319	0.0002	0.2345	Tcfap2b	transcription factor AP-2 beta	AV237028	21419	1 A2-A4	
1442884_at	22	58	44	126	2.1839	0.3756	0.3463	2.0137	1E-04	0.0318	0.0007	0.1092	Hgf	hepatocyte growth factor	BB476818	15234	5 4.0 cM	
1418340_at	754	572	369	1248	2.1831	1.3183	0.2956	0.4895	1E-08	0.0023	1E-06	0.0003	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide	NM_010185	14127	1 H3	
1427126_at	935	1028	1113	2244	2.183	0.9093	0.4959	1.1905	1E-05	0.3012	8E-05	0.1322	Hspa1b	heat shock protein 1B	M12573	15511	17 B1	
1453837_at	75	64	65	140	2.1812	1.1625	0.4603	0.8637	0.0065	0.5356	0.0048	0.5308	6330500D04Rik	RIKEN cDNA 6330500D04 gene	BB867666	193385	13 A3.2	
1452250_a_at	1757	2416	2221	5269	2.1811	0.7273	0.4216	1.2643	7E-07	0.0073	8E-08	0.0226	Col6a2	collagen, type VI, alpha 2	BI455189	12834	10 41.1 cM	

Table S1 - M vs F (WT)

Probe Set ID	Female Cd82- /-	Female Cd82 +/+	Male Cd82- /-	Male Cd82+ +/	Male Cd82+/- /+	Female Cd82+/- /+	Male Cd82+/- /+	Male Cd82+/- /+	p-value Male Cd82+/- /+ vs Female Cd82+/- /+	p-value Female Cd82+/- /+ vs Female Cd82+/- /+	p-value Male Cd82+/- /+ vs Male Cd82+/- /+	p-value MFemale Cd82+/- /+ vs Female Cd82+/- /+	Gene	Description	GB	Entrez Id	Cytoband
	signal	signal	signal	signal	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio	Ratio					
1439015_at	300	390	366	849	2.1806	0.7696	0.4312	1.2217	5E-07	0.0787	1E-10	0.0989	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	AV221299	14585	19 D2-D3
1452426_x_at	131	154	131	336	2.1795	0.8497	0.3902	1.0009	1E-06	0.3172	9E-08	0.9951			BC004065		
1458802_at	142	204	165	445	2.179	0.6945	0.3697	1.1601	3E-08	0.002	1E-11	0.064	Hivep3	human immunodeficiency virus type I enhancer binding protein	BB164127	16656	4 D1
1427754_a_at	55	77	79	168	2.1787	0.708	0.4672	1.4377	4E-05	0.0348	7E-06	0.014	Dnm1	dynamin 1	L29457	13429	2 B
1423593_a_at	384	269	226	584	2.1731	1.4299	0.387	0.5882	3E-05	0.0036	7E-08	4E-06	Csf1r	colony stimulating factor 1 receptor	AK004947	12978	18 D
1417822_at	497	804	705	1746	2.1717	0.6184	0.4039	1.4183	3E-07	3E-05	4E-09	6E-05	D17H6S56E-5	DNA segment, Chr 17, human D6S56E 5	NM_033075	110956	17 B1
1455961_at	122	69	76	150	2.1715	1.7617	0.5072	0.6252	7E-05	0.0029	4E-05	0.0034			AV174022		
1441333_at	46	47	43	102	2.17	0.9689	0.416	0.9317	1E-07	0.8315	0.0009	0.7596			BB485544		
1454159_a_at	12775	7709	7799	16699	2.1661	1.6572	0.467	0.6105	5E-11	0.0039	3E-08	0.0031	Igfbp2	insulin-like growth factor binding protein 2	AK011784	16008	1 C3
1419397_at	235	397	294	859	2.1657	0.5922	0.3423	1.2517	3E-08	2E-06	2E-09	0.0027	Pola1	polymerase (DNA directed), alpha 1	NM_008892	18968	X C-D
1419603_at	185	235	91	508	2.1654	0.7872	0.1797	0.4943	9E-06	0.0764	1E-06	0.003	Ifi204	interferon activated gene 204	NM_008329	15951	1 H3
1442101_at	201	68	106	147	2.1643	2.9662	0.7241	0.5283	3E-05	2E-05	0.0014	0.0002	Elf1	leucine rich repeat and fibronectin type III, extracellular 1	BB279531	243312	5 G2
1415999_at	196	164	176	353	2.1609	1.1996	0.4969	0.895	1E-06	0.0111	3E-07	0.0553	Hey1	hair/enhancer-of-split related with YRPW motif 1	NM_010423	15213	3 A1
1437313_x_at	535	895	601	1933	2.1609	0.5982	0.3111	1.1239	9E-06	0.0002	4E-07	0.265	Hmgb2	high mobility group box 2	C85885	97165	8 B2
1435504_at	62	49	56	105	2.1605	1.2678	0.5297	0.9027	1E-05	0.0387	9E-05	0.3666	Clp4	CAP-GLY domain containing linker protein family, member 4	BM217861	78785	17 E2
1423252_at	129	155	134	335	2.1581	0.829	0.3999	1.0411	7E-08	0.0737	5E-06	0.7551	Hdgfrp3	hepatoma-derived growth factor, related protein 3	BB291880	29877	7 D3
1433930_at	45	53	56	115	2.1579	0.8429	0.4842	1.2397	0.0017	0.5041	0.0006	0.3389	Hpse	heparanase	BG094050	15442	5 E4
1455269_a_at	173	114	111	246	2.1564	1.5137	0.4501	0.6411	2E-07	0.0005	0.0122	0.5011	Coro1a	coronin, actin binding protein 1A	BB740218	12721	7 F3
1425527_at	778	814	826	1755	2.1551	0.9548	0.4704	1.0618	3E-06	0.4407	2E-06	0.3605	Prrx1	paired related homeobox 1	L06502	18933	1 H2.1
1418454_at	614	644	729	1388	2.154	0.9526	0.5252	1.1876	9E-09	0.4781	5E-08	0.0257	Mfap5	microfibrillar associated protein 5	NM_015776	50530	6 F1
1449699_s_at	285	456	364	982	2.1537	0.6251	0.3706	1.2771	1E-06	0.0005	2E-08	0.0139	C330027C09Rik	RIKEN cDNA C330027C09 gene	AU018569	22471	16 B5
1418718_at	335	251	213	540	2.1473	1.334	0.3944	0.6349	1E-06	0.0031	4E-07	0.0003	Cxcl16	chemokine (C-X-C motif) ligand 16	BC019961	66102	11 B4
1450020_at	209	119	79	255	2.1461	1.7563	0.3079	0.3762	4E-05	0.0036	6E-08	1E-05	Cx3cr1	chemokine (C-X3-C) receptor 1	BC012653	13051	9 F4
1415802_at	755	1069	864	2292	2.145	0.7062	0.3771	1.1453	7E-08	2E-05	2E-09	0.0128	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), men	NM_009196	20501	3 F.2
1419905_s_at	92	55	50	117	2.1411	1.6758	0.4302	0.5497	0.0011	0.0207	1E-05	0.0011	Hpgd	hydroxyprostaglandin dehydrogenase 15 (NAD)	AV026552	15446	8 B3.2
1427086_at	569	328	470	701	2.1399	1.7374	0.6698	0.825	5E-06	0.0003	0.0009	0.0857	Slit3	slit homolog 3 (Drosophila)	BM570006	20564	
1443968_at	23	79	56	169	2.1397	0.2976	0.3295	2.3694	0.0033	0.0272	4E-05	0.0618	Adarb1	adenosine deaminase, RNA-specific, B1	BI202667	110532	10 41.4 cM
1421991_a_at	373	519	429	1109	2.1373	0.7182	0.387	1.1515	4E-07	0.0004	2E-06	0.1844	Igfbp4	insulin-like growth factor binding protein 4	NM_010517	16010	11 D
1449401_at	1170	964	523	2061	2.1373	1.2137	0.2536	0.4466	2E-10	0.0007	8E-08	1E-05	C1qc	complement component 1, q subcomponent, C chain	NM_007574	12262	4 D3
1418167_at	57	100	83	213	2.1317	0.5669	0.3892	1.4637	4E-06	0.0039	5E-07	0.0219	Tcfap4	transcription factor AP4	NM_031182	83383	16 A1
1423804_a_at	434	532	531	1132	2.1303	0.8166	0.4692	1.2239	2E-06	0.0312	7E-06	0.0601	Idi1	isopentenyl-diphosphate delta isomerase	BC004801	319554	13 A1
1438081_at	164	184	155	391	2.1257	0.8927	0.3958	0.9425	2E-06	0.1101	2E-05	0.6285	Mcc	mutated in colorectal cancers	BB794635	328949	18 B3
1417926_at	433	672	494	1428	2.1251	0.6448	0.346	1.1403	4E-08	7E-06	2E-09	0.0378	Ncapg2	non-SMC condensin II complex, subunit G2	NM_133762	76044	12 F2
1421106_at	207	209	208	444	2.1239	0.9931	0.4689	1.0028	0.0002	0.9591	8E-05	0.9826	Jag1	jagged 1	AA880220	16449	2 F3
1416710_at	122	58	65	122	2.12	1.2102	0.5324	0.5324	0.0018	0.0008	0.0151	0.011	Tmem35	transmembrane protein 35	NM_026239	67564	X E3
1453214_at	758	1012	895	2143	2.1182	0.7494	0.4175	1.1802	1E-05	0.0146	4E-06	0.1341	Lrrc15	leucine rich repeat containing 15	AK017350	74488	16 B2
1439345_at	94	63	58	133	2.1168	1.5059	0.4386	0.6165	0.0001	0.0087	1E-05	0.001	Gpnmb	glycoprotein (transmembrane) nmb	BB113177	93695	6 B2.3
1456359_at	113	127	112	268	2.1159	0.8939	0.4181	0.9896	0.0008	0.5311	0.0006	0.9575	Ppwd1	peptidylprolyl isomerase domain and WD repeat containing 1	AV233215	238831	13 D1
1423974_at	441	447	607	946	2.1156	0.9855	0.641	1.3762	6E-10	0.8121	0.0038	0.0316	Numa1	nuclear mitotic apparatus protein 1	BC006631	101706	7 E3
1421038_a_at	49	93	84	197	2.1153	0.5261	0.4256	1.7112	6E-06	4E-05	1E-07	2E-05	Kcnn4	potassium intermediate/small conductance calcium-activated ch	NM_008433	16534	7 A3
1448160_at	387	316	197	667	2.1129	1.2248	0.2958	0.5103	2E-10	0.0024	2E-07	7E-05	Lcp1	lymphocyte cytosolic protein 1	NM_008879	18826	14 D3
1415864_at	910	620	658	1309	2.111	1.4674	0.5027	0.7232	6E-06	0.0194	2E-05	0.0359	Bpgm	2,3-bisphosphoglycerate mutase	NM_007563	12183	6 B1
1460365_a_at	399	471	437	993	2.1088	0.848	0.4397	1.0935	7E-07	0.0962	1E-05	0.4624	Dnm1	dynamin 1	L31397	13429	2 B
1426906_at	213	264	121	556	2.1059	0.8079	0.217	0.5656	3E-05	0.0388	2E-08	9E-05	Ifi205	interferon activated gene 205	M74124	226695	1 H3
1448250_at	291	433	412	910	2.1018	0.6727	0.4529	1.415	8E-09	2E-05	8E-09	8E-05	9030425E11Rik	RIKEN cDNA 9030425E11 gene	BG072972	71566	9 A5.1
1419627_s_at	68	57	55	120	2.1005	1.1783	0.4561	0.813	0.0015	0.3281	0.0002	0.1434	Clec4n	C-type lectin domain family 4, member n	NM_020001	56620	6 F3
1437939_s_at	129	90	85	188	2.1003	1.4394	0.4546	0.6633	1E-05	0.0017	1E-06	0.0003	Ctsc	cathepsin C	BM237633	13032	7 D3-E.1
1426258_at	167	64	87	135	2.0974	2.5897	0.6442	0.5218	7E-05	0.0004	0.0006	0.0015	Sor11	sortilin-related receptor, LDLR class A repeats-containing	BI648081	20660	
1424965_at	217	195	111	409	2.0967	1.1142	0.2712	0.5103	3E-06	0.1255	9E-06	0.0014	Lpxn	leupaxin	BC026563	107321	19 A
1459552_at	89	58	79	121	2.096	1.5293	0.6508	0.8919	0.0007	0.0248	0.0578	0.5942			BB404047		
1450440_at	102	123	106	257	2.0924	0.8291	0.4126	1.0413	1E-08	0.1173	1E-07	0.7301	Gfra1	glial cell line derived neurotrophic factor family receptor alpha 1	BE534815	14585	19 D2-D3
1417063_at	1451	1121	625	2342	2.0894	1.2947	0.2671	0.431	7E-09	0.0006	5E-07	4E-05	C1qb	complement component 1, q subcomponent, beta polypeptide	NM_009777	12260	4 D3
1448119_at	551	350	406	731	2.0877	1.5715	0.5546	0.7368	5E-07	0.0013	1E-05	0.015	Bpgm	2,3-bisphosphoglycerate mutase	NM_007563	12183	6 B1
1451161_a_at	540	437	270	912	2.0869	1.2357	0.2959	0.4997	9E-11	0.0029	1E-07	4E-05	Emr1	EGF-like module containing, mucin-like, hormone receptor-like s	U66888	13733	17 D
1416986_a_at	150	152	101	316	2.085	0.991	0.3181	0.6691	6E-07	0.8572	1E-06	0.0034	Sirpa	signal-regulatory protein alpha	AB018194	19261	2 F3
1451931_x_at	3153	3705	2114	7718	2.0833	0.8511	0.274	0.6706	7E-06	0.0864	1E-08	0.0006	H2-L	histocompatibility 2, D region	M69068	14980	17.19.13 cM

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82- /- avera ge signal	Femal e Cd82 +/+ avera ge signal	Male Cd82- /- avera ge signal	Male Cd82+ /+ avera ge signal	Male Cd82+/ /+ Ratio	Female Cd82-/ /- Ratio	Male Cd82-/ /+ Ratio	Male Cd82-/ /+ Ratio	p-value Male Cd82+/ /+ vs Female Cd82+/ /+	p-value Female Cd82+/ /+ vs Female Cd82-/ /-	p-value Male Cd82+/ /+ vs Male Cd82-/ /-	p-value MFemale Cd82-/ /- vs Female Cd82-/ /-	Gene	Description	GB	Entrez Id	Cytoband
	1420559_a_at	81	96	102	200	2.0823	0.8431	0.5092	1.2578	0.0003	0.4174	0.0026	0.3212	Shox2	short stature homeobox 2	NM_013665	20429
1450678_at	331	276	185	574	2.0797	1.1989	0.3213	0.5574	8E-07	0.0638	6E-07	0.0005	Itgb2	integrin beta 2	NM_008404	16414	10 C1
1431213_a_at	266	283	287	588	2.0754	0.9391	0.4889	1.0805	7E-06	0.4834	6E-07	0.2993	LOC67527	murine leukemia retrovirus	BG297038	67527	18 B1
1442287_at	32	50	49	104	2.0725	0.6397	0.4759	1.5419	0.0009	0.3019	0.001	0.2796			BB483068		
1419703_at	866	1321	1192	2736	2.0718	0.6556	0.4356	1.3764	3E-05	0.0007	5E-06	0.0042	Col5a3	collagen, type V, alpha 3	NM_016919	53867	9 A3
1420768_a_at	35	58	18	120	2.0707	0.6047	0.1498	0.5131	0.002	0.0286	0.0005	0.1104	Dhx58	DEXH (Asp-Glu-X-His) box polypeptide 58	NM_030150	80861	11 D
1417019_a_at	169	331	242	685	2.0691	0.5103	0.3535	1.4335	2E-07	1E-06	6E-09	0.0002	Cdc6	cell division cycle 6 homolog (S. cerevisiae)	NM_011799	23834	11 D
1448950_at	86	164	140	339	2.0651	0.5212	0.4131	1.6369	6E-05	0.0136	1E-05	0.0336	Il1r1	interleukin 1 receptor, type I	NM_008362	16177	1 B
1451767_at	111	90	44	185	2.0636	1.2419	0.2372	0.3941	0.0001	0.1178	0.0052	0.0457	Ncf1	neutrophil cytosolic factor 1	BE370703	17969	5 G2
1421792_s_at	233	190	72	391	2.0628	1.2257	0.1831	0.3082	4E-05	0.0526	0.0003	0.0035	Trem2	triggering receptor expressed on myeloid cells 2	NM_031254	83433	17 C
1427017_at	148	164	148	339	2.0612	0.9014	0.4381	1.0018	9E-07	0.1698	5E-08	0.9787	Satb2	special AT-rich sequence binding protein 2	BB104560	212712	1 C1.3
1458299_s_at	122	121	133	248	2.0598	1.0122	0.5353	1.0893	9E-09	0.8866	1E-06	0.3687	Nfkbie	nuclear factor of kappa light polypeptide gene enhancer in B-ce	BB820441	18037	17 C
1415865_s_at	1012	651	735	1340	2.0585	1.5544	0.5488	0.7268	2E-07	0.0007	1E-07	0.0023	Bpgm	2,3-bisphosphoglycerate mutase	NM_007563	12183	6 B1
1448061_at	206	192	131	394	2.0493	1.0725	0.3313	0.6331	6E-06	0.5358	4E-06	0.0091	Msr1	macrophage scavenger receptor 1	AA183642	20288	8 A4
1452279_at	165	132	86	270	2.0465	1.2546	0.3188	0.52	8E-05	0.1897	0.0002	0.0157	Cfp	complement factor properdin	BB800282	18636	X A3
1441071_at	78	50	58	102	2.0456	1.558	0.5693	0.7475	0.0008	0.0318	0.0008	0.0767	Kcnq5	potassium voltage-gated channel, subfamily Q, member 5	BB181225	226922	1 A5
1436055_at	606	770	711	1574	2.0435	0.7863	0.452	1.1746	1E-04	0.0697	1E-05	0.1598	Lrrc15	leucine rich repeat containing 15	AI506528	74488	16 B2
1419292_at	108	72	105	146	2.0348	1.5091	0.7192	0.9697	0.0001	0.0321	0.0729	0.8781	Htra3	Htra serine peptidase 3	NM_030127	78558	5 B1
1451045_at	112	77	83	157	2.0345	1.4484	0.5306	0.7454	0.0002	0.0116	0.0008	0.0563	Syt13	synaptotagmin XIII	BE648447	80976	2 E1
1438838_at	46	62	61	126	2.0323	0.7418	0.4852	1.3294	0.0046	0.3064	0.0044	0.3135	B230206F22Rik	RIKEN cDNA B230206F22 gene	BG141977	78878	X D
1438833_at	28	74	25	150	2.0313	0.3828	0.1651	0.8758	0.0002	0.0004	0.0205	0.8461	Casc5	cancer susceptibility candidate 5	BB818947	76464	2 E5
1430228_at	53	88	61	179	2.0311	0.6043	0.3403	1.1439	0.0007	0.0289	0.0002	0.5531	Dtl	denticleless homolog (Drosophila)	AV308327	76843	1 H6
1417095_a_at	156	150	138	305	2.0304	1.0361	0.4528	0.8874	0.0044	0.8069	0.001	0.3784	Hspa14	heat shock protein 14	NM_015765	50497	2 A1
1453753_at	32	61	38	123	2.0302	0.5192	0.3055	1.1944	0.0002	0.0151	2E-06	0.4044	Dtl	denticleless homolog (Drosophila)	AK012919	76843	1 H6
1448534_at	282	271	201	550	2.0298	1.0408	0.3656	0.713	3E-07	0.2621	5E-09	1E-05	Sirpa	signal-regulatory protein alpha	AB018194	19261	2 F3
1452318_a_at	1333	1379	1437	2792	2.0248	0.9663	0.5145	1.078	4E-07	0.1351	7E-06	0.2618	Hspa1b	heat shock protein 1B	M12573	15511	17 B1
1421228_at	584	556	602	1124	2.0241	1.0508	0.5358	1.0321	9E-07	0.5582	3E-06	0.7109	Ccl7	chemokine (C-C motif) ligand 7	AF128193	20306	11 C
1422477_at	77	69	64	140	2.0239	1.1204	0.459	0.8291	0.0017	0.5844	0.0003	0.3206	Cables1	Cdk5 and Abl enzyme substrate 1	AF328140	63955	18 A2
1440884_s_at	112	160	124	323	2.0213	0.6998	0.3835	1.1077	4E-05	0.0095	5E-05	0.5116	A530047J11Rik	RIKEN cDNA A530047J11 gene	BB218047	103767	
1424367_a_at	78	96	78	195	2.0211	0.8106	0.4014	1.0007	4E-05	0.0228	1E-05	0.9949	Homer2	homer homolog 2 (Drosophila)	AB017136	26557	7 D3
1429490_at	49	100	71	202	2.0204	0.4907	0.3507	1.4438	0.0006	0.0047	0.001	0.187	Rif1	Rap1 interacting factor 1 homolog (yeast)	AK018316	51869	2 C.1
1422239_at	179	143	175	289	2.0201	1.2533	0.6072	0.9787	2E-06	0.0076	6E-05	0.7803	Hoxd13	homeo box D13	NM_008275	15433	2 C3
1425854_x_at	117	72	87	146	2.0196	1.6093	0.5934	0.7447	8E-05	0.0002	0.0053	0.0528	Tcrb-J	T-cell receptor beta, joining region	U07661	21580	6 20.5 cM
1443445_at	40	57	32	116	2.0194	0.689	0.2727	1.1994	6E-06	0.1383	0.0085	0.6242			BM238212		
1455332_x_at	50	67	16	136	2.018	0.7414	0.1213	0.33	0.0003	0.4277	3E-05	0.0258	Fcgr2b	Fc receptor, IgG, low affinity IIb	BM224327	14130	1 H3
1454699_at	138	99	137	200	2.0168	1.3927	0.6869	0.9947	0.0003	0.0983	0.0013	0.9711	Sesn1	sestrin 1	BG076140	140724	10 B2
1448710_at	164	74	70	149	2.0164	2.2137	0.4662	0.4247	0.0001	0.0008	8E-06	0.0001	Cxcr4	chemokine (C-X-C motif) receptor 4	D87747	12767	1 E4
1453064_at	125	168	142	339	2.016	0.746	0.4187	1.1315	5E-08	0.0015	7E-09	0.0942	Eta1	Ewing's tumor-associated antigen 1	AK018594	68145	11 A3.1
1451716_at	209	157	153	316	2.016	1.3325	0.484	0.7323	8E-06	0.0311	2E-05	0.0256	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, prote	AW412521	16658	2 H2
1454744_at	111	128	117	259	2.0149	0.8643	0.4515	1.0525	0.0011	0.355	0.0002	0.7204	F630043A04Rik	RIKEN cDNA F630043A04 gene	BG073400	219114	14 C3
1459374_at	52	77	59	156	2.0149	0.671	0.3751	1.1265	0.0001	0.0037	2E-06	0.246			BB133363		
1425423_at	75	68	59	138	2.0147	1.0976	0.4302	0.7896	0.0008	0.529	0.0062	0.358	Glis1	GLIS family zinc finger 1	AF220434	230587	4 C6
1429524_at	157	106	64	213	2.0122	1.4807	0.2989	0.4062	3E-06	0.0003	7E-06	9E-05	Myo1f	myosin IF	AK021181	17916	17 B-C
1424727_at	86	64	50	128	2.0061	1.3388	0.3868	0.5796	0.0004	0.0717	0.0002	0.0108	Ccr5	chemokine (C-C motif) receptor 5	D83648	12774	9 72.0 cM
1427127_x_at	1445	1514	1722	3034	2.0035	0.9545	0.5676	1.1913	2E-05	0.5306	8E-05	0.0462	Hspa1b	heat shock protein 1B	M12573	15511	17 B1
1455724_at	155	171	144	342	2.003	0.9104	0.4221	0.9286	0.0005	0.4018	8E-05	0.5329	Prrg1	proline rich Gla (G-carboxyglutamic acid) 1	BM230193	546336	X B
1419152_at	351	661	464	1324	2.0023	0.5303	0.3508	1.3244	8E-09	2E-05	2E-07	0.0226	2810417H13Rik	RIKEN cDNA 2810417H13 gene	AK017673	68026	9 C
1454783_at	262	313	289	626	2.0019	0.8359	0.4619	1.1064	2E-05	0.0635	3E-06	0.2357	Il13ra1	interleukin 13 receptor, alpha 1	BI081033	16164	X A3.3
1438169_a_at	145	82	58	164	2.0009	1.7774	0.3533	0.3978	0.0002	0.0009	7E-06	3E-05	Frm4b	FERM domain containing 4B	BB009122	232288	6 D3
1420928_at	919	800	900	400	0.4999	1.1488	2.2514	0.9797	2E-06	0.0903	1E-07	0.771	St6gal1	beta galactoside alpha 2,6 sialyltransferase 1	BG075800	20440	16 B1
1448942_at	5938	4990	5465	2489	0.4989	1.1901	2.1955	0.9204	4E-07	0.0046	7E-09	0.0451	Gng11	guanine nucleotide binding protein (G protein), gamma 11	NM_025331	66066	6 A1
1443485_at	223	164	196	82	0.498	1.3595	2.3958	0.8776	0.0002	0.003	1E-05	0.1118	Epha7	Eph receptor A7	BB361326	13841	4 A4
1441107_at	289	239	299	119	0.4979	1.2091	2.5154	1.0357	0.0001	0.0339	4E-07	0.4377	Dmrt2	doublesex and mab-3 related transcription factor like family A2	BB292639	242620	C7
1449473_s_at	117	107	120	53	0.4956	1.0864	2.2485	1.0258	0.0006	0.6198	2E-05	0.8526	Cd40	CD40 antigen	NM_011611	21939	2 H3
1433769_at	434	468	453	231	0.4941	0.9266	1.9602	1.0453	6E-06	0.304	5E-06	0.5573	Als2cl	ALS2 C-terminal like	BM201174	235633	9 F3
1429196_at	231	201	252	99	0.4937	1.1513	2.544	1.0909	0.0003	0.2374	5E-07	0.2283	Rabgap1l	RAB GTPase activating protein 1-like	BB431654	29809	1 H2.1

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82- /-	Femal e Cd82 +/+	Male Cd82- /	Male Cd82+ /+	Male Cd82+/- /	Male Cd82-/- /	p-value Male Cd82+/- + vs Female Cd82+/- + Ratio	p-value Female Cd82+/- + vs Female Cd82+/- + Ratio	p-value Male Cd82+/- + vs Male Cd82+/- + Ratio	p-value MFemale Cd82+/- - vs Female Cd82+/- + Ratio	Gene	Description	GB	Entrez Id	Cytoband		
	averag e signal	averag e signal	averag e signal	averag e signal	FMale Cd82+/- + Ratio	Female Cd82+/- + Ratio	/ Male Cd82+/- + Ratio	Female Cd82+/- + Ratio	Female Cd82+/- + Ratio	Female Cd82+/- + Ratio							
1422592_at	552	507	464	251	0.4937	1.0877	1.8526	0.8409	3E-06	0.2618	3E-06	0.029	Ctrnd2	catenin (cadherin associated protein), delta 2	NM_008729	18163	15 B2
1429764_at	5317	6416	5620	3152	0.4913	0.8288	1.7827	1.0569	5E-07	0.0297	0.0003	0.6398	1500005K14Rik	RIKEN cDNA 1500005K14 gene	BF101721	76566	11 B4
1422644_at	217	138	174	67	0.4895	1.5722	2.5876	0.8057	1E-04	0.004	1E-06	0.0584	Sh3bgr	SH3-binding domain glutamic acid-rich protein	NM_015825	50795	16 C4
1442223_at	1003	892	791	436	0.4892	1.1248	1.8121	0.7882	0.0006	0.239	0.001	0.0231	Enah	enabled homolog (Drosophila)	AV329519	13800	1 H5
1434975_x_at	4086	2991	3064	1459	0.4879	1.3663	2.1003	0.75	5E-09	1E-05	1E-08	8E-05	4933439C20Rik	RIKEN cDNA 4933439C20 gene	AA673371	66776	
1447812_x_at	1669	1708	1962	832	0.4873	0.9771	2.3568	1.1753	0.0003	0.8413	5E-06	0.0749	Flncl	filamin C, gamma (actin binding protein 280)	AV014577	68794	6 A3.3
1457899_at	111	136	121	66	0.4873	0.8168	1.8193	1.0853	0.0003	0.0721	0.0012	0.4858	Kalrn	kalirin, RhoGEF kinase	BG066934	545156	16 B3
1448321_at	403	576	658	280	0.4863	0.6987	2.347	1.6337	3E-05	0.0005	3E-06	5E-05	Smoc1	SPARC related modular calcium binding 1	NM_022316	64075	12 D1
1432826_a_at	195	176	205	85	0.4862	1.1086	2.3955	1.0505	2E-06	0.2186	2E-07	0.5458	Cd80	CD80 antigen	AK019867	12519	16 B5
1422948_s_at	1819	1152	1593	559	0.4854	1.5786	2.848	0.8758	2E-05	0.0003	3E-07	0.1303	Hist1h3a	histone cluster 1, H3a	NM_013550	360198	13 A2-A3
1427009_at	822	686	786	332	0.4836	1.1975	2.3693	0.9568	4E-07	0.0132	4E-08	0.4856	Lama5	laminin, alpha 5	AV224009	16776	2 H4
1449133_at	95	122	135	59	0.4835	0.7808	2.2906	1.4184	8E-05	0.0253	2E-05	0.0043	Sprr1a	small proline-rich protein 1A	NM_009264	20753	3 F1
1438370_x_at	779	613	714	296	0.4832	1.272	2.4103	0.9156	4E-06	0.0008	4E-07	0.1547	Stk11	serine/threonine kinase 11	BB357126	20869	10 C1
1426498_at	351	437	258	211	0.4823	0.8035	1.2254	0.7354	6E-07	0.0534	0.0535	0.0253	Jarid1c	jumonji, AT rich interactive domain 1C (Rbp2 like)	AK011577	20591	X F2-F4
1426758_s_at	6727	5881	5596	2836	0.4822	1.144	1.9734	0.8318	0.0001	0.0608	0.002	0.2126	Meg3	maternally expressed 3	Y13832	17263	12 F1
1426122_x_at	132	123	133	59	0.4816	1.07	2.2407	1.0086	0.0006	0.64	0.0001	0.9498	Coro6	coronin, actin binding protein 6	AB070896	216961	11 B5
1456526_at	825	964	893	464	0.4809	0.8562	1.9261	1.0819	1E-06	0.2453	1E-08	0.4681	Hoxa9	homeo box A9	AA987181	15405	6 B3
1424568_at	792	623	741	299	0.4805	1.272	2.4761	0.9354	7E-07	0.0005	1E-08	0.1256	Tspan2	tetraspanin 2	BC007185	70747	3 F3
1432092_a_at	431	438	428	210	0.4803	0.9834	2.0354	0.9942	7E-07	0.826	3E-06	0.9467	Gulp1	GULP, engulfment adaptor PTB domain containing 1	AK017798	70676	1 C1
1452412_at	782	713	905	342	0.4802	1.0979	2.6433	1.1562	1E-06	0.3205	4E-08	0.1235	Hoxc8	homeo box C8	BB283726	15426	15 F3
1450482_a_at	122	134	133	64	0.4795	0.9129	2.0665	1.0853	1E-05	0.1793	1E-05	0.2977	Pitx2	paired-like homeodomain transcription factor 2	AB006320	18741	3 G3
1418412_at	420	307	352	147	0.4792	1.367	2.3902	0.838	8E-05	0.002	2E-06	0.0075	Tpd521l	tumor protein D52-like 1	NM_009413	21987	10 A4-B2
1428357_at	173	114	139	54	0.479	1.5244	2.5557	0.803	0.0002	0.0006	2E-05	0.0409	2610019F03Rik	RIKEN cDNA 2610019F03 gene	AK011462	72148	8 A1.1
1440617_at	477	389	431	186	0.4774	1.2253	2.3174	0.903	1E-06	0.0116	2E-05	0.3666	Cpa6	carboxypeptidase A6	BB072673	329093	1 A2
1438115_a_at	1376	1205	1275	575	0.4773	1.1416	2.2157	0.9264	9E-07	0.0928	2E-09	0.1461	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), member 3	BB805362	26941	11 E2
1426387_x_at	3275	2634	2619	1256	0.4769	1.2434	2.0854	0.7998	3E-06	0.0004	1E-06	0.0006	4933439C20Rik	RIKEN cDNA 4933439C20 gene	BB085906	66776	
1449959_x_at	2944	1802	2039	856	0.4752	1.6339	2.3815	0.6926	1E-05	0.0027	2E-05	0.0231	Lce1h	late cornified envelope 1H	NM_026335	67718	3 F1
1424927_at	5245	4413	5348	2093	0.4742	1.1885	2.5554	1.0196	3E-09	0.0074	2E-10	0.7047	Glpr1	GLI pathogenesis-related 1 (glioma)	BC025083	73690	10 D1
1431162_a_at	358	339	287	160	0.4732	1.0565	1.7896	0.8016	0.0007	0.6128	0.0024	0.0697	Enah	enabled homolog (Drosophila)	AK020248	13800	1 H5
1416666_at	7707	5177	6903	2449	0.4731	1.4888	2.8182	0.8956	6E-05	0.0003	9E-07	0.1118	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	NM_009255	20720	1 C4
1419613_at	2316	2420	2265	1144	0.4726	0.9569	1.9797	0.9777	8E-05	0.2115	0.0006	0.824	Col7a1	collagen, type VII, alpha 1	NM_007738	12836	9 F2
1450803_at	354	227	304	107	0.4711	1.5618	2.8464	0.8585	0.002	0.0017	8E-05	0.1622	Ntf3	neurotrophin 3	NM_008742	18205	6 F3
1416688_at	246	137	170	65	0.4707	1.7887	2.6269	0.6912	1E-06	0.0004	1E-06	0.0121	Snap91	synaptosomal-associated protein 91	NM_013669	20616	
1426791_at	1980	1413	1716	665	0.4707	1.4014	2.581	0.8668	3E-06	8E-05	9E-08	0.0148	Rusc2	RUN and SH3 domain containing 2	BC024790	100213	4 A5
1425092_at	881	1085	1178	510	0.4701	0.8121	2.31	1.3372	3E-08	0.013	2E-07	0.0055	Cdh10	cadherin 10	AF183946	320873	15 A2
1437502_x_at	2389	1806	1937	848	0.4699	1.3232	2.2831	0.8108	6E-07	0.0026	4E-08	0.0074	Cd24a	CD24a antigen	BB560574	12484	10 B2
1442880_at	238	228	252	107	0.4697	1.042	2.3507	1.0597	4E-05	0.6163	2E-06	0.4001			AV319882		
1435132_at	348	310	302	145	0.469	1.1249	2.0777	0.8663	7E-06	0.2434	6E-06	0.1583	Disp1	dispatched homolog 1 (Drosophila)	AI505698	68897	
1457044_at	112	131	127	61	0.4658	0.8568	2.0766	1.129	0.0002	0.2347	0.0011	0.4571	4732474O15Rik	RIKEN cDNA 4732474O15 gene	BB007136	238455	12 F2
1454224_at	799	696	756	324	0.4656	1.1471	2.3313	0.9464	3E-07	0.0183	3E-07	0.4154	2010300F17Rik	RIKEN cDNA 2010300F17 gene	AK008491	69884	
1440108_at	194	198	214	92	0.4648	0.983	2.3282	1.1007	1E-05	0.8224	7E-07	0.1788	Foxp2	forkhead box P2	BM964154	114142	6 A2
1435510_at	149	118	136	55	0.4646	1.265	2.4846	0.9125	7E-06	0.0367	3E-07	0.3185	Ppm1h	protein phosphatase 1H (PP2C domain containing)	BB283101	319468	10 D2
1435584_at	230	151	155	70	0.4629	1.5274	2.226	0.6747	0.0067	0.0029	0.003	0.0043	A630033H20Rik	RIKEN cDNA A630033H20 gene	BB034567	213438	X D
1424797_a_at	414	363	431	168	0.4622	1.1416	2.5702	1.0405	1E-06	0.0737	2E-07	0.6091	Pitx2	paired-like homeodomain transcription factor 2	U80011	18741	3 G3
1437932_a_at	133	120	132	55	0.462	1.1122	2.3907	0.9931	7E-05	0.2106	9E-06	0.9295	Cldn1	claudin 1	AV227581	12737	16 B2
1443814_x_at	643	592	643	274	0.4618	1.0859	2.3516	0.9999	2E-09	0.0319	8E-11	0.9981	Ctsh	cathepsin H	BB542535	13036	9 E3.1
1427361_at	521	506	643	233	0.4614	1.0292	2.7519	1.2338	2E-05	0.6133	2E-07	0.0007	Hoxc6	homeo box C6	BB440143	15425	15 E2
1438232_at	355	371	411	171	0.4596	0.9554	2.4073	1.1581	3E-06	0.3764	3E-07	0.0132	Foxp2	forkhead box P2	AV322952	114142	6 A2
1434802_s_at	361	229	278	105	0.458	1.577	2.6499	0.7697	4E-06	3E-05	1E-07	0.0007	Ntf3	neurotrophin 3	BE945709	18205	6 F3
1427354_at	159	128	146	59	0.4574	1.2404	2.488	0.9176	0.0002	0.0062	4E-05	0.3153	Hoxa4	homeo box A4	AV135424	15401	6 B3
1416689_at	509	324	371	147	0.4557	1.5732	2.5189	0.7297	0.0001	0.0012	3E-05	0.0154	Tuft1	tuftelin 1	NM_011656	22156	3 F2
1433909_at	194	155	176	71	0.4556	1.2462	2.4823	0.9075	0.0027	0.0165	0.0006	0.3316	Syt17	synaptotagmin XVII	AW048713	110058	7 F2
1448823_at	10674	10311	11983	4692	0.4551	1.0353	2.5541	1.1226	7E-09	0.3456	2E-11	0.001	Cxcl12	chemokine (C-X-C motif) ligand 12	BC006640	20315	6 F1
1420992_at	6507	5951	6909	2691	0.4523	1.0934	2.5674	1.0619	3E-08	0.1877	4E-09	0.3687	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	AK009959	107765	19 C3
1417109_at	5328	3919	4757	1769	0.4513	1.3595	2.6896	0.8928	1E-06	0.0016	8E-09	0.0734	Tinagl1	tubulointerstitial nephritis antigen-like 1	BC005738	9424	4 D3
1449036_at	2908	2339	2457	1054	0.4504	1.2432	2.3324	0.845	1E-08	0.0006	3E-09	0.0034	Rnf128	ring finger protein 128	AK004847	66889	X F1

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82-/-	Femal e Cd82+/-	Male Cd82-/-	Male Cd82+/-	Male Cd82+/-	Male Cd82+/-	Male Cd82+/-	p-value Male Cd82+/-	p-value Female Cd82+/-	p-value Male Cd82+/-	p-value Female Cd82+/-	Gene	Description	GB	Entrez Id	Cytoband
	averag e signal	averag e signal	averag e signal	averag e signal	+/+ Ratio	+/- Ratio	+/- Ratio	+ vs Cd82+/-	+ vs Cd82+/-	+ vs Cd82+/-	+ vs Cd82+/-					
1457198_at	1641	2098	1861	944	0.4498	0.7824	1.9724	1.1339	3E-07	0.0033	3E-06	0.1179	Nrp1	neuropilin 1	AV291009	18186 8 E
1455679_at	177	107	141	48	0.4494	1.6539	2.9254	0.7949	0.0019	0.0012	6E-05	0.0328			BE457727	
1439757_s_at	376	274	301	123	0.4489	1.3747	2.4535	0.8012	5E-06	0.0002	0.0004	0.2002	Epha4	Eph receptor A4	AI385584	13838 1 C1-C5
1450469_at	312	250	297	112	0.4481	1.2488	2.6552	0.9528	5E-06	0.0677	6E-08	0.6114	RP23-394O9.3	differential display clone 8	NM_021440	58251 11 E2
1418762_at	363	198	230	89	0.4476	1.8321	2.5922	0.6332	5E-05	0.0006	2E-05	0.0059	Cd55	CD55 antigen	NM_010016	13136 1 E4
1423362_at	672	443	547	198	0.447	1.5173	2.7613	0.8134	4E-06	0.0002	6E-08	0.0065	Sort1	sortilin 1	AV247637	20661 3 F3
1416754_at	217	150	217	67	0.447	1.4471	3.2321	0.9983	0.0078	0.0141	0.0002	0.9842	Prkar1b	protein kinase, cAMP dependent regulatory, type I beta	NM_008923	19085 5 G2
1460242_at	353	194	226	86	0.4463	1.8242	2.6133	0.6393	8E-05	0.0002	1E-05	0.0017	Cd55	CD55 antigen	NM_010016	13136 1 E4
1454674_at	1459	1495	1584	666	0.4454	0.976	2.379	1.0856	2E-08	0.6514	1E-09	0.1159	Fez1	fasciculation and elongation protein zeta 1 (zygin I)	AU067669	235180 9 A4
1453708_a_at	95	123	109	55	0.4445	0.7722	1.9923	1.1469	0.0008	0.0132	0.0008	0.0871	Gsto2	glutathione S-transferase omega 2	AK019582	68214 19 D2
1419486_at	1359	1306	1416	579	0.4434	1.0404	2.4458	1.0422	6E-10	0.3826	5E-11	0.342	Foxc1	forkhead box C1	BB759833	17300 13 A3.2
1441070_at	360	282	321	125	0.4423	1.2782	2.5713	0.8898	9E-07	0.003	3E-08	0.0576			BB660130	
1456220_at	458	440	455	194	0.4409	1.0403	2.3451	0.9939	1E-05	0.5874	3E-06	0.9311	Fbxl7	F-box and leucine-rich repeat protein 7	BB446014	448987 15 B1
1435756_at	174	134	139	59	0.4396	1.2977	2.3613	0.8	3E-05	0.0374	3E-07	0.0127	Samd10	sterile alpha motif domain containing 10	BB526577	229011 2 H4
1428794_at	2464	2672	2826	1174	0.4394	0.922	2.4065	1.1469	2E-09	0.0769	9E-09	0.0304	Specc1	sperm antigen with calponin homology and coiled-coil domains	BQ175052	432572 11 B2
1418486_at	901	434	608	190	0.439	2.0771	3.191	0.6744	2E-07	0.0007	2E-09	0.0139	Vnn1	vanin 1	NM_011704	22661 10 A1-B2
1429052_at	499	446	474	196	0.4386	1.1178	2.425	0.9516	2E-06	0.1307	3E-07	0.4563	Ptprd	protein tyrosine phosphatase, receptor type, D	AK003303	19266 4 C3
1457825_x_at	2265	1257	1704	550	0.4378	1.8021	3.0967	0.7524	5E-06	0.0002	4E-07	0.0231	Tcn2	transcobalamin 2	BB515151	21452 11 A1
1419032_at	206	173	181	76	0.437	1.1922	2.3934	0.8773	6E-05	0.1267	2E-06	0.0951	Papola	poly (A) polymerase alpha	AW556821	18789 12 F1
1428671_at	921	792	894	346	0.4366	1.1622	2.5848	0.9712	2E-08	0.0465	1E-08	0.6859	2200002D01Rik	RIKEN cDNA 2200002D01 gene	AK008617	72275 7 A3
1422155_at	673	362	494	158	0.4351	1.8593	3.1325	0.733	1E-04	1E-06	4E-06	0.0023	Hist2h3c2	histone cluster 2, H3c2	BC015270	97114 3 F.2.1
1423915_at	2778	2391	2665	1040	0.435	1.1618	2.5626	0.9594	1E-08	0.0935	4E-10	0.5817	Olfml2b	olfactomedin-like 2B	BC025654	320078 1 H3
1432205_a_at	228	244	217	106	0.434	0.9346	2.0424	0.9485	4E-05	0.4143	5E-05	0.5094	C130038G02Rik	RIKEN cDNA C130038G02 gene	AK002529	77521 5 G3
1418366_at	1002	480	710	208	0.4335	2.0886	3.4156	0.709	1E-05	1E-04	2E-06	0.0304	Hist2h2aa1	histone cluster 2, H2aa1	BC010564	15267 3 F1-F2
1419485_at	639	580	664	251	0.4333	1.1014	2.6413	1.0391	4E-08	0.1543	5E-09	0.5554	Foxc1	forkhead box C1	BB759833	17300 13 A3.2
1449151_at	1146	962	979	416	0.4323	1.1916	2.3542	0.8541	4E-07	0.0136	8E-08	0.02	Pctk3	PCTAIRE-motif protein kinase 3	NM_008795	18557 1 E4
1418357_at	842	648	684	280	0.4322	1.2993	2.4423	0.8124	3E-07	0.0007	2E-07	0.009	Foxg1	forkhead box G1	NM_008241	15228 12 B3
1435695_a_at	965	1160	969	501	0.4319	0.8317	1.9353	1.0049	3E-07	0.1624	2E-07	0.9646	A030007L17Rik	RIKEN cDNA A030007L17 gene	AA673177	68252 6 B3
1436613_at	152	108	126	47	0.4312	1.4061	2.7041	0.8292	0.0003	0.0057	4E-05	0.0905	Coro6	coronin, actin binding protein 6	AI507196	216961 11 B5
1456721_at	270	242	250	104	0.4309	1.1123	2.3959	0.9282	4E-05	0.095	2E-05	0.3047	Thsd7a	thrombospondin, type I, domain containing 7A	BE690988	330267 6 A1
1427362_x_at	662	562	701	242	0.4301	1.1764	2.8959	1.0589	2E-06	0.0198	5E-08	0.3208	Hoxc6	homeo box C6	BB440143	15425 15 E2
1435353_a_at	1050	832	886	356	0.4284	1.2622	2.487	0.8441	2E-07	0.0141	1E-07	0.0596	Sfi1	Sfi1 homolog, spindle assembly associated (yeast)	BI454991	78887 11 A1
1424567_at	2089	1515	1795	648	0.4277	1.3787	2.7699	0.8593	1E-08	8E-06	2E-10	0.001	Tspan2	tetraspanin 2	BC007185	70747 3 F3
1429830_a_at	464	1395	368	596	0.4272	0.3323	0.6181	0.7945	6E-07	4E-08	2E-05	0.0042	Cd59a	CD59a antigen	AK005507	12509 2 55.0 cM
1427605_at	354	294	331	125	0.4268	1.2046	2.643	0.9365	1E-05	0.1307	5E-06	0.5903	Hoxb3	homeo box B3	X66177	15410 11 D
1450325_at	225	159	221	68	0.4256	1.4136	3.2622	0.9822	0.0006	0.0163	2E-05	0.874	Angpt4	angiopoietin 4	NM_009641	11602 2 G3
1427735_a_at	5100	4136	5534	1759	0.4253	1.2332	3.1461	1.0851	1E-09	0.0004	4E-12	0.0413	Acta1	actin, alpha 1, skeletal muscle	M12233	11459 8 E2
1416242_at	433	257	326	109	0.4249	1.6841	2.9865	0.7535	2E-07	6E-05	6E-08	0.0078	Klhl13	kelch-like 13 (Drosophila)	NM_026167	67455 X A2
1420693_at	388	329	381	139	0.4223	1.1805	2.7464	0.9825	4E-05	0.1938	3E-08	0.8113	Myom13	myomesin 1	NM_010867	17929 17 E1.3
1460379_at	296	216	280	91	0.4217	1.3741	3.0766	0.9442	7E-05	0.0017	6E-07	0.1937	Hoxb4	homeo box B4	AV307188	15412 11 D
1439878_at	398	207	244	87	0.4215	1.9185	2.7912	0.6133	2E-05	6E-05	3E-05	0.0047	Ivi	involutrin	AV009441	16447 3 F1
1428433_at	2891	3110	3199	1307	0.4202	0.9296	2.4473	1.1063	6E-11	0.3027	3E-10	0.1616	Hipk2	homeodomain interacting protein kinase 2	AK003718	15258 6 B
1453127_at	193	182	180	76	0.4199	1.0634	2.3579	0.931	0.0003	0.6421	4E-05	0.4717	Ppm1j	protein phosphatase 1J	AK009235	71887 3 F3
1456022_at	1101	1167	1200	489	0.4194	0.944	2.4534	1.09	0.0003	0.5132	2E-06	0.4053	Hipk2	homeodomain interacting protein kinase 2	BB554636	15258 6 B
1417156_at	755	993	795	416	0.4192	0.7601	1.9106	1.0536	3E-07	0.0028	1E-06	0.4392	Krt19	keratin 19	NM_008471	16669 11 D
1420991_at	6910	6797	7709	2841	0.418	1.0166	2.7131	1.1156	2E-08	0.8057	2E-09	0.1162	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	AK009959	107765 19 C3
1416034_at	5286	4308	4306	1796	0.417	1.2272	2.3976	0.8146	5E-09	0.0003	1E-08	0.0019	Cd24a	CD24a antigen	NM_009846	10040 10 B2
1447886_at	602	428	639	178	0.416	1.4065	3.5889	1.0615	4E-05	0.0067	8E-07	0.5702	0610040B09Rik	RIKEN cDNA 0610040B09 gene	AV302770	75395
1418393_a_at	881	735	815	304	0.414	1.1984	2.6799	0.9257	9E-07	0.0001	1E-07	0.0958	Itga7	integrin alpha 7	NM_008398	16404 10 D3
1448260_at	2751	1958	2750	804	0.4106	1.4049	3.4202	0.9997	2E-09	3E-07	9E-11	0.9936	Uchl1	ubiquitin carboxy-terminal hydrolase L1	NM_011670	22223 5 C3.1
1429135_at	198	122	160	50	0.41	1.6238	3.2028	0.8086	0.0047	0.0087	0.0001	0.0236	1110059M19Rik	RIKEN cDNA 1110059M19 gene	AV015858	68800 X A4
1425463_at	198	278	237	114	0.4098	0.7119	2.0784	1.1964	2E-07	0.0022	1E-07	0.0309	Gata6	GATA binding protein 6	BM214048	14465 18 A1
1425217_at	271	247	333	101	0.409	1.0979	3.2913	1.2261	0.0003	0.3002	0.0005	0.3376	Hoxb9	homeo box B9	AA386586	15417 11 D
1435426_s_at	164	120	154	49	0.4081	1.3723	3.1471	0.9359	9E-05	0.0033	7E-06	0.5	Pisd	phosphatidylserine decarboxylase	AV212090	320951 5 B1
1418415_at	270	216	261	88	0.4071	1.2538	2.9716	0.9649	0.0002	0.0068	2E-05	0.6241	Hoxb5	homeo box B5	NM_008268	15413 11 D
1424863_a_at	1201	1272	1431	515	0.405	0.9443	2.7778	1.1915	5E-07	0.4051	1E-08	0.0092	Hipk2	homeodomain interacting protein kinase 2	AF170301	15258 6 B

Table S1 - M vs F (WT)

Probe Set ID	Femal e Cd82- /- avera ge signal	Femal e Cd82 +/ avera ge signal	Male Cd82- /- avera ge signal	Male Cd82+ /+ avera ge signal	Male Cd82+/ /+ Ratio	Female Cd82-/ /- Ratio	Male Cd82-/ /- Ratio	Male Cd82+/ /+ Ratio	p-value Male Cd82+/ /+ vs Female Cd82+/ /+	p-value Female Cd82+/ /+ vs Female Cd82-/ /-	p-value Male Cd82+/ /+ vs Male Cd82-/ /-	p-value MFemale Cd82-/ /- vs Female Cd82-/ /-	Gene	Description	GB	Entrez Id	Cytoband
	1420558_at	179	118	142	48	0.4044	1.5218	2.987	0.7938	8E-05	0.0162	7E-07	0.064	Selp	selectin, platelet	M72332	20344
1418072_at	10949	7496	9638	3027	0.4039	1.4606	3.1837	0.8803	2E-06	6E-08	3E-08	0.0006	Hist1h2bc	histone cluster 1, H2bc	NM_023422	68024	13 A3.1
1422668_at	2394	1759	2140	710	0.4037	1.3611	3.0132	0.8938	2E-07	8E-05	3E-08	0.0931	Serpinh9b	serine (or cysteine) peptidase inhibitor, clade B, member 9b	NM_011452	20706	13 A3.3
1434913_at	235	106	163	43	0.4037	2.2208	3.821	0.6945	0.0004	2E-05	2E-06	0.0006	Hmgcl1	3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase-like 1	BF471959	208982	9 D
1451991_at	294	226	267	91	0.4028	1.3026	2.9345	0.9073	0.0019	0.0319	0.0001	0.1798	Epha7	Eph receptor A7	BC026153	13841	4 A4
1435421_at	265	191	242	77	0.4027	1.3872	3.1479	0.9139	0.0056	0.0068	0.0007	0.4138	Fsd1	fibronectin type 3 and SPRY domain-containing protein	BQ175318	240121	17 D
1429718_at	255	167	165	67	0.4025	1.5267	2.4561	0.6475	0.0005	0.0094	0.0002	0.0048	Slitrk5	SLIT and NTRK-like family, member 5	BB782729	75409	14 E3
1449357_at	266	196	241	79	0.4015	1.3577	3.0635	0.906	2E-05	0.0085	8E-07	0.2584	2310030G06Rik	RIKEN cDNA 2310030G06 gene	NM_025865	66952	9 A5.3
1422870_at	315	244	295	97	0.3971	1.2878	3.044	0.9387	1E-05	0.0074	6E-07	0.3959	Hoxc4	homeo box C4	NM_013553	15423	15 F3
1425240_a_at	10146	7094	9393	2799	0.3946	1.4303	3.3553	0.9258	5E-07	5E-06	1E-08	0.0879	Hist1h2bp	histone cluster 1, H2bp	M25487	319188	13 A3.1
1448631_a_at	552	525	532	206	0.3928	1.0519	2.5789	0.963	0.0001	0.6301	5E-05	0.7185	Hipk2	homeodomain interacting protein kinase 2	NM_010433	15258	6 B
1433683_at	163	139	149	54	0.39	1.1683	2.7459	0.9167	0.0001	0.1021	8E-06	0.1521	Rbm35b	RNA binding motif protein 35b	BF124648	77411	8 D3
1420872_at	562	484	548	189	0.3899	1.1601	2.8996	0.9745	1E-06	0.1114	3E-08	0.7184	Gucy1b3	guanylate cyclase 1, soluble, beta 3	BF472806	54195	3 E3
1423561_at	225	148	160	58	0.3895	1.5204	2.7807	0.7124	9E-05	0.004	5E-05	0.0264	Nell2	NEL-like 2 (chicken)	AI838010	54003	
1451019_at	301	173	258	67	0.3893	1.735	3.8294	0.8593	1E-05	0.0021	7E-07	0.2919	Ctsf	cathepsin F	AK017474	56464	19 A
1442051_at	947	540	696	210	0.3887	1.7535	3.3146	0.7347	1E-06	1E-07	2E-07	0.0009	Hist2h3c1	histone cluster 2, H3c1	BE691662	15077	3 F1-F2
1460314_s_at	2078	1144	1843	443	0.3874	1.8175	4.1601	0.8668	1E-07	7E-06	1E-11	0.0212	Hist2h3c1	histone cluster 2, H3c1	NM_019469	15077	3 F1-F2
1424966_at	308	302	310	117	0.3872	1.0198	2.6515	1.0067	0.0003	0.8061	9E-05	0.9343	Tmem40	transmembrane protein 40	BC019416	93436	6 E3
1450567_a_at	1416	1594	1566	617	0.387	0.8881	2.539	1.1066	1E-06	0.255	4E-06	0.3915	Col2a1	collagen, type II, alpha 1	NM_031163	12824	15 F1
1425464_at	547	607	573	235	0.3862	0.8997	2.4443	1.0492	2E-07	0.2712	2E-07	0.5954	Gata6	GATA binding protein 6	BM214048	14465	18 A1
1418365_at	1587	1577	1673	609	0.3859	1.0064	2.7489	1.0541	2E-08	0.8797	5E-09	0.2942	Ctsh	cathepsin H	NM_007801	13036	9 E3.1
1439885_at	372	278	423	107	0.3842	1.3394	3.9665	1.1378	2E-06	0.0013	8E-08	0.1555	Hoxc5	homeo box C5	AA051236	15424	15 F3
1418318_at	4641	4004	3987	1531	0.3824	1.159	2.6039	0.8591	4E-10	0.0067	5E-11	0.0033	Rnf128	ring finger protein 128	AK004847	66889	X F1
1451440_at	191	123	117	47	0.3822	1.5521	2.4933	0.6139	1E-06	0.0073	0.0002	0.0205	Chodl	chondrolectin	AF311699	246048	16 C3.2
1439109_at	569	566	582	215	0.3788	1.0045	2.7151	1.0239	7E-08	0.9369	2E-08	0.6852	Ccdc68	coiled-coil domain containing 68	AV378320	381175	18 E2
1448182_a_at	8765	7252	7677	2741	0.3779	1.2086	2.8011	0.8758	8E-09	0.0003	4E-09	0.0145	Cd24a	CD24a antigen	NM_009846	12484	10 B2
1433924_at	4396	3123	3673	1170	0.3745	1.4074	3.14	0.8356	8E-09	0.0016	1E-09	0.0419			BM200248		
1456229_at	720	577	690	216	0.374	1.2467	3.1961	0.9588	2E-06	0.0004	3E-07	0.5288	Hoxb3	homeo box B3	BG073383	15410	11 D
1427760_s_at	301	139	210	52	0.3721	2.1692	4.0599	0.6964	0.0002	0.0005	4E-06	0.0249	Prl2c2	prolactin family 2, subfamily c, member 2	X75557	18811	13 A1
1439627_at	232	135	142	50	0.3706	1.7187	2.8433	0.6131	9E-06	0.0021	3E-05	0.0101	Zic1	zinc finger protein of the cerebellum 1	AV031691	22771	9 E3.3
1416023_at	2403	1688	2049	616	0.3648	1.4232	3.3269	0.8527	4E-09	6E-06	2E-10	0.0031	Fabp3	fatty acid binding protein 3, muscle and heart	NM_010174	14077	4 D.2
1424886_at	1275	1122	1202	409	0.3646	1.1369	2.939	0.9426	8E-10	0.0021	4E-11	0.0712	Ptprd	protein tyrosine phosphatase, receptor type, D	BC025145	19266	4 C3
1447845_s_at	333	154	215	56	0.3646	2.1571	3.8192	0.6455	2E-06	0.0009	3E-08	0.0124	Vnn1	vanin 1	AV360029	22361	10 A1-B2
1451718_at	405	172	340	63	0.3645	2.3549	5.4164	0.8385	0.0021	0.0017	4E-07	0.0556	Plp1	proteolipid protein (myelin) 1	BB768495	18823	X F1-F2
1422168_a_at	2927	2483	2523	905	0.3643	1.1784	2.7879	0.8619	4E-09	0.0029	2E-09	0.0093	Bdnf	brain derived neurotrophic factor	AY057913	12064	2 E3
1419675_at	4026	4006	4689	1450	0.3619	1.005	3.234	1.1647	2E-08	0.9273	6E-10	0.0105	Ngf	nerve growth factor	NM_013609	18049	3 F.2
1451999_at	226	207	215	75	0.3611	1.0963	2.8801	0.9486	5E-05	0.3111	3E-05	0.6325	Ldb3	LIM domain binding 3	AF114378	24131	14 B
1418367_x_at	1728	892	1332	322	0.3609	1.9367	4.1362	0.7708	2E-05	3E-05	3E-07	0.0142	Hist2h2aa1	histone cluster 2, H2aa1	BC010564	15267	3 F1-F2
1458482_at	236	209	222	75	0.3596	1.1315	2.9577	0.9399	5E-06	0.0586	2E-06	0.4439	Tnni3k	TNNI3 interacting kinase	BB480482	435766	3 H4
1448595_a_at	3461	850	982	305	0.3587	4.0696	3.2185	0.2837	5E-08	4E-06	3E-09	2E-06	Bex1	brain expressed gene 1	NM_009052	19716	X F1
1448269_a_at	1721	1096	1263	393	0.3582	1.5704	3.2165	0.7337	4E-08	8E-09	2E-07	0.0024	Klhl13	kelch-like 13 (Drosophila)	NM_026167	67455	X A2
1446524_at	297	200	235	71	0.3564	1.4819	3.2909	0.7914	3E-05	0.0006	3E-05	0.1109			BB396283		
1420940_x_at	258	173	192	62	0.3561	1.492	3.119	0.7444	2E-06	0.0225	4E-08	0.0428	Rgs5	regulator of G-protein signaling 5	BF585144	19737	1 H2
1434780_at	170	166	142	59	0.3551	1.0234	2.4121	0.837	6E-05	0.7869	0.0001	0.0801	C130038G02Rik	RIKEN cDNA C130038G02 gene	AU067634	77521	5 G3
1449153_at	1001	602	566	213	0.3549	1.6634	2.6537	0.5661	4E-06	8E-05	3E-06	4E-05	Mmp12	matrix metalloproteinase 12	BC019135	17381	9 A1
1433919_at	115	108	100	38	0.3536	1.0675	2.6318	0.8718	8E-05	0.2553	4E-05	0.0182	Asb4	ankyrin repeat and SOCS box-containing 4	AV302111	65255	6 A1
1444650_at	126	100	102	35	0.3475	1.2601	2.9403	0.8108	0.0073	0.223	0.0019	0.1252	Arhgef18	rho/rac guanine nucleotide exchange factor (GEF) 18	BF151040	102098	8 A1.1
1450171_x_at	405	183	259	64	0.347	2.2096	4.0642	0.6382	5E-05	2E-06	9E-05	0.039	Gzme	granzyme E	NM_010373	14942	14 C3
1451245_at	286	157	201	54	0.3457	1.8229	3.9668	0.7011	1E-06	3E-05	2E-08	0.0004	Lrrc3b	leucine rich repeat containing 3B	BC019794	218763	14 A2
1423477_at	1179	825	914	285	0.3448	1.4283	3.2127	0.7757	8E-09	0.0119	1E-08	0.0499	Zic1	zinc finger protein of the cerebellum 1	BB361162	22771	9 E3.3
1449359_at	215	245	242	85	0.3445	0.8752	2.8599	1.1258	4E-07	0.2703	4E-07	0.3211	Pax1	paired box gene 1	NM_008780	18503	2 G2
1428891_at	2140	718	1188	247	0.3437	2.9826	4.8181	0.5552	3E-06	7E-05	1E-06	0.0096	9130213B05Rik	RIKEN cDNA 9130213B05 gene	AK008716	231440	5 E2
1423506_a_at	1018	445	706	152	0.342	2.2867	4.6366	0.6934	1E-07	0.0002	7E-12	0.0099	Nnat	neuronatin	AV218841	18111	2 H1
1418933_at	1271	1287	1316	440	0.3418	0.9879	2.9926	1.0355	6E-06	0.8182	7E-07	0.398	Slc1a6	solute carrier family 1 (high affinity aspartate/glutamate transpor	NM_009200	20513	10 C1
1421594_a_at	940	701	730	239	0.3411	1.341	3.0504	0.7759	3E-07	0.0027	3E-08	0.0031	Sytl2	synaptotagmin-like 2	NM_031394	83671	7 E1
1450303_at	103	125	130	42	0.3375	0.8309	3.0885	1.2544	0.0006	0.5046	0.0002	0.3777	Vax2	ventral anterior homeobox containing gene 2	NM_011912	24113	6 C3

Table S1 - M vs F (WT)

Probe Set ID	Female Cd82-/- average signal	Female Cd82+/+ average signal	Male Cd82-/- average signal	Male Cd82+/+ average signal	Male Cd82+/+ Ratio	Female Cd82-/- Ratio	Male Cd82+/+ Ratio	Female Cd82-/- Ratio	p-value Male Cd82+/+ vs Female Cd82+/+	p-value Male Cd82+/+ vs Male Cd82-/-	p-value Female Cd82-/- vs Male Cd82-/-	Gene	Description	GB	Entrez Id	Cytoband
1420942_s_at	271	148	171	17	0.1186	1.8372	9.7849	0.6317	0.0008	0.0094	0.0002	Rgs5	regulator of G-protein signaling 5	BF585144	19737	1 H2
1418105_at	344	251	278	22	0.088	1.3722	12.612	0.8084	0.0013	0.0015	0.0003	Stmn4	stathmin-like 4	NM_019675	56471	14 D1
1449499_at	245	232	270	16	0.0706	1.0549	16.514	1.1054	3E-08	0.5373	2E-09	Hoxa7	homeo box A7	NM_010455	15404	6 B3
1425672_a_at	97	101	15	3	0.0306	0.9622	4.7105	0.15	2E-08	0.8527	0.0911	Trpc2	transient receptor potential cation channel, subfamily C, member 2	AF230802	22064	7 F1
1436936_s_at	3887	5799	51	58	0.0101	0.6703	0.8779	0.0132	2E-11	0.0015	0.448	Tsix	X (inactive)-specific transcript, antisense	BG806300	22097	X D
1427263_at	166	224	6	2	0.0081	0.7391	3.41	0.0374	1E-07	0.0115	0.042	Xist	inactive X specific transcripts	L04961	213742	X D
1427262_at	766	1046	8	6	0.006	0.7325	1.2991	0.0107	9E-07	0.0434	0.6224	Xist	inactive X specific transcripts	L04961	213742	X D

Table S1 - M vs F (WT)