

Figure S1. Boxplots of normalized samples in five datasets. (A) GSE25604, (B) GSE50161, (C) GSE66354, (D) GSE74195 and (E) GSE86574. The x-axes indicate samples, and the y-axes represent the expression of genes.

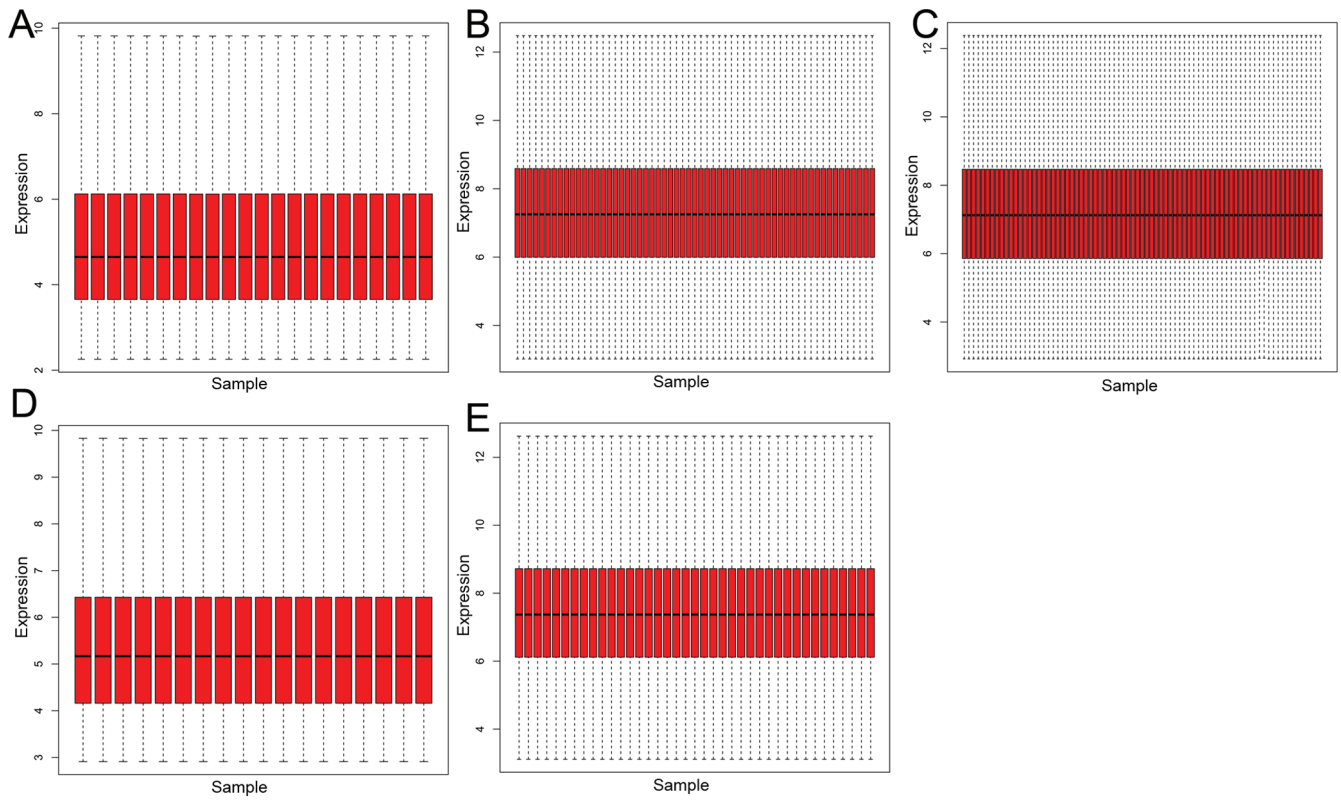


Figure S2. Volcano plots of DEGs in five datasets. (A) GSE25604, (B) GSE50161, (C) GSE66354, (D) GSE74195 and (E) GSE86574. Red nodes represent upregulated DEGs and green nodes indicate downregulated DEGs. Cut-off criteria were $P < 0.05$ and $|\log_2 FC| > 1$. DEGs, differentially expressed genes; FC, fold change; adj.P.Val, adjusted P-value.

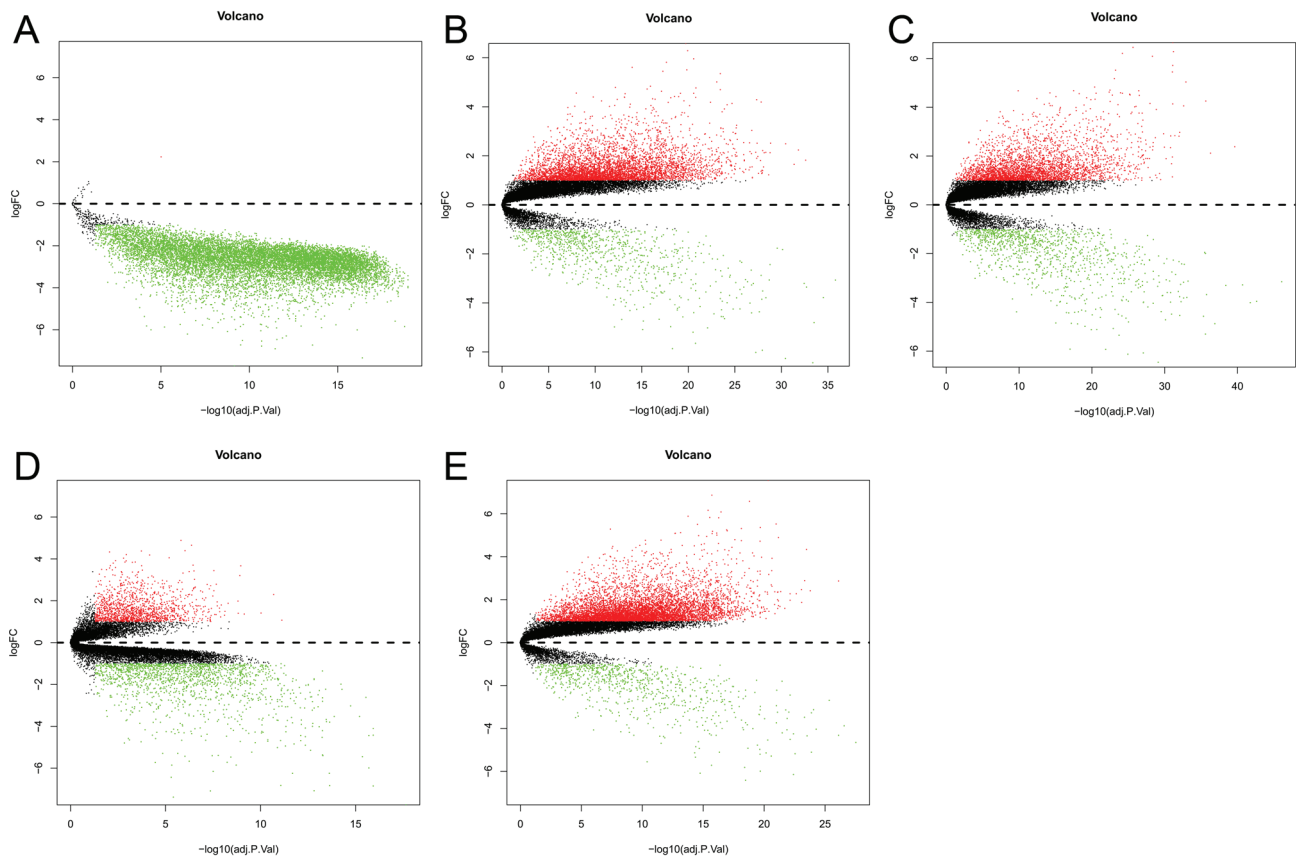


Figure S3. Transcription factor-gene regulatory network constructed using the Cytoscape iRegulion plug-in.

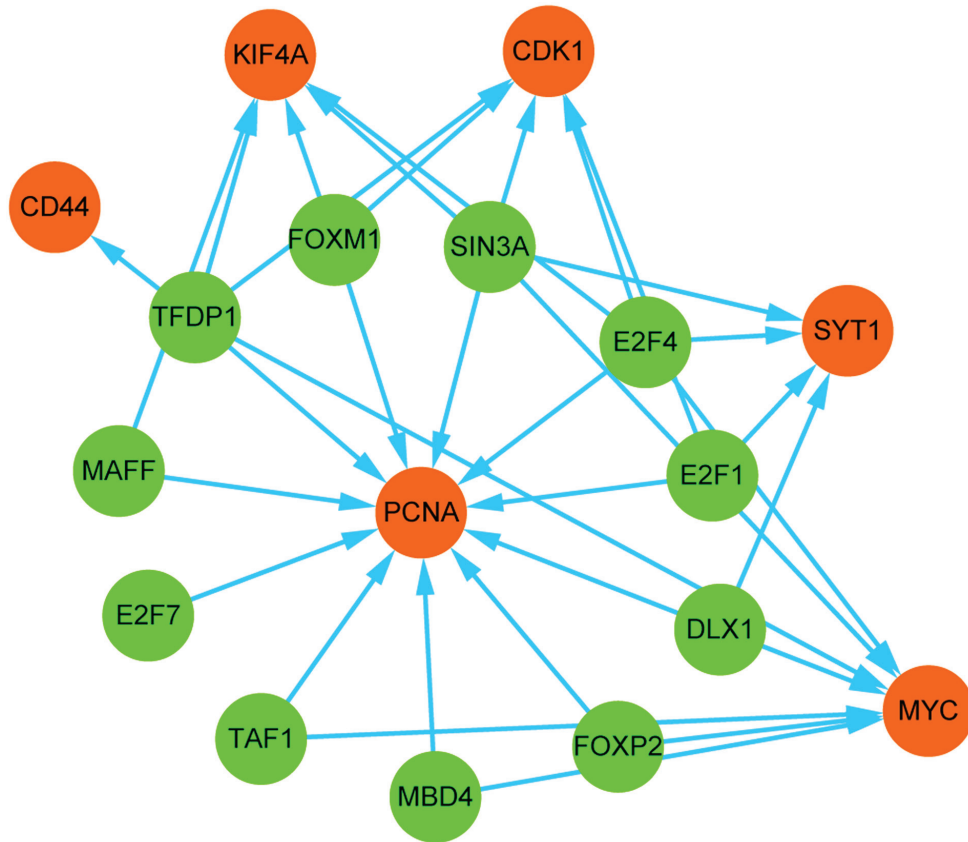


Table SI. Primer sequences for reverse transcription-quantitative polymerase chain reaction.

Genes	Sequences
hsa-miR-124	F: 5'-ACACTCCAGCTGGGCAGCAGCAATTCATGTTT-3' R: 5'-CTCAACTGGTGTCTGTGGA-3'
hsa-miR-330-3p	F: 5'-CATGAATTCACTCTCCCCGTTTCTCCCTCTGC-3' R: 5'-CCTGCGGCCGCGAGCCGCCCTGTTTGTCTGAG-3'
hsa-miR-34a-5p	F: 5'-TGGCAGTGTCTTAGCTGGTTGT-3' R: 5'-GCGAGCACAGAATTAATACGAC-3'
hsa-miR-449a	F: 5'-TGCGGTGGCAGTGTATTGTTAGC-3' R: 5'-CCAGTGCAGGGTCCGAGGT-3'
CD44	F: 5'-CGGACACCATGGACAAGTTT-3' R: 5'-TGTC AATCCAGTTTCAGCATCA-3'
PCNA	F: 5'-GAACTGGTTCATTCATCTCTATGG-3' F: 5'-TGTCACAGACAAGTAATGTCGATAAAA-3'
SYT1	F: 5'-CAATAGCCATAGTCGCAGTCCT-3' R: 5'-TGTC AATCCAGTTTCAGCATCA-3'
U6	F: 5'-GCTTCGGCAGCACATATACTAAAAT-3' R: 5'-CGCTTCACGAATTTGCGTGTTCAT-3'
GAPDH	F: 5'-GGAAAGCTGTGGCGTGAT-3' R: 5'-AAGGTGGAAGAATGGGAGTT-3'

hsa, *homo sapiens*; miR, microRNA; CD44, CD44 molecule (Indian blood group); PCNA, proliferating cell nuclear antigen; SYT1, synaptotagmin 1.

Table SII. Downregulated and upregulated differentially expressed miRNAs in the GSE42657 dataset.

miRNA_ID	adj.P.val	P-value	t	B	logFC	Expression
hsa-miR-124a:9.1	3.06x10 ⁻⁸	6.97x10 ⁻¹¹	-12.20530	15.136710	-4.398000	Down
hsa-miR-128b:9.1	4.83x10 ⁻⁸	2.11x10 ⁻¹⁰	-11.47940	14.049030	-4.368078	Down
hsa-miR-129-3p	4.61x10 ⁻⁵	8.46x10 ⁻⁷	-6.93222	5.773031	-4.324756	Down
hsa-miR-128a:9.1	3.06x10 ⁻⁸	8.03x10 ⁻¹¹	-12.11100	14.998540	-4.094944	Down
hsa-miR-124	7.24x10 ⁻⁵	1.71x10 ⁻⁶	-6.60268	5.065821	-4.067027	Down
hsa-miR-1224-5p	6.00x10 ⁻¹⁴	5.24x10 ⁻¹⁷	-25.38230	28.136500	-3.884722	Down
hsa-miR-129 ^a	3.17x10 ⁻⁴	1.38x10 ⁻⁵	-5.66109	2.971619	-3.588282	Down
hsa-miR-433	5.69x10 ⁻⁵	1.16x10 ⁻⁶	-6.78273	5.453998	-3.508976	Down
hsa-miR-219-2-3p	3.87x10 ⁻⁸	1.35x10 ⁻¹⁰	-11.76620	14.485540	-3.481658	Down
hsa-miR-326	7.24x10 ⁻⁵	1.81x10 ⁻⁶	-6.57766	5.011556	-3.384371	Down
hsa-miR-876-3p	1.27x10 ⁻⁴	3.89x10 ⁻⁶	-6.22635	4.241239	-3.267747	Down
hsa-miR-329	2.98x10 ⁻⁵	4.95x10 ⁻⁷	-7.18774	6.311459	-3.241901	Down
hsa-miR-873	6.62x10 ⁻⁶	5.78x10 ⁻⁸	-8.25560	8.464584	-3.211621	Down
hsa-miR-138	7.24x10 ⁻⁵	1.83x10 ⁻⁶	-6.57067	4.996379	-3.208415	Down
hsa-miR-137	8.10x10 ⁻⁴	4.26x10 ⁻⁵	-5.17132	1.846386	-3.065793	Down
hsa-miR-383	5.83x10 ⁻⁶	4.58x10 ⁻⁸	-8.37650	8.698425	-3.058894	Down
hsa-miR-1296	2.25x10 ⁻⁴	7.85x10 ⁻⁶	-5.91151	3.538382	-2.928583	Down
hsa-miR-656	1.84x10 ⁻⁵	2.25x10 ⁻⁷	-7.57040	7.101129	-2.858111	Down
hsa-miR-187	2.65x10 ⁻⁴	1.11x10 ⁻⁵	-5.75805	3.191826	-2.850080	Down
hsa-miR-668	2.37x10 ⁻⁴	9.11x10 ⁻⁶	-5.84528	3.389111	-2.688792	Down
hsa-miR-410	6.80x10 ⁻³	6.53x10 ⁻⁴	-4.01181	-0.861090	-2.570598	Down
hsa-miR-299-5p	9.73x10 ⁻⁶	1.02x10 ⁻⁷	-7.96585	7.895943	-2.499440	Down
hsa-miR-330-3p	8.24x10 ⁻⁶	7.92x10 ⁻⁸	-8.09464	8.150126	-2.490239	Down
hsa-miR-770-5p	3.09x10 ⁻⁵	5.40x10 ⁻⁷	-7.14569	6.223453	-2.470578	Down
hsa-miR-874	7.54x10 ⁻⁴	3.88x10 ⁻⁵	-5.21126	1.938849	-2.465748	Down
hsa-miR-485-3p	2.69x10 ⁻⁵	3.54x10 ⁻⁷	-7.34978	6.648292	-2.418290	Down
hsa-miR-487b	7.24x10 ⁻⁵	1.77x10 ⁻⁶	-6.58839	5.034846	-2.341674	Down
hsa-miR-379	1.34x10 ⁻²	1.48x10 ⁻³	-3.66470	-1.664200	-2.283603	Down
hsa-miR-323-3p	2.37x10 ⁻⁴	9.12x10 ⁻⁶	-5.84505	3.388584	-2.275284	Down
hsa-miR-409-3p	6.39x10 ⁻⁴	3.13x10 ⁻⁵	-5.30497	2.155375	-2.272903	Down
hsa-miR-642	3.24x10 ⁻²	5.09x10 ⁻³	-3.13516	-2.857160	-2.250881	Down
hsa-miR-1249	1.33x10 ⁻²	1.46x10 ⁻³	-3.67057	-1.650740	-2.215154	Down
hsa-miR-598	4.95x10 ⁻⁴	2.29x10 ⁻⁵	-5.43959	2.465225	-2.205659	Down
hsa-miR-490-5p	3.94x10 ⁻³	3.34x10 ⁻⁴	-4.29486	-0.200100	-2.188138	Down
hsa-miR-885-5p	3.13x10 ⁻³	2.40x10 ⁻⁴	-4.43420	0.126142	-2.147553	Down
hsa-miR-7	2.54x10 ⁻⁴	1.04x10 ⁻⁵	-5.78609	3.255333	-2.061466	Down
hsa-miR-409-5p	3.94x10 ⁻³	3.32x10 ⁻⁴	-4.29729	-0.194420	-2.008801	Down
hsa-miR-889	2.37x10 ⁻⁴	9.09x10 ⁻⁶	-5.84644	3.391726	-1.993087	Down
hsa-miR-154 ^a	2.04x10 ⁻²	2.68x10 ⁻³	-3.41152	-2.240880	-1.966815	Down
hsa-miR-128	3.12x10 ⁻³	2.37x10 ⁻⁴	-4.43938	0.138281	-1.957274	Down
hsa-miR-330-5p	1.64x10 ⁻⁴	5.31x10 ⁻⁶	-6.08604	3.929393	-1.933395	Down
hsa-miR-7-2 ^a	1.16x10 ⁻²	1.22x10 ⁻³	-3.74697	-1.474950	-1.831817	Down
hsa-miR-369-3p	4.12x10 ⁻²	7.24x10 ⁻³	-2.98063	-3.194010	-1.827947	Down
hsa-miR-33b	4.53x10 ⁻²	8.45x10 ⁻³	-2.91225	-3.340960	-1.822507	Down
hsa-miR-539	1.66x10 ⁻³	1.04x10 ⁻⁴	-4.78750	0.953022	-1.821063	Down
hsa-miR-379 ^a	9.36x10 ⁻³	9.56x10 ⁻⁴	-3.85061	-1.235450	-1.813168	Down
hsa-miR-1179	3.64x10 ⁻²	6.12x10 ⁻³	-3.05427	-3.034270	-1.778167	Down
hsa-miR-206	2.28x10 ⁻²	3.17x10 ⁻³	-3.34004	-2.401770	-1.772400	Down
hsa-miR-577	9.17x10 ⁻⁴	5.04x10 ⁻⁵	-5.09875	1.678088	-1.749504	Down
hsa-miR-124 ^a	1.74x10 ⁻⁵	1.97x10 ⁻⁷	-7.63621	7.234902	-1.704053	Down
hsa-miR-495	6.51x10 ⁻³	6.14x10 ⁻⁴	-4.03773	-0.800720	-1.668726	Down
hsa-miR-488 ^a	3.64x10 ⁻²	6.11x10 ⁻³	-3.05485	-3.033010	-1.655069	Down
hsa-miR-154	2.90x10 ⁻²	4.49x10 ⁻³	-3.18975	-2.736750	-1.641024	Down
hsa-miR-127-3p	1.75x10 ⁻³	1.14x10 ⁻⁴	-4.74849	0.861836	-1.615866	Down
hsa-miR-655	2.65x10 ⁻²	3.81x10 ⁻³	-3.26030	-2.580090	-1.592616	Down
hsa-miR-628-5p	1.61x10 ⁻²	1.90x10 ⁻³	-3.55964	-1.904660	-1.541800	Down
hsa-miR-744	1.89x10 ⁻³	1.29x10 ⁻⁴	-4.69880	0.745644	-1.537217	Down
hsa-miR-584	1.61x10 ⁻²	1.91x10 ⁻³	-3.55697	-1.910760	-1.537108	Down
hsa-miR-133b	1.00x10 ⁻³	5.59x10 ⁻⁵	-5.05426	1.574767	-1.523298	Down

Table SII. Continued.

miRNA_ID	adj.P.val	P-value	t	B	logFC	Expression
hsa-miR-769-3p	3.89x10 ⁻²	6.73x10 ⁻³	-3.01244	-3.125180	-1.515118	Down
hsa-miR-107	5.90x10 ⁻³	5.45x10 ⁻⁴	-4.08852	-0.682330	-1.503248	Down
hsa-miR-338-3p	3.72x10 ⁻⁴	1.69x10 ⁻⁵	-5.57293	2.770594	-1.486301	Down
hsa-miR-29c ^a	7.33x10 ⁻³	7.16x10 ⁻⁴	-3.97289	-0.951670	-1.443588	Down
hsa-miR-340 ^a	5.66x10 ⁻³	5.14x10 ⁻⁴	-4.11297	-0.625260	-1.404232	Down
hsa-miR-138-1 ^a	7.82x10 ⁻³	7.85x10 ⁻⁴	-3.93402	-1.042010	-1.329171	Down
hsa-miR-548k	4.68x10 ⁻⁷	2.46x10 ⁻⁹	-9.98282	11.618980	-1.302216	Down
hsa-miR-139-3p	2.78x10 ⁻²	4.07x10 ⁻³	-3.23184	-2.643430	-1.290689	Down
hsa-miR-548o	3.64x10 ⁻²	6.08x10 ⁻³	-3.05745	-3.027340	-1.271591	Down
hsa-miR-342-3p	1.89x10 ⁻⁴	6.29x10 ⁻⁶	-6.01066	3.760928	-1.248232	Down
hsa-miR-138-2 ^a	2.62x10 ⁻³	1.88x10 ⁻⁴	-4.53820	0.369723	-1.240113	Down
hsa-miR-181b	1.28x10 ⁻⁴	4.01x10 ⁻⁶	-6.21261	4.210803	-1.231861	Down
hsa-miR-136 ^a	3.57x10 ⁻²	5.77x10 ⁻³	-3.08050	-2.977030	-1.210438	Down
hsa-miR-487a	2.87x10 ⁻²	4.34x10 ⁻³	-3.20459	-2.703870	-1.186042	Down
hsa-miR-132 ^a	4.81x10 ⁻²	9.20x10 ⁻³	-2.87457	-3.421340	-1.093071	Down
hsa-miR-197	4.12x10 ⁻²	7.20x10 ⁻³	-2.98305	-3.188770	-1.089135	Down
hsa-miR-491-5p	2.04x10 ⁻²	2.73x10 ⁻³	-3.40487	-2.255880	-1.083874	Down
hsa-miR-328	2.87x10 ⁻²	4.31x10 ⁻³	-3.20714	-2.698240	-1.065684	Down
hsa-miR-342-5p	4.71x10 ⁻²	8.97x10 ⁻³	-2.88550	-3.398070	-1.039282	Down
hsa-miR-885-3p	2.70x10 ⁻²	3.92x10 ⁻³	-3.24879	-2.605730	-1.025146	Down
hsa-miR-671-3p	4.95x10 ⁻²	9.52x10 ⁻³	-2.85925	-3.453910	-1.005048	Down
hsa-miR-450a	2.90x10 ⁻²	4.53x10 ⁻³	3.18579	-2.745500	1.020921	Up
hsa-miR-193a-3p	4.15x10 ⁻²	7.32x10 ⁻³	2.97566	-3.204720	1.087457	Up
hsa-miR-148a	8.15x10 ⁻⁵	2.28x10 ⁻⁶	6.47120	4.779735	1.097744	Up
hsa-miR-199a-5p	4.11x10 ⁻³	3.51x10 ⁻⁴	4.27347	-0.250150	1.112635	Up
hsa-miR-106a	1.49x10 ⁻³	9.00x10 ⁻⁵	4.85101	1.101323	1.125590	Up
hsa-miR-363	6.50x10 ⁻³	6.07x10 ⁻⁴	4.04250	-0.789600	1.125833	Up
hsa-miR-545:9.1	2.92x10 ⁻³	2.19x10 ⁻⁴	4.47324	0.217586	1.156359	Up
hsa-miR-92b	1.17x10 ⁻²	1.24x10 ⁻³	3.74008	-1.490830	1.191967	Up
hsa-miR-17 ^a	1.61x10 ⁻²	1.94x10 ⁻³	3.55130	-1.923700	1.223239	Up
hsa-miR-18a	5.90x10 ⁻³	5.46x10 ⁻⁴	4.08761	-0.684430	1.241874	Up
hsa-miR-503	4.21x10 ⁻²	7.47x10 ⁻³	2.96689	-3.223650	1.248250	Up
hsa-miR-339-5p	1.71x10 ⁻³	1.09x10 ⁻⁴	4.76987	0.911809	1.271402	Up
hsa-miR-18b	1.72x10 ⁻²	2.15x10 ⁻³	3.50642	-2.025890	1.273376	Up
hsa-miR-16-1 ^a	2.04x10 ⁻²	2.70x10 ⁻³	3.40837	-2.248000	1.326431	Up
hsa-miR-592	2.78x10 ⁻³	2.07x10 ⁻⁴	4.49782	0.275145	1.374665	Up
hsa-miR-24-2 ^a	9.29x10 ⁻⁷	5.68x10 ⁻⁹	9.50396	10.783770	1.399102	Up
hsa-miR-34a	1.25x10 ⁻⁶	8.76x10 ⁻⁹	9.26296	10.352250	1.450013	Up
hsa-miR-1246	2.11x10 ⁻²	2.85x10 ⁻³	3.38632	-2.297720	1.457936	Up
hsa-miR-603	1.81x10 ⁻²	2.31x10 ⁻³	3.47634	-2.094180	1.478898	Up
hsa-miR-141	2.44x10 ⁻³	1.73x10 ⁻⁴	4.57434	0.454354	1.550393	Up
hsa-miR-142-3p	6.54x10 ⁻⁵	1.43x10 ⁻⁶	6.68694	5.248004	1.551637	Up
hsa-miR-19a	5.69x10 ⁻⁵	1.19x10 ⁻⁶	6.77089	5.428586	1.586584	Up
hsa-miR-199a ^a :9.1	1.31x10 ⁻³	7.69x10 ⁻⁵	4.91776	1.257033	1.586803	Up
hsa-miR-135a	5.66x10 ⁻³	5.13x10 ⁻⁴	4.11388	-0.623150	1.592555	Up
hsa-miR-146b-5p	5.09x10 ⁻³	4.44x10 ⁻⁴	4.17458	-0.481390	1.598980	Up
hsa-miR-155	2.75x10 ⁻⁴	1.17x10 ⁻⁵	5.73272	3.134383	1.627800	Up
hsa-miR-1251	4.48x10 ⁻²	8.08x10 ⁻³	2.93226	-3.298100	1.629974	Up
hsa-miR-32	3.58x10 ⁻²	5.84x10 ⁻³	3.07499	-2.989060	1.655588	Up
hsa-miR-100 ^a	3.86x10 ⁻³	3.17x10 ⁻⁴	4.31705	-0.148160	1.683209	Up
hsa-miR-449a	3.81x10 ⁻²	6.46x10 ⁻³	3.03101	-3.084880	1.685879	Up
hsa-miR-92b ^a	3.28x10 ⁻²	5.22x10 ⁻³	3.12400	-2.881710	1.689690	Up
hsa-miR-10a ^a	8.05x10 ⁻³	8.16x10 ⁻⁴	3.91778	-1.079720	1.711922	Up
hsa-miR-16-2 ^a	1.90x10 ⁻³	1.31x10 ⁻⁴	4.69125	0.727978	1.779191	Up
hsa-miR-210	2.90x10 ⁻²	4.53x10 ⁻³	3.18614	-2.744720	1.787449	Up
hsa-miR-34a ^a	5.99x10 ⁻⁴	2.83x10 ⁻⁵	5.34867	2.256127	1.860500	Up
hsa-miR-214	3.94x10 ⁻³	3.31x10 ⁻⁴	4.29813	-0.192450	1.903700	Up
hsa-miR-610	2.11x10 ⁻²	2.85x10 ⁻³	3.38569	-2.299130	1.952833	Up
hsa-miR-301a	7.80x10 ⁻⁵	2.11x10 ⁻⁶	6.50600	4.855662	1.981815	Up

Table SII. Continued.

miRNA_ID	adj.P.val	P-value	t	B	logFC	Expression
hsa-miR-551b	1.75x10 ⁻³	1.14x10 ⁻⁴	4.75033	0.866148	2.091346	Up
hsa-miR-31 ^a	2.87x10 ⁻²	4.26x10 ⁻³	3.21278	-2.685730	2.179291	Up
hsa-miR-10b	1.62x10 ⁻²	1.99x10 ⁻³	3.53932	-1.951000	2.280868	Up
hsa-miR-1247	1.53x10 ⁻²	1.75x10 ⁻³	3.59483	-1.824300	2.377220	Up
hsa-miR-142-5p	5.40x10 ⁻³	4.77x10 ⁻⁴	4.14479	-0.550980	2.395549	Up
hsa-miR-20a ^a	8.15x10 ⁻⁵	2.35x10 ⁻⁶	6.45679	4.748252	2.489395	Up
hsa-miR-34c-5p	1.85x10 ⁻³	1.23x10 ⁻⁴	4.71854	0.791820	2.949769	Up
hsa-miR-144:9.1	9.78x10 ⁻³	1.02x10 ⁻³	3.82467	-1.295490	3.046745	Up
hsa-miR-34b ^a	1.89x10 ⁻³	1.28x10 ⁻⁴	4.70256	0.754432	3.072460	Up
hsa-miR-483-3p	1.25x10 ⁻³	7.19x10 ⁻⁵	4.94696	1.325087	3.192252	Up
hsa-miR-923	2.98x10 ⁻⁵	4.75x10 ⁻⁷	7.20772	6.353177	3.231787	Up

hsa, *homo sapiens*; miR, microRNA; adj.P.val; adjusted P-value; FC, fold change; ^alowly expressed miRNA.

Table SIII. Top 5 significant Gene Ontology terms of up- and downregulated differentially expressed genes.

A, Upregulated				
Category	Term	Count	%	P-value
CC	GO:0070062~extracellular exosome	171	28.73950	1.22x10 ⁻¹⁹
CC	GO:0031012~extracellular matrix	44	7.39496	1.78x10 ⁻¹⁷
CC	GO:0005578~proteinaceous extracellular matrix	33	5.54622	6.18x10 ⁻¹¹
CC	GO:0005604~basement membrane	16	2.68908	1.61x10 ⁻⁸
CC	GO:0005783~endoplasmic reticulum	56	9.41177	7.49x10 ⁻⁸
BP	GO:0030198~extracellular matrix organization	38	6.38656	1.47x10 ⁻¹⁸
BP	GO:0007155~cell adhesion	38	6.38656	2.70x10 ⁻⁷
BP	GO:0042493~response to drug	28	4.70588	1.85x10 ⁻⁶
BP	GO:0051301~cell division	29	4.87395	8.95x10 ⁻⁶
BP	GO:0007067~mitotic nuclear division	23	3.86555	1.70x10 ⁻⁵
MF	GO:0005201~extracellular matrix structural constituent	18	3.02521	2.36x10 ⁻¹¹
MF	GO:0005515~protein binding	356	59.83193	5.87x10 ⁻¹¹
MF	GO:0005178~integrin binding	18	3.02521	3.72x10 ⁻⁸
MF	GO:0005509~calcium ion binding	47	7.89916	6.05x10 ⁻⁶
MF	GO:0004859~phospholipase inhibitor activity	6	1.00840	1.31x10 ⁻⁵
B, Downregulated				
Category	Term	Count	%	P-value
CC	GO:0030054~cell junction	59	17.77108	3.14x10 ⁻³³
CC	GO:0005886~plasma membrane	139	41.86747	5.47x10 ⁻¹⁷
CC	GO:0045211~postsynaptic membrane	29	8.73494	5.56x10 ⁻¹⁷
CC	GO:0045202~synapse	26	7.83133	1.17x10 ⁻¹⁵
CC	GO:0014069~postsynaptic density	25	7.53012	1.65x10 ⁻¹⁴
BP	GO:0007268~chemical synaptic transmission	45	13.55422	1.22x10 ⁻³¹
BP	GO:0007269~neurotransmitter secretion	17	5.12048	3.51x10 ⁻¹⁶
BP	GO:0014047~glutamate secretion	14	4.21687	5.00x10 ⁻¹⁶
BP	GO:0007399~nervous system development	28	8.43374	2.56x10 ⁻¹²
BP	GO:0016079~synaptic vesicle exocytosis	10	3.01205	7.51x10 ⁻¹¹
MF	GO:0005509~calcium ion binding	37	11.14458	1.92x10 ⁻⁸
MF	GO:0004890~GABA-A receptor activity	8	2.40964	2.19x10 ⁻⁸
MF	GO:0044325~ion channel binding	13	3.91566	7.95x10 ⁻⁷
MF	GO:0005230~extracellular ligand-gated ion channel activity	8	2.40964	1.50x10 ⁻⁶
MF	GO:0005246~calcium channel regulator activity	7	2.10843	6.48x10 ⁻⁶

GO, gene ontology; CC, cellular component; BP, biological process; MF, molecular function.

Table SIV. Top 10 significant Kyoto Encyclopedia of Genes and Genomes terms of the up- and downregulated differentially expressed genes.

A, Upregulated			
Term	Count	P-value	Genes
hsa04512:ECM-receptor interaction	19	9.70x10 ⁻⁹	<i>COL4A2, COL4A1, TNC, COL3A1, ITGB4, COL5A2, COL5A1, COL4A5, LAMA2, LAMA1, LAMB2, ITGA6, CD44, ITGA7, COL6A2, COL1A2, COL1A1, LAMC1, FN1</i>
hsa04510:Focal adhesion	23	3.41x10 ⁻⁵	<i>COL4A2, CAV1, COL4A1, TNC, COL3A1, ITGB4, FLNC, COL5A2, FLNA, COL5A1, KDR, COL4A5, LAMA2, LAMA1, VEGFC, LAMB2, ITGA6, ITGA7, COL1A2, COL6A2, COL1A1, LAMC1, FN1</i>
hsa05332:Graft-versus-host disease	9	4.17x10 ⁻⁵	<i>HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, FAS, HLA-DMA, HLA-G, HLA-DRA</i>
hsa05330:Allograft rejection	9	1.01x10 ⁻⁴	<i>HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, FAS, HLA-DMA, HLA-G, HLA-DRA</i>
hsa04940:Type I diabetes mellitus	9	2.57x10 ⁻⁴	<i>HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, FAS, HLA-DMA, HLA-G, HLA-DRA</i>
hsa05416:Viral myocarditis	10	4.67x10 ⁻⁴	<i>CAV1, HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, ABL1, HLA-DMA, HLA-G, HLA-DRA</i>
hsa05222:Small cell lung cancer	12	6.60x10 ⁻⁴	<i>LAMA2, CKS1B, LAMA1, COL4A2, COL4A1, LAMB2, ITGA6, LAMC1, CDK4, MYC, COL4A5, FN1</i>
hsa04151:PI3K-Akt signaling pathway	28	8.87x10 ⁻⁴	<i>PPP2R3A, TNC, COL3A1, ITGB4, GNG12, G6PC3, LAMB2, COL6A2, GNG5, MYC, FN1, COL4A2, COL4A1, CDK4, COL5A2, COL5A1, KDR, COL4A5, LAMA2, NRAS, VEGFC, LAMA1, ITGA6, LPAR6, ITGA7, COL1A2, COL1A1, LAMC1</i>
hsa05320:Autoimmune thyroid disease	9	1.148x10 ⁻³	<i>HLA-DRB1, HLA-A, HLA-C, HLA-DPA1, HLA-B, FAS, HLA-DMA, HLA-G, HLA-DRA</i>
hsa05146:Amoebiasis	13	1.277x10 ⁻³	<i>LAMA2, LAMA1, COL4A2, COL4A1, LAMB2, COL3A1, COL1A2, COL1A1, LAMC1, COL5A2, COL5A1, COL4A5, FN1</i>
B, Downregulated			
Term	Count	P-value	Genes
hsa04727:GABAergic synapse	21	1.12x10 ⁻¹⁶	<i>GABRD, GABRG2, GABRA2, GABARAPL1, ADCY1, GABRA1, GNAO1, GABRB3, GABRA4, GABRB2, GABRB1, GNG13, GABBR2, PRKCB, GLS2, PLCL1, KCNJ6, GNB5, GNG3, GAD1, CACNA1B</i>
hsa04723:Retrograde endocannabinoid signaling	22	2.74x10 ⁻¹⁶	<i>GABRD, GABRG2, GABRA2, ADCY1, GABRA1, GNAO1, GABRB3, GABRA4, GABRB2, GABRB1, GNG13, RIMS1, ITPR1, PRKCB, SLC17A7, KCNJ6, PLCB4, KCNJ9, GRIA2, GNB5, GNG3, CACNA1B</i>
hsa05032:Morphine addiction	20	7.79x10 ⁻¹⁵	<i>GABRD, GABRG2, GABRA2, ADCY1, GABRA1, GNAO1, GABRB3, GABRA4, GABRB2, GABRB1, GNG13, GABBR2, PRKCB, KCNJ6, KCNJ9, ARRB1, PDE1A, GNB5, GNG3, CACNA1B</i>
hsa04724:Glutamatergic synapse	18	6.81x10 ⁻¹¹	<i>DLGAPI, ADCY1, GNAO1, GNG13, HOMER1, ITPR1, PRKCB, SLC17A7, GLS2, GRM3, SLC1A2, PLCB4, GRIA2, SLC1A6, GNB5, GNG3, PPP3CA, SLC1A1</i>
hsa04721:Synaptic vesicle cycle	13	2.78x10 ⁻⁹	<i>RAB3A, SYT1, STX1A, CPLX2, STXBPI, ATP6V1G2, RIMS1, SLC17A7, VAMP2, SNAP25, DNMI, UNC13A, CACNA1B</i>
hsa05033:Nicotine addiction	11	3.70x10 ⁻⁹	<i>SLC17A7, GABRD, GABRG2, GABRA2, GABRA1, GRIA2, GABRB3, GABRA4, GABRB2, GABRB1, CACNA1B</i>
hsa04713:Circadian entrainment	15	4.26x10 ⁻⁹	<i>ADCY1, GNAO1, GNG13, ITPR1, PRKCB, PLCB4, KCNJ6, KCNJ9, GRIA2, GUCY1A2, RYR2, GNB5, CAMK2B, GUCY1B3, GNG3</i>
hsa04921:Oxytocin signaling pathway	17	7.89x10 ⁻⁸	<i>ADCY1, GNAO1, CACNB2, CACNG2, CACNB4, ITPR1, PRKCB, CAMKK2, KCNJ6, PLCB4, CAMK4, KCNJ9, GUCY1A2, RYR2, CAMK2B, GUCY1B3, PPP3CA</i>
hsa04911:Insulin secretion	13	9.44x10 ⁻⁸	<i>KCNMB4, RAB3A, STX1A, ADCY1, RIMS2, PCLO, PRKCB, PLCB4, RYR2, CAMK2B, RAPGEF4, VAMP2, SNAP25</i>
hsa04728:Dopaminergic synapse	15	2.07x10 ⁻⁷	<i>SCN1A, GNAO1, KIF5C, GNG13, ITPR1, PRKCB, KCNJ6, PLCB4, KCNJ9, GRIA2, GNB5, CAMK2B, GNG3, PPP3CA, CACNA1B</i>

hsa, *homo sapiens*.

Table SV. Topology of the protein-protein interaction network of differentially expressed genes.

Node 1	Node 2	Combined_score
VAMP2	SNAP25	0.999
CDK1	BUB1B	0.999
SYT1	STX1A	0.999
SNAP25	STX1A	0.999
SYT1	SNAP25	0.999
POLI	PCNA	0.999
SNRPG	SNRPD3	0.999
VEGFC	KDR	0.999
LSM7	SNRPD3	0.999
CDK1	CCNB1	0.999
CDK1	CKS1B	0.999
PRMT5	WDR77	0.999
PSMB8	PSMB9	0.999
WEE1	CDK1	0.998
CDK1	CCNA1	0.998
DDOST	DAD1	0.998
VAMP2	STX1A	0.998
WASF1	CYFIP2	0.998
TTK	BUB1B	0.998
NUP37	NUP107	0.998
STXBP1	STX1A	0.998
COL4A1	COL4A2	0.998
ACTL6A	RUVBL1	0.998
ZWINT	BUB1B	0.997
CACNG2	GRIA2	0.997
CCNB1	CCNA1	0.997
S100A10	ANXA2	0.997
PRKCZ	PARD3	0.997
WEE1	CCNB1	0.997
DDOST	SEC61A1	0.997
PCNA	KIAA0101	0.997
SCN2A	SCN3A	0.996
SNAP25	VAMP3	0.996
VAMP2	SYT1	0.996
CDK1	RRM2	0.996
NID1	LAMC1	0.996
MIS12	ZWINT	0.995
CKS1B	CCNB1	0.995
CDK1	TPX2	0.995
RGS7	GNB5	0.995
SCN8A	SCN2A	0.995
CDK1	FOXM1	0.995
FKBP1B	RYR2	0.995
FOXM1	CCNB1	0.995
CDK1	PCNA	0.995
VAMP8	SNAP25	0.994
BUB1B	CCNB1	0.994
TUBB4A	TUBA4A	0.994
STT3A	DDOST	0.994
UBE2C	BUB1B	0.994
CDK4	CCNB1	0.994
PMF1	ZWINT	0.993
STXBP1	SNAP25	0.993
PCNA	CDK4	0.993
KIF13B	ADAP1	0.993
UBE2C	PTTG1	0.992
DCTD	TYMS	0.992
PCNA	MCM2	0.992

Table SV. Continued.

Node 1	Node 2	Combined_score
PMF1	MIS12	0.992
BMP7	ACVR1	0.992
UBE2C	CCNB1	0.992
CENPF	FOXM1	0.991
PCNA	RRM2	0.991
COL1A2	COL1A1	0.991
STXBP1	VAMP2	0.991
MYC	CDK4	0.990
COL3A1	COL1A1	0.990
STT3A	DAD1	0.990
CENPF	CCNB1	0.990
KIF20A	KIF4A	0.990
CENPF	BUB1B	0.990
FBLN5	ELN	0.990
CDK1	SMC4	0.990
ELN	LOX	0.989
RHOBTB3	PLIN3	0.989
HLA-DRA	HLA-DMA	0.989
IFT88	IFT57	0.989
CDK1	UBE2C	0.989
CDK1	CENPF	0.989
MIS12	BUB1B	0.989
SCN1A	SCN3A	0.988
COL3A1	COL1A2	0.988
SCN8A	SCN1A	0.988
FBN1	ELN	0.987
MFAP2	ELN	0.987
SNAP25	RAB3A	0.987
P4HB	CALR	0.987
FBLN5	LOXL1	0.986
ITGA6	ITGB4	0.986
SYT1	RAB3A	0.986
SCN8A	SCN3A	0.986
COL5A2	COL3A1	0.985
STXBP1	APBA1	0.985
CTNNA1	CDH2	0.985
SCN1B	SCN1A	0.985
DNM1	AMPH	0.985
GNG3	GNB5	0.985
CDK1	ZWINT	0.985
ARG2	ODC1	0.984
LAMB2	NID1	0.984
RRM2	TYMS	0.984
RIMS1	RAB3A	0.984
MYC	CCNB1	0.984
WEE1	CCNA1	0.984
GNG5	GNB5	0.983
TEAD3	YAP1	0.983
MYC	ODC1	0.983
STK3	YAP1	0.983
GANAB	CALR	0.983
HLA-DRA	HLA-G	0.982
PCNA	TYMS	0.982
PAK1	ARHGEF6	0.982
SYT1	VAMP3	0.982
KCNAB1	KCNA1	0.981
C1R	SERPING1	0.981
DDOST	SSR4	0.981
ZWINT	CCNB1	0.981

Table SV. Continued.

Node 1	Node 2	Combined_score
RIMS2	RAPGEF4	0.980
ACTL6A	MYC	0.980
TCF7L2	TCF7L1	0.979
LAMA1	NID1	0.979
SCN2A	ANK3	0.979
SYN1	RAB3A	0.979
COL5A2	COL1A2	0.979
VAMP2	RAB3A	0.978
SH3GL2	AMPH	0.978
BGN	VCAN	0.978
TRIM22	GBP1	0.978
FBLN5	LOX	0.978
TNC	VCAN	0.977
MAPRE1	TUBB4A	0.977
CDK1	PTTG1	0.977
PCNA	RBBP8	0.977
NRXN1	LRRTM2	0.976
DLG2	DLGAP1	0.976
SNRPG	LSM7	0.976
LOXL1	ELN	0.976
ARRB1	ADRB2	0.976
ZWINT	CENPF	0.975
E2F5	CCNA1	0.975
MAPRE1	TUBA4A	0.975
HOMER1	DLGAP1	0.974
SCN1A	SCN2B	0.974
SNAP91	AMPH	0.974
GNAO1	GNG13	0.974
FLNA	ITGB4	0.973
SCN1B	SCN2A	0.973
ISG15	PCNA	0.973
COL5A1	COL1A1	0.972
RBBP8	BARD1	0.972
MFAP2	FBN1	0.972
FAS	EZR	0.971
GNG3	GNG13	0.971
FOS	CCL2	0.971
CDK1	FOS	0.971
PPP4R1	PPP4C	0.971
E2F5	CDK4	0.971
GNG12	GNG13	0.971
LAMA2	NID1	0.971
TCF7L2	MYC	0.970
KCNQ2	ANK3	0.970
COL4A2	COL4A5	0.970
P4HB	PPIB	0.970
IFT27	IFT88	0.970
MYC	RUVBL1	0.970
SYN1	SNAP25	0.970
NRXN1	APBA1	0.969
C5AR1	C5	0.969
SH3GL2	DNM1	0.969
IFT88	DYNC2LI1	0.969
STX1A	RAB3A	0.969
CTGF	YAP1	0.968
SYN1	SYT1	0.968
PRMT5	SNRPD3	0.968
IMPDH2	GMPR	0.967
SCN1B	SCN3A	0.967

Table SV. Continued.

Node 1	Node 2	Combined_score
P4HB	PDIA6	0.967
IQGAP1	KDR	0.967
CETN2	TUBA4A	0.967
COL5A2	COL1A1	0.967
KDELR1	TMED10	0.967
STX18	VAMP8	0.967
CXCR4	CCL2	0.967
FLNA	PAK1	0.967
WDR77	SNRPD3	0.967
PCNA	ERCC1	0.966
RIMS1	SNAP25	0.966
RGS1	GNAO1	0.966
NRAS	KIT	0.966
CDK4	WDR77	0.966
DOLK	DPAGT1	0.966
CASP7	FAS	0.965
COL4A1	PLOD3	0.965
CDK1	TTK	0.965
NOTCH2	JAG1	0.965
DNM1	SYT1	0.965
DNAJC6	SNAP91	0.965
SH3GL2	SNAP91	0.964
COL5A1	COL1A2	0.964
TKTL1	ALDOC	0.964
FAS	FAIM2	0.964
SMC4	CCNB1	0.964
PRMT5	CDK4	0.964
COL3A1	COL6A2	0.964
TCF7L2	HDAC1	0.964
PCNA	BARD1	0.963
TCTN1	B9D1	0.962
HDAC1	TCF7L1	0.962
AAK1	SNAP91	0.962
NOTCH2	HES1	0.962
CTGF	WWTR1	0.961
PTTG1	CCNB1	0.961
HLA-B	HLA-C	0.961
PENK	FOS	0.961
MCM2	CCNA1	0.961
IFT27	IFT57	0.960
COL5A1	COL3A1	0.960
INHBB	ACVR1	0.960
TCTN3	B9D1	0.960
SCN1B	SCN2B	0.959
SCG5	PCSK2	0.959
AK5	NME5	0.959
CDH2	GRIA2	0.959
TTC30A	IFT57	0.959
E2F5	CDK1	0.959
PLCB4	ITPR1	0.959
GNG3	GNAO1	0.959
CDK1	NUP37	0.958
COL6A2	COL1A2	0.958
PAK6	ARHGEF6	0.958
DNM1	SNAP91	0.958
SCN1B	ANK3	0.958
E2F5	PCNA	0.957
SYT1	SLC17A7	0.957
COL5A2	COL5A1	0.957

Table SV. Continued.

Node 1	Node 2	Combined_score
PCNA	RAD51AP1	0.956
CTNNA1	TJP1	0.956
NRXN1	SYT1	0.956
FANCF	ERCC1	0.956
SCN8A	ANK3	0.956
CACNA1B	CACNG2	0.956
KDELR1	STX18	0.956
PAK7	ARHGEF6	0.956
AK1	NME5	0.956
SSR4	SEC11A	0.955
SEC11A	SEC61A1	0.955
VAMP2	SYN1	0.955
SNAP25	SLC17A7	0.955
NRAS	PAK1	0.955
RPH3A	RAB3A	0.955
ITGA6	CD9	0.955
AMPD3	IMPDH2	0.954
MAPRE1	BUB1B	0.954
APBA1	STX1A	0.954
RIMS2	RAB3A	0.954
SNAP91	SYT1	0.954
HDAC1	RUVBL1	0.954
CAMK2B	PPP3CA	0.954
UBE2C	TYMS	0.954
HDAC1	HMG20B	0.954
KCNAB1	KCND2	0.954
HLA-A	CALR	0.954
TTK	SMC4	0.953
SCN3A	SCN2B	0.953
CAMKK2	CAMK4	0.953
WWTR1	TEAD3	0.953
TTC30A	IFT88	0.953
CDK1	TUBB4A	0.953
VAMP8	SYT1	0.953
SCN2A	SCN2B	0.952
PENK	SST	0.952
FBLN5	FBN1	0.952
FANCF	HES1	0.952
ISG15	PSMB8	0.952
GSTP1	PRDX6	0.952
IFT88	KIF3C	0.951
CDK1	TUBA4A	0.951
AK1	RRM2	0.951
PIIB	COL1A1	0.951
AGPAT5	PPAP2A	0.951
RIMS1	STX1A	0.951
DNAJC6	AMPH	0.951
L1CAM	ANK1	0.951
IFT57	DYNC2LI1	0.951
FN1	VEGFC	0.950
KCNN3	KCNMB4	0.950
CETN2	TUBB4A	0.950
COL6A2	COL1A1	0.950
RAPGEF4	PCLO	0.950
NPHP1	B9D1	0.950
LAMA1	LAMB2	0.950
HDAC1	CDK4	0.950
CDK1	KIF20A	0.950
CENPF	NUP107	0.949

Table SV. Continued.

Node 1	Node 2	Combined_score
RRM2	AK5	0.949
KCNAB1	KCNC1	0.949
GPC4	GLCE	0.949
MYC	TCF7L1	0.949
SLC25A4	PPIF	0.949
RRM2	NME5	0.949
SNAP91	VAMP2	0.949
ARRB1	CXCR4	0.949
LAMB2	ITGB4	0.948
HLA-A	PSMB8	0.948
LAMB2	LAMC1	0.948
SCN1B	SCN8A	0.948
HNRNPF	EIF4A3	0.948
EIF4A3	SNRPD3	0.948
RIMS1	SYT1	0.948
VAMP2	SLC17A7	0.948
LAMA2	LAMB2	0.948
COL1A2	PLOD2	0.947
SCN1A	ANK3	0.947
CACNB4	CACNG2	0.947
SSR4	SEC61A1	0.947
COL4A1	PLOD2	0.947
GNG5	GNAO1	0.947
HDAC1	ZNF217	0.947
CYR61	FOS	0.947
EXT2	GPC4	0.946
HLA-C	CALR	0.946
CTNNA1	IQGAP1	0.946
PCNA	CCNB1	0.946
SST	OPRK1	0.946
FOS	TIMP1	0.946
HOXB3	EGR2	0.946
CD44	FN1	0.946
SCP2	HSD17B10	0.946
COL4A1	COL3A1	0.946
HSD17B6	SRD5A1	0.946
MFAP2	LOX	0.946
HLA-B	PSMB8	0.945
PLOD2	COL1A1	0.945
UBE2C	CCNA1	0.945
TCTN1	NPHP1	0.945
GNAO1	GNB5	0.945
TTK	CCNB1	0.945
ALDH7A1	GAD1	0.945
PIIB	COL1A2	0.944
SOX2	SALL1	0.944
L1CAM	EZR	0.944
PTTG1	BUB1B	0.944
E2F5	HDAC1	0.944
ENO2	ALDOC	0.944
FN1	TIMP1	0.944
P4HB	COL1A1	0.943
RIMS1	SYN1	0.943
SERPINH1	COL1A1	0.943
COL5A1	COL6A2	0.943
SERPINH1	COL1A2	0.943
GNB5	GNG13	0.943
DNAJC6	DNM1	0.943
PRKAR1B	ADCY1	0.943

Table SV. Continued.

Node 1	Node 2	Combined_score
COL4A1	COL5A2	0.942
PSMB8	SHFM1	0.942
TOB1	CPEB3	0.942
DGKZ	PLCB4	0.942
SCN8A	SCN2B	0.942
PUF60	HNRNPF	0.942
AAK1	DNAJC6	0.942
ANXA2	ANXA1	0.941
DNM1	VAMP2	0.941
CXCR4	CCL4	0.941
GPX7	P4HB	0.941
GUCY1A2	GUCY1B3	0.941
ABL1	WASF1	0.941
COL4A5	COL1A2	0.941
PRKAR1B	PRKX	0.941
GAD1	SNAP25	0.941
PLCB4	GNAO1	0.941
L1CAM	MSN	0.941
GNG12	GNAO1	0.941
CDK1	TYMS	0.941
HDAC1	PRMT5	0.941
FANCF	BARD1	0.941
E2F5	MYC	0.940
ITGA6	LAMB2	0.940
PPP3CA	DNM1	0.940
CDH12	CDH18	0.940
HLA-A	HLA-C	0.940
AMPH	SYT1	0.940
STK3	WWTR1	0.940
SNAP91	REPS2	0.940
CCNB1	NUP37	0.940
SCN3A	ANK3	0.940
WWTR1	YAP1	0.940
PENK	OPRK1	0.940
GABRG2	GABRA1	0.940
ITGA7	LAMA2	0.940
GOT1	AGA	0.940
ROR2	FZD6	0.940
CETN2	NPHP1	0.940
COL4A1	COL1A1	0.939
SYN1	STX1A	0.939
TMED10	KDEL2	0.939
POLI	ISG15	0.939
SH3GL2	SYT1	0.939
VAMP2	VAMP8	0.939
CASP7	VIM	0.939
VAMP8	VAMP3	0.938
HDAC1	HES1	0.938
CALB2	PVALB	0.938
BDNF	CDH2	0.938
SPTBN2	ANK3	0.938
RRM2	CCNB1	0.938
NRAS	YES1	0.938
DDOST	SEC11A	0.938
FN1	LGALS3BP	0.938
TF	SNAP91	0.938
AAK1	AMPH	0.938
P4HB	COL1A2	0.938
HLA-C	PSMB8	0.937

Table SV. Continued.

Node 1	Node 2	Combined_score
CDK1	HDAC1	0.937
COL5A1	PLOD2	0.937
CTNNA1	CDH10	0.937
TF	AMPH	0.937
KIF20A	CCNB1	0.937
MAPT	CDK5R1	0.937
ADCY1	GNAO1	0.937
COL4A1	COL1A2	0.936
NRAS	PRKCB	0.936
RIMS1	VAMP2	0.936
COL5A2	COL6A2	0.936
CENPF	NUP37	0.936
GABRB2	GABRA1	0.936
TRAM1	SEC61A1	0.936
CAT	DECR1	0.936
COL4A2	PLOD2	0.936
MIS12	CENPF	0.936
ACTL6A	CETN2	0.936
COL4A1	COL5A1	0.935
KCNAB1	KCNQ2	0.935
P4HB	PLOD3	0.935
COL4A2	COL3A1	0.935
MYC	FOS	0.935
TYMS	MCM2	0.935
MYC	LGALS1	0.935
COL3A1	PLOD2	0.935
PLCD1	DGKZ	0.935
COL1A2	PLOD3	0.935
DGKZ	PLCE1	0.935
AMPH	VAMP2	0.935
FLNC	ITGB4	0.935
SNRPG	NUP37	0.934
TF	VAMP3	0.934
NRXN3	LRRTM2	0.934
VAMP2	PPFIA4	0.934
GEMIN8	SNRPD3	0.934
DERA	RBKS	0.934
FBLN2	MFAP2	0.934
SERPINH1	COL3A1	0.934
GABRG2	GABRB2	0.934
CETN2	ERCC1	0.934
PRKCZ	PRKCB	0.934
ISG15	IFI44L	0.934
COL1A1	PLOD3	0.934
MSN	EZR	0.934
WWTR1	TJP1	0.934
TF	VAMP2	0.933
SNAP91	VAMP3	0.933
APBA1	SNAP25	0.933
TTC30A	DYNC2LI1	0.933
GABRA2	GABRB2	0.933
COL4A2	COL1A2	0.933
CDK5R1	PAK1	0.933
MFAP4	FBLN1	0.933
AMPD3	AK1	0.933
COL4A2	COL1A1	0.933
SPTBN2	ANK1	0.933
RAB3A	SLC17A7	0.932
AMPD3	GMPT	0.932

Table SV. Continued.

Node 1	Node 2	Combined_score
LRRTM2	NRXN2	0.932
SERPINH1	PPIB	0.932
HDAC1	AES	0.932
MFAP4	MFAP2	0.932
GPC4	NDST3	0.932
LAMA1	LAMC1	0.932
CACNG2	ADAM23	0.932
COL3A1	PLOD3	0.932
RAB13	VAMP2	0.932
KCNJ9	GABBR2	0.932
COL4A2	PLOD3	0.931
VAMP2	VAMP3	0.931
UBE2C	BARD1	0.931
L1CAM	ANK3	0.931
GAD1	SYT1	0.931
CD44	ANK1	0.931
YES1	EFNB3	0.931
TF	DNM1	0.931
MFAP4	FBLN5	0.931
MIS12	NUP107	0.931
PI4KA	CCNB1	0.931
GRM3	GABBR2	0.931
HLA-B	CALR	0.930
DLG2	HOMER1	0.930
ABL1	BARD1	0.930
GABRG2	GABRA2	0.930
MFAP2	FBLN5	0.930
COL4A5	PLOD3	0.930
PI4KA	CDK1	0.930
ABL1	CDK4	0.930
COL4A5	PLOD2	0.930
RIMS1	SLC17A7	0.929
HNRNPF	SNRPD3	0.929
VEGFC	TIMP1	0.929
GABRG2	GABRB1	0.929
NRXN1	DLG2	0.929
HLA-DPA1	HLA-G	0.929
REPS2	AMPH	0.929
MFAP2	FBLN1	0.929
STX18	TMED10	0.929
ITGA7	LAMB2	0.928
COL5A1	PLOD3	0.928
CDK1	NUP107	0.928
CAMK2B	GRIA2	0.928
COL5A1	SERPINH1	0.928
TF	REPS2	0.928
ANK3	SCN2B	0.928
ARRB1	TF	0.928
KIF3C	IFT57	0.928
PSMB8	HLA-G	0.928
GABRA2	GABRB1	0.928
HDAC1	ABL1	0.928
HLA-DPA1	HLA-A	0.928
COL5A2	COL4A2	0.928
CERS2	PPAP2A	0.928
HSD17B6	ALDH1A1	0.928
ADRB2	ADCY1	0.927
CXCR4	SST	0.927
ZWINT	NUP37	0.927

Table SV. Continued.

Node 1	Node 2	Combined_score
CDK1	CDK4	0.927
CDK1	MIS12	0.927
COL4A1	SERPINH1	0.927
STX1A	SLC17A7	0.927
GABRB1	GABRA1	0.927
LAMA2	LAMC1	0.927
BUB1B	CCNA1	0.926
COL4A5	COL1A1	0.926
BUB1B	NUP107	0.926
NEDD4L	FBXW7	0.926
GAD1	ALDH9A1	0.926
SEC11A	TRAM1	0.926
CD44	HLA-A	0.926
AAK1	DNM1	0.926
PRK CZ	CTNNA1	0.925
SSR4	TRAM1	0.925
CKS1B	CDK4	0.925
MIS12	CCNB1	0.925
LAMA2	ITGA6	0.925
BUB1B	NUP37	0.925
PRKCB	DECR1	0.925
MFAP2	LOXL1	0.925
NRXN1	STXBP1	0.925
LAMC1	ITGB4	0.925
B4GALNT1	ST8SIA5	0.925
FBLN2	MFAP4	0.925
STX18	KDEL R2	0.925
ACTL6A	PRMT5	0.925
CPLX2	VAMP2	0.925
RBBP8	ERCC1	0.924
COL5A2	PLOD2	0.924
P4HB	SEC61A1	0.924
HMG N1	PCNA	0.924
CXCR4	GNAO1	0.924
TF	ADRB2	0.924
PTRF	CAV1	0.924
KIF20A	TPX2	0.924
SLIT2	ABL1	0.924
COL5A1	COL4A2	0.924
SCN8A	ANK1	0.924
ITGA6	LAMA1	0.924
APBA1	RAB3A	0.924
SGPL1	PPAP2A	0.923
PI4KA	PLCD1	0.923
PROS1	TIMP1	0.923
COL4A2	COL6A2	0.923
KCNJ6	GABBR2	0.923
ELAVL2	HNRNPF	0.923
ARRB1	DNM1	0.923
POLR2G	SNRPD3	0.923
BARD1	CCNA1	0.923
NRXN1	DLGAP1	0.923
KIF4A	TPX2	0.923
HLA-DRA	HLA-A	0.922
HLA-B	HLA-DRA	0.922
CDK1	CETN2	0.922
GAD1	VAMP2	0.922
ARRB1	SNAP91	0.922
ACTL6A	CDK4	0.922

Table SV. Continued.

Node 1	Node 2	Combined_score
TCF7L2	FOS	0.922
CD44	HLA-G	0.922
NRAS	IQGAP1	0.922
CAMK2B	MAPT	0.922
COL5A2	SERPINH1	0.922
SH3GL2	VAMP2	0.922
YES1	KIT	0.921
SERPINH1	COL4A5	0.921
PROS1	SERPING1	0.921
DNM1	ADRB2	0.921
NRXN2	APBA1	0.921
COL4A2	SERPINH1	0.921
ITGA6	MYC	0.921
HLA-B	HLA-DPA1	0.921
CCNB1	NUP107	0.921
FOXMI	CCNA1	0.921
HLA-DPA1	HLA-DMA	0.921
PUF60	EIF4A3	0.921
DNM1	VAMP3	0.920
DLG2	NRXN3	0.920
SNAP91	VAMP8	0.920
ABL1	CDH2	0.920
RHOBTB3	VAMP3	0.920
GRM3	ADCY1	0.920
TCTN1	TCTN3	0.920
P4HB	PLOD2	0.920
CTNNA1	CDH18	0.920
SERPINH1	COL6A2	0.920
ITGA6	LAMC1	0.920
TKTL1	RBKS	0.919
SERPING1	LGALS3BP	0.919
COL4A1	COL4A5	0.919
EDNRA	COL3A1	0.919
MAPRE1	CCNB1	0.919
CDK1	MAPRE1	0.919
GABRG2	GABRB3	0.919
GABRB2	GABRA4	0.919
LAMA1	ITGB4	0.919
PROS1	FN1	0.919
NPHP1	TCTN3	0.919
HLA-DPA1	HLA-C	0.919
IIFT27	DYNC2LI1	0.919
IIFT27	TTC30A	0.919
GPC4	BGN	0.919
NRXN3	SYT1	0.919
GABRB3	GABRA4	0.919
GABRA2	GABRA1	0.919
NRAS	FN1	0.919
TPX2	CCNB1	0.919
SST	GABBR2	0.919
GABRB1	GABRA4	0.919
ITGA7	LAMC1	0.918
TKTL1	ENO2	0.918
POLR2G	LSM7	0.918
SCN3A	ANK1	0.918
TF	DNAJC6	0.918
DLG2	NRXN2	0.918
BARD1	ERCC1	0.918
RIMS1	APBA1	0.918

Table SV. Continued.

Node 1	Node 2	Combined_score
HLA-DRA	HLA-C	0.918
KCNQ2	SPTBN2	0.918
FOXMI	MELK	0.918
APBA1	SYT1	0.918
MYC	COL1A2	0.918
DNAJC6	SH3GL2	0.918
HDAC1	CCNA1	0.918
COL4A1	COL6A2	0.918
GABRA2	GABRB3	0.917
ITGA7	TNC	0.917
NOTCH2	PSENEN	0.917
NRXN2	SYT1	0.917
DNM1	VAMP8	0.917
PI4KA	MTM1	0.917
HLA-B	HLA-A	0.917
LOXL1	LOX	0.917
EZR	ADRB2	0.917
ABL1	CTNNA1	0.917
HLA-G	CALR	0.917
FBXW7	WSB1	0.917
COL9A2	PLOD2	0.917
DNAJC6	SYT1	0.917
EIF4A3	NUP107	0.917
FOS	IGFBP7	0.917
GABRB3	GABRA1	0.917
CDH18	CDH10	0.917
RIMS1	PPFIA4	0.917
ITPR1	PLCE1	0.917
KIF4A	KIF3C	0.916
PRKAR1B	CDK4	0.916
YES1	PAK1	0.916
CACNB4	CACNA1B	0.916
KIF13B	KIF3C	0.916
KIF20A	FOXMI	0.916
TF	SYT1	0.916
UNC13A	RIMS2	0.916
COL4A5	COL3A1	0.916
ITGA7	LAMA1	0.916
HMGNI	ERCC1	0.916
TF	VAMP8	0.916
TF	SH3GL2	0.916
BARD1	RAD51AP1	0.916
ZWINT	NUP107	0.916
LAMA2	ITGB4	0.916
ITPR1	SNAP25	0.916
CXCR4	CXCR7	0.916
GSTP1	GPX7	0.915
DNM1	GABRA2	0.915
COL9A2	PLOD3	0.915
HLA-C	HLA-G	0.915
AMPH	VAMP3	0.915
NRXN3	APBA1	0.915
BUB1B	SHFM1	0.915
SLIT2	PAK1	0.915
SCN2A	ANK1	0.915
COL5A2	PLOD3	0.915
NRXN1	STX1A	0.915
LPCAT4	AGPAT5	0.915
PLIN3	VAMP3	0.915

Table SV. Continued.

Node 1	Node 2	Combined_score
ODF2	B9D1	0.915
MYC	ITGB4	0.915
ARRB1	AMPH	0.915
CACNB2	CACNG2	0.915
PSMB8	ODC1	0.915
SCN8A	SPTBN2	0.915
LGALS3BP	TIMP1	0.915
PRMT5	ACTL6B	0.915
IQGAP2	IQGAP1	0.915
RBBP8	CCNA1	0.915
MELK	CCNB1	0.915
ID1	HDAC1	0.915
CDK1	MCM2	0.915
ARRB1	DNAJC6	0.915
DNM1	GABRA1	0.915
AAK1	TF	0.915
ITPR1	PRKCB	0.914
DDOST	TRAM1	0.914
GAD1	RAB3A	0.914
STXBP1	NRXN2	0.914
CD44	HLA-C	0.914
PPP3CA	PPP2R3A	0.914
AMPD3	AK5	0.914
DLGAP1	NRXN2	0.914
RGS7	GNAO1	0.914
ALDH7A1	CAT	0.914
KCNJ9	GNG3	0.914
CXCR4	ANXA1	0.914
COL9A2	COL3A1	0.914
RASGRP1	ITPR1	0.914
NRXN1	HOMER1	0.914
PRKCZ	VAMP2	0.914
HLA-B	CD44	0.914
ADCY1	GNG13	0.914
STX1A	VAMP3	0.914
GAD1	STX1A	0.914
CXCR4	APLNR	0.914
VAMP2	APBA1	0.913
KIF13B	KIF4A	0.913
ADCY1	VIPR2	0.913
EDNRA	COL1A2	0.913
AAK1	SH3GL2	0.913
SST	APLNR	0.913
PI4KA	PLCE1	0.913
GPC4	VCAN	0.913
PI4KA	PLCB4	0.913
NUP37	SNRPD3	0.913
PPFIA4	APBA1	0.913
PCNA	POLR2G	0.913
CAMK2B	CAMK4	0.913
ODF2	CETN2	0.913
CAMK2B	CAV1	0.912
GNG12	GNB5	0.912
GNG12	ADRB2	0.912
HLA-A	HLA-G	0.912
GABRG2	GABRA4	0.912
SPTBN2	KIF3C	0.912
HDAC1	HIST1H4J	0.912
CACNB2	SNAP25	0.912

Table SV. Continued.

Node 1	Node 2	Combined_score
NRAS	RASGRP1	0.912
SERPING1	TIMP1	0.912
POLR2G	SNRPG	0.912
UBE2C	FBXW7	0.912
EDNRA	GNG3	0.912
CXCR4	GABBR2	0.912
PPFIA4	RAB3A	0.912
MYC	AES	0.911
ABL1	CYFIP2	0.911
COL5A1	COL4A5	0.911
SNRPG	NUP107	0.911
CXCR4	ADRB2	0.911
EIF4A3	NUP37	0.911
SH3GL2	VAMP3	0.911
GNG5	PLCB4	0.911
SPOCK3	TIMP2	0.911
HLA-A	VAMP3	0.911
MIS12	NUP37	0.911
GRM3	SST	0.911
NME5	GUCY1B3	0.911
CXCR4	OPRK1	0.911
CXCR4	DNM1	0.911
PMF1	BUB1B	0.911
VAMP8	STX1A	0.911
CETN2	TPX2	0.911
KCNQ2	ANK1	0.911
PLCB4	EDNRA	0.911
DERA	TKTL1	0.911
GUCY1A2	NME5	0.911
CXCR4	GNG5	0.910
PLCD1	ITPR1	0.910
MYOF	KDR	0.910
GNG5	CXCR7	0.910
CXCR4	GNG12	0.910
CTGF	TEAD3	0.910
STXBP1	NRXN3	0.910
GNG3	CXCR7	0.910
GNG5	OPRK1	0.910
HLA-DPA1	GBP1	0.910
HLA-B	VAMP3	0.910
GNG5	EDNRA	0.910
PENK	GABBR2	0.910
EDNRA	GNG13	0.910
SNCA	YES1	0.910
VAMP2	ITPR1	0.910
MYC	SERPINI1	0.910
GNG3	APLNR	0.910
ADRB2	GNG3	0.910
COL5A2	COL4A5	0.910
P4HB	COL3A1	0.910
ODF2	TUBB4A	0.910
GNG12	APLNR	0.910
CXCR4	GNG13	0.910
SCN1A	ANK1	0.910
GNG5	APLNR	0.910
POLR2G	EIF4A3	0.910
CXCR4	GNG3	0.910
CXCR7	GNG13	0.910
PLCD1	MTM1	0.910

Table SV. Continued.

Node 1	Node 2	Combined_score
PSMB9	ODC1	0.910
PROS1	LGALS3BP	0.910
SLIT2	PAK6	0.910
AAK1	REPS2	0.910
HLA-DRA	GBP1	0.910
OPRK1	GNG13	0.910
GNG3	OPRK1	0.910
CDH12	CTNNA1	0.910
COL4A5	COL6A2	0.910
GNG12	CXCR7	0.910
ADRB2	GNG13	0.910
RAPGEF4	IQGAP1	0.910
C5AR1	ANXA1	0.910
GNG5	ADRB2	0.910
APLNR	GNG13	0.910
COL9A2	BGN	0.910
GNG12	OPRK1	0.910
PLCD1	PLCE1	0.910
GNG12	EDNRA	0.910
CDK4	ACTL6B	0.910
NEDD4L	UBE2C	0.909
FN1	SERPING1	0.909
GNG3	GABBR2	0.909
CDK1	PSMB8	0.909
ADRB2	VIPR2	0.909
KIF20A	SPTBN2	0.909
PRKCZ	NRAS	0.909
CDH12	CDH2	0.909
PPFIA4	SYT1	0.909
RBBP8	RAD51AP1	0.909
CAMK2B	NRAS	0.909
MDK	NOTCH2	0.908
ISG15	HLA-A	0.908
TUBB4A	B9D1	0.908
FAS	NMI	0.908
GRM3	GNG3	0.908
EIF4A3	LSM7	0.908
HLA-B	ISG15	0.908
PDE1A	GMPR	0.908
HDAC1	FAM60A	0.908
LPCAT4	PEMT	0.908
CDH18	CDH2	0.908
ISG15	HLA-C	0.908
FBXL7	WSB1	0.908
GNB5	GABBR2	0.908
BDNF	CTNNA1	0.908
ITPR1	IQGAP1	0.908
CD44	HLA-DRA	0.908
SPTBN2	SCN1A	0.908
FOS	TRIP6	0.908
GNG3	KCNJ6	0.908
CTNNA1	KDR	0.908
PEX11A	PEX12	0.908
DNAJC6	VAMP2	0.908
LAMB2	PAK1	0.908
MAPRE1	CETN2	0.908
PMF1	CDK1	0.908
PTTG1	SHFM1	0.908
PRKAR1B	ADRB2	0.908

Table SV. Continued.

Node 1	Node 2	Combined_score
PLCB4	PLCE1	0.908
SST	CXCR7	0.907
HLA-B	GBP1	0.907
SPTBN2	SCN2A	0.907
NRXN1	NRXN3	0.907
HLA-DPA1	HLA-DRA	0.907
MAMLD1	MYC	0.907
FOS	AKR7A2	0.907
NRXN2	STX1A	0.907
SH3GL2	ADRB2	0.907
ASUN	SNAPC1	0.907
SLIT2	PAK7	0.907
AP1S2	VAMP2	0.907
POLR2G	SNAPC1	0.907
CDH2	CDH10	0.907
HNRNPF	POLR2G	0.907
AAK1	VAMP2	0.907
AZIN1	ODC1	0.907
TCF7L2	RUVBL1	0.907
LPCAT4	LPCAT1	0.907
B9D1	TUBA4A	0.907
PLCB4	GNB5	0.907
CYFIP2	ELMO1	0.907
UGT8	CERS2	0.907
GNG12	PLCB4	0.907
KDELRL1	KDELRL2	0.907
PTTG1	TPX2	0.907
AMPH	VAMP8	0.907
STXBP1	CACNB2	0.907
FN1	IQGAP1	0.907
CXCR4	C5AR1	0.907
PAK7	PAK6	0.907
KIF3C	DYNC2LI1	0.907
KIF4A	SPTBN2	0.907
GRM3	PENK	0.907
CXCR4	C5	0.907
COL5A2	COL9A2	0.907
ELMO1	PAK1	0.907
RAPGEF4	PRKAR1B	0.907
MAPRE1	ODF2	0.907
NUP107	SNRPD3	0.906
KIF20A	CENPF	0.906
STMN4	TUBB4A	0.906
COL5A1	P4HB	0.906
COL4A1	P4HB	0.906
NRAS	SPTBN2	0.906
COL9A2	COL5A1	0.906
HLA-C	GBP1	0.906
FBXL7	UBE2C	0.906
HLA-A	GBP1	0.906
HNRNPF	SNRPG	0.906
DNM1	JAG1	0.906
CNKSR2	NRAS	0.906
PAK1	PAK6	0.906
FZD6	GNAO1	0.906
CDH12	CDH10	0.906
GRM3	GNB5	0.906
DNM1	AP1S2	0.906
DNAJC6	VAMP3	0.906

Table SV. Continued.

Node 1	Node 2	Combined_score
HMGN1	POLR2G	0.906
GBP1	HLA-G	0.906
GNG5	KCNJ6	0.906
GRM3	OPRK1	0.906
PUF60	LSM7	0.906
GNG12	KCNJ9	0.906
CXCR4	PENK	0.906
SCN2B	ANK1	0.906
GNG5	KCNJ9	0.906
KIF20A	STX18	0.906
CAMK2B	CAMKK2	0.906
GNG12	KCNJ6	0.906
COL9A2	COL1A1	0.906
SCN1B	ANK1	0.906
SYN1	PPFIA4	0.906
HSD17B8	SRD5A1	0.905
COL4A2	P4HB	0.905
PAK7	PAK1	0.905
CETN2	B9D1	0.905
NRXN3	STX1A	0.905
NRXN3	DLGAP1	0.905
ITGA6	MDK	0.905
PIPOX	CRYM	0.905
RUVBL1	TCF7L1	0.905
MAPRE1	TPX2	0.905
TRIM22	HLA-C	0.905
PRKAR1B	EZR	0.905
WASF1	KDR	0.905
ODF2	TUBA4A	0.905
TTC30A	KIF3C	0.905
MAPRE1	NUP37	0.905
COL9A2	COL1A2	0.905
STX18	KIF3C	0.905
ACTL6A	WDR77	0.905
SST	ANXA1	0.905
TPX2	MELK	0.905
PPFIA4	SNAP25	0.905
COL5A2	P4HB	0.905
PRMT5	SNRPG	0.905
RIMS1	GAD1	0.905
COL4A5	P4HB	0.905
YES1	ELMO1	0.905
PLCD1	PLCB4	0.905
AP1S2	VAMP8	0.905
KIF13B	KIF20A	0.905
PUF60	POLR2G	0.905
FBXL7	FBXW7	0.904
ARRB1	SYT1	0.904
ACVR1	CDK4	0.904
GNG3	SST	0.904
OPRK1	GABBR2	0.904
CALR	PDIA4	0.904
CD44	GBP1	0.904
GNG12	GNG3	0.904
CDH2	BNIP2	0.904
KIF20A	DYNC2LI1	0.904
ARRB1	IQGAP1	0.904
L1CAM	SPTBN2	0.904
ISG15	HLA-G	0.904

Table SV. Continued.

Node 1	Node 2	Combined_score
ABL1	BNIP2	0.904
CD44	COL1A1	0.904
DNAJC6	VAMP8	0.904
CTNNA1	PAK1	0.904
GUCY1A2	PDE1A	0.904
IFT27	KIF3C	0.904
UBE2C	TPX2	0.904
SLIT2	PFN1	0.904
ODF2	NPHP1	0.904
CXCR4	GRM3	0.904
HECW1	PSMB8	0.904
PENK	GNG3	0.904
KIF4A	DYNC2LI1	0.904
COL5A2	PPIB	0.904
MAPRE1	NPHP1	0.904
POLR2G	NME5	0.904
SNAP91	ADRB2	0.903
ADCY1	GABBR2	0.903
ABL1	YES1	0.903
CKS1B	CCNA1	0.903
PSMB9	SHFM1	0.903
SYN1	APBA1	0.903
PSMB8	CCNA1	0.903
ARRB1	AAK1	0.903
PDE1A	GUCY1B3	0.903
GNG5	GNG3	0.903
ANK3	ANK1	0.903
RAPGEF4	RAP1GAP2	0.903
PROS1	VEGFC	0.903
RUVBL1	CCNA1	0.903
FAM60A	ZNF217	0.903
COL9A2	COL6A2	0.903
SPTBN2	SCN3A	0.903
GPC4	B3GAT1	0.903
TCTN1	ODF2	0.903
KIF20A	KIF3C	0.903
COL9A2	SERPINH1	0.903
PPFIA4	SLC17A7	0.903
NRXN3	HOMER1	0.903
CDK1	PSMB9	0.903
PRKCB	GRIA2	0.903
ITPR1	STX1A	0.903
SH3GL2	VAMP8	0.903
CDK1	KIF4A	0.903
POLR2G	ASUN	0.903
CACNB2	STX1A	0.903
CDK1	MELK	0.903
GPC4	RBP1	0.903
MAPRE1	ZWINT	0.903
AMPH	ADRB2	0.903
PAK1	EFNB3	0.903
CTNNA1	BNIP2	0.903
GNG12	FZD6	0.903
LPCAT1	PEMT	0.903
HNRNPF	LSM7	0.903
PENK	GNB5	0.903
KIF4A	STX18	0.902
EDNRA	ANXA1	0.902
ADCY1	OPRK1	0.902

Table SV. Continued.

Node 1	Node 2	Combined_score
CAMK2B	HDAC1	0.902
PRKAR1B	ITPR1	0.902
VEGFC	SERPING1	0.902
GRM3	APLNR	0.902
GRM3	C5AR1	0.902
POLR2G	ERCC1	0.902
LAMA2	PAK6	0.902
MTM1	PLCB4	0.902
LAMA2	PAK1	0.902
GNG5	ITPR1	0.902
PPFIA4	STX1A	0.902
KIF13B	STX18	0.902
GRM3	CXCR7	0.902
GNG12	ITPR1	0.902
SCN1B	SPTBN2	0.902
LAMA2	PAK7	0.902
AAK1	VAMP8	0.902
ITPR1	GNAO1	0.902
PMF1	CCNB1	0.902
UBE2C	SHFM1	0.902
CDK1	TCTN3	0.902
ITPR1	GNG3	0.902
LAMA2	LAMA1	0.902
UGT8	PPAP2A	0.902
GNG5	GABBR2	0.902
BGN	B3GAT1	0.902
PAK6	LAMC1	0.902
AAK1	VAMP3	0.902
C5AR1	CXCR7	0.902
PAK1	LAMC1	0.902
CACNB2	VAMP2	0.902
NRXN1	NRXN2	0.902
PAK7	LAMC1	0.902
PLOD2	PLOD3	0.902
C5AR1	GNG3	0.902
GNG12	C5AR1	0.902
ARRB1	SH3GL2	0.902
DNM1	L1CAM	0.902
MAPKAPK3	KDR	0.902
CAMK2B	CACNG2	0.902
MTM1	PLCE1	0.902
ELAVL2	EIF4A3	0.902
ITPR1	GNG13	0.902
POLR2G	EGR2	0.902
C5AR1	GNG13	0.902
CTNNA1	GRIA2	0.902
DPYSL3	CDK5R1	0.902
GNG5	C5AR1	0.902
VIPR2	GNB5	0.902
ANXA1	C5	0.902
DNM1	EFNB3	0.902
SHFM1	ODC1	0.901
ANK1	DYNC2LI1	0.901
COL4A1	PPIB	0.901
CDK1	SHFM1	0.901
COL6A2	PLOD2	0.901
AMPD3	PDE1A	0.901
COL6A2	PPIB	0.901
ELAVL2	SNRPD3	0.901

Table SV. Continued.

Node 1	Node 2	Combined_score
AP1S2	GNS	0.901
MAPRE1	CENPF	0.901
DNAJC6	AP1S2	0.901
ARRB1	VAMP8	0.901
ADCY1	GNB5	0.901
C5AR1	SST	0.901
COL9A2	COL4A2	0.901
KIF4A	MELK	0.901
MAPRE1	NUP107	0.901
ADRB2	GNB5	0.901
HLA-DRA	TRIM22	0.901
ODF2	TCTN3	0.901
PRKAR1B	IQGAP1	0.901
HLA-B	HLA-G	0.901
AK1	PDE1A	0.901
CXCR7	GABBR2	0.901
CTSO	HLA-DPA1	0.901
PSMB9	UBE2C	0.901
NEDD4L	TRIM9	0.901
TPX2	TUBB4A	0.901
LAMB2	PAK6	0.901
PMF1	CENPF	0.901
MAMLD1	HEY2	0.901
COL4A5	PPIB	0.901
GNG12	GNG5	0.901
GABBR2	GNG13	0.901
GABBR2	APLNR	0.901
NPHP1	TUBA4A	0.901
BDNF	DYNLT1	0.901
ANK3	DYNC2LI1	0.901
HECW1	PSMB9	0.901
COL5A1	PPIB	0.901
AK5	PDE1A	0.901
ARRB1	VAMP3	0.901
ADCY1	GNG3	0.901
CDK1	ODF2	0.901
CACNB2	GNG3	0.901
CYFIP2	KDR	0.901
ELMO1	KDR	0.901
CTSO	HLA-DRA	0.901
SH3GL2	AP1S2	0.901
SH3GL2	L1CAM	0.901
PAK7	LAMB2	0.901
NRXN3	NRXN2	0.901
TMOD2	VIM	0.901
LPAR6	ANXA1	0.901
GNG12	ANXA1	0.901
MYC	ALDH9A1	0.901
PLCB4	GNG3	0.901
ELAVL2	SNRPG	0.901
FZD6	GNG3	0.901
P4HB	COL6A2	0.901
LPAR6	PLCB4	0.901
TPX2	TUBA4A	0.901
PUF60	SNRPD3	0.901
COL4A2	PPIB	0.901
HDAC1	WDR77	0.901
CD44	TRIM2	0.901
ISG15	KIAA0101	0.901

Table SV. Continued.

Node 1	Node 2	Combined_score
PENK	CXCR7	0.901
LAMA1	L1CAM	0.901
CD44	HLA-DPA1	0.901
HLA-DPA1	TRIM22	0.901
PUF60	ELAVL2	0.901
MAPRE1	B9D1	0.901
CXCR4	GNB5	0.901
SNRPG	EIF4A3	0.901
ARRB1	VAMP2	0.901
PLCB4	GNG13	0.901
CACNB2	GNB5	0.901
L1CAM	LAMC1	0.901
FOLR1	TMED10	0.901
MIS12	MAPRE1	0.901
COL3A1	PPIB	0.901
AAK1	SYT1	0.901
PMF1	NUP37	0.901
SST	GNB5	0.901
DERA	ALDOC	0.901
CXCR7	APLNR	0.901
EDNRA	GNB5	0.900
GNG12	LPAR6	0.900
STXBP1	ITPR1	0.900
TCTN1	TUBA4A	0.900
PSMB9	PTTG1	0.900
CNKSR2	FN1	0.900
C5AR1	ADCY1	0.900
GNG12	VIPR2	0.900
MAPRE1	TCTN3	0.900
SPTBN2	SCN2B	0.900
CETN2	TCTN3	0.900
L1CAM	KIAA1598	0.900
ARRB1	NRAS	0.900
FBXL7	TRIM9	0.900
PSMB9	TNFRSF12A	0.900
VEGFC	LGALS3BP	0.900
CNTN6	PSENN	0.900
UBE2C	WSB1	0.900
SPTBN2	KDEL2	0.900
KIF20A	KDEL2	0.900
HLA-DMA	KIF4A	0.900
GNG12	GABBR2	0.900
GNG3	C5	0.900
CASP7	ITGB4	0.900
GNG3	VIPR2	0.900
GNG12	SST	0.900
KIF4A	TMED10	0.900
OPRK1	GNB5	0.900
GNG5	SST	0.900
PSMB8	UBE2C	0.900
C5AR1	OPRK1	0.900
KIF20A	KDEL2	0.900
HLA-DRA	SPTBN2	0.900
CDK1	KIAA0101	0.900
LPAR6	GNG13	0.900
GNG5	FZD6	0.900
PRKAR1B	ACVR1	0.900
KIF4A	KDEL2	0.900
GBP1	TRIM2	0.900

Table SV. Continued.

Node 1	Node 2	Combined_score
HLA-DPA1	TRIM2	0.900
REPS2	VAMP2	0.900
CCNA1	SHFM1	0.900
ADCY1	APLNR	0.900
HLA-DPA1	DYNC2LI1	0.900
SPTBN2	FOLR1	0.900
GNG3	ANXA1	0.900
AAK1	ADRB2	0.900
GNG5	GNG13	0.900
TMED10	ANK3	0.900
B4GALT4	PRELP	0.900
HLA-C	TRIM2	0.900
CXCR4	ADCY1	0.900
REPS2	ADRB2	0.900
OPRK1	ANXA1	0.900
HLA-DPA1	DNM1	0.900
ADRB2	VAMP8	0.900
WDR77	ACTL6B	0.900
COL9A2	PPIB	0.900
DNM1	REPS2	0.900
TMED10	DYNC2LI1	0.900
C5AR1	APLNR	0.900
ELAVL2	POLR2G	0.900
GNG12	C5	0.900
CNKSR2	IQGAP1	0.900
ANK3	KDEL2	0.900
ADCY1	SST	0.900
PSMB8	TNFRSF12A	0.900
GNB5	APLNR	0.900
ADCY1	C5	0.900
HLA-DPA1	KIF3C	0.900
CETN2	RUVBL1	0.900
ITPR1	GNB5	0.900
ARRB1	REPS2	0.900
GUCY1A2	POLR2G	0.900
SST	GNG13	0.900
GNB5	ANXA1	0.900
HLA-B	VAMP8	0.900
SPTBN2	DYNC2LI1	0.900
ADCY1	CXCR7	0.900
ODF2	TPX2	0.900
NRAS	EFNB3	0.900
HLA-DRA	AP1S2	0.900
DNAJC6	ADRB2	0.900
DDX60	IFI44L	0.900
POLR2G	GUCY1B3	0.900
SH3GL2	REPS2	0.900
CCNB1	NMI	0.900
KIF13B	TMED10	0.900
GRM3	C5	0.900
TCTN3	TUBA4A	0.900
LAMA2	ARHGEF6	0.900
LPAR6	GNB5	0.900
CXCR7	OPRK1	0.900
HLA-DPA1	SPTBN2	0.900
FOLR1	ANK1	0.900
SH3GL2	GNS	0.900
GEMIN8	SNRPG	0.900
LPAR6	EDNRA	0.900

Table SV. Continued.

Node 1	Node 2	Combined_score
PLCB4	ANXA1	0.900
HLA-DPA1	KIF20A	0.900
FOLR1	KDELR2	0.900
CXCR7	ANXA1	0.900
KIF13B	KDELR2	0.900
COL9A2	P4HB	0.900
LPAR6	GNG3	0.900
KIF4A	L1CAM	0.900
PSMB8	BUB1B	0.900
PSMB9	BUB1B	0.900
HLA-DRA	SH3GL2	0.900
HLA-C	VAMP8	0.900
HLA-DMA	SPTBN2	0.900
DYNC2LI1	KDELR2	0.900
KDELR1	KIF3C	0.900
ELAVL2	LSM7	0.900
GRM3	ANXA1	0.900
SNRPG	WDR77	0.900
FOLR1	DYNC2LI1	0.900
TNFRSF12A	SHFM1	0.900
ITGA6	CASP7	0.900
ARRB1	AP1S2	0.900
GNG5	CACNB2	0.900
HLA-DRA	KIF4A	0.900
GNG5	VIPR2	0.900
GABBR2	ANXA1	0.900
TCTN1	TUBB4A	0.900
ARRB1	FN1	0.900
PUF60	SNRPG	0.900
FZD6	GNG13	0.900
HLA-DRA	DNM1	0.900
KIF20A	TMED10	0.900
KDELR1	ANK1	0.900
TRIM22	HLA-G	0.900
UBE2C	TRIM9	0.900
GNG5	PENK	0.900
KDELR1	FOLR1	0.900
NEDD4L	WSB1	0.900
UGT8	GLA	0.900
HLA-A	TRIM2	0.900
KIF20A	HLA-DMA	0.900
HLA-DPA1	AP1S2	0.900
TCTN1	CDK1	0.900
CXCR7	GNB5	0.900
FZD6	GNB5	0.900
REPS2	SYT1	0.900
HLA-G	VAMP8	0.900
ANXA1	GNG13	0.900
CDK1	B9D1	0.900
MAMLD1	HDAC1	0.900
LPCAT4	PPAP2A	0.900
REPS2	VAMP3	0.900
COL9A2	COL4A5	0.900
TRIM22	HLA-A	0.900
CXCR7	C5	0.900
CD44	TRIM22	0.900
NPHP1	TUBB4A	0.900
GNB5	C5	0.900
SH3GL2	KIF4A	0.900

Table SV. Continued.

Node 1	Node 2	Combined_score
C5AR1	PENK	0.900
WASF1	ELMO1	0.900
ADRB2	SYT1	0.900
HLA-DPA1	SH3GL2	0.900
GNG5	GRM3	0.900
GNG5	ADCY1	0.900
PCNA	NMI	0.900
HLA-A	VAMP8	0.900
PENK	APLNR	0.900
OPRK1	APLNR	0.900
DNAJC6	REPS2	0.900
GNG12	CACNB2	0.900
KDELR1	ANK3	0.900
CDK1	NPHP1	0.900
HLA-DRA	KIF3C	0.900
HLA-B	TRIM22	0.900
DGKZ	AGPAT5	0.900
PENK	C5	0.900
KIF13B	KDELR1	0.900
PENK	GNG13	0.900
TF	ATP6V1G2	0.900
CACNB2	GNG13	0.900
KDELR1	SPTBN2	0.900
HLA-DMA	KIF3C	0.900
HLA-C	VAMP3	0.900
GABBR2	C5	0.900
B3GAT1	VCAN	0.900
PSMB9	CCNA1	0.900
KIF3C	KDELR2	0.900
HLA-G	TRIM2	0.900
TMED10	KIF3C	0.900
REPS2	VAMP8	0.900
SST	C5	0.900
GNG5	ANXA1	0.900
OPRK1	C5	0.900
TCTN1	MAPRE1	0.900
HLA-DPA1	KIF4A	0.900
HLA-B	TRIM2	0.900
PSMB8	PTTG1	0.900
TCTN3	TUBB4A	0.900
PENK	ADCY1	0.900
HLA-G	VAMP3	0.900
FBXL7	NEDD4L	0.900
RRM2	MELK	0.900
ADRB2	VAMP3	0.900
HLA-DRA	KIF20A	0.900
GNG12	GRM3	0.900
TCTN1	CETN2	0.900
C5AR1	GABBR2	0.900
KIF4A	KDELR1	0.900
CENPF	PTTG1	0.900
TRIM9	FBXW7	0.900
ADCY1	ANXA1	0.900
VAMP8	GNS	0.900
CCNA1	NMI	0.900
GNG12	ADCY1	0.900
ANK1	KDELR2	0.900
C5AR1	GNB5	0.900
HLA-DMA	DYNC2LI1	0.900

Table SV. Continued.

Node 1	Node 2	Combined_score
ARRB1	CNKS2R2	0.900
MAMLD1	HES1	0.900
COL4A1	COL9A2	0.900
VIPR2	GNG13	0.900
PRKAR1B	FN1	0.900
COL6A2	PLOD3	0.900
HOXB3	POLR2G	0.900
VAMP2	GNS	0.900
SPTBN2	TMED10	0.900
SOX2	POLR2G	0.900
GNG5	C5	0.900
PMF1	NUP107	0.900
GNG5	LPAR6	0.900
EDNRA	ADCY1	0.900
LAMC1	ARHGEF6	0.900
TRIM9	WSB1	0.900
HOMER1	NRXN2	0.900
PENK	ANXA1	0.900
GRM3	GNG13	0.900
VAMP2	ADRB2	0.900
GNG12	PENK	0.900
ARRB1	GNS	0.900
HLA-DRA	DYNC2LI1	0.900
MAMLD1	NOTCH2	0.900
GNG13	C5	0.900
LAMB2	ARHGEF6	0.900
FOLR1	ANK3	0.900
ANXA1	APLNR	0.900
TMED10	ANK1	0.900
APLNR	C5	0.900
GPC4	LRP10	0.900
HLA-DRA	TRIM2	0.900
KDELR1	DYNC2LI1	0.900
DNAJC6	GNS	0.900
PMF1	MAPRE1	0.900
HECW1	SHFM1	0.900
CACNA1B	CACNB2	0.899
CENPF	TPX2	0.897
RRM2	MCM2	0.897
TPX2	BUB1B	0.897
CD44	LAMB2	0.895
CACNA1B	GNB5	0.894
CDK4	CCNA1	0.894
RRM2	TPX2	0.893
CDH2	VIM	0.892
NRAS	PLCE1	0.892
KIF20A	BUB1B	0.892
TTK	CENPF	0.891
KIF20A	PTTG1	0.891
CD44	COL1A2	0.890
KIF4A	BUB1B	0.889
CACNA1B	GNAO1	0.888
KIF20A	MELK	0.888
CD44	IQGAP1	0.888
CPLX2	SNAP25	0.887
KIAA0101	MELK	0.887
FOXM1	TPX2	0.886
KIF4A	CCNB1	0.886
PDIA4	SEC61A1	0.886

Table SV. Continued.

Node 1	Node 2	Combined_score
SCN1A	SCN2A	0.885
ABCA1	PLTP	0.885
KIF20A	TTK	0.884
CENPF	MELK	0.884
UBE2C	KIAA0101	0.884
GABRG2	EFHC1	0.884
KIT	VEGFC	0.883
MELK	BUB1B	0.882
ITGA7	ITGB4	0.881
CAMK2B	RYR2	0.881
CAMK4	ATF1	0.881
MCM2	CCNB1	0.881
S100A11	ANXA1	0.880
MAPK7	PTPRR	0.880
TPX2	KIAA0101	0.878
PRKCB	GNAO1	0.877
HSD17B6	DECR1	0.877
CENPF	UBE2C	0.876
TMEM231	B9D1	0.875
CD44	MSN	0.874
TTK	MELK	0.874
RRM2	KIAA0101	0.874
PTTG1	MELK	0.874
TTK	CKS1B	0.873
ZWINT	KIAA0101	0.873
PCNA	DAD1	0.872
RAPGEF4	RYR2	0.872
STT3A	SEC61A1	0.871
FGF12	KDR	0.871
KIF20A	UBE2C	0.871
RRM2	PTTG1	0.871
RIMS2	PCLO	0.871
PCLO	RAB3A	0.870
RRM2	UBE2C	0.869
STX18	VAMP3	0.869
MCM2	CDK4	0.869
CD44	EZR	0.868
DERA	ENO2	0.868
FZD6	VANGL1	0.867
MYC	ABL1	0.867
PTTG1	KIAA0101	0.866
RRM2	BUB1B	0.866
KIF20A	RRM2	0.866
TTK	TPX2	0.865
UBE2C	MELK	0.865
TYMS	KIAA0101	0.864
CDK1	RAD51AP1	0.863
FOS	PRKCB	0.862
TTK	PTTG1	0.861
ANXA2	LGALS1	0.861
SCP2	FDX1	0.861
ITGA6	FN1	0.861
FOS	CCL4	0.860
PTTG1	TYMS	0.860
BDNF	FOS	0.859
HLA-DRA	VIM	0.858
VAMP2	STX18	0.858
PRMT3	PRMT5	0.858
DAD1	SEC61A1	0.857

Table SV. Continued.

Node 1	Node 2	Combined_score
TTK	UBE2C	0.855
UNC13A	RIMS1	0.855
CD44	LAMA1	0.854
KIAA0101	CCNB1	0.854
ZWINT	UBE2C	0.853
TMEM231	TCTN1	0.852
GANAB	P4HB	0.852
RYR2	PPP2R3A	0.852
ITGA6	TNC	0.852
P4HB	RCN1	0.851
CACNA1B	RYR2	0.851
UBE2C	FOXM1	0.850
MELK	RAD51AP1	0.850
ITGA7	COL4A2	0.850
ZWINT	RRM2	0.848
TTK	RAD51AP1	0.848
PLCB4	PRKCB	0.848
PLCD1	PRKCB	0.848
ITGA7	FN1	0.847
GAD1	PVALB	0.846
STX18	SNAP25	0.846
TJP1	NOTCH2	0.846
LAMA2	CD44	0.845
UNC13A	BSN	0.845
PRKCB	PLCE1	0.845
GABRG2	GABARAPL1	0.844
ITGA7	COL6A2	0.844
HS2ST1	GLCE	0.844
HSD17B8	HSD17B6	0.844
ITPR1	ANK1	0.844
TYMS	MELK	0.843
FGF14	KDR	0.843
DNAJC10	SEC61A1	0.843
STMN4	TUBA4A	0.843
ITGA6	COL1A1	0.843
FN1	ITGB4	0.841
ZWINT	MELK	0.841
GNAO1	GABBR2	0.841
KCNJ9	GNAO1	0.841
SIGMAR1	LBR	0.840
CENPF	KIAA0101	0.839
FGF14	KIT	0.838
FGF12	KIT	0.837
KIF5C	GRIA2	0.837
SCP2	CAV1	0.837
CD44	COL4A5	0.836
ZWINT	TPX2	0.836
FBN1	VCAN	0.836
STK3	CAB39L	0.836
CD44	VCAN	0.834
ITGA7	COL1A2	0.833
TTK	KIAA0101	0.832
ITGA6	COL4A2	0.832
CD44	LAMC1	0.832
RIMS1	BSN	0.832
CD44	VIM	0.831
CD44	COL4A2	0.831
KIF20A	KIAA0101	0.831
RGS3	EFNB3	0.831

Table SV. Continued.

Node 1	Node 2	Combined_score
FN1	COL1A1	0.831
COL4A2	ITGB4	0.830
KIAA0101	BUB1B	0.830
NRXN1	SYT13	0.830
CAMK2B	FLNA	0.830
KIF4A	TTK	0.830
CYBA	DECR1	0.829
TTK	RRM2	0.829
KCNJ6	GNB5	0.828
CAV1	ITGB4	0.828
DYNLT1	DNALI1	0.828
ITGA7	COL4A1	0.828
ITGA6	COL4A1	0.827
CD44	COL4A1	0.827
RRM2	FOXM1	0.826
ITGA7	COL1A1	0.826
CAMK2B	FLNC	0.826
ITGA7	COL4A5	0.826
COL4A5	ITGB4	0.826
MYC	FBXW7	0.825
NEDD4L	KDR	0.825
CAMK2B	PLCB4	0.825
CALR	RCN1	0.825
NEDD4L	KIT	0.825
ITGA6	COL1A2	0.825
PARP4	CASP7	0.824
BUB1B	BARD1	0.824
PRDX6	DNAJC10	0.824
PPP3CA	RCAN2	0.824
KCNJ6	GNAO1	0.823
CXCR4	KIT	0.823
COL1A2	ITGB4	0.823
KCNJ9	GNB5	0.823
COL1A1	ITGB4	0.823
COL4A1	ITGB4	0.823
TCF7L2	YAP1	0.822
SPTBN2	SLC1A6	0.822
KIF4A	UBE2C	0.822
SPAG8	HSD17B6	0.822
FLNC	PAK1	0.821
CLN5	CLN3	0.821
PROM1	CD44	0.821
DLG2	SCRIB	0.820
EZR	PRKCB	0.820
CD44	COL6A2	0.820
KIF4A	FOXM1	0.820
PRKCB	PRKD2	0.820
TNC	ITGB4	0.819
PIIB	PDIA4	0.819
PRDX6	CAT	0.819
GABRB1	GABRB2	0.817
UBE2C	CKS1B	0.817
CACNA1B	GNG3	0.817
ITGA6	COL4A5	0.817
TMED10	PSENEN	0.816
HOOK1	CLN3	0.816
SLC25A24	SLC25A4	0.816
ST6GALNAC2	EEF1A2	0.815
PPP3CA	PLCB4	0.815

Table SV. Continued.

Node 1	Node 2	Combined_score
ITGA6	COL6A2	0.815
MELK	MCM2	0.815
CYR61	IGFBP7	0.815
CACNA1B	GNG13	0.815
GOT1	GAD1	0.815
SLC1A1	SLC1A6	0.814
HIST1H4J	HAT1	0.814
CPLX2	NEUROD2	0.814
FOXM1	BUB1B	0.814
ENOSF1	TYMS	0.814
KCNJ6	GNG13	0.813
KCNJ9	GNG13	0.813
PLCL1	GABRB2	0.813
PRKCB	TJP1	0.813
PLP2	PLP1	0.813
PLCL1	GABRB1	0.813
PLCL1	GABRB3	0.813
ZWINT	PTTG1	0.812
PLCB4	KDR	0.812
RGL2	NRAS	0.812
RRM2	RAD51AP1	0.812
PLCB4	KIT	0.812
NRAS	ARHGEF6	0.812
HLA-DRA	ABL1	0.811
CAMK2B	CACNB2	0.811
KIF4A	CENPF	0.811
CACNB4	CAMK2B	0.810
RPH3A	SNAP25	0.810
PRMT8	PRMT5	0.810
ITGA6	FLNA	0.809
COL6A2	ITGB4	0.809
PRKCB	ITGB4	0.809
TCF7L2	TEAD3	0.808
SCN1B	CAMK2B	0.808
TEAD3	TCF7L1	0.808
CAMK2B	ATF1	0.808
G6PC3	ALDOC	0.808
PLCL1	GABRD	0.807
TYMS	TPX2	0.807
RASGRP1	CACNG2	0.807
GABRG2	PLCL1	0.807
GABARAPL1	GABRA1	0.807
PRKCB	GNB5	0.807
GABARAPL1	GABRA4	0.807
GABRA2	GABARAPL1	0.807
COL9A2	ITGB4	0.806
KIF20A	FAM64A	0.806
PDE1A	GNG13	0.806
PRKCB	GNG3	0.806
TAGLN3	ENO2	0.806
SCN1A	GNAO1	0.806
GABRB1	GABARAPL1	0.805
TPX2	RAD51AP1	0.805
FLNA	FLNC	0.805
KIF20A	RAD51AP1	0.805
SH3GL2	KIT	0.805
SH3GL2	KDR	0.805
GABRB3	GABRB1	0.805
GABRB3	GABRB2	0.805

Table SV. Continued.

Node 1	Node 2	Combined_score
SV2B	LAMB2	0.805
CD44	CXCR4	0.805
GABRB2	GABARAPL1	0.804
GABRB3	GABARAPL1	0.804
TSPO	SLC25A4	0.804
CENPF	RRM2	0.804
CACNA1B	GNG5	0.804
TTK	TYMS	0.804
ITGA6	FLNC	0.803
BDNF	SYN1	0.803
ITGA7	FLNA	0.803
UGT8	AGA	0.803
PLCL1	GABRA2	0.803
PLCL1	GABRA4	0.803
LAMA1	SV2B	0.802
NSDHL	LBR	0.802
GABRD	GABARAPL1	0.802
PCNA	CKS1B	0.802
KDELRL1	RCN1	0.802
CACNB4	RASGRP1	0.802
ITGA7	FLNC	0.802
GNG12	PAK6	0.802
PRKD2	ATF1	0.802
SV2B	LAMC1	0.802
CACNA1B	RASGRP1	0.802
FKBP1B	ENO2	0.802
CACNA1B	GNG12	0.802
LAMA2	SV2B	0.802
PRKCB	GNG13	0.801
CACNB2	RASGRP1	0.801
PLCL1	GABRA1	0.801
SH3GLB1	KIT	0.800
CACNB4	PPP2R3A	0.800
YAP1	TCF7L1	0.800
PCNA	RNASEH2A	0.800
TKTL1	G6PC3	0.800
KIF20A	ZWINT	0.800
GNG5	PRKCB	0.800
ITGA7	COL9A2	0.800
SCN1A	GNB5	0.800
GNG5	SCN1A	0.800
CD44	COL9A2	0.800
GNG12	PAK1	0.800
ITGA6	COL9A2	0.800
SCN1A	GNG13	0.800
CACNG2	PPP2R3A	0.800
GNG12	SCN1A	0.800
SCN1A	GNG3	0.800
HECW1	SSR4	0.800
RRM2	PDIA6	0.800
GNG12	PRKCB	0.800
DERA	G6PC3	0.800
GNG12	PAK7	0.800
SH3GLB1	KDR	0.800
PARD3	PRSS3	0.800
ARRB1	OR10J1	0.800
OR10J1	GNG13	0.800
HLA-DRA	PPFIA4	0.800
CACNB2	PPP2R3A	0.800

Table SV. Continued.

Node 1	Node 2	Combined_score
EMILIN1	ELN	0.798
FN1	COL1A2	0.798
NSDHL	SIGMAR1	0.798
PRDX6	P4HB	0.798
ABL1	FOS	0.797
CYR61	CTGF	0.796
SMC4	MCM2	0.796
KIF4A	RRM2	0.795
TYMS	CCNB1	0.795
PCNA	ANXA2	0.794
GAD1	AGXT2L1	0.794
TTK	FOXMI	0.793
MCM2	HAT1	0.793
PTTG1	CKS1B	0.793
PALLD	EZR	0.792
BUB1B	RAD51AP1	0.792
SPEF1	MAPRE1	0.792
CTGF	IGFBP7	0.792
RUVBL1	ACTL6B	0.791
C5	WFDC1	0.791
TCF7L1	AES	0.791
CCL2	DECR1	0.791
ZWINT	HNRNPF	0.790
CDK1	VIM	0.790
SST	PVALB	0.790
PRSS3	ZMYND10	0.790
DDX60	ISG15	0.789
FBXW7	CCNB1	0.789
MYC	SOX2	0.789
TPX2	MCM2	0.788
AZIN1	ARG2	0.788
MCM2	RNASEH2A	0.787
KIAA0101	RAD51AP1	0.787
FOXMI	FAM64A	0.787
PROM1	KDR	0.786
SGPL1	AGXT2L1	0.785
CALR	PDIA6	0.784
LBR	EIF4A3	0.784
MAMLD1	MTM1	0.783
MYC	KIT	0.783
RYR2	CACNB2	0.783
KIF20A	TYMS	0.783
QKI	ELAVL4	0.782
CYR61	ZWINT	0.782
PRDX6	PDIA6	0.782
FOS	SST	0.781
FBLN1	VCAN	0.781
ZWINT	RCN1	0.781
UBE2C	YAP1	0.781
FAS	ANXA5	0.780
FKBP1B	TAGLN3	0.780
STXBP1	RAB3A	0.779
QKI	ELAVL3	0.779
ABL1	YAP1	0.779
TAGLN2	TAGLN3	0.779
CAV1	KDR	0.778
SV2A	SYT1	0.777
GAD1	CALB2	0.777
TPX2	FAM64A	0.777

Table SV. Continued.

Node 1	Node 2	Combined_score
DYNLT1	DNAH9	0.776
CDYL	ACOX2	0.775
FOXMI	MCM2	0.775
ELAVL2	QKI	0.775
ZWINT	RAD51AP1	0.775
UBE2C	TRIP6	0.774
SMC4	BUB1B	0.774
PSAT1	KIAA1598	0.774
ZWINT	TTK	0.774
TF	MIS12	0.774
TMEM123	DNAJC6	0.774
BDNF	SLC12A5	0.774
PPP4R1	ANXA5	0.774
PTTG1	DECR1	0.774
MAPT	SNCA	0.771
KIF20A	SMC4	0.769
TTK	MCM2	0.769
RRM2	CKS1B	0.769
KIF4A	PTTG1	0.768
CACNB4	EFHC1	0.768
CPLX2	VAMP8	0.768
CACNA1B	OLFM1	0.766
CDK1	MYC	0.766
PCNA	ABL1	0.766
UNC13A	STX1A	0.765
CDK1	FAM64A	0.765
MAPK7	FOS	0.764
PRDX6	PDIA4	0.764
MSN	PPP1R16B	0.763
IFI44L	GBP1	0.763
KIT	CD9	0.763
CPLX2	VAMP3	0.763
DYNLT1	DYNC2LI1	0.762
KIF4A	RAD51AP1	0.762
FAT4	PKP4	0.762
NR4A2	FOS	0.762
PCNA	HDAC1	0.762
KIF4A	KIAA0101	0.760
KDELR1	SEC61A1	0.760
TUBB4A	GNB5	0.759
RGL2	HSD17B8	0.759
UNC13A	STXBP1	0.758
RIMS1	ELOVL4	0.758
TTK	FAM64A	0.758
EMP2	IMPDH2	0.758
CPLX2	NUP107	0.758
SOX2	VIM	0.758
ANXA2	S100A11	0.758
ZWINT	MCM2	0.757
UBE2C	FAM64A	0.757
CDK1	FBXW7	0.757
ZWINT	FOXMI	0.756
SULT4A1	RIT2	0.755
MYC	MAPK7	0.755
IFT27	RAB3A	0.755
DALRD3	IMPDH2	0.755
HIST1H4J	PRMT5	0.754
CDK1	TACC3	0.754
CENPF	TYMS	0.754

Table SV. Continued.

Node 1	Node 2	Combined_score
STXBP1	SYT1	0.754
EXT2	NDST3	0.753
PPP4R1	PPP3CA	0.752
MAPRE1	DNAH9	0.752
MFAP2	BGN	0.752
FOXMI	RAD51AP1	0.751
PPP3CA	PVALB	0.751
TYMS	CKS1B	0.751
TYMS	RNASEH2A	0.751
SPAG8	HSD11B1	0.749
PCNA	ZWINT	0.749
RRM2	ODC1	0.749
MEST	SLC22A4	0.749
DDX60	GBP1	0.748
FOS	ODC1	0.748
PTTG1	FOXMI	0.747
SV2B	SYT1	0.746
FBLN2	VCAN	0.745
ZWINT	TYMS	0.745
PCNA	SMC4	0.745
SOX2	NEUROD1	0.745
P4HB	PDIA4	0.744
PPP4R1	PPP2R3A	0.744
HS2ST1	NDST3	0.744
CACNB4	RYR2	0.744
DDX60	TRIM22	0.743
PTTG1	RNASEH2A	0.743
ENO2	VIM	0.743
MYC	HIST1H4J	0.742
GPX7	CAT	0.742
LAMA2	COL6A2	0.741
GABRG2	SCN1A	0.741
CD44	TIMP1	0.740
TF	VIM	0.740
ALDH7A1	AGXT2L1	0.739
VANGL1	CELSR3	0.739
KIF20A	MCM2	0.739
GABRD	GLRB	0.739
ALDH9A1	AGXT2L1	0.739
ALDH7A1	DECR1	0.738
HOMER1	ITPR1	0.738
AGXT2L1	ALDH8A1	0.737
CENPF	FAM64A	0.737
FBLN1	ELN	0.737
ALDH1A1	AGXT2L1	0.737
CTGF	COL1A1	0.736
CTGF	FN1	0.735
PPP3CA	CALB2	0.735
GABRB1	GLRB	0.735
TRIM22	IFI44L	0.735
FLNA	CAV1	0.735
PROM1	SOX2	0.735
SMC4	RAD51AP1	0.735
GABRD	EFHC1	0.734
GABRG2	SCN1B	0.734
VSNL1	KCNC1	0.734
SLC1A2	PAMR1	0.734
FKBP1B	CACNA1B	0.734
CDK5R1	CDK4	0.734

Table SV. Continued.

Node 1	Node 2	Combined_score
TMED10	SEC11A	0.733
CD63	TIMP1	0.733
UBE2C	MCM2	0.733
UNC13A	SYT1	0.733
PARD3	BAZ1A	0.733
FBLN2	ELN	0.732
GABRB2	GLRB	0.732
SMC4	MELK	0.732
ANXA2	CAV1	0.731
FKBP1B	CACNB2	0.731
ACTL6A	PCNA	0.730
PPP3CA	EFCAB2	0.730
HLF	AES	0.730
PPP3CA	CABP1	0.730
B4GALNT1	GALNT10	0.729
STXBP1	KCNQ2	0.729
ABL1	CAV1	0.728
PTTG1	MCM2	0.728
FOXMI	KIAA0101	0.728
CACNB4	FKBP1B	0.728
PLCE1	MPV17	0.727
COL4A1	NID1	0.727
TCF7L2	AES	0.727
PPIC	LGALS3BP	0.726
STXBP1	VAMP3	0.726
CACNB4	CACNB2	0.725
PCNA	PTTG1	0.725
MYC	HDAC1	0.725
MYC	CAV1	0.725
UBE2C	CBX7	0.724
CTGF	CCL2	0.723
HPCA	KCNC1	0.723
FKBP1B	CACNG2	0.723
SCN8A	PVALB	0.723
HIST1H4J	PRMT3	0.723
ACTL6A	ACTL6B	0.722
GMPR	DECR1	0.722
RYR2	CACNG2	0.722
LRBA	GABARAPL1	0.722
ISG15	GBP1	0.721
UNC13A	RAB3A	0.721
EMILIN1	MFAP2	0.721
ABL1	MAPT	0.721
CACNA1B	SCN2A	0.721
FBN1	COL3A1	0.721
NAIP	HPCA	0.721
BUB1B	CBX7	0.720
BARD1	CBX7	0.720
INA	DLGAP1	0.720
RRM2	SMC4	0.719
TRIM9	SNAP25	0.719
ELN	TIMP1	0.719
CCNB1	RAD51AP1	0.719
PCNA	MYC	0.718
VCAN	CCL2	0.718
MYC	CDH2	0.717
CAT	HSPE1	0.716
DNALI1	DNAH9	0.716
DNAH9	DYNC2LI1	0.716

Table SV. Continued.

Node 1	Node 2	Combined_score
CALB2	SST	0.716
BGN	ELN	0.716
FOS	EGR2	0.716
PROM1	KIT	0.715
PEG3	MEST	0.715
GABRB3	GLRB	0.714
KCND2	VSNL1	0.713
CD44	KIT	0.713
CACNA1B	SCN1A	0.712
TYMS	BUB1B	0.711
SUCLG2	IMPDH2	0.711
MYC	ANXA5	0.710
BDNF	CALB2	0.710
CADPS	VSNL1	0.710
PCNA	HAT1	0.710
HSD17B6	CAT	0.708
PDLIM1	ELN	0.708
RAB40B	TIMP2	0.706
CLIC1	DECR1	0.706
KIF4A	ZWINT	0.706
INA	NEFM	0.706
BCAS1	QKI	0.705
DNALI1	DYNC2LI1	0.704
SCN1A	PVALB	0.703
ANXA5	LGALS1	0.703
TACC3	TPX2	0.703
CENPF	RAD51AP1	0.703
CAMK2B	CABP1	0.702
MELK	FAM64A	0.702
PROM1	ALDH1A1	0.702
FBN1	LOX	0.702
WEE1	CKS1B	0.701
CAT	ODC1	0.701
PROM1	CXCR4	0.701
BDNF	SLC17A7	0.701
SOX2	CDH2	0.701
HLA-C	CNNM1	0.700
FOS	CAMK4	0.700
UNC13A	SNAP25	0.700
PCNA	MELK	0.700
RRM2	RNASEH2A	0.700

Table SVI. Characteristics of hub genes in the protein-protein interaction network according to Degree and Betweenness.

Gene	Gene description	Expression	Degree	Betweenness score
<i>CDK1</i>	Cyclin dependent kinase 1	Up	48	22558.62579
<i>CD44</i>	CD44 antigen	Up	31	23637.23444
<i>PCNA</i>	Proliferating cell nuclear antigen	Up	30	14249.79057
<i>MYC</i>	Myelocytomatosis oncogene	Up	29	24736.11759
<i>SYT1</i>	Synaptotagmin 1	Down	29	8371.00425
<i>KIF4A</i>	Kinesin family member 4A	Up	28	9911.58477

CDK1, cyclin dependent kinase 1; *CD44*, CD44 molecule (Indian blood group); *PCNA*, proliferating cell nuclear antigen; *SYT1*, synaptotagmin 1; *KIF4A*, kinesin family member 4A.

Table SVII. Top three significant Gene Ontology Biological Process and Kyoto Encyclopedia of Genes and Genomes terms of the top five modules from the protein-protein interaction network.

Module	Category	Term	P value	Genes
Module 1	KEGG	hsa05032:Morphine addiction	1.40x10 ⁻⁷	ADCY1, ARRB1, GNG13, GNB5, GABBR2, GNG3, GNG12, GNG5
	KEGG	hsa04727:GABAergic synapse	2.03x10 ⁻⁶	ADCY1, GNG13, GNB5, GABBR2, GNG3, GNG12, GNG5
	GO_BP	GO:0007268~chemical synaptic transmission	3.72x10 ⁻⁶	SYT1, GRM3, SNAP91, PENK, OPRK1, GABBR2, SST, AMPH
Module 2	GO_BP	GO:0030574~collagen catabolic process	8.32x10 ⁻¹⁷	COL4A2, COL4A1, COL3A1, COL1A2, COL6A2, COL1A1, COL5A2, COL5A1, COL4A5
	KEGG	hsa04974:Protein digestion and absorption	1.23x10 ⁻¹⁵	COL4A2, COL9A2, COL4A1, COL3A1, COL1A2, COL6A2, COL1A1, COL5A2, COL5A1, COL4A5
GO_BP	GO:0030198~extracellular matrix organization	6.33x10 ⁻¹⁵	COL4A2, COL9A2, COL4A1, COL3A1, COL1A2, COL6A2, COL1A1, COL5A2, COL5A1, COL4A5	
Module 3	GO_BP	GO:0000086~G2/M transition of mitotic cell cycle	1.82x10 ⁻⁵	CETN2, TUBA4A, ODF2, TUBB4A
	GO_BP	GO:0060271~cilium morphogenesis	0.001331506	B9D1, TCTN3, TCTN1
	KEGG	hsa05130:Pathogenic Escherichia coli infection	0.014707803	TUBA4A, TUBB4A
Module 4	GO_BP	GO:0000398~mRNA splicing, via spliceosome	3.46x10 ⁻¹¹	POLR2G, EIF4A3, HNRNPF, SNRPD3, LSM7, ELAVL2, SNRPG
	KEGG	hsa03040:Spliceosome	6.46x10 ⁻⁷	EIF4A3, SNRPD3, LSM7, PUF60, SNRPG
GO_BP	GO:0008380~RNA splicing	3.23x10 ⁻⁵	EIF4A3, SNRPD3, PUF60, SNRPG	
Module 5	KEGG	hsa04727:GABAergic synapse	3.32x10 ⁻¹⁴	PLCL1, GABRG2, GABARAPL1, GABRA2, GABRA1, GABRB3, GABRB2, GABRB1
	GO_BP	GO:0071420~cellular response to histamine	7.40x10 ⁻¹³	GABRG2, GABRA1, GABRB3, GABRB2, GABRB1
	GO_BP	GO:0007214~gamma-aminobutyric acid signaling pathway	7.71x10 ⁻¹¹	PLCL1, GABRG2, GABRA2, GABRA1, GABRB2

GO, Gene Ontology; BP, biological process; KEGG, Kyoto encyclopedia of genes and genomes