

Figure S1. Kaplan-Meier survival curves of patients with ovarian cancer, stratified by gene expression levels. (A) EFNB2, cisplatin plus paclitaxel. (B) EFNB2, others. (C) TFPI2, cisplatin plus paclitaxel. (D) TFPI2, others. Others, sequential doxorubicin-cisplatin/paclitaxel and sequential topotecan-cisplatin/paclitaxel; EFNB2, ephrin B2; TFPI2, tissue factor pathway inhibitor 2.

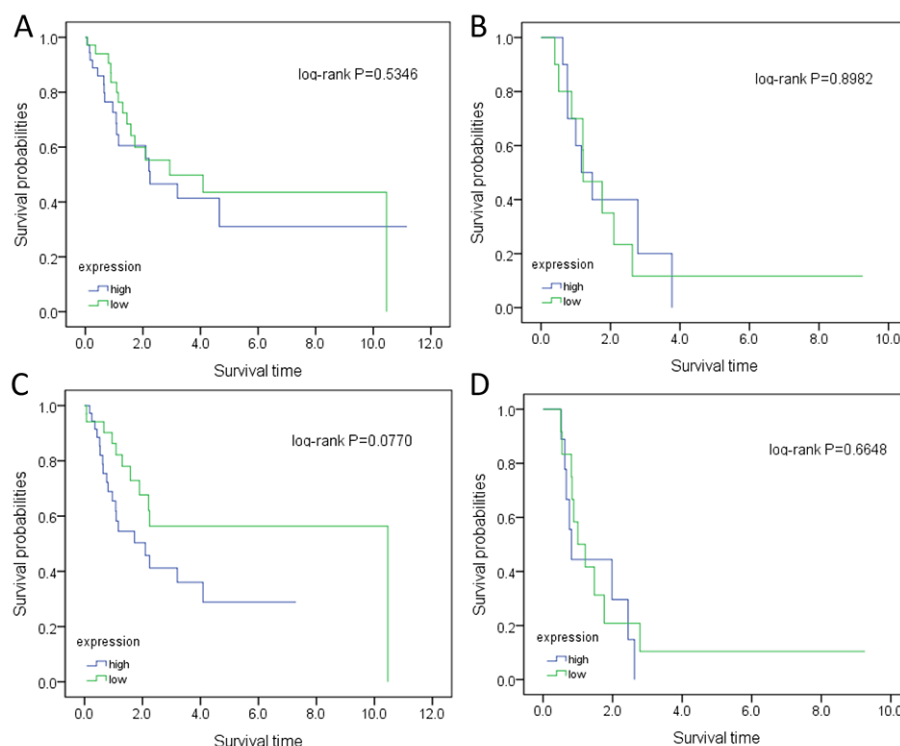


Table SI. Real time-quantitative PCR primer sequences.

Gene	Sequence (5'→3')
<i>ACTB</i>	F: CTTAGTTGCGTTACACCCTTTCTTG R: CTGTCACCTTCACCGTTCCAGTTT
<i>CDKN2A</i>	F: GATCCAGGTGGGTAGAAGGTC R: CCCCTGCAAACCTTCGTCCT
<i>DLG1</i>	F: GCAGGAGGTACGGACAACC R: ATTGACCCGCAATCTTCCATC
<i>CTGF</i>	F: CAGCATGGACGTTTCGTCTG R: AACCACGGTTTGGTCCTTGG
<i>MET</i>	F: AGCGTCAACAGAGGGACCT R: GCAGTGAACCTCCGACTGTATG
<i>MAF</i>	F: CTGGCAATGAGCAACTCCGA R: AGCCGGTCATCCAGTAGTAGT
<i>FGFR3</i>	F: TGCGTCTGTGGAGAACAAGTTT R: GCACGGTAACGTAGGGTGTG
<i>PIK3R1</i>	F: TGGACGGCGAAGTAAAGCATT R: AGTGTGACATTGAGGGAGTCG
<i>FAS</i>	F: AGATTGTGTGATGAAGGACATGG R: TGTTGCTGGTGAGTGTGCATT
<i>PTAFR</i>	F: ATGGAGCCACATGACTCCTC R: AATGACCCCGAGCACAAAGAT
<i>ABAC1</i>	F: CCCGGCGGAGTAGAAAGG R: AGGGCGATGCAAACAAAGAC
<i>TNFAIP3</i>	F: TTGTCCTCAGTTTCGGGAGAT R: ACTTCTCGACACCAGTTGAGTT
<i>CDK14</i>	F: GAGTTAAAGCTGGCAGATTTTCGG R: CAAGGTAACCACTTCGTTGGAG
<i>TUBB3</i>	F: GGCCAAGGGTCACTACACG R: GCAGTCGCAGTTTTTCACACTC
<i>COL1A2</i>	F: GGCCCTCAAGGTTTCCAAGG R: CACCCTGTGGTCCAACAACCTC
<i>RHOBTB1</i>	F: TGGAGCGTTCTCGGGATGT R: CGAAAAACAGAGGACCACAACA

ABCB1, ATP binding cassette subfamily B member 1; *CDKN2A*, cyclin dependent kinase inhibitor 2A; *CDK14*, cyclin dependent kinase 14; *COL1A2*, collagen type I alpha 2 chain; *CTGF*, connective tissue growth factor; *DLG1*, disks large homolog 1; *FAS*, Fas cell surface death receptor; *FGFR3*, fibroblast growth factor receptor 3; *MAF*, MAF bZIP transcription factor; *MET*, MET proto-oncogene, receptor tyrosine kinase; *PIK3R1*, phosphoinositide-3-kinase regulatory subunit 1; *PTAFR*, platelet activating factor receptor; *RHOBTB1*, Rho related BTB domain containing 1; *TNFAIP3*, TNF alpha induced protein 3; *TUBB3*, tubulin beta 3 class III.

Table SII. Differentially expressed genes in the cisplatin resistant group.

Gene symbol	Log ₂ (fold change)	P-value
Upregulated		
<i>TRIM53AP</i>	8.051013	1.85E-15
<i>MYL10</i>	6.535632	6.64E-11
<i>KCNMA1</i>	5.210379	2.67E-05
<i>AUTS2</i>	4.44547	9.04E-07
<i>SAGE1</i>	4.422235	3.33E-23
<i>NTNG1</i>	4.261986	2.67E-17
<i>TIMP3</i>	4.154971	1.45E-06
<i>PRSS12</i>	3.97902	6.74E-04
<i>AKR1C1</i>	3.93372	2.15E-05
<i>SLC25A24</i>	3.811169	1.80E-14
<i>IGF1R</i>	3.64108	1.97E-11
<i>ADGRL2</i>	3.51922	3.14E-10
<i>NAALAD2</i>	3.506801	2.19E-11
<i>VAV3</i>	3.314487	6.26E-05
<i>BMP7</i>	3.270986	4.64E-13
<i>FAM198B</i>	3.156795	3.48E-09
<i>MAGEA1</i>	3.138632	1.47E-07
<i>PROCR</i>	3.113334	2.46E-04
<i>BASP1</i>	3.092006	5.75E-04
<i>S100A3</i>	3.062618	7.23E-06
<i>EPHA7</i>	3.059732	5.39E-04
<i>HNMT</i>	3.052566	6.78E-12
<i>PDE4B</i>	3.000804	4.20E-03
<i>CD68</i>	2.962745	7.29E-04
<i>AKR1C3</i>	2.931011	7.53E-03
<i>STC1</i>	2.911922	9.54E-03
<i>FGF10</i>	2.888486	7.22E-10
<i>SOX18</i>	2.874594	3.13E-12
<i>PCDH7</i>	2.821827	7.59E-03
<i>ABCC2</i>	2.804555	2.21E-08
<i>GSN</i>	2.725365	1.18E-08
<i>KCNJ2</i>	2.693067	5.93E-03
<i>DNAJC6</i>	2.654405	2.49E-03
<i>EDIL3</i>	2.651271	5.16E-06
<i>AMOTL1</i>	2.601684	1.68E-04
<i>UBTFL1</i>	2.591646	4.43E-09
<i>RGL1</i>	2.540607	2.05E-08
<i>ITM2A</i>	2.523403	1.40E-04
<i>UBASH3B</i>	2.505784	1.11E-05
<i>NECTIN3</i>	2.466094	9.25E-07
<i>SEMA5A</i>	2.456867	4.12E-05
<i>HAPLN1</i>	2.409391	3.10E-04
<i>SLITRK5</i>	2.408781	9.46E-05
<i>BBX</i>	2.398808	7.22E-08
<i>ABCG1</i>	2.37503	2.59E-06
<i>ARHGAP28</i>	2.349535	6.15E-04
<i>NES</i>	2.34119	7.58E-03
<i>TRIM71</i>	2.327833	4.42E-11
<i>CDKN1A</i>	2.324349	2.25E-03
<i>BTG2</i>	2.272209	1.72E-04
<i>MLLT3</i>	2.189362	1.63E-05
<i>DPYSL4</i>	2.144886	3.55E-05
<i>LINC00518</i>	2.127924	1.79E-06
<i>VWA5A</i>	2.122828	3.86E-05
<i>ATRNL1</i>	2.103324	6.63E-05
<i>TMEM2</i>	2.102978	5.75E-05
<i>IGSF3</i>	2.102505	2.10E-04

Table SII. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>WNK1</i>	2.084726	3.21E-05
<i>FDXR</i>	2.069188	1.19E-04
<i>PLK2</i>	2.035827	5.13E-03
<i>WDR63</i>	2.028013	5.36E-06
<i>GHR</i>	2.013758	7.45E-04
Downregulated		
<i>ESRP1</i>	-2.00597	8.78E-03
<i>ARG2</i>	-2.01073	8.37E-03
<i>GKAP1</i>	-2.01384	7.23E-05
<i>FGFBP3</i>	-2.01629	4.23E-05
<i>DLG3</i>	-2.0256	1.66E-04
<i>TMEM200C</i>	-2.03369	9.90E-03
<i>RAB3IP</i>	-2.04699	9.73E-07
<i>TUBE1</i>	-2.0637	8.04E-03
<i>PRTFDC1</i>	-2.08446	9.36E-03
<i>MYEF2</i>	-2.10134	7.56E-09
<i>PELI1</i>	-2.11029	2.90E-04
<i>SHROOM3</i>	-2.11163	3.23E-06
<i>MLKL</i>	-2.11181	2.45E-03
<i>CNKSR2</i>	-2.12405	6.36E-03
<i>C7orf31</i>	-2.12407	7.18E-03
<i>NELL2</i>	-2.13353	6.41E-04
<i>KBTBD3</i>	-2.1416	8.85E-08
<i>TFPI2</i>	-2.1504	3.03E-04
<i>CEBPD</i>	-2.15098	1.12E-07
<i>OCLN</i>	-2.16381	4.89E-06
<i>PRICKLE1</i>	-2.16582	2.39E-04
<i>PLEKHA2</i>	-2.16743	2.45E-06
<i>IL18</i>	-2.16985	1.40E-04
<i>BEND7</i>	-2.17989	2.09E-11
<i>PLA2G3</i>	-2.19085	1.98E-03
<i>LGALS1</i>	-2.19706	2.61E-04
<i>ARMC9</i>	-2.20358	7.64E-07
<i>IDNK</i>	-2.23992	9.51E-05
<i>SLC25A21</i>	-2.24123	3.84E-09
<i>AMIGO2</i>	-2.2531	9.89E-04
<i>ASAP2</i>	-2.25337	3.46E-05
<i>B3GNT5</i>	-2.27446	1.22E-04
<i>SLAIN1</i>	-2.28566	7.60E-07
<i>PXK</i>	-2.29996	2.01E-07
<i>TSC22D3</i>	-2.32122	1.34E-03
<i>FZD6</i>	-2.3385	8.76E-03
<i>TNFSF10</i>	-2.34611	7.70E-05
<i>PRDM8</i>	-2.37494	3.57E-09
<i>AKAP12</i>	-2.4015	1.35E-05
<i>RNF157</i>	-2.40742	4.97E-04
<i>ZNF385D</i>	-2.42024	1.55E-04
<i>AP1M2</i>	-2.42386	2.84E-06
<i>NPAS3</i>	-2.42469	1.44E-03
<i>KCNMB4</i>	-2.4901	2.42E-08
<i>ERAP2</i>	-2.49116	1.07E-05
<i>HHEX</i>	-2.52304	8.23E-11
<i>FHIT</i>	-2.5513	4.86E-04
<i>CD53</i>	-2.58914	4.72E-18
<i>SOCS2</i>	-2.59559	2.13E-05
<i>NPVF</i>	-2.60405	3.13E-09
<i>SLC43A1</i>	-2.61983	1.58E-05
<i>NRAS</i>	-2.6335	5.62E-05
<i>EFNB2</i>	-2.63635	5.87E-04

Table SII. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>TMEM56</i>	-2.67051	5.80E-08
<i>SLC40A1</i>	-2.68116	4.65E-12
<i>THSD7A</i>	-2.68785	4.84E-03
<i>KIAA0825</i>	-2.6916	1.21E-12
<i>TRIB3</i>	-2.69625	6.41E-03
<i>MECOM</i>	-2.71702	1.81E-11
<i>FGF18</i>	-2.7227	1.32E-04
<i>STAU2</i>	-2.74922	2.04E-06
<i>WIF1</i>	-2.76947	2.83E-07
<i>SLC8A1</i>	-2.77499	8.39E-05
<i>CAV1</i>	-2.79248	5.28E-03
<i>STC2</i>	-2.79327	2.52E-04
<i>RIMS2</i>	-2.80194	6.82E-06
<i>TMSB4X</i>	-2.81605	4.43E-03
<i>PCDH10</i>	-2.8454	2.85E-04
<i>IFT74</i>	-2.86644	6.24E-10
<i>MDF1C</i>	-2.87757	5.73E-03
<i>METTL7A</i>	-2.90267	7.00E-10
<i>SLC6A15</i>	-2.91359	1.20E-06
<i>KERA</i>	-2.93829	2.74E-06
<i>SCN3A</i>	-2.95644	2.56E-04
<i>TMTC2</i>	-2.95659	2.43E-06
<i>MSANTD4</i>	-3.00283	7.56E-08
<i>ARID5B</i>	-3.00409	4.45E-12
<i>RRAGD</i>	-3.06922	6.42E-06
<i>RERGL</i>	-3.08951	2.09E-03
<i>GRIA4</i>	-3.13171	1.23E-08
<i>NHSL1</i>	-3.14765	1.27E-04
<i>SLC1A4</i>	-3.17643	1.30E-04
<i>TMEM47</i>	-3.17689	5.85E-08
<i>LONRF1</i>	-3.20708	1.30E-08
<i>NR0B1</i>	-3.21773	8.36E-03
<i>COLEC11</i>	-3.23721	1.55E-07
<i>CSTA</i>	-3.27358	9.22E-03
<i>MCTP1</i>	-3.29391	9.56E-05
<i>MAP1B</i>	-3.3117	9.68E-05
<i>SLC27A2</i>	-3.33999	1.12E-06
<i>ABCA3</i>	-3.3651	8.61E-08
<i>CLGN</i>	-3.41109	2.50E-03
<i>BEX2</i>	-3.41368	2.49E-04
<i>JAM2</i>	-3.46303	3.14E-07
<i>FBN1</i>	-3.47343	9.06E-09
<i>MANSC1</i>	-3.51781	1.11E-09
<i>PAX9</i>	-3.5791	2.36E-06
<i>PTPRZ1</i>	-3.5796	4.83E-03
<i>HTR2B</i>	-3.58978	1.87E-06
<i>MAGEA12</i>	-3.67742	5.24E-07
<i>PYGL</i>	-3.70986	1.19E-13
<i>GATM</i>	-3.75534	5.28E-04
<i>NRK</i>	-3.88906	1.71E-04
<i>SLIT2</i>	-3.93542	2.28E-14
<i>TMEM26</i>	-4.06715	2.34E-12
<i>ERRF11</i>	-4.09099	5.25E-06
<i>CAV2</i>	-4.27463	2.26E-04
<i>CD55</i>	-4.35555	9.80E-10
<i>ROBO2</i>	-4.37707	2.92E-03
<i>SVIL</i>	-4.51337	1.68E-09
<i>MDGA2</i>	-4.54509	3.01E-11
<i>LIN28A</i>	-4.67339	2.74E-09

Table SII. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>TCEAL8</i>	-4.68696	5.14E-15
<i>LRP1B</i>	-4.71864	5.02E-05
<i>BCAT1</i>	-4.73031	8.17E-08
<i>GOLPH3L</i>	-4.76765	1.48E-14
<i>NEBL</i>	-4.79971	9.33E-07
<i>MGST1</i>	-5.00942	1.40E-12
<i>FAM129A</i>	-5.19911	1.47E-03
<i>ARMCX2</i>	-5.22868	2.05E-17
<i>BST2</i>	-5.4939	1.02E-04
<i>TES</i>	-5.70947	5.00E-05
<i>ZPLD1</i>	-6.01572	8.90E-09
<i>PTPRK</i>	-6.09872	3.04E-11
<i>LHX8</i>	-6.1519	3.52E-09
<i>COL11A1</i>	-6.27367	5.27E-04

Table SIII. Differentially expressed genes in the doxorubicin resistant group.

Gene symbol	Log ₂ (fold change)	P-value
Upregulated		
<i>ABCB1</i>	5.899172	2.07E-17
<i>IFI16</i>	5.688752	2.00E-03
<i>GCG</i>	4.918503	9.03E-06
<i>ADGRL2</i>	4.903931	3.27E-13
<i>RUNX2</i>	4.606079	4.05E-04
<i>C1QTNF3</i>	4.328399	1.52E-03
<i>GHR</i>	4.255047	2.22E-08
<i>PTGS2</i>	4.190079	8.00E-06
<i>CYP1B1</i>	4.103811	8.59E-03
<i>STAMBPL1</i>	4.076743	1.20E-05
<i>NKX3-2</i>	4.061657	5.77E-05
<i>MSX1</i>	3.950309	2.39E-05
<i>IFIH1</i>	3.639784	3.89E-04
<i>FAS</i>	3.633238	7.51E-08
<i>DMRT1</i>	3.595177	4.11E-03
<i>ABCB4</i>	3.481095	8.55E-03
<i>SMPDL3A</i>	3.463366	2.31E-05
<i>EPYC</i>	3.438972	8.64E-07
<i>ATP1B1</i>	3.343814	1.82E-06
<i>KCNMA1</i>	3.207151	4.13E-03
<i>FAM155A</i>	3.123902	2.82E-03
<i>DMRT3</i>	3.108451	8.91E-03
<i>METTL7A</i>	2.998023	3.72E-10
<i>PDE4B</i>	2.933608	4.98E-03
<i>DSG2</i>	2.901877	6.28E-03
<i>MGARP</i>	2.885348	1.36E-03
<i>FSTL5</i>	2.877697	1.55E-04
<i>PALLD</i>	2.829702	3.00E-03
<i>MYO6</i>	2.822658	2.54E-05
<i>ITM2A</i>	2.808305	3.83E-05
<i>BICC1</i>	2.697197	9.46E-04
<i>PLA2G4A</i>	2.692697	2.94E-04
<i>EDIL3</i>	2.677896	4.47E-06
<i>CCDC85A</i>	2.655237	1.00E-04
<i>FABP4</i>	2.652401	9.47E-03
<i>DDX60</i>	2.611742	8.05E-04
<i>NRK</i>	2.596255	5.15E-03
<i>NSG1</i>	2.590918	1.88E-04
<i>NAV3</i>	2.536024	4.92E-11
<i>ANKRD22</i>	2.51605	7.66E-03
<i>PRKCH</i>	2.483945	9.60E-03
<i>SLITRK5</i>	2.478889	6.70E-05
<i>HAPLN1</i>	2.446491	2.63E-04
<i>ASB9</i>	2.427522	2.97E-03
<i>CROT</i>	2.351305	2.74E-05
<i>GREB1</i>	2.302331	9.44E-09
<i>RALGPS2</i>	2.22325	1.97E-04
<i>CCDC152</i>	2.219556	2.07E-06
<i>TNFAIP3</i>	2.210008	6.54E-03
<i>BMPRI1B</i>	2.194387	4.70E-10
<i>LAMB1</i>	2.189219	3.92E-03
<i>TACSTD2</i>	2.175639	2.78E-04
<i>HS3ST3B1</i>	2.148473	2.47E-06
<i>DCLK1</i>	2.14075	1.44E-06
<i>CXADR</i>	2.134141	1.51E-04
<i>AKAP12</i>	2.127937	6.45E-05
<i>KIAA1217</i>	2.122421	9.83E-03

Table SIII. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>CCND2</i>	2.10742	1.36E-04
<i>EPHA7</i>	2.100855	1.16E-08
<i>PCDH7</i>	2.081296	1.86E-03
<i>EPS8</i>	2.073437	1.24E-03
<i>RUNDC3B</i>	2.071024	2.19E-03
<i>GJA3</i>	2.026741	1.05E-03
<i>BBX</i>	2.020634	2.12E-06
<i>ANGPTL1</i>	2.015702	2.11E-03
<i>GPR84</i>	2.006219	4.54E-03
Downregulated		
<i>PTPRK</i>	-2.04784	1.11E-05
<i>MDK</i>	-2.06096	2.49E-04
<i>SLC6A15</i>	-2.08328	1.16E-04
<i>SLC27A2</i>	-2.13961	3.74E-04
<i>PDE4D</i>	-2.15889	4.29E-05
<i>SHROOM3</i>	-2.23115	2.59E-03
<i>KBTBD3</i>	-2.30282	1.63E-07
<i>KIAA0825</i>	-2.303	3.14E-11
<i>MAGEA12</i>	-2.48621	1.21E-04
<i>TMTC2</i>	-2.49431	2.65E-05
<i>LRFN5</i>	-2.50912	5.27E-04
<i>NDN</i>	-2.54511	2.53E-03
<i>CD53</i>	-2.57556	5.33E-18
<i>MECOM</i>	-2.6171	3.91E-11
<i>TFPI2</i>	-2.67271	2.25E-05
<i>TMEM47</i>	-2.69494	8.91E-07
<i>NRAS</i>	-2.71596	3.82E-05
<i>MSANTD4</i>	-2.72749	3.79E-07
<i>LIN28A</i>	-2.78864	1.32E-05
<i>ZC3H12C</i>	-2.81235	7.04E-05
<i>SCN3A</i>	-2.95739	2.55E-04
<i>FREM2</i>	-3.08557	6.63E-06
<i>C11orf87</i>	-3.12614	1.32E-03
<i>TNFSF10</i>	-3.21668	9.58E-07
<i>GRIA4</i>	-3.2313	6.94E-09
<i>ARID5B</i>	-3.39051	3.40E-13
<i>SLC8A1</i>	-3.50531	3.70E-06
<i>CDH10</i>	-3.66091	2.29E-03
<i>NEBL</i>	-3.71133	3.65E-05
<i>SLIT2</i>	-3.88166	3.09E-14
<i>TMEM26</i>	-3.97863	3.72E-12
<i>ZPLD1</i>	-6.12878	6.32E-09

Table SIV. Differentially expressed genes in the paclitaxel resistant group.

Gene symbol	Log ₂ (fold change)	P-value
Upregulated		
<i>ABCB1</i>	6.934653	4.97E-19
<i>MAGEA4</i>	5.644649	2.33E-23
<i>LAMB1</i>	5.26633	6.50E-08
<i>ADGRL2</i>	5.026778	1.92E-13
<i>RUNDC3B</i>	4.940088	2.12E-08
<i>PCDH18</i>	4.606775	3.53E-05
<i>PTPRR</i>	4.417658	8.18E-09
<i>MYO6</i>	4.383266	2.73E-08
<i>IGFBP6</i>	4.352941	2.93E-07
<i>CD47</i>	4.301568	4.69E-05
<i>SLC25A24</i>	4.291201	1.28E-15
<i>DSG2</i>	4.162612	2.49E-04
<i>ANXA1</i>	4.052021	2.10E-04
<i>CROT</i>	4.038843	4.84E-09
<i>SERPINB2</i>	3.996541	8.36E-03
<i>SPATS2L</i>	3.939662	3.74E-07
<i>GIMAP2</i>	3.923938	8.90E-06
<i>ACSS1</i>	3.913259	2.88E-15
<i>ADGRG6</i>	3.824702	6.69E-03
<i>MET</i>	3.795597	2.74E-04
<i>SP100</i>	3.676323	1.14E-05
<i>FOXF2</i>	3.629535	4.85E-03
<i>PTPN3</i>	3.55735	1.00E-09
<i>ABCB4</i>	3.553053	7.44E-03
<i>MAGEA10</i>	3.476633	2.70E-12
<i>PPP3CA</i>	3.450408	6.85E-05
<i>EPHA7</i>	3.445863	5.86E-13
<i>AMOTL1</i>	3.441281	4.51E-06
<i>MARCKS</i>	3.408964	1.19E-04
<i>AIM2</i>	3.366581	8.04E-03
<i>AKAP12</i>	3.360445	3.02E-10
<i>EPDR1</i>	3.340305	4.22E-12
<i>BMP7</i>	3.32172	3.33E-13
<i>S100A10</i>	3.252416	6.72E-04
<i>HIVEP2</i>	3.222602	1.07E-07
<i>GJA3</i>	3.209994	4.33E-06
<i>SOX8</i>	3.187569	9.51E-07
<i>CBLN2</i>	3.182942	1.48E-08
<i>GLUL</i>	3.164806	8.90E-03
<i>CLCN4</i>	3.118548	1.58E-17
<i>CTGF</i>	3.011358	2.68E-03
<i>CAVI</i>	3.009392	2.55E-03
<i>PSMB9</i>	2.996434	1.00E-05
<i>DDX60</i>	2.994468	1.94E-04
<i>EPB41L4B</i>	2.979065	3.71E-10
<i>ELFN1</i>	2.941309	9.68E-11
<i>SH3BP4</i>	2.939692	6.68E-07
<i>DLX4</i>	2.91254	2.15E-05
<i>CD9</i>	2.908538	2.27E-07
<i>PLA2G4A</i>	2.900116	1.29E-04
<i>ATP1B1</i>	2.894592	1.46E-05
<i>AKR1C1</i>	2.864932	8.05E-04
<i>TMEM98</i>	2.853059	5.04E-06
<i>VDR</i>	2.850065	2.00E-05
<i>SPHK1</i>	2.825409	1.50E-04
<i>PROCR</i>	2.788819	7.64E-04
<i>UBE2L6</i>	2.787012	6.41E-06

Table SIV. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>AKR1C2</i>	2.783449	7.34E-05
<i>PALLD</i>	2.763415	3.62E-03
<i>FSCN1</i>	2.71772	1.28E-04
<i>TTC39C</i>	2.701711	2.38E-15
<i>PDLIM1</i>	2.696474	1.45E-07
<i>SAMD4A</i>	2.687207	7.39E-13
<i>PPIC</i>	2.662679	8.59E-06
<i>LGALS3BP</i>	2.603275	1.24E-06
<i>EPB41L4A</i>	2.590761	9.95E-03
<i>SLC16A14</i>	2.581545	3.97E-07
<i>ZNF423</i>	2.577269	5.22E-03
<i>CEP126</i>	2.564925	1.43E-03
<i>TBC1D9</i>	2.559141	4.21E-06
<i>TUBB3</i>	2.551329	2.90E-04
<i>MYOC</i>	2.551213	3.62E-07
<i>AK4</i>	2.502794	6.34E-04
<i>PTAFR</i>	2.493281	7.42E-03
<i>SDK2</i>	2.473536	1.80E-09
<i>ST8SIA4</i>	2.439857	7.99E-06
<i>CABLES1</i>	2.421449	9.94E-03
<i>NKX3-2</i>	2.411389	8.01E-03
<i>LHFP</i>	2.394147	4.86E-05
<i>ERAP2</i>	2.393612	2.29E-06
<i>SLC39A8</i>	2.392128	5.04E-04
<i>CDK14</i>	2.37822	3.37E-03
<i>HHAT</i>	2.355106	4.77E-06
<i>PLOD2</i>	2.343944	8.53E-03
<i>MT1A</i>	2.34107	8.92E-07
<i>CDKN2A</i>	2.334344	4.88E-06
<i>TNFAIP3</i>	2.327869	4.48E-03
<i>SCIN</i>	2.323187	7.97E-03
<i>STMN3</i>	2.322592	1.21E-06
<i>COL17A1</i>	2.286768	3.40E-03
<i>JAZF1</i>	2.264757	8.20E-03
<i>LTBR</i>	2.214859	8.52E-03
<i>AIG1</i>	2.212162	3.81E-05
<i>MCTP2</i>	2.211694	5.49E-03
<i>FGFR3</i>	2.211127	5.50E-04
<i>IRF1</i>	2.203007	1.50E-06
<i>ITM2A</i>	2.201283	9.54E-04
<i>CDK6</i>	2.193792	9.95E-03
<i>KIF26A</i>	2.189086	9.02E-03
<i>SLITRK5</i>	2.187356	2.82E-04
<i>CXXC5</i>	2.187003	3.60E-06
<i>KAZN</i>	2.169332	6.45E-06
<i>AHNAK</i>	2.166832	2.29E-05
<i>AHNAK2</i>	2.159551	1.05E-03
<i>TAGLN2</i>	2.158727	4.40E-08
<i>KLF13</i>	2.146075	4.57E-06
<i>ANKH</i>	2.137941	3.25E-03
<i>TCF7</i>	2.134628	1.01E-07
<i>LOX</i>	2.127317	7.12E-03
<i>FAM83H</i>	2.11868	2.40E-05
<i>HSPB1</i>	2.114557	1.92E-06
<i>SRPX</i>	2.112447	3.21E-04
<i>DBF4</i>	2.108449	1.28E-03
<i>ALCAM</i>	2.107931	1.54E-03
<i>PIK3R1</i>	2.08757	4.45E-05
<i>FAS</i>	2.075117	2.18E-04

Table SIV. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>MYO1B</i>	2.07468	1.91E-07
<i>HLA-B</i>	2.071207	2.78E-03
<i>NFE2L3</i>	2.06491	1.66E-06
<i>FEZ1</i>	2.06348	3.42E-03
<i>DNAJB5</i>	2.050055	7.89E-03
<i>TMEM159</i>	2.036158	1.24E-06
<i>LGR5</i>	2.02887	1.00E-04
<i>COL1A2</i>	2.028178	1.00E-03
<i>NFKBIZ</i>	2.020997	9.81E-04
<i>DHRS3</i>	2.019881	4.08E-04
<i>DMKN</i>	2.01462	1.62E-06
<i>TAP1</i>	2.01286	3.20E-05
<i>PMP22</i>	2.01206	2.28E-04
<i>SHTN1</i>	2.011532	6.72E-07
<i>METRNL</i>	2.009878	6.63E-04
Downregulated		
<i>MGST1</i>	-2.00156	1.84E-05
<i>SSX2IP</i>	-2.00838	5.86E-07
<i>ADAMTS3</i>	-2.01464	1.63E-05
<i>SPAG1</i>	-2.01624	5.55E-04
<i>RHOBTB1</i>	-2.02143	6.72E-03
<i>RFXAP</i>	-2.02801	5.44E-08
<i>SCN3A</i>	-2.07906	6.01E-03
<i>LRFN5</i>	-2.09673	2.71E-03
<i>ABCC2</i>	-2.09854	2.62E-06
<i>ATP11C</i>	-2.11773	2.66E-06
<i>ASAP2</i>	-2.13054	6.97E-05
<i>CCDC50</i>	-2.13973	2.33E-03
<i>SHROOM3</i>	-2.14141	9.60E-05
<i>FGFBP3</i>	-2.1746	1.57E-05
<i>DLG1</i>	-2.18834	1.12E-07
<i>SLAIN1</i>	-2.21654	1.23E-06
<i>EFNB2</i>	-2.25912	7.28E-04
<i>ERMP1</i>	-2.2709	6.30E-09
<i>STC2</i>	-2.27225	1.89E-03
<i>PRICKLE1</i>	-2.29347	1.25E-04
<i>PRDM8</i>	-2.29848	6.57E-09
<i>TMEM56</i>	-2.31366	2.92E-10
<i>AP1M2</i>	-2.3506	4.46E-06
<i>GRIA4</i>	-2.36279	1.41E-06
<i>PARD6B</i>	-2.38265	8.17E-04
<i>CTH</i>	-2.39276	4.81E-05
<i>CHN1</i>	-2.39521	6.33E-09
<i>JAM2</i>	-2.40365	6.03E-05
<i>SLC1A4</i>	-2.40882	2.08E-03
<i>KIAA0825</i>	-2.43228	1.02E-11
<i>STAU2</i>	-2.43752	1.98E-07
<i>TMEM100</i>	-2.45393	1.51E-03
<i>CD160</i>	-2.46736	1.56E-03
<i>TOX</i>	-2.49101	7.06E-03
<i>HMGN5</i>	-2.50066	5.87E-09
<i>SH3BGR</i>	-2.50384	6.39E-06
<i>TFPI2</i>	-2.52813	4.61E-05
<i>PLA2G3</i>	-2.57238	4.36E-04
<i>CRNDE</i>	-2.58492	1.64E-04
<i>MAP2K6</i>	-2.61375	2.04E-03
<i>CD53</i>	-2.61811	3.65E-18
<i>MECOM</i>	-2.62705	3.62E-11
<i>CNKSR2</i>	-2.64467	1.06E-03

Table SIV. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>MYEF2</i>	-2.65119	8.52E-11
<i>PCDH10</i>	-2.66913	5.54E-04
<i>NPVF</i>	-2.72912	1.29E-09
<i>HOXB9</i>	-2.72999	1.24E-03
<i>GPC6</i>	-2.7557	4.83E-03
<i>NHSL1</i>	-2.77817	4.93E-04
<i>CBR3</i>	-2.79081	2.94E-04
<i>SLC6A15</i>	-2.85102	1.67E-06
<i>PKP2</i>	-2.89461	1.61E-09
<i>TMEM47</i>	-2.93896	2.19E-07
<i>LIPG</i>	-2.93949	2.30E-05
<i>GLDC</i>	-2.94702	1.56E-03
<i>METTL7A</i>	-2.9531	5.00E-10
<i>POSTN</i>	-2.95723	1.83E-03
<i>ATRNL1</i>	-2.95737	5.29E-07
<i>LUM</i>	-2.99086	4.70E-03
<i>MLIP</i>	-3.13219	8.07E-03
<i>FAM46A</i>	-3.1584	1.13E-06
<i>HAPLN1</i>	-3.16708	5.64E-06
<i>KERA</i>	-3.21056	7.01E-07
<i>ARID5B</i>	-3.26776	7.50E-13
<i>SLC27A2</i>	-3.27749	1.50E-06
<i>TNFSF10</i>	-3.38193	4.31E-07
<i>TMTC2</i>	-3.39853	2.70E-07
<i>UACA</i>	-3.41331	1.11E-13
<i>NRAS</i>	-3.46251	6.32E-07
<i>BRINP3</i>	-3.48588	1.08E-06
<i>RERGL</i>	-3.49352	6.78E-04
<i>MDGA2</i>	-3.5172	4.57E-09
<i>ARHGAP28</i>	-3.5192	7.88E-03
<i>NEBL</i>	-3.62102	4.98E-05
<i>WNT16</i>	-3.64201	4.56E-03
<i>NAALAD2</i>	-3.65595	3.83E-12
<i>IKZF2</i>	-3.75931	2.83E-08
<i>NRK</i>	-3.79774	2.23E-04
<i>MAGEA12</i>	-3.85351	2.44E-07
<i>SEMA3A</i>	-3.8987	3.35E-07
<i>EDIL3</i>	-3.98896	5.93E-09
<i>SERPINF1</i>	-4.0248	2.72E-03
<i>TMEM26</i>	-4.05349	2.51E-12
<i>CTNNA2</i>	-4.11825	1.08E-13
<i>SCN2A</i>	-4.12133	5.26E-06
<i>PTPRZ1</i>	-4.27817	1.09E-03
<i>SLIT2</i>	-4.29632	3.26E-15
<i>MAF</i>	-4.31216	8.46E-08
<i>MCTP1</i>	-4.32517	6.50E-05
<i>PTGER2</i>	-4.58674	1.15E-08
<i>SLC8A1</i>	-4.62684	4.17E-08
<i>LRP1B</i>	-4.65154	6.00E-05
<i>FN1</i>	-4.66403	6.00E-08
<i>GRIN3A</i>	-4.68789	2.39E-08
<i>ERRF11</i>	-4.89238	3.34E-07
<i>LIN28A</i>	-4.94046	9.51E-10
<i>PTPRK</i>	-5.00817	1.50E-09
<i>TFAP2A</i>	-5.43585	3.91E-15
<i>SEMA3D</i>	-5.57451	1.20E-16
<i>COL11A1</i>	-6.04827	7.58E-04

Table SV. Differentially expressed genes in the topotecan resistant group.

Gene symbol	Log ₂ (fold change)	P-value
Upregulated		
<i>ABCG2</i>	7.53272	4.52E-28
<i>FABP7</i>	7.023987	3.64E-06
<i>SPP1</i>	6.547056	7.87E-06
<i>F2RL1</i>	5.899826	1.36E-18
<i>TGFB1</i>	5.780521	1.72E-17
<i>TRIM53AP</i>	5.312622	1.48E-11
<i>COL1A2</i>	5.017905	4.55E-16
<i>ART5</i>	4.875114	6.13E-20
<i>PRSS23</i>	4.798264	4.76E-08
<i>S100A3</i>	4.789493	4.48E-09
<i>MARCKS</i>	4.64525	2.90E-07
<i>SMPDL3A</i>	4.573848	3.80E-07
<i>RGS1</i>	4.50622	2.95E-11
<i>S100A9</i>	4.296875	1.57E-10
<i>IFI27</i>	4.256946	9.41E-04
<i>CYP1B1</i>	4.254178	4.40E-03
<i>TM4SF1</i>	4.218229	1.18E-14
<i>AKR1C1</i>	4.215575	8.35E-06
<i>LCP1</i>	4.202313	1.73E-07
<i>FAM198B</i>	4.018332	1.58E-06
<i>CAMK2N1</i>	3.990716	3.65E-04
<i>IL1R1</i>	3.618882	5.48E-09
<i>HERC5</i>	3.552554	2.59E-07
<i>RALGPS2</i>	3.439322	5.09E-07
<i>ADRB2</i>	3.41847	2.22E-04
<i>SEMA6D</i>	3.41732	2.55E-03
<i>SYNPO2</i>	3.407539	4.52E-05
<i>TMEM30B</i>	3.397063	8.82E-04
<i>ARHGD1B</i>	3.393527	1.60E-05
<i>ITGB8</i>	3.370497	7.50E-08
<i>IQGAP2</i>	3.328669	2.41E-20
<i>RGL1</i>	3.291996	1.50E-10
<i>PDGFD</i>	3.271938	1.07E-08
<i>IER3</i>	3.219902	2.88E-11
<i>OTOR</i>	3.206005	3.50E-06
<i>LAMA4</i>	3.205237	5.04E-15
<i>ITM2A</i>	3.200156	6.58E-06
<i>PRKCH</i>	3.199916	2.78E-03
<i>CCR1</i>	3.127966	8.61E-12
<i>PRKCB</i>	3.11018	1.29E-06
<i>S100A10</i>	3.101826	1.06E-03
<i>MYOT</i>	3.08369	3.23E-05
<i>GPC3</i>	3.081675	6.31E-06
<i>WNT5A</i>	3.070087	4.93E-03
<i>SAMD4A</i>	3.042913	5.00E-14
<i>SPARC</i>	3.034308	9.14E-08
<i>PCLO</i>	2.972949	7.63E-04
<i>AKR1C2</i>	2.955028	3.48E-05
<i>MGP</i>	2.935201	1.56E-06
<i>RGS5</i>	2.926909	3.41E-06
<i>JAKMIP2</i>	2.909949	2.93E-03
<i>HAPLN1</i>	2.874554	2.15E-05
<i>CD48</i>	2.872221	1.25E-03
<i>SEMA3E</i>	2.865353	7.19E-05
<i>CXADR</i>	2.86335	2.09E-08
<i>ASB9</i>	2.860539	6.86E-04
<i>SYT14</i>	2.853749	4.47E-08

Table SV. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>C11orf87</i>	2.829903	3.08E-03
<i>RHOBTB1</i>	2.799504	1.06E-06
<i>DLK1</i>	2.799125	3.17E-11
<i>ANK3</i>	2.787842	6.99E-05
<i>IFIH1</i>	2.778589	4.38E-03
<i>CPA2</i>	2.776402	8.56E-08
<i>RGS13</i>	2.752032	1.01E-03
<i>ACTA2</i>	2.741854	1.34E-07
<i>TBX18</i>	2.737173	5.90E-11
<i>FGFBP2</i>	2.721859	3.94E-03
<i>PSMB9</i>	2.704211	3.93E-05
<i>GHR</i>	2.68238	2.88E-05
<i>BDKRB1</i>	2.663652	3.41E-09
<i>DDX60</i>	2.656345	6.83E-04
<i>SP100</i>	2.60027	6.78E-04
<i>RERG</i>	2.583579	4.31E-04
<i>LRRTM1</i>	2.58231	7.09E-14
<i>GSTM3</i>	2.577037	1.40E-10
<i>TPM1</i>	2.576056	1.99E-07
<i>S1PR3</i>	2.573691	8.98E-06
<i>TMEM170B</i>	2.565728	1.24E-12
<i>SLC25A24</i>	2.557735	8.48E-11
<i>KIAA1324L</i>	2.544112	3.73E-04
<i>F2RL2</i>	2.541421	1.40E-16
<i>AMBN</i>	2.524498	9.16E-08
<i>KLHL13</i>	2.504081	3.75E-04
<i>EDIL3</i>	2.497366	1.20E-05
<i>RFPL4B</i>	2.496557	7.15E-04
<i>RGS2</i>	2.484943	9.54E-04
<i>ANGPT1</i>	2.480201	1.50E-07
<i>PALLD</i>	2.479919	7.98E-03
<i>PIMI</i>	2.438856	7.93E-07
<i>SLC38A4</i>	2.431709	8.06E-03
<i>TNS3</i>	2.407693	4.16E-04
<i>CADM1</i>	2.400311	1.03E-08
<i>BMP7</i>	2.390293	3.03E-10
<i>CD24</i>	2.380971	6.57E-04
<i>GTSF1</i>	2.380489	1.18E-13
<i>ADAMTS1</i>	2.374859	6.92E-04
<i>EMP1</i>	2.372551	3.30E-05
<i>XK</i>	2.372299	1.34E-12
<i>USP53</i>	2.367561	2.19E-03
<i>NFKBIZ</i>	2.355356	2.04E-04
<i>CD9</i>	2.353227	9.99E-04
<i>FGFBP3</i>	2.346837	5.43E-06
<i>EPDR1</i>	2.336494	5.12E-09
<i>MYO6</i>	2.327581	2.57E-04
<i>LUZP2</i>	2.310412	7.12E-04
<i>AMIGO2</i>	2.309423	1.01E-04
<i>FAS</i>	2.261495	4.01E-04
<i>GPC4</i>	2.259913	6.38E-03
<i>ISG20</i>	2.259314	2.21E-06
<i>SLC39A8</i>	2.255257	8.99E-04
<i>IFITM1</i>	2.247297	6.95E-03
<i>ARHGAP29</i>	2.238004	3.11E-06
<i>SESN3</i>	2.237422	1.72E-03
<i>NES</i>	2.236319	2.42E-04
<i>TMEM2</i>	2.230602	8.15E-06
<i>LONRF2</i>	2.227154	1.06E-04

Table SV. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>HDAC9</i>	2.205601	2.69E-03
<i>BDNF</i>	2.202899	3.12E-05
<i>CLU</i>	2.20236	1.14E-07
<i>SLITRK5</i>	2.193552	2.74E-04
<i>TPD52L1</i>	2.18914	2.59E-03
<i>CRIM1</i>	2.172478	1.34E-08
<i>CD68</i>	2.168848	9.18E-03
<i>HNMT</i>	2.1688	5.83E-09
<i>CALCA</i>	2.163064	2.19E-06
<i>AMOTL1</i>	2.145085	1.21E-03
<i>OLFML3</i>	2.134021	2.99E-04
<i>MTCL1</i>	2.133069	1.87E-06
<i>FBN2</i>	2.120103	9.17E-06
<i>LITD1</i>	2.116214	1.13E-08
<i>ESRRG</i>	2.110513	2.12E-04
<i>TNNC1</i>	2.104441	5.48E-03
<i>AARD</i>	2.0946	5.44E-04
<i>FZD7</i>	2.092517	5.44E-07
<i>PTGER2</i>	2.091748	6.36E-06
<i>PPIC</i>	2.043475	6.60E-04
<i>RPS6KA3</i>	2.04296	6.47E-03
<i>CALCB</i>	2.041604	3.88E-07
<i>PRKG1</i>	2.039876	6.16E-04
<i>KRT18</i>	2.039149	6.05E-03
<i>TNFSF10</i>	2.039047	2.02E-05
<i>SIX1</i>	2.028902	1.21E-03
<i>UBE2L6</i>	2.025851	3.38E-04
<i>NAALAD2</i>	2.022148	5.77E-07
<i>HEY1</i>	2.021561	4.94E-04
<i>TAP1</i>	2.012201	3.22E-05
<i>KANK4</i>	2.009275	2.34E-03
<i>TWISTNB</i>	2.004875	5.55E-05
Downregulated		
<i>SLC6A15</i>	-2.01867	4.42E-03
<i>MEOX2</i>	-2.13052	1.18E-06
<i>TRPC4</i>	-2.14492	2.74E-04
<i>IGDCC4</i>	-2.17598	2.25E-05
<i>JAM2</i>	-2.18381	1.86E-04
<i>RIMS1</i>	-2.18471	6.40E-03
<i>EPHA7</i>	-2.19819	4.86E-03
<i>KCNMB4</i>	-2.21021	1.90E-07
<i>MIPOL1</i>	-2.23275	3.02E-06
<i>TRPS1</i>	-2.24837	1.66E-10
<i>TMEM26</i>	-2.29031	1.46E-07
<i>MSANTD4</i>	-2.32828	4.36E-06
<i>SGCZ</i>	-2.36323	6.91E-07
<i>CD53</i>	-2.4077	2.50E-17
<i>MECOM</i>	-2.41337	2.11E-11
<i>BRINP3</i>	-2.47397	1.17E-04
<i>PTPRK</i>	-2.57827	3.42E-07
<i>FILIP1L</i>	-2.59596	6.03E-03
<i>NPVF</i>	-2.60186	3.18E-09
<i>NRAS</i>	-2.60426	6.45E-05
<i>ARMC9</i>	-2.61871	4.28E-08
<i>KIAA0825</i>	-2.69628	1.17E-12
<i>SLC25A21</i>	-2.71112	9.52E-11
<i>EFNB2</i>	-2.79247	3.24E-04
<i>TSPAN8</i>	-2.94059	9.40E-03
<i>SLIT2</i>	-2.98126	8.83E-12

Table SV. Continued.

Gene symbol	Log ₂ (fold change)	P-value
<i>SLC1A3</i>	-3.03344	1.02E-04
<i>GPC6</i>	-3.10343	1.86E-03
<i>MAGEA12</i>	-3.10935	6.67E-06
<i>MDFIC</i>	-3.11074	3.17E-03
<i>RERGL</i>	-3.14833	1.78E-03
<i>GRIA4</i>	-3.17843	9.40E-09
<i>AGMO</i>	-3.19155	6.27E-05
<i>WNT16</i>	-3.3777	7.83E-03
<i>NR0B1</i>	-3.41242	5.54E-03
<i>HTR2B</i>	-3.66429	1.36E-06
<i>EPHA3</i>	-3.7243	7.37E-04
<i>ANO3</i>	-3.82168	4.38E-07
<i>PAX9</i>	-4.02707	3.72E-07
<i>PTPRZ1</i>	-4.0361	1.84E-03
<i>ROBO2</i>	-4.12056	4.67E-03
<i>MDGA2</i>	-4.21232	1.40E-10
<i>MCTP1</i>	-4.33861	6.25E-05
<i>COL11A1</i>	-4.58866	2.77E-03
<i>LRP1B</i>	-4.7334	4.83E-05
<i>LGR5</i>	-5.79547	5.26E-06

Table SVI. GO and KEGG enrichment analysis of DEGs in ovarian cancer.

Group	ID	Description	Count	P-value
Cisplatin-resistant	Upregulated			
	GOTERM_BP			
	GO:0019065	Receptor-mediated endocytosis of virus by host cell	2	1.53E-04
	GO:0061364	Apoptotic process involved in luteolysis	2	1.53E-04
	GO:0075509	Endocytosis involved in viral entry into host cell	2	1.53E-04
	GO:0048731	System development	49	1.56E-04
	GO:0009888	Tissue development	27	1.65E-04
	GO:0007275	Multicellular organism development	53	2.01E-04
	GO:0050923	Regulation of negative chemotaxis	2	3.05E-04
	GO:0070836	Caveola assembly	2	3.05E-04
	GO:0044707	Single-multicellular organism process	60	3.70E-04
	GO:0001554	Luteolysis	2	5.05E-04
	GO:0044854	Plasma membrane raft assembly	2	5.05E-04
	GO:0044857	Plasma membrane raft organization	2	5.05E-04
	GO:0048856	Anatomical structure development	55	5.32E-04
	GO:0003018	Vascular process in circulatory system	6	7.74E-04
	GO:0048513	Animal organ development	37	8.90E-04
	GO:0032434	Regulation of proteasomal ubiquitin-dependent protein catabolic process	5	9.19E-04
	GO:0032502	Developmental process	57	9.93E-04
	GOTERM_CC			
	GO:0030667	Secretory granule membrane	9	2.39E-04
	KEGG			
	map4360	Axon guidance	4	9.23E-03
	map5223	Non-small cell lung cancer	2	4.73E-02
	map0330	Arginine and proline metabolism	2	4.73E-02
	map4530	Tight junction	3	5.30E-02
	map4910	Insulin signaling pathway	3	5.90E-02
	map290	Valine, leucine and isoleucine biosynthesis	1	6.90E-02
	map5120	Epithelial cell signaling in Helicobacter pylori infection	2	7.12E-02
	map4310	Wnt signaling pathwa	3	7.21E-02
	map5416	Viral myocarditis	2	7.49E-02
	map4730	Long-term depression	2	7.49E-02
	map5100	Bacterial invasion of epithelial cells	2	7.49E-02
	map5218	Melanoma	2	7.68E-02
	map5220	Chronic myeloid leukemia	2	8.05E-02
	map4370	VEGF signaling pathway	2	8.63E-02
	map4664	Fc epsilon RI signaling pathway	2	9.22E-02
	map4010	MAPK signaling pathway	4	9.33E-02
	map4974	Protein digestion and absorption	2	9.62E-02
	map770	Pantothenate and CoA biosynthesis	1	9.88E-02
	Downregulated			
	GOTERM_BP			
	GO:0032501	Multicellular organismal process	40	2.97E-06
	GO:0044707	Single-multicellular organism process	36	9.73E-06
	GO:0044699	Single-organism process	53	5.81E-05
	GO:0009753	Response to jasmonic acid	2	6.92E-05
	GO:0071395	Cellular response to jasmonic acid stimulus	2	6.92E-05
	GO:0009725	Response to hormone	11	8.89E-05
	GO:0009719	Response to endogenous stimulus	15	1.35E-04
	GO:0032808	Lacrimal gland development	2	1.72E-04
	GO:0072338	Cellular lactam metabolic process	2	1.72E-04
	GO:0031960	Response to corticosteroid	5	1.99E-04
	GO:0008207	C21-steroid hormone metabolic process	3	2.13E-04
	GO:0031076	Embryonic camera-type eye development	3	2.13E-04
	GO:0086004	Regulation of cardiac muscle cell contraction	3	2.32E-04
	GO:0051261	Protein depolymerization	4	2.34E-04
	GO:0010941	Regulation of cell death	14	2.41E-04
	GO:1901700	Response to oxygen-containing compound	14	2.73E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0044767	Single-organism developmental process	32	2.73E-04
	GO:0010243	Response to organonitrogen compound	10	2.81E-04
	GO:0030007	Cellular potassium ion homeostasis	2	3.20E-04
	GO:0030638	Polyketide metabolic process	2	3.20E-04
	GO:0044597	Daunorubicin metabolic process	2	3.20E-04
	GO:0044598	Doxorubicin metabolic process	2	3.20E-04
	GO:1903115	Regulation of actin filament-based movement	3	3.21E-04
	GO:0044765	Single-organism transport	21	3.44E-04
	GO:0007275	Multicellular organism development	29	3.48E-04
	GO:0032502	Developmental process	32	3.76E-04
	GO:0030647	Aminoglycoside antibiotic metabolic process	2	4.11E-04
	GO:0042981	Regulation of apoptotic process	13	4.20E-04
	GO:0007389	Pattern specification process	7	4.60E-04
	GO:0043067	Regulation of programmed cell death	13	4.65E-04
	GO:0003014	Renal system process	4	4.77E-04
	GO:0071156	Regulation of cell cycle arrest	4	4.77E-04
	GO:0060513	Prostatic bud formation	2	5.12E-04
	GO:0019748	Secondary metabolic process	3	5.59E-04
	GO:0035272	Exocrine system development	3	5.59E-04
	GO:0042135	Neurotransmitter catabolic process	2	6.25E-04
	GO:0042574	Retinal metabolic process	2	6.25E-04
	GO:0048856	Anatomical structure development	30	6.56E-04
	GO:0007417	Central nervous system development	10	6.60E-04
	GO:1902578	Single-organism localization	21	6.65E-04
	GO:1901698	Response to nitrogen compound	10	7.47E-04
	GO:0032970	Regulation of actin filament-based process	6	7.59E-04
	GO:0014070	Response to organic cyclic compound	10	7.87E-04
	GO:0048731	System development	26	8.22E-04
	GO:0060601	Lateral sprouting from an epithelium	2	8.82E-04
	GO:0065008	Regulation of biological quality	22	9.66E-04
	GOTERM_MF			
	GO:0018636	Phenanthrene 9,10-monooxygenase activity	2	3.47E-05
	GO:0047023	Androsterone dehydrogenase activity	2	3.47E-05
	GO:0047086	Ketosteroid monooxygenase activity	2	3.47E-05
	GO:0047718	Indanol dehydrogenase activity	2	3.47E-05
	GO:0047115	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	2	6.92E-05
	GO:0004032	Alditol:NADP+ 1-oxidoreductase activity	2	2.41E-04
	KEGG			
	map5218	Melanoma	3	2.53E-03
	map4810	Regulation of actin cytoskeleton	4	8.68E-03
	map2010	ABC transporters	2	1.26E-02
	map0140	Steroid hormone biosynthesis	2	1.99E-02
	map5214	Glioma	2	2.63E-02
	map0980	Metabolism of xenobiotics by cytochrome P450	2	3.10E-02
	map4520	Adherens junction	2	3.26E-02
	map4510	Focal adhesion	3	4.18E-02
	map5215	Prostate cancer	2	4.68E-02
	map4666	Fc gamma R-mediated phagocytosis	2	5.16E-02
	map4670	Leukocyte transendothelial migration	2	7.48E-02
	map4360	Axon guidance	2	8.99E-02
	map4530	Tight junction	2	9.35E-02
Doxorubicin-resistant	Upregulated			
	GOTERM_BP			
	GO:0010649	Regulation of cell communication by electrical coupling	2	9.41E-05
	GO:0055119	Relaxation of cardiac muscle	2	3.53E-04
	GO:0086064	Cell communication by electrical coupling involved in cardiac conduction	2	4.91E-04
	GO:0010880	Regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	2	5.96E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0010644	Cell communication by electrical coupling	2	7.10E-04
	GO:0014808	Release of sequestered calcium ion into cytosol by sarcoplasmic reticulum	2	8.35E-04
	GO:1903514	Calcium ion transport from endoplasmic reticulum to cytosol	2	9.01E-04
GOTERM_CC	GO:0005911	Cell-cell junction	5	7.59E-04
KEGG	map5220	Chronic myeloid leukemia	2	4.07E-03
	map4360	Axon guidance	2	1.23E-02
	map4650	Natural killer cell mediated cytotoxicity	2	1.36E-02
	map5216	Thyroid cancer	1	3.89E-02
	map4010	MAPK signaling pathway	2	4.85E-02
	map5219	Bladder cancer	1	5.59E-02
	map5213	Endometrial cancer	1	6.88E-02
	map5200	Pathways in cancer	2	6.90E-02
	map5223	Non-small cell lung cancer	1	7.13E-02
	map5221	Acute myeloid leukemia	1	7.51E-02
	map5214	Glioma	1	8.53E-02
	map4720	Long-term potentiation	1	9.16E-02
	map4730	Long-term depression	1	9.16E-02
	map5211	Renal cell carcinoma	1	9.16E-02
	map3320	PPAR signaling pathway	1	9.16E-02
	map5218	Melanoma	1	9.28E-02
	map5412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	1	9.66E-02
	map4662	B cell receptor signaling pathway	1	9.78E-02
	map4370	VEGF signaling pathway	1	9.91E-02
Downregulated				
GOTERM_BP	GO:0051239	Regulation of multicellular organismal process	24	6.57E-06
	GO:0044707	Single-multicellular organism process	38	1.86E-05
	GO:0044699	Single-organism process	58	1.98E-05
	GO:0032501	Multicellular organismal process	41	2.98E-05
	GO:0048518	Positive regulation of biological process	34	4.27E-05
	GO:0035556	Intracellular signal transduction	22	4.86E-05
	GO:0048513	Animal organ development	25	6.91E-05
	GO:0035633	Maintenance of permeability of blood-brain barrier	2	8.27E-05
	GO:0010226	Response to lithium ion	3	8.44E-05
	GO:0008283	Cell proliferation	18	9.84E-05
	GO:0042481	Regulation of odontogenesis	3	1.09E-04
	GO:0006970	Response to osmotic stress	4	1.29E-04
	GO:0048583	Regulation of response to stimulus	26	1.31E-04
	GO:0048584	Positive regulation of response to stimulus	18	1.50E-04
	GO:0044700	Single organism signaling	36	1.67E-04
	GO:0023052	Signaling	36	1.71E-04
	GO:0007154	Cell communication	36	1.83E-04
	GO:0086042	Cardiac muscle cell-cardiac muscle cell adhesion	2	2.88E-04
	GO:0050896	Response to stimulus	43	2.88E-04
	GO:0000902	Cell morphogenesis	11	3.51E-04
	GO:0030007	Cellular potassium ion homeostasis	2	3.82E-04
	GO:0001816	Cytokine production	9	4.70E-04
	GO:0008354	Germ cell migration	2	4.90E-04
	GO:0039530	MDA-5 signaling pathway	2	4.90E-04
	GO:0051240	Positive regulation of multicellular organismal process	14	5.00E-04
	GO:0001819	Positive regulation of cytokine production	7	5.12E-04
	GO:0006928	Movement of cell or subcellular component	16	6.02E-04
	GO:0042908	Xenobiotic transport	2	6.12E-04
	GO:0047484	Regulation of response to osmotic stress	2	6.12E-04
	GO:0032330	Regulation of chondrocyte differentiation	3	6.38E-04
	GO:0051716	Cellular response to stimulus	37	6.47E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
Paclitaxel-resistant	GO:0019369	Arachidonic acid metabolic process	3	6.80E-04
	GO:0048731	System development	28	7.04E-04
	GO:0023051	Regulation of signaling	22	7.44E-04
	GO:0045836	Positive regulation of meiotic nuclear division	2	7.46E-04
	GO:0032989	Cellular component morphogenesis	11	8.08E-04
	GO:0086065	Cell communication involved in cardiac conduction	3	8.19E-04
	GO:2000026	Regulation of multicellular organismal development	15	9.15E-04
	GO:0044767	Single-organism developmental process	33	9.31E-04
	GO:0042476	Odontogenesis	4	9.38E-04
	GOTERM_MF			
	GO:0090554	Phosphatidylcholine-translocating ATPase activity	2	8.55E-05
	GO:0008525	Phosphatidylcholine transporter activity	2	2.13E-04
	GO:0008559	Xenobiotic-transporting ATPase activity	2	2.97E-04
	GO:0042910	Xenobiotic transporter activity	2	5.07E-04
	GO:0061578	Lys63-specific deubiquitinase activity	2	5.07E-04
	GO:0086080	Protein binding involved in heterotypic cell-cell adhesion	2	7.71E-04
	GO:0032559	Adenyl ribonucleotide binding	14	8.69E-04
	GO:0030554	Adenyl nucleotide binding	14	9.36E-04
	GOTERM_CC			
	GO:0044459	Plasma membrane part	21	1.30E-04
	GO:0098590	Plasma membrane region	12	1.38E-04
	GO:0098589	Membrane region	7	3.46E-04
	GO:0045121	Membrane raft	6	6.11E-04
	GO:0098857	Membrane microdomain	6	6.23E-04
	GO:0016328	Lateral plasma membrane	3	9.03E-04
	GO:0005887	Integral component of plasma membrane	14	9.61E-04
	KEGG			
	map4976	Bile secretion	3	2.22E-03
	map4972	Pancreatic secretion	3	6.01E-03
	map4270	Vascular smooth muscle contraction	3	8.81E-03
	map2010	ABC transporters	2	1.15E-02
	map0590	Arachidonic acid metabolism	2	2.02E-02
	map4115	p53 signaling pathway	2	2.63E-02
	map4370	VEGF signaling pathway	2	3.23E-02
	map5222	Small cell lung cancer	2	3.97E-02
	map4970	Salivary secretion	2	4.32E-02
	map0592	alpha-Linolenic acid metabolism	1	7.25E-02
	map4060	Cytokine-cytokine receptor interaction	3	7.44E-02
	map4964	Proximal tubule bicarbonate reclamation	1	8.29E-02
	map5145	Toxoplasmosis	2	8.66E-02
	map0534	Glycosaminoglycan biosynthesis-heparan sulfate/heparin	1	9.32E-02
	Upregulated			
	GOTERM_BP			
	GO:0048731	System development	45	5.14E-06
	GO:0032501	Multicellular organismal process	59	1.74E-05
	GO:0007399	Nervous system development	27	4.12E-05
	GO:0007275	Multicellular organism development	46	5.59E-05
	GO:0044707	Single-multicellular organism process	52	7.74E-05
	GO:0003008	System process	24	1.02E-04
	GO:0048856	Anatomical structure development	48	1.07E-04
	GO:1901655	Cellular response to ketone	5	1.19E-04
	GO:0021825	Substrate-dependent cerebral cortex tangential migration	2	1.97E-04
	GO:0008045	Motor neuron axon guidance	3	3.94E-04
	GO:0050793	Regulation of developmental process	25	4.21E-04
	GO:0044767	Single-organism developmental process	48	4.67E-04
	GO:0006929	Substrate-dependent cell migration	3	4.97E-04
	GO:0045595	Regulation of cell differentiation	19	5.54E-04
	GO:1901654	Response to ketone	6	5.66E-04
	GO:0048729	Tissue morphogenesis	11	6.80E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0035524	Proline transmembrane transport	2	6.83E-04
	GO:0032502	Developmental process	48	6.94E-04
	GO:0030154	Cell differentiation	35	8.01E-04
	GO:0048869	Cellular developmental process	36	8.91E-04
	GO:0071549	Cellular response to dexamethasone stimulus	3	9.04E-04
	GO:0002072	Optic cup morphogenesis involved in camera-type eye development	2	9.08E-04
	GO:0021800	Cerebral cortex tangential migration	2	9.08E-04
	GO:0060078	Regulation of postsynaptic membrane potential	5	9.44E-04
	GO:0022008	Neurogenesis	18	9.92E-04
GOTERM_MF				
	GO:1901681	Sulfur compound binding	8	2.80E-05
	GO:0005539	Glycosaminoglycan binding	7	1.18E-04
	GO:0008201	Heparin binding	6	1.88E-04
	GO:0015193	L-proline transmembrane transporter activity	2	6.39E-04
	GO:0005201	Extracellular matrix structural constituent	4	8.65E-04
GOTERM_CC				
	GO:0005578	Proteinaceous extracellular matrix	14	7.82E-09
	GO:0031012	Extracellular matrix	16	1.47E-08
	GO:0005911	Cell-cell junction	13	3.39E-07
	GO:0044420	Extracellular matrix component	6	4.98E-05
	GO:0014704	Intercalated disc	4	1.19E-04
	GO:0005615	Extracellular space	18	3.38E-04
	GO:0044291	Cell-cell contact zone	4	4.14E-04
	GO:0044421	Extracellular region part	34	7.39E-04
KEGG				
	map5412	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	3	8.00E-03
	map0260	Glycine, serine and threonine metabolism	2	1.37E-02
	map4360	Axon guidance	3	3.50E-02
	map4530	Tight junction	3	3.71E-02
	map0590	Arachidonic acid metabolism	2	4.30E-02
	map5120	Epithelial cell signaling in Helicobacter pylori infection	2	5.55E-02
	map5100	Bacterial invasion of epithelial cells	2	5.84E-02
	map4520	Adherens junction	2	6.29E-02
	map4664	Fc epsilon RI signaling pathway	2	7.22E-02
	map4974	Protein digestion and absorption	2	7.54E-02
	map4512	ECM-receptor interaction	2	8.20E-02
	map0450	Selenocompound metabolism	1	9.15E-02
Downregulated				
GOTERM_BP				
	GO:0007155	Cell adhesion	27	2.61E-07
	GO:0022610	Biological adhesion	27	2.91E-07
	GO:0044707	Single-multicellular organism process	68	3.12E-07
	GO:0061572	Actin filament bundle organization	9	3.44E-07
	GO:0006928	Movement of cell or subcellular component	32	4.13E-07
	GO:0048856	Anatomical structure development	63	5.31E-07
	GO:0032502	Developmental process	65	1.31E-06
	GO:0040011	Locomotion	28	2.26E-06
	GO:0009653	Anatomical structure morphogenesis	36	2.46E-06
	GO:0051239	Regulation of multicellular organismal process	38	3.40E-06
	GO:0051017	Actin filament bundle assembly	8	3.43E-06
	GO:0044767	Single-organism developmental process	63	4.45E-06
	GO:0007275	Multicellular organism development	57	5.85E-06
	GO:0032501	Multicellular organismal process	71	8.30E-06
	GO:0016477	Cell migration	23	8.69E-06
	GO:0042127	Regulation of cell proliferation	26	9.71E-06
	GO:0048731	System development	52	1.02E-05
	GO:0030029	Actin filament-based process	16	1.36E-05
	GO:0007166	Cell surface receptor signaling pathway	36	1.94E-05

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0097435	Supramolecular fiber organization	14	2.61E-05
	GO:0008283	Cell proliferation	29	2.93E-05
	GO:0048513	Animal organ development	41	2.95E-05
	GO:0051240	Positive regulation of multicellular organismal process	24	3.62E-05
	GO:0048870	Cell motility	23	4.36E-05
	GO:0051674	Localization of cell	23	4.36E-05
	GO:0032652	Regulation of interleukin-1 production	5	4.81E-05
	GO:0048522	Positive regulation of cellular process	52	5.80E-05
	GO:0044089	Positive regulation of cellular component biogenesis	12	8.16E-05
	GO:0030335	Positive regulation of cell migration	11	8.25E-05
	GO:0050896	Response to stimulus	76	9.54E-05
	GO:0051270	Regulation of cellular component movement	16	9.57E-05
	GO:0032612	Interleukin-1 production	5	1.06E-04
	GO:2000147	Positive regulation of cell motility	11	1.16E-04
	GO:0007015	Actin filament organization	10	1.24E-04
	GO:0044763	Single-organism cellular process	90	1.36E-04
	GO:0051492	Regulation of stress fiber assembly	5	1.41E-04
	GO:0051272	Positive regulation of cellular component movement	11	1.45E-04
	GO:0036337	Fas signaling pathway	2	1.50E-04
	GO:0000904	Cell morphogenesis involved in differentiation	14	1.53E-04
	GO:0030036	Actin cytoskeleton organization	13	1.84E-04
	GO:0050793	Regulation of developmental process	30	1.93E-04
	GO:0030334	Regulation of cell migration	14	1.96E-04
	GO:0040017	Positive regulation of locomotion	11	2.07E-04
	GO:2000026	Regulation of multicellular organismal development	25	2.08E-04
	GO:0006925	Inflammatory cell apoptotic process	3	2.23E-04
	GO:0032651	Regulation of interleukin-1 beta production	4	2.66E-04
	GO:0030038	Contractile actin filament bundle assembly	5	2.80E-04
	GO:0043149	Stress fiber assembly	5	2.80E-04
	GO:0009753	Response to jasmonic acid	2	2.99E-04
	GO:0044860	Protein localization to plasma membrane raft	2	2.99E-04
	GO:0071395	Cellular response to jasmonic acid stimulus	2	2.99E-04
	GO:1901529	Positive regulation of anion channel activity	2	2.99E-04
	GO:0098609	Cell-cell adhesion	15	3.06E-04
	GO:0048583	Regulation of response to stimulus	41	3.06E-04
	GO:0032231	Regulation of actin filament bundle assembly	5	3.14E-04
	GO:0048545	Response to steroid hormone	10	3.18E-04
	GO:0051130	Positive regulation of cellular component organization	19	3.21E-04
	GO:0048584	Positive regulation of response to stimulus	27	3.40E-04
	GO:0009888	Tissue development	26	3.52E-04
	GO:0044087	Regulation of cellular component biogenesis	15	3.61E-04
	GO:0007160	Cell-matrix adhesion	7	3.82E-04
	GO:2000145	Regulation of cell motility	14	4.18E-04
	GO:0032879	Regulation of localization	31	4.38E-04
	GO:0000902	Cell morphogenesis	16	4.53E-04
	GO:0032970	Regulation of actin filament-based process	9	4.60E-04
	GO:0032989	Cellular component morphogenesis	17	4.61E-04
	GO:0030154	Cell differentiation	42	4.76E-04
	GO:0008285	Negative regulation of cell proliferation	13	4.88E-04
	GO:1903961	Positive regulation of anion transmembrane transport	2	4.96E-04
	GO:0048518	Positive regulation of biological process	53	5.00E-04
	GO:0098602	Single organism cell adhesion	13	5.03E-04
	GO:0090257	Regulation of muscle system process	7	5.07E-04
	GO:0010035	Response to inorganic substance	11	5.18E-04
	GO:0006937	Regulation of muscle contraction	6	5.34E-04
	GO:0050789	Regulation of biological process	89	5.63E-04
	GO:0044700	Single organism signaling	59	5.67E-04
	GO:0023052	Signaling	59	5.87E-04
	GO:0032611	Interleukin-1 beta production	4	5.88E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0048869	Cellular developmental process	43	6.30E-04
	GO:0007154	Cell communication	59	6.39E-04
	GO:0065008	Regulation of biological quality	39	6.72E-04
	GO:0022607	Cellular component assembly	32	6.83E-04
	GO:0097191	Extrinsic apoptotic signaling pathway	7	7.01E-04
	GO:0010359	Regulation of anion channel activity	2	7.41E-04
	GO:0051179	Localization	58	8.00E-04
	GO:0065007	Biological regulation	92	8.86E-04
	GO:0035556	Intracellular signal transduction	31	9.24E-04
	GO:0008219	Cell death	26	9.73E-04
	GO:0040012	Regulation of locomotion	14	9.78E-04
	GO:0051128	Regulation of cellular component organization	28	9.86E-04
GOTERM_MF				
	GO:0032052	Bile acid binding	3	3.02E-05
	GO:0019900	Kinase binding	14	8.66E-05
	GO:0018636	Phenanthrene 9,10-monooxygenase activity	2	1.56E-04
	GO:0047086	Ketosteroid monooxygenase activity	2	1.56E-04
	GO:0008106	Alcohol dehydrogenase (NADP+) activity	3	1.59E-04
	GO:0047115	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	2	3.10E-04
	GO:0090554	Phosphatidylcholine-translocating ATPase activity	2	3.10E-04
	GO:0050839	Cell adhesion molecule binding	11	3.26E-04
	GO:0051015	Actin filament binding	6	5.04E-04
	GO:0004033	Aldo-keto reductase (NADP) activity	3	7.61E-04
	GO:0008525	Phosphatidylcholine transporter activity	2	7.67E-04
	GO:0005488	Binding	108	8.22E-04
GOTERM_CC				
	GO:0030054	Cell junction	27	3.62E-08
	GO:0030055	Cell-substrate junction	14	5.97E-07
	GO:0005911	Cell-cell junction	14	1.01E-06
	GO:0070161	Anchoring junction	15	2.37E-06
	GO:0005925	Focal adhesion	13	2.77E-06
	GO:0005924	Cell-substrate adherens junction	13	3.03E-06
	GO:0005912	Adherens junction	13	3.45E-05
	GO:0070062	Extracellular exosome	35	1.07E-04
	GO:1903561	Extracellular vesicle	35	1.20E-04
	GO:0043230	Extracellular organelle	35	1.21E-04
	GO:0045177	Apical part of cell	10	1.85E-04
	GO:0031982	Vesicle	45	5.68E-04
	GO:0044421	Extracellular region part	41	8.57E-04
KEGG				
	map4370	VEGF signaling pathway	5	2.09E-04
	map4666	Fc gamma R-mediated phagocytosis	5	5.64E-04
	map2010	ABC transporters	3	3.94E-03
	map5146	Amoebiasis	4	7.22E-03
	map5200	Pathways in cancer	7	8.74E-03
	map4010	MAPK signaling pathway	6	1.26E-02
	map5100	Bacterial invasion of epithelial cells	3	1.43E-02
	map4510	Focal adhesion	5	1.47E-02
	map4976	Bile secretion	3	1.48E-02
	map5218	Melanoma	3	1.48E-02
	map4650	Natural killer cell mediated cytotoxicity	4	1.69E-02
	map4974	Protein digestion and absorption	3	2.10E-02
	map4512	ECM-receptor interaction	3	2.39E-02
	map4210	Apoptosis	3	2.54E-02
	map5330	Allograft rejection	2	2.97E-02
	map5332	Graft-versus-host disease	2	3.59E-02
	map5219	Bladder cancer	2	3.75E-02
	map4960	Aldosterone-regulated sodium reabsorption	2	3.75E-02
	map4940	Type I diabetes mellitus	2	3.92E-02

Table SVI. Continued.

Group	ID	Description	Count	P-value
Topotecan-resistant	map4973	Carbohydrate digestion and absorption	2	4.09E-02
	map5213	Endometrial cancer	2	5.52E-02
	map5320	Autoimmune thyroid disease	2	5.52E-02
	map4144	Endocytosis	4	5.83E-02
	map5223	Non-small cell lung cancer	2	5.90E-02
	map140	Steroid hormone biosynthesis	2	6.30E-02
	map5221	Acute myeloid leukemia	2	6.50E-02
	map4360	Axon guidance	3	6.78E-02
	map5145	Toxoplasmosis	3	7.16E-02
	map5210	Colorectal cancer	2	7.52E-02
	map5214	Glioma	2	8.16E-02
	map4115	p53 signaling pathway	2	8.82E-02
	map5212	Pancreatic cancer	2	9.27E-02
	map5211	Renal cell carcinoma	2	9.27E-02
	map5416	Viral myocarditis	2	9.27E-02
	map980	Metabolism of xenobiotics by cytochrome P450	2	9.49E-02
	map4520	Adherens junction	2	9.95E-02
	map5220	Chronic myeloid leukemia	2	9.95E-02
	Upregulated			
	GOTERM_BP			
	GO:0048731	System development	24	1.37E-05
	GO:0030154	Cell differentiation	22	1.41E-05
	GO:0061364	Apoptotic process involved in luteolysis	2	1.89E-05
	GO:0009888	Tissue development	15	1.95E-05
	GO:0031290	Retinal ganglion cell axon guidance	3	1.97E-05
	GO:0050919	Negative chemotaxis	3	1.97E-05
	GO:0030182	Neuron differentiation	12	2.45E-05
	GO:0022008	Neurogenesis	13	2.58E-05
	GO:0048869	Cellular developmental process	22	3.01E-05
	GO:0050923	Regulation of negative chemotaxis	2	3.78E-05
	GO:0001554	Luteolysis	2	6.29E-05
	GO:0051964	Negative regulation of synapse assembly	2	6.29E-05
	GO:0048699	Generation of neurons	12	6.36E-05
	GO:0002042	Cell migration involved in sprouting angiogenesis	3	7.20E-05
	GO:0009653	Anatomical structure morphogenesis	16	8.63E-05
	GO:0044707	Single-multicellular organism process	27	9.15E-05
	GO:0048468	Cell development	14	1.02E-04
	GO:0007275	Multicellular organism development	24	1.15E-04
	GO:0007399	Nervous system development	15	1.19E-04
	GO:0035385	Roundabout signaling pathway	2	1.32E-04
	GO:0043616	Keratinocyte proliferation	3	1.41E-04
	GO:0048856	Anatomical structure development	25	1.53E-04
	GO:0021891	Olfactory bulb interneuron development	2	1.75E-04
	GO:0051239	Regulation of multicellular organismal process	16	2.83E-04
	GO:0048513	Animal organ development	18	2.87E-04
	GO:0006865	Amino acid transport	4	3.64E-04
	GO:0022603	Regulation of anatomical structure morphogenesis	9	3.66E-04
	GO:0044767	Single-organism developmental process	25	4.07E-04
	GO:0072073	Kidney epithelium development	4	4.07E-04
	GO:0072178	Nephric duct morphogenesis	2	4.10E-04
	GO:1905809	Negative regulation of synapse organization	2	4.10E-04
	GO:0021889	Olfactory bulb interneuron differentiation	2	4.84E-04
	GO:0048666	Neuron development	9	4.87E-04
	GO:0032502	Developmental process	25	5.32E-04
	GO:0010839	Negative regulation of keratinocyte proliferation	2	5.64E-04
	GO:0072176	Nephric duct development	2	5.64E-04
	GO:0050793	Regulation of developmental process	14	5.77E-04
	GO:2000026	Regulation of multicellular organismal development	12	5.96E-04
	GO:0072001	Renal system development	5	6.52E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0002040	Sprouting angiogenesis	3	6.54E-04
	GO:0048729	Tissue morphogenesis	7	7.10E-04
	GO:0045595	Regulation of cell differentiation	11	7.46E-04
	GO:0031175	Neuron projection development	8	7.84E-04
	GO:0046942	Carboxylic acid transport	5	8.27E-04
	GO:0061564	Axon development	6	8.35E-04
	GO:0007166	Cell surface receptor signaling pathway	15	8.82E-04
	GO:0043534	Blood vessel endothelial cell migration	3	9.09E-04
	GO:0015849	Organic acid transport	5	9.33E-04
GOTERM_MF				
	GO:0005004	GPI-linked ephrin receptor activity	2	1.12E-04
	GO:0008046	Axon guidance receptor activity	2	1.12E-04
	GO:0004872	Receptor activity	11	4.64E-04
	GO:0060089	Molecular transducer activity	11	4.64E-04
	GO:0038023	Signaling receptor activity	10	4.82E-04
	GO:0005001	Transmembrane receptor protein tyrosine phosphatase activity	2	6.34E-04
	GO:0019198	Transmembrane receptor protein phosphatase activity	2	6.34E-04
	GO:0005003	Ephrin receptor activity	2	8.99E-04
GOTERM_CC				
	GO:0005887	Integral component of plasma membrane	15	4.61E-06
	GO:0031226	Intrinsic component of plasma membrane	15	7.49E-06
	GO:0044459	Plasma membrane part	18	3.19E-05
	GO:0031224	Intrinsic component of membrane	26	1.15E-04
	GO:0016021	Integral component of membrane	25	2.38E-04
	GO:0005886	Plasma membrane	24	5.25E-04
	GO:0071944	Cell periphery	24	7.17E-04
KEGG				
	map4360	Axon guidance	6	2.61E-07
	map5120	Epithelial cell signaling in Helicobacter pylori infection	2	1.10E-02
	map5220	Chronic myeloid leukemia	2	1.26E-02
	map4540	Gap junction	2	1.88E-02
	map4916	Melanogenesis	2	2.33E-02
	map4530	Tight junction	2	3.83E-02
	map5200	Pathways in cancer	3	3.91E-02
	map5216	Thyroid cancer	1	6.71E-02
	map5219	Bladder cancer	1	9.58E-02
Downregulated				
GOTERM_BP				
	GO:0051239	Regulation of multicellular organismal process	51	2.21E-09
	GO:0044707	Single-multicellular organism process	83	1.86E-08
	GO:0032502	Developmental process	81	2.17E-08
	GO:0044767	Single-organism developmental process	80	2.63E-08
	GO:0007275	Multicellular organism development	72	7.02E-08
	GO:0048856	Anatomical structure development	76	8.21E-08
	GO:0032501	Multicellular organismal process	89	1.23E-07
	GO:0050896	Response to stimulus	98	2.22E-07
	GO:0051240	Positive regulation of multicellular organismal process	32	2.56E-07
	GO:0009888	Tissue development	37	4.89E-07
	GO:0072359	Circulatory system development	24	9.50E-07
	GO:0016477	Cell migration	28	1.05E-06
	GO:0070887	Cellular response to chemical stimulus	45	1.75E-06
	GO:0048731	System development	63	1.87E-06
	GO:0007165	Signal transduction	73	2.91E-06
	GO:0051716	Cellular response to stimulus	83	3.06E-06
	GO:0048583	Regulation of response to stimulus	54	3.09E-06
	GO:2000026	Regulation of multicellular organismal development	33	3.96E-06
	GO:0071310	Cellular response to organic substance	39	4.20E-06
	GO:0072358	Cardiovascular system development	18	4.28E-06

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0045986	Negative regulation of smooth muscle contraction	4	5.17E-06
	GO:0065008	Regulation of biological quality	52	6.26E-06
	GO:0048870	Cell motility	28	7.41E-06
	GO:0051674	Localization of cell	28	7.41E-06
	GO:0001568	Blood vessel development	17	8.68E-06
	GO:0035556	Intracellular signal transduction	42	9.05E-06
	GO:0044700	Single organism signaling	76	9.32E-06
	GO:0023052	Signaling	76	9.79E-06
	GO:0009653	Anatomical structure morphogenesis	40	1.00E-05
	GO:0007154	Cell communication	76	1.10E-05
	GO:0050793	Regulation of developmental process	38	1.23E-05
	GO:0048518	Positive regulation of biological process	68	1.27E-05
	GO:0001944	Vasculature development	17	1.39E-05
	GO:0048519	Negative regulation of biological process	63	1.50E-05
	GO:0031214	Biomineral tissue development	8	1.52E-05
	GO:0007155	Cell adhesion	27	1.58E-05
	GO:0006928	Movement of cell or subcellular component	33	1.63E-05
	GO:0022610	Biological adhesion	27	1.75E-05
	GO:0040011	Locomotion	30	1.75E-05
	GO:0010033	Response to organic substance	44	1.87E-05
	GO:0042221	Response to chemical	56	2.06E-05
	GO:0045932	Negative regulation of muscle contraction	4	2.40E-05
	GO:0048513	Animal organ development	48	2.47E-05
	GO:0044089	Positive regulation of cellular component biogenesis	14	3.61E-05
	GO:1901342	Regulation of vasculature development	10	3.62E-05
	GO:0065009	Regulation of molecular function	44	3.64E-05
	GO:0022603	Regulation of anatomical structure morphogenesis	21	3.71E-05
	GO:0009966	Regulation of signal transduction	42	4.03E-05
	GO:0071229	Cellular response to acid chemical	9	4.15E-05
	GO:0032879	Regulation of localization	39	4.39E-05
	GO:0030334	Regulation of cell migration	17	4.60E-05
	GO:0010646	Regulation of cell communication	45	4.79E-05
	GO:0044699	Single-organism process	126	5.07E-05
	GO:0072012	Glomerulus vasculature development	4	5.13E-05
	GO:0003018	Vascular process in circulatory system	8	5.30E-05
	GO:0051963	Regulation of synapse assembly	6	6.04E-05
	GO:0019221	Cytokine-mediated signaling pathway	15	6.40E-05
	GO:0061437	Renal system vasculature development	4	7.12E-05
	GO:0061440	Kidney vasculature development	4	7.12E-05
	GO:0045778	Positive regulation of ossification	6	8.00E-05
	GO:0001101	Response to acid chemical	11	8.60E-05
	GO:0072507	Divalent inorganic cation homeostasis	13	9.25E-05
	GO:0006955	Immune response	31	9.37E-05
	GO:0051241	Negative regulation of multicellular organismal process	21	9.58E-05
	GO:0097755	Positive regulation of blood vessel diameter	5	9.60E-05
	GO:0042311	Vasodilation	4	9.62E-05
	GO:0051270	Regulation of cellular component movement	18	1.09E-04
	GO:2000145	Regulation of cell motility	17	1.15E-04
	GO:0048523	Negative regulation of cellular process	56	1.18E-04
	GO:0034097	Response to cytokine	18	1.26E-04
	GO:0048522	Positive regulation of cellular process	60	1.32E-04
	GO:0070493	Thrombin-activated receptor signaling pathway	3	1.35E-04
	GO:0050900	Leukocyte migration	12	1.46E-04
	GO:0023051	Regulation of signaling	44	1.55E-04
	GO:0072001	Renal system development	10	1.58E-04
	GO:0003156	Regulation of animal organ formation	4	1.64E-04
	GO:0065007	Biological regulation	113	1.70E-04
	GO:0007166	Cell surface receptor signaling pathway	39	1.79E-04
	GO:0050790	Regulation of catalytic activity	36	1.85E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:0030282	Bone mineralization	6	1.92E-04
	GO:0030278	Regulation of ossification	8	1.95E-04
	GO:0072006	Nephron development	7	1.97E-04
	GO:0010647	Positive regulation of cell communication	27	2.08E-04
	GO:0007416	Synapse assembly	7	2.15E-04
	GO:0032835	Glomerulus development	5	2.19E-04
	GO:0002739	Regulation of cytokine secretion involved in immune response	3	2.20E-04
	GO:0036337	Fas signaling pathway	2	2.25E-04
	GO:0072503	Cellular divalent inorganic cation homeostasis	12	2.33E-04
	GO:0008283	Cell proliferation	31	2.42E-04
	GO:0051130	Positive regulation of cellular component organization	22	2.54E-04
	GO:0050808	Synapse organization	9	2.64E-04
	GO:0006875	Cellular metal ion homeostasis	13	2.64E-04
	GO:0050789	Regulation of biological process	108	2.71E-04
	GO:0030500	Regulation of bone mineralization	5	2.73E-04
	GO:0072109	Glomerular mesangium development	3	2.73E-04
	GO:0055065	Metal ion homeostasis	14	2.75E-04
	GO:0071345	Cellular response to cytokine stimulus	16	2.86E-04
	GO:0051336	Regulation of hydrolase activity	24	2.95E-04
	GO:0008015	Blood circulation	13	2.98E-04
	GO:0030198	Extracellular matrix organization	10	3.08E-04
	GO:0009611	Response to wounding	15	3.12E-04
	GO:0009967	Positive regulation of signal transduction	25	3.12E-04
	GO:0001503	Ossification	11	3.16E-04
	GO:0043062	Extracellular structure organization	10	3.16E-04
	GO:0040012	Regulation of locomotion	17	3.21E-04
	GO:0003013	Circulatory system process	13	3.22E-04
	GO:0006952	Defense response	25	3.30E-04
	GO:0010595	Positive regulation of endothelial cell migration	5	3.36E-04
	GO:0007507	Heart development	13	3.56E-04
	GO:0043542	Endothelial cell migration	7	3.57E-04
	GO:0030155	Regulation of cell adhesion	15	3.69E-04
	GO:0002376	Immune system process	38	3.73E-04
	GO:0044087	Regulation of cellular component biogenesis	17	3.79E-04
	GO:0001655	Urogenital system development	10	3.99E-04
	GO:0002374	Cytokine secretion involved in immune response	3	4.03E-04
	GO:1902531	Regulation of intracellular signal transduction	28	4.15E-04
	GO:0048585	Negative regulation of response to stimulus	24	4.33E-04
	GO:0009753	Response to jasmonic acid	2	4.48E-04
	GO:0060686	Negative regulation of prostatic bud formation	2	4.48E-04
	GO:0071395	Cellular response to jasmonic acid stimulus	2	4.48E-04
	GO:0002687	Positive regulation of leukocyte migration	6	4.63E-04
	GO:0070167	Regulation of biomineral tissue development	5	4.65E-04
	GO:1905331	Negative regulation of morphogenesis of an epithelium	3	4.81E-04
	GO:0030335	Positive regulation of cell migration	11	4.87E-04
	GO:0010594	Regulation of endothelial cell migration	6	5.08E-04
	GO:0006950	Response to stress	47	5.16E-04
	GO:0030029	Actin filament-based process	15	5.22E-04
	GO:0023056	Positive regulation of signaling	26	5.40E-04
	GO:0009607	Response to biotic stimulus	17	5.45E-04
	GO:0002682	Regulation of immune system process	23	5.48E-04
	GO:0050807	Regulation of synapse organization	6	5.57E-04
	GO:0042060	Wound healing	13	5.59E-04
	GO:0060337	Type I interferon signaling pathway	5	5.59E-04
	GO:0071357	Cellular response to type I interferon	5	5.59E-04
	GO:0045995	Regulation of embryonic development	6	5.83E-04
	GO:0003206	Cardiac chamber morphogenesis	6	6.10E-04
	GO:0008217	Regulation of blood pressure	7	6.30E-04

Table SVI. Continued.

Group	ID	Description	Count	P-value
	GO:1901700	Response to oxygen-containing compound	25	6.48E-04
	GO:0072111	Cell proliferation involved in kidney development	3	6.63E-04
	GO:0050803	Regulation of synapse structure or activity	6	6.66E-04
	GO:2000147	Positive regulation of cell motility	11	6.73E-04
	GO:0072132	Mesenchyme morphogenesis	4	6.79E-04
	GO:0014706	Striated muscle tissue development	10	6.95E-04
	GO:0035296	Regulation of tube diameter	6	6.95E-04
	GO:0097746	Regulation of blood vessel diameter	6	6.95E-04
	GO:0034340	Response to type I interferon	5	7.05E-04
	GO:0010463	Mesenchymal cell proliferation	4	7.37E-04
	GO:0019748	Secondary metabolic process	4	7.37E-04
	GO:0032020	ISG15-protein conjugation	2	7.42E-04
	GO:0044093	Positive regulation of molecular function	29	7.45E-04
	GO:0051128	Regulation of cellular component organization	33	7.45E-04
	GO:0003007	Heart morphogenesis	8	7.78E-04
	GO:0061383	Trabecula morphogenesis	4	7.99E-04
	GO:0051272	Positive regulation of cellular component movement	11	8.26E-04
	GO:0051094	Positive regulation of developmental process	21	8.54E-04
	GO:1905330	Regulation of morphogenesis of an epithelium	7	8.90E-04
	GO:0051707	Response to other organism	16	9.17E-04
	GO:0061448	Connective tissue development	8	9.24E-04
	GO:0043207	Response to external biotic stimulus	16	9.30E-04
	GO:0050776	Regulation of immune response	17	9.30E-04
	GO:0009968	Negative regulation of signal transduction	20	9.37E-04
	GO:0001501	Skeletal system development	12	9.40E-04
	GO:0060537	Muscle tissue development	10	9.50E-04
	GO:0050880	Regulation of blood vessel size	6	9.69E-04
GOTERM_MF				
	GO:0005102	Receptor binding	27	5.17E-05
	GO:0005201	Extracellular matrix structural constituent	6	5.20E-05
	GO:0018636	Phenanthrene 9,10-monooxygenase activity	2	2.25E-04
	GO:0047086	Ketosteroid monooxygenase activity	2	2.25E-04
	GO:0042296	ISG15 transferase activity	2	4.47E-04
	GO:0047115	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase activity	2	4.47E-04
	GO:0001965	G-protein alpha-subunit binding	3	4.80E-04
	GO:0030165	PDZ domain binding	5	6.65E-04
	GO:0015057	Thrombin-activated receptor activity	2	7.41E-04
GOTERM_CC				
	GO:0031012	Extracellular matrix	18	2.84E-07
	GO:0005576	Extracellular region	64	9.47E-07
	GO:0044421	Extracellular region part	56	1.77E-06
	GO:0005578	Proteinaceous extracellular matrix	12	4.84E-05
	GO:0005615	Extracellular space	26	5.89E-05
	GO:0071944	Cell periphery	65	6.80E-05
	GO:1903561	Extracellular vesicle	41	7.19E-05
	GO:0043230	Extracellular organelle	41	7.25E-05
	GO:0070062	Extracellular exosome	40	1.38E-04
	GO:0005886	Plasma membrane	61	5.10E-04
	GO:0044420	Extracellular matrix component	6	5.33E-04
	GO:0031982	Vesicle	52	7.62E-04
	GO:0005884	Actin filament	5	7.88E-04
KEGG				
	map5143	African trypanosomiasis	4	3.58E-04
	map980	Metabolism of xenobiotics by cytochrome P450	4	5.10E-03
	map4512	ECM-receptor interaction	4	9.60E-03
	map4510	Focal adhesion	6	1.35E-02
	map4080	Neuroactive ligand-receptor interaction	7	1.69E-02
	map140	Steroid hormone biosynthesis	3	1.75E-02
	map5146	Amoebiasis	4	2.02E-02

Table SVI. Continued.

Group	ID	Description	Count	P-value
	map4270	Vascular smooth muscle contraction	4	2.71E-02
	map4650	Natural killer cell mediated cytotoxicity	4	4.47E-02
	map4060	Cytokine-cytokine receptor interaction	6	4.55E-02
	map5410	Hypertrophic cardiomyopathy (HCM)	3	4.83E-02
	map4210	Apoptosis	3	5.42E-02
	map4640	Hematopoietic cell lineage	3	5.57E-02
	map4970	Salivary secretion	3	5.73E-02
	map4540	Gap junction	3	5.88E-02
	map5414	Dilated cardiomyopathy (DCM)	3	5.88E-02
	map2010	ABC transporters	2	6.97E-02
	map4916	Melanogenesis	3	7.74E-02
	map4020	Calcium signaling pathway	4	9.67E-02