Table SI. Co-expression analysis results of KIF family genes in LUAD tumor tissues.

ID	KIF11	KIF12	KIF13A	KIF13B	KIF14	KIF15	KIF16B	KIF17	KIF18A	KIF18B	KIF19	KIF1A	KIF1B	KIF1BP	KIF1C	KIF20A	KIF20B	KIF21A	KIF21B	KIF22	KIF23	KIF24	KIF25	KIF26A	KIF26B	KIF27	KIF2A	KIF2C	KIF3A	KIF3B	KIF3C	KIF4A	KIF4B	KIF5A	KIF5B	KIF5C	KIF6	KIF7	KIF9	KIFAP3	KIFC1	KIFC2	KIFC3
KIF11	1.000	-0.221	-0.196	-0.089	0.861	0.797	-0.173	-0.031	0.724	0.755	0.068	0.316	0.328	0.325	-0.256	0.779	0.865	0.365	0.079	0.406	0.765	0.547	-0.032	0.130	0.000	-0.081	0.429	0.785	0.026	0.317	0.330	0.846	0.419	0.191	0.418	0.268	-0.192	0.190	-0.212	-0.032	0.757	-0.049	-0.137
KIF12	-0.221	1.000	-0.033	0.133	-0.194	-0.196	0.085	-0.081	-0.220	-0.136	0.094	-0.115	-0.156	-0.059	0.109	-0.201	-0.235	0.047	0.145	-0.073	-0.196	-0.165	0.109	0.004	0.058	-0.049	-0.190	-0.219	0.126	-0.005	-0.134	-0.223	-0.161	-0.035	-0.136	0.007	0.071	-0.087	0.126	-0.080	-0.152	0.192	0.215
KIF13A	-0.196	-0.033	1.000	0.085	-0.173	-0.221	0.287	0.018	-0.078	-0.282	-0.081	-0.106	0.267	0.028	0.277	-0.234	-0.059	-0.056	-0.069	-0.279	-0.250	-0.113	-0.126	-0.079	0.009	0.248	0.059	-0.264	0.050	-0.030	-0.171	-0.222	0.012	-0.051	0.054	-0.194	0.123	0.075	0.005	0.178	-0.251	-0.181	0.026
KIF13B	-0.089	0.133	0.085	1.000	-0.064	-0.157	0.186	-0.025	-0.148	-0.144	0.029	0.010	0.085	0.066	0.312	-0.179	-0.069	0.220	0.141	-0.255	-0.103	-0.052	-0.148	0.000	0.027	0.117	-0.054	-0.177	0.024	0.294	-0.065	-0.122	-0.079	-0.152	0.225	-0.036	-0.008	-0.137	0.143	-0.157	-0.139	-0.109	0.053
KIF14	0.861	-0.194	-0.173	-0.064	1.000	0.757	-0.121	-0.003	0.726	0.713	0.010	0.342	0.371	0.234	-0.205	0.760	0.750	0.421	0.148	0.377	0.712	0.563	-0.029	0.090	0.062	-0.041	0.390	0.786	0.090	0.314	0.327	0.795	0.406	0.152	0.447	0.344	-0.215	0.245	-0.209	0.006	0.732	-0.008	-0.037
KIF15	0.797	-0.196	-0.221	-0.157	0.757	1.000	-0.156	-0.007	0.668	0.717	0.134	0.327	0.380	0.122	-0.237	0.765	0.637	0.229	0.081	0.488	0.644	0.577	-0.028	0.229	-0.051	-0.030	0.433	0.809	0.059	0.242	0.303	0.782	0.393	0.255	0.353	0.389	-0.207	0.249	-0.116	-0.001	0.794	0.036	-0.191
KIF16B	-0.173	0.085	0.287	0.186	-0.121	-0.156	1.000	-0.096	-0.171	-0.225	-0.038	-0.096	0.183	0.048	0.184	-0.209	-0.102	0.138	-0.037	-0.242	-0.169	-0.067	-0.080	-0.047	0.090	0.220	0.065	-0.188	0.165	0.092	-0.091	-0.220	-0.090	-0.021	0.163	-0.040	0.017	-0.016	0.023	0.264	-0.163	-0.127	-0.040
KIF17	-0.031	-0.081	0.018	-0.025	-0.003	-0.007	-0.096	1.000	0.016	-0.065	0.269	-0.001	0.076	-0.109	0.124	-0.035	-0.096	-0.003	0.091	-0.087	-0.028	0.211	-0.044	0.084	-0.154	0.170	0.014	0.007	0.125	0.036	-0.015	-0.078	-0.013	0.022	-0.056	0.098	0.361	0.172	0.237	-0.028	-0.002	-0.140	-0.017
KIF18A	0.724	-0.220	-0.078	-0.148	0.726	0.668	-0.171	0.016	1.000	0.549	0.002	0.335	0.260	0.186	-0.246	0.663	0.648	0.304	-0.047	0.326	0.629	0.480	-0.096	0.091	-0.099	-0.018	0.400	0.657	0.023	0.197	0.211	0.693	0.426	0.069	0.307	0.282	-0.171	0.149	-0.146	0.022	0.648	-0.076	-0.129
KIF18B	0.755	-0.136	-0.282	-0.144	0.713	0.717	-0.225	-0.065	0.549	1.000	0.096	0.374	0.198	0.106	-0.274	0.722	0.566	0.229	0.151	0.523	0.635	0.512	0.074	0.168	-0.045	-0.144	0.266	0.788	-0.062	0.226	0.367	0.790	0.313	0.172	0.207	0.255	-0.196	0.272	-0.240	-0.116	0.799	0.199	-0.001
KIF19	0.068	0.094	-0.081	0.029	0.010	0.134	-0.038	0.269	0.002	0.096	1.000	0.056	-0.015	0.027	0.010	0.069	-0.009	0.161	0.047	0.088	-0.003	0.285	-0.019	0.331	0.113	0.275	0.082	0.034	0.278	0.213	0.071	0.030	-0.075	0.047	0.024	0.106	0.390	-0.025	0.315	0.011	0.150	0.011	0.041
KIF1A	0.316	-0.115	-0.106	0.010	0.342	0.327	-0.096	-0.001	0.335	0.374	0.056	1.000	0.231	0.078	-0.153	0.193	0.168	0.265	0.097	0.238	0.237	0.244	0.041	0.099	0.085	-0.068	0.111	0.336	0.027	0.194	0.351	0.357	0.226	0.144	0.166	0.354	-0.065	0.132	-0.132	-0.041	0.345	0.059	-0.022
KIF1B	0.328	-0.156	0.267	0.085	0.371	0.380	0.183	0.076	0.260	0.198	-0.015	0.231	1.000	0.234	0.093	0.246	0.274	0.248	0.112	0.007	0.214	0.302	-0.094	0.070	0.098	0.178	0.370	0.303	0.312	0.359	0.149	0.266	0.188	0.181	0.435	0.308	-0.063	0.214	-0.059	0.120	0.266	-0.087	-0.096
KIF1BP	0.325	-0.059	0.028	0.066	0.234	0.122	0.048	-0.109	0.186	0.106	0.027	0.078	0.234	1.000	0.079	0.137	0.338	0.234	-0.057	-0.050	0.203	0.108	-0.076	-0.010	0.147	-0.065	0.169	0.142	0.143	0.238	0.126	0.199	0.128	0.031	0.366	0.064	-0.022	-0.080	-0.060	0.066	0.148	-0.088	-0.022
KIF1C	-0.256	0.109	0.277	0.312	-0.205	-0.237	0.184	0.124	-0.246	-0.274	0.010	-0.153	0.093	0.079	1.000	-0.265	-0.199	0.025	0.050	-0.219	-0.233	-0.106	-0.113	0.042	-0.053	0.008	-0.198	-0.240	0.100	0.071	-0.143	-0.294	-0.127	-0.122	0.048	-0.075	0.166	0.023	0.234	0.019	-0.198	-0.011	0.162
KIF20A	0.779	-0.201	-0.234	-0.179	0.760	0.765	-0.209	-0.035	0.663	0.722	0.069	0.193	0.246	0.137	-0.265	1.000	0.608	0.175	0.074	0.501	0.688	0.510	-0.018	0.194	-0.028	-0.123	0.332	0.796	0.048	0.182	0.283	0.770	0.329	0.114	0.271	0.285	-0.192	0.194	-0.174	-0.038	0.804	0.041	-0.156
KIF20B	0.865	-0.235	-0.059	-0.069	0.750	0.637	-0.102	-0.096	0.648	0.566	-0.009	0.168	0.274	0.338	-0.199	0.608	1.000	0.371	0.013	0.211	0.655	0.433	-0.081	0.077	0.016	0.025	0.485	0.606	0.019	0.262	0.238	0.730	0.410	0.160	0.418	0.096	-0.188	0.051	-0.223	0.004	0.549	-0.086	-0.103
KIF21A	0.365	0.047	-0.056	0.220	0.421	0.229	0.138	-0.003	0.304	0.229	0.161	0.265	0.248	0.234	0.025	0.175	0.371	1.000	0.012	0.016	0.291	0.293	-0.096	0.020	0.055	0.227	0.295	0.228	0.295	0.359	0.111	0.299	0.159	0.015	0.392	0.188	0.141	-0.065	0.078	-0.045	0.211	-0.092	0.032
KIF21B	0.079	0.145	-0.069	0.141	0.148	0.081	-0.037	0.091	-0.047	0.151	0.047	0.097	0.112	-0.057	0.050	0.074	0.013	0.012	1.000	-0.024	-0.042	0.087	0.039	0.141	0.113	-0.015	0.106	0.037	0.120	0.061	0.069	0.045	-0.014	0.107	-0.003	0.132	-0.048	0.082	-0.126	-0.085	0.071	0.133	0.046
KIF22	0.406	-0.073	-0.279	-0.255	0.377	0.488	-0.242	-0.087	0.326	0.523	0.088	0.238	0.007	-0.050	-0.219	0.501	0.211	0.016	-0.024	1.000	0.398	0.343	0.202	0.128	-0.192	-0.115	-0.058	0.535	-0.122	-0.015	0.198	0.431	0.183	0.130	0.013	0.220	-0.096	0.191	-0.026	-0.109	0.560	0.274	0.034
KIF23	0.765	-0.196	-0.250	-0.103	0.712	0.644	-0.169	-0.028	0.629	0.635	-0.003	0.237	0.214	0.203	-0.233	0.688	0.655	0.291	-0.042	0.398	1.000	0.454	-0.012	0.037	-0.064	-0.070	0.261	0.722	-0.038	0.242	0.267	0.729	0.327	0.074	0.345	0.264	-0.202	0.241	-0.149	-0.119	0.680	-0.021	-0.085
KIF24	0.547	-0.165	-0.113	-0.052	0.563	0.577	-0.067	0.211	0.480	0.512	0.285	0.244	0.302	0.108	-0.106	0.510	0.433	0.293	0.087	0.343	0.454	1.000	-0.042	0.060	-0.057	0.364	0.339	0.523	0.251	0.312	0.153	0.509	0.256	0.123	0.285	0.276	0.214	0.251	0.151	-0.008	0.526	0.044	-0.138
KIF25	-0.032	0.109	-0.126	-0.148	-0.029	-0.028	-0.080	-0.044	-0.096	0.074	-0.019	0.041	-0.094	-0.076	-0.113	-0.018	-0.081	-0.096	0.039	0.202	-0.012	-0.042	1.000	-0.052	0.000	-0.072	-0.139	-0.007	-0.024	-0.087	0.064	0.026	0.054	0.040	-0.118	0.084	-0.045	0.058	-0.111	-0.052	-0.003	0.168	0.169
KIF26A	0.130	0.004	-0.079	0.000	0.090	0.229	-0.047	0.084	0.091	0.168	0.331	0.099	0.070	-0.010	0.042	0.194	0.077	0.020	0.141	0.128	0.037	0.060	-0.052	1.000	0.103	-0.011	0.089	0.136	0.129	0.083	0.100	0.091	0.037	0.111	0.008	0.169	0.163	0.054	-0.029	0.050	0.274	0.030	-0.033
KIF26B	0.000	0.058	0.009	0.027	0.062	-0.051	0.090	-0.154	-0.099	-0.045	0.113	0.085	0.098	0.147	-0.053	-0.028	0.016	0.055	0.113	-0.192	-0.064	-0.057	0.000	0.103	1.000	-0.046	0.085	-0.103	0.108	0.216	0.167	-0.011	0.060	0.028	0.145	0.073	-0.097	0.011	-0.197	0.119	-0.050	-0.075	0.027
KIF27	-0.081	-0.049	0.248	0.117	-0.041	-0.030	0.220	0.170	-0.018	-0.144	0.275	-0.068	0.178	-0.065	0.008	-0.123	0.025	0.227	-0.015	-0.115	-0.070	0.364	-0.072	-0.011	-0.046	1.000	0.272	-0.128	0.335	0.090	-0.122	-0.119	-0.021	-0.041	0.179	-0.039	0.384	-0.050	0.323	0.098	-0.142	-0.051	-0.045
KIF2A	0.429	-0.190	0.059	-0.054	0.390	0.433	0.065	0.014	0.400	0.266	0.082	0.111	0.370	0.169	-0.198	0.332	0.485	0.295	0.106	-0.058	0.261	0.339	-0.139	0.089	0.085	0.272	1.000	0.295	0.276	0.240	0.164	0.386	0.256	0.176	0.359	0.185	-0.081	0.015	-0.151	0.175	0.279	-0.177	-0.279
KIF2C	0.785	-0.219	-0.264	-0.177	0.786	0.809	-0.188	0.007	0.657	0.788	0.034	0.336	0.303	0.142	-0.240	0.796	0.606	0.228	0.037	0.535	0.722	0.523	-0.007	0.136	-0.103	-0.128	0.295	1.000	-0.064	0.206	0.317	0.793	0.320	0.183	0.254	0.343	-0.213	0.303	-0.170	-0.044	0.863	0.070	-0.113
KIF3A	0.026	0.126	0.050	0.024	0.090	0.059	0.165	0.125	0.023	-0.062	0.278	0.027	0.312	0.143	0.100	0.048	0.019	0.295	0.120	-0.122	-0.038	0.251	-0.024	0.129	0.108	0.335	0.276	-0.064	1.000	0.297	-0.055	-0.049	0.088	0.156	0.223	0.267	0.346	-0.033	0.212	0.167	-0.038	-0.025	-0.032
KIF3B	0.317	-0.005	-0.030	0.294	0.314	0.242	0.092	0.036	0.197	0.226	0.213	0.194	0.359	0.238	0.071	0.182	0.262	0.359	0.061	-0.015	0.242	0.312	-0.087	0.083	0.216	0.090	0.240	0.206	0.297	1.000	0.256	0.294	0.182	0.045	0.427	0.234	0.101	0.106	0.040	0.109	0.256	-0.156	-0.083
KIF3C	0.330	-0.134	-0.171	-0.065	0.327	0.303	-0.091	-0.015	0.211	0.367	0.071	0.351	0.149	0.126	-0.143	0.283	0.238	0.111	0.069	0.198	0.267	0.153	0.064	0.100	0.167	-0.122	0.164	0.317	-0.055	0.256	1.000	0.351	0.188	0.152	0.150	0.150	-0.116	0.166	-0.121	-0.028	0.309	0.037	0.035
KIF4A	0.846	-0.223	-0.222	-0.122	0.795	0.782	-0.220	-0.078	0.693	0.790	0.030	0.357	0.266	0.199	-0.294	0.770	0.730	0.299	0.045	0.431	0.729	0.509	0.026	0.091	-0.011	-0.119	0.386	0.793	-0.049	0.294	0.351	1.000	0.508	0.117	0.317	0.260	-0.239	0.165	-0.255	-0.044	0.746	0.013	-0.114
KIF4B	0.419	-0.161	0.012	-0.079	0.406	0.393	-0.090	-0.013	0.426	0.313	-0.075	0.226	0.188	0.128	-0.127	0.329	0.410	0.159	-0.014	0.183	0.327	0.256	0.054	0.037	0.060	-0.021	0.256	0.320	0.088	0.182	0.188	0.508	1.000	0.057	0.259	0.085	-0.115	0.063	-0.169	0.019	0.286	-0.037	-0.105
KIF5A	0.191	-0.035	-0.051	-0.152	0.152	0.255	-0.021	0.022	0.069	0.172	0.047	0.144	0.181	0.031	-0.122	0.114	0.160	0.015	0.107	0.130	0.074	0.123	0.040	0.111	0.028	-0.041	0.176	0.183	0.156	0.045	0.152	0.117	0.057	1.000	0.066	0.192	-0.032	0.101	-0.114	0.074	0.177	-0.003	-0.087
KIF5B	0.418	-0.136	0.054	0.225	0.447	0.353	0.163	-0.056	0.307	0.207	0.024	0.166	0.435	0.366	0.048	0.271	0.418	0.392	-0.003	0.013	0.345	0.285	-0.118	0.008	0.145	0.179	0.359	0.254	0.223	0.427	0.150	0.317	0.259	0.066	1.000	0.189	-0.103	-0.051	-0.012	0.101	0.223	-0.204	-0.148
KIF5C	0.268	0.007	-0.194	-0.036	0.344	0.389	-0.040	0.098	0.282	0.255	0.106	0.354	0.308	0.064	-0.075	0.285	0.096	0.188	0.132	0.220	0.264	0.276	0.084	0.169	0.073	-0.039	0.185	0.343	0.267	0.234	0.150	0.260	0.085	0.192	0.189	1.000	-0.052	0.137	-0.012	-0.047	0.415	0.059	-0.140
KIF6	-0.192	0.071	0.123	-0.008	-0.215	-0.207	0.017	0.361	-0.171	-0.196	0.390	-0.065	-0.063	-0.022	0.166	-0.192	-0.188	0.141	-0.048	-0.096	-0.202	0.214	-0.045	0.163	-0.097	0.384	-0.081	-0.213	0.346	0.101	-0.116	-0.239	-0.115	-0.032	-0.103	-0.052	1.000	0.004	0.471	0.101	-0.175	-0.077	0.004
KIF7	0.190	-0.087	0.075	-0.137	0.245	0.249	-0.016	0.172	0.149	0.272	-0.025	0.132	0.214	-0.080	0.023	0.194	0.051	-0.065	0.082	0.191	0.241	0.251	0.058	0.054	0.011	-0.050	0.015	0.303	-0.033	0.106	0.166	0.165	0.063	0.101	-0.051	0.137	0.004	1.000	-0.046	-0.021	0.292	0.116	0.018
KIF9	-0.212	0.126	0.005	0.143	-0.209	-0.116	0.023	0.237	-0.146	-0.240	0.315	-0.132	-0.059	-0.060	0.234	-0.174	-0.223	0.078	-0.126	-0.026	-0.149	0.151	-0.111	-0.029	-0.197	0.323	-0.151	-0.170	0.212	0.040	-0.121	-0.255	-0.169	-0.114	-0.012	-0.012	0.471	-0.046	1.000	-0.041	-0.171	0.029	0.014
KIFAP3	-0.032	-0.080	0.178	-0.157	0.006	-0.001	0.264	-0.028	0.022	-0.116	0.011	-0.041	0.120	0.066	0.019	-0.038	0.004	-0.045	-0.085	-0.109	-0.119	-0.008	-0.052	0.050	0.119	0.098	0.175	-0.044	0.167	0.109	-0.028	-0.044	0.019	0.074	0.101	-0.047	0.101	-0.021	-0.041	1.000	-0.028	-0.171	-0.162
KIFC1	0.757	-0.152	-0.251	-0.139	0.732	0.794	-0.163	-0.002	0.648	0.799	0.150	0.345	0.266	0.148	-0.198	0.804	0.549	0.211	0.071	0.560	0.680	0.526	-0.003	0.274	-0.050	-0.142	0.279	0.863	-0.038	0.256	0.309	0.746	0.286	0.177	0.223	0.415	-0.175	0.292	-0.171	-0.028	1.000	0.088	-0.107
KIFC2	-0.049	0.192	-0.181	-0.109	-0.008	0.036	-0.127	-0.140	-0.076	0.199	0.011	0.059	-0.087	-0.088	-0.011	0.041	-0.086	-0.092	0.133	0.274	-0.021	0.044	0.168	0.030	-0.075	-0.051	-0.177	0.070	-0.025	-0.156	0.037	0.013	-0.037	-0.003	-0.204	0.059	-0.077	0.116	0.029	-0.171	0.088	1.000	0.388
KIFC3	-0.137	0.215	0.026	0.053	-0.037	-0.191	-0.040	-0.017	-0.129	-0.001	0.041	-0.022	-0.096	-0.022	0.162	-0.156	-0.103	0.032	0.046	0.034	-0.085	-0.138	0.169	-0.033	0.027	-0.045	-0.279	-0.113	-0.032	-0.083	0.035	-0.114	-0.105	-0.087	-0.148	-0.140	0.004	0.018	0.014	-0.162	-0.107	0.388	1.000

Abbreviations: LUAD, lung adenocarcinoma; KIF, kinesin.

Table SII. **GSEA results of c5 reference gene set of high *KIF14* expression group.**

Name	Size	ES	NES	NOM P-value	FDR q-value
GO MITOTIC NUCLEAR DIVISION	337	0.712098	2.682246	<0.0001	<0.0001
GO ORGANELLE FISSION	449	0.675969	2.667881	<0.0001	<0.0001
GO SPINDLE MICROTUBULE	56	0.783062	2.663053	<0.0001	<0.0001
GO REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	164	0.66438	2.650518	<0.0001	<0.0001
GO CHROMOSOME SEGREGATION	247	0.752335	2.645015	<0.0001	<0.0001
GO CELL DIVISION	423	0.656167	2.634596	<0.0001	<0.0001
GO SPINDLE	267	0.647816	2.632039	<0.0001	<0.0001
GO MITOTIC SISTER CHROMATID SEGREGATION	88	0.82701	2.629891	<0.0001	<0.0001
GO NUCLEAR CHROMOSOME SEGREGATION	204	0.773826	2.619981	<0.0001	<0.0001
GO CONDENSED CHROMOSOME	169	0.763499	2.596428	<0.0001	<0.0001
GO SISTER CHROMATID SEGREGATION	163	0.801452	2.591617	<0.0001	<0.0001
GO REGULATION OF MICROTUBULE BASED PROCESS	226	0.628592	2.589697	<0.0001	<0.0001
GO CELL CYCLE CHECKPOINT	179	0.651547	2.556352	<0.0001	<0.0001
GO MITOTIC SPINDLE ORGANIZATION	64	0.770373	2.556195	<0.0001	<0.0001
GO REGULATION OF NUCLEAR DIVISION	153	0.623087	2.550648	<0.0001	<0.0001
GO CHROMOSOMAL REGION	297	0.716265	2.548625	<0.0001	<0.0001
GO CHROMOSOME CENTROMERIC REGION	153	0.779618	2.540278	<0.0001	<0.0001
GO DNA RECOMBINATION	189	0.708108	2.539063	<0.0001	<0.0001
GO CYTOKINESIS	80	0.659796	2.525565	<0.0001	<0.0001
GO KINETOCHORE	103	0.798729	2.523413	<0.0001	<0.0001
GO NEGATIVE REGULATION OF PROTEIN COMPLEX DISASSEMBLY	156	0.607188	2.518233	<0.0001	<0.0001
GO MEIOTIC CELL CYCLE	162	0.655327	2.511826	<0.0001	<0.0001
GO MEIOTIC CELL CYCLE PROCESS	130	0.673755	2.511794	<0.0001	<0.0001
GO CONDENSED CHROMOSOME CENTROMERIC REGION	83	0.836371	2.507111	<0.0001	<0.0001
GO CONDENSED NUCLEAR CHROMOSOME	74	0.742605	2.506965	<0.0001	<0.0001
GO MIDBODY	121	0.6022	2.505331	<0.0001	<0.0001
GO DNA REPLICATION	192	0.731864	2.500598	<0.0001	<0.0001
GO CELL CYCLE PHASE TRANSITION	248	0.673171	2.472004	<0.0001	<0.0001
GO REGULATION OF CHROMOSOME SEGREGATION	77	0.746082	2.471076	<0.0001	<0.0001
GO SPINDLE POLE	113	0.669898	2.46671	<0.0001	<0.0001
GO MITOTIC SPINDLE	50	0.719176	2.464137	<0.0001	<0.0001
GO REGULATION OF SISTER CHROMATID SEGREGATION	61	0.735854	2.462449	<0.0001	<0.0001
GO G2 DNA DAMAGE CHECKPOINT	31	0.742472	2.456178	<0.0001	<0.0001
GO CELL CYCLE G2 M PHASE TRANSITION	134	0.647235	2.455047	<0.0001	<0.0001
GO CHROMOSOME LOCALIZATION	56	0.738878	2.452304	<0.0001	<0.0001
GO SISTER CHROMATID COHESION	100	0.814757	2.448755	<0.0001	<0.0001
GO MEMBRANE DISASSEMBLY	44	0.772361	2.445921	<0.0001	<0.0001
GO DNA DEPENDENT DNA REPLICATION	90	0.792206	2.4393	<0.0001	<0.0001

GO DNA INTEGRITY CHECKPOINT	136	0.616455	2.435896	<0.0001	<0.0001
GO SPINDLE ASSEMBLY	67	0.675513	2.430131	<0.0001	<0.0001
GO REGULATION OF CELL DIVISION	250	0.561616	2.428758	<0.0001	<0.0001
GO MITOTIC CELL CYCLE CHECKPOINT	129	0.623171	2.428147	<0.0001	<0.0001
GO REGULATION OF DNA REPLICATION	152	0.607312	2.424847	<0.0001	<0.0001
GO DNA BIOSYNTHETIC PROCESS	108	0.679865	2.42479	<0.0001	<0.0001
GO REGULATION OF PROTEIN COMPLEX DISASSEMBLY	198	0.561611	2.423981	<0.0001	<0.0001
GO NEGATIVE REGULATION OF ORGANELLE ORGANIZATION	361	0.524476	2.414919	<0.0001	<0.0001
GO DNA REPAIR	433	0.608988	2.414044	<0.0001	<0.0001
GO NEGATIVE REGULATION OF CYTOSKELETON ORGANIZATION	205	0.537606	2.401888	<0.0001	<0.0001
GO NUCLEAR ENVELOPE ORGANIZATION	75	0.644243	2.399201	<0.0001	<0.0001
GO CYTOSKELETON DEPENDENT CYTOKINESIS	38	0.726307	2.39768	<0.0001	<0.0001
GO DNA DEPENDENT ATPASE ACTIVITY	76	0.75211	2.397585	<0.0001	<0.0001
GO REPLICATION FORK	62	0.788078	2.395891	<0.0001	<0.0001
GO PROTEIN SUMOYLATION	112	0.675924	2.395123	<0.0001	<0.0001
GO SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS	37	0.731896	2.393728	<0.0001	<0.0001
GO MULTI ORGANISM LOCALIZATION	65	0.695134	2.392456	<0.0001	<0.0001
GO NUCLEUS ORGANIZATION	124	0.597255	2.389481	<0.0001	<0.0001
GO DNA SYNTHESIS INVOLVED IN DNA REPAIR	67	0.738807	2.388248	<0.0001	<0.0001
GO MITOTIC SPINDLE ASSEMBLY	39	0.730121	2.384423	<0.0001	<0.0001
GO ATPASE ACTIVITY	412	0.546545	2.38414	<0.0001	<0.0001
GO HISTONE KINASE ACTIVITY	18	0.869347	2.381841	<0.0001	<0.0001
GO HISTONE PHOSPHORYLATION	24	0.768077	2.379646	<0.0001	<0.0001
GO SPINDLE MIDZONE	25	0.822831	2.376028	<0.0001	<0.0001
GO METAPHASE PLATE CONGRESSION	41	0.778993	2.371539	<0.0001	<0.0001
GO REGULATION OF DNA DEPENDENT DNA REPLICATION	39	0.800185	2.365752	<0.0001	<0.0001
GO NUCLEAR PERIPHERY	118	0.616942	2.364359	<0.0001	<0.0001
GO NEGATIVE REGULATION OF CELL DIVISION	56	0.670046	2.357604	<0.0001	<0.0001
GO MICROTUBULE CYTOSKELETON ORGANIZATION	314	0.567429	2.356141	<0.0001	<0.0001
GO RNA LOCALIZATION	173	0.615701	2.349783	<0.0001	1.05E-05
GO MEIOTIC CHROMOSOME SEGREGATION	49	0.680336	2.349619	<0.0001	1.03E-05
GO REGULATION OF MITOTIC CELL CYCLE	444	0.528076	2.346507	<0.0001	1.02E-05
GO NEGATIVE REGULATION OF CHROMOSOME ORGANIZATION	93	0.647127	2.340031	<0.0001	1.00E-05
GO CELL CYCLE G1 S PHASE TRANSITION	108	0.717898	2.338962	<0.0001	9.91E-06
GO NEGATIVE REGULATION OF MITOTIC CELL CYCLE	184	0.54229	2.334017	<0.0001	9.77E-06
GO NUCLEAR EXPORT	139	0.625466	2.332653	<0.0001	9.64E-06
GO MEIOSIS I	73	0.664922	2.329829	<0.0001	9.51E-06
GO REGULATION OF CHROMOSOME ORGANIZATION	263	0.546924	2.328474	<0.0001	9.39E-06
GO SOMATIC DIVERSIFICATION OF IMMUNOGLOBULINS	26	0.741615	2.327723	<0.0001	9.26E-06

GO CENTROSOME CYCLE	44	0.710459	2.325169	<0.0001	9.14E-06
GO NEGATIVE REGULATION OF CELL CYCLE PROCESS	199	0.538433	2.323229	<0.0001	9.03E-06
GO DNA GEOMETRIC CHANGE	77	0.721333	2.322284	<0.0001	8.92E-06
GO REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	156	0.569462	2.321441	<0.0001	8.81E-06
GO REGULATION OF DNA METABOLIC PROCESS	318	0.531544	2.321098	<0.0001	8.70E-06
GO NEGATIVE REGULATION OF DNA REPLICATION	50	0.652957	2.320175	<0.0001	8.59E-06
GO MICROTUBULE ORGANIZING CENTER ORGANIZATION	79	0.646021	2.315917	<0.0001	1.97E-05
GO DOUBLE STRAND BREAK REPAIR	151	0.652402	2.312146	<0.0001	1.94E-05
GO NEGATIVE REGULATION OF NUCLEAR DIVISION	42	0.692808	2.310467	<0.0001	1.92E-05
GO RECOMBINATIONAL REPAIR	70	0.70894	2.305188	<0.0001	1.90E-05
GO HELICASE ACTIVITY	148	0.675157	2.303484	<0.0001	1.88E-05
GO POSITIVE REGULATION OF CELL CYCLE PROCESS	227	0.538833	2.303124	<0.0001	1.85E-05
GO MITOTIC CYTOKINESIS	31	0.718289	2.295251	<0.0001	2.76E-05
GO POSITIVE REGULATION OF MITOTIC CELL CYCLE	118	0.587833	2.294271	<0.0001	2.73E-05
GO CENTROSOME	457	0.516237	2.293944	<0.0001	2.70E-05
GO NUCLEAR PORE	73	0.671182	2.286681	<0.0001	6.17E-05
GO NEGATIVE REGULATION OF MITOTIC NUCLEAR DIVISION	32	0.732843	2.285027	<0.0001	6.10E-05
GO SOMATIC CELL DNA RECOMBINATION	31	0.724322	2.284676	<0.0001	6.04E-05
GO REGULATION OF TELOMERE MAINTENANCE	64	0.635078	2.278184	<0.0001	8.37E-05
GO DNA STRAND ELONGATION	29	0.879653	2.277452	<0.0001	8.28E-05
GO REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	57	0.618936	2.275083	<0.0001	9.05E-05
GO REGULATION OF CELL CYCLE PHASE TRANSITION	308	0.530402	2.273736	<0.0001	1.04E-04
GO TRNA TRANSPORT	32	0.812964	2.273654	<0.0001	1.03E-04
GO CHROMOSOME CONDENSATION	26	0.820715	2.272898	<0.0001	1.02E-04
GO REGULATION OF CENTROSOME CYCLE	38	0.739239	2.272252	<0.0001	1.01E-04
GO REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	49	0.660699	2.271119	<0.0001	1.08E-04
GO RIBONUCLEOPROTEIN COMPLEX LOCALIZATION	112	0.649751	2.270998	<0.0001	1.07E-04
GO DNA DEPENDENT DNA REPLICATION MAINTENANCE OF FIDELITY	19	0.841238	2.270667	<0.0001	1.06E-04
GO DNA CONFORMATION CHANGE	243	0.654861	2.267809	<0.0001	1.05E-04
GO RECIPROCAL DNA RECOMBINATION	34	0.723155	2.264945	<0.0001	1.04E-04
GO POSITIVE REGULATION OF CELL CYCLE	308	0.497873	2.26184	<0.0001	1.26E-04
GO SPINDLE LOCALIZATION	36	0.704923	2.261765	<0.0001	1.24E-04
GO MITOTIC RECOMBINATION	41	0.853253	2.260345	<0.0001	1.30E-04
GO MITOTIC DNA INTEGRITY CHECKPOINT	93	0.568916	2.259875	<0.0001	1.29E-04
GO NUCLEAR CHROMOSOME	488	0.56416	2.255939	<0.0001	1.70E-04
GO POSITIVE REGULATION OF CHROMOSOME	23	0.774029	2.254839	<0.0001	1.76E-04

SEGREGATION					
GO CHROMATIN REMODELING	139	0.596132	2.254539	<0.0001	1.74E-04
GO KINESIN COMPLEX	53	0.68674	2.253981	<0.0001	1.73E-04
GO DNA HELICASE ACTIVITY	50	0.78077	2.253384	<0.0001	1.80E-04
GO PURINE NTP DEPENDENT HELICASE ACTIVITY	95	0.668325	2.251719	<0.0001	1.92E-04
GO POSITIVE REGULATION OF CELL CYCLE PHASE TRANSITION	66	0.612909	2.247219	<0.0001	2.52E-04
GO STRAND DISPLACEMENT	25	0.857924	2.244335	<0.0001	2.60E-04
GO NUCLEAR MATRIX	95	0.571998	2.243401	<0.0001	2.58E-04
GO DNA STRAND ELONGATION INVOLVED IN DNA REPLICATION	25	0.904276	2.242602	<0.0001	2.63E-04
GO MICROTUBULE	382	0.493602	2.240029	<0.0001	2.87E-04
GO MICROTUBULE BINDING	189	0.520415	2.237755	<0.0001	2.85E-04
GO RESPONSE TO IONIZING RADIATION	137	0.543534	2.234383	<0.0001	2.96E-04
GO SOMATIC RECOMBINATION OF IMMUNOGLOBULIN GENE SEGMENTS	21	0.753897	2.234008	<0.0001	2.94E-04
GO REGULATION OF DOUBLE STRAND BREAK REPAIR	33	0.683869	2.21987	<0.0001	3.78E-04
GO ATP DEPENDENT DNA HELICASE ACTIVITY	32	0.769188	2.214459	<0.0001	4.10E-04
GO NEGATIVE REGULATION OF CHROMOSOME SEGREGATION	25	0.787655	2.212827	<0.0001	4.07E-04
GO PROTEIN LOCALIZATION TO CYTOSKELETON	28	0.668449	2.211528	<0.0001	4.10E-04
GO SINGLE STRANDED DNA BINDING	78	0.637339	2.209148	<0.0001	4.28E-04
GO ANAPHASE PROMOTING COMPLEX	20	0.78991	2.207604	<0.0001	4.32E-04
GO ATPASE ACTIVITY COUPLED	307	0.498259	2.205396	<0.0001	4.41E-04
GO REGULATION OF TRANSCRIPTION INVOLVED IN G1 S TRANSITION OF MITOTIC CELL CYCLE	25	0.844392	2.204197	<0.0001	4.45E-04
GO CHROMOSOME SEPARATION	16	0.825543	2.203816	<0.0001	4.42E-04
GO SPINDLE CHECKPOINT	23	0.810519	2.200688	<0.0001	4.58E-04
GO NEGATIVE REGULATION OF CELL CYCLE PHASE TRANSITION	137	0.527435	2.197703	<0.0001	4.84E-04
GO RNA 3 END PROCESSING	96	0.632007	2.195773	<0.0001	4.80E-04
GO NUCLEOBASE CONTAINING COMPOUND TRANSPORT	187	0.544178	2.195028	<0.0001	4.83E-04
GO DNA REPLICATION INITIATION	29	0.86371	2.189515	<0.0001	5.16E-04
GO REGULATION OF CELLULAR RESPONSE TO HEAT	72	0.643045	2.187421	<0.0001	5.50E-04
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE	44	0.624996	2.186949	<0.0001	5.46E-04
GO DNA DIRECTED DNA POLYMERASE ACTIVITY	26	0.69116	2.183641	<0.0001	5.49E-04
GO REGULATION OF CYTOKINESIS	56	0.60157	2.183209	<0.0001	5.58E-04
GO MRNA 3 END PROCESSING	71	0.653102	2.183206	<0.0001	5.54E-04
GO POSITIVE REGULATION OF DNA METABOLIC PROCESS	174	0.500897	2.179585	<0.0001	5.78E-04
GO SIGNAL TRANSDUCTION IN RESPONSE TO	91	0.560032	2.17819	<0.0001	5.96E-04

DNA DAMAGE					
GO TELOMERE MAINTENANCE VIA RECOMBINATION	32	0.845018	2.177901	<0.0001	5.92E-04
GO MICROTUBULE END	21	0.762806	2.177106	<0.0001	5.88E-04
GO ATP DEPENDENT MICROTUBULE MOTOR ACTIVITY	18	0.821186	2.173439	<0.0001	6.26E-04
GO INTERSTRAND CROSS LINK REPAIR	38	0.686513	2.173382	<0.0001	6.22E-04
GO MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	38	0.623258	2.173214	<0.0001	6.25E-04
GO HETEROCHROMATIN	65	0.61276	2.170755	<0.0001	6.37E-04
GO NEGATIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	60	0.579122	2.169545	<0.0001	6.55E-04
GO HEAT SHOCK PROTEIN BINDING	86	0.557312	2.167885	<0.0001	6.51E-04
GO PROTEIN EXPORT FROM NUCLEUS	29	0.655804	2.166861	<0.0001	6.77E-04
GO EXONUCLEASE ACTIVITY	70	0.580711	2.161916	<0.0001	7.27E-04
GO POSITIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	57	0.583944	2.161853	<0.0001	7.22E-04
GO RNA POLYADENYLATION	29	0.704223	2.160275	<0.0001	7.29E-04
GO FEMALE MEIOTIC DIVISION	22	0.724275	2.159829	<0.0001	7.25E-04
GO NUCLEAR REPLICATION FORK	39	0.738987	2.158608	<0.0001	7.42E-04
GO PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	127	0.528314	2.158536	<0.0001	7.37E-04
GO POSITIVE REGULATION OF MITOTIC NUCLEAR DIVISION	46	0.609649	2.155905	<0.0001	8.01E-04
GO REGULATION OF DNA BIOSYNTHETIC PROCESS	90	0.537845	2.154432	<0.0001	8.16E-04
GO REGULATION OF DNA REPAIR	68	0.591068	2.14987	<0.0001	8.68E-04
GO NEGATIVE REGULATION OF CELL CYCLE	404	0.439902	2.143356	<0.0001	9.52E-04
GO REGULATION OF CHROMATIN SILENCING	21	0.747849	2.142313	<0.0001	9.47E-04
GO TUBULIN BINDING	255	0.47973	2.138896	<0.0001	9.95E-04
GO RESPONSE TO GAMMA RADIATION	49	0.577475	2.137084	<0.0001	0.001013
GO REGULATION OF DOUBLE STRAND BREAK REPAIR VIA HOMOLOGOUS RECOMBINATION	17	0.780716	2.136381	<0.0001	0.001013
GO MICROTUBULE BASED PROCESS	478	0.49037	2.135001	<0.0001	0.001046
GO BLASTOCYST GROWTH	15	0.798958	2.13441	<0.0001	0.001047
GO CHROMOSOME TELOMERIC REGION	150	0.613272	2.130309	<0.0001	0.001123
GO ATP DEPENDENT CHROMATIN REMODELING	67	0.688353	2.130273	<0.0001	0.001117
GO NUCLEAR IMPORT	126	0.51719	2.130023	<0.0001	0.001116
GO PRONUCLEUS	15	0.869304	2.126436	<0.0001	0.001158
GO REPLISOME	29	0.739198	2.125365	<0.0001	0.001156
GO REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	141	0.506234	2.120427	<0.0001	0.001258
GO DNA SECONDARY STRUCTURE BINDING	24	0.737121	2.120405	<0.0001	0.00125
GO NUCLEAR TRANSPORT	341	0.466141	2.116048	<0.0001	0.00135
GO MICROTUBULE ASSOCIATED COMPLEX	141	0.525455	2.112357	<0.0001	0.00143
GO TETRAHYDROFOLATE METABOLIC PROCESS	19	0.742573	2.110568	<0.0001	0.001437
GO REGULATION OF CENTROSOME	31	0.673565	2.109085	<0.0001	0.001469

DUPLICATION					
GO PEPTIDYL LYSINE MODIFICATION	278	0.507345	2.107943	<0.0001	0.001476
GO RAN GTPASE BINDING	31	0.734209	2.107892	<0.0001	0.001472
GO MITOTIC G2 M TRANSITION CHECKPOINT	17	0.727178	2.107629	<0.0001	0.001471
GO NUCLEAR HETEROCHROMATIN	31	0.687675	2.107301	<0.0001	0.001469
GO PROTEIN LOCALIZATION TO CHROMOSOME	37	0.676805	2.104992	<0.0001	0.001513
GO REGULATION OF DNA RECOMBINATION	53	0.586606	2.102456	<0.0001	0.001559
GO NUCLEAR LOCALIZATION SEQUENCE BINDING	20	0.778758	2.101085	<0.0001	0.001565
GO HISTONE METHYLTRANSFERASE COMPLEX	64	0.603817	2.100345	<0.0001	0.001575
GO SIGNAL SEQUENCE BINDING	36	0.642677	2.098635	<0.0001	0.001619
GO MICROTUBULE ORGANIZING CENTER PART	133	0.54475	2.097315	<0.0001	0.001661
GO PROTEIN PHOSPHATASE 2A BINDING	27	0.642852	2.095832	<0.0001	0.001712
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	32	0.64283	2.092268	<0.0001	0.001775
GO BASE EXCISION REPAIR	39	0.627767	2.091925	0.001996	0.00178
GO NEGATIVE REGULATION OF DNA METABOLIC PROCESS	104	0.528153	2.090345	<0.0001	0.001834
GO NUCLEAR UBIQUITIN LIGASE COMPLEX	39	0.622718	2.089995	<0.0001	0.001828
GO CYTOPLASMIC MICROTUBULE	51	0.531455	2.086745	<0.0001	0.001903
GO POSITIVE REGULATION OF CHROMOSOME ORGANIZATION	141	0.499468	2.086528	<0.0001	0.001908
GO DNA REPLICATION INDEPENDENT NUCLEOSOME ORGANIZATION	47	0.739084	2.086273	0.002008	0.001911
GO RNA HELICASE ACTIVITY	67	0.62087	2.085402	<0.0001	0.00193
GO G1 DNA DAMAGE CHECKPOINT	68	0.543067	2.084571	<0.0001	0.001952
GO POSITIVE REGULATION OF CYTOKINESIS	28	0.667476	2.082158	<0.0001	0.002019
GO HISTONE MRNA METABOLIC PROCESS	28	0.699677	2.082111	<0.0001	0.002009
GO NUCLEAR BODY	334	0.472133	2.08111	<0.0001	0.002023
GO MICROTUBULE PLUS END	16	0.782717	2.07877	<0.0001	0.002096
GO NCRNA TRANSCRIPTION	80	0.569304	2.078149	<0.0001	0.002117
GO DNA POLYMERASE ACTIVITY	33	0.641351	2.07579	<0.0001	0.002182
GO NUCLEAR ENVELOPE	381	0.440081	2.073704	<0.0001	0.002246
GO NUCLEIC ACID PHOSPHODIESTER BOND HYDROLYSIS	230	0.49755	2.072707	<0.0001	0.002301
GO CELLULAR RESPONSE TO GAMMA RADIATION	19	0.680358	2.067889	0.001992	0.002425
GO CENTROMERE COMPLEX ASSEMBLY	42	0.782528	2.066985	<0.0001	0.002442
GO POSITIVE REGULATION OF DNA REPLICATION	84	0.520644	2.063836	<0.0001	0.002582
GO RETROGRADE VESICLE MEDIATED TRANSPORT GOLGI TO ER	75	0.57885	2.063153	<0.0001	0.002592
GO ESTABLISHMENT OF MITOTIC SPINDLE LOCALIZATION	23	0.684882	2.062194	<0.0001	0.0026
GO REGULATION OF MRNA METABOLIC PROCESS	113	0.55388	2.060332	<0.0001	0.00265
GO METHYLTRANSFERASE COMPLEX	83	0.606673	2.059736	<0.0001	0.002666
GO DNA PACKAGING	168	0.634984	2.05899	0.001961	0.002673
GO CHROMATIN MODIFICATION	490	0.479084	2.056361	<0.0001	0.002761

GO CENTRIOLE	91	0.564999	2.054757	0.002041	0.002819
GO NUCLEAR MEMBRANE	254	0.438168	2.05342	<0.0001	0.002857
GO RNA SPLICING VIA TRANSESTERIFICATION REACTIONS	259	0.567014	2.052311	<0.0001	0.002909
GO POSTREPLICATION REPAIR	48	0.620328	2.051865	<0.0001	0.002909
GO TERMINATION OF RNA POLYMERASE II TRANSCRIPTION	61	0.633137	2.051615	<0.0001	0.002905
GO CATALYTIC STEP 2 SPLICEOSOME	84	0.63399	2.051142	<0.0001	0.002907
GO MRNA CLEAVAGE FACTOR COMPLEX	17	0.759932	2.050455	<0.0001	0.002926
GO NUCLEOTIDE EXCISION REPAIR DNA GAP FILLING	24	0.721295	2.048837	0.002016	0.00297
GO PROTEIN DEPOLYMERIZATION	23	0.662483	2.048375	<0.0001	0.002984
GO HSP70 PROTEIN BINDING	28	0.621915	2.048138	<0.0001	0.002978
GO MISMATCH REPAIR	26	0.699113	2.048065	<0.0001	0.002965
GO DEOXYRIBONUCLEASE ACTIVITY	63	0.572157	2.047669	<0.0001	0.002966
GO POSITIVE REGULATION OF CELL DIVISION	117	0.501527	2.046629	<0.0001	0.002968
GO REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	134	0.491593	2.046034	<0.0001	0.003002
GO CELLULAR RESPONSE TO IONIZING RADIATION	50	0.559121	2.044637	<0.0001	0.003043
GO REGULATION OF CYTOSKELETON ORGANIZATION	470	0.423661	2.044242	<0.0001	0.003037
GO CHROMOSOME ORGANIZATION INVOLVED IN MEIOTIC CELL CYCLE	40	0.604767	2.043671	0.002123	0.00303
GO ISOTYPE SWITCHING	16	0.702461	2.041907	<0.0001	0.003121
GO FOUR WAY JUNCTION DNA BINDING	15	0.808127	2.041414	<0.0001	0.003128
GO NUCLEAR CHROMOSOME TELOMERIC REGION	122	0.612332	2.040933	<0.0001	0.003121
GO DNA REPAIR COMPLEX	37	0.619853	2.040891	<0.0001	0.003108
GO CHROMATIN BINDING	408	0.47666	2.039593	<0.0001	0.003159
GO DNA TEMPLATED TRANSCRIPTION TERMINATION	97	0.598075	2.037204	<0.0001	0.003256
GO NUCLEASE ACTIVITY	185	0.477699	2.03691	<0.0001	0.003255
GO CELL DIVISION SITE	47	0.577241	2.028183	<0.0001	0.003674
GO ENDODEOXYRIBONUCLEASE ACTIVITY	48	0.587723	2.025692	<0.0001	0.003753
GO NEGATIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	23	0.62163	2.024815	<0.0001	0.003793
GO MRNA PROCESSING	405	0.523069	2.02164	<0.0001	0.003954
GO RNA SPLICING	347	0.54014	2.01721	<0.0001	0.004176
GO STRUCTURE SPECIFIC DNA BINDING	114	0.522247	2.014924	<0.0001	0.0043
GO DNA DAMAGE RESPONSE DETECTION OF DNA DAMAGE	36	0.693493	2.012533	<0.0001	0.004419
GO NUCLEOCYTOPLASMIC TRANSPORTER ACTIVITY	23	0.745203	2.010531	<0.0001	0.004553
GO PROTEIN LOCALIZATION TO CENTROSOME	15	0.708968	2.008624	<0.0001	0.004699
GO MRNA CIS SPLICING VIA SPLICEOSOME	18	0.731885	2.008383	<0.0001	0.004705
GO POSITIVE REGULATION OF NUCLEAR DIVISION	57	0.540259	2.008326	<0.0001	0.004692
GO POSITIVE REGULATION OF CELL CYCLE	79	0.495278	2.007417	<0.0001	0.004712

ARREST					
GO NUCLEOBASE BIOSYNTHETIC PROCESS	17	0.780294	2.006151	<0.0001	0.004778
GO NEGATIVE REGULATION OF CHROMATIN MODIFICATION	44	0.582162	2.005816	0.002096	0.004798
GO SEX CHROMOSOME	27	0.679758	2.00037	<0.0001	0.005153
GO CELLULAR RESPONSE TO HEAT	33	0.593175	1.994971	<0.0001	0.005475
GO SNRNA PROCESSING	20	0.699159	1.993753	<0.0001	0.005532
GO CENTROSOME DUPLICATION	31	0.6538	1.992964	0.002024	0.005555
GO SPLICEOSOMAL COMPLEX	162	0.567743	1.992657	<0.0001	0.005551
GO UBIQUITIN LIKE PROTEIN BINDING	113	0.490234	1.991558	<0.0001	0.005579
GO REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	93	0.474244	1.990771	<0.0001	0.0056
GO DOUBLE STRANDED RNA BINDING	59	0.565659	1.989945	<0.0001	0.005644
GO REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	140	0.455297	1.986695	<0.0001	0.005874
GO CAJAL BODY	49	0.587838	1.985149	<0.0001	0.005961
GO HISTONE EXCHANGE	46	0.73396	1.984435	0.002058	0.005966
GO PROTEIN K63 LINKED UBIQUITINATION	34	0.57288	1.98191	<0.0001	0.006134
GO GAMMA TUBULIN COMPLEX	19	0.669204	1.981785	0.002096	0.006125
GO CYCLIN DEPENDENT PROTEIN KINASE HOLOENZYME COMPLEX	30	0.594797	1.979752	<0.0001	0.006273
GO REGULATION OF GLUCOSE TRANSPORT	93	0.493705	1.975881	<0.0001	0.006485
GO REGULATION OF UBIQUITIN PROTEIN LIGASE ACTIVITY	17	0.669785	1.973125	0.002049	0.006683
GO REGULATION OF CELL CYCLE CHECKPOINT	27	0.650903	1.973067	0.00404	0.006662
GO RRNA TRANSCRIPTION	17	0.690885	1.972289	<0.0001	0.006711
GO DNA LIGATION	16	0.723128	1.971955	<0.0001	0.006713
GO EXONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	40	0.579127	1.971129	<0.0001	0.006778
GO NEGATIVE REGULATION OF PROTEIN CATABOLIC PROCESS	103	0.452858	1.969879	<0.0001	0.006834
GO MICROTUBULE MOTOR ACTIVITY	75	0.589855	1.96985	<0.0001	0.006813
GO DNA TEMPLATED TRANSCRIPTION ELONGATION	86	0.56271	1.968954	0.002008	0.006848
GO POLY PYRIMIDINE TRACT BINDING	17	0.728195	1.968503	<0.0001	0.006856
GO TRANSLESION SYNTHESIS	36	0.596081	1.967985	<0.0001	0.006861
GO NEGATIVE REGULATION OF DNA DEPENDENT DNA REPLICATION	15	0.773595	1.967123	<0.0001	0.006899
GO CHROMATIN	407	0.486591	1.963476	0.00202	0.007223
GO NEGATIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	134	0.546519	1.963432	<0.0001	0.007197
GO SNRNA METABOLIC PROCESS	74	0.556635	1.962609	<0.0001	0.00725
GO RIBONUCLEOPROTEIN COMPLEX BINDING	89	0.531998	1.961532	0.002041	0.007342
GO HOMOLOGOUS CHROMOSOME SEGREGATION	37	0.594856	1.956747	0.002183	0.007777
GO REGULATION OF PROTEIN EXPORT FROM NUCLEUS	33	0.547334	1.956635	<0.0001	0.007768

GO REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	173	0.45571	1.954466	<0.0001	0.007994
GO RNA SECONDARY STRUCTURE UNWINDING	40	0.601168	1.95406	<0.0001	0.008009
GO EUCHROMATIN	30	0.599649	1.953466	0.00202	0.008065
GO SYNAPTONEMAL COMPLEX	31	0.601978	1.953426	0.002101	0.008044
GO TRANSFERASE COMPLEX TRANSFERRING PHOSPHORUS CONTAINING GROUPS	230	0.452708	1.95308	<0.0001	0.008048
GO DAMAGED DNA BINDING	62	0.558051	1.952278	0.004184	0.008097
GO NUCLEAR TRANSCRIPTION FACTOR COMPLEX	125	0.465011	1.946358	<0.0001	0.008652
GO SWI SNF SUPERFAMILY TYPE COMPLEX	71	0.556771	1.941781	<0.0001	0.009093
GO PML BODY	93	0.46955	1.941196	<0.0001	0.00912
GO PROTEIN IMPORT	150	0.440816	1.939846	<0.0001	0.009263
GO TELOMERE ORGANIZATION	101	0.599753	1.935023	<0.0001	0.009839
GO NUCLEOLAR PART	59	0.636255	1.933081	0.005906	0.010053
GO MATURATION OF 5 8S RRNA FROM TRICISTRONIC RRNA TRANSCRIPT SSU RRNA 5 8S RRNA LSU RRNA	19	0.728647	1.930914	<0.0001	0.010265
GO PROTEIN K11 LINKED UBIQUITINATION	26	0.658576	1.930709	<0.0001	0.010279
GO NUCLEOTIDYLTRANSFERASE ACTIVITY	123	0.482525	1.929282	<0.0001	0.010438
GO TRNA METABOLIC PROCESS	166	0.557165	1.928585	0.007984	0.010474
GO REGULATION OF CELL CYCLE ARREST	100	0.461459	1.927339	<0.0001	0.010648
GO SMALL SUBUNIT PROCESSOME	32	0.681872	1.927079	0.006073	0.01063
GO NEGATIVE REGULATION OF DNA RECOMBINATION	15	0.692229	1.925733	0.006085	0.010748
GO NUCLEOBASE METABOLIC PROCESS	37	0.582812	1.921916	<0.0001	0.011306
GO RNA PHOSPHODIESTER BOND HYDROLYSIS	107	0.496908	1.920012	<0.0001	0.011547
GO MALE MEIOSIS I	15	0.67099	1.917993	0.002066	0.011816
GO 90S PRERIBOSOME	23	0.723413	1.917468	0.005976	0.011842
GO REGULATION OF TELOMERASE ACTIVITY	41	0.519909	1.915489	<0.0001	0.012009
GO REGULATION OF MRNA SPLICING VIA SPLICEOSOME	60	0.572947	1.914435	<0.0001	0.012097
GO MALE MEIOSIS	34	0.586112	1.914209	0.002137	0.012097
GO SITE OF DOUBLE STRAND BREAK	28	0.619545	1.913298	<0.0001	0.012214
GO MRNA BINDING	143	0.483458	1.910893	0.006073	0.012482
GO BLASTOCYST DEVELOPMENT	58	0.534723	1.908463	<0.0001	0.012829
GO POSITIVE REGULATION OF MRNA METABOLIC PROCESS	42	0.559521	1.906602	<0.0001	0.013045
GO TELOMERASE HOLOENZYME COMPLEX	19	0.682356	1.906222	<0.0001	0.013053
GO NON RECOMBINATIONAL REPAIR	65	0.588037	1.906148	<0.0001	0.013021
GO POSITIVE REGULATION OF MRNA PROCESSING	30	0.590228	1.902495	<0.0001	0.013507
GO NUCLEOSOME BINDING	44	0.589376	1.902061	<0.0001	0.0135
GO KINESIN BINDING	30	0.590016	1.899891	0.00432	0.013753
GO MLL1 2 COMPLEX	26	0.634347	1.897575	0.006122	0.014027
GO REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	266	0.448642	1.896672	<0.0001	0.014127
GO REGULATION OF TELOMERASE RNA	15	0.824613	1.895117	0.001984	0.014293

LOCALIZATION TO CAJAL BODY					
GO SINGLE STRANDED RNA BINDING	63	0.503819	1.893925	0.004274	0.014495
GO CENTRIOLE ASSEMBLY	18	0.713908	1.89333	0.006276	0.014529
GO CELLULAR RESPONSE TO RADIATION	130	0.435298	1.893117	<0.0001	0.014522
GO ANAPHASE PROMOTING COMPLEX DEPENDENT CATABOLIC PROCESS	75	0.676796	1.887743	<0.0001	0.015268
GO UBIQUITIN LIKE PROTEIN CONJUGATING ENZYME ACTIVITY	29	0.637061	1.883956	0.002066	0.015849
GO INTERCELLULAR BRIDGE	40	0.52002	1.883849	0.006098	0.015824
GO ENDONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	34	0.610515	1.882334	<0.0001	0.016016
GO COVALENT CHROMATIN MODIFICATION	309	0.444392	1.877049	0.002128	0.016903
GO TRANSCRIPTION ELONGATION FROM RNA POLYMERASE II PROMOTER	71	0.543671	1.876523	0.002012	0.016928
GO NUCLEAR SPECK	188	0.455373	1.875969	0.002053	0.016944
GO RNA POLYMERASE II CARBOXY TERMINAL DOMAIN KINASE ACTIVITY	16	0.674287	1.875679	0.007937	0.016943
GO NLS BEARING PROTEIN IMPORT INTO NUCLEUS	22	0.668471	1.873533	0.002066	0.017281
GO ENDORIBONUCLEASE ACTIVITY PRODUCING 5 PHOSPHOMONOESTERS	26	0.655121	1.870329	0.002033	0.017814
GO CORE PROMOTER BINDING	146	0.441218	1.86935	<0.0001	0.017943
GO PORE COMPLEX ASSEMBLY	15	0.735202	1.869193	<0.0001	0.017928
GO REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	262	0.436465	1.864555	0.002079	0.018815
GO REGULATION OF CELL AGING	32	0.555262	1.864374	0.008282	0.018804
GO NUCLEAR CYCLIN DEPENDENT PROTEIN KINASE HOLOENZYME COMPLEX	15	0.677438	1.863766	0.004184	0.018844
GO ORGANELLE LOCALIZATION	393	0.386607	1.863514	<0.0001	0.018839
GO BASAL TRANSCRIPTION MACHINERY BINDING	23	0.626006	1.863509	0.004032	0.018784
GO PROTEIN DNA COMPLEX SUBUNIT ORGANIZATION	208	0.534491	1.863119	0.002	0.018799
GO PROTEIN LOCALIZATION TO NUCLEUS	151	0.424184	1.861604	<0.0001	0.019029
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	17	0.67086	1.860122	0.007921	0.019276
GO REGULATION OF RNA STABILITY	135	0.491163	1.857657	0.002083	0.019757
GO ACETYLTRANSFERASE COMPLEX	84	0.505237	1.856431	0.002212	0.019944
GO CELL DIFFERENTIATION INVOLVED IN EMBRYONIC PLACENTA DEVELOPMENT	25	0.609406	1.856358	0.004292	0.019904
GO TRANSCRIPTION ELONGATION FACTOR COMPLEX	36	0.547939	1.854068	0.00404	0.020289
GO SPERMATID NUCLEUS DIFFERENTIATION	15	0.648862	1.851105	<0.0001	0.020858
GO POSITIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	18	0.616072	1.850314	0.004008	0.020957
GO DNA DOUBLE STRAND BREAK PROCESSING	19	0.646722	1.847508	0.010225	0.021506
GO LAMIN BINDING	17	0.574237	1.841921	0.004175	0.022699
GO PROTEIN MONOUBIQUITINATION	49	0.541169	1.841176	0.004301	0.022778

GO IMMUNOGLOBULIN PRODUCTION	40	0.540793	1.840476	0.004082	0.022911
GO ENDONUCLEASE ACTIVITY	115	0.451229	1.838041	<0.0001	0.023445
GO MRNA CLEAVAGE	17	0.644799	1.838017	0.00823	0.02338
GO HISTONE BINDING	164	0.501355	1.837831	0.00404	0.023367
GO SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	120	0.420295	1.83697	<0.0001	0.023498
GO MOTOR ACTIVITY	128	0.461552	1.83641	<0.0001	0.023563
GO REGULATION OF SPINDLE ORGANIZATION	19	0.638296	1.834773	<0.0001	0.023848
GO OXIDOREDUCTASE ACTIVITY ACTING ON THE CH NH GROUP OF DONORS NAD OR NADP AS ACCEPTOR	16	0.605585	1.833589	0.004008	0.024072
GO RESPONSE TO X RAY	30	0.577522	1.83339	0.002028	0.024053
GO SAGA TYPE COMPLEX	30	0.565796	1.831048	0.00641	0.024511
GO GENE SILENCING BY RNA	128	0.520093	1.828089	0.004057	0.025175
GO MITOCHONDRIAL RNA METABOLIC PROCESS	23	0.641993	1.825639	0.007968	0.025692
GO CEREBRAL CORTEX DEVELOPMENT	103	0.457922	1.8217	<0.0001	0.02664
GO RNA STABILIZATION	29	0.579155	1.820595	0.00818	0.026827
GO CLEAVAGE INVOLVED IN RRNA PROCESSING	19	0.689687	1.818022	0.004107	0.027386
GO RESPONSE TO RADIATION	387	0.362234	1.817479	<0.0001	0.027487
GO CELL AGING	66	0.454905	1.817015	<0.0001	0.02752
GO HISTONE DEACETYLASE BINDING	102	0.439297	1.815694	0.01002	0.027726
GO RESPONSE TO HEAT	85	0.441508	1.814727	<0.0001	0.027903
GO REGULATION OF MITOPHAGY	40	0.482817	1.810389	<0.0001	0.029025
GO CHROMATIN ASSEMBLY OR DISASSEMBLY	155	0.566448	1.808385	0.012	0.029564
GO TELOMERIC DNA BINDING	28	0.595841	1.806751	0.008264	0.030012
GO RESPONSE TO UV	119	0.418879	1.806737	<0.0001	0.029938
GO NUCLEOSOMAL DNA BINDING	29	0.614415	1.806138	0.010204	0.030008
GO FOLIC ACID CONTAINING COMPOUND METABOLIC PROCESS	27	0.582835	1.805726	0.004237	0.030052
GO NEGATIVE REGULATION OF CELL AGING	16	0.632737	1.804551	0.008368	0.030292
GO INO80 TYPE COMPLEX	21	0.60723	1.804072	0.002066	0.030324
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE	26	0.58631	1.804044	0.009921	0.030251
GO PRERIBOSOME	58	0.627094	1.803694	0.012295	0.030266
GO REGULATION OF PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	101	0.537812	1.802484	0.00409	0.030526
GO ESTABLISHMENT OF SPINDLE ORIENTATION	24	0.588106	1.798344	0.01004	0.031628
GO OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN 2 OXOGLUTARATE AS ONE DONOR AND INCORPORATION OF ONE ATOM EACH OF OXYGEN INTO BOTH DONORS	38	0.518082	1.79786	0.006237	0.031682
GO NEGATIVE REGULATION OF GENE SILENCING	18	0.586601	1.796649	0.004175	0.031979
GO POSITIVE REGULATION OF TELOMERASE	27	0.527978	1.795541	0.009804	0.032224

ACTIVITY					
GO RNA POLYMERASE COMPLEX	118	0.486551	1.794492	0.006186	0.032466
GO ESC E Z COMPLEX	16	0.678413	1.7924	0.008658	0.033015
GO POSTTRANSCRIPTIONAL REGULATION OF GENE EXPRESSION	417	0.410785	1.79141	0.004184	0.033214
GO PROTEIN PHOSPHATASE BINDING	117	0.407577	1.791014	0.002062	0.033223
GO POSITIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	28	0.546467	1.789346	0.004219	0.033686
GO POSITIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	58	0.469998	1.78797	<0.0001	0.03402
GO RNA POLYMERASE CORE ENZYME BINDING	19	0.612397	1.787954	0.004032	0.033939
GO REGULATION OF LIGASE ACTIVITY	126	0.521045	1.787589	0.00616	0.033958
GO MATURATION OF 5 8S RRNA	28	0.642094	1.787453	0.022449	0.033928
GO GLUCOSYLTRANSFERASE ACTIVITY	16	0.654954	1.787037	0.012024	0.033978
GO PROTEASOMAL PROTEIN CATABOLIC PROCESS	263	0.433438	1.78677	0.002101	0.033963
GO PROTEIN C TERMINUS BINDING	182	0.379622	1.786564	0.002075	0.033959
GO PROTEIN POLYUBIQUITINATION	234	0.423322	1.783803	<0.0001	0.03473
GO PALLIUM DEVELOPMENT	148	0.431592	1.783653	0.002066	0.03469
GO REGULATION OF CHROMATIN ORGANIZATION	146	0.418252	1.783644	0.004167	0.034611
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	23	0.59403	1.783627	0.005988	0.034529
GO XY BODY	15	0.653156	1.783359	0.006098	0.034553
GO TRNA BINDING	43	0.569248	1.783061	0.008163	0.034565
GO CELLULAR COMPONENT DISASSEMBLY	488	0.388554	1.782927	0.004124	0.034512
GO AMINO ACID ACTIVATION	51	0.594877	1.782845	0.02	0.034437
GO LIGASE ACTIVITY FORMING CARBON OXYGEN BONDS	44	0.593745	1.777014	0.013944	0.036248
GO NEGATIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	92	0.423099	1.776326	0.002004	0.036369
GO APOPTOTIC NUCLEAR CHANGES	24	0.553531	1.776237	0.006329	0.036327
GO POSITIVE REGULATION OF NEURON DEATH	66	0.451662	1.776029	0.001961	0.036288
GO REGULATION OF RETINOIC ACID RECEPTOR SIGNALING PATHWAY	16	0.593088	1.775504	0.002012	0.03636
GO REGULATION OF HISTONE METHYLATION	51	0.523337	1.774247	0.006073	0.036703
GO GENE SILENCING	183	0.487875	1.773266	0.01626	0.036947
GO POSITIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	185	0.444973	1.772933	0.006224	0.036959
GO PROTEASOME BINDING	16	0.644995	1.770949	0.010163	0.037481
GO POSITIVE REGULATION OF HISTONE METHYLATION	29	0.554896	1.770422	0.004124	0.037589
GO PROTEIN SERINE THREONINE KINASE ACTIVITY	425	0.366917	1.768459	<0.0001	0.038122
GO PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	28	0.514191	1.768199	0.001965	0.038114
GO AXON CYTOPLASM	29	0.539711	1.766658	0.008351	0.038521
GO N ACETYLTRANSFERASE ACTIVITY	76	0.463594	1.765644	0.004211	0.038768

GO 3 5 EXONUCLEASE ACTIVITY	44	0.495949	1.76459	0.004292	0.03904
GO PEPTIDYL SERINE MODIFICATION	146	0.395281	1.7628	<0.0001	0.039583
GO TRNA PROCESSING	106	0.516662	1.762798	0.021696	0.039491
GO REGULATION OF PROTEIN CATABOLIC PROCESS	376	0.381468	1.762529	<0.0001	0.039483
GO NEGATIVE REGULATION OF MRNA METABOLIC PROCESS	34	0.558685	1.759989	0.004098	0.040275
GO REGULATION OF CELLULAR SENESCENCE	26	0.55267	1.759684	0.008421	0.040303
GO PEPTIDE N ACETYLTRANSFERASE ACTIVITY	58	0.493388	1.756889	0.010526	0.041229
GO LIGASE ACTIVITY FORMING CARBON NITROGEN BONDS	52	0.499128	1.755615	0.004149	0.041599
GO REGULATION OF GENE EXPRESSION EPIGENETIC	202	0.468252	1.754901	0.016032	0.041745
GO NUCLEAR CHROMATIN	275	0.439152	1.753116	0.006098	0.042304
GO OOCYTE MATURATION	17	0.576679	1.751095	0.006383	0.043038
GO NUCLEAR TRANSCRIPTIONAL REPRESSOR COMPLEX	22	0.605594	1.750897	0.012579	0.043017
GO POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	185	0.429115	1.74917	0.004073	0.043564
GO LIGAND DEPENDENT NUCLEAR RECEPTOR TRANSCRIPTION COACTIVATOR ACTIVITY	51	0.468999	1.748208	0.012474	0.043829
GO CHD TYPE COMPLEX	17	0.641239	1.747277	0.020121	0.044087
GO RNA PHOSPHODIESTER BOND HYDROLYSIS ENDONUCLEOLYTIC	54	0.500068	1.746873	0.012245	0.04412
GO NUCLEOID	39	0.607604	1.74565	0.014199	0.04443
GO NEGATIVE REGULATION OF HISTONE MODIFICATION	35	0.519433	1.745242	0.019068	0.044504
GO LIGASE ACTIVITY	375	0.380547	1.744227	0.002114	0.044762
GO N ACYLTRANSFERASE ACTIVITY	92	0.437785	1.74394	0.004264	0.044782
GO RNA POLYMERASE II CORE BINDING	15	0.64141	1.743722	0.006061	0.044753
GO REGULATION OF HISTONE H3 K9 METHYLATION	17	0.641086	1.742544	0.01217	0.045101
GO REGULATION OF RNA SPLICING	92	0.469625	1.741095	<0.0001	0.045511
GO RNA POLYMERASE II TRANSCRIPTION FACTOR COMPLEX	100	0.430705	1.740693	0.00202	0.045565
GO PROTEASOME COMPLEX	73	0.585858	1.738807	0.020576	0.046183
GO REGULATION OF GENE SILENCING	50	0.552785	1.735845	0.01417	0.047258
GO ACETYLTRANSFERASE ACTIVITY	92	0.439301	1.73524	0.00431	0.047439
GO DESMOSOME	26	0.62161	1.733601	0.021097	0.047943
GO REGULATION OF PROTEIN PHOSPHATASE TYPE 2A ACTIVITY	23	0.546366	1.732707	0.012024	0.048198
GO MICROTUBULE BASED MOVEMENT	192	0.439082	1.729608	0.01417	0.049259
GO SMALL NUCLEOLAR RIBONUCLEOPROTEIN COMPLEX	18	0.698941	1.728988	0.014113	0.04941
GO CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	34	0.483041	1.728626	0.008114	0.049473
GO PERICENTRIOLAR MATERIAL	18	0.611819	1.727773	0.018711	0.049741
GO DEMETHYLATION	51	0.462979	1.726086	0.001934	0.050309
GO PYRIMIDINE NUCLEOBASE METABOLIC	19	0.559585	1.725858	0.00823	0.05029

PROCESS					
GO POSITIVE REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	36	0.518121	1.725565	0.004008	0.050312
GO POSITIVE REGULATION OF VIRAL GENOME REPLICATION	29	0.508976	1.724485	0.010846	0.050629
GO PCG PROTEIN COMPLEX	43	0.513687	1.722924	0.011062	0.051207
GO CELL PROJECTION CYTOPLASM	48	0.455185	1.72224	0.004158	0.051405
GO TRNA MODIFICATION	53	0.544739	1.721648	0.022541	0.051521
GO RNA POLYMERASE II DISTAL ENHANCER SEQUENCE SPECIFIC DNA BINDING	61	0.453857	1.721296	0.015123	0.051577
GO NUCLEAR EUCHROMATIN	23	0.549064	1.721216	0.004032	0.051501
GO POLY PURINE TRACT BINDING	18	0.636183	1.721203	0.014523	0.051401
GO POSITIVE REGULATION OF LIGASE ACTIVITY	106	0.529908	1.72118	0.014433	0.051302
GO TRNA METHYLATION	20	0.5976	1.721026	0.012097	0.051267
GO POSITIVE REGULATION OF DNA REPAIR	33	0.529551	1.718758	0.012097	0.052204
GO POSITIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	335	0.343776	1.7183	<0.0001	0.052305
GO HISTONE UBIQUITINATION	34	0.536641	1.716497	0.02454	0.053043
GO CELLULAR PROTEIN COMPLEX LOCALIZATION	21	0.547553	1.716102	0.00616	0.053124
GO HSP90 PROTEIN BINDING	27	0.483502	1.714929	0.01	0.053479
GO ERROR FREE TRANSLESION SYNTHESIS	17	0.654881	1.714768	0.016162	0.053445
GO SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX	59	0.53413	1.711769	0.023013	0.054703
GO PEPTIDYL THREONINE MODIFICATION	44	0.485037	1.709942	0.01378	0.055399
GO REGULATION OF PROTEIN INSERTION INTO MITOCHONDRIAL MEMBRANE INVOLVED IN APOPTOTIC SIGNALING PATHWAY	29	0.52647	1.707634	0.002033	0.056352
GO POSITIVE REGULATION OF NEURON APOPTOTIC PROCESS	46	0.455744	1.705892	0.007968	0.056966
GO REGULATION OF DNA METHYLATION	15	0.640389	1.705703	0.020408	0.056946
GO UBIQUITIN LIKE PROTEIN LIGASE BINDING	255	0.370035	1.705372	<0.0001	0.056998
GO NUCLEOTIDE EXCISION REPAIR DNA INCISION	39	0.541769	1.705138	0.006211	0.056991
GO EXECUTION PHASE OF APOPTOSIS	53	0.436349	1.703735	0.002128	0.057491
GO ANDROGEN RECEPTOR SIGNALING PATHWAY	40	0.517774	1.702676	0.017204	0.057906
GO PROTEIN ACETYLATION	112	0.41814	1.701586	0.016771	0.058254
GO AXO DENDRITIC TRANSPORT	33	0.501757	1.699614	0.010352	0.059083
GO HISTONE MONOUBIQUITINATION	23	0.577518	1.698593	0.026915	0.059478
GO CARBOXY TERMINAL DOMAIN PROTEIN KINASE COMPLEX	22	0.589622	1.698421	0.01992	0.05944
GO NEGATIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	30	0.502541	1.698411	0.00789	0.059324
GO REGULATION OF CELL MATURATION	18	0.558616	1.697853	0.015238	0.059455
GO PROTEIN MODIFICATION BY SMALL	107	0.429823	1.695193	0.017131	0.060638

PROTEIN REMOVAL					
GO PROTEIN TRANSPORTER ACTIVITY	96	0.435064	1.695106	0.006237	0.060559
GO CELLULAR COMPONENT DISASSEMBLY INVOLVED IN EXECUTION PHASE OF APOPTOSIS	41	0.465221	1.694488	0.002165	0.060788
GO RIBOSOME BINDING	43	0.484631	1.693543	0.02459	0.061139
GO SPLICEOSOMAL COMPLEX ASSEMBLY	52	0.531451	1.693248	0.023158	0.061169
GO RESPONSE TO PLATELET DERIVED GROWTH FACTOR	18	0.606853	1.692001	0.016427	0.061609
GO ENDORIBONUCLEASE ACTIVITY	45	0.476362	1.690794	0.01	0.062075
GO REGULATION OF TRANSLATIONAL INITIATION	79	0.470238	1.690304	0.02449	0.062154
GO HISTONE DEMETHYLASE ACTIVITY	23	0.627776	1.688996	0.026694	0.062713
GO DSRNA FRAGMENTATION	18	0.616727	1.68815	0.015695	0.063039
GO REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	321	0.374259	1.688124	0.010373	0.062919
GO FOLIC ACID METABOLIC PROCESS	17	0.57794	1.686295	0.020921	0.063706
GO PURINE NUCLEOBASE METABOLIC PROCESS	19	0.601447	1.685386	0.025532	0.064043
GO RNA MODIFICATION	106	0.461232	1.685052	0.025896	0.064075
GO ORGAN REGENERATION	82	0.410953	1.683537	0.005894	0.064742
GO POSITIVE REGULATION OF G1 S TRANSITION OF MITOTIC CELL CYCLE	24	0.52668	1.681583	0.004202	0.065653
GO TRANSCRIPTIONALLY ACTIVE CHROMATIN	16	0.569552	1.679862	0.008197	0.066387
GO NCRNA METABOLIC PROCESS	499	0.484679	1.679413	0.040323	0.066456
GO METHYL CPG BINDING	15	0.600475	1.677749	0.022869	0.067204
GO FEMALE GAMETE GENERATION	84	0.387163	1.677052	0.002088	0.067427
GO NEGATIVE REGULATION OF MRNA SPLICING VIA SPLICEOSOME	19	0.624996	1.67607	0.012474	0.067807
GO NUCLEOTIDE EXCISION REPAIR	111	0.461951	1.674103	0.012526	0.068732
GO MAGNESIUM ION BINDING	188	0.353884	1.673683	0.002123	0.068856
GO NEURAL PRECURSOR CELL PROLIFERATION	70	0.448762	1.67129	0.011976	0.070025
GO POSITIVE REGULATION OF CHROMATIN MODIFICATION	81	0.418499	1.670909	0.010204	0.070124
GO PROTEASOME ACCESSORY COMPLEX	23	0.695905	1.668222	0.018443	0.071382
GO CELLULAR RESPONSE TO ESTRADIOL STIMULUS	28	0.513131	1.667228	0.014463	0.071785
GO NEGATIVE REGULATION OF CELLULAR CATABOLIC PROCESS	148	0.364522	1.666522	<0.0001	0.072023
GO MITOCHONDRIAL MEMBRANE ORGANIZATION	90	0.449344	1.664287	0.01992	0.073054
GO MATURATION OF SSU RRNA	40	0.596838	1.658933	0.030738	0.075963
GO NEGATIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	49	0.423146	1.658304	0.008114	0.076166
GO DNA DIRECTED RNA POLYMERASE II HOLOENZYME	93	0.448119	1.6575	0.024341	0.076492
GO DNA METHYLATION OR DEMETHYLATION	56	0.455769	1.654925	0.022917	0.077783
GO ESTABLISHMENT OF MITOTIC SPINDLE ORIENTATION	19	0.562116	1.653455	0.018182	0.078422
GO CELLULAR RESPONSE TO UV	65	0.41634	1.653069	0.016194	0.07848

GO DNA BINDING BENDING	19	0.556546	1.651186	0.01165	0.079509
GO CELLULAR RESPONSE TO ESTROGEN STIMULUS	38	0.451561	1.6502	0.016393	0.079957
GO REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	42	0.479111	1.649638	0.011742	0.080119
GO UBIQUITIN LIKE PROTEIN LIGASE ACTIVITY	188	0.37851	1.649326	0.006237	0.080181
GO ADP BINDING	31	0.476247	1.648984	0.016495	0.080228
GO INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY	66	0.438883	1.648802	0.008386	0.080198
GO CELLULAR RESPONSE TO ALCOHOL	110	0.400376	1.64835	0.004149	0.080303
GO MRNA 3 UTR BINDING	47	0.483866	1.648043	0.035714	0.080331
GO POSITIVE REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	126	0.377586	1.647785	0.002088	0.080345
GO TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	38	0.493837	1.647501	0.016949	0.080366
GO RNA POLYMERASE ACTIVITY	43	0.51065	1.645742	0.024096	0.08121
GO CHROMATIN DNA BINDING	76	0.437382	1.645688	0.015936	0.081116
GO ALPHA AMINO ACID BIOSYNTHETIC PROCESS	73	0.452561	1.643778	0.018634	0.082106
GO UNFOLDED PROTEIN BINDING	89	0.488486	1.642347	0.03681	0.082809
GO CYTOSKELETON DEPENDENT INTRACELLULAR TRANSPORT	109	0.396906	1.642311	0.015873	0.082683
GO CYTOPLASMIC EXOSOME RNASE COMPLEX	15	0.612582	1.642188	0.022869	0.082622
GO EXOSOME RNASE COMPLEX	21	0.566638	1.64166	0.024194	0.082799
GO CHROMATIN DISASSEMBLY	16	0.62584	1.641423	0.034274	0.082792
GO BINDING OF SPERM TO ZONA PELLUCIDA	30	0.519745	1.641179	0.012658	0.082794
GO NEGATIVE REGULATION OF HISTONE METHYLATION	16	0.636391	1.638989	0.026749	0.084067
GO RIBONUCLEOPROTEIN GRANULE	139	0.397476	1.637066	0.013015	0.08509
GO INCLUSION BODY	65	0.404667	1.636662	0.01581	0.08519
GO HYDROLASE ACTIVITY ACTING ON CARBON NITROGEN BUT NOT PEPTIDE BONDS IN CYCLIC AMIDINES	32	0.488636	1.635353	0.03252	0.085831
GO METHYLATED HISTONE BINDING	46	0.482599	1.635293	0.025532	0.085706
GO REGULATION OF MRNA 3 END PROCESSING	26	0.545129	1.633913	0.034908	0.086188
GO NEGATIVE REGULATION OF RNA SPLICING	24	0.575723	1.633337	0.018443	0.086422
GO TOR SIGNALING	16	0.55784	1.632981	0.033195	0.086471
GO ACID AMINO ACID LIGASE ACTIVITY	19	0.524982	1.632263	0.021912	0.086749
GO PROTEIN DEALKYLATION	26	0.546552	1.629428	0.024691	0.08839
GO RNA METHYLATION	45	0.493269	1.629373	0.027833	0.088267
GO TRANSCRIPTION FACTOR COMPLEX	288	0.347448	1.628983	0.008214	0.088328
GO TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	34	0.519463	1.628567	0.034951	0.088448
GO MULTICELLULAR ORGANISM GROWTH	75	0.410357	1.628489	0.019608	0.08835
GO POLYSOME	38	0.519257	1.628345	0.035417	0.088283
GO SIN3 TYPE COMPLEX	16	0.614028	1.627947	0.036403	0.088389
GO SYNAPTONEMAL COMPLEX ORGANIZATION	18	0.5567	1.627094	0.035941	0.088852
GO NCRNA CATABOLIC PROCESS	22	0.53646	1.626228	0.026258	0.089214

GO DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION RESULTING IN TRANSCRIPTION	15	0.552918	1.625246	0.02454	0.089754
GO MITOCHONDRIAL GENOME MAINTENANCE	20	0.516461	1.623295	0.026316	0.090831
GO RNA SPLICING VIA ENDONUCLEOLYTIC CLEAVAGE AND LIGATION	15	0.617744	1.622264	0.029046	0.091297
GO REGULATION OF MAMMARY GLAND EPITHELIAL CELL PROLIFERATION	16	0.55494	1.620239	0.033543	0.09246
GO MICROTUBULE NUCLEATION	18	0.557829	1.618936	0.026694	0.093183
GO REGULATION OF MEMBRANE PERMEABILITY	69	0.430321	1.618074	0.02004	0.093568
GO P53 BINDING	66	0.410499	1.618068	0.015414	0.093408
GO GLUTAMINE METABOLIC PROCESS	22	0.528355	1.61689	0.036325	0.09404
GO RRNA CATABOLIC PROCESS	17	0.555383	1.616809	0.027837	0.093928
GO TRANSCRIPTION FACTOR TFIID COMPLEX	23	0.529721	1.615166	0.033755	0.094843
GO ORGANELLE TRANSPORT ALONG MICROTUBULE	54	0.435048	1.614964	0.016667	0.094823
GO EXON EXON JUNCTION COMPLEX	20	0.564771	1.614485	0.024742	0.095027
GO RESPONSE TO GONADOTROPIN	26	0.504191	1.612787	0.028571	0.095851
GO PROTEIN KINASE C BINDING	47	0.426233	1.61239	0.022495	0.096002
GO WIDE PORE CHANNEL ACTIVITY	22	0.523549	1.612131	0.023305	0.096041
GO NUCLEAR INNER MEMBRANE	45	0.418954	1.610805	0.020534	0.096594
GO HORMONE RECEPTOR BINDING	146	0.363517	1.610159	0.012474	0.096867
GO MODULATION BY VIRUS OF HOST MORPHOLOGY OR PHYSIOLOGY	36	0.463727	1.608897	0.025263	0.097496
GO POLYUBIQUITIN BINDING	38	0.457441	1.608217	0.023061	0.097797
GO REGULATION OF MICROTUBULE POLYMERIZATION	31	0.470797	1.606227	0.014403	0.099032
GO TRANSLATION INITIATION FACTOR BINDING	27	0.516101	1.605989	0.044625	0.098845
GO NITROGEN COMPOUND TRANSPORT	476	0.325319	1.605925	0.00207	0.098733
GO REGULATION OF ALTERNATIVE MRNA SPLICING VIA SPLICEOSOME	34	0.496063	1.604572	0.027368	0.099342
GO ALDITOL METABOLIC PROCESS	18	0.571724	1.603562	0.042596	0.099829
GO SNRNA BINDING	33	0.496187	1.603515	0.047131	0.099689
GO DEMETHYLASE ACTIVITY	31	0.522996	1.603114	0.03373	0.099774
GO PHOSPHATASE BINDING	159	0.347101	1.603099	0.010246	0.099616
GO PROTEIN KINASE COMPLEX	88	0.394083	1.601629	0.019027	0.100446
GO REGULATION OF HISTONE H3 K4 METHYLATION	24	0.537702	1.601139	0.037422	0.100615
GO POSITIVE REGULATION OF RNA SPLICING	22	0.530222	1.600834	0.030928	0.100632
GO OOCYTE DIFFERENTIATION	34	0.456057	1.599409	0.024845	0.101216
GO N TERMINAL PROTEIN AMINO ACID MODIFICATION	24	0.494629	1.598458	0.031042	0.101721
GO PROTEIN ACYLATION	142	0.368566	1.597997	0.021598	0.101865
GO U12 TYPE SPLICEOSOMAL COMPLEX	25	0.577243	1.597785	0.048729	0.101807
GO APOPTOTIC DNA FRAGMENTATION	15	0.548178	1.593512	0.045549	0.104679
GO ANATOMICAL STRUCTURE ARRANGEMENT	17	0.564604	1.593129	0.038855	0.104758
GO PRODUCTION OF MOLECULAR MEDIATOR	57	0.423097	1.592583	0.027778	0.104969

OF IMMUNE RESPONSE					
GO CRANIAL NERVE MORPHOGENESIS	23	0.537322	1.591606	0.041841	0.105475
GO DNA CATABOLIC PROCESS ENDONUCLEOLYTIC	18	0.516798	1.590975	0.036093	0.105704
GO IN UTERO EMBRYONIC DEVELOPMENT	301	0.337014	1.589694	0.004073	0.106405
GO HISTONE H4 ACETYLATION	42	0.455196	1.589017	0.036585	0.106716
GO ADENYLYLTRANSFERASE ACTIVITY	24	0.489131	1.589009	0.044872	0.106545
GO UBIQUITIN LIGASE COMPLEX	247	0.351935	1.58773	0.012397	0.107081
GO POSITIVE REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	95	0.378961	1.586071	0.010246	0.107737
GO POSITIVE REGULATION OF PROTEIN CATABOLIC PROCESS	253	0.360262	1.585804	0.016667	0.107782
GO MACROMOLECULE METHYLATION	171	0.384751	1.58409	0.012712	0.108626
GO ANATOMICAL STRUCTURE HOMEOSTASIS	263	0.334782	1.58334	<0.0001	0.108968
GO ORGANELLE ASSEMBLY	450	0.350489	1.582516	0.01833	0.109373
GO NF KAPPAB BINDING	30	0.47285	1.581748	0.03397	0.10975
GO PYRIMIDINE NUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	17	0.56249	1.581052	0.035417	0.110043
GO RESPONSE TO CAFFEINE	17	0.519854	1.580823	0.037182	0.110045
GO REGULATION OF DNA BINDING	92	0.376367	1.580106	0.01222	0.110373
GO CUL4 RING E3 UBIQUITIN LIGASE COMPLEX	25	0.510485	1.580047	0.033403	0.110227
GO RIBONUCLEASE ACTIVITY	86	0.40584	1.577534	0.045267	0.111907
GO TBP CLASS PROTEIN BINDING	20	0.546808	1.577258	0.029106	0.111764
GO REGULATION OF RECEPTOR BIOSYNTHETIC PROCESS	21	0.498902	1.576915	0.022869	0.111853
GO REGULATION OF MEIOTIC CELL CYCLE	38	0.448704	1.576612	0.020921	0.111895
GO CULLIN RING UBIQUITIN LIGASE COMPLEX	139	0.357735	1.575633	0.012371	0.112436
GO PROTEIN N TERMINUS BINDING	101	0.372243	1.575054	0.016913	0.112537
GO TRNA METHYLTRANSFERASE ACTIVITY	18	0.545286	1.57465	0.045635	0.112684
GO METENCEPHALON DEVELOPMENT	99	0.42598	1.57444	0.016529	0.112655
GO SYMPATHETIC NERVOUS SYSTEM DEVELOPMENT	21	0.540659	1.574432	0.03681	0.112485
GO TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	24	0.499055	1.573398	0.044	0.113164
GO REGULATION OF ANOIKIS	24	0.483519	1.57306	0.029644	0.113207
GO ANTEROGRADE AXONAL TRANSPORT	22	0.502584	1.572573	0.035417	0.113386
GO CYTOPLASMIC STRESS GRANULE	31	0.511792	1.572486	0.043668	0.113283
GO DNA MODIFICATION	76	0.390364	1.572112	0.034137	0.113383
GO REGULATION OF TRANSCRIPTION ELONGATION FROM RNA POLYMERASE II PROMOTER	20	0.514785	1.572043	0.034413	0.113263
GO RNA PHOSPHODIESTER BOND HYDROLYSIS EXONUCLEOLYTIC	33	0.474597	1.568199	0.042373	0.11577
GO GAMETE GENERATION	488	0.316273	1.567451	0.002151	0.11611
GO RNA POLYMERASE BINDING	32	0.468837	1.567138	0.040486	0.116138
GO REGULATION OF GENE EXPRESSION BY GENETIC IMPRINTING	15	0.579103	1.563112	0.040568	0.118865
GO REGULATION OF MYELINATION	29	0.469328	1.560832	0.023762	0.120312
GO OOGENESIS	57	0.394052	1.560476	0.012245	0.120387

GO CELLULAR RESPONSE TO LIGHT STIMULUS	86	0.369324	1.560463	0.012097	0.120219
GO EMBRYONIC PLACENTA DEVELOPMENT	82	0.396865	1.558775	0.024096	0.120835
GO PROTEIN FOLDING	201	0.40299	1.55825	0.047521	0.121085
GO DNA ALKYLATION	42	0.471771	1.556764	0.046025	0.122102
GO NEGATIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	119	0.37952	1.551532	0.015054	0.125722
GO COP9 SIGNALOSOME	31	0.451412	1.551347	0.02988	0.125656
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO ENDOPLASMIC RETICULUM STRESS	28	0.468023	1.54975	0.041096	0.12675
GO CELLULAR SENESCENCE	32	0.440978	1.549348	0.040936	0.126876
GO REGULATION OF PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	21	0.470472	1.548561	0.04008	0.127121
GO MALE GAMETE GENERATION	392	0.320675	1.54443	0.008386	0.130123
GO PROTEIN K48 LINKED UBIQUITINATION	45	0.428311	1.542981	0.042254	0.131215
GO PTERIDINE CONTAINING COMPOUND BIOSYNTHETIC PROCESS	16	0.606068	1.54201	0.047521	0.131844
GO GLUCOSE 6 PHOSPHATE METABOLIC PROCESS	21	0.547287	1.541852	0.04277	0.13179
GO NEGATIVE REGULATION OF CATABOLIC PROCESS	193	0.318975	1.541159	0.002058	0.132167
GO REGULATION OF INTERFERON BETA PRODUCTION	43	0.44405	1.540874	0.041257	0.132014
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY	147	0.328652	1.54077	0.008247	0.131712
GO PYRUVATE METABOLIC PROCESS	59	0.437057	1.54002	0.046122	0.132129
GO TRANSFERASE ACTIVITY TRANSFERRING PENTOSYL GROUPS	51	0.39998	1.539424	0.033543	0.132432
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	20	0.481001	1.538624	0.048583	0.13293
GO POSITIVE REGULATION OF TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER	17	0.513009	1.53841	0.042424	0.132924
GO MICROTUBULE POLYMERIZATION	26	0.457684	1.537219	0.034836	0.133543
GO GAMMA TUBULIN BINDING	23	0.446165	1.534939	0.034413	0.135039
GO RNA METHYLTRANSFERASE ACTIVITY	38	0.480636	1.534902	0.040816	0.13487
GO UBIQUITIN LIKE PROTEIN TRANSFERASE ACTIVITY	394	0.323678	1.534068	0.020661	0.135427
GO POSITIVE REGULATION OF PROTEOLYSIS	349	0.335386	1.529676	0.02863	0.138917
GO SINGLE FERTILIZATION	92	0.369086	1.528726	0.019802	0.139496
GO DEVELOPMENTAL PROGRAMMED CELL DEATH	26	0.478741	1.526705	0.026804	0.140663
GO POSITIVE REGULATION OF TELOMERE CAPPING	15	0.510929	1.523399	0.048485	0.142852
GO CORE PROMOTER SEQUENCE SPECIFIC DNA BINDING	99	0.362366	1.518946	0.020704	0.146452
GO REGULATION OF CIRCADIAN RHYTHM	94	0.364781	1.516516	0.020661	0.148004
GO REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION	120	0.33891	1.513953	0.014768	0.149782

GO CRANIAL NERVE DEVELOPMENT	42	0.435581	1.512836	0.035124	0.150589
GO AGGRESOME	30	0.413069	1.507019	0.023669	0.154513
GO POSITIVE REGULATION OF DNA TEMPLATED TRANSCRIPTION INITIATION	24	0.472285	1.506019	0.035865	0.154774
GO RESPONSE TO ESTRADIOL	143	0.328843	1.504607	0.012397	0.155603
GO HIPPOCAMPUS DEVELOPMENT	70	0.384394	1.503733	0.028571	0.156161
GO RESPONSE TO DSRNA	54	0.391743	1.501191	0.049896	0.158293
GO POSITIVE REGULATION OF PEPTIDYL THREONINE PHOSPHORYLATION	24	0.472836	1.499517	0.045635	0.159734
GO CELLULAR AMINO ACID BIOSYNTHETIC PROCESS	87	0.38629	1.499382	0.045361	0.159638
GO ENHANCER BINDING	88	0.37271	1.491476	0.043912	0.165269
GO PLACENTA DEVELOPMENT	134	0.345041	1.489867	0.028747	0.166406
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	70	0.354927	1.489228	0.01875	0.166778
GO STRUCTURAL CONSTITUENT OF CYTOSKELETON	94	0.386527	1.488349	0.034409	0.166923
GO POSITIVE REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	33	0.408751	1.484099	0.042194	0.169859
GO POSITIVE REGULATION OF MITOCHONDRION ORGANIZATION	151	0.333508	1.483998	0.022267	0.169749
GO ESTABLISHMENT OF LOCALIZATION BY MOVEMENT ALONG MICROTUBULE	90	0.369138	1.483559	0.047244	0.169942
GO CELLULAR PROCESS INVOLVED IN REPRODUCTION IN MULTICELLULAR ORGANISM	212	0.315249	1.483266	0.012526	0.170005
GO HEPATICOBILIARY SYSTEM DEVELOPMENT	126	0.342623	1.479651	0.02	0.172014
GO CELLULAR RESPONSE TO NITRIC OXIDE	15	0.491214	1.478887	0.04931	0.172574
GO NEGATIVE REGULATION OF PROTEIN BINDING	78	0.347381	1.478556	0.022222	0.172663
GO SPERM EGG RECOGNITION	40	0.432847	1.475055	0.037694	0.175981
GO RHYTHMIC PROCESS	278	0.317623	1.472359	0.01046	0.177916
GO TELENCEPHALON DEVELOPMENT	222	0.336323	1.470762	0.03937	0.179272
GO OVARIAN FOLLICLE DEVELOPMENT	55	0.363584	1.457777	0.032854	0.189787
GO REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	214	0.309971	1.455988	0.019763	0.191202
GO RESPONSE TO TEMPERATURE STIMULUS	140	0.315911	1.454281	0.022044	0.192775
GO POSITIVE REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	22	0.455514	1.453588	0.046939	0.193322
GO FERTILIZATION	122	0.338354	1.44801	0.016293	0.197822
GO RESPONSE TO TESTOSTERONE	37	0.392696	1.444499	0.032	0.200194
GO REGULATION OF NEURON APOPTOTIC PROCESS	184	0.312847	1.443397	0.019531	0.200978
GO BETA TUBULIN BINDING	35	0.406344	1.440658	0.04931	0.203208
GO METHYLATION	236	0.33858	1.43943	0.049896	0.203754
GO POSITIVE REGULATION OF CATABOLIC PROCESS	383	0.296921	1.439308	0.041494	0.203645
GO PHOSPHOPROTEIN BINDING	59	0.358151	1.438831	0.049485	0.20395
GO CELL CYCLE ARREST	142	0.309409	1.43822	0.04008	0.204054

GO HINDBRAIN DEVELOPMENT	135	0.366692	1.436938	0.045738	0.204624
GO MULTICELLULAR ORGANISM AGING	30	0.394195	1.432142	0.048327	0.208692
GO REGULATION OF NEURON DEATH	240	0.299804	1.431397	0.017308	0.208536
GO RNA POLYMERASE II CORE PROMOTER SEQUENCE SPECIFIC DNA BINDING	53	0.368938	1.426651	0.041322	0.212396
GO TRANSCRIPTION COREPRESSOR ACTIVITY	208	0.311606	1.423678	0.040816	0.214727
GO MAINTENANCE OF CELL NUMBER	130	0.339352	1.423451	0.037624	0.214721
GO TRANSCRIPTION FACTOR BINDING	498	0.28992	1.421787	0.020202	0.215893
GO NEGATIVE REGULATION OF BINDING	129	0.313446	1.420904	0.021097	0.216656
GO CELLULAR RESPONSE TO KETONE	72	0.365326	1.41762	0.046414	0.219163
GO REPRODUCTIVE SYSTEM DEVELOPMENT	390	0.290034	1.414235	0.022044	0.222667
GO REGENERATION	154	0.311328	1.411096	0.035088	0.22594
GO RESPONSE TO LIGHT STIMULUS	263	0.280481	1.409458	0.034137	0.226649
GO AGING	256	0.292188	1.408693	0.025292	0.226513
GO PROTEIN DEPHOSPHORYLATION	180	0.292287	1.403264	0.036609	0.23125
GO INTRACELLULAR RECEPTOR SIGNALING PATHWAY	160	0.311649	1.402683	0.045267	0.231389

ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate; GSEA, gene set enrichment analysis; KIF, kinesin.

Table SIII. GSEA results of c2 reference gene set of high *KIF14* expression group.

Name	Size	ES	NES	NOM P-value	FDR q-value
SHEPARD BMYB TARGETS	70	0.818884	2.664855	<0.0001	<0.0001
SHEPARD BMYB MORPHOLINO DN	193	0.65088	2.578635	<0.0001	<0.0001
WHITFIELD CELL CYCLE G2	169	0.705651	2.570494	<0.0001	<0.0001
FLORIO NEOCORTEX BASAL RADIAL GLIA DN	187	0.85642	2.565327	<0.0001	<0.0001
CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	164	0.81638	2.562315	<0.0001	<0.0001
WHITFIELD CELL CYCLE G2 M	196	0.675931	2.561875	<0.0001	<0.0001
DUTERTRE ESTRADIOL RESPONSE 24HR UP	309	0.830081	2.546488	<0.0001	<0.0001
ZHENG GLIOBLASTOMA PLASTICITY UP	240	0.621794	2.535723	<0.0001	<0.0001
TOYOTA TARGETS OF MIR34B AND MIR34C	409	0.665883	2.532558	<0.0001	<0.0001
WANG RESPONSE TO GSK3 INHIBITOR SB216763 DN	332	0.675787	2.531132	<0.0001	<0.0001
SHEPARD CRUSH AND BURN MUTANT DN	174	0.667064	2.518277	<0.0001	<0.0001
AFFAR YY1 TARGETS DN	226	0.628908	2.500055	<0.0001	<0.0001
BLUM RESPONSE TO SALIRASIB DN	336	0.731556	2.498425	<0.0001	<0.0001
LINDGREN BLADDER CANCER CLUSTER 1 DN	356	0.577445	2.493411	<0.0001	<0.0001
BASAKI YBX1 TARGETS UP	268	0.747538	2.493154	<0.0001	<0.0001
ODONNELL TFRC TARGETS DN	123	0.814665	2.489543	<0.0001	<0.0001
ZHANG TLX TARGETS 60HR DN	263	0.831575	2.484256	<0.0001	<0.0001
DUTERTRE ESTRADIOL RESPONSE 6HR UP	218	0.613941	2.473439	<0.0001	<0.0001
LI WILMS TUMOR VS FETAL KIDNEY 1 DN	159	0.817373	2.464465	<0.0001	<0.0001
GAVIN FOXP3 TARGETS CLUSTER P6	88	0.81008	2.464099	<0.0001	<0.0001
FURUKAWA DUSP6 TARGETS PCI35 DN	67	0.828011	2.464026	<0.0001	<0.0001
VILLANUEVA LIVER CANCER KRT19 UP	162	0.751999	2.462688	<0.0001	<0.0001
RUIZ TNC TARGETS DN	136	0.79689	2.462005	<0.0001	<0.0001
FERREIRA EWINGS SARCOMA UNSTABLE VS STABLE UP	148	0.779458	2.459651	<0.0001	<0.0001
MARKEY RB1 ACUTE LOF UP	223	0.752566	2.453993	<0.0001	<0.0001
KEGG CELL CYCLE	124	0.734303	2.453143	<0.0001	<0.0001
FOURNIER ACINAR DEVELOPMENT LATE 2	265	0.749801	2.448522	<0.0001	<0.0001
CHEMNITZ RESPONSE TO PROSTAGLANDIN E2 UP	129	0.756192	2.442144	<0.0001	<0.0001
KAUFFMANN DNA REPLICATION GENES	141	0.686977	2.437814	<0.0001	<0.0001
FUJII YBX1 TARGETS DN	193	0.781675	2.436416	<0.0001	<0.0001
MITSIADES RESPONSE TO APLIDIN DN	239	0.751172	2.43588	<0.0001	<0.0001
BENPORATH ES 1	356	0.657202	2.434668	<0.0001	<0.0001
SARRIO EPITHELIAL MESENCHYMAL TRANSITION UP	171	0.7807	2.434058	<0.0001	<0.0001
VECCHI GASTRIC CANCER EARLY UP	384	0.693793	2.425952	<0.0001	<0.0001
FISCHER G2 M CELL CYCLE	220	0.768768	2.424458	<0.0001	<0.0001
CHANG CYCLING GENES	138	0.879557	2.423594	<0.0001	<0.0001
SHEDDEN LUNG CANCER POOR SURVIVAL A6	427	0.816478	2.415649	<0.0001	<0.0001
HORIUCHI WTAP TARGETS DN	293	0.728973	2.415397	<0.0001	<0.0001
REACTOME CELL CYCLE MITOTIC	299	0.73335	2.414615	<0.0001	<0.0001
GRAHAM CML DIVIDING VS NORMAL QUIESCENT UP	176	0.794351	2.40974	<0.0001	<0.0001
HOFFMANN LARGE TO SMALL PRE BII LYMPHOCYTE UP	158	0.795924	2.405677	<0.0001	<0.0001
LE EGR2 TARGETS UP	104	0.80024	2.405358	<0.0001	<0.0001
LEE EARLY T LYMPHOCYTE UP	97	0.844579	2.399977	<0.0001	<0.0001
PUJANA BRCA2 PCC NETWORK	401	0.733439	2.399403	<0.0001	<0.0001

KOBAYASHI EGFR SIGNALING 24HR DN	242	0.858716	2.392327	<0.0001	<0.0001
BURTON ADIPOGENESIS 3	100	0.854862	2.391245	<0.0001	<0.0001
LINDGREN BLADDER CANCER CLUSTER 3 UP	305	0.704228	2.390668	<0.0001	<0.0001
PUJANA BREAST CANCER LIT INT NETWORK	97	0.713468	2.38424	<0.0001	1.85E-05
MANALO HYPOXIA DN	271	0.765634	2.381619	<0.0001	1.82E-05
REACTOME MITOTIC PROMETAPHASE	78	0.822793	2.367637	<0.0001	6.19E-05
REACTOME MITOTIC G2 G2 M PHASES	77	0.694932	2.365062	<0.0001	6.07E-05
PYEON CANCER HEAD AND NECK VS CERVICAL UP	169	0.689481	2.362038	<0.0001	5.96E-05
MORI PRE BI LYMPHOCYTE UP	78	0.7633	2.361567	<0.0001	5.84E-05
WEST ADRENOCORTICAL TUMOR UP	282	0.670382	2.359493	<0.0001	5.74E-05
FISCHER G1 S CELL CYCLE	192	0.64337	2.353799	<0.0001	5.63E-05
TARTE PLASMA CELL VS PLASMABLAST DN	300	0.686566	2.353118	<0.0001	5.53E-05
RIZ ERYTHROID DIFFERENTIATION	72	0.684927	2.352404	<0.0001	5.43E-05
KAUFFMANN DNA REPAIR GENES	219	0.639908	2.350098	<0.0001	5.34E-05
REACTOME CELL CYCLE	386	0.693068	2.34536	<0.0001	6.65E-05
TANG SENESCENCE TP53 TARGETS DN	54	0.889923	2.34484	<0.0001	6.54E-05
PEART HDAC PROLIFERATION CLUSTER DN	73	0.697289	2.343508	<0.0001	6.43E-05
PID AURORA A PATHWAY	30	0.783023	2.33772	<0.0001	6.33E-05
PID AURORA B PATHWAY	37	0.845793	2.335224	<0.0001	6.23E-05
CROONQUIST IL6 DEPRIVATION DN	96	0.910438	2.334166	<0.0001	6.13E-05
PAL PRMT5 TARGETS UP	195	0.641676	2.333921	<0.0001	6.04E-05
CROONQUIST NRAS VS STROMAL STIMULATION DN	98	0.654713	2.329878	<0.0001	5.94E-05
WINNEPENNINCKX MELANOMA METASTASIS UP	151	0.836517	2.327474	<0.0001	5.86E-05
MUELLER PLURINET	296	0.691944	2.327251	<0.0001	5.77E-05
ZHANG TLX TARGETS DN	87	0.910856	2.327075	<0.0001	5.69E-05
BURTON ADIPOGENESIS PEAK AT 24HR	42	0.889311	2.326663	<0.0001	5.60E-05
NAKAYAMA SOFT TISSUE TUMORS PCA2 UP	86	0.778926	2.322817	<0.0001	7.13E-05
REACTOME RECRUITMENT OF MITOTIC CENTROSOME PROTEINS AND COMPLEXES	62	0.663006	2.321396	<0.0001	7.03E-05
OLSSON E2F3 TARGETS DN	45	0.724699	2.31756	<0.0001	6.94E-05
ZHANG TLX TARGETS 36HR DN	182	0.81015	2.315679	<0.0001	6.84E-05
GRADE COLON AND RECTAL CANCER UP	272	0.657404	2.312434	<0.0001	6.75E-05
SENGUPTA NASOPHARYNGEAL CARCINOMA UP	275	0.679703	2.312428	<0.0001	6.66E-05
NADERI BREAST CANCER PROGNOSIS UP	46	0.794386	2.312046	<0.0001	6.58E-05
GEORGES CELL CYCLE MIR192 TARGETS	61	0.755207	2.311957	<0.0001	6.49E-05
REACTOME MRNA PROCESSING	151	0.677944	2.310748	<0.0001	6.41E-05
KONG E2F3 TARGETS	94	0.893101	2.308986	<0.0001	6.33E-05
GARCIA TARGETS OF FLI1 AND DAX1 DN	163	0.670404	2.307959	<0.0001	6.25E-05
CHICAS RB1 TARGETS GROWING	225	0.656	2.305482	<0.0001	7.57E-05
BOYAULT LIVER CANCER SUBCLASS G23 UP	49	0.842025	2.304992	<0.0001	7.48E-05
PUJANA XPRSS INT NETWORK	161	0.801418	2.304236	<0.0001	7.39E-05
VANTVEER BREAST CANCER METASTASIS DN	111	0.736104	2.302841	<0.0001	7.30E-05
WU APOPTOSIS BY CDKN1A VIA TP53	54	0.888194	2.300104	<0.0001	7.21E-05
PID FOXM1 PATHWAY	40	0.748312	2.298363	<0.0001	7.13E-05
ALCALAY AML BY NPM1 LOCALIZATION DN	180	0.544985	2.294987	<0.0001	8.39E-05
REACTOME GLUCOSE TRANSPORT	37	0.743485	2.294825	<0.0001	8.29E-05
STEIN ESRRA TARGETS RESPONSIVE TO ESTROGEN DN	39	0.81439	2.294499	<0.0001	8.20E-05
MOLENAAR TARGETS OF CCND1 AND CDK4 DN	51	0.8837	2.286442	<0.0001	1.01E-04
XU HGF SIGNALING NOT VIA AKT1 48HR DN	20	0.808827	2.28584	<0.0001	9.99E-05

GENTILE RESPONSE CLUSTER D3	61	0.658938	2.284339	<0.0001	9.88E-05
GOLDRATH ANTIGEN RESPONSE	331	0.614894	2.284271	<0.0001	9.78E-05
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS UP	121	0.624373	2.280433	<0.0001	1.07E-04
BENPORATH PROLIFERATION	136	0.814502	2.280209	<0.0001	1.06E-04
REACTOME DNA REPLICATION	180	0.793046	2.27984	<0.0001	1.05E-04
REACTOME LOSS OF NLP FROM MITOTIC CENTROSOMES	55	0.678061	2.279517	<0.0001	1.15E-04
VERNELL RETINOBLASTOMA PATHWAY UP	68	0.80927	2.278211	<0.0001	1.13E-04
MISSIAGLIA REGULATED BY METHYLATION DN	115	0.817003	2.277496	<0.0001	1.12E-04
PID E2F PATHWAY	73	0.672305	2.275194	<0.0001	1.11E-04
REACTOME MITOTIC M M G1 PHASES	160	0.779826	2.272403	<0.0001	1.17E-04
BHATTACHARYA EMBRYONIC STEM CELL	86	0.708858	2.269721	<0.0001	1.31E-04
ZHOU CELL CYCLE GENES IN IR RESPONSE 24HR	119	0.850134	2.266954	<0.0001	1.41E-04
YU BAP1 TARGETS	29	0.768103	2.266531	<0.0001	1.40E-04
BIDUS METASTASIS UP	204	0.719619	2.265172	<0.0001	1.38E-04
MORI EMU MYC LYMPHOMA BY ONSET TIME UP	99	0.676762	2.264455	<0.0001	1.60E-04
WANG CISPLATIN RESPONSE AND XPC UP	190	0.562129	2.261287	<0.0001	1.71E-04
WHITEFORD PEDIATRIC CANCER MARKERS	111	0.862278	2.260581	<0.0001	1.69E-04
MORI IMMATURE B LYMPHOCYTE DN	90	0.841432	2.259593	<0.0001	1.78E-04
BENPORATH ES CORE NINE CORRELATED	98	0.630887	2.259514	<0.0001	1.76E-04
GRAHAM CML QUIESCENT VS NORMAL QUIESCENT UP	80	0.658461	2.258753	<0.0001	1.75E-04
PID ATR PATHWAY	39	0.833682	2.258667	<0.0001	1.73E-04
BENPORATH ES 2	39	0.72723	2.257777	<0.0001	1.72E-04
KAUFFMANN MELANOMA RELAPSE UP	59	0.884929	2.256542	<0.0001	1.70E-04
PUJANA BRCA CENTERED NETWORK	114	0.814561	2.256107	<0.0001	1.69E-04
LIAO METASTASIS	495	0.501986	2.255941	<0.0001	1.67E-04
LY AGING OLD DN	55	0.820124	2.255255	<0.0001	1.66E-04
PENG LEUCINE DEPRIVATION DN	182	0.654905	2.25395	<0.0001	1.64E-04
HU GENOTOXIC DAMAGE 4HR	35	0.7872	2.25334	<0.0001	1.63E-04
PID FANCONI PATHWAY	43	0.796392	2.252355	<0.0001	1.62E-04
CROONQUIST NRAS SIGNALING DN	71	0.926879	2.251029	<0.0001	1.68E-04
WEST ADRENOCORTICAL TUMOR MARKERS UP	21	0.862136	2.250474	<0.0001	1.67E-04
SU TESTIS	67	0.682402	2.249822	<0.0001	1.65E-04
PID PLK1 PATHWAY	43	0.80469	2.249556	<0.0001	1.64E-04
CHANG CORE SERUM RESPONSE UP	198	0.6738	2.249262	<0.0001	1.63E-04
REACTOME PROCESSING OF CAPPED INTRON CONTAINING PRE MRNA	132	0.689805	2.248208	<0.0001	1.61E-04
LABBE WNT3A TARGETS UP	108	0.539421	2.246352	<0.0001	1.60E-04
REN BOUND BY E2F	60	0.894843	2.246019	<0.0001	1.59E-04
ZHOU CELL CYCLE GENES IN IR RESPONSE 6HR	80	0.890253	2.242706	<0.0001	1.58E-04
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS TURQUOISE DN	50	0.744311	2.241454	<0.0001	1.65E-04
PENG GLUTAMINE DEPRIVATION DN	324	0.613118	2.240468	<0.0001	1.64E-04
PYEON HPV POSITIVE TUMORS UP	84	0.700808	2.237365	<0.0001	1.86E-04
MOHANKUMAR HOXA1 TARGETS UP	384	0.533987	2.23503	<0.0001	1.84E-04
CHANDRAN METASTASIS UP	191	0.533844	2.234377	<0.0001	1.83E-04
THILLAINADESAN ZNF217 TARGETS UP	42	0.696334	2.231721	<0.0001	2.11E-04
XU HGF TARGETS INDUCED BY AKT1 48HR DN	24	0.799407	2.228777	<0.0001	2.17E-04
KARLSSON TGFB1 TARGETS UP	118	0.646269	2.227601	<0.0001	2.22E-04
KIM WT1 TARGETS DN	427	0.534994	2.226837	<0.0001	2.21E-04

REACTOME HIV LIFE CYCLE	105	0.646826	2.224949	<0.0001	2.26E-04
ZHANG BREAST CANCER PROGENITORS UP	399	0.62057	2.224277	<0.0001	2.32E-04
BOYAULT LIVER CANCER SUBCLASS G3 UP	181	0.732087	2.22399	<0.0001	2.30E-04
GREENBAUM E2A TARGETS UP	32	0.868471	2.223044	<0.0001	2.29E-04
WHITFIELD CELL CYCLE G1 S	128	0.603238	2.222478	<0.0001	2.34E-04
EPPERT PROGENITOR	125	0.658069	2.219506	<0.0001	2.44E-04
WHITFIELD CELL CYCLE S	147	0.606982	2.217655	<0.0001	2.42E-04
REACTOME TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM	51	0.729971	2.21592	<0.0001	2.45E-04
SERVITJA LIVER HNF1A TARGETS UP	132	0.515127	2.215804	<0.0001	2.44E-04
STEIN ESR1 TARGETS	82	0.587358	2.212768	<0.0001	2.66E-04
DANG REGULATED BY MYC UP	71	0.684629	2.212471	<0.0001	2.64E-04
GRAHAM NORMAL QUIESCENT VS NORMAL DIVIDING DN	85	0.877635	2.211792	<0.0001	2.69E-04
REACTOME REGULATION OF GLUCOKINASE BY GLUCOKINASE REGULATORY PROTEIN	26	0.806491	2.210947	<0.0001	2.72E-04
BURTON ADIPOGENESIS PEAK AT 16HR	40	0.798562	2.208908	<0.0001	2.80E-04
PUJANA BREAST CANCER WITH BRCA1 MUTATED UP	54	0.877099	2.208528	<0.0001	2.78E-04
PID MYC ACTIV PATHWAY	78	0.670096	2.200786	<0.0001	3.12E-04
MARKEY RB1 CHRONIC LOF UP	111	0.576633	2.198618	<0.0001	3.18E-04
CHEN ETV5 TARGETS TESTIS	21	0.85175	2.198446	<0.0001	3.16E-04
NAKAMURA CANCER MICROENVIRONMENT DN	43	0.801437	2.196281	<0.0001	3.35E-04
REACTOME LATE PHASE OF HIV LIFE CYCLE	92	0.651908	2.196273	<0.0001	3.33E-04
PID ATM PATHWAY	33	0.715714	2.195678	<0.0001	3.31E-04
REACTOME TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRONLESS TRANSCRIPT	31	0.794525	2.194744	<0.0001	3.36E-04
MORI MATURE B LYMPHOCYTE DN	72	0.645012	2.190867	<0.0001	3.60E-04
SOTIRIOU BREAST CANCER GRADE 1 VS 3 UP	141	0.906792	2.190187	<0.0001	3.58E-04
OXFORD RALA OR RALB TARGETS UP	45	0.839893	2.188002	<0.0001	3.71E-04
ROSTY CERVICAL CANCER PROLIFERATION CLUSTER	133	0.903303	2.186217	<0.0001	3.80E-04
BORCZUK MALIGNANT MESOTHELIOMA UP	291	0.627247	2.186204	<0.0001	3.77E-04
MORI LARGE PRE BII LYMPHOCYTE UP	84	0.813722	2.18572	<0.0001	3.75E-04
WAKASUGI HAVE ZNF143 BINDING SITES	56	0.678475	2.185088	<0.0001	3.78E-04
ODONNELL TARGETS OF MYC AND TFRC DN	43	0.851083	2.181835	<0.0001	4.02E-04
SCIBETTA KDM5B TARGETS DN	77	0.614466	2.181623	<0.0001	4.08E-04
FRASOR RESPONSE TO SERM OR FULVESTRANT DN	50	0.847613	2.181508	<0.0001	4.06E-04
LY AGING PREMATURE DN	29	0.817715	2.180502	<0.0001	4.27E-04
REACTOME TRANSPORT OF RIBONUCLEOPROTEINS INTO THE HOST NUCLEUS	26	0.824211	2.180265	<0.0001	4.29E-04
RHODES CANCER META SIGNATURE	63	0.752764	2.17843	<0.0001	4.45E-04
YUAN ZNF143 PARTNERS	21	0.797695	2.177093	<0.0001	4.53E-04
DELPUECH FOXO3 TARGETS DN	39	0.762981	2.176658	<0.0001	4.57E-04
JAEGER METASTASIS UP	43	0.730693	2.175459	<0.0001	4.63E-04
WANG METASTASIS OF BREAST CANCER ESR1 UP	19	0.899648	2.175379	<0.0001	4.60E-04
CHANDRAN METASTASIS TOP50 UP	34	0.691174	2.172908	<0.0001	4.91E-04
PETROVA ENDOTHELIUM LYMPHATIC VS BLOOD UP	126	0.550446	2.17231	<0.0001	4.89E-04
REACTOME INTERACTIONS OF VPR WITH HOST CELLULAR PROTEINS	31	0.760647	2.170238	<0.0001	5.15E-04
BOYAULT LIVER CANCER SUBCLASS G123 UP	44	0.753895	2.168304	<0.0001	5.38E-04
REACTOME DNA REPAIR	101	0.628646	2.167815	<0.0001	5.35E-04

WONG EMBRYONIC STEM CELL CORE	330	0.71035	2.167248	<0.0001	5.32E-04
PETROVA PROX1 TARGETS UP	27	0.79695	2.166576	<0.0001	5.29E-04
REACTOME DOUBLE STRAND BREAK REPAIR	21	0.795255	2.165606	<0.0001	5.39E-04
YAMAZAKI TCEB3 TARGETS DN	204	0.551047	2.16489	<0.0001	5.49E-04
FERRANDO T ALL WITH MLL ENL FUSION DN	83	0.624372	2.163714	<0.0001	5.56E-04
REACTOME METABOLISM OF NON CODING RNA	47	0.742599	2.160016	<0.0001	6.06E-04
MATTIOLI MGUS VS PCL	93	0.605428	2.159106	<0.0001	6.09E-04
VANTVEER BREAST CANCER ESR1 DN	226	0.560046	2.15587	<0.0001	6.50E-04
WILCOX RESPONSE TO PROGESTERONE UP	140	0.595077	2.154259	<0.0001	6.67E-04
FOURNIER ACINAR DEVELOPMENT LATE DN	21	0.847551	2.154185	<0.0001	6.64E-04
UDAYAKUMAR MED1 TARGETS UP	129	0.566115	2.15414	<0.0001	6.67E-04
GARY CD5 TARGETS DN	414	0.584464	2.152362	<0.0001	6.73E-04
REACTOME APC CDC20 MEDIATED DEGRADATION OF NEK2A	21	0.855183	2.152212	<0.0001	6.69E-04
REACTOME NEP NS2 INTERACTS WITH THE CELLULAR EXPORT MACHINERY	26	0.822461	2.152121	<0.0001	6.66E-04
PID BARD1 PATHWAY	28	0.796554	2.145886	<0.0001	7.14E-04
DAIRKEE CANCER PRONE RESPONSE BPA	49	0.609662	2.145401	<0.0001	7.10E-04
SONG TARGETS OF IE86 CMV PROTEIN	58	0.840351	2.143159	<0.0001	7.40E-04
WHITFIELD CELL CYCLE LITERATURE	44	0.908925	2.142448	<0.0001	7.36E-04
REACTOME KINESINS	23	0.825208	2.141724	<0.0001	7.51E-04
MARTINEZ RESPONSE TO TRABECTEDIN DN	265	0.566944	2.141457	<0.0001	7.51E-04
NUNODA RESPONSE TO DASATINIB IMATINIB UP	29	0.664982	2.141399	<0.0001	7.48E-04
REACTOME E2F MEDIATED REGULATION OF DNA REPLICATION	33	0.820768	2.14092	<0.0001	7.48E-04
SUNG METASTASIS STROMA DN	49	0.686454	2.140358	<0.0001	7.55E-04
KANG DOXORUBICIN RESISTANCE UP	50	0.960602	2.139787	<0.0001	7.57E-04
REACTOME G2 M CHECKPOINTS	41	0.856706	2.1397	<0.0001	7.53E-04
KEGG OOCYTE MEIOSIS	107	0.541611	2.13967	<0.0001	7.49E-04
WILLIAMS ESR1 TARGETS UP	26	0.675222	2.139384	<0.0001	7.46E-04
ISHIDA E2F TARGETS	50	0.924684	2.137164	<0.0001	7.58E-04
REACTOME ANTIVIRAL MECHANISM BY IFN STIMULATED GENES	64	0.645225	2.136975	<0.0001	7.58E-04
REACTOME INHIBITION OF THE PROTEOLYTIC ACTIVITY OF APC C REQUIRED FOR THE ONSET OF ANAPHASE BY MITOTIC SPINDLE CHECKPOINT COMPONENTS	18	0.852275	2.136087	<0.0001	7.65E-04
ZAMORA NOS2 TARGETS UP	64	0.655794	2.133023	<0.0001	8.04E-04
LEE LIVER CANCER SURVIVAL DN	165	0.673741	2.131174	<0.0001	8.26E-04
BIOCARTA ATRBRCA PATHWAY	19	0.803318	2.128207	<0.0001	8.64E-04
LI WILMS TUMOR ANAPLASTIC UP	19	0.937158	2.128053	<0.0001	8.61E-04
KEGG DNA REPLICATION	36	0.869243	2.125047	<0.0001	8.99E-04
PUIFFE INVASION INHIBITED BY ASCITES UP	81	0.572121	2.124737	<0.0001	8.99E-04
SASAKI ADULT T CELL LEUKEMIA	168	0.550264	2.124196	<0.0001	9.07E-04
KEGG ONE CARBON POOL BY FOLATE	17	0.746395	2.123496	<0.0001	9.11E-04
RHODES UNDIFFERENTIATED CANCER	67	0.81671	2.122367	<0.0001	9.33E-04
SMIRNOV RESPONSE TO IR 6HR DN	108	0.598424	2.121625	<0.0001	9.59E-04
BHATI G2M ARREST BY 2METHOXYESTRADIOL UP	108	0.547504	2.121505	<0.0001	9.55E-04
REICHERT MITOSIS LIN9 TARGETS	27	0.937563	2.11949	<0.0001	9.72E-04
REACTOME MRNA SPLICING	104	0.658175	2.119412	<0.0001	9.67E-04
TURASHVILI BREAST DUCTAL CARCINOMA VS LOBULAR	71	0.66102	2.118949	<0.0001	9.73E-04

NORMAL UP					
KAMMINGA EZH2 TARGETS	41	0.888495	2.113548	<0.0001	0.001035
BIOCARTA G2 PATHWAY	24	0.72111	2.112303	0.001976	0.00105
REACTOME G1 S SPECIFIC TRANSCRIPTION	17	0.899431	2.111586	<0.0001	0.001046
REACTOME PHOSPHORYLATION OF THE APC C	17	0.8417	2.111012	<0.0001	0.001053
SMID BREAST CANCER LUMINAL A DN	18	0.928521	2.110611	<0.0001	0.001057
AMUNDSON GAMMA RADIATION RESPONSE	40	0.868888	2.107679	<0.0001	0.00115
MONNIER POSTRADIATION TUMOR ESCAPE UP	374	0.482796	2.106114	<0.0001	0.00118
SCHLOSSER MYC TARGETS AND SERUM RESPONSE DN	45	0.722332	2.104194	<0.0001	0.001217
YANG BREAST CANCER ESR1 LASER DN	49	0.610732	2.100824	<0.0001	0.001285
REACTOME CELL CYCLE CHECKPOINTS	111	0.729286	2.098385	<0.0001	0.001338
JUBAN TARGETS OF SPI1 AND FLI1 DN	84	0.569549	2.098272	<0.0001	0.001333
REACTOME DNA STRAND ELONGATION	30	0.919092	2.097477	<0.0001	0.001327
KEGG HOMOLOGOUS RECOMBINATION	26	0.774813	2.093362	<0.0001	0.001431
BIOCARTA G1 PATHWAY	28	0.675212	2.092306	<0.0001	0.001448
YU MYC TARGETS UP	39	0.860119	2.089476	<0.0001	0.001513
HONRADO BREAST CANCER BRCA1 VS BRCA2	18	0.750159	2.087336	<0.0001	0.001533
ENK UV RESPONSE KERATINOCYTE DN	479	0.50511	2.084076	<0.0001	0.001601
SHAFFER IRF4 TARGETS IN ACTIVATED B LYMPHOCYTE	76	0.598363	2.082454	<0.0001	0.001626
REACTOME APC C CDC20 MEDIATED DEGRADATION OF CYCLIN B	19	0.82178	2.079784	<0.0001	0.001731
REACTOME MITOTIC G1 G1 S PHASES	130	0.6897	2.077138	<0.0001	0.001778
NAKAMURA TUMOR ZONE PERIPHERAL VS CENTRAL UP	267	0.559954	2.0759	<0.0001	0.001834
OUELLET OVARIAN CANCER INVASIVE VS LMP UP	117	0.622279	2.075105	<0.0001	0.001831
SIMBULAN PARP1 TARGETS DN	17	0.888615	2.072002	<0.0001	0.001923
BOYLAN MULTIPLE MYELOMA C D UP	129	0.491912	2.07141	<0.0001	0.001929
GROSS HYPOXIA VIA ELK3 UP	198	0.471301	2.069197	<0.0001	0.001982
VANTVEER BREAST CANCER POOR PROGNOSIS	50	0.600746	2.068319	0.006036	0.001996
ABRAMSON INTERACT WITH AIRE	44	0.733943	2.066511	<0.0001	0.002065
MATZUK MEIOTIC AND DNA REPAIR	35	0.627007	2.066183	<0.0001	0.002056
REACTOME G0 AND EARLY G1	23	0.806231	2.063543	<0.0001	0.002138
YANG BCL3 TARGETS UP	344	0.443605	2.061485	<0.0001	0.002181
REACTOME FANCONI ANEMIA PATHWAY	19	0.848344	2.061417	<0.0001	0.00218
ZHAN MULTIPLE MYELOMA PR UP	43	0.93328	2.060436	<0.0001	0.002199
SCHLOSSER MYC TARGETS REPRESSED BY SERUM	153	0.648982	2.060364	<0.0001	0.00219
BOYLAN MULTIPLE MYELOMA C CLUSTER UP	37	0.59411	2.058488	<0.0001	0.002244
BILANGES SERUM SENSITIVE VIA TSC2	37	0.671963	2.056884	<0.0001	0.00229
CHIARETTI T ALL RELAPSE PROGNOSIS	19	0.750839	2.056361	<0.0001	0.002308
REACTOME ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS	35	0.848436	2.052634	<0.0001	0.002445
BOHN PRIMARY IMMUNODEFICIENCY SYNDROM UP	45	0.629882	2.051573	<0.0001	0.002459
BASSO B LYMPHOCYTE NETWORK	135	0.532313	2.0499	0.001957	0.002502
GROSS HYPOXIA VIA ELK3 ONLY DN	41	0.563094	2.049859	<0.0001	0.002493
REACTOME CONVERSION FROM APC C CDC20 TO APC C CDH1 IN LATE ANAPHASE	16	0.769687	2.04824	<0.0001	0.002543
CUI TCF21 TARGETS 2 UP	404	0.469723	2.04728	<0.0001	0.002557
REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX	30	0.880281	2.047278	<0.0001	0.002547
KEGG SPLICEOSOME	123	0.614674	2.046917	<0.0001	0.002547

SLEBOS HEAD AND NECK CANCER WITH HPV UP	78	0.668341	2.046518	0.004	0.002552
KRASNOSELSKAYA ILF3 TARGETS DN	44	0.578547	2.045805	<0.0001	0.002587
SCHUHMACHER MYC TARGETS UP	77	0.673086	2.045094	<0.0001	0.002591
SCHLOSSER MYC TARGETS AND SERUM RESPONSE UP	46	0.661722	2.044917	<0.0001	0.002585
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 11	95	0.585354	2.043413	<0.0001	0.002631
LE NEURONAL DIFFERENTIATION DN	19	0.806641	2.041215	<0.0001	0.002708
GAL LEUKEMIC STEM CELL DN	233	0.521663	2.037668	<0.0001	0.002857
KEGG MISMATCH REPAIR	23	0.792861	2.036774	<0.0001	0.002892
ZHAN MULTIPLE MYELOMA SUBGROUPS	30	0.783434	2.034444	<0.0001	0.00296
IWANAGA E2F1 TARGETS INDUCED BY SERUM	29	0.748001	2.03212	<0.0001	0.003046
WELCSH BRCA1 TARGETS DN	139	0.582613	2.030536	<0.0001	0.003134
REACTOME G1 S TRANSITION	106	0.701458	2.024296	<0.0001	0.003411
LI WILMS TUMOR VS FETAL KIDNEY 2 UP	29	0.692672	2.024231	<0.0001	0.003406
CAIRO PML TARGETS BOUND BY MYC UP	23	0.71123	2.023444	<0.0001	0.00344
GENTILE UV HIGH DOSE DN	300	0.482203	2.023252	<0.0001	0.003439
REACTOME HIV INFECTION	184	0.571172	2.019885	0.002024	0.003615
PENG RAPAMYCIN RESPONSE DN	230	0.577971	2.019522	<0.0001	0.003621
REACTOME CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION REGION	42	0.675376	2.018684	<0.0001	0.003667
BIOCARTA CELLCYCLE PATHWAY	23	0.70707	2.018089	<0.0001	0.003679
RAMASWAMY METASTASIS UP	64	0.555347	2.017182	<0.0001	0.003707
KOKKINAKIS METHIONINE DEPRIVATION 96HR DN	75	0.552112	2.015791	<0.0001	0.003786
REACTOME RNA POL II TRANSCRIPTION	93	0.595103	2.014864	<0.0001	0.00382
REACTOME PROCESSING OF CAPPED INTRONLESS PRE MRNA	23	0.755274	2.013584	<0.0001	0.003897
HEDENFALK BREAST CANCER BRCA1 VS BRCA2	156	0.494516	2.012398	<0.0001	0.003938
PID TELOMERASE PATHWAY	67	0.540832	2.012027	<0.0001	0.003944
REACTOME S PHASE	106	0.714839	2.011464	<0.0001	0.003962
ELVIDGE HYPOXIA DN	136	0.526811	2.009907	<0.0001	0.004024
CAIRO HEPATOBLASTOMA UP	197	0.488101	2.00944	<0.0001	0.004041
KEGG PROGESTERONE MEDIATED OOCYTE MATURATION	83	0.497293	2.006977	<0.0001	0.004153
FARMER BREAST CANCER CLUSTER 2	32	0.908979	2.00511	<0.0001	0.004237
REACTOME EXTENSION OF TELOMERES	27	0.844126	2.004778	<0.0001	0.004276
REACTOME LAGGING STRAND SYNTHESIS	19	0.888307	2.003379	<0.0001	0.004345
REACTOME FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC	21	0.742653	2.002449	<0.0001	0.004389
WINTER HYPOXIA UP	88	0.615224	2.000517	0.007663	0.004508
REACTOME SYNTHESIS OF DNA	90	0.739965	1.993704	<0.0001	0.004969
JEON SMAD6 TARGETS DN	19	0.740631	1.993601	0.002016	0.004958
EGUCHI CELL CYCLE RB1 TARGETS	23	0.97528	1.993144	<0.0001	0.004973
KUROKAWA LIVER CANCER CHEMOTHERAPY DN	39	0.551187	1.991965	<0.0001	0.005036
HESS TARGETS OF HOXA9 AND MEIS1 UP	63	0.587435	1.990295	<0.0001	0.005167
SESTO RESPONSE TO UV C2	53	0.602597	1.989025	<0.0001	0.005232
REACTOME CYTOSOLIC TRNA AMINOACYLATION	24	0.772669	1.987639	<0.0001	0.005307
SENESE HDAC2 TARGETS UP	107	0.561417	1.982967	<0.0001	0.005625
WONG PROTEASOME GENE MODULE	49	0.644623	1.979534	<0.0001	0.005892
BIOCARTA MCM PATHWAY	18	0.871783	1.979429	<0.0001	0.005881
MENSSEN MYC TARGETS	51	0.678415	1.975998	0.001969	0.006134
REACTOME CYCLIN A B1 ASSOCIATED EVENTS DURING G2 M TRANSITION	15	0.873892	1.975945	<0.0001	0.006118

GROSS HYPOXIA VIA ELK3 AND HIF1A DN	100	0.466381	1.974088	<0.0001	0.006227
REACTOME HOMOLOGOUS RECOMBINATION REPAIR OF REPLICATION INDEPENDENT DOUBLE STRAND BREAKS	15	0.781991	1.971643	<0.0001	0.00638
ONDER CDH1 TARGETS 1 DN	163	0.52004	1.970277	<0.0001	0.006494
BURTON ADIPOGENESIS 4	44	0.599456	1.970258	<0.0001	0.006474
MATZUK SPERMATOCYTE	68	0.508975	1.964937	<0.0001	0.00683
MEINHOLD OVARIAN CANCER LOW GRADE DN	20	0.763136	1.963936	<0.0001	0.006888
CHIBA RESPONSE TO TSA DN	22	0.689952	1.962235	<0.0001	0.00703
BIOCARTA ATM PATHWAY	19	0.656755	1.961606	<0.0001	0.007077
MOREAUX MULTIPLE MYELOMA BY TACI DN	154	0.571631	1.960743	0.004008	0.007125
BROWNE HCMV INFECTION 2HR DN	48	0.600096	1.957341	0.003876	0.007412
FINETTI BREAST CANCER KINOME RED	16	0.975179	1.955877	<0.0001	0.007528
WANG RECURRENT LIVER CANCER UP	20	0.661706	1.955834	0.005825	0.00751
REACTOME HOST INTERACTIONS OF HIV FACTORS	117	0.589509	1.953403	0.00202	0.007752
LAU APOPTOSIS CDKN2A UP	55	0.532113	1.952813	<0.0001	0.007792
JI RESPONSE TO FSH DN	57	0.595134	1.951937	<0.0001	0.007843
IIZUKA LIVER CANCER PROGRESSION G1 G2 DN	24	0.683785	1.948953	<0.0001	0.008141
RAMALHO STEMNESS UP	196	0.507734	1.947663	<0.0001	0.008251
REACTOME M G1 TRANSITION	78	0.727732	1.947418	<0.0001	0.008235
KEGG BASE EXCISION REPAIR	33	0.665263	1.947016	0.001953	0.008278
CREIGHTON ENDOCRINE THERAPY RESISTANCE 1	483	0.425214	1.945143	<0.0001	0.008441
PID P73PATHWAY	76	0.511262	1.94442	0.002049	0.008483
HERNANDEZ MITOTIC ARREST BY DOCETAXEL 1 DN	36	0.612238	1.943955	0.003883	0.008504
REACTOME MRNA 3 END PROCESSING	33	0.669538	1.942417	0.00789	0.008606
RHEIN ALL GLUCOCORTICOID THERAPY DN	349	0.553248	1.942108	0.002033	0.008611
XU RESPONSE TO TRETINOIN AND NSC682994 DN	15	0.808174	1.941696	<0.0001	0.008635
MOREAUX B LYMPHOCYTE MATURATION BY TACI DN	66	0.637039	1.941485	0.001996	0.00862
ACOSTA PROLIFERATION INDEPENDENT MYC TARGETS UP	75	0.519791	1.940781	<0.0001	0.008673
JOHANSSON GLIOMAGENESIS BY PDGFB UP	57	0.578771	1.939908	<0.0001	0.008745
JIANG HYPOXIA VIA VHL	33	0.597939	1.939604	0.003937	0.008771
LY AGING MIDDLE DN	16	0.962931	1.934212	<0.0001	0.009335
DEN INTERACT WITH LCA5	25	0.686135	1.93151	<0.0001	0.009568
COLDREN GEFITINIB RESISTANCE UP	74	0.529267	1.930096	0.001972	0.009702
VANHARANTA UTERINE FIBROID WITH 7Q DELETION UP	65	0.529358	1.929423	0.002028	0.009737
REACTOME PROCESSIVE SYNTHESIS ON THE LAGGING STRAND	15	0.866633	1.928926	<0.0001	0.009754
TIEN INTESTINE PROBIOTICS 2HR DN	85	0.511781	1.924996	<0.0001	0.010201
WHITFIELD CELL CYCLE M G1	140	0.484977	1.923445	<0.0001	0.010349
RICKMAN TUMOR DIFFERENTIATED MODERATELY VS POORLY DN	15	0.753345	1.923022	<0.0001	0.010381
GENTILE UV RESPONSE CLUSTER D5	37	0.569663	1.921625	<0.0001	0.010511
MARIADASON RESPONSE TO BUTYRATE SULINDAC 4	21	0.644317	1.92145	<0.0001	0.01051
GALE APL WITH FLT3 MUTATED UP	53	0.519535	1.919877	<0.0001	0.010682
LIU SOX4 TARGETS DN	293	0.429582	1.919009	<0.0001	0.010757
DANG MYC TARGETS UP	138	0.608306	1.918042	0.002024	0.01083
BOYLAN MULTIPLE MYELOMA C UP	44	0.525446	1.917899	0.001965	0.010826
VANTVEER BREAST CANCER BRCA1 UP	31	0.592304	1.917018	0.006048	0.01093
SCIAN CELL CYCLE TARGETS OF TP53 AND TP73 DN	22	0.872963	1.91647	<0.0001	0.010977
JAIN NFKB SIGNALING	71	0.505407	1.915647	0.002016	0.011053

REACTOME REGULATION OF MITOTIC CELL CYCLE	77	0.683042	1.913993	<0.0001	0.011248
DACOSTA UV RESPONSE VIA ERCC3 COMMON DN	467	0.539437	1.913581	0.00996	0.011271
BROWNE HCMV INFECTION 14HR UP	151	0.437797	1.906344	<0.0001	0.012227
BACOLOD RESISTANCE TO ALKYLATING AGENTS DN	57	0.50437	1.905139	<0.0001	0.01235
REACTOME TRNA AMINOACYLATION	42	0.665197	1.904617	0.002066	0.012382
GENTLES LEUKEMIC STEM CELL DN	18	0.708551	1.904339	0.001976	0.012387
KEGG AMINOACYL TRNA BIOSYNTHESIS	41	0.635608	1.904024	0.002028	0.012401
REACTOME GLOBAL GENOMIC NER GG NER	32	0.637705	1.903426	0.004	0.012474
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION MONOCYTE UP	195	0.453977	1.901624	0.004032	0.012695
GENTILE UV RESPONSE CLUSTER D4	54	0.545071	1.900842	0.001996	0.012769
LEE METASTASIS AND RNA PROCESSING UP	17	0.751445	1.89972	<0.0001	0.012891
REACTOME FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION	111	0.482313	1.898117	0.00381	0.013122
KEGG UBIQUITIN MEDIATED PROTEOLYSIS	130	0.463645	1.897385	<0.0001	0.01322
CHOW RASSF1 TARGETS UP	26	0.60129	1.894908	0.003953	0.013568
GROSS HYPOXIA VIA HIF1A UP	75	0.510389	1.894526	<0.0001	0.013603
ZHAN VARIABLE EARLY DIFFERENTIATION GENES DN	30	0.601802	1.892928	<0.0001	0.013823
AMIT EGF RESPONSE 480 MCF10A	40	0.552028	1.889329	0.00396	0.014372
COLINA TARGETS OF 4EBP1 AND 4EBP2	346	0.418017	1.887206	<0.0001	0.014708
WANG SMARCE1 TARGETS DN	348	0.444288	1.885691	0.002028	0.014937
AIYAR COBRA1 TARGETS DN	28	0.55724	1.884096	0.002016	0.015115
PEART HDAC PROLIFERATION CLUSTER UP	55	0.52685	1.883687	<0.0001	0.015155
BILD MYC ONCOGENIC SIGNATURE	187	0.465488	1.881166	0.002004	0.015558
SHIPP DLBCL VS FOLLICULAR LYMPHOMA UP	44	0.668241	1.879387	0.005917	0.015797
MODY HIPPOCAMPUS NEONATAL	35	0.605354	1.879214	0.008	0.015799
DAZARD UV RESPONSE CLUSTER G6	142	0.53311	1.877704	0.002012	0.016032
LOPEZ TRANSLATION VIA FN1 SIGNALING	34	0.55338	1.876149	0.007905	0.016279
PID P53 REGULATION PATHWAY	57	0.508715	1.87551	<0.0001	0.016372
IVANOVA HEMATOPOIESIS EARLY PROGENITOR	489	0.40054	1.875404	<0.0001	0.016353
ELVIDGE HIF1A TARGETS UP	63	0.53071	1.873746	0.004237	0.016613
REACTOME PROTEIN FOLDING	51	0.543924	1.872548	0.007937	0.016777
SAKAI TUMOR INFILTRATING MONOCYTES DN	79	0.544897	1.87183	0.004	0.016879
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 14	134	0.547888	1.869837	0.008147	0.017238
HOSHIDA LIVER CANCER SUBCLASS S2	113	0.532722	1.868546	0.008264	0.017413
REACTOME PREFOLDIN MEDIATED TRANSFER OF SUBSTRATE TO CCT TRIC	27	0.66543	1.868371	0.009671	0.017404
PRAMOONJAGO SOX4 TARGETS DN	50	0.569142	1.865758	<0.0001	0.017844
SHAFFER IRF4 TARGETS IN ACTIVATED DENDRITIC CELL	61	0.530798	1.865253	<0.0001	0.017882
CHICAS RB1 TARGETS LOW SERUM	84	0.561924	1.863312	0.001965	0.018225
SMID BREAST CANCER RELAPSE IN LUNG UP	20	0.663588	1.86314	<0.0001	0.018203
CONCANNON APOPTOSIS BY EPOXOMICIN DN	159	0.454962	1.860777	<0.0001	0.018625
NAGY TFTC COMPONENTS HUMAN	18	0.670555	1.860558	0.003984	0.018631
KEGG BASAL TRANSCRIPTION FACTORS	35	0.567192	1.857848	<0.0001	0.019076
CHAUHAN RESPONSE TO METHOXYESTRADIOL UP	50	0.553921	1.857844	0.004115	0.019031
NEMETH INFLAMMATORY RESPONSE LPS DN	32	0.551292	1.856437	0.003953	0.019248
REACTOME ASSEMBLY OF THE PRE REPLICATIVE COMPLEX	63	0.695611	1.854654	0.011881	0.019536
REACTOME CHROMOSOME MAINTENANCE	112	0.650034	1.854429	0.001946	0.01954
COLLIS PRKDC SUBSTRATES	19	0.664233	1.848502	<0.0001	0.020772
BROWNE HCMV INFECTION 48HR UP	174	0.400962	1.848036	<0.0001	0.020807

BILD E2F3 ONCOGENIC SIGNATURE	222	0.418463	1.847621	0.004082	0.020841
PEDERSEN METASTASIS BY ERBB2 ISOFORM 7	362	0.388932	1.847026	<0.0001	0.0209
HUANG GATA2 TARGETS DN	67	0.465132	1.845021	<0.0001	0.021251
REACTOME ORC1 REMOVAL FROM CHROMATIN	65	0.675034	1.844886	0.009785	0.02123
REACTOME BASE EXCISION REPAIR	19	0.704913	1.844277	<0.0001	0.021293
DOANE BREAST CANCER CLASSES DN	32	0.603842	1.842963	0.004141	0.02152
DAZARD RESPONSE TO UV SCC DN	119	0.474362	1.836879	0.002033	0.022798
COLLER MYC TARGETS UP	25	0.710431	1.834533	<0.0001	0.023313
CUI GLUCOSE DEPRIVATION	58	0.521446	1.833758	<0.0001	0.023464
YANG BREAST CANCER ESR1 BULK DN	22	0.610128	1.832945	0.005825	0.023609
VANDESLUIS COMMD1 TARGETS GROUP 2 UP	15	0.656657	1.832333	0.005906	0.023735
MARIADASON REGULATED BY HISTONE ACETYLATION DN	48	0.483704	1.827729	0.004016	0.024793
KATSANOU ELAVL1 TARGETS DN	141	0.418613	1.827106	<0.0001	0.024898
CAFFAREL RESPONSE TO THC 24HR 5 UP	30	0.632439	1.825481	0.006098	0.025289
FAELT B CLL WITH VH3 21 UP	42	0.589339	1.824419	0.00956	0.025547
REACTOME MRNA SPLICING MINOR PATHWAY	40	0.634329	1.824131	0.006024	0.025595
LEE CALORIE RESTRICTION NEOCORTEX DN	83	0.447936	1.821395	0.001942	0.026196
BIOCARTA P53 PATHWAY	16	0.633242	1.820757	0.004024	0.026289
BERTUCCI MEDULLARY VS DUCTAL BREAST CANCER UP	187	0.493624	1.820208	0.009921	0.026348
PID FOXO PATHWAY	49	0.504749	1.819531	0.003937	0.026468
NGUYEN NOTCH1 TARGETS DN	84	0.45355	1.817667	0.006237	0.026969
RASHI RESPONSE TO IONIZING RADIATION 4	57	0.454953	1.815458	<0.0001	0.027471
SESTO RESPONSE TO UV C4	20	0.619513	1.81434	0.00404	0.027691
DAIRKEE CANCER PRONE RESPONSE BPA E2	113	0.462271	1.813857	<0.0001	0.027744
DITTMER PTHLH TARGETS UP	110	0.46692	1.813625	0.003968	0.027767
PENG GLUCOSE DEPRIVATION DN	163	0.425335	1.810238	<0.0001	0.028716
GRADE METASTASIS DN	42	0.621716	1.808554	0.003992	0.029112
CAFFAREL RESPONSE TO THC DN	29	0.654343	1.80552	0.012072	0.029849
GINESTIER BREAST CANCER 20Q13 AMPLIFICATION DN	151	0.503784	1.80388	0.022222	0.030246
TOMIDA METASTASIS UP	26	0.59838	1.803788	0.013645	0.030205
SMITH TERT TARGETS UP	141	0.440728	1.803614	0.004024	0.030182
KEGG NUCLEOTIDE EXCISION REPAIR	44	0.57315	1.803144	0.012097	0.030254
SANSOM APC TARGETS UP	113	0.431182	1.802453	<0.0001	0.030369
SANSOM APC TARGETS REQUIRE MYC	192	0.456086	1.802067	0.003929	0.03042
WANG LMO4 TARGETS DN	326	0.418273	1.802056	<0.0001	0.030356
REACTOME TRANSCRIPTIONAL ACTIVITY OF SMAD2 SMAD3 SMAD4 HETEROTRIMER	36	0.544208	1.801772	0.006036	0.030366
SENGUPTA NASOPHARYNGEAL CARCINOMA WITH LMP1 UP	375	0.442444	1.801458	<0.0001	0.030403
SILIGAN TARGETS OF EWS FLI1 FUSION DN	17	0.634452	1.800188	0.004167	0.030704
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS RED UP	16	0.676106	1.799742	0.01002	0.03076
REACTOME APC C CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC C CDH1 TARGETED PROTEINS IN LATE MITOSIS EARLY G1	64	0.656154	1.799011	0.009804	0.030907
SENESE HDAC1 TARGETS UP	425	0.437943	1.797798	0.009709	0.031177
JAZAG TGFB1 SIGNALING UP	104	0.414879	1.796938	<0.0001	0.03138
REACTOME APC C CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS	65	0.662565	1.796022	0.007874	0.031625
MULLIGAN NTF3 SIGNALING VIA INSR AND IGF1R UP	23	0.616338	1.793555	0.00198	0.03224

BROWN MYELOID CELL DEVELOPMENT DN	119	0.42822	1.792586	0.002008	0.032431
KIM MYCL1 AMPLIFICATION TARGETS DN	19	0.599645	1.79035	0.007859	0.033071
REACTOME POST CHAPERONIN TUBULIN FOLDING PATHWAY	18	0.647657	1.789697	0.011928	0.033205
REACTOME ANTIGEN PROCESSING UBIQUITINATION PROTEASOME DEGRADATION	192	0.45398	1.789484	0.006024	0.033225
SA G1 AND S PHASES	15	0.6574	1.788893	0.005964	0.033355
ZHANG RESPONSE TO IKK INHIBITOR AND TNF DN	100	0.450021	1.788685	0.004167	0.033329
VERHAAK GLIOBLASTOMA PRONEURAL	167	0.481945	1.787275	0.009921	0.033671
LASTOWSKA NEUROBLASTOMA COPY NUMBER UP	163	0.49957	1.786955	0.018762	0.033691
WEIGEL OXIDATIVE STRESS BY HNE AND H2O2	39	0.497943	1.785722	0.005871	0.034037
PIONTEK PKD1 TARGETS DN	16	0.66367	1.783604	0.01	0.034663
MAYBURD RESPONSE TO L663536 UP	27	0.52913	1.783244	0.003992	0.03471
WATANABE COLON CANCER MSI VS MSS UP	27	0.545412	1.781706	0.004032	0.035103
CHIN BREAST CANCER COPY NUMBER UP	24	0.629027	1.781215	0.008032	0.035183
STANELLE E2F1 TARGETS	27	0.522403	1.778581	0.007968	0.03596
MARTORIATI MDM4 TARGETS FETAL LIVER DN	495	0.412415	1.778176	0.002053	0.036003
TOOKER GEMCITABINE RESISTANCE DN	119	0.454145	1.776444	0.008	0.0365
KAMMINGA SENESCENCE	39	0.513728	1.775628	0.013514	0.036659
LOCKWOOD AMPLIFIED IN LUNG CANCER	205	0.472079	1.773483	0.016632	0.037359
BENPORATH OCT4 TARGETS	274	0.380914	1.77203	<0.0001	0.037773
DAZARD RESPONSE TO UV NHEK DN	301	0.480219	1.771112	0.035573	0.038047
GRESHOCK CANCER COPY NUMBER UP	313	0.399372	1.769583	<0.0001	0.038534
REACTOME ASSOCIATION OF TRIC CCT WITH TARGET PROTEINS DURING BIOSYNTHESIS	26	0.550117	1.768524	0.012097	0.038838
MATSUDA NATURAL KILLER DIFFERENTIATION	455	0.361808	1.76741	<0.0001	0.039152
BONOME OVARIAN CANCER POOR SURVIVAL DN	20	0.614894	1.766414	0.011834	0.039404
REACTOME RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATCH REPLACEMENT PATHWAY	17	0.700982	1.763146	0.002016	0.04048
REACTOME TRANSCRIPTION COUPLED NER TC NER	43	0.573218	1.761344	0.024242	0.041027
MMS MOUSE LYMPH HIGH 4HRS UP	31	0.593276	1.760869	0.015748	0.041122
NIKOLSKY BREAST CANCER 12Q24 AMPLICON	15	0.786594	1.760698	0.013972	0.041126
DORMOY ELAVL1 TARGETS	16	0.636704	1.76029	0.006211	0.041206
OUELLET CULTURED OVARIAN CANCER INVASIVE VS LMP UP	65	0.510015	1.758884	0.002096	0.041618
YANAGIHARA ESX1 TARGETS	29	0.558055	1.757296	0.004167	0.042167
RAHMAN TP53 TARGETS PHOSPHORYLATED	21	0.696858	1.75633	0.010142	0.042431
ZHANG RESPONSE TO CANTHARIDIN DN	67	0.586782	1.756311	0.013861	0.042349
BURTON ADIPOGENESIS 12	31	0.633779	1.756028	0.020704	0.042374
LIAO HAVE SOX4 BINDING SITES	40	0.487452	1.754347	0.006276	0.042969
HEIDENBLAD AMPLICON 8Q24 UP	34	0.506113	1.754154	0.005747	0.042956
WANG TUMOR INVASIVENESS UP	362	0.422517	1.753477	0.007692	0.043095
FARMER BREAST CANCER BASAL VS LULMINAL	317	0.372322	1.751602	<0.0001	0.043758
CAFFAREL RESPONSE TO THC 24HR 5 DN	55	0.5424	1.750371	0.01751	0.044157
KENNY CTNNB1 TARGETS UP	46	0.466248	1.749652	<0.0001	0.044315
GENTILE UV RESPONSE CLUSTER D8	39	0.555961	1.749345	0.004274	0.044325
MORI SMALL PRE BII LYMPHOCYTE DN	74	0.441043	1.747196	0.011583	0.045
SCHAEFFER PROSTATE DEVELOPMENT 6HR DN	482	0.37942	1.746934	0.003953	0.045025
PANGAS TUMOR SUPPRESSION BY SMAD1 AND SMAD5 DN	142	0.385688	1.746443	0.002058	0.045144
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS	31	0.575021	1.746114	0.012346	0.045182

YELLOW UP					
ELVIDGE HIF1A AND HIF2A TARGETS UP	38	0.532076	1.745029	0.008214	0.045525
HEDENFALK BREAST CANCER HEREDITARY VS SPORADIC	46	0.510439	1.744883	0.012931	0.045492
DING LUNG CANCER EXPRESSION BY COPY NUMBER	96	0.522323	1.741925	0.02079	0.04658
SYED ESTRADIOL RESPONSE	19	0.567053	1.741695	0.003914	0.046594
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 10	64	0.554322	1.738372	0.009862	0.047833
KORKOLA TERATOMA	39	0.521538	1.736379	0.002066	0.048542
BENPORATH NOS TARGETS	167	0.394158	1.735487	<0.0001	0.048808
REACTOME RNA POL II PRE TRANSCRIPTION EVENTS	51	0.536591	1.73453	0.022088	0.049143
PID PI3KCI AKT PATHWAY	35	0.517671	1.730794	0.008547	0.050573
BLALOCK ALZHEIMERS DISEASE INCIPIENT DN	161	0.423464	1.729327	<0.0001	0.051089
AMUNDSON RESPONSE TO ARSENITE	211	0.361445	1.728605	0.002041	0.051243
GRYDER PAX3FOXO1 TOP ENHANCERS	429	0.380099	1.726814	0.00202	0.051803
MILI PSEUDOPODIA HAPTOTAXIS UP	483	0.478654	1.726012	0.020833	0.052022
YIH RESPONSE TO ARSENITE C3	35	0.513379	1.724346	0.013514	0.052628
GOTZMANN EPITHELIAL TO MESENCHYMAL TRANSITION UP	68	0.49008	1.724127	0.024048	0.052635
SANSOM APC TARGETS	192	0.370204	1.724123	<0.0001	0.052533
REACTOME SIGNALING BY TGF BETA RECEPTOR COMPLEX	60	0.476028	1.724074	0.013672	0.052459
BIOCARTA TEL PATHWAY	18	0.594007	1.724068	0.017822	0.052363
GAZIN EPIGENETIC SILENCING BY KRAS	24	0.530104	1.721906	0.016949	0.053168
KARAKAS TGFB1 SIGNALING	18	0.653596	1.721183	0.018256	0.053392
REACTOME REGULATION OF MRNA STABILITY BY PROTEINS THAT BIND AU RICH ELEMENTS	81	0.534093	1.720097	0.023762	0.053774
JIANG VHL TARGETS	130	0.424455	1.717976	0.00404	0.054626
REACTOME DESTABILIZATION OF MRNA BY AUF1 HNRNP D0	50	0.639686	1.717617	0.029412	0.054663
KEGG PYRIMIDINE METABOLISM	96	0.471784	1.716585	0.016097	0.054958
MARKS HDAC TARGETS DN	15	0.636935	1.716012	0.009615	0.055123
REACTOME CDT1 ASSOCIATION WITH THE CDC6 ORC ORIGIN COMPLEX	54	0.65589	1.716	0.025591	0.055023
KEGG RNA DEGRADATION	56	0.51927	1.715115	0.026477	0.055308
ENK UV RESPONSE EPIDERMIS UP	277	0.396653	1.71478	0.003839	0.055362
SANSOM APC MYC TARGETS	198	0.391441	1.714559	0.003953	0.055379
TAYLOR METHYLATED IN ACUTE LYMPHOBLASTIC LEUKEMIA	73	0.449887	1.713326	0.008032	0.055865
SMID BREAST CANCER RELAPSE IN BONE DN	293	0.393585	1.712422	0.002008	0.05618
ZEMBUTSU SENSITIVITY TO METHOTREXATE	16	0.585476	1.711834	0.006122	0.056327
BONCI TARGETS OF MIR15A AND MIR16 1	88	0.455043	1.709993	0.015779	0.057015
ZUCCHI METASTASIS UP	38	0.508496	1.709634	0.005803	0.05706
ALFANO MYC TARGETS	230	0.384211	1.709342	0.006085	0.057078
WATANABE RECTAL CANCER RADIOTHERAPY RESPONSIVE DN	89	0.448667	1.708183	0.014286	0.057529
RICKMAN TUMOR DIFFERENTIATED WELL VS POORLY UP	219	0.44463	1.707944	0.022267	0.057539
REACTOME SHC1 EVENTS IN EGFR SIGNALING	15	0.626948	1.70774	0.011765	0.057526
REACTOME CLASS I MHC MEDIATED ANTIGEN PROCESSING PRESENTATION	229	0.413844	1.706487	0.007767	0.058032
FERRANDO HOX11 NEIGHBORS	23	0.62554	1.706106	0.022	0.058088
MCBRYAN PUBERTAL BREAST 6 7WK DN	76	0.426278	1.705047	0.00396	0.058458
BURTON ADIPOGENESIS PEAK AT 8HR	39	0.494526	1.703544	0.015717	0.059112
REACTOME AUTODEGRADATION OF CDH1 BY CDH1 APC C	56	0.628255	1.703088	0.021442	0.059224
DORN ADENOVIRUS INFECTION 12HR DN	33	0.505449	1.702581	0.013566	0.059348
VETTER TARGETS OF PRKCA AND ETS1 UP	15	0.603878	1.701816	0.021739	0.059581

SAKAI CHRONIC HEPATITIS VS LIVER CANCER UP	79	0.497029	1.70124	0.020243	0.059765
PID MYC PATHWAY	25	0.551098	1.700995	0.019231	0.05978
REACTOME TRANSCRIPTION	188	0.5167	1.70089	0.030769	0.059728
PID BETA CATENIN NUC PATHWAY	74	0.428773	1.699252	<0.0001	0.060403
BIOCARTA CASPASE PATHWAY	23	0.546091	1.69897	0.022634	0.060432
REACTOME AMINO ACID SYNTHESIS AND INTERCONVERSION TRANSAMINATION	15	0.639634	1.698237	0.02045	0.060687
BIOCARTA TNFR1 PATHWAY	29	0.499905	1.693128	0.009901	0.062986
AZARE STAT3 TARGETS	23	0.578007	1.692447	0.034951	0.063226
KEGG GLYOXYLATE AND DICARBOXYLATE METABOLISM	16	0.621381	1.692134	0.021401	0.063253
HOFMANN CELL LYMPHOMA UP	46	0.47245	1.690977	0.019841	0.063748
PODAR RESPONSE TO ADAPHOSTIN DN	18	0.625287	1.690159	0.03	0.063966
KEGG SMALL CELL LUNG CANCER	84	0.424916	1.690009	0.009671	0.063918
REACTOME APOPTOSIS	141	0.441803	1.688153	0.014141	0.064708
KIM WT1 TARGETS 8HR DN	114	0.367602	1.687968	<0.0001	0.064702
BROWNE HCMV INFECTION 18HR UP	171	0.40397	1.687676	0.00625	0.064768
REACTOME DOWNREGULATION OF SMAD2 3 SMAD4 TRANSCRIPTIONAL ACTIVITY	19	0.58538	1.687628	0.021442	0.064689
IVANOVA HEMATOPOIESIS STEM CELL SHORT TERM	29	0.506089	1.687402	0.01378	0.064653
DEBIASI APOPTOSIS BY REOVIRUS INFECTION UP	303	0.423488	1.687207	0.008351	0.064646
BOYAULT LIVER CANCER SUBCLASS G2	27	0.495766	1.686316	0.004008	0.064983
LIN MELANOMA COPY NUMBER UP	67	0.473821	1.686184	0.017822	0.064929
KOINUMA COLON CANCER MSI UP	16	0.626124	1.686045	0.013699	0.064876
MILI PSEUDOPODIA CHEMOTAXIS UP	69	0.429895	1.684119	0.010267	0.065686
PROVENZANI METASTASIS UP	183	0.40015	1.683638	0.009804	0.065785
MARZEC IL2 SIGNALING UP	110	0.422339	1.682607	0.013436	0.066183
FIRESTEIN CTNNB1 PATHWAY	32	0.494589	1.682464	0.011605	0.066128
SCHAEFFER SOX9 TARGETS IN PROSTATE DEVELOPMENT DN	44	0.519023	1.682038	0.031373	0.066261
XU CREBBP TARGETS UP	24	0.534615	1.679093	0.01232	0.067797
SHAFFER IRF4 TARGETS IN MYELOMA VS MATURE B LYMPHOCYTE	99	0.445432	1.677055	0.022	0.06873
KOKKINAKIS METHIONINE DEPRIVATION 48HR DN	64	0.42631	1.676694	0.011696	0.068758
REACTOME GLYCOLYSIS	25	0.579583	1.676492	0.031068	0.068741
REACTOME P53 INDEPENDENT G1 S DNA DAMAGE CHECKPOINT	48	0.638372	1.676365	0.023904	0.068702
WEST ADRENOCORTICAL CARCINOMA VS ADENOMA UP	18	0.568753	1.674831	0.017893	0.06942
REACTOME CYCLIN E ASSOCIATED EVENTS DURING G1 S TRANSITION	62	0.599862	1.67442	0.039216	0.069487
HASLINGER B CLL WITH CHROMOSOME 12 TRISOMY	22	0.589413	1.674138	0.029586	0.069513
KEGG P53 SIGNALING PATHWAY	66	0.437661	1.671067	0.015905	0.071007
BHAT ESR1 TARGETS VIA AKT1 UP	267	0.383494	1.671063	0.019194	0.070885
ELVIDGE HYPOXIA BY DMOG DN	54	0.442393	1.670696	0.008264	0.070981
SMID BREAST CANCER RELAPSE IN BRAIN UP	39	0.507199	1.670125	0.016227	0.071179
REACTOME DESTABILIZATION OF MRNA BY KSRP	17	0.583577	1.669474	0.022177	0.071476
ZHENG IL22 SIGNALING DN	37	0.459242	1.669029	0.012371	0.071538
DE YY1 TARGETS DN	90	0.469888	1.666946	0.028	0.072512
REACTOME NUCLEOTIDE EXCISION REPAIR	48	0.520226	1.66664	0.034553	0.07257
GAJATE RESPONSE TO TRABECTEDIN DN	18	0.591151	1.664867	0.023346	0.073436
FARMER BREAST CANCER CLUSTER 5	18	0.732468	1.663821	0.033865	0.073843

REACTOME G1 PHASE	35	0.50546	1.662827	0.023529	0.074266
TCGA GLIOBLASTOMA COPY NUMBER UP	66	0.467425	1.660534	0.018828	0.07536
STAMBOLSKY TARGETS OF MUTATED TP53 UP	46	0.447634	1.660451	0.008114	0.075257
OUILLETTE CLL 13Q14 DELETION UP	69	0.427047	1.659901	0.013514	0.075401
PID RB 1PATHWAY	65	0.42723	1.659408	0.011811	0.075576
DOANE RESPONSE TO ANDROGEN DN	225	0.348679	1.659151	0.001949	0.075572
REACTOME P53 DEPENDENT G1 DNA DAMAGE RESPONSE	53	0.604504	1.65892	0.035785	0.075585
HAHTOLA SEZARY SYNDROM UP	92	0.430003	1.658449	0.015656	0.075731
GAZDA DIAMOND BLACKFAN ANEMIA PROGENITOR DN	62	0.475799	1.65785	0.01848	0.075901
KEGG PROTEASOME	42	0.651967	1.65695	0.029412	0.076312
KIM WT1 TARGETS 12HR DN	200	0.391558	1.656898	0.005976	0.07619
SIG REGULATION OF THE ACTIN CYTOSKELETON BY RHO GTPASES	34	0.524591	1.655948	0.035928	0.076606
TSENG IRS1 TARGETS UP	106	0.403401	1.653592	0.018293	0.077854
WIERENGA PML INTERACTOME	40	0.513588	1.652293	0.025845	0.078457
OSMAN BLADDER CANCER UP	383	0.398818	1.651791	0.029183	0.078594
MCBRYAN PUBERTAL BREAST 5 6WK DN	127	0.400125	1.65131	0.017578	0.078743
BHAT ESR1 TARGETS NOT VIA AKT1 UP	204	0.376136	1.650532	0.007634	0.079063
RAY TUMORIGENESIS BY ERBB2 CDC25A UP	99	0.381187	1.650404	0.003839	0.079009
SCHLOSSER MYC AND SERUM RESPONSE SYNERGY	31	0.590989	1.648224	0.036735	0.080162
SHIN B CELL LYMPHOMA CLUSTER 8	36	0.530104	1.646891	0.023952	0.080756
WONG ENDMETRIUM CANCER UP	25	0.519694	1.644474	0.009804	0.082115
FLECHNER PBL KIDNEY TRANSPLANT REJECTED VS OK UP	62	0.41146	1.643248	0.008016	0.082744
AMUNDSON GENOTOXIC SIGNATURE	99	0.3757	1.640345	0.011905	0.084355
LIU VMYB TARGETS UP	114	0.382195	1.639758	0.010526	0.084548
MARIADASON RESPONSE TO BUTYRATE SULINDAC 6	46	0.474213	1.639427	0.031373	0.084617
HOFMANN MYELODYSPLASTIC SYNDROM LOW RISK DN	30	0.531183	1.638773	0.031621	0.084872
FLOTHO PEDIATRIC ALL THERAPY RESPONSE DN	27	0.499248	1.636458	0.021401	0.086038
POMEROY MEDULLOBLASTOMA PROGNOSIS DN	43	0.57809	1.635835	0.049801	0.086282
KUMAR PATHOGEN LOAD BY MACROPHAGES	245	0.321681	1.635697	<0.0001	0.08622
ZHONG RESPONSE TO AZACITIDINE AND TSA DN	63	0.465464	1.635426	0.033663	0.086261
STEIN ESRRA TARGETS RESPONSIVE TO ESTROGEN UP	29	0.484024	1.633561	0.025641	0.087285
KORKOLA YOLK SAC TUMOR UP	19	0.643292	1.632927	0.040777	0.087605
GOLDRATH HOMEOSTATIC PROLIFERATION	163	0.42393	1.632349	0.025794	0.087816
HU GENOTOXIN ACTION DIRECT VS INDIRECT 24HR	51	0.45042	1.631855	0.014228	0.087994
GEISS RESPONSE TO DSRNA DN	15	0.573206	1.631693	0.029703	0.087959
BROWNE HCMV INFECTION 16HR UP	217	0.383509	1.631379	0.023605	0.08802
RIZ ERYTHROID DIFFERENTIATION CCNE1	39	0.466142	1.630702	0.010204	0.088318
KIM TIAL1 TARGETS	31	0.504676	1.630118	0.020408	0.088558
BROWNE HCMV INFECTION 20HR UP	230	0.348789	1.629245	0.006148	0.088915
REACTOME SMAD2 SMAD3 SMAD4 HETEROTRIMER REGULATES TRANSCRIPTION	25	0.519864	1.627145	0.024952	0.090188
JAERVINEN AMPLIFIED IN LARYNGEAL CANCER	37	0.478422	1.625893	0.030992	0.090827
REACTOME INTRINSIC PATHWAY FOR APOPTOSIS	29	0.526158	1.625654	0.030303	0.090809
REACTOME CDK MEDIATED PHOSPHORYLATION AND REMOVAL OF CDC6	46	0.6389	1.624869	0.04	0.09111
YAGI AML SURVIVAL	119	0.359624	1.623065	0.006048	0.092076
ST FAS SIGNALING PATHWAY	63	0.399853	1.621458	0.025341	0.093009
YIH RESPONSE TO ARSENITE C1	23	0.53364	1.62096	0.016495	0.093186

LU EZH2 TARGETS DN	356	0.367171	1.61638	0.010204	0.09598
FARMER BREAST CANCER APOCRINE VS BASAL	316	0.346667	1.613765	0.011952	0.097569
KAPOSI LIVER CANCER MET UP	17	0.593801	1.613735	0.03012	0.097431
BENPORATH MYC TARGETS WITH EBOX	219	0.370799	1.612224	0.017751	0.098274
DITTMER PTHLH TARGETS DN	72	0.419333	1.612067	0.014257	0.098229
PID DNA PK PATHWAY	16	0.561749	1.611967	0.037849	0.098136
CHENG IMPRINTED BY ESTRADIOL	100	0.36815	1.609978	0.008	0.099279
HOLLEMAN PREDNISOLONE RESISTANCE B ALL UP	22	0.561948	1.608265	0.049505	0.100329
BUCKANOVICH T LYMPHOCYTE HOMING ON TUMOR DN	19	0.51839	1.607094	0.025794	0.100969
KAN RESPONSE TO ARSENIC TRIOXIDE	118	0.412375	1.605869	0.023622	0.10133
TERAO AOX4 TARGETS SKIN UP	35	0.463012	1.605396	0.035019	0.101492
FLECHNER BIOPSY KIDNEY TRANSPLANT OK VS DONOR DN	25	0.476014	1.605174	0.018868	0.10146
WOOD EBV EBNA1 TARGETS UP	109	0.398263	1.604507	0.024242	0.101754
AMIT SERUM RESPONSE 480 MCF10A	34	0.522424	1.603219	0.038697	0.102526
PARK HSC VS MULTIPOTENT PROGENITORS DN	18	0.541898	1.602923	0.035785	0.102521
RIZ ERYTHROID DIFFERENTIATION HBZ	40	0.464598	1.602743	0.02268	0.102507
BROWNE HCMV INFECTION 10HR UP	95	0.36663	1.602081	0.011905	0.102773
BYSTROEM CORRELATED WITH IL5 DN	63	0.461639	1.602062	0.036145	0.102631
NIELSEN LIPOSARCOMA DN	19	0.500428	1.601659	0.037698	0.102737
PID LKB1 PATHWAY	46	0.432082	1.601294	0.020161	0.102882
BLUM RESPONSE TO SALIRASIB UP	236	0.38965	1.599729	0.021956	0.103503
REACTOME METABOLISM OF CARBOHYDRATES	228	0.355934	1.599639	0.00998	0.103413
ZHU CMV 24 HR UP	93	0.423945	1.598979	0.031746	0.103689
SMIRNOV RESPONSE TO IR 2HR DN	52	0.43491	1.597758	0.03012	0.104412
KANNAN TP53 TARGETS DN	21	0.518352	1.59535	0.04251	0.105786
CHEN HOXA5 TARGETS 9HR DN	36	0.475814	1.593394	0.035565	0.106848
STAMBOLSKY BOUND BY MUTATED TP53	17	0.533212	1.592761	0.022495	0.107007
JACKSON DNMT1 TARGETS DN	24	0.555331	1.592614	0.046332	0.106936
TIEN INTESTINE PROBIOTICS 6HR DN	158	0.378613	1.590721	0.024845	0.108007
REACTOME SIGNALING BY CONSTITUTIVELY ACTIVE EGFR	17	0.545932	1.590347	0.037624	0.10814
KIM MYC AMPLIFICATION TARGETS UP	186	0.409196	1.590281	0.028455	0.108037
WU HBX TARGETS 2 UP	22	0.512302	1.590024	0.013462	0.108072
SENESE HDAC3 TARGETS DN	481	0.324994	1.589872	0.010438	0.108029
SCHLOSSER SERUM RESPONSE AUGMENTED BY MYC	101	0.405214	1.588321	0.025845	0.108766
HIRSCH CELLULAR TRANSFORMATION SIGNATURE DN	95	0.381182	1.586471	0.010267	0.109937
WEI MIR34A TARGETS	141	0.367921	1.585311	0.018182	0.110588
DORSAM HOXA9 TARGETS UP	35	0.446791	1.584984	0.024242	0.110671
REACTOME PYRUVATE METABOLISM	18	0.540195	1.582334	0.04065	0.112131
QI HYPOXIA TARGETS OF HIF1A AND FOXA2	36	0.501433	1.582225	0.038986	0.112052
LU TUMOR ANGIOGENESIS UP	25	0.504791	1.582141	0.045098	0.111964
SIG PIP3 SIGNALING IN CARDIAC MYOCTES	66	0.400405	1.581374	0.015564	0.112419
MILI PSEUDOPODIA	41	0.424873	1.579452	0.030303	0.113724
REACTOME DEADENYLATION DEPENDENT MRNA DECAY	42	0.491756	1.577539	0.039683	0.114976
YANG BREAST CANCER ESR1 DN	24	0.49262	1.576019	0.035928	0.115959
BIOCARTA VEGF PATHWAY	29	0.470594	1.575019	0.03937	0.116361
PHONG TNF RESPONSE VIA P38 COMPLETE	221	0.345624	1.573374	0.007813	0.117145
PID AR PATHWAY	61	0.409093	1.572359	0.025641	0.117706
CONRAD STEM CELL	39	0.441007	1.568667	0.035789	0.119943
TURASHVILI BREAST CARCINOMA DUCTAL VS LOBULAR UP	19	0.528365	1.56845	0.026263	0.119939

WANG CLIM2 TARGETS UP	217	0.33065	1.567843	0.011173	0.120262
ZHAN EARLY DIFFERENTIATION GENES DN	42	0.478918	1.567609	0.035156	0.120259
JOHNSTONE PARVB TARGETS 2 DN	315	0.401319	1.567086	0.047817	0.120304
KYNG ENVIRONMENTAL STRESS RESPONSE DN	19	0.512273	1.566585	0.042084	0.120472
REACTOME RNA POL I TRANSCRIPTION TERMINATION	19	0.597967	1.563401	0.043388	0.12267
WANG RESPONSE TO FORSKOLIN UP	22	0.51664	1.563149	0.036217	0.12269
OZEN MIR125B1 TARGETS	25	0.477198	1.562725	0.036072	0.12285
BAE BRCA1 TARGETS DN	32	0.448326	1.561732	0.027237	0.123436
REACTOME PRE NOTCH EXPRESSION AND PROCESSING	38	0.438524	1.561665	0.028681	0.123334
MULLIGHAN NPM1 MUTATED SIGNATURE 2 UP	127	0.367212	1.560194	0.026157	0.124289
PID DELTA NP63 PATHWAY	45	0.441436	1.55967	0.026585	0.124484
LIU COMMON CANCER GENES	67	0.39207	1.558317	0.012346	0.125208
BYSTRYKH HEMATOPOIESIS STEM CELL AND BRAIN QTL TRANS	175	0.330511	1.557717	0.004082	0.125363
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS GREEN DN	22	0.488344	1.556341	0.044574	0.12629
PID MTOR 4PATHWAY	69	0.39131	1.552611	0.047893	0.128754
SPIELMAN LYMPHOBLAST EUROPEAN VS ASIAN UP	467	0.390019	1.55152	0.048096	0.129204
SENESE HDAC1 AND HDAC2 TARGETS UP	220	0.381878	1.547474	0.026871	0.131794
AUNG GASTRIC CANCER	53	0.422567	1.546632	0.015968	0.132246
DOANE BREAST CANCER ESR1 DN	47	0.460401	1.545565	0.034483	0.132745
HELLER HDAC TARGETS DN	275	0.341707	1.541225	0.023762	0.135545
RICKMAN TUMOR DIFFERENTIATED MODERATELY VS POORLY UP	114	0.372841	1.540628	0.025918	0.135672
PID PRL SIGNALING EVENTS PATHWAY	23	0.490748	1.539611	0.043478	0.136331
YEGNASUBRAMANIAN PROSTATE CANCER	117	0.388272	1.539252	0.022267	0.136289
WANG RESPONSE TO ANDROGEN UP	27	0.493984	1.539088	0.032653	0.136262
CEBALLOS TARGETS OF TP53 AND MYC DN	37	0.428256	1.53883	0.016293	0.136301
KYNG WERNER SYNDROM AND NORMAL AGING UP	87	0.374516	1.536424	0.017613	0.137926
WANG TARGETS OF MLL CBP FUSION DN	42	0.451813	1.536386	0.04008	0.137792
KYNG ENVIRONMENTAL STRESS RESPONSE NOT BY 4NQO IN WS	39	0.400106	1.534646	0.032819	0.139045
ZHU CMV ALL UP	119	0.39732	1.534112	0.037475	0.13933
BRUINS UVC RESPONSE EARLY LATE	292	0.32024	1.532619	0.008163	0.140356
PID NFAT 3PATHWAY	53	0.411672	1.531804	0.048	0.140939
LEE LIVER CANCER MYC UP	51	0.412772	1.531745	0.046243	0.140802
HOLLEMAN VINCRISTINE RESISTANCE ALL UP	25	0.482779	1.529622	0.038618	0.142
GENTILE UV RESPONSE CLUSTER D1	18	0.508266	1.528893	0.04918	0.142424
ROESSLER LIVER CANCER METASTASIS UP	102	0.355223	1.52781	0.01378	0.142963
LIANG HEMATOPOIESIS STEM CELL NUMBER LARGE VS TINY DN	40	0.419267	1.527717	0.034137	0.142837
DACOSTA UV RESPONSE VIA ERCC3 XPCS UP	25	0.471035	1.527198	0.042339	0.14272
REACTOME SIGNALING BY SCF KIT	75	0.389868	1.527054	0.041096	0.142489
BOYAULT LIVER CANCER SUBCLASS G1 UP	106	0.399934	1.525078	0.046122	0.143868
KEGG CHRONIC MYELOID LEUKEMIA	73	0.387383	1.52252	0.042065	0.145828
WANG TUMOR INVASIVENESS DN	200	0.341181	1.51853	0.032882	0.148878
BURTON ADIPOGENESIS 2	72	0.39755	1.515559	0.039216	0.151301
KEGG PANCREATIC CANCER	69	0.388184	1.514839	0.034749	0.151679
RAO BOUND BY SALL4 ISOFORM B	480	0.317776	1.514425	0.010504	0.151873

PID NOTCH PATHWAY	58	0.396508	1.512504	0.042885	0.15274
JACKSON DNMT1 TARGETS UP	74	0.395422	1.512036	0.035363	0.152911
CARD MIR302A TARGETS	77	0.402312	1.510654	0.045635	0.153927
JAZAERI BREAST CANCER BRCA1 VS BRCA2 UP	47	0.434109	1.50923	0.045726	0.154593
APRELIKOVA BRCA1 TARGETS	48	0.424253	1.505852	0.039666	0.156934
PID CDC42 PATHWAY	69	0.401321	1.505354	0.045545	0.157137
AMUNDSON POOR SURVIVAL AFTER GAMMA RADIATION 2G	161	0.334007	1.504761	0.035052	0.157336
SANSOM WNT PATHWAY REQUIRE MYC	57	0.401949	1.503344	0.046559	0.157967
MATZUK MALE REPRODUCTION SERTOLI	28	0.434846	1.502245	0.03876	0.158691
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 15	31	0.433252	1.497727	0.047817	0.162092
FLECHNER PBL KIDNEY TRANSPLANT REJECTED VS OK DN	50	0.404961	1.497522	0.027451	0.162076
KOYAMA SEMA3B TARGETS DN	370	0.304585	1.493319	0.014028	0.165129
BROWNE HCMV INFECTION 8HR DN	44	0.412397	1.489224	0.04845	0.167397
SHETH LIVER CANCER VS TXNIP LOSS PAM1	221	0.323902	1.486541	0.018293	0.169201
BROWNE HCMV INFECTION 30MIN DN	136	0.328255	1.484028	0.012097	0.171305
BAKKER FOXO3 TARGETS DN	168	0.323115	1.482407	0.020161	0.172384
CREIGHTON ENDOCRINE THERAPY RESISTANCE 4	278	0.307611	1.481572	0.010142	0.17294
SHIPP DLBCL CURED VS FATAL DN	42	0.385979	1.481241	0.044146	0.173025
KEGG PURINE METABOLISM	152	0.342204	1.479581	0.049383	0.174054
MULLIGHAN NPM1 SIGNATURE 3 UP	311	0.302873	1.479113	0.023715	0.174293
REACTOME SIGNALING BY NOTCH	95	0.343089	1.475223	0.020325	0.177146
GRYDER PAX3FOXO1 ENHANCERS KO DOWN	426	0.324932	1.471148	0.046	0.180045
PASINI SUZ12 TARGETS UP	102	0.33258	1.47112	0.027505	0.179851
BROWNE HCMV INFECTION 12HR UP	104	0.347793	1.467365	0.034343	0.182405
BROWNE HCMV INFECTION 24HR UP	139	0.322127	1.457753	0.031373	0.190306
LINSLEY MIR16 TARGETS	190	0.334743	1.454722	0.049213	0.192201
LIN NPAS4 TARGETS UP	146	0.325163	1.448942	0.026423	0.196818
DEURIG T CELL PROLYMPHOCYTIC LEUKEMIA UP	340	0.30133	1.447941	0.028226	0.197356
HOFFMANN SMALL PRE BII TO IMMATURE B LYMPHOCYTE DN	45	0.368485	1.445439	0.041754	0.198977
KEGG PROSTATE CANCER	89	0.352522	1.444957	0.042636	0.199044
OKUMURA INFLAMMATORY RESPONSE LPS	171	0.315914	1.443961	0.025845	0.199091
WALLACE PROSTATE CANCER RACE DN	74	0.347913	1.443845	0.04321	0.198982
ST PHOSPHOINOSITIDE 3 KINASE PATHWAY	37	0.400296	1.442385	0.03854	0.200005
FORTSCHEGGER PHF8 TARGETS UP	248	0.312259	1.436562	0.046559	0.204157
YOSHIMURA MAPK8 TARGETS DN	350	0.308065	1.432228	0.028112	0.206833
CADWELL ATG16L1 TARGETS DN	63	0.358065	1.430796	0.045833	0.207804
SHEPARD BMYB MORPHOLINO UP	201	0.312314	1.429427	0.018036	0.20901
RAO BOUND BY SALL4	218	0.312793	1.415285	0.043912	0.218891
IWANAGA CARCINOGENESIS BY KRAS PTEN UP	163	0.311604	1.413827	0.029586	0.219995
DARWICHE PAPILLOMA RISK LOW UP	149	0.333083	1.408046	0.049808	0.223985
BROWNE HCMV INFECTION 1HR DN	208	0.28726	1.407956	0.019531	0.223845
BROWNE HCMV INFECTION 8HR UP	100	0.322791	1.390408	0.043299	0.235521
FIRESTEIN PROLIFERATION	166	0.30195	1.388269	0.04918	0.236965
LEE AGING NEOCORTEX DN	75	0.342268	1.386387	0.043299	0.237327
GAUSSMANN MLL AF4 FUSION TARGETS A UP	176	0.311393	1.381745	0.047525	0.240275

ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate; GSEA, gene set enrichment analysis; KIF, kinesin.

Table SIV. **GSEA results of c5 reference gene set of high *KIF18B* expression group.**

Name	Size	ES	NES	NOM P-value	FDR q-value
GO MITOTIC NUCLEAR DIVISION	337	0.695214	2.533665	<0.0001	<0.0001
GO MITOTIC SISTER CHROMATID SEGREGATION	88	0.824457	2.504	<0.0001	<0.0001
GO ORGANELLE FISSION	449	0.65348	2.487347	<0.0001	<0.0001
GO REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	164	0.630036	2.466409	<0.0001	<0.0001
GO REGULATION OF MICROTUBULE BASED PROCESS	226	0.613028	2.45458	<0.0001	<0.0001
GO CHROMOSOME SEGREGATION	247	0.733279	2.453065	<0.0001	<0.0001
GO CELL DIVISION	423	0.622785	2.432042	<0.0001	<0.0001
GO CELL CYCLE CHECKPOINT	179	0.639043	2.423801	<0.0001	<0.0001
GO SPINDLE POLE	113	0.665984	2.41154	<0.0001	<0.0001
GO CONDENSED CHROMOSOME	169	0.745587	2.399401	<0.0001	7.85E-05
GO SISTER CHROMATID SEGREGATION	163	0.786773	2.398867	<0.0001	7.14E-05
GO NUCLEAR CHROMOSOME SEGREGATION	204	0.744149	2.390345	<0.0001	6.55E-05
GO DNA RECOMBINATION	189	0.692473	2.387913	<0.0001	6.04E-05
GO SPINDLE	267	0.605558	2.381053	<0.0001	5.61E-05
GO DNA REPLICATION	192	0.719517	2.377038	<0.0001	5.24E-05
GO REGULATION OF NUCLEAR DIVISION	153	0.613795	2.372078	<0.0001	4.91E-05
GO MITOTIC CELL CYCLE CHECKPOINT	129	0.615084	2.365139	<0.0001	4.62E-05
GO DNA INTEGRITY CHECKPOINT	136	0.604388	2.364059	<0.0001	4.36E-05
GO CELL CYCLE PHASE TRANSITION	248	0.658892	2.362131	<0.0001	4.13E-05
GO MITOTIC SPINDLE	50	0.708673	2.353799	<0.0001	3.93E-05
GO REGULATION OF CHROMOSOME SEGREGATION	77	0.732982	2.335761	<0.0001	3.74E-05
GO MITOTIC RECOMBINATION	41	0.892067	2.330344	<0.0001	7.05E-05
GO REGULATION OF SISTER CHROMATID SEGREGATION	61	0.71342	2.329753	<0.0001	6.74E-05
GO POSITIVE REGULATION OF CELL CYCLE PHASE TRANSITION	66	0.652319	2.324191	<0.0001	6.46E-05
GO MITOTIC SPINDLE ORGANIZATION	64	0.734191	2.323057	<0.0001	6.21E-05
GO NEGATIVE REGULATION OF PROTEIN COMPLEX DISASSEMBLY	156	0.580054	2.318141	<0.0001	5.97E-05
GO NEGATIVE REGULATION OF MITOTIC CELL CYCLE	184	0.545554	2.317627	<0.0001	5.75E-05
GO DNA DEPENDENT DNA REPLICATION	90	0.776615	2.315754	<0.0001	5.54E-05
GO CELL CYCLE G1 S PHASE TRANSITION	108	0.731461	2.309636	<0.0001	5.35E-05
GO CONDENSED NUCLEAR CHROMOSOME	74	0.72556	2.30792	<0.0001	5.17E-05
GO CHROMOSOME CENTROMERIC REGION	153	0.743936	2.306779	<0.0001	5.00E-05
GO CHROMOSOMAL REGION	297	0.679537	2.300972	<0.0001	4.85E-05
GO DNA BIOSYNTHETIC PROCESS	108	0.652386	2.294378	<0.0001	4.70E-05
GO KINETOCHORE	103	0.75897	2.292932	<0.0001	4.56E-05
GO NEGATIVE REGULATION OF CELL CYCLE PROCESS	199	0.540729	2.292379	<0.0001	4.43E-05
GO DNA REPAIR	433	0.590051	2.282094	<0.0001	7.41E-05
GO MEIOTIC CELL CYCLE	162	0.620952	2.28104	<0.0001	7.21E-05

GO CENTROSOME CYCLE	44	0.725436	2.279923	<0.0001	7.02E-05
GO REGULATION OF CELL DIVISION	250	0.543265	2.279514	<0.0001	6.84E-05
GO MEIOTIC CELL CYCLE PROCESS	130	0.639148	2.272672	<0.0001	6.66E-05
GO CELL CYCLE G2 M PHASE TRANSITION	134	0.613278	2.266491	<0.0001	6.50E-05
GO PROTEIN SUMOYLATION	112	0.650545	2.258938	<0.0001	6.35E-05
GO SPINDLE MICROTUBULE	56	0.699954	2.251328	<0.0001	6.20E-05
GO CONDENSED CHROMOSOME CENTROMERIC REGION	83	0.802744	2.250374	<0.0001	6.06E-05
GO CHROMOSOME LOCALIZATION	56	0.713117	2.248999	<0.0001	5.92E-05
GO SISTER CHROMATID COHESION	100	0.788677	2.242098	<0.0001	9.45E-05
GO MICROTUBULE CYTOSKELETON ORGANIZATION	314	0.549524	2.23961	<0.0001	1.45E-04
GO MITOTIC DNA INTEGRITY CHECKPOINT	93	0.576269	2.23897	<0.0001	1.42E-04
GO DOUBLE STRAND BREAK REPAIR	151	0.656316	2.237831	<0.0001	1.40E-04
GO TELOMERE MAINTENANCE VIA RECOMBINATION	32	0.883217	2.236518	<0.0001	1.81E-04
GO POSITIVE REGULATION OF MITOTIC CELL CYCLE	118	0.588028	2.235824	<0.0001	1.78E-04
GO MIDBODY	121	0.567507	2.222937	<0.0001	2.70E-04
GO POSITIVE REGULATION OF CELL CYCLE PROCESS	227	0.534526	2.221087	<0.0001	2.65E-04
GO METAPHASE PLATE CONGRESSION	41	0.760706	2.218585	<0.0001	2.60E-04
GO NEGATIVE REGULATION OF CYTOSKELETON ORGANIZATION	205	0.517592	2.212474	<0.0001	2.90E-04
GO REGULATION OF TRANSCRIPTION INVOLVED IN G1 S TRANSITION OF MITOTIC CELL CYCLE	25	0.860641	2.212003	<0.0001	2.84E-04
GO POSITIVE REGULATION OF MITOTIC NUCLEAR DIVISION	46	0.652065	2.203988	<0.0001	3.43E-04
GO REGULATION OF MITOTIC CELL CYCLE	444	0.516949	2.198882	<0.0001	4.59E-04
GO SPINDLE MIDZONE	25	0.798669	2.198844	<0.0001	4.51E-04
GO REGULATION OF DNA DEPENDENT DNA REPLICATION	39	0.766749	2.198039	<0.0001	4.80E-04
GO RECOMBINATIONAL REPAIR	70	0.696163	2.197403	<0.0001	4.72E-04
GO RNA LOCALIZATION	173	0.594813	2.196538	<0.0001	5.06E-04
GO REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	156	0.557775	2.196347	<0.0001	4.98E-04
GO REGULATION OF PROTEIN COMPLEX DISASSEMBLY	198	0.53506	2.193278	<0.0001	5.78E-04
GO MITOTIC SPINDLE ASSEMBLY	39	0.696308	2.192221	<0.0001	5.87E-04
GO REPLICATION FORK	62	0.753177	2.191554	<0.0001	5.95E-04
GO REGULATION OF CENTROSOME CYCLE	38	0.727174	2.187337	<0.0001	6.82E-04
GO MICROTUBULE ORGANIZING CENTER ORGANIZATION	79	0.620049	2.18608	<0.0001	6.93E-04
GO REGULATION OF DNA REPLICATION	152	0.567544	2.186019	<0.0001	6.83E-04
GO DEOXYRIBONUCLEASE ACTIVITY	63	0.618961	2.183639	<0.0001	7.00E-04
GO RESPONSE TO IONIZING RADIATION	137	0.545946	2.183277	<0.0001	7.11E-04
GO NUCLEAR CHROMOSOME	488	0.569787	2.180921	<0.0001	7.21E-04
GO DNA STRAND ELONGATION	29	0.861615	2.175984	<0.0001	7.62E-04
GO DNA SYNTHESIS INVOLVED IN DNA REPAIR	67	0.690984	2.173705	<0.0001	8.09E-04

GO NEGATIVE REGULATION OF CELL DIVISION	56	0.651914	2.167547	<0.0001	8.76E-04
GO SPINDLE ASSEMBLY	67	0.632129	2.164428	<0.0001	8.99E-04
GO POSITIVE REGULATION OF CELL CYCLE	308	0.48716	2.161335	<0.0001	9.58E-04
GO REGULATION OF DNA METABOLIC PROCESS	318	0.506619	2.158969	<0.0001	9.64E-04
GO ENDODEOXYRIBONUCLEASE ACTIVITY	48	0.636288	2.158758	<0.0001	9.62E-04
GO HELICASE ACTIVITY	148	0.632376	2.153421	<0.0001	0.001014
GO NEGATIVE REGULATION OF CELL CYCLE	404	0.444209	2.153408	<0.0001	0.00101
GO NUCLEAR PERIPHERY	118	0.576716	2.153239	<0.0001	9.98E-04
GO REGULATION OF CELL CYCLE PHASE TRANSITION	308	0.519991	2.146266	<0.0001	0.001149
GO G2 DNA DAMAGE CHECKPOINT	31	0.676847	2.144829	<0.0001	0.001145
GO HETEROCHROMATIN	65	0.622782	2.144475	<0.0001	0.001132
GO PURINE NTP DEPENDENT HELICASE ACTIVITY	95	0.639972	2.143051	<0.0001	0.001161
GO DNA STRAND ELONGATION INVOLVED IN DNA REPLICATION	25	0.892482	2.139555	<0.0001	0.001264
GO RIBONUCLEOPROTEIN COMPLEX LOCALIZATION	112	0.624821	2.136743	<0.0001	0.001319
GO NUCLEAR ENVELOPE ORGANIZATION	75	0.594105	2.132639	<0.0001	0.001367
GO MEIOSIS I	73	0.633108	2.130637	<0.0001	0.001419
GO MEMBRANE DISASSEMBLY	44	0.70757	2.130143	<0.0001	0.001421
GO REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	57	0.602969	2.129376	<0.0001	0.001413
GO POSITIVE REGULATION OF DNA METABOLIC PROCESS	174	0.497878	2.129143	<0.0001	0.001406
GO DNA GEOMETRIC CHANGE	77	0.668556	2.128682	<0.0001	0.001391
GO MULTI ORGANISM LOCALIZATION	65	0.644368	2.128169	<0.0001	0.001396
GO DNA HELICASE ACTIVITY	50	0.754319	2.12734	<0.0001	0.001406
GO NEGATIVE REGULATION OF CELL CYCLE PHASE TRANSITION	137	0.526797	2.12709	<0.0001	0.001413
GO NEGATIVE REGULATION OF ORGANELLE ORGANIZATION	361	0.472241	2.124627	<0.0001	0.001452
GO ATPASE ACTIVITY	412	0.481783	2.119326	<0.0001	0.001585
GO G1 DNA DAMAGE CHECKPOINT	68	0.554537	2.118361	<0.0001	0.001656
GO PROTEIN DEPOLYMERIZATION	23	0.710478	2.116016	<0.0001	0.001669
GO DNA DEPENDENT ATPASE ACTIVITY	76	0.699925	2.112583	<0.0001	0.00179
GO POSITIVE REGULATION OF CHROMOSOME SEGREGATION	23	0.758324	2.111786	<0.0001	0.001787
GO CELL DIVISION SITE	47	0.616768	2.111476	<0.0001	0.001769
GO DNA SECONDARY STRUCTURE BINDING	24	0.764532	2.110131	<0.0001	0.001819
GO DNA REPLICATION INITIATION	29	0.881483	2.109485	<0.0001	0.001817
GO MICROTUBULE ORGANIZING CENTER PART	133	0.549249	2.107216	<0.0001	0.001903
GO CYTOKINESIS	80	0.578635	2.106981	<0.0001	0.001903
GO CENTROSOME	457	0.475096	2.102207	<0.0001	0.001984
GO REGULATION OF CHROMOSOME ORGANIZATION	263	0.501659	2.096891	<0.0001	0.00218
GO FOUR WAY JUNCTION DNA BINDING	15	0.881299	2.095665	<0.0001	0.002192
GO NUCLEAR EXPORT	139	0.578038	2.094703	<0.0001	0.00224
GO PROTEIN LOCALIZATION TO CHROMOSOME	37	0.697169	2.094514	<0.0001	0.00223

GO DNA CONFORMATION CHANGE	243	0.63699	2.09248	<0.0001	0.002281
GO MRNA CIS SPLICING VIA SPLICEOSOME	18	0.756928	2.091661	0.001976	0.002277
GO NUCLEAR PORE	73	0.629965	2.089824	<0.0001	0.002333
GO NUCLEOBASE CONTAINING COMPOUND TRANSPORT	187	0.520372	2.087582	<0.0001	0.002383
GO HISTONE PHOSPHORYLATION	24	0.708495	2.085798	<0.0001	0.002402
GO NEGATIVE REGULATION OF NUCLEAR DIVISION	42	0.655814	2.084938	<0.0001	0.002403
GO HISTONE METHYLTRANSFERASE COMPLEX	64	0.618044	2.084155	<0.0001	0.002415
GO CHROMOSOME CONDENSATION	26	0.785578	2.082687	<0.0001	0.00243
GO EUCHROMATIN	30	0.655879	2.081471	<0.0001	0.002416
GO ATP DEPENDENT DNA HELICASE ACTIVITY	32	0.75186	2.074272	<0.0001	0.002738
GO NUCLEAR MATRIX	95	0.553035	2.073893	<0.0001	0.002725
GO FEMALE MEIOTIC DIVISION	22	0.711161	2.071821	0.002041	0.002769
GO MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	38	0.60511	2.071089	<0.0001	0.002777
GO SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS	37	0.643358	2.068766	<0.0001	0.002814
GO POSITIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	57	0.579024	2.067949	<0.0001	0.002864
GO KINESIN COMPLEX	53	0.641915	2.067668	<0.0001	0.002842
GO STRAND DISPLACEMENT	25	0.826647	2.067544	<0.0001	0.002832
GO SIGNAL TRANSDUCTION IN RESPONSE TO DNA DAMAGE	91	0.537019	2.066748	<0.0001	0.002846
GO CENTRIOLE ASSEMBLY	18	0.786683	2.066114	<0.0001	0.002838
GO NUCLEUS ORGANIZATION	124	0.517449	2.064895	<0.0001	0.002885
GO NUCLEAR REPLICATION FORK	39	0.705708	2.06335	<0.0001	0.002919
GO REGULATION OF CELLULAR RESPONSE TO HEAT	72	0.608696	2.063044	<0.0001	0.002898
GO SINGLE STRANDED DNA BINDING	78	0.621227	2.062861	<0.0001	0.002884
GO REGULATION OF CYTOKINESIS	56	0.587097	2.06231	<0.0001	0.002863
GO POSITIVE REGULATION OF NUCLEAR DIVISION	57	0.581425	2.062231	<0.0001	0.002842
GO PEPTIDYL LYSINE MODIFICATION	278	0.503187	2.057316	<0.0001	0.003018
GO RAN GTPASE BINDING	31	0.710154	2.047662	<0.0001	0.003542
GO POSITIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	18	0.686553	2.046552	<0.0001	0.003571
GO NUCLEAR HETEROCHROMATIN	31	0.678994	2.045704	<0.0001	0.003597
GO REGULATION OF DNA REPAIR	68	0.57582	2.043149	<0.0001	0.003704
GO MICROTUBULE BASED PROCESS	478	0.472544	2.04242	<0.0001	0.00371
GO STRUCTURE SPECIFIC DNA BINDING	114	0.544633	2.040823	<0.0001	0.003742
GO RECIPROCAL DNA RECOMBINATION	34	0.666303	2.039668	0.001916	0.003813
GO HISTONE KINASE ACTIVITY	18	0.789801	2.038862	<0.0001	0.003814
GO REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	140	0.471591	2.038328	<0.0001	0.003823
GO DNA REPLICATION INDEPENDENT NUCLEOSOME ORGANIZATION	47	0.751357	2.038056	<0.0001	0.003806
GO GAMMA TUBULIN COMPLEX	19	0.68484	2.037439	<0.0001	0.003822
GO INTERSTRAND CROSS LINK REPAIR	38	0.663361	2.035212	<0.0001	0.003915

GO NEGATIVE REGULATION OF CHROMOSOME ORGANIZATION	93	0.577197	2.033347	<0.0001	0.003961
GO METHYLTRANSFERASE COMPLEX	83	0.603993	2.028147	<0.0001	0.004307
GO CENTROSOME DUPLICATION	31	0.68743	2.027841	<0.0001	0.004302
GO HEAT SHOCK PROTEIN BINDING	86	0.518859	2.023387	<0.0001	0.004636
GO BASE EXCISION REPAIR	39	0.632842	2.022947	<0.0001	0.004638
GO MICROTUBULE	382	0.449923	2.021772	<0.0001	0.004703
GO CENTRIOLE	91	0.560001	2.020459	<0.0001	0.004781
GO CENTROMERE COMPLEX ASSEMBLY	42	0.801922	2.016399	<0.0001	0.005102
GO MICROTUBULE END	21	0.710149	2.012335	<0.0001	0.005349
GO REGULATION OF DNA BIOSYNTHETIC PROCESS	90	0.510264	2.010707	<0.0001	0.00546
GO MICROTUBULE BINDING	189	0.478265	2.010579	<0.0001	0.005433
GO POSITIVE REGULATION OF CELL CYCLE ARREST	79	0.507431	2.008409	0.001988	0.005541
GO REGULATION OF UBIQUITIN PROTEIN LIGASE ACTIVITY	17	0.70127	2.006411	0.004065	0.005654
GO NEGATIVE REGULATION OF MITOTIC NUCLEAR DIVISION	32	0.680643	2.005052	<0.0001	0.005713
GO MEIOTIC CHROMOSOME SEGREGATION	49	0.622079	2.00423	0.00207	0.005758
GO SOMATIC DIVERSIFICATION OF IMMUNOGLOBULINS	26	0.653444	2.004062	<0.0001	0.005732
GO DNA PACKAGING	168	0.650433	2.001988	<0.0001	0.005845
GO NEGATIVE REGULATION OF CHROMOSOME SEGREGATION	25	0.737592	2.001595	<0.0001	0.005838
GO NUCLEOTIDE EXCISION REPAIR DNA GAP FILLING	24	0.733661	1.999863	<0.0001	0.005906
GO REGULATION OF CELL CYCLE ARREST	100	0.488065	1.999712	<0.0001	0.005887
GO RNA SPLICING VIA TRANSESTERIFICATION REACTIONS	259	0.55264	1.999272	<0.0001	0.005869
GO REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	49	0.601568	1.998778	<0.0001	0.005883
GO CAJAL BODY	49	0.602197	1.993868	<0.0001	0.00623
GO DNA DIRECTED DNA POLYMERASE ACTIVITY	26	0.650977	1.9928	<0.0001	0.006292
GO NUCLEAR UBIQUITIN LIGASE COMPLEX	39	0.621619	1.99272	<0.0001	0.006281
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE	44	0.588677	1.99174	0.00207	0.006335
GO REGULATION OF CENTROSOME DUPLICATION	31	0.647044	1.987476	<0.0001	0.006635
GO POSITIVE REGULATION OF CELL DIVISION	117	0.497792	1.983063	<0.0001	0.007006
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	32	0.637505	1.982239	0.002053	0.007019
GO MICROTUBULE ASSOCIATED COMPLEX	141	0.492313	1.976872	<0.0001	0.007461
GO POSITIVE REGULATION OF CHROMOSOME ORGANIZATION	141	0.478981	1.976612	0.001953	0.007444
GO CHROMATIN	407	0.504658	1.974624	<0.0001	0.007563
GO CHROMOSOME TELOMERIC REGION	150	0.586916	1.973622	<0.0001	0.007647
GO SOMATIC CELL DNA RECOMBINATION	31	0.639973	1.972911	<0.0001	0.007722

GO REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	134	0.479004	1.97029	<0.0001	0.007913
GO SEX CHROMOSOME	27	0.692076	1.969114	0.002033	0.007953
GO NEGATIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	92	0.472068	1.965732	<0.0001	0.008167
GO CHROMATIN REMODELING	139	0.551518	1.963479	<0.0001	0.00831
GO TRNA TRANSPORT	32	0.726221	1.961654	<0.0001	0.008424
GO PROTEIN LOCALIZATION TO CYTOSKELETON	28	0.613842	1.960205	<0.0001	0.008483
GO DNA POLYMERASE ACTIVITY	33	0.601722	1.95998	0.001992	0.008451
GO ATP DEPENDENT CHROMATIN REMODELING	67	0.682513	1.959655	<0.0001	0.00844
GO CYTOSKELETON DEPENDENT CYTOKINESIS	38	0.629121	1.95923	<0.0001	0.008453
GO POSITIVE REGULATION OF CYTOKINESIS	28	0.632393	1.958116	<0.0001	0.008529
GO HISTONE EXCHANGE	46	0.751313	1.958035	<0.0001	0.008514
GO ANAPHASE PROMOTING COMPLEX	20	0.718019	1.956704	<0.0001	0.008636
GO MLL1 2 COMPLEX	26	0.672906	1.955337	<0.0001	0.008785
GO DNA DEPENDENT DNA REPLICATION MAINTENANCE OF FIDELITY	19	0.74737	1.955322	0.002004	0.008745
GO POSITIVE REGULATION OF DNA REPLICATION	84	0.50823	1.95523	<0.0001	0.008707
GO CYTOPLASMIC MICROTUBULE	51	0.513117	1.953852	<0.0001	0.008795
GO ATPASE ACTIVITY COUPLED	307	0.440032	1.953424	<0.0001	0.008788
GO RNA SPLICING	347	0.515388	1.951778	<0.0001	0.008943
GO TUBULIN BINDING	255	0.444353	1.950899	<0.0001	0.008987
GO CHROMOSOME SEPARATION	16	0.763343	1.95014	<0.0001	0.009032
GO EXONUCLEASE ACTIVITY	70	0.531533	1.947153	<0.0001	0.009343
GO SPLICEOSOMAL COMPLEX	162	0.550271	1.947023	0.001976	0.009303
GO NEGATIVE REGULATION OF DNA REPLICATION	50	0.563802	1.945711	<0.0001	0.009319
GO REGULATION OF MRNA SPLICING VIA SPLICEOSOME	60	0.577026	1.945565	<0.0001	0.009287
GO MITOTIC CYTOKINESIS	31	0.647185	1.944002	0.001934	0.009416
GO MRNA PROCESSING	405	0.495268	1.943403	<0.0001	0.00943
GO PRONUCLEUS	15	0.850921	1.943232	<0.0001	0.009398
GO REGULATION OF TELOMERASE ACTIVITY	41	0.544635	1.942316	0.001946	0.009473
GO BLASTOCYST GROWTH	15	0.746431	1.942142	0.002016	0.009445
GO ENDONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	34	0.648212	1.94201	<0.0001	0.009417
GO MRNA 3 END PROCESSING	71	0.593629	1.941784	<0.0001	0.009402
GO REGULATION OF CHROMATIN SILENCING	21	0.691355	1.940697	<0.0001	0.009483
GO REGULATION OF TELOMERE MAINTENANCE	64	0.554244	1.937471	0.002092	0.0098
GO TELOMERE ORGANIZATION	101	0.621529	1.935654	<0.0001	0.009958
GO RNA HELICASE ACTIVITY	67	0.578993	1.935323	<0.0001	0.009964
GO TERMINATION OF RNA POLYMERASE II TRANSCRIPTION	61	0.604972	1.930117	0.001984	0.010582
GO EXONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	40	0.580679	1.927201	<0.0001	0.01085
GO ATP DEPENDENT MICROTUBULE MOTOR	18	0.753385	1.927108	0.002	0.01081

ACTIVITY					
GO REGULATION OF MRNA METABOLIC PROCESS	113	0.514245	1.925224	<0.0001	0.011049
GO SPINDLE LOCALIZATION	36	0.626319	1.923467	0.003891	0.011236
GO CHROMOSOME ORGANIZATION INVOLVED IN MEIOTIC CELL CYCLE	40	0.59764	1.918758	0.002028	0.011895
GO REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	93	0.458955	1.917206	<0.0001	0.012102
GO SPINDLE CHECKPOINT	23	0.744945	1.916597	<0.0001	0.012131
GO HSP70 PROTEIN BINDING	28	0.577432	1.916277	<0.0001	0.012115
GO CHROMATIN BINDING	408	0.457331	1.913063	0.001988	0.012468
GO RESPONSE TO GAMMA RADIATION	49	0.521189	1.913042	<0.0001	0.012417
GO REGULATION OF DOUBLE STRAND BREAK REPAIR	33	0.614142	1.910851	0.002045	0.012712
GO POSTREPLICATION REPAIR	48	0.593163	1.910466	0.002008	0.012734
GO PROTEIN DNA COMPLEX SUBUNIT ORGANIZATION	208	0.565468	1.909632	<0.0001	0.012812
GO REGULATION OF CELL CYCLE CHECKPOINT	27	0.640725	1.909536	<0.0001	0.012764
GO MICROTUBULE PLUS END	16	0.733785	1.909207	0.003854	0.012746
GO NEGATIVE REGULATION OF CHROMATIN MODIFICATION	44	0.559616	1.907574	0.003992	0.012953
GO REPLISOME	29	0.679307	1.904793	0.00396	0.01335
GO SYNAPTONEMAL COMPLEX	31	0.618171	1.904786	0.002041	0.013294
GO SITE OF DOUBLE STRAND BREAK	28	0.621918	1.904251	<0.0001	0.01331
GO RNA 3 END PROCESSING	96	0.568402	1.902459	<0.0001	0.013534
GO CHROMATIN ASSEMBLY OR DISASSEMBLY	155	0.610262	1.900685	<0.0001	0.013791
GO NUCLEOSOME BINDING	44	0.601008	1.90063	0.003945	0.013738
GO NUCLEOBASE BIOSYNTHETIC PROCESS	17	0.725841	1.89965	0.001938	0.013867
GO NEGATIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	134	0.548366	1.898058	0.002123	0.014065
GO NUCLEASE ACTIVITY	185	0.453742	1.896295	0.001961	0.014332
GO MRNA CLEAVAGE FACTOR COMPLEX	17	0.722851	1.895265	<0.0001	0.014472
GO REGULATION OF TELOMERASE RNA LOCALIZATION TO CAJAL BODY	15	0.828849	1.894692	<0.0001	0.014499
GO NUCLEAR CHROMOSOME TELOMERIC REGION	122	0.583828	1.893977	0.003953	0.014535
GO INTERCELLULAR BRIDGE	40	0.539819	1.89222	<0.0001	0.014754
GO HOMOLOGOUS CHROMOSOME SEGREGATION	37	0.597179	1.887803	0.006173	0.015401
GO REGULATION OF DNA RECOMBINATION	53	0.529242	1.884841	0.001934	0.015843
GO NUCLEIC ACID PHOSPHODIESTER BOND HYDROLYSIS	230	0.464022	1.880139	<0.0001	0.016614
GO ESTABLISHMENT OF MITOTIC SPINDLE LOCALIZATION	23	0.659775	1.877274	0.003937	0.017077
GO PCG PROTEIN COMPLEX	43	0.562044	1.877104	0.003984	0.017046
GO MICROTUBULE MOTOR ACTIVITY	75	0.549739	1.876132	0.00198	0.017193
GO NUCLEAR TRANSPORT	341	0.417966	1.86901	<0.0001	0.018761
GO NUCLEAR CHROMATIN	275	0.478557	1.868697	0.002045	0.018771

GO REGULATION OF DOUBLE STRAND BREAK REPAIR VIA HOMOLOGOUS RECOMBINATION	17	0.700887	1.866341	0.00404	0.019254
GO REGULATION OF DNA METHYLATION	15	0.706243	1.865896	0.003861	0.019278
GO CELL DIFFERENTIATION INVOLVED IN EMBRYONIC PLACENTA DEVELOPMENT	25	0.602164	1.862792	0.003802	0.019925
GO POSITIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	58	0.485864	1.86093	0.004237	0.020303
GO REGULATION OF MITOPHAGY	40	0.507571	1.860367	0.006135	0.020349
GO CELLULAR RESPONSE TO IONIZING RADIATION	50	0.514886	1.859509	<0.0001	0.020459
GO NEGATIVE REGULATION OF DNA DEPENDENT DNA REPLICATION	15	0.735466	1.858615	0.001976	0.020605
GO CHROMATIN MODIFICATION	490	0.442852	1.857248	0.006	0.020875
GO TETRAHYDROFOLATE METABOLIC PROCESS	19	0.666423	1.856837	0.002053	0.020891
GO DNA DAMAGE RESPONSE DETECTION OF DNA DAMAGE	36	0.650046	1.85424	0.004024	0.021418
GO NUCLEAR TRANSCRIPTION FACTOR COMPLEX	125	0.449126	1.852158	<0.0001	0.021842
GO INO80 TYPE COMPLEX	21	0.632164	1.850495	0.003922	0.022152
GO XY BODY	15	0.691813	1.847089	0.002049	0.023058
GO DNA TEMPLATED TRANSCRIPTION TERMINATION	97	0.557233	1.844482	0.006036	0.023614
GO BLASTOCYST DEVELOPMENT	58	0.525007	1.843357	0.002028	0.023869
GO NUCLEOTIDYLTRANSFERASE ACTIVITY	123	0.463679	1.843153	0.001988	0.023854
GO SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	120	0.42971	1.841111	<0.0001	0.024265
GO MISMATCH REPAIR	26	0.643013	1.837668	0.003922	0.025029
GO NUCLEAR ENVELOPE	381	0.390322	1.837366	0.001908	0.025031
GO ENDONUCLEASE ACTIVITY	115	0.459825	1.834794	0.001996	0.025611
GO DOUBLE STRANDED RNA BINDING	59	0.527021	1.831624	0.006024	0.026383
GO ANAPHASE PROMOTING COMPLEX DEPENDENT CATABOLIC PROCESS	75	0.677952	1.8279	0.002058	0.027331
GO NUCLEAR BODY	334	0.419035	1.827334	0.003922	0.027384
GO REGULATION OF CYTOSKELETON ORGANIZATION	470	0.387108	1.82515	<0.0001	0.027874
GO LIGAND DEPENDENT NUCLEAR RECEPTOR TRANSCRIPTION COACTIVATOR ACTIVITY	51	0.49242	1.824727	0.003922	0.027915
GO TRANSLESION SYNTHESIS	36	0.564277	1.82425	0.003922	0.027961
GO GLUCOSE CATABOLIC PROCESS	27	0.622431	1.823228	0.012766	0.028168
GO NUCLEAR IMPORT	126	0.44884	1.822489	0.009901	0.028294
GO DAMAGED DNA BINDING	62	0.536131	1.820461	0.005964	0.028775
GO MITOTIC G2 M TRANSITION CHECKPOINT	17	0.648439	1.820438	0.010163	0.028687
GO HISTONE MRNA METABOLIC PROCESS	28	0.621966	1.820354	0.007984	0.028612
GO CATALYTIC STEP 2 SPLICEOSOME	84	0.565815	1.819656	0.006073	0.028663
GO 3 5 EXONUCLEASE ACTIVITY	44	0.517897	1.81815	0.005837	0.029021
GO NEGATIVE REGULATION OF HISTONE METHYLATION	16	0.708159	1.817382	0.007859	0.029173
GO UBIQUITIN LIKE PROTEIN CONJUGATING ENZYME ACTIVITY	29	0.618951	1.816876	<0.0001	0.02923

GO PROTEIN ACETYLATION	112	0.453408	1.814955	0.005964	0.029668
GO CELL AGING	66	0.453044	1.813908	0.004115	0.029874
GO RESPONSE TO HEAT	85	0.448278	1.813829	0.004219	0.029793
GO CELLULAR RESPONSE TO GAMMA RADIATION	19	0.599839	1.813789	0.003953	0.029702
GO COVALENT CHROMATIN MODIFICATION	309	0.42754	1.810516	0.005929	0.030734
GO NEGATIVE REGULATION OF CELL AGING	16	0.626328	1.799643	0.007648	0.034204
GO SOMATIC RECOMBINATION OF IMMUNOGLOBULIN GENE SEGMENTS	21	0.626999	1.797247	0.012712	0.034942
GO PROTEIN PHOSPHATASE 2A BINDING	27	0.563725	1.79607	0.009416	0.035216
GO PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	127	0.442055	1.793316	0.008	0.036109
GO REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	141	0.429992	1.792834	0.003984	0.036151
GO POSITIVE REGULATION OF TELOMERASE ACTIVITY	27	0.547519	1.787689	0.010081	0.038053
GO REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	266	0.427133	1.785777	0.004115	0.038672
GO RESPONSE TO X RAY	30	0.575432	1.785515	0.006073	0.038639
GO REGULATION OF LIGASE ACTIVITY	126	0.538859	1.782006	0.004211	0.039873
GO NON RECOMBINATIONAL REPAIR	65	0.564155	1.781894	0.01217	0.039767
GO PROTEIN K11 LINKED UBIQUITINATION	26	0.617413	1.780033	0.004008	0.040382
GO REGULATION OF CELL AGING	32	0.519255	1.779968	0.012195	0.040272
GO NUCLEAR MEMBRANE	254	0.381785	1.779763	0.001949	0.040224
GO NEGATIVE REGULATION OF HISTONE MODIFICATION	35	0.530651	1.779571	0.015656	0.04016
GO REGULATION OF SPINDLE ORGANIZATION	19	0.627794	1.777349	0.004175	0.040962
GO CYCLIN DEPENDENT PROTEIN KINASE HOLOENZYME COMPLEX	30	0.529523	1.777017	<0.0001	0.040947
GO U2 TYPE SPLICEOSOMAL COMPLEX	29	0.581785	1.77459	0.012024	0.041711
GO MALE MEIOSIS I	15	0.623856	1.774553	0.010101	0.041594
GO NUCLEOSOMAL DNA BINDING	29	0.621686	1.774498	0.005906	0.041483
GO DNA LIGATION	16	0.662429	1.771212	0.002049	0.04263
GO NUCLEAR LOCALIZATION SEQUENCE BINDING	20	0.662614	1.769362	0.008114	0.043353
GO RETROGRADE VESICLE MEDIATED TRANSPORT GOLGI TO ER	75	0.49923	1.76719	0.009709	0.044127
GO REGULATION OF RETINOIC ACID RECEPTOR SIGNALING PATHWAY	16	0.605541	1.766643	<0.0001	0.044231
GO PML BODY	93	0.428366	1.766308	0.004049	0.044281
GO KINESIN BINDING	30	0.560245	1.765165	0.008097	0.044591
GO REGULATION OF HISTONE H3 K9 METHYLATION	17	0.665372	1.764913	0.003976	0.044574
GO NEGATIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	60	0.483221	1.764034	<0.0001	0.044835
GO ENDORIBONUCLEASE ACTIVITY PRODUCING 5 PHOSPHOMONOESTERS	26	0.637989	1.762623	0.003984	0.045242

GO POSITIVE REGULATION OF NEURON APOPTOTIC PROCESS	46	0.466252	1.762235	0.001976	0.045254
GO POSITIVE REGULATION OF NEURON DEATH	66	0.441425	1.762017	<0.0001	0.045199
GO DNA DOUBLE STRAND BREAK PROCESSING	19	0.624737	1.759188	0.011834	0.046298
GO DSRNA FRAGMENTATION	18	0.649702	1.759006	0.012346	0.046239
GO POLY PYRIMIDINE TRACT BINDING	17	0.645035	1.757854	0.002024	0.046646
GO RESPONSE TO RADIATION	387	0.351811	1.756062	<0.0001	0.047224
GO GAMMA TUBULIN BINDING	23	0.508971	1.755962	0.007874	0.047126
GO SAGA TYPE COMPLEX	30	0.556508	1.752979	0.017928	0.048234
GO ATP GENERATION FROM ADP	35	0.550378	1.752127	0.016529	0.048507
GO SPLICEOSOMAL COMPLEX ASSEMBLY	52	0.548662	1.751859	0.019531	0.048495
GO REGULATION OF GLUCOSE TRANSPORT	93	0.434143	1.751708	0.003824	0.048433
GO NEGATIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	23	0.558485	1.751675	0.012146	0.0483
GO REGULATION OF PROTEIN EXPORT FROM NUCLEUS	33	0.487741	1.751663	0.004124	0.04816
GO VIRAL GENOME REPLICATION	19	0.542231	1.751095	0.006024	0.048287
GO HISTONE BINDING	164	0.487502	1.750468	0.00998	0.048417
GO HISTONE DEACETYLASE BINDING	102	0.430481	1.749458	0.004024	0.048764
GO PROTEIN EXPORT FROM NUCLEUS	29	0.52686	1.746546	0.013487	0.049858
GO MOTOR ACTIVITY	128	0.438766	1.745523	0.004	0.050223
GO MALE MEIOSIS	34	0.540361	1.744635	0.006186	0.050478
GO NEGATIVE REGULATION OF HISTONE ACETYLATION	15	0.577075	1.74397	0.003824	0.050661
GO ACID AMINO ACID LIGASE ACTIVITY	19	0.56995	1.743816	0.011858	0.050589
GO POSITIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	185	0.453404	1.742916	0.008351	0.050836
GO 90S PRERIBOSOME	23	0.661889	1.742273	0.015686	0.050977
GO BINDING OF SPERM TO ZONA PELLUCIDA	30	0.546771	1.740965	0.008316	0.051402
GO MITOCHONDRIAL RNA METABOLIC PROCESS	23	0.635786	1.74073	0.026585	0.051365
GO CELLULAR RESPONSE TO HEAT	33	0.519102	1.740493	0.010288	0.051335
GO REGULATION OF RNA SPLICING	92	0.465362	1.739125	0.016	0.051838
GO PROTEIN LOCALIZATION TO CENTROSOME	15	0.621837	1.738324	0.01165	0.05206
GO SNRNA METABOLIC PROCESS	74	0.502474	1.737493	0.020534	0.052335
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	23	0.594121	1.737345	0.00998	0.052253
GO NEGATIVE REGULATION OF DNA METABOLIC PROCESS	104	0.444817	1.734873	0.008016	0.053355
GO PROTEASOME BINDING	16	0.629629	1.73458	0.017822	0.05336
GO CORE PROMOTER BINDING	146	0.420888	1.734178	0.00404	0.053403
GO NCRNA TRANSCRIPTION	80	0.491256	1.732749	0.018405	0.053912
GO MRNA CLEAVAGE	17	0.623046	1.730657	0.012397	0.054744
GO NUCLEOLAR PART	59	0.580881	1.728135	0.032454	0.055856
GO HISTONE H4 ACETYLATION	42	0.498431	1.727242	0.007952	0.056113
GO PROTEASOME ACCESSORY COMPLEX	23	0.741598	1.719856	0.004132	0.059716
GO MODULATION BY VIRUS OF HOST MORPHOLOGY OR PHYSIOLOGY	36	0.495764	1.719356	0.005882	0.059828
GO NUCLEOBASE METABOLIC PROCESS	37	0.525913	1.719299	0.017787	0.059692

GO NUCLEOCYTOPLASMIC TRANSPORTER ACTIVITY	23	0.628483	1.716766	0.021359	0.060953
GO REGULATION OF PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	101	0.536708	1.716236	0.021053	0.06113
GO CELLULAR RESPONSE TO RADIATION	130	0.397308	1.714092	0.002058	0.062161
GO CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	34	0.486063	1.713921	0.004098	0.062091
GO POSITIVE REGULATION OF TELOMERE CAPPING	15	0.590285	1.71286	0.013725	0.06253
GO LRR DOMAIN BINDING	16	0.595509	1.712166	0.022177	0.062757
GO SIGNAL SEQUENCE BINDING	36	0.534595	1.711012	0.008	0.063206
GO NEGATIVE REGULATION OF MRNA SPLICING VIA SPLICEOSOME	19	0.646439	1.709862	0.011765	0.063629
GO POSITIVE REGULATION OF LIGASE ACTIVITY	106	0.543527	1.708865	0.023061	0.063993
GO RNA SECONDARY STRUCTURE UNWINDING	40	0.526357	1.707131	0.01992	0.064714
GO RNA POLYMERASE II CARBOXY TERMINAL DOMAIN KINASE ACTIVITY	16	0.646089	1.70641	0.014463	0.0649
GO PERICENTRIOLAR MATERIAL	18	0.608053	1.70621	0.013592	0.064837
GO REGULATION OF DNA BINDING	92	0.408634	1.704836	<0.0001	0.065382
GO REGULATION OF GENE EXPRESSION EPIGENETIC	202	0.464621	1.702896	0.010081	0.066267
GO POSITIVE REGULATION OF DNA REPAIR	33	0.523541	1.702372	0.014315	0.06639
GO CHD TYPE COMPLEX	17	0.62802	1.697399	0.026769	0.068915
GO TRANSCRIPTION FACTOR COMPLEX	288	0.368924	1.697225	0.006342	0.068839
GO CELLULAR RESPONSE TO ESTROGEN STIMULUS	38	0.476226	1.696599	0.00404	0.069018
GO NEGATIVE REGULATION OF MRNA METABOLIC PROCESS	34	0.554485	1.694569	0.018072	0.069973
GO ESC E Z COMPLEX	16	0.653419	1.693952	0.003976	0.070185
GO GENE SILENCING	183	0.475892	1.693475	0.013889	0.070288
GO SINGLE STRANDED RNA BINDING	63	0.453645	1.692115	0.01004	0.070959
GO DNA BINDING BENDING	19	0.578908	1.691428	0.014706	0.071225
GO UBIQUITIN LIKE PROTEIN LIGASE BINDING	255	0.367148	1.689241	0.001996	0.072313
GO POSITIVE REGULATION OF HISTONE METHYLATION	29	0.538829	1.686885	0.013972	0.07353
GO SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX	59	0.527515	1.686872	0.039095	0.073349
GO REGULATION OF CHROMATIN ORGANIZATION	146	0.394492	1.686553	0.011905	0.073345
GO SMALL NUCLEOLAR RIBONUCLEOPROTEIN COMPLEX	18	0.698641	1.686346	0.014553	0.073266
GO PROTEASOME COMPLEX	73	0.570885	1.683987	0.034274	0.074499
GO RIBONUCLEOPROTEIN COMPLEX BINDING	89	0.45535	1.683845	0.031809	0.074397
GO N ACYLTRANSFERASE ACTIVITY	92	0.427953	1.683592	0.012048	0.074379
GO NUCLEOTIDE EXCISION REPAIR DNA INCISION	39	0.531228	1.680682	0.016194	0.075933
GO PROTEIN ACYLATION	142	0.394167	1.679421	0.010101	0.07659
GO REGULATION OF RNA STABILITY	135	0.452856	1.678117	0.016632	0.077264

GO LIGASE ACTIVITY FORMING CARBON NITROGEN BONDS	52	0.476419	1.677874	0.025896	0.077228
GO PROTEIN C TERMINUS BINDING	182	0.36281	1.67757	0.001992	0.077201
GO GENE SILENCING BY RNA	128	0.48847	1.676417	0.015686	0.077763
GO PROTEIN POLYUBIQUITINATION	234	0.39708	1.67604	0.020661	0.077817
GO REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	173	0.388696	1.674597	0.008197	0.078269
GO RNA POLYMERASE II TRANSCRIPTION FACTOR COMPLEX	100	0.421008	1.674518	0.002096	0.078125
GO PROTEASOMAL PROTEIN CATABOLIC PROCESS	263	0.409115	1.67423	0.012371	0.07808
GO NUCLEAR EUCHROMATIN	23	0.539271	1.673783	0.016194	0.078167
GO SMALL SUBUNIT PROCESSOME	32	0.601021	1.673631	0.020921	0.078085
GO REGULATION OF HISTONE METHYLATION	51	0.49906	1.673335	0.025591	0.078079
GO TOR SIGNALING	16	0.57272	1.672169	0.017341	0.078604
GO INTRACELLULAR ESTROGEN RECEPTOR SIGNALING PATHWAY	17	0.563483	1.670995	0.023622	0.079106
GO RNA POLYMERASE II CORE PROMOTER SEQUENCE SPECIFIC DNA BINDING	53	0.43583	1.666751	0.010101	0.081707
GO DNA REPAIR COMPLEX	37	0.506046	1.664791	0.028169	0.082809
GO APOPTOTIC NUCLEAR CHANGES	24	0.523923	1.663991	0.019493	0.083065
GO IMMUNOGLOBULIN PRODUCTION	40	0.478885	1.663936	0.020921	0.082903
GO AXON CYTOPLASM	29	0.50491	1.663033	0.015842	0.083269
GO POSITIVE REGULATION OF MRNA PROCESSING	30	0.522612	1.660284	0.018595	0.084918
GO MRNA SPLICE SITE SELECTION	26	0.568173	1.660076	0.049808	0.084872
GO METHYL CPG BINDING	15	0.590235	1.659652	0.025692	0.084915
GO RESPONSE TO UV	119	0.390948	1.658081	0.00818	0.085673
GO SIN3 TYPE COMPLEX	16	0.621161	1.656476	0.03876	0.086588
GO TRNA METABOLIC PROCESS	166	0.482884	1.654583	0.043912	0.087727
GO OOCYTE MATURATION	17	0.560351	1.652414	0.021318	0.089013
GO N ACETYLTRANSFERASE ACTIVITY	76	0.440102	1.651893	0.01833	0.089132
GO POSITIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	28	0.501337	1.651322	0.012526	0.08936
GO SWI SNF SUPERFAMILY TYPE COMPLEX	71	0.476373	1.649547	0.026515	0.090511
GO POSITIVE REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	36	0.500576	1.649258	0.027368	0.090508
GO P53 BINDING	66	0.420242	1.648637	0.01354	0.090686
GO NUCLEAR INNER MEMBRANE	45	0.438317	1.647532	0.009862	0.091279
GO REGULATION OF CELLULAR SENESCENCE	26	0.499545	1.645707	0.02994	0.092223
GO UBIQUITIN LIKE PROTEIN BINDING	113	0.403673	1.642633	0.021739	0.094145
GO UNFOLDED PROTEIN BINDING	89	0.487867	1.64228	0.028017	0.094202
GO CHROMATIN DNA BINDING	76	0.448922	1.64214	0.021318	0.094095
GO 4 IRON 4 SULFUR CLUSTER BINDING	40	0.490891	1.641797	0.028169	0.094173
GO HEXOSE CATABOLIC PROCESS	45	0.473236	1.641481	0.023952	0.094188
GO PROTEIN KINASE C BINDING	47	0.440678	1.641091	0.015873	0.094256
GO ANATOMICAL STRUCTURE HOMEOSTASIS	263	0.345165	1.640907	0.003992	0.094173
GO NUCLEOTIDE EXCISION REPAIR	111	0.455461	1.640795	0.022449	0.094025

GO ACETYLTRANSFERASE COMPLEX	84	0.452731	1.640681	0.03055	0.093884
GO CELLULAR RESPONSE TO ESTRADIOL STIMULUS	28	0.501723	1.640649	0.016194	0.093701
GO REGULATION OF GENE SILENCING	50	0.537253	1.640078	0.030801	0.093933
GO PROTEIN K63 LINKED UBIQUITINATION	34	0.478582	1.639388	0.026694	0.094231
GO NEGATIVE REGULATION OF RNA SPLICING	24	0.595878	1.638791	0.021912	0.094418
GO CYCLIN DEPENDENT PROTEIN SERINE THREONINE KINASE REGULATOR ACTIVITY	27	0.518314	1.635404	0.025751	0.096602
GO ESTABLISHMENT OF SPINDLE ORIENTATION	24	0.555838	1.63523	0.013699	0.096512
GO PYRUVATE METABOLIC PROCESS	59	0.464302	1.631605	0.02079	0.098911
GO SPERM EGG RECOGNITION	40	0.473869	1.629339	0.010638	0.100405
GO TRANSFERASE COMPLEX TRANSFERRING PHOSPHORUS CONTAINING GROUPS	230	0.374601	1.628394	0.022133	0.100874
GO METHYLATED HISTONE BINDING	46	0.475691	1.627601	0.025243	0.101255
GO NEGATIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	49	0.418	1.626376	0.012448	0.101951
GO CELLULAR SENESCENCE	32	0.466332	1.626337	0.02459	0.101743
GO MODULATION BY SYMBIONT OF HOST CELLULAR PROCESS	27	0.494681	1.62456	0.023529	0.102857
GO TRNA MODIFICATION	53	0.516353	1.623186	0.048	0.103669
GO EXON EXON JUNCTION COMPLEX	20	0.556405	1.62315	0.035849	0.103477
GO NADH METABOLIC PROCESS	33	0.52091	1.623064	0.043659	0.103305
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	17	0.598399	1.62294	0.030426	0.103171
GO NUCLEAR SPECK	188	0.396927	1.62166	0.023715	0.103989
GO CYTOPLASMIC EXOSOME RNASE COMPLEX	15	0.625546	1.62165	0.035789	0.103776
GO PEPTIDYL SERINE MODIFICATION	146	0.380568	1.621519	0.009901	0.103634
GO CELLULAR COMPONENT DISASSEMBLY INVOLVED IN EXECUTION PHASE OF APOPTOSIS	41	0.452817	1.621243	0.017787	0.103611
GO REGULATION OF HISTONE H3 K4 METHYLATION	24	0.545077	1.620947	0.037475	0.103596
GO NAD METABOLIC PROCESS	49	0.46621	1.61793	0.047423	0.105169
GO DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION RESULTING IN TRANSCRIPTION	15	0.559931	1.615229	0.026263	0.107021
GO REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	42	0.470382	1.61498	0.03527	0.107026
GO POSITIVE REGULATION OF MRNA METABOLIC PROCESS	42	0.466938	1.614796	0.024742	0.106946
GO FOLIC ACID CONTAINING COMPOUND METABOLIC PROCESS	27	0.52306	1.614168	0.032653	0.107211
GO MATURATION OF 5 8S RRNA FROM TRICISTRONIC RRNA TRANSCRIPT SSU RRNA 5 8S RRNA LSU RRNA	19	0.63202	1.61405	0.04908	0.107072
GO RNA POLYADENYLATION	29	0.544795	1.611653	0.02459	0.108714
GO MRNA BINDING	143	0.406967	1.611327	0.029528	0.108702
GO OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN 2	38	0.462565	1.609781	0.018109	0.109682

OXOGLUTARATE AS ONE DONOR AND INCORPORATION OF ONE ATOM EACH OF OXYGEN INTO BOTH DONORS					
GO SYNAPTONEMAL COMPLEX ORGANIZATION	18	0.570751	1.609353	0.027888	0.1098
GO REGULATION OF MEMBRANE PERMEABILITY	69	0.425854	1.609268	0.024793	0.109636
GO DNA MODIFICATION	76	0.40915	1.608402	0.01833	0.110119
GO HSP90 PROTEIN BINDING	27	0.467777	1.60792	0.018519	0.110318
GO PROTEIN REFOLDING	19	0.585005	1.607608	0.034043	0.110326
GO IN UTERO EMBRYONIC DEVELOPMENT	301	0.346253	1.607321	0.004	0.110347
GO REGULATION OF PROTEIN INSERTION INTO MITOCHONDRIAL MEMBRANE INVOLVED IN APOPTOTIC SIGNALING PATHWAY	29	0.496517	1.606397	0.02449	0.110821
GO SYNAPSIS	28	0.52518	1.606385	0.036364	0.110599
GO EXECUTION PHASE OF APOPTOSIS	53	0.415665	1.605737	0.013384	0.110898
GO ERROR FREE TRANSLESION SYNTHESIS	17	0.632181	1.604453	0.033797	0.111786
GO MICROTUBULE BASED MOVEMENT	192	0.398073	1.599462	0.034765	0.115714
GO DNA CATABOLIC PROCESS	26	0.481089	1.598767	0.027559	0.116071
GO ISOTYPE SWITCHING	16	0.570794	1.59787	0.033264	0.116348
GO PYRIMIDINE NUCLEOSIDE TRIPHOSPHATE BIOSYNTHETIC PROCESS	17	0.587847	1.595108	0.04661	0.118261
GO NEGATIVE REGULATION OF DNA RECOMBINATION	15	0.558827	1.594683	0.037475	0.118403
GO ORGANELLE LOCALIZATION	393	0.330308	1.592694	0.01518	0.119757
GO RNA POLYMERASE II DISTAL ENHANCER SEQUENCE SPECIFIC DNA BINDING	61	0.431502	1.592058	0.023211	0.12008
GO POSTTRANSCRIPTIONAL REGULATION OF GENE EXPRESSION	417	0.36652	1.591161	0.028747	0.120595
GO REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	262	0.379188	1.590152	0.029046	0.121173
GO CELLULAR PROTEIN COMPLEX LOCALIZATION	21	0.501586	1.590129	0.035156	0.120941
GO TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	24	0.509431	1.589813	0.03681	0.120963
GO PROTEIN LOCALIZATION TO NUCLEUS	151	0.364499	1.587519	0.022774	0.12244
GO PORE COMPLEX ASSEMBLY	15	0.62296	1.58742	0.045833	0.122263
GO HYDROLASE ACTIVITY ACTING ON CARBON NITROGEN BUT NOT PEPTIDE BONDS IN CYCLIC AMIDINES	32	0.49158	1.586432	0.031381	0.122847
GO NUCLEAR TRANSCRIPTIONAL REPRESSOR COMPLEX	22	0.551278	1.586268	0.038314	0.122751
GO PROTEIN IMPORT	150	0.370048	1.583494	0.020704	0.124709
GO RESPONSE TO TESTOSTERONE	37	0.425941	1.583486	0.015905	0.124473
GO ENDORIBONUCLEASE COMPLEX	17	0.59136	1.58022	0.033797	0.127159
GO NEGATIVE REGULATION OF DNA BINDING	46	0.428822	1.579294	0.030426	0.127728
GO RESPONSE TO CAFFEINE	17	0.518458	1.576671	0.020661	0.129504
GO RRNA TRANSCRIPTION	17	0.580251	1.574638	0.044625	0.130292
GO NUCLEAR ENVELOPE REASSEMBLY	17	0.568899	1.574309	0.04817	0.130318
GO POSITIVE REGULATION OF VIRAL GENOME REPLICATION	29	0.465615	1.574018	0.044266	0.130066

GO REGULATION OF CELL MATURATION	18	0.520363	1.573624	0.031434	0.130155
GO REGULATION OF PROTEIN PHOSPHATASE TYPE 2A ACTIVITY	23	0.514276	1.573291	0.038153	0.130209
GO POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	185	0.398118	1.572266	0.046218	0.130818
GO MULTICELLULAR ORGANISM AGING	30	0.426614	1.571733	0.016097	0.131081
GO MODIFICATION BY SYMBIONT OF HOST MORPHOLOGY OR PHYSIOLOGY	44	0.450837	1.568534	0.021739	0.133624
GO POSITIVE REGULATION OF RNA SPLICING	22	0.529438	1.568522	0.046939	0.133375
GO ACETYLTRANSFERASE ACTIVITY	92	0.402573	1.567502	0.024691	0.133991
GO GLUCOSE 6 PHOSPHATE METABOLIC PROCESS	21	0.563066	1.563586	0.043137	0.137066
GO PROTEIN SERINE THREONINE KINASE ACTIVITY	425	0.323065	1.561703	0.009434	0.138224
GO NEGATIVE REGULATION OF PROTEIN ACETYLATION	20	0.481625	1.561565	0.025743	0.138106
GO DNA CATABOLIC PROCESS ENDONUCLEOLYTIC	18	0.513371	1.560898	0.038911	0.138474
GO CELLULAR COMPONENT DISASSEMBLY	488	0.344172	1.560675	0.03055	0.138419
GO HISTONE METHYLTRANSFERASE ACTIVITY	47	0.440995	1.559927	0.038384	0.138872
GO ALDITOL METABOLIC PROCESS	18	0.559822	1.559636	0.03937	0.13891
GO RNA STABILIZATION	29	0.500046	1.558303	0.045545	0.139872
GO CRANIAL NERVE MORPHOGENESIS	23	0.536053	1.557115	0.034137	0.140685
GO PRE MRNA BINDING	24	0.526258	1.555345	0.046693	0.142144
GO REGULATION OF MAMMARY GLAND EPITHELIAL CELL PROLIFERATION	16	0.5383	1.55502	0.041833	0.142175
GO DEVELOPMENTAL PROGRAMMED CELL DEATH	26	0.481542	1.554506	0.037698	0.142355
GO MITOCHONDRIAL MEMBRANE ORGANIZATION	90	0.416129	1.551527	0.037344	0.144631
GO NEURAL PRECURSOR CELL PROLIFERATION	70	0.414361	1.551003	0.025845	0.144819
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY	147	0.326404	1.548475	0.010081	0.147032
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	20	0.489466	1.546822	0.045361	0.148128
GO NEGATIVE REGULATION OF GENE SILENCING	18	0.509661	1.546218	0.045455	0.148435
GO OOCYTE DIFFERENTIATION	34	0.452072	1.545829	0.022358	0.148554
GO CRANIAL NERVE DEVELOPMENT	42	0.450946	1.54538	0.034816	0.148742
GO L ALPHA AMINO ACID TRANSMEMBRANE TRANSPORT	30	0.482206	1.542854	0.049281	0.150081
GO PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	28	0.457084	1.541084	0.043933	0.151209
GO ADP BINDING	31	0.444737	1.536849	0.034286	0.154483
GO ENDORIBONUCLEASE ACTIVITY	45	0.45567	1.536706	0.049689	0.154376
GO POSITIVE REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	126	0.344116	1.536172	0.018405	0.154396
GO HORMONE RECEPTOR BINDING	146	0.347855	1.529838	0.020121	0.159147
GO PROTEIN MONOUBIQUITINATION	49	0.453037	1.529269	0.04277	0.159102
GO OXIDOREDUCTASE ACTIVITY ACTING ON	16	0.510637	1.524861	0.046939	0.162887

THE CH NH GROUP OF DONORS NAD OR NADP AS ACCEPTOR					
GO REGULATION OF TYPE I INTERFERON MEDIATED SIGNALING PATHWAY	25	0.491582	1.523489	0.045635	0.163927
GO POSITIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	335	0.298118	1.522932	0.001961	0.1642
GO ESTABLISHMENT OF MITOTIC SPINDLE ORIENTATION	19	0.525008	1.517628	0.041016	0.169439
GO NEGATIVE REGULATION OF BINDING	129	0.337844	1.516241	0.014028	0.170576
GO REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION	120	0.34131	1.515087	0.022449	0.171471
GO POSITIVE REGULATION OF CHROMATIN MODIFICATION	81	0.384956	1.513425	0.04902	0.172789
GO PALLIUM DEVELOPMENT	148	0.360975	1.512546	0.016	0.172868
GO MACROMOLECULE DEACYLATION	66	0.38652	1.508687	0.036364	0.175108
GO CEREBRAL CORTEX DEVELOPMENT	103	0.378168	1.507116	0.025896	0.176162
GO ANATOMICAL STRUCTURE ARRANGEMENT	17	0.534651	1.506784	0.04277	0.176244
GO CELLULAR RESPONSE TO UV	65	0.37759	1.506528	0.046939	0.176244
GO CELLULAR RESPONSE TO HYDROGEN PEROXIDE	60	0.378247	1.506035	0.034836	0.176426
GO REGULATION OF PROTEIN CATABOLIC PROCESS	376	0.330624	1.505527	0.030738	0.176352
GO NEGATIVE REGULATION OF PROTEIN CATABOLIC PROCESS	103	0.349017	1.502487	0.032922	0.178804
GO NITROGEN COMPOUND TRANSPORT	476	0.300897	1.500996	0.005736	0.180131
GO RESPONSE TO GONADOTROPIN	26	0.472858	1.500551	0.034068	0.180316
GO PROTEIN PHOSPHATASE BINDING	117	0.346367	1.494817	0.015504	0.18528
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	70	0.352472	1.492845	0.031373	0.187213
GO ORGAN REGENERATION	82	0.363604	1.492764	0.025263	0.186695
GO ORGANELLE ASSEMBLY	450	0.329846	1.492388	0.032854	0.186508
GO NEGATIVE REGULATION OF PROTEIN BINDING	78	0.357497	1.49208	0.030612	0.186571
GO POSITIVE REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	95	0.3494	1.491917	0.038306	0.186432
GO POSITIVE REGULATION OF PROTEOLYSIS	349	0.332446	1.487456	0.041068	0.18991
GO MAGNESIUM ION BINDING	188	0.315254	1.484554	0.014056	0.19196
GO OVARIAN FOLLICLE DEVELOPMENT	55	0.370953	1.483198	0.024845	0.19319
GO MALE GAMETE GENERATION	392	0.30732	1.482003	0.008147	0.194205
GO POSITIVE REGULATION OF G1 S TRANSITION OF MITOTIC CELL CYCLE	24	0.456614	1.481508	0.045064	0.194459
GO REGULATION OF PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	21	0.452743	1.480863	0.04277	0.194852
GO SINGLE FERTILIZATION	92	0.348239	1.479414	0.024793	0.19581
GO REGULATION OF MEIOTIC CELL CYCLE	38	0.418345	1.476862	0.048096	0.19836
GO AGING	256	0.30723	1.4759	0.014675	0.19926
GO PROTEIN N TERMINUS BINDING	101	0.345558	1.473382	0.045635	0.201295
GO STRUCTURAL CONSTITUENT OF CYTOSKELETON	94	0.379992	1.470907	0.04829	0.203131

GO CELLULAR RESPONSE TO LIGHT STIMULUS	86	0.347879	1.470624	0.031646	0.203118
GO POSITIVE REGULATION OF MITOCHONDRION ORGANIZATION	151	0.329367	1.46222	0.041068	0.209599
GO HYDROLASE ACTIVITY HYDROLYZING N GLYCOSYL COMPOUNDS	22	0.479561	1.460692	0.040568	0.211156
GO RESPONSE TO DSRNA	54	0.380661	1.459333	0.040404	0.212181
GO GAMETE GENERATION	488	0.293725	1.459058	0.004107	0.212169
GO TRANSFERASE ACTIVITY TRANSFERRING PENTOSYL GROUPS	51	0.365533	1.457853	0.042017	0.213306
GO RIBONUCLEOPROTEIN GRANULE	139	0.351907	1.452017	0.047325	0.218014
GO CELLULAR RESPONSE TO OXIDATIVE STRESS	177	0.309304	1.44906	0.027426	0.220634
GO CELLULAR RESPONSE TO ALKALOID	32	0.411007	1.447818	0.049896	0.22116
GO METENCEPHALON DEVELOPMENT	99	0.382518	1.447195	0.048356	0.221221
GO CELLULAR RESPONSE TO REACTIVE OXYGEN SPECIES	102	0.333436	1.442002	0.023061	0.226021
GO CELL CYCLE ARREST	142	0.307337	1.438642	0.020161	0.22848
GO REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	321	0.31972	1.437991	0.041068	0.228961
GO OOGENESIS	57	0.370357	1.431047	0.039916	0.233608
GO FEMALE GAMETE GENERATION	84	0.333072	1.430269	0.031558	0.23426
GO CELLULAR RESPONSE TO ALCOHOL	110	0.346435	1.427815	0.025743	0.236065
GO RESPONSE TO VITAMIN	95	0.335466	1.425134	0.04898	0.238041
GO RESPONSE TO ESTRADIOL	143	0.310524	1.421045	0.022634	0.241204
GO LIMBIC SYSTEM DEVELOPMENT	94	0.348151	1.419289	0.046693	0.242089
GO LIGASE ACTIVITY	375	0.308517	1.411824	0.043121	0.24861

ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate; GSEA, gene set enrichment analysis; KIF, kinesin.

Table SV. **GSEA results of c2 reference gene set of high *KIF18B* expression group.**

Name	Size	ES	NES	NOM P-val	FDR q-value
LINDGREN BLADDER CANCER CLUSTER 1 DN	356	0.608203	2.651989	<0.0001	<0.0001
SHEPARD BMYB TARGETS	70	0.789135	2.556192	<0.0001	<0.0001
SHEPARD BMYB MORPHOLINO DN	193	0.642768	2.548583	<0.0001	<0.0001
DUTERTRE ESTRADIOL RESPONSE 24HR UP	309	0.843362	2.51653	<0.0001	<0.0001
TOYOTA TARGETS OF MIR34B AND MIR34C	409	0.654658	2.505821	<0.0001	<0.0001
GAVIN FOXP3 TARGETS CLUSTER P6	88	0.819558	2.504447	<0.0001	<0.0001
WHITFIELD CELL CYCLE G2	169	0.690554	2.501407	<0.0001	<0.0001
ZHENG GLIOBLASTOMA PLASTICITY UP	240	0.62588	2.494126	<0.0001	<0.0001
RUIZ TNC TARGETS DN	136	0.795786	2.484866	<0.0001	<0.0001
KAUFFMANN DNA REPLICATION GENES	141	0.689284	2.483981	<0.0001	<0.0001
BASAKI YBX1 TARGETS UP	268	0.754848	2.483411	<0.0001	<0.0001
BLUM RESPONSE TO SALIRASIB DN	336	0.725009	2.482629	<0.0001	<0.0001
VECCHI GASTRIC CANCER EARLY UP	384	0.714576	2.482614	<0.0001	<0.0001
AFFAR YY1 TARGETS DN	226	0.620023	2.476123	<0.0001	<0.0001
CHEMNITZ RESPONSE TO PROSTAGLANDIN E2 UP	129	0.767644	2.475762	<0.0001	<0.0001
CROONQUIST NRAS VS STROMAL STIMULATION DN	98	0.694698	2.474264	<0.0001	<0.0001
ODONNELL TFRC TARGETS DN	123	0.813105	2.472898	<0.0001	<0.0001
SARRIO EPITHELIAL MESENCHYMAL TRANSITION UP	171	0.786611	2.472442	<0.0001	<0.0001
CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	164	0.804616	2.470043	<0.0001	<0.0001
WANG RESPONSE TO GSK3 INHIBITOR SB216763 DN	332	0.656208	2.464246	<0.0001	<0.0001
LIAO METASTASIS	495	0.532635	2.437502	<0.0001	<0.0001
FLORIO NEOCORTEX BASAL RADIAL GLIA DN	187	0.84075	2.435493	<0.0001	<0.0001
FURUKAWA DUSP6 TARGETS PCI35 DN	67	0.822387	2.433345	<0.0001	<0.0001
PUJANA BRCA2 PCC NETWORK	401	0.721308	2.424555	<0.0001	3.31E-05
LE EGR2 TARGETS UP	104	0.803958	2.42148	<0.0001	3.18E-05
GRAHAM CML DIVIDING VS NORMAL QUIESCENT UP	176	0.799011	2.421	<0.0001	3.06E-05
ALCALAY AML BY NPM1 LOCALIZATION DN	180	0.558588	2.409388	<0.0001	2.94E-05
KEGG CELL CYCLE	124	0.721007	2.408469	<0.0001	2.84E-05
WHITFIELD CELL CYCLE G2 M	196	0.653129	2.407541	<0.0001	2.74E-05
ZHANG TLX TARGETS 60HR DN	263	0.815048	2.40398	<0.0001	2.65E-05
LINDGREN BLADDER CANCER CLUSTER 3 UP	305	0.717653	2.400535	<0.0001	2.56E-05
SHEPARD CRUSH AND BURN MUTANT DN	174	0.635677	2.399899	<0.0001	2.48E-05
RIZ ERYTHROID DIFFERENTIATION	72	0.699786	2.395906	<0.0001	2.41E-05
HOFFMANN LARGE TO SMALL PRE BII LYMPHOCYTE UP	158	0.790739	2.394133	<0.0001	2.34E-05
FUJII YBX1 TARGETS DN	193	0.774218	2.394083	<0.0001	2.27E-05
FOURNIER ACINAR DEVELOPMENT LATE 2	265	0.738993	2.392198	<0.0001	2.21E-05
MARKEY RB1 ACUTE LOF UP	223	0.728226	2.386909	<0.0001	4.68E-05
MORI PRE BI LYMPHOCYTE UP	78	0.769408	2.38381	<0.0001	4.56E-05

FISCHER G2 M CELL CYCLE	220	0.763198	2.383128	<0.0001	4.44E-05
LI WILMS TUMOR VS FETAL KIDNEY 1 DN	159	0.79942	2.379187	<0.0001	4.33E-05
LEE EARLY T LYMPHOCYTE UP	97	0.834666	2.378463	<0.0001	4.23E-05
BURTON ADIPOGENESIS PEAK AT 24HR	42	0.895226	2.376109	<0.0001	4.13E-05
KOBAYASHI EGFR SIGNALING 24HR DN	242	0.85161	2.374535	<0.0001	4.03E-05
BURTON ADIPOGENESIS 3	100	0.858249	2.369379	<0.0001	5.43E-05
CHANG CYCLING GENES	138	0.873537	2.366816	<0.0001	5.31E-05
FERREIRA EWINGS SARCOMA UNSTABLE VS STABLE UP	148	0.756718	2.363326	<0.0001	5.19E-05
STEIN ESRRA TARGETS RESPONSIVE TO ESTROGEN DN	39	0.831171	2.363122	<0.0001	5.08E-05
DUTERTRE ESTRADIOL RESPONSE 6HR UP	218	0.588938	2.353324	<0.0001	9.94E-05
REACTOME CELL CYCLE MITOTIC	299	0.721819	2.350134	<0.0001	9.74E-05
SHEDDEN LUNG CANCER POOR SURVIVAL A6	427	0.798459	2.348762	<0.0001	9.54E-05
MORI MATURE B LYMPHOCYTE DN	72	0.674875	2.345805	<0.0001	9.36E-05
PUJANA BREAST CANCER LIT INT NETWORK	97	0.708693	2.344361	<0.0001	9.18E-05
PID E2F PATHWAY	73	0.696553	2.343881	<0.0001	9.00E-05
REACTOME CELL CYCLE	386	0.69674	2.336957	<0.0001	8.84E-05
VILLANUEVA LIVER CANCER KRT19 UP	162	0.737877	2.336815	<0.0001	8.68E-05
NADERI BREAST CANCER PROGNOSIS UP	46	0.802431	2.336593	<0.0001	8.52E-05
CROONQUIST NRAS SIGNALING DN	71	0.945903	2.330528	<0.0001	9.66E-05
BENPORATH ES CORE NINE CORRELATED	98	0.643199	2.329801	<0.0001	9.49E-05
FISCHER G1 S CELL CYCLE	192	0.639166	2.324182	<0.0001	1.07E-04
HU GENOTOXIC DAMAGE 4HR	35	0.797247	2.317543	<0.0001	1.18E-04
CROONQUIST IL6 DEPRIVATION DN	96	0.907253	2.314846	<0.0001	1.16E-04
MANALO HYPOXIA DN	271	0.755888	2.313522	<0.0001	1.14E-04
OXFORD RALA OR RALB TARGETS UP	45	0.865834	2.313378	<0.0001	1.13E-04
MORI IMMATURE B LYMPHOCYTE DN	90	0.84193	2.311813	<0.0001	1.11E-04
PEART HDAC PROLIFERATION CLUSTER DN	73	0.661291	2.311469	<0.0001	1.09E-04
MORI EMU MYC LYMPHOMA BY ONSET TIME UP	99	0.683707	2.305759	<0.0001	1.23E-04
WHITFIELD CELL CYCLE G1 S	128	0.632909	2.305621	<0.0001	1.21E-04
PID ATR PATHWAY	39	0.835218	2.305482	<0.0001	1.19E-04
KAUFFMANN DNA REPAIR GENES	219	0.635751	2.303722	<0.0001	1.17E-04
PID AURORA A PATHWAY	30	0.755255	2.302697	<0.0001	1.16E-04
PENG LEUCINE DEPRIVATION DN	182	0.669002	2.297153	<0.0001	1.45E-04
MUELLER PLURINET	296	0.674754	2.296901	<0.0001	1.43E-04
MISSIAGLIA REGULATED BY METHYLATION DN	115	0.821504	2.29341	<0.0001	1.65E-04
NAKAYAMA SOFT TISSUE TUMORS PCA2 UP	86	0.783035	2.293213	<0.0001	1.62E-04
GRAHAM CML QUIESCENT VS NORMAL QUIESCENT UP	80	0.659527	2.291676	<0.0001	1.84E-04
PUJANA BRCA CENTERED NETWORK	114	0.82377	2.289912	<0.0001	1.81E-04
PETROVA PROX1 TARGETS UP	27	0.830786	2.286639	<0.0001	1.79E-04
PAL PRMT5 TARGETS UP	195	0.628681	2.285923	<0.0001	1.77E-04
WU APOPTOSIS BY CDKN1A VIA TP53	54	0.898918	2.28489	<0.0001	1.74E-04
HORIUCHI WTAP TARGETS DN	293	0.69568	2.284683	<0.0001	1.72E-04
ZHOU CELL CYCLE GENES IN IR RESPONSE 24HR	119	0.848455	2.284447	<0.0001	1.70E-04
BENPORATH ES 2	39	0.743048	2.283872	<0.0001	1.68E-04
PUJANA XPRSS INT NETWORK	161	0.794019	2.283369	<0.0001	1.66E-04
KONG E2F3 TARGETS	94	0.886932	2.280455	<0.0001	1.94E-04

BENPORATH ES 1	356	0.622392	2.278398	<0.0001	1.91E-04
WHITEFORD PEDIATRIC CANCER MARKERS	111	0.871876	2.275522	<0.0001	2.09E-04
WINNEPENNINCKX MELANOMA METASTASIS UP	151	0.817942	2.274679	<0.0001	2.06E-04
PID FOXM1 PATHWAY	40	0.759672	2.27461	<0.0001	2.04E-04
MORI LARGE PRE BII LYMPHOCYTE UP	84	0.831443	2.274032	<0.0001	2.02E-04
TANG SENESCENCE TP53 TARGETS DN	54	0.88528	2.27163	<0.0001	2.08E-04
GOLDRATH ANTIGEN RESPONSE	331	0.603479	2.271496	<0.0001	2.05E-04
LABBE WNT3A TARGETS UP	108	0.544691	2.271423	<0.0001	2.03E-04
GARCIA TARGETS OF FLI1 AND DAX1 DN	163	0.651642	2.26735	<0.0001	2.01E-04
MOLENAAR TARGETS OF CCND1 AND CDK4 DN	51	0.866696	2.260139	<0.0001	2.26E-04
VERNELL RETINOBLASTOMA PATHWAY UP	68	0.801729	2.259285	<0.0001	2.40E-04
PENG GLUTAMINE DEPRIVATION DN	324	0.616227	2.255061	<0.0001	2.77E-04
GRAHAM NORMAL QUIESCENT VS NORMAL DIVIDING DN	85	0.886554	2.250934	<0.0001	2.74E-04
ZHANG TLX TARGETS DN	87	0.892133	2.250629	<0.0001	2.79E-04
FERRANDO T ALL WITH MLL ENL FUSION DN	83	0.633776	2.249271	0.002004	2.76E-04
TARTE PLASMA CELL VS PLASMABLAST DN	300	0.665856	2.247513	0.002033	2.81E-04
REACTOME DNA REPLICATION	180	0.770362	2.246521	<0.0001	2.94E-04
MITSIADES RESPONSE TO APLIDIN DN	239	0.699376	2.245892	<0.0001	2.99E-04
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS TURQUOISE DN	50	0.749052	2.244419	<0.0001	2.96E-04
MARKEY RB1 CHRONIC LOF UP	111	0.582982	2.244265	<0.0001	2.93E-04
WANG CISPLATIN RESPONSE AND XPC UP	190	0.548017	2.244199	<0.0001	2.91E-04
XU HGF SIGNALING NOT VIA AKT1 48HR DN	20	0.805235	2.243348	<0.0001	2.88E-04
OLSSON E2F3 TARGETS DN	45	0.706133	2.240486	<0.0001	2.85E-04
ZHOU CELL CYCLE GENES IN IR RESPONSE 6HR	80	0.886257	2.233605	<0.0001	3.43E-04
FAELT B CLL WITH VH3 21 UP	42	0.702863	2.231728	<0.0001	3.46E-04
PYEON HPV POSITIVE TUMORS UP	84	0.715883	2.229796	<0.0001	3.59E-04
YU BAP1 TARGETS	29	0.753985	2.229632	<0.0001	3.56E-04
LY AGING PREMATURE DN	29	0.836252	2.229195	<0.0001	3.52E-04
GAL LEUKEMIC STEM CELL DN	233	0.552276	2.223748	<0.0001	3.65E-04
PID AURORA B PATHWAY	37	0.800533	2.223034	<0.0001	3.61E-04
SCIBETTA KDM5B TARGETS DN	77	0.624447	2.222436	<0.0001	3.58E-04
REACTOME MITOTIC G2 G2 M PHASES	77	0.664858	2.222397	<0.0001	3.55E-04
PUJANA BREAST CANCER WITH BRCA1 MUTATED UP	54	0.869048	2.221128	<0.0001	3.65E-04
PID PLK1 PATHWAY	43	0.799871	2.218306	<0.0001	3.78E-04
REACTOME GLUCOSE TRANSPORT	37	0.7291	2.215784	<0.0001	3.98E-04
BURTON ADIPOGENESIS PEAK AT 16HR	40	0.791977	2.21548	<0.0001	4.08E-04
BENPORATH PROLIFERATION	136	0.786101	2.21383	<0.0001	4.04E-04
STEIN ESR1 TARGETS	82	0.588458	2.213415	<0.0001	4.01E-04
REN BOUND BY E2F	60	0.88408	2.210404	<0.0001	4.05E-04
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS UP	121	0.622287	2.20852	<0.0001	4.21E-04
ODONNELL TARGETS OF MYC AND TFRC DN	43	0.869258	2.206679	<0.0001	4.40E-04
CHANG CORE SERUM RESPONSE UP	198	0.666035	2.198774	<0.0001	5.36E-04
BIDUS METASTASIS UP	204	0.702124	2.196377	<0.0001	5.52E-04
ZHANG TLX TARGETS 36HR DN	182	0.782349	2.195435	<0.0001	5.55E-04

VANTVEER BREAST CANCER METASTASIS DN	111	0.723795	2.19513	<0.0001	5.51E-04
REACTOME G2 M CHECKPOINTS	41	0.878442	2.193896	<0.0001	5.63E-04
REACTOME MITOTIC M M G1 PHASES	160	0.754996	2.193351	<0.0001	5.59E-04
REACTOME TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM	51	0.723601	2.19295	<0.0001	5.60E-04
ABRAMSON INTERACT WITH AIRE	44	0.781407	2.191665	<0.0001	5.61E-04
CHICAS RB1 TARGETS GROWING	225	0.621861	2.191629	<0.0001	5.57E-04
BHATTACHARYA EMBRYONIC STEM CELL	86	0.692871	2.191613	<0.0001	5.53E-04
WEST ADRENOCORTICAL TUMOR UP	282	0.62801	2.190665	<0.0001	5.60E-04
GEORGES CELL CYCLE MIR192 TARGETS	61	0.727622	2.189875	<0.0001	5.64E-04
KEGG DNA REPLICATION	36	0.881792	2.188927	<0.0001	5.79E-04
BOYAULT LIVER CANCER SUBCLASS G3 UP	181	0.719776	2.186208	<0.0001	5.99E-04
VANTVEER BREAST CANCER ESR1 DN	226	0.574753	2.183449	<0.0001	6.48E-04
LY AGING OLD DN	55	0.793099	2.182936	<0.0001	6.44E-04
DANG REGULATED BY MYC UP	71	0.656173	2.181595	<0.0001	6.51E-04
SENGUPTA NASOPHARYNGEAL CARCINOMA UP	275	0.64308	2.178788	<0.0001	6.58E-04
REACTOME MITOTIC PROMETAPHASE	78	0.768087	2.176139	<0.0001	6.86E-04
RHODES CANCER META SIGNATURE	63	0.75136	2.175686	<0.0001	6.87E-04
SONG TARGETS OF IE86 CMV PROTEIN	58	0.839873	2.171904	<0.0001	7.27E-04
REACTOME MRNA PROCESSING	151	0.637036	2.17165	<0.0001	7.22E-04
ROSTY CERVICAL CANCER PROLIFERATION CLUSTER	133	0.904753	2.170918	<0.0001	7.29E-04
FRASOR RESPONSE TO SERM OR FULVESTRANT DN	50	0.848255	2.168967	<0.0001	7.45E-04
GREENBAUM E2A TARGETS UP	32	0.884223	2.168952	<0.0001	7.40E-04
KEGG HOMOLOGOUS RECOMBINATION	26	0.811003	2.166975	<0.0001	7.54E-04
GROSS HYPOXIA VIA ELK3 UP	198	0.497359	2.165637	<0.0001	7.67E-04
GRADE COLON AND RECTAL CANCER UP	272	0.628431	2.163404	<0.0001	8.11E-04
THILLAINADESAN ZNF217 TARGETS UP	42	0.663378	2.160018	<0.0001	8.46E-04
JAEGER METASTASIS UP	43	0.719422	2.159601	<0.0001	8.40E-04
KAUFFMANN MELANOMA RELAPSE UP	59	0.858715	2.15951	<0.0001	8.35E-04
CHEN ETV5 TARGETS TESTIS	21	0.848038	2.158898	<0.0001	8.35E-04
RHODES UNDIFFERENTIATED CANCER	67	0.846356	2.15832	<0.0001	8.41E-04
REACTOME HIV LIFE CYCLE	105	0.625698	2.156117	<0.0001	8.79E-04
PID ATM PATHWAY	33	0.723995	2.152404	<0.0001	9.45E-04
WEST ADRENOCORTICAL TUMOR MARKERS UP	21	0.827331	2.151475	<0.0001	9.58E-04
SOTIRIOU BREAST CANCER GRADE 1 VS 3 UP	141	0.911728	2.150769	<0.0001	9.58E-04
REACTOME TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRONLESS TRANSCRIPT	31	0.78993	2.150719	<0.0001	9.52E-04
REACTOME ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS	35	0.876601	2.150423	<0.0001	9.46E-04
REACTOME PROCESSING OF CAPPED INTRON CONTAINING PRE MRNA	132	0.65681	2.149792	<0.0001	9.80E-04
SANSOM APC TARGETS REQUIRE MYC	192	0.54353	2.149358	<0.0001	9.74E-04
REACTOME RECRUITMENT OF MITOTIC CENTROSOME PROTEINS AND COMPLEXES	62	0.633393	2.147291	<0.0001	1.00E-03
BOYAULT LIVER CANCER SUBCLASS G23 UP	49	0.78964	2.14394	<0.0001	0.001058
PUIFFE INVASION INHIBITED BY ASCITES UP	81	0.571522	2.142774	<0.0001	0.001063
WHITFIELD CELL CYCLE LITERATURE	44	0.913939	2.141911	<0.0001	0.001057

WELCSH BRCA1 TARGETS DN	139	0.609454	2.140259	<0.0001	0.001085
REACTOME DNA REPAIR	101	0.629986	2.139719	<0.0001	0.001095
DELPUECH FOXO3 TARGETS DN	39	0.756195	2.137588	<0.0001	0.001135
REACTOME EXTENSION OF TELOMERES	27	0.881087	2.13467	<0.0001	0.001191
REACTOME DNA STRAND ELONGATION	30	0.929324	2.133741	<0.0001	0.001214
WHITFIELD CELL CYCLE S	147	0.591354	2.130671	<0.0001	0.001287
ISHIDA E2F TARGETS	50	0.921924	2.128528	<0.0001	0.00132
REACTOME E2F MEDIATED REGULATION OF DNA REPLICATION	33	0.805744	2.127428	<0.0001	0.00133
XU HGF TARGETS INDUCED BY AKT1 48HR DN	24	0.76192	2.126319	<0.0001	0.001362
FOURNIER ACINAR DEVELOPMENT LATE DN	21	0.836678	2.126291	<0.0001	0.001355
KANG DOXORUBICIN RESISTANCE UP	50	0.959832	2.12497	<0.0001	0.001378
BIOCARTA MCM PATHWAY	18	0.894425	2.124591	<0.0001	0.001375
PID MYC ACTIV PATHWAY	78	0.630986	2.123963	<0.0001	0.001385
ZAMORA NOS2 TARGETS UP	64	0.658205	2.122983	<0.0001	0.001412
WONG EMBRYONIC STEM CELL CORE	330	0.685597	2.112932	0.001931	0.001619
AMUNDSON GAMMA RADIATION RESPONSE	40	0.866518	2.112331	<0.0001	0.001637
SUNG METASTASIS STROMA DN	49	0.669221	2.11179	<0.0001	0.001656
KOKKINAKIS METHIONINE DEPRIVATION 96HR DN	75	0.571024	2.111435	<0.0001	0.001657
WILLIAMS ESR1 TARGETS UP	26	0.673158	2.111164	<0.0001	0.001658
BIOCARTA G2 PATHWAY	24	0.74592	2.110856	<0.0001	0.001654
GINESTIER BREAST CANCER 20Q13 AMPLIFICATION DN	151	0.588402	2.108311	<0.0001	0.001702
YU MYC TARGETS UP	39	0.866203	2.10712	<0.0001	0.001709
REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX	30	0.895076	2.106946	<0.0001	0.0017
KAMMINGA EZH2 TARGETS	41	0.881167	2.106422	<0.0001	0.001695
HESS TARGETS OF HOXA9 AND MEIS1 UP	63	0.602291	2.105219	<0.0001	0.001705
REACTOME MITOTIC G1 G1 S PHASES	130	0.689553	2.103447	0.00198	0.001735
REACTOME SYNTHESIS OF DNA	90	0.75547	2.103255	0.001946	0.001726
WANG METASTASIS OF BREAST CANCER ESR1 UP	19	0.85497	2.103049	<0.0001	0.001722
REACTOME REGULATION OF GLUCOKINASE BY GLUCOKINASE REGULATORY PROTEIN	26	0.771778	2.099896	<0.0001	0.001785
KEGG MISMATCH REPAIR	23	0.800884	2.099178	<0.0001	0.00179
NUNODA RESPONSE TO DASATINIB IMATINIB UP	29	0.652181	2.09755	<0.0001	0.001821
STANELLE E2F1 TARGETS	27	0.594432	2.095453	<0.0001	0.001877
CUI TCF21 TARGETS 2 UP	404	0.486541	2.093327	<0.0001	0.001933
MATTIOLI MGUS VS PCL	93	0.578283	2.09257	0.002008	0.00194
ZHAN MULTIPLE MYELOMA SUBGROUPS	30	0.806344	2.09204	<0.0001	0.001931
REACTOME S PHASE	106	0.719442	2.090513	0.001931	0.001971
REACTOME LOSS OF NLP FROM MITOTIC CENTROSOMES	55	0.634169	2.090493	<0.0001	0.001962
REACTOME LATE PHASE OF HIV LIFE CYCLE	92	0.616493	2.089722	<0.0001	0.001971
PID FANCONI PATHWAY	43	0.762282	2.089032	<0.0001	0.001968
REACTOME ANTIVIRAL MECHANISM BY IFN STIMULATED GENES	64	0.624437	2.087877	<0.0001	0.002011

REICHERT MITOSIS LIN9 TARGETS	27	0.921414	2.085688	<0.0001	0.002063
SLEBOS HEAD AND NECK CANCER WITH HPV UP	78	0.678077	2.084783	<0.0001	0.002062
WINTER HYPOXIA UP	88	0.636414	2.08418	<0.0001	0.002065
REACTOME INTERACTIONS OF VPR WITH HOST CELLULAR PROTEINS	31	0.743304	2.08228	<0.0001	0.002134
REACTOME NEP NS2 INTERACTS WITH THE CELLULAR EXPORT MACHINERY	26	0.798508	2.081939	<0.0001	0.002146
REACTOME TRANSPORT OF RIBONUCLEOPROTEINS INTO THE HOST NUCLEUS	26	0.79971	2.08071	<0.0001	0.002186
BOYAULT LIVER CANCER SUBCLASS G123 UP	44	0.741986	2.080435	<0.0001	0.002185
SU TESTIS	67	0.640624	2.079646	<0.0001	0.002191
MOHANKUMAR HOXA1 TARGETS UP	384	0.497657	2.079488	<0.0001	0.002185
REACTOME CELL CYCLE CHECKPOINTS	111	0.724142	2.077745	<0.0001	0.00222
PID BARD1 PATHWAY	28	0.776418	2.07737	<0.0001	0.002214
SERVITJA LIVER HNF1A TARGETS UP	132	0.480138	2.076758	<0.0001	0.002218
SASAKI ADULT T CELL LEUKEMIA	168	0.541987	2.07645	<0.0001	0.002216
REACTOME FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC	21	0.790064	2.074503	<0.0001	0.002284
VANTVEER BREAST CANCER POOR PROGNOSIS	50	0.615508	2.072005	<0.0001	0.002374
NAKAMURA CANCER MICROENVIRONMENT DN	43	0.77325	2.071477	<0.0001	0.002387
PYEON CANCER HEAD AND NECK VS CERVICAL UP	169	0.622744	2.067814	0.001901	0.002527
SIMBULAN PARP1 TARGETS DN	17	0.891198	2.066801	<0.0001	0.002564
GENTILE RESPONSE CLUSTER D3	61	0.597491	2.066162	<0.0001	0.002581
HONRADO BREAST CANCER BRCA1 VS BRCA2	18	0.751023	2.064675	<0.0001	0.002622
REACTOME LAGGING STRAND SYNTHESIS	19	0.906143	2.060474	<0.0001	0.002824
NAKAMURA TUMOR ZONE PERIPHERAL VS CENTRAL UP	267	0.556121	2.057963	<0.0001	0.00293
REACTOME HOST INTERACTIONS OF HIV FACTORS	117	0.611248	2.054864	0.001984	0.00304
PETROVA ENDOTHELIUM LYMPHATIC VS BLOOD UP	126	0.527579	2.054503	<0.0001	0.003051
SMID BREAST CANCER LUMINAL A DN	18	0.906986	2.046908	<0.0001	0.003367
MATZUK MEIOTIC AND DNA REPAIR	35	0.625582	2.044516	0.002016	0.003486
KEGG BASE EXCISION REPAIR	33	0.66736	2.041335	<0.0001	0.003611
SMIRNOV RESPONSE TO IR 6HR DN	108	0.576037	2.036821	<0.0001	0.00381
WILCOX RESPONSE TO PROGESTERONE UP	140	0.558499	2.036707	<0.0001	0.003807
REACTOME HIV INFECTION	184	0.574529	2.033981	0.002024	0.003928
LE NEURONAL DIFFERENTIATION DN	19	0.785866	2.033888	<0.0001	0.003926
WAKASUGI HAVE ZNF143 BINDING SITES	56	0.640048	2.033449	<0.0001	0.003931
REACTOME G1 S TRANSITION	106	0.705011	2.033273	0.001961	0.003926
SHIPP DLBCL VS FOLLICULAR LYMPHOMA UP	44	0.715433	2.0317	<0.0001	0.004019
REACTOME G1 S SPECIFIC TRANSCRIPTION	17	0.887317	2.031275	<0.0001	0.004022
YAMAZAKI TCEB3 TARGETS DN	204	0.51882	2.028697	<0.0001	0.004127
JEON SMAD6 TARGETS DN	19	0.753473	2.027249	<0.0001	0.004151
ZHAN MULTIPLE MYELOMA PR UP	43	0.9348	2.026491	<0.0001	0.00416
REACTOME KINESINS	23	0.787591	2.024085	0.002012	0.004296
MATZUK SPERMATOCYTE	68	0.526375	2.022173	<0.0001	0.004388

LI WILMS TUMOR ANAPLASTIC UP	19	0.928738	2.020802	<0.0001	0.004485
SA G1 AND S PHASES	15	0.723232	2.018772	0.00202	0.004604
BOYLAN MULTIPLE MYELOMA C CLUSTER UP	37	0.582256	2.017723	<0.0001	0.004658
GROSS HYPOXIA VIA ELK3 ONLY DN	41	0.550316	2.014632	<0.0001	0.004829
CAFFAREL RESPONSE TO THC DN	29	0.713056	2.014072	<0.0001	0.004829
CHAUHAN RESPONSE TO METHOXYESTRADIOL UP	50	0.598643	2.012912	<0.0001	0.004873
REACTOME G0 AND EARLY G1	23	0.782151	2.010308	<0.0001	0.005011
BIOCARTA G1 PATHWAY	28	0.658731	2.010183	<0.0001	0.005002
KEGG SPLICEOSOME	123	0.593228	2.007755	<0.0001	0.005142
REACTOME PROCESSIVE SYNTHESIS ON THE LAGGING STRAND	15	0.887818	2.005355	<0.0001	0.005267
SCIAN CELL CYCLE TARGETS OF TP53 AND TP73 DN	22	0.879797	2.005096	<0.0001	0.005257
KEGG OOCYTE MEIOSIS	107	0.513166	2.002527	0.002045	0.005389
PENG RAPAMYCIN RESPONSE DN	230	0.5871	2.002149	<0.0001	0.005425
REACTOME APC CDC20 MEDIATED DEGRADATION OF NEK2A	21	0.783271	1.999412	<0.0001	0.005595
PID P73PATHWAY	76	0.511208	1.99822	<0.0001	0.00567
SANSOM APC MYC TARGETS	198	0.441858	1.997603	<0.0001	0.005701
LY AGING MIDDLE DN	16	0.9695	1.99711	<0.0001	0.005707
BASSO B LYMPHOCYTE NETWORK	135	0.521596	1.996411	0.001972	0.005742
LAU APOPTOSIS CDKN2A UP	55	0.535261	1.995455	<0.0001	0.005797
REACTOME CHROMOSOME MAINTENANCE	112	0.704528	1.992625	<0.0001	0.005991
REACTOME MRNA SPLICING	104	0.620392	1.992351	<0.0001	0.005991
GROSS HYPOXIA VIA ELK3 AND HIF1A DN	100	0.468281	1.992147	<0.0001	0.005984
KEGG PROGESTERONE MEDIATED OOCYTE MATURATION	83	0.494061	1.991438	<0.0001	0.006005
REACTOME METABOLISM OF NON CODING RNA	47	0.702641	1.989715	<0.0001	0.006114
REACTOME HOMOLOGOUS RECOMBINATION REPAIR OF REPLICATION INDEPENDENT DOUBLE STRAND BREAKS	15	0.795836	1.988127	0.001901	0.006189
REACTOME M G1 TRANSITION	78	0.740495	1.985265	0.00198	0.006396
BIOCARTA ATRBRCA PATHWAY	19	0.762603	1.979125	<0.0001	0.006858
BILD MYC ONCOGENIC SIGNATURE	187	0.476209	1.977043	0.002079	0.007043
ELVIDGE HYPOXIA DN	136	0.520392	1.976719	<0.0001	0.007049
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 11	95	0.566186	1.976506	0.002062	0.007043
RAMASWAMY METASTASIS UP	64	0.546034	1.976347	<0.0001	0.007042
JOHANSSON GLIOMAGENESIS BY PDGFB UP	57	0.576944	1.975038	0.002083	0.007111
ENK UV RESPONSE EPIDERMIS UP	277	0.457464	1.973899	<0.0001	0.007174
PID RB 1PATHWAY	65	0.496958	1.97231	0.002062	0.007291
MEINHOLD OVARIAN CANCER LOW GRADE DN	20	0.776498	1.970919	<0.0001	0.007416
SCHLOSSER SERUM RESPONSE AUGMENTED BY MYC	101	0.486546	1.96799	<0.0001	0.007669
CHANDRAN METASTASIS UP	191	0.466812	1.967911	<0.0001	0.007652
REACTOME INHIBITION OF THE PROTEOLYTIC ACTIVITY OF APC C REQUIRED FOR THE ONSET OF ANAPHASE BY MITOTIC SPINDLE	18	0.79346	1.966908	<0.0001	0.007763

CHECKPOINT COMPONENTS					
REACTOME BASE EXCISION REPAIR	19	0.736942	1.965773	<0.0001	0.007849
BHAT ESR1 TARGETS VIA AKT1 UP	267	0.440362	1.963363	<0.0001	0.008057
YANG BCL3 TARGETS UP	344	0.419185	1.961807	<0.0001	0.008198
EPPERT PROGENITOR	125	0.589314	1.960984	0.006012	0.008234
REACTOME CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION REGION	42	0.644429	1.957844	<0.0001	0.008602
REACTOME DOUBLE STRAND BREAK REPAIR	21	0.741136	1.952599	0.001931	0.009115
EGUCHI CELL CYCLE RB1 TARGETS	23	0.969321	1.949859	<0.0001	0.009362
BIOCARTA CELLCYCLE PATHWAY	23	0.685744	1.949435	<0.0001	0.009383
REACTOME CYCLIN A B1 ASSOCIATED EVENTS DURING G2 M TRANSITION	15	0.849242	1.949138	0.002012	0.0094
RICKMAN TUMOR DIFFERENTIATED MODERATELY VS POORLY DN	15	0.758615	1.947434	<0.0001	0.009551
SCHUHMACHER MYC TARGETS UP	77	0.634432	1.946798	0.003914	0.009609
LASTOWSKA NEUROBLASTOMA COPY NUMBER UP	163	0.532851	1.943121	0.003992	0.010075
JUBAN TARGETS OF SPI1 AND FLI1 DN	84	0.52183	1.942098	0.001972	0.010154
IWANAGA E2F1 TARGETS INDUCED BY SERUM	29	0.711711	1.940305	0.001927	0.010309
REACTOME PHOSPHORYLATION OF THE APC C	17	0.782124	1.939369	<0.0001	0.010389
BURTON ADIPOGENESIS 4	44	0.575164	1.938206	0.004167	0.010525
HERNANDEZ MITOTIC ARREST BY DOCETAXEL 1 DN	36	0.60557	1.937816	<0.0001	0.010512
BHATI G2M ARREST BY 2METHOXYESTRADIOL UP	108	0.497994	1.936528	<0.0001	0.010634
REACTOME PROCESSING OF CAPPED INTRONLESS PRE MRNA	23	0.712659	1.934703	<0.0001	0.010773
JIANG HYPOXIA VIA VHL	33	0.610943	1.934451	0.00198	0.010758
GINESTIER BREAST CANCER ZNF217 AMPLIFIED DN	303	0.55689	1.932361	0.008403	0.011003
KIM WT1 TARGETS DN	427	0.471465	1.932234	<0.0001	0.01099
NIKOLSKY BREAST CANCER 12Q24 AMPLICON	15	0.847804	1.929698	0.002088	0.011272
RIZ ERYTHROID DIFFERENTIATION CCNE1	39	0.53327	1.928633	<0.0001	0.011413
REACTOME MRNA 3 END PROCESSING	33	0.656334	1.924507	0.001916	0.011951
SANSOM APC TARGETS UP	113	0.453162	1.924256	<0.0001	0.011964
REACTOME FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION	111	0.487684	1.923137	<0.0001	0.012068
REACTOME ASSEMBLY OF THE PRE REPLICATIVE COMPLEX	63	0.724831	1.921464	0.001976	0.012279
FARMER BREAST CANCER CLUSTER 2	32	0.916967	1.919269	<0.0001	0.01256
NAGY TFTC COMPONENTS HUMAN	18	0.658953	1.918653	<0.0001	0.012624
BILD E2F3 ONCOGENIC SIGNATURE	222	0.431774	1.917682	<0.0001	0.012713
LEE LIVER CANCER SURVIVAL DN	165	0.613091	1.917151	0.002024	0.012742
WONG PROTEASOME GENE MODULE	49	0.650704	1.915606	<0.0001	0.01295
REACTOME GLOBAL GENOMIC NER GG NER	32	0.646461	1.91298	<0.0001	0.013271
KEGG GLYOXYLATE AND DICARBOXYLATE METABOLISM	16	0.72315	1.912502	0.001957	0.01332
OUELLET OVARIAN CANCER INVASIVE VS LMP	117	0.584398	1.912028	0.00404	0.013357

UP					
BOHN PRIMARY IMMUNODEFICIENCY SYNDROM UP	45	0.58582	1.909768	0.001988	0.013632
GENTLES LEUKEMIC STEM CELL DN	18	0.709169	1.908006	0.002037	0.01388
PEART HDAC PROLIFERATION CLUSTER UP	55	0.531517	1.90765	<0.0001	0.013901
REACTOME FANCONI ANEMIA PATHWAY	19	0.786802	1.907609	0.001976	0.013864
PID TELOMERASE PATHWAY	67	0.514617	1.905231	0.004032	0.014149
LI WILMS TUMOR VS FETAL KIDNEY 2 UP	29	0.652867	1.903723	0.005803	0.014376
MONNIER POSTRADIATION TUMOR ESCAPE UP	374	0.431026	1.898734	0.002053	0.01516
PIONTEK PKD1 TARGETS DN	16	0.710243	1.89749	<0.0001	0.015304
KRASNOSELSKAYA ILF3 TARGETS DN	44	0.546053	1.896969	<0.0001	0.015331
REACTOME APC C CDC20 MEDIATED DEGRADATION OF CYCLIN B	19	0.750141	1.896512	0.001965	0.015375
SMID BREAST CANCER RELAPSE IN LUNG UP	20	0.666454	1.89343	0.002024	0.015846
SHIN B CELL LYMPHOMA CLUSTER 8	36	0.599433	1.892346	0.002058	0.015948
REACTOME GLYCOLYSIS	25	0.640644	1.890798	0.002088	0.01626
MORI SMALL PRE BII LYMPHOCYTE DN	74	0.474081	1.890609	0.00198	0.016243
LOPEZ TRANSLATION VIA FN1 SIGNALING	34	0.553193	1.889538	0.00404	0.016358
CAIRO PML TARGETS BOUND BY MYC UP	23	0.654825	1.888087	0.01227	0.016569
MODY HIPPOCAMPUS NEONATAL	35	0.607488	1.887457	0.007843	0.016632
REACTOME RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATCH REPLACEMENT PATHWAY	17	0.7289	1.887273	0.004024	0.01663
FINETTI BREAST CANCER KINOME RED	16	0.956155	1.887021	<0.0001	0.016627
REACTOME RNA POL II TRANSCRIPTION	93	0.553349	1.886383	0.001931	0.016667
DOANE BREAST CANCER CLASSES DN	32	0.601599	1.886329	0.002058	0.01662
REACTOME ORC1 REMOVAL FROM CHROMATIN	65	0.702322	1.884071	0.002012	0.017005
REACTOME REGULATION OF MITOTIC CELL CYCLE	77	0.685013	1.883218	0.002016	0.017095
MENSSEN MYC TARGETS	51	0.655932	1.882209	0.006122	0.017221
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION MONOCYTE UP	195	0.466716	1.881605	0.004158	0.017313
SESTO RESPONSE TO UV C4	20	0.63672	1.880775	0.004219	0.017425
HEDENFALK BREAST CANCER BRCA1 VS BRCA2	156	0.470417	1.880102	0.003976	0.017501
WALLACE JAK2 TARGETS UP	25	0.632531	1.875817	0.002066	0.018272
REACTOME PREFOLDIN MEDIATED TRANSFER OF SUBSTRATE TO CCT TRIC	27	0.686418	1.871294	0.004073	0.019122
LEE METASTASIS AND RNA PROCESSING UP	17	0.7356	1.870598	0.001965	0.019207
REACTOME POST CHAPERONIN TUBULIN FOLDING PATHWAY	18	0.672857	1.870263	0.006012	0.019237
FARMER BREAST CANCER CLUSTER 5	18	0.786578	1.866916	0.001953	0.019888
REACTOME TRANSCRIPTION COUPLED NER TC NER	43	0.607443	1.866313	0.00198	0.019951
CHOW RASSF1 TARGETS UP	26	0.59771	1.864912	0.004024	0.020155
KARAKAS TGFB1 SIGNALING	18	0.696527	1.864268	0.004149	0.020217
SMITH TERT TARGETS UP	141	0.464406	1.863065	0.001972	0.020474
TOMIDA METASTASIS UP	26	0.631341	1.862824	0.004175	0.020459
COLINA TARGETS OF 4EBP1 AND 4EBP2	346	0.40879	1.861381	0.001934	0.020702
GRAESSMANN RESPONSE TO MC AND SERUM	78	0.438816	1.861151	<0.0001	0.020692

DEPRIVATION DN					
SCHLOSSER MYC TARGETS AND SERUM RESPONSE DN	45	0.643542	1.860431	0.014085	0.020765
REACTOME CONVERSION FROM APC C CDC20 TO APC C CDH1 IN LATE ANAPHASE	16	0.709278	1.858078	0.001976	0.021259
UDAYAKUMAR MED1 TARGETS UP	129	0.491122	1.857105	<0.0001	0.021387
BROWNE HCMV INFECTION 2HR DN	48	0.565526	1.854565	0.003992	0.021878
YUAN ZNF143 PARTNERS	21	0.690491	1.854281	0.002016	0.02191
CHIARETTI T ALL RELAPSE PROGNOSIS	19	0.691591	1.854114	0.001942	0.021893
KARLSSON TGFB1 TARGETS UP	118	0.554544	1.852094	0.006048	0.022247
WEIGEL OXIDATIVE STRESS BY HNE AND H2O2	39	0.50648	1.844822	0.001949	0.023823
ZHANG BREAST CANCER PROGENITORS UP	399	0.526447	1.844558	0.009506	0.023816
ZHAN VARIABLE EARLY DIFFERENTIATION GENES DN	30	0.576495	1.843922	0.01222	0.023926
MARIADASON RESPONSE TO BUTYRATE SULINDAC 4	21	0.638055	1.840878	<0.0001	0.024633
BROWNE HCMV INFECTION 14HR UP	151	0.429471	1.8378	<0.0001	0.025324
CHIN BREAST CANCER COPY NUMBER UP	24	0.642377	1.837327	0.006036	0.02537
CHANDRAN METASTASIS TOP50 UP	34	0.599966	1.835718	0.008529	0.025764
AMIT EGF RESPONSE 480 MCF10A	40	0.549684	1.834165	0.004032	0.026162
PID MYC PATHWAY	25	0.58743	1.832561	0.002041	0.02647
KOKKINAKIS METHIONINE DEPRIVATION 48HR DN	64	0.468072	1.831878	<0.0001	0.026574
OUYANG PROSTATE CANCER MARKERS	19	0.598903	1.82692	0.003984	0.027808
RHEIN ALL GLUCOCORTICOID THERAPY DN	349	0.52694	1.826612	0.013917	0.027803
COLLER MYC TARGETS UP	25	0.688274	1.824542	0.00994	0.028272
FERRANDO HOX11 NEIGHBORS	23	0.665388	1.824189	0.008097	0.028276
MOREAUX B LYMPHOCYTE MATURATION BY TACI DN	66	0.610888	1.823406	0.015444	0.028441
REACTOME APC C CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS	65	0.68184	1.822773	0.013944	0.028526
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 14	134	0.533481	1.82163	0.014315	0.02878
SHAFFER IRF4 TARGETS IN ACTIVATED B LYMPHOCYTE	76	0.534984	1.817887	0.00996	0.029723
QI HYPOXIA TARGETS OF HIF1A AND FOXA2	36	0.562575	1.815728	0.012959	0.030264
GRADE METASTASIS DN	42	0.632338	1.81546	0.010101	0.030267
ZHANG RESPONSE TO CANTHARIDIN DN	67	0.595862	1.811645	0.016194	0.031294
BONOME OVARIAN CANCER POOR SURVIVAL DN	20	0.607782	1.810324	0.008316	0.03162
TURASHVILI BREAST DUCTAL CARCINOMA VS LOBULAR NORMAL UP	71	0.574818	1.808855	0.006012	0.031939
LOCKWOOD AMPLIFIED IN LUNG CANCER	205	0.466003	1.807801	0.00998	0.032154
GROSS HYPOXIA VIA HIF1A UP	75	0.488037	1.807693	0.009862	0.032112
ZHANG RESPONSE TO IKK INHIBITOR AND TNF DN	100	0.463692	1.807535	<0.0001	0.032067
ZHAN EARLY DIFFERENTIATION GENES DN	42	0.528242	1.806294	0.006036	0.032346
GARY CD5 TARGETS DN	414	0.503119	1.806287	0.009843	0.032267
WANG RECURRENT LIVER CANCER UP	20	0.617381	1.805788	0.009671	0.032317

CONCANNON APOPTOSIS BY EPOXOMICIN DN	159	0.443199	1.805061	0.004008	0.032457
REACTOME APC C CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC C CDH1 TARGETED PROTEINS IN LATE MITOSIS EARLY G1	64	0.678872	1.801255	0.006198	0.033611
KENNY CTNNB1 TARGETS UP	46	0.47911	1.798506	0.002083	0.034422
HUANG GATA2 TARGETS DN	67	0.456913	1.798502	0.005988	0.034336
KATSANOU ELAVL1 TARGETS DN	141	0.411378	1.798093	0.002037	0.034376
KORKOLA TERATOMA	39	0.522011	1.796968	0.005682	0.034607
CAFFAREL RESPONSE TO THC 24HR 5 DN	55	0.564307	1.796131	0.011858	0.034799
PRAMOONJAGO SOX4 TARGETS DN	50	0.542804	1.795203	0.014286	0.035024
BIOCARTA ATM PATHWAY	19	0.607166	1.793747	0.00994	0.035413
ACOSTA PROLIFERATION INDEPENDENT MYC TARGETS UP	75	0.484334	1.791232	<0.0001	0.036201
YANG BREAST CANCER ESR1 BULK DN	22	0.589339	1.787586	0.004008	0.037347
KAMMINGA SENESCENCE	39	0.510462	1.785717	0.006073	0.037869
HEIDENBLAD AMPLICON 8Q24 UP	34	0.513789	1.784153	0.002033	0.038296
DOANE RESPONSE TO ANDROGEN DN	225	0.377645	1.782836	<0.0001	0.038629
XU RESPONSE TO TRETINOIN AND NSC682994 DN	15	0.749218	1.782828	0.007952	0.038536
DAIRKEE CANCER PRONE RESPONSE BPA	49	0.5149	1.78255	0.008163	0.038531
YANG BREAST CANCER ESR1 LASER DN	49	0.51411	1.782425	0.009766	0.038496
GENTILE UV RESPONSE CLUSTER D5	37	0.538302	1.781632	0.004049	0.038691
DAIRKEE CANCER PRONE RESPONSE BPA E2	113	0.454566	1.780891	0.007937	0.038834
AGUIRRE PANCREATIC CANCER COPY NUMBER UP	271	0.422701	1.780223	0.006036	0.03895
REACTOME TELOMERE MAINTENANCE	72	0.717516	1.779141	0.009862	0.039168
KOINUMA COLON CANCER MSI UP	16	0.680834	1.777525	0.008	0.039635
MULLIGAN NTF3 SIGNALING VIA INSR AND IGF1R UP	23	0.613226	1.775819	0.013889	0.040098
BORCZUK MALIGNANT MESOTHELIOMA UP	291	0.534062	1.77549	0.018293	0.040138
REACTOME NUCLEOTIDE EXCISION REPAIR	48	0.551427	1.775326	0.011858	0.040091
CREIGHTON ENDOCRINE THERAPY RESISTANCE 1	483	0.388255	1.774407	0.001969	0.040293
BIOCARTA P53 PATHWAY	16	0.6195	1.772056	0.014085	0.041034
BOYLAN MULTIPLE MYELOMA C UP	44	0.489699	1.771714	0.002028	0.041066
PEDERSEN METASTASIS BY ERBB2 ISOFORM 7	362	0.374922	1.769196	0.002016	0.041819
SHIPP DLBCL CURED VS FATAL DN	42	0.454515	1.768747	0.004211	0.041875
BIOCARTA MTA3 PATHWAY	19	0.601146	1.768595	0.006316	0.041814
MARKS HDAC TARGETS DN	15	0.650421	1.761765	0.005882	0.044272
AUNG GASTRIC CANCER	53	0.483991	1.761633	0.002004	0.044214
JAIN NFKB SIGNALING	71	0.450145	1.760884	0.005988	0.044359
MARTINEZ RESPONSE TO TRABECTEDIN DN	265	0.470591	1.757903	0.009804	0.04541
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS RED UP	16	0.674322	1.757627	0.00969	0.045389
BOYLAN MULTIPLE MYELOMA C D UP	129	0.412027	1.750828	0.001949	0.04793
MCBRYAN PUBERTAL BREAST 6 7WK DN	76	0.432564	1.750524	0.003914	0.047915
FIRESTEIN CTNNB1 PATHWAY	32	0.522313	1.750299	0.010482	0.047874
RASHI RESPONSE TO IONIZING RADIATION 4	57	0.428119	1.749433	0.006048	0.048117

COLLIS PRKDC SUBSTRATES	19	0.629469	1.748729	0.012048	0.048256
SCHLOSSER MYC TARGETS AND SERUM RESPONSE UP	46	0.582833	1.748623	0.008282	0.048189
ALFANO MYC TARGETS	230	0.387894	1.744518	<0.0001	0.049764
VANDESLUIS COMMD1 TARGETS GROUP 2 UP	15	0.632077	1.743413	0.010482	0.050116
DANG MYC TARGETS UP	138	0.558517	1.743166	0.022133	0.050106
IIZUKA LIVER CANCER PROGRESSION G1 G2 DN	24	0.606108	1.741579	0.014113	0.050655
KRIGE AMINO ACID DEPRIVATION	28	0.579764	1.741358	0.014028	0.050614
HASLINGER B CLL WITH CHROMOSOME 12 TRISOMY	22	0.625503	1.739008	0.010101	0.051462
HEDENFALK BREAST CANCER HEREDITARY VS SPORADIC	46	0.510327	1.738706	0.016064	0.051486
NEMETH INFLAMMATORY RESPONSE LPS DN	32	0.514624	1.738703	0.009785	0.051375
KEGG NUCLEOTIDE EXCISION REPAIR	44	0.564056	1.738524	0.014315	0.05133
REACTOME SHC1 EVENTS IN EGFR SIGNALING	15	0.637525	1.736871	0.010267	0.051851
REACTOME REGULATION OF KIT SIGNALING	16	0.625786	1.73376	0.01581	0.052997
KORKOLA YOLK SAC TUMOR UP	19	0.688392	1.730922	0.0125	0.054076
CHICAS RB1 TARGETS LOW SERUM	84	0.52153	1.729963	0.025341	0.054305
REACTOME CDT1 ASSOCIATION WITH THE CDC6 ORC ORIGIN COMPLEX	54	0.671975	1.728596	0.029821	0.054781
SYED ESTRADIOL RESPONSE	19	0.552392	1.727593	0.001953	0.055147
DORMOY ELAVL1 TARGETS	16	0.600263	1.726545	0.014	0.055477
KIM TIAL1 TARGETS	31	0.529722	1.72588	0.016162	0.055626
SCHLOSSER MYC TARGETS REPRESSED BY SERUM	153	0.558718	1.724649	0.023669	0.056053
BHAT ESR1 TARGETS NOT VIA AKT1 UP	204	0.391497	1.722863	0.004292	0.056667
WANG SMARCE1 TARGETS DN	348	0.413368	1.722439	0.009747	0.056741
SCHLOSSER MYC AND SERUM RESPONSE SYNERGY	31	0.621273	1.715185	0.016701	0.060069
BIOCARTA VEGF PATHWAY	29	0.502447	1.710731	0.01	0.062121
ELVIDGE HIF1A AND HIF2A TARGETS UP	38	0.513299	1.710603	0.013672	0.062049
GAZIN EPIGENETIC SILENCING BY KRAS	24	0.536963	1.707667	0.02004	0.063299
PID PRL SIGNALING EVENTS PATHWAY	23	0.541884	1.707621	0.011696	0.063191
DACOSTA UV RESPONSE VIA ERCC3 UP	296	0.423989	1.706927	0.013333	0.063388
MATSUDA NATURAL KILLER DIFFERENTIATION	455	0.348894	1.704425	<0.0001	0.064484
TSENG IRS1 TARGETS UP	106	0.424004	1.701628	0.004141	0.065767
SPIELMAN LYMPHOBLAST EUROPEAN VS ASIAN UP	467	0.421584	1.701536	0.029046	0.065666
CHEN HOXA5 TARGETS 9HR DN	36	0.502367	1.701035	0.023158	0.065765
BENPORATH MYC TARGETS WITH EBOX	219	0.391862	1.700512	0.008264	0.06587
REACTOME MRNA SPLICING MINOR PATHWAY	40	0.585225	1.698687	0.044922	0.066606
WOOD EBV EBNA1 TARGETS UP	109	0.415678	1.696567	0.017621	0.067623
WU HBX TARGETS 2 UP	22	0.534293	1.695216	0.017241	0.0682
KEGG ONE CARBON POOL BY FOLATE	17	0.616594	1.694383	0.014199	0.068486
LIAO HAVE SOX4 BINDING SITES	40	0.479374	1.691486	0.008065	0.069656
SHETH LIVER CANCER VS TXNIP LOSS PAM1	221	0.359227	1.688762	0.008097	0.07092
VANHARANTA UTERINE FIBROID WITH 7Q DELETION UP	65	0.469301	1.688505	0.009311	0.070937
WHITFIELD CELL CYCLE M G1	140	0.430909	1.685723	0.009881	0.07228

ROESSLER LIVER CANCER METASTASIS UP	102	0.380249	1.68114	0.006466	0.074694
WEST ADRENOCORTICAL CARCINOMA VS ADENOMA UP	18	0.563082	1.680375	0.015842	0.074945
CUI GLUCOSE DEPRIVATION	58	0.474211	1.679451	0.021739	0.075299
SANSOM APC TARGETS	192	0.361143	1.679052	<0.0001	0.075357
REACTOME APOPTOSIS	141	0.434313	1.679024	0.022	0.075222
REACTOME G1 PHASE	35	0.509178	1.67761	0.018293	0.075877
VANTVEER BREAST CANCER BRCA1 UP	31	0.522712	1.676921	0.014644	0.076069
LIU SOX4 TARGETS DN	293	0.368142	1.674423	0.008147	0.077422
JACKSON DNMT1 TARGETS DN	24	0.580639	1.671261	0.030675	0.078966
BROWNE HCMV INFECTION 48HR UP	174	0.366618	1.670898	0.007707	0.07903
MMS MOUSE LYMPH HIGH 4HRS UP	31	0.577448	1.669948	0.026369	0.079362
XU CREBBP TARGETS UP	24	0.522459	1.669384	0.021569	0.079532
AMUNDSON GENOTOXIC SIGNATURE	99	0.378593	1.668514	0.006122	0.079889
DEN INTERACT WITH LCA5	25	0.606244	1.667957	0.036437	0.080035
HOFMANN MYELODYSPLASTIC SYNDROM RISK UP	24	0.552774	1.667232	0.026971	0.080299
KAPOSI LIVER CANCER MET UP	17	0.617205	1.66397	0.030864	0.081786
PARK HSC VS MULTIPOTENT PROGENITORS DN	18	0.578936	1.663548	0.024048	0.081896
PODAR RESPONSE TO ADAPHOSTIN DN	18	0.588823	1.663177	0.034979	0.081988
REACTOME ANTIGEN PROCESSING UBIQUITINATION PROTEASOME DEGRADATION	192	0.431399	1.660313	0.021739	0.083498
BURTON ADIPOGENESIS 2	72	0.434288	1.658349	0.02714	0.084485
SIG REGULATION OF THE ACTIN CYTOSKELETON BY RHO GTPASES	34	0.51478	1.657486	0.026052	0.084828
VERHAAK GLIOBLASTOMA PRONEURAL	167	0.454466	1.655961	0.016791	0.085439
SHAFFER IRF4 TARGETS IN ACTIVATED DENDRITIC CELL	61	0.468219	1.65402	0.030769	0.08641
MACLACHLAN BRCA1 TARGETS UP	21	0.587358	1.653751	0.031579	0.086405
STAMBOLSKY BOUND BY MUTATED TP53	17	0.559684	1.65369	0.019685	0.086266
ZUCCHI METASTASIS UP	38	0.506389	1.651958	0.028056	0.087209
REACTOME GLUCONEOGENESIS	29	0.553363	1.650653	0.030738	0.087935
KEGG PYRIMIDINE METABOLISM	96	0.454016	1.646759	0.022044	0.090304
REACTOME GLUCOSE METABOLISM	61	0.457947	1.645502	0.02454	0.090967
STEIN ESRRA TARGETS RESPONSIVE TO ESTROGEN UP	29	0.498494	1.645105	0.019763	0.09107
GENTILE UV HIGH DOSE DN	300	0.393233	1.644563	0.01341	0.091225
PURBEY TARGETS OF CTBP1 AND SATB1 UP	76	0.411234	1.638322	0.014085	0.094873
GAJATE RESPONSE TO TRABECTEDIN DN	18	0.567216	1.638186	0.02907	0.094792
MOREAUX MULTIPLE MYELOMA BY TACI DN	154	0.489631	1.637983	0.044747	0.094753
CAFFAREL RESPONSE TO THC 24HR 5 UP	30	0.563796	1.636167	0.035088	0.095771
REACTOME P53 INDEPENDENT G1 S DNA DAMAGE CHECKPOINT	48	0.645389	1.635859	0.047228	0.095775
LEE TARGETS OF PTCH1 AND SUFU UP	48	0.471272	1.63417	0.028807	0.096733
LI LUNG CANCER	41	0.489513	1.634072	0.034765	0.096644
YIH RESPONSE TO ARSENITE C3	35	0.487537	1.633819	0.021442	0.096605
HOFMANN MYELODYSPLASTIC SYNDROM LOW RISK DN	30	0.534486	1.633768	0.036247	0.09646
BACOLOD RESISTANCE TO ALKYLATING	57	0.436501	1.631495	0.017717	0.097409

AGENTS DN					
REACTOME INTRINSIC PATHWAY FOR APOPTOSIS	29	0.506254	1.630883	0.02947	0.097658
HOLLEMAN PREDNISOLONE RESISTANCE ALL UP	19	0.56937	1.629767	0.041916	0.09817
OUELLET CULTURED OVARIAN CANCER INVASIVE VS LMP UP	65	0.466339	1.623623	0.02863	0.102045
FLOTHO PEDIATRIC ALL THERAPY RESPONSE DN	27	0.492507	1.623287	0.028902	0.102086
HONMA DOCETAXEL RESISTANCE	30	0.610885	1.622961	0.042596	0.102105
KIM MYCL1 AMPLIFICATION TARGETS DN	19	0.549036	1.621311	0.020484	0.102997
KEGG BLADDER CANCER	40	0.432286	1.620543	0.010661	0.103338
FLECHNER BIOPSY KIDNEY TRANSPLANT OK VS DONOR DN	25	0.480215	1.620483	0.013861	0.103179
DITTMER PTHLH TARGETS UP	110	0.42746	1.619487	0.036885	0.103498
KEGG BASAL TRANSCRIPTION FACTORS	35	0.506228	1.618743	0.021318	0.103758
REACTOME SHC MEDIATED SIGNALLING	15	0.561212	1.614165	0.039683	0.106735
SAKAI TUMOR INFILTRATING MONOCYTES DN	79	0.486758	1.613951	0.046512	0.106713
JIANG VHL TARGETS	130	0.396838	1.613075	0.020704	0.107153
YAGI AML RELAPSE PROGNOSIS	34	0.481919	1.613002	0.026915	0.107021
RIZ ERYTHROID DIFFERENTIATION HBZ	40	0.468207	1.61249	0.02381	0.107183
PID DNA PK PATHWAY	16	0.561255	1.611381	0.022133	0.107569
KAN RESPONSE TO ARSENIC TRIOXIDE	118	0.414642	1.611206	0.01581	0.107473
DORN ADENOVIRUS INFECTION 12HR DN	33	0.48512	1.610997	0.032129	0.107407
ZEMBUTSU SENSITIVITY TO METHOTREXATE	16	0.542896	1.609612	0.030948	0.108235
DORSAM HOXA9 TARGETS UP	35	0.469132	1.608232	0.019157	0.108805
KEGG UBIQUITIN MEDIATED PROTEOLYSIS	130	0.398562	1.608094	0.023669	0.108724
DIRMEIER LMP1 RESPONSE LATE UP	55	0.464157	1.607486	0.045064	0.10875
PENG GLUCOSE DEPRIVATION DN	163	0.382865	1.604813	0.016427	0.110463
LIN APC TARGETS	75	0.45452	1.603297	0.049438	0.111148
REACTOME METABOLISM OF CARBOHYDRATES	228	0.35001	1.602403	0.004141	0.111562
BANDRES RESPONSE TO CARMUSTIN WITHOUT MGMT 48HR DN	29	0.477178	1.598209	0.038618	0.11433
KANNAN TP53 TARGETS DN	21	0.518945	1.597191	0.031558	0.114901
JACKSON DNMT1 TARGETS UP	74	0.411704	1.596822	0.027944	0.114973
PID ILK PATHWAY	45	0.46215	1.595919	0.044266	0.115256
AMIT SERUM RESPONSE 480 MCF10A	34	0.518867	1.594374	0.024691	0.115837
DACOSTA UV RESPONSE VIA ERCC3 TTD UP	62	0.429759	1.593814	0.027311	0.116049
KEGG P53 SIGNALING PATHWAY	66	0.412606	1.586298	0.034483	0.121101
GHO ATF5 TARGETS DN	16	0.582184	1.585551	0.040773	0.121263
REACTOME SHC RELATED EVENTS	17	0.540824	1.585015	0.028112	0.121426
REACTOME RNA POL II PRE TRANSCRIPTION EVENTS	51	0.488548	1.5836	0.043222	0.122093
YAGI AML SURVIVAL	119	0.351863	1.582957	0.008264	0.122396
YIH RESPONSE TO ARSENITE C1	23	0.511724	1.582521	0.031936	0.12248
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 15	31	0.456327	1.579098	0.040161	0.124971
RAY TUMORIGENESIS BY ERBB2 CDC25A UP	99	0.364849	1.576795	0.004184	0.126606
CHEN LUNG CANCER SURVIVAL	26	0.5199	1.576677	0.039501	0.126487

ONDER CDH1 TARGETS 1 DN	163	0.419621	1.571548	0.030769	0.130425
SMID BREAST CANCER RELAPSE IN BONE DN	293	0.368597	1.569138	0.010288	0.132103
SMID BREAST CANCER RELAPSE IN BRAIN UP	39	0.475131	1.567573	0.035433	0.133129
REACTOME CLASS I MHC MEDIATED ANTIGEN PROCESSING PRESENTATION	229	0.393769	1.567127	0.043478	0.133252
FARMER BREAST CANCER BASAL VS LULMINAL	317	0.343699	1.56651	0.009785	0.133526
LU TUMOR ANGIOGENESIS UP	25	0.510078	1.566007	0.032653	0.133714
PID P53 REGULATION PATHWAY	57	0.423841	1.562963	0.048733	0.135978
JI RESPONSE TO FSH DN	57	0.488766	1.560851	0.041502	0.137101
LIN MELANOMA COPY NUMBER UP	67	0.437154	1.560371	0.044	0.137279
REACTOME DESTABILIZATION OF MRNA BY KSRP	17	0.543378	1.56019	0.036072	0.137214
PID PI3KCI AKT PATHWAY	35	0.46228	1.559266	0.034836	0.137528
JAZAG TGFB1 SIGNALING UP	104	0.358152	1.558575	0.01341	0.137582
FOSTER KDM1A TARGETS DN	195	0.343706	1.55472	0.018109	0.140648
OZEN MIR125B1 TARGETS	25	0.47698	1.554058	0.048733	0.141021
NGUYEN NOTCH1 TARGETS DN	84	0.38837	1.552365	0.038462	0.142055
WATANABE COLON CANCER MSI VS MSS UP	27	0.478435	1.551096	0.041257	0.142611
PID DELTA NP63 PATHWAY	45	0.439802	1.550394	0.039139	0.143011
PID LKB1 PATHWAY	46	0.417719	1.549038	0.017167	0.143946
BYSTRYKH HEMATOPOIESIS STEM CELL AND BRAIN QTL TRANS	175	0.324096	1.546719	0.008065	0.145441
HATADA METHYLATED IN LUNG CANCER DN	28	0.476138	1.544298	0.036511	0.147344
HOFMANN CELL LYMPHOMA UP	46	0.428368	1.542343	0.049618	0.148056
BIOCARTA CARM ER PATHWAY	35	0.447378	1.53739	0.042596	0.151881
BIOCARTA TNFR1 PATHWAY	29	0.460219	1.535701	0.048096	0.153243
AIYAR COBRA1 TARGETS DN	28	0.451191	1.534458	0.042857	0.154202
SENESE HDAC3 TARGETS DN	481	0.317207	1.531563	0.008368	0.156398
CEBALLOS TARGETS OF TP53 AND MYC DN	37	0.426576	1.530657	0.045064	0.156978
ZHU CMV 24 HR UP	93	0.418076	1.530502	0.032129	0.156857
PID HDAC CLASSI PATHWAY	65	0.386848	1.526282	0.030426	0.160336
HIRSCH CELLULAR TRANSFORMATION SIGNATURE DN	95	0.366637	1.520931	0.019646	0.164539
MUELLER COMMON TARGETS OF AML FUSIONS DN	29	0.460486	1.520771	0.04829	0.164145
SATO SILENCED BY METHYLATION IN PANCREATIC CANCER 2	44	0.414175	1.51848	0.043478	0.16584
BROWNE HCMV INFECTION 8HR DN	44	0.428655	1.512252	0.031809	0.170622
SUZUKI RESPONSE TO TSA AND DECITABINE 1B	21	0.464547	1.508993	0.046875	0.173202
ST FAS SIGNALING PATHWAY	63	0.373409	1.505988	0.034553	0.175949
AMUNDSON RESPONSE TO ARSENITE	211	0.319293	1.505967	0.013619	0.175698
IVANOVA HEMATOPOIESIS EARLY PROGENITOR	489	0.325484	1.505455	0.031936	0.175643
DEURIG T CELL PROLYMPHOCYTIC LEUKEMIA UP	340	0.306213	1.502455	0.015748	0.177463
REACTOME SIGNALLING TO RAS	27	0.462607	1.495756	0.047917	0.182348
GRADE COLON VS RECTAL CANCER DN	49	0.376338	1.495199	0.031847	0.182338
KYNG WERNER SYNDROM AND NORMAL AGING UP	87	0.357155	1.489897	0.016097	0.186848
SIG PIP3 SIGNALING IN CARDIAC MYOCTES	66	0.368876	1.489332	0.031189	0.186843

HAHTOLA SEZARY SYNDROM UP	92	0.38984	1.487074	0.032	0.188279
DACOSTA UV RESPONSE VIA ERCC3 COMMON UP	70	0.380407	1.486032	0.04	0.188455
BROWNE HCMV INFECTION 24HR UP	139	0.324547	1.478919	0.019685	0.19425
KEGG PANCREATIC CANCER	69	0.374507	1.470288	0.048485	0.200665
FIGUEROA AML METHYLATION CLUSTER 4 UP	97	0.324782	1.453892	0.031128	0.212344
BAKKER FOXO3 TARGETS DN	168	0.314701	1.44876	0.02907	0.216734
HELLER HDAC TARGETS DN	275	0.316792	1.445236	0.038388	0.219097
FERNANDEZ BOUND BY MYC	179	0.321616	1.431034	0.041237	0.232664
PANGAS TUMOR SUPPRESSION BY SMAD1 AND SMAD5 DN	142	0.318249	1.427508	0.038536	0.233941
CHENG IMPRINTED BY ESTRADIOL	100	0.33281	1.427413	0.038306	0.23342
BROWNE HCMV INFECTION 20HR UP	230	0.30354	1.426112	0.036822	0.234641
PENG LEUCINE DEPRIVATION UP	134	0.315465	1.424267	0.046278	0.236144
LEE AGING NEOCORTEX DN	75	0.349563	1.424074	0.031311	0.235706
AMUNDSON POOR SURVIVAL AFTER GAMMA RADIATION 2G	161	0.307236	1.416233	0.046843	0.241085
BROWNE HCMV INFECTION 10HR UP	95	0.333986	1.407838	0.038835	0.246995
BRUINS UVC RESPONSE EARLY LATE	292	0.295554	1.405713	0.037549	0.248156

ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate; GSEA, gene set enrichment analysis; KIF, kinesin.

Table SVI. **GSEA results of c5 reference gene set of high *KIF20A* expression group.**

Name	Size	ES	NES	NOM P-value	FDR q-value
GO CELL DIVISION	423	0.660811	2.630137	<0.0001	<0.0001
GO ORGANELLE FISSION	449	0.680021	2.60867	<0.0001	<0.0001
GO MITOTIC SISTER CHROMATID SEGREGATION	88	0.827501	2.605532	<0.0001	<0.0001
GO CELL CYCLE PHASE TRANSITION	248	0.704605	2.593259	<0.0001	<0.0001
GO CHROMOSOME SEGREGATION	247	0.755327	2.592687	<0.0001	<0.0001
GO MITOTIC NUCLEAR DIVISION	337	0.709956	2.585621	<0.0001	<0.0001
GO NUCLEAR CHROMOSOME SEGREGATION	204	0.777326	2.581268	<0.0001	<0.0001
GO DNA RECOMBINATION	189	0.723569	2.576992	<0.0001	<0.0001
GO SPINDLE	267	0.639977	2.567176	<0.0001	<0.0001
GO CONDENSED CHROMOSOME	169	0.775263	2.553432	<0.0001	<0.0001
GO SISTER CHROMATID SEGREGATION	163	0.801726	2.524628	<0.0001	<0.0001
GO CELL CYCLE CHECKPOINT	179	0.658174	2.518347	<0.0001	<0.0001
GO DNA REPLICATION	192	0.733677	2.518005	<0.0001	<0.0001
GO SPINDLE POLE	113	0.689469	2.504815	<0.0001	<0.0001
GO REGULATION OF MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	164	0.636036	2.504704	<0.0001	<0.0001
GO MITOTIC SPINDLE	50	0.74303	2.503505	<0.0001	<0.0001
GO CHROMOSOME CENTROMERIC REGION	153	0.776734	2.501119	<0.0001	<0.0001
GO SPINDLE MICROTUBULE	56	0.761647	2.500701	<0.0001	<0.0001
GO REGULATION OF MITOTIC CELL CYCLE	444	0.56376	2.499029	<0.0001	<0.0001
GO MITOTIC CELL CYCLE CHECKPOINT	129	0.643888	2.496368	<0.0001	<0.0001
GO CHROMOSOMAL REGION	297	0.705116	2.484785	<0.0001	<0.0001
GO DNA REPAIR	433	0.629087	2.482185	<0.0001	<0.0001
GO CELL CYCLE G1 S PHASE TRANSITION	108	0.753415	2.476977	<0.0001	<0.0001
GO REGULATION OF MICROTUBULE BASED PROCESS	226	0.606974	2.474004	<0.0001	<0.0001
GO SPINDLE MIDZONE	25	0.852275	2.468379	<0.0001	<0.0001
GO MITOTIC SPINDLE ORGANIZATION	64	0.748675	2.465732	<0.0001	<0.0001
GO MIDBODY	121	0.617822	2.465511	<0.0001	<0.0001
GO CHROMOSOME LOCALIZATION	56	0.750433	2.454397	<0.0001	<0.0001
GO REGULATION OF CELL CYCLE PHASE TRANSITION	308	0.581206	2.45415	<0.0001	<0.0001
GO CYTOKINESIS	80	0.640975	2.453465	<0.0001	<0.0001
GO REGULATION OF NUCLEAR DIVISION	153	0.61796	2.449809	<0.0001	<0.0001
GO REGULATION OF DNA REPLICATION	152	0.615301	2.448988	<0.0001	<0.0001
GO REGULATION OF DNA DEPENDENT DNA REPLICATION	39	0.821107	2.443355	<0.0001	<0.0001
GO CONDENSED CHROMOSOME CENTROMERIC REGION	83	0.846639	2.441495	<0.0001	<0.0001
GO CELL CYCLE G2 M PHASE TRANSITION	134	0.652451	2.438719	<0.0001	<0.0001
GO CONDENSED NUCLEAR CHROMOSOME	74	0.736769	2.437688	<0.0001	<0.0001
GO MEIOTIC CELL CYCLE	162	0.652896	2.434834	<0.0001	<0.0001
GO NEGATIVE REGULATION OF PROTEIN COMPLEX DISASSEMBLY	156	0.601239	2.434196	<0.0001	<0.0001
GO DNA INTEGRITY CHECKPOINT	136	0.620797	2.429499	<0.0001	<0.0001

GO POSITIVE REGULATION OF DNA METABOLIC PROCESS	174	0.551989	2.428966	<0.0001	<0.0001
GO DNA BIOSYNTHETIC PROCESS	108	0.686832	2.428841	<0.0001	<0.0001
GO REGULATION OF DNA METABOLIC PROCESS	318	0.553886	2.428423	<0.0001	<0.0001
GO RECOMBINATIONAL REPAIR	70	0.743982	2.416813	<0.0001	<0.0001
GO KINETOCHORE	103	0.788082	2.407898	<0.0001	<0.0001
GO REGULATION OF CHROMOSOME SEGREGATION	77	0.734029	2.406588	<0.0001	<0.0001
GO MEIOTIC CELL CYCLE PROCESS	130	0.660201	2.405313	<0.0001	<0.0001
GO NEGATIVE REGULATION OF CHROMOSOME ORGANIZATION	93	0.659019	2.404744	<0.0001	<0.0001
GO SISTER CHROMATID COHESION	100	0.806746	2.396744	<0.0001	<0.0001
GO DNA DEPENDENT DNA REPLICATION	90	0.791862	2.385005	<0.0001	<0.0001
GO POSITIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	57	0.638467	2.380365	<0.0001	<0.0001
GO NEGATIVE REGULATION OF CELL CYCLE PROCESS	199	0.55008	2.37442	<0.0001	<0.0001
GO NEGATIVE REGULATION OF MITOTIC CELL CYCLE	184	0.548421	2.370377	<0.0001	<0.0001
GO NEGATIVE REGULATION OF ORGANELLE ORGANIZATION	361	0.519748	2.362648	<0.0001	<0.0001
GO REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	57	0.649513	2.362177	<0.0001	<0.0001
GO DNA SYNTHESIS INVOLVED IN DNA REPAIR	67	0.73598	2.356527	<0.0001	1.34E-05
GO SPINDLE ASSEMBLY	67	0.673932	2.350369	<0.0001	1.31E-05
GO DOUBLE STRAND BREAK REPAIR	151	0.662951	2.344767	<0.0001	2.58E-05
GO RNA LOCALIZATION	173	0.611908	2.34285	<0.0001	2.53E-05
GO REGULATION OF CELL DIVISION	250	0.542589	2.337131	<0.0001	6.05E-05
GO REGULATION OF SISTER CHROMATID SEGREGATION	61	0.696144	2.336224	<0.0001	7.83E-05
GO REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	156	0.585316	2.332175	<0.0001	7.70E-05
GO MITOTIC DNA INTEGRITY CHECKPOINT	93	0.588111	2.330566	<0.0001	7.58E-05
GO PROTEIN SUMOYLATION	112	0.658692	2.330413	<0.0001	7.46E-05
GO METAPHASE PLATE CONGRESSION	41	0.771644	2.328486	<0.0001	7.34E-05
GO REPLICATION FORK	62	0.778807	2.32353	<0.0001	7.23E-05
GO POSITIVE REGULATION OF DNA REPLICATION	84	0.576722	2.314016	<0.0001	7.12E-05
GO DNA STRAND ELONGATION	29	0.905697	2.312734	<0.0001	7.01E-05
GO NUCLEAR PERIPHERY	118	0.60151	2.312341	<0.0001	6.91E-05
GO NEGATIVE REGULATION OF CELL CYCLE PHASE TRANSITION	137	0.547533	2.308296	<0.0001	8.65E-05
GO MEIOTIC CHROMOSOME SEGREGATION	49	0.695876	2.307551	<0.0001	8.52E-05
GO DNA GEOMETRIC CHANGE	77	0.702514	2.305371	<0.0001	8.40E-05
GO SINGLE STRANDED DNA BINDING	78	0.674893	2.30118	<0.0001	8.29E-05
GO NUCLEAR EXPORT	139	0.618033	2.29859	<0.0001	8.17E-05
GO MEIOSIS I	73	0.666714	2.298146	<0.0001	8.06E-05
GO NUCLEAR TRANSPORT	341	0.500081	2.294754	<0.0001	9.53E-05
GO REGULATION OF PROTEIN COMPLEX	198	0.551694	2.293829	<0.0001	9.40E-05

DISASSEMBLY					
GO NEGATIVE REGULATION OF CYTOSKELETON ORGANIZATION	205	0.525655	2.293532	<0.0001	1.03E-04
GO NUCLEAR CHROMOSOME	488	0.582026	2.289451	<0.0001	1.12E-04
GO CYTOSKELETON DEPENDENT CYTOKINESIS	38	0.697478	2.288011	<0.0001	1.11E-04
GO DNA STRAND ELONGATION INVOLVED IN DNA REPLICATION	25	0.923112	2.286211	<0.0001	1.09E-04
GO RIBONUCLEOPROTEIN COMPLEX LOCALIZATION	112	0.644312	2.278178	<0.0001	1.28E-04
GO MULTI ORGANISM LOCALIZATION	65	0.662595	2.276624	<0.0001	1.26E-04
GO NUCLEAR IMPORT	126	0.553295	2.272512	<0.0001	1.24E-04
GO POSITIVE REGULATION OF MITOTIC CELL CYCLE	118	0.586146	2.271782	<0.0001	1.32E-04
GO NUCLEAR ENVELOPE ORGANIZATION	75	0.613021	2.27102	<0.0001	1.30E-04
GO MITOTIC RECOMBINATION	41	0.84238	2.270988	<0.0001	1.29E-04
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE	44	0.650351	2.270476	<0.0001	1.27E-04
GO MITOTIC SPINDLE ASSEMBLY	39	0.700745	2.270003	<0.0001	1.26E-04
GO SOMATIC DIVERSIFICATION OF IMMUNE RECEPTORS	37	0.679425	2.268409	<0.0001	1.37E-04
GO CHROMOSOME SEPARATION	16	0.869264	2.268388	<0.0001	1.35E-04
GO POSITIVE REGULATION OF CELL CYCLE PROCESS	227	0.536314	2.266594	<0.0001	1.34E-04
GO BLASTOCYST GROWTH	15	0.841951	2.266136	<0.0001	1.32E-04
GO REGULATION OF CHROMOSOME ORGANIZATION	263	0.538688	2.265021	<0.0001	1.31E-04
GO DNA DEPENDENT ATPASE ACTIVITY	76	0.717595	2.263071	<0.0001	1.39E-04
GO REGULATION OF TELOMERE MAINTENANCE	64	0.628213	2.262557	<0.0001	1.38E-04
GO SOMATIC DIVERSIFICATION OF IMMUNOGLOBULINS	26	0.709056	2.260429	<0.0001	1.36E-04
GO POSITIVE REGULATION OF CELL CYCLE PHASE TRANSITION	66	0.620311	2.260365	<0.0001	1.35E-04
GO REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	49	0.654718	2.256848	<0.0001	1.47E-04
GO REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	134	0.532934	2.254433	<0.0001	1.77E-04
GO REGULATION OF DNA BIOSYNTHETIC PROCESS	90	0.553583	2.252117	<0.0001	1.97E-04
GO HETEROCHROMATIN	65	0.625897	2.249072	<0.0001	2.18E-04
GO DNA DAMAGE RESPONSE DETECTION OF DNA DAMAGE	36	0.782489	2.245896	<0.0001	2.30E-04
GO ATPASE ACTIVITY	412	0.502777	2.245846	<0.0001	2.28E-04
GO REGULATION OF DNA REPAIR	68	0.623786	2.245409	<0.0001	2.26E-04
GO METHYLTRANSFERASE COMPLEX	83	0.655215	2.245314	<0.0001	2.24E-04
GO SIGNAL TRANSDUCTION IN RESPONSE TO DNA DAMAGE	91	0.576429	2.245174	<0.0001	2.29E-04
GO POSITIVE REGULATION OF CELL CYCLE	308	0.494018	2.240261	<0.0001	2.35E-04
GO REGULATION OF RNA STABILITY	135	0.585796	2.239057	<0.0001	2.40E-04
GO SNRNA METABOLIC PROCESS	74	0.65691	2.238053	<0.0001	2.38E-04

GO POSTREPLICATION REPAIR	48	0.680209	2.235532	<0.0001	2.36E-04
GO NUCLEUS ORGANIZATION	124	0.549594	2.234064	<0.0001	2.34E-04
GO SOMATIC CELL DNA RECOMBINATION	31	0.70252	2.228734	<0.0001	2.44E-04
GO POSITIVE REGULATION OF CHROMOSOME SEGREGATION	23	0.775953	2.228108	<0.0001	2.41E-04
GO REGULATION OF DOUBLE STRAND BREAK REPAIR	33	0.684693	2.224732	<0.0001	2.39E-04
GO CHROMOSOME CONDENSATION	26	0.808006	2.223898	<0.0001	2.37E-04
GO DNA CONFORMATION CHANGE	243	0.655499	2.222279	<0.0001	2.35E-04
GO POSITIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	185	0.555419	2.220613	<0.0001	2.46E-04
GO CHROMATIN REMODELING	139	0.601242	2.217792	<0.0001	2.63E-04
GO NEGATIVE REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	134	0.619873	2.214668	<0.0001	2.68E-04
GO REGULATION OF CELLULAR RESPONSE TO HEAT	72	0.645582	2.214477	<0.0001	2.66E-04
GO NEGATIVE REGULATION OF CELL CYCLE	404	0.449473	2.211326	<0.0001	2.89E-04
GO HEAT SHOCK PROTEIN BINDING	86	0.551754	2.211092	<0.0001	2.93E-04
GO SOMATIC RECOMBINATION OF IMMUNOGLOBULIN GENE SEGMENTS	21	0.738018	2.210279	<0.0001	2.98E-04
GO MICROTUBULE CYTOSKELETON ORGANIZATION	314	0.536841	2.209822	<0.0001	2.95E-04
GO REGULATION OF TRANSCRIPTION INVOLVED IN G1 S TRANSITION OF MITOTIC CELL CYCLE	25	0.843398	2.209002	<0.0001	2.93E-04
GO CATALYTIC STEP 2 SPLICEOSOME	84	0.670652	2.206736	<0.0001	2.96E-04
GO REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	262	0.501767	2.204877	<0.0001	2.94E-04
GO G2 DNA DAMAGE CHECKPOINT	31	0.691886	2.201896	<0.0001	3.11E-04
GO REGULATION OF PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	101	0.652653	2.200525	<0.0001	3.33E-04
GO RECIPROCAL DNA RECOMBINATION	34	0.715683	2.199213	<0.0001	3.30E-04
GO NEGATIVE REGULATION OF DNA REPLICATION	50	0.61944	2.197801	<0.0001	3.28E-04
GO NUCLEAR PORE	73	0.651928	2.197411	<0.0001	3.30E-04
GO RNA SPLICING VIA TRANSESTERIFICATION REACTIONS	259	0.601223	2.196343	<0.0001	3.28E-04
GO NEGATIVE REGULATION OF CELL DIVISION	56	0.644598	2.194553	<0.0001	3.41E-04
GO RNA SPLICING	347	0.576644	2.194118	<0.0001	3.39E-04
GO REGULATION OF PROTEASOMAL UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	141	0.51394	2.193323	<0.0001	3.42E-04
GO PROTEIN LOCALIZATION TO CHROMOSOME	37	0.712133	2.192314	<0.0001	3.44E-04
GO POSITIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	32	0.677586	2.191353	<0.0001	3.56E-04
GO MITOTIC CYTOKINESIS	31	0.699218	2.189471	<0.0001	3.61E-04
GO DNA REPLICATION INDEPENDENT NUCLEOSOME ORGANIZATION	47	0.793965	2.189197	<0.0001	3.58E-04

GO MEMBRANE DISASSEMBLY	44	0.704564	2.188619	<0.0001	3.56E-04
GO REGULATION OF PROTEIN MODIFICATION BY SMALL PROTEIN CONJUGATION OR REMOVAL	266	0.5109	2.183276	<0.0001	3.66E-04
GO DNA HELICASE ACTIVITY	50	0.754049	2.180905	<0.0001	3.76E-04
GO POSITIVE REGULATION OF CHROMOSOME ORGANIZATION	141	0.524285	2.17459	<0.0001	3.99E-04
GO MISMATCH REPAIR	26	0.742196	2.174211	<0.0001	3.96E-04
GO HISTONE METHYLTRANSFERASE COMPLEX	64	0.628203	2.173017	<0.0001	3.93E-04
GO RESPONSE TO IONIZING RADIATION	137	0.529132	2.170958	<0.0001	4.20E-04
GO DNA DIRECTED DNA POLYMERASE ACTIVITY	26	0.684234	2.170379	<0.0001	4.17E-04
GO RAN GTPASE BINDING	31	0.725659	2.168248	<0.0001	4.50E-04
GO NUCLEAR REPLICATION FORK	39	0.730183	2.168062	<0.0001	4.47E-04
GO INTERSTRAND CROSS LINK REPAIR	38	0.684814	2.165138	<0.0001	4.79E-04
GO DNA POLYMERASE ACTIVITY	33	0.65677	2.164661	<0.0001	4.81E-04
GO EXONUCLEASE ACTIVITY	70	0.581509	2.163279	<0.0001	4.91E-04
GO NCRNA TRANSCRIPTION	80	0.624406	2.162111	<0.0001	4.98E-04
GO CENTROSOME	457	0.490232	2.161983	<0.0001	4.95E-04
GO REGULATION OF LIGASE ACTIVITY	126	0.623796	2.160618	<0.0001	5.06E-04
GO SPLICEOSOMAL COMPLEX	162	0.605047	2.159803	<0.0001	5.07E-04
GO STRAND DISPLACEMENT	25	0.829354	2.15841	<0.0001	5.14E-04
GO NUCLEOBASE CONTAINING COMPOUND TRANSPORT	187	0.5325	2.156588	<0.0001	5.11E-04
GO NUCLEAR HETEROCHROMATIN	31	0.69716	2.155668	<0.0001	5.15E-04
GO HISTONE PHOSPHORYLATION	24	0.725683	2.15392	<0.0001	5.20E-04
GO NEGATIVE REGULATION OF NUCLEAR DIVISION	42	0.67103	2.150547	<0.0001	5.72E-04
GO CHROMOSOME TELOMERIC REGION	150	0.619044	2.15001	<0.0001	5.73E-04
GO HELICASE ACTIVITY	148	0.631913	2.149751	<0.0001	5.85E-04
GO SNRNA PROCESSING	20	0.772736	2.149612	<0.0001	5.82E-04
GO HISTONE KINASE ACTIVITY	18	0.805996	2.149449	<0.0001	5.78E-04
GO EUCHROMATIN	30	0.679637	2.147882	<0.0001	6.01E-04
GO NUCLEAR MATRIX	95	0.554528	2.14748	<0.0001	6.03E-04
GO CENTROSOME CYCLE	44	0.67298	2.146653	<0.0001	6.10E-04
GO NEGATIVE REGULATION OF MITOTIC NUCLEAR DIVISION	32	0.705531	2.145708	<0.0001	6.16E-04
GO MRNA PROCESSING	405	0.541885	2.145683	<0.0001	6.13E-04
GO POSITIVE REGULATION OF LIGASE ACTIVITY	106	0.653795	2.143097	<0.0001	6.47E-04
GO TERMINATION OF RNA POLYMERASE II TRANSCRIPTION	61	0.650438	2.1428	<0.0001	6.44E-04
GO TELOMERE MAINTENANCE VIA RECOMBINATION	32	0.840974	2.14104	<0.0001	6.57E-04
GO RNA 3 END PROCESSING	96	0.62139	2.139404	<0.0001	6.72E-04
GO CELLULAR RESPONSE TO IONIZING RADIATION	50	0.575638	2.138971	<0.0001	6.69E-04
GO FEMALE MEIOTIC DIVISION	22	0.716946	2.137508	<0.0001	6.94E-04
GO DNA REPLICATION INITIATION	29	0.875282	2.137183	<0.0001	6.90E-04
GO ANAPHASE PROMOTING COMPLEX	75	0.769971	2.137161	<0.0001	6.86E-04

DEPENDENT CATABOLIC PROCESS					
GO BASE EXCISION REPAIR	39	0.657567	2.137023	<0.0001	6.82E-04
GO NEGATIVE REGULATION OF CHROMOSOME SEGREGATION	25	0.774654	2.136937	<0.0001	6.85E-04
GO REGULATION OF CENTROSOME CYCLE	38	0.696025	2.136375	<0.0001	6.91E-04
GO POSITIVE REGULATION OF MITOTIC NUCLEAR DIVISION	46	0.611603	2.135852	<0.0001	6.93E-04
GO DNA DEPENDENT DNA REPLICATION MAINTENANCE OF FIDELITY	19	0.792324	2.134392	<0.0001	7.33E-04
GO REGULATION OF PROTEASOMAL PROTEIN CATABOLIC PROCESS	173	0.482434	2.133965	<0.0001	7.29E-04
GO PROTEIN POLYUBIQUITINATION	234	0.498647	2.133929	<0.0001	7.25E-04
GO POSITIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	185	0.513657	2.125878	<0.0001	8.35E-04
GO MICROTUBULE BINDING	189	0.504059	2.12562	<0.0001	8.31E-04
GO DNA TEMPLATED TRANSCRIPTION TERMINATION	97	0.619712	2.124853	<0.0001	8.51E-04
GO PRONUCLEUS	15	0.876588	2.124475	<0.0001	8.47E-04
GO NEGATIVE REGULATION OF CELLULAR PROTEIN CATABOLIC PROCESS	60	0.555375	2.123024	<0.0001	8.64E-04
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	17	0.764254	2.12233	<0.0001	8.64E-04
GO REGULATION OF DNA RECOMBINATION	53	0.600588	2.121909	<0.0001	8.69E-04
GO CHROMOSOME ORGANIZATION INVOLVED IN MEIOTIC CELL CYCLE	40	0.648128	2.120865	<0.0001	8.77E-04
GO PROTEIN UBIQUITINATION INVOLVED IN UBIQUITIN DEPENDENT PROTEIN CATABOLIC PROCESS	127	0.519567	2.11974	<0.0001	8.84E-04
GO SITE OF DOUBLE STRAND BREAK	28	0.665192	2.119519	<0.0001	8.79E-04
GO HOMOLOGOUS CHROMOSOME SEGREGATION	37	0.656093	2.118767	<0.0001	8.79E-04
GO DNA PACKAGING	168	0.663263	2.117413	<0.0001	8.85E-04
GO PROTEASOME COMPLEX	73	0.694556	2.112586	<0.0001	9.17E-04
GO KINESIN COMPLEX	53	0.646585	2.109551	<0.0001	9.87E-04
GO HISTONE MRNA METABOLIC PROCESS	28	0.716639	2.109461	<0.0001	9.82E-04
GO ATP DEPENDENT CHROMATIN REMODELING	67	0.701622	2.10939	<0.0001	9.77E-04
GO G1 DNA DAMAGE CHECKPOINT	68	0.546826	2.107086	<0.0001	0.001005
GO MITOTIC G2 M TRANSITION CHECKPOINT	17	0.750913	2.106567	<0.0001	0.001016
GO CYTOPLASMIC MICROTUBULE	51	0.535228	2.105276	<0.0001	0.001039
GO PROTEASOMAL PROTEIN CATABOLIC PROCESS	263	0.504103	2.103537	<0.0001	0.001064
GO MICROTUBULE POLYMERIZATION OR DEPOLYMERIZATION	38	0.604628	2.102253	<0.0001	0.001076
GO NUCLEOTIDYLTRANSFERASE ACTIVITY	123	0.522834	2.101443	<0.0001	0.001081
GO MRNA CIS SPLICING VIA SPLICEOSOME	18	0.769609	2.101046	<0.0001	0.001075
GO SEX CHROMOSOME	27	0.721345	2.100896	<0.0001	0.001075
GO PROTEIN K63 LINKED UBIQUITINATION	34	0.60511	2.100563	<0.0001	0.001078
GO REGULATION OF DOUBLE STRAND BREAK REPAIR VIA HOMOLOGOUS RECOMBINATION	17	0.749607	2.099855	<0.0001	0.001077

GO NUCLEAR ENVELOPE	381	0.444484	2.097347	<0.0001	0.001134
GO MICROTUBULE ORGANIZING CENTER ORGANIZATION	79	0.587396	2.094939	<0.0001	0.001161
GO POSITIVE REGULATION OF CYTOKINESIS	28	0.677782	2.092981	<0.0001	0.001183
GO DAMAGED DNA BINDING	62	0.600791	2.092563	<0.0001	0.001181
GO ENDONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	34	0.687019	2.092477	<0.0001	0.001176
GO PROTEIN K11 LINKED UBIQUITINATION	26	0.720149	2.092397	<0.0001	0.001175
GO CENTROMERE COMPLEX ASSEMBLY	42	0.83007	2.091972	<0.0001	0.00117
GO NUCLEAR MEMBRANE	254	0.442553	2.090459	<0.0001	0.0012
GO NEGATIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	23	0.650065	2.09025	<0.0001	0.001205
GO NUCLEAR TRANSCRIPTION FACTOR COMPLEX	125	0.497975	2.08997	<0.0001	0.001215
GO MICROTUBULE	382	0.466857	2.089097	<0.0001	0.001226
GO REGULATION OF PROTEIN CATABOLIC PROCESS	376	0.440554	2.087006	<0.0001	0.001255
GO REGULATION OF CYTOKINESIS	56	0.594412	2.08659	0.002033	0.001257
GO NUCLEIC ACID PHOSPHODIESTER BOND HYDROLYSIS	230	0.505722	2.085398	<0.0001	0.00128
GO REGULATION OF CELL CYCLE ARREST	100	0.50346	2.084802	<0.0001	0.001278
GO ATPASE ACTIVITY COUPLED	307	0.462702	2.083445	<0.0001	0.001295
GO SPINDLE LOCALIZATION	36	0.658816	2.082772	<0.0001	0.001311
GO SPINDLE CHECKPOINT	23	0.789185	2.081658	<0.0001	0.001342
GO STRUCTURE SPECIFIC DNA BINDING	114	0.547135	2.080812	<0.0001	0.001343
GO REPLISOME	29	0.729958	2.079841	<0.0001	0.001351
GO TETRAHYDROFOLATE METABOLIC PROCESS	19	0.752778	2.079126	<0.0001	0.00138
GO ANAPHASE PROMOTING COMPLEX	20	0.759091	2.07903	<0.0001	0.001379
GO NUCLEOBASE METABOLIC PROCESS	37	0.617506	2.078126	<0.0001	0.001392
GO SMALL NUCLEAR RIBONUCLEOPROTEIN COMPLEX	59	0.652356	2.077093	<0.0001	0.001401
GO NEGATIVE REGULATION OF DNA METABOLIC PROCESS	104	0.518733	2.074403	<0.0001	0.001466
GO HISTONE EXCHANGE	46	0.782576	2.074084	<0.0001	0.00146
GO RIBONUCLEOPROTEIN COMPLEX BINDING	89	0.561971	2.072373	<0.0001	0.001482
GO PURINE NTP DEPENDENT HELICASE ACTIVITY	95	0.620812	2.070938	<0.0001	0.001525
GO TRNA TRANSPORT	32	0.73912	2.069882	<0.0001	0.001541
GO NUCLEAR UBIQUITIN LIGASE COMPLEX	39	0.643382	2.067242	<0.0001	0.001578
GO MRNA 3 END PROCESSING	71	0.614101	2.064766	<0.0001	0.00161
GO NEGATIVE REGULATION OF CHROMATIN MODIFICATION	44	0.588164	2.062891	0.002033	0.001667
GO POSITIVE REGULATION OF CELL CYCLE ARREST	79	0.514629	2.061679	<0.0001	0.001699
GO CAJAL BODY	49	0.599402	2.061581	<0.0001	0.001692
GO MICROTUBULE BASED PROCESS	478	0.478984	2.059913	<0.0001	0.001736
GO NUCLEAR CHROMOSOME TELOMERIC REGION	122	0.623248	2.058962	<0.0001	0.001766

GO REGULATION OF CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	93	0.489607	2.058285	<0.0001	0.00178
GO INNATE IMMUNE RESPONSE ACTIVATING CELL SURFACE RECEPTOR SIGNALING PATHWAY	104	0.574565	2.055366	<0.0001	0.001868
GO NUCLEAR BODY	334	0.466245	2.053154	<0.0001	0.001906
GO REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	140	0.467089	2.05264	<0.0001	0.001898
GO NUCLEASE ACTIVITY	185	0.487587	2.0515	<0.0001	0.001906
GO PEPTIDYL LYSINE MODIFICATION	278	0.491665	2.050568	<0.0001	0.001926
GO PROTEIN IMPORT	150	0.466603	2.050474	<0.0001	0.001925
GO NUCLEOTIDE EXCISION REPAIR DNA GAP FILLING	24	0.749686	2.049907	<0.0001	0.001931
GO ENDODEOXYRIBONUCLEASE ACTIVITY	48	0.59768	2.047833	<0.0001	0.002002
GO POSTTRANSCRIPTIONAL REGULATION OF GENE EXPRESSION	417	0.470535	2.046749	<0.0001	0.002034
GO SIN3 TYPE COMPLEX	16	0.755286	2.045962	<0.0001	0.002059
GO GLUCOSE CATABOLIC PROCESS	27	0.68746	2.045804	<0.0001	0.00206
GO NUCLEOBASE BIOSYNTHETIC PROCESS	17	0.79253	2.04479	<0.0001	0.002076
GO BLASTOCYST DEVELOPMENT	58	0.573738	2.044439	<0.0001	0.002074
GO REGULATION OF ESTABLISHMENT OF PLANAR POLARITY	109	0.539472	2.042935	<0.0001	0.002145
GO POSITIVE REGULATION OF NUCLEAR DIVISION	57	0.566496	2.04152	<0.0001	0.002171
GO TRANSLESION SYNTHESIS	36	0.630423	2.041181	<0.0001	0.002174
GO DEOXYRIBONUCLEASE ACTIVITY	63	0.578395	2.040374	0.001976	0.002207
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	23	0.68993	2.035615	0.002088	0.00235
GO RESPONSE TO GAMMA RADIATION	49	0.558019	2.033648	<0.0001	0.002393
GO PURINE NUCLEOBASE METABOLIC PROCESS	19	0.722068	2.033642	<0.0001	0.002384
GO POSITIVE REGULATION OF CELL DIVISION	117	0.502408	2.030531	<0.0001	0.002512
GO SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	120	0.463386	2.028517	<0.0001	0.00258
GO TELOMERE ORGANIZATION	101	0.62577	2.027951	<0.0001	0.002608
GO TUBULIN BINDING	255	0.459135	2.027368	<0.0001	0.002612
GO CHROMATIN	407	0.508486	2.026913	<0.0001	0.002613
GO TRNA METABOLIC PROCESS	166	0.601979	2.026295	<0.0001	0.002647
GO DOUBLE STRANDED RNA BINDING	59	0.563095	2.022902	0.004049	0.00276
GO AMINO ACID ACTIVATION	51	0.675329	2.022626	<0.0001	0.002766
GO RETROGRADE VESICLE MEDIATED TRANSPORT GOLGI TO ER	75	0.564983	2.022472	<0.0001	0.002756
GO DNA SECONDARY STRUCTURE BINDING	24	0.709612	2.021259	<0.0001	0.002805
GO MICROTUBULE END	21	0.722394	2.0212	<0.0001	0.0028
GO DNA TEMPLATED TRANSCRIPTION ELONGATION	86	0.583727	2.020248	<0.0001	0.002837
GO RNA POLYMERASE II TRANSCRIPTION FACTOR COMPLEX	100	0.497652	2.018995	<0.0001	0.002893
GO REGULATION OF CHROMATIN SILENCING	21	0.693397	2.018679	0.002037	0.002887
GO LIGASE ACTIVITY FORMING CARBON	44	0.669263	2.013368	<0.0001	0.003115

OXYGEN BONDS					
GO MICROTUBULE ORGANIZING CENTER PART	133	0.530512	2.012034	<0.0001	0.003147
GO SIGNAL SEQUENCE BINDING	36	0.617951	2.009804	0.001961	0.003217
GO CENTRIOLE	91	0.559179	2.007612	<0.0001	0.003313
GO NUCLEOSOME BINDING	44	0.628761	2.007399	<0.0001	0.003316
GO EXOSOME RNASE COMPLEX	21	0.72222	2.007186	<0.0001	0.003308
GO RNA POLYMERASE COMPLEX	118	0.548817	2.005213	<0.0001	0.003412
GO NON CANONICAL WNT SIGNALING PATHWAY	134	0.494763	2.004289	<0.0001	0.003439
GO REGULATION OF TELOMERASE RNA LOCALIZATION TO CAJAL BODY	15	0.849887	2.002976	<0.0001	0.003474
GO ENDORIBONUCLEASE ACTIVITY PRODUCING 5 PHOSPHOMONOESTERS	26	0.725648	2.000846	<0.0001	0.003587
GO CELLULAR COMPONENT DISASSEMBLY	488	0.444763	1.997593	<0.0001	0.003757
GO NEGATIVE REGULATION OF HISTONE MODIFICATION	35	0.579851	1.997108	0.001992	0.003774
GO NUCLEAR LOCALIZATION SEQUENCE BINDING	20	0.728355	1.996613	<0.0001	0.003795
GO NEGATIVE REGULATION OF MRNA METABOLIC PROCESS	34	0.645281	1.995869	<0.0001	0.003841
GO ESTABLISHMENT OF MITOTIC SPINDLE LOCALIZATION	23	0.667858	1.995189	<0.0001	0.003846
GO UNFOLDED PROTEIN BINDING	89	0.587009	1.991007	<0.0001	0.004014
GO PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	28	0.596557	1.990693	<0.0001	0.004029
GO CELLULAR RESPONSE TO HEAT	33	0.591322	1.990574	<0.0001	0.004025
GO TRANSFERASE COMPLEX TRANSFERRING PHOSPHORUS CONTAINING GROUPS	230	0.457449	1.989615	<0.0001	0.004049
GO ISOTYPE SWITCHING	16	0.693633	1.989613	<0.0001	0.004036
GO PRERIBOSOME	58	0.706518	1.9866	<0.0001	0.004197
GO NIK NF KAPPAB SIGNALING	82	0.610002	1.985987	<0.0001	0.004222
GO POSITIVE REGULATION OF PROTEIN CATABOLIC PROCESS	253	0.439146	1.981675	<0.0001	0.004453
GO REGULATION OF MRNA SPLICING VIA SPLICEOSOME	60	0.597332	1.978694	0.001972	0.004591
GO CELL DIVISION SITE	47	0.570848	1.978354	<0.0001	0.004606
GO PROTEIN MONOUBIQUITINATION	49	0.581073	1.976087	0.002024	0.004734
GO POLY PYRIMIDINE TRACT BINDING	17	0.712145	1.975975	<0.0001	0.004726
GO HSP70 PROTEIN BINDING	28	0.586135	1.975079	<0.0001	0.004793
GO MLL1 2 COMPLEX	26	0.667424	1.972742	<0.0001	0.004955
GO INO80 TYPE COMPLEX	21	0.671806	1.972387	<0.0001	0.004969
GO NUCLEOTIDE EXCISION REPAIR DNA INCISION	39	0.619028	1.97208	<0.0001	0.004974
GO NEGATIVE REGULATION OF MRNA SPLICING VIA SPLICEOSOME	19	0.736555	1.971953	0.001905	0.004974
GO DNA DOUBLE STRAND BREAK PROCESSING	19	0.690377	1.970552	0.003839	0.005045
GO POSITIVE REGULATION OF CELL CYCLE G2 M PHASE TRANSITION	18	0.666374	1.969115	<0.0001	0.005129
GO PCG PROTEIN COMPLEX	43	0.576323	1.969029	<0.0001	0.00513

GO SNRNA BINDING	33	0.61198	1.967201	0.001898	0.005235
GO NUCLEOSOMAL DNA BINDING	29	0.675457	1.962143	0.005917	0.00559
GO ATP DEPENDENT MICROTUBULE MOTOR ACTIVITY	18	0.757944	1.958766	0.002079	0.005794
GO CYCLIN DEPENDENT PROTEIN KINASE HOLOENZYME COMPLEX	30	0.578602	1.958431	<0.0001	0.005797
GO REGULATION OF CELLULAR AMINO ACID METABOLIC PROCESS	65	0.645287	1.957956	0.001908	0.005819
GO POSITIVE REGULATION OF DNA REPAIR	33	0.609803	1.957251	0.004057	0.005844
GO BINDING OF SPERM TO ZONA PELLUCIDA	30	0.603644	1.956881	<0.0001	0.005842
GO REGULATION OF TELOMERASE ACTIVITY	41	0.538606	1.956742	0.001957	0.005826
GO PROTEIN EXPORT FROM NUCLEUS	29	0.597052	1.95665	0.00211	0.005816
GO RNA HELICASE ACTIVITY	67	0.581054	1.953531	0.008081	0.006006
GO NEGATIVE REGULATION OF TELOMERE MAINTENANCE	26	0.626078	1.951759	0.001934	0.006148
GO PROTEIN LOCALIZATION TO CYTOSKELETON	28	0.611033	1.95158	0.002101	0.006143
GO RIBONUCLEOPROTEIN GRANULE	139	0.47102	1.951298	0.006061	0.006147
GO REGULATION OF CYTOSKELETON ORGANIZATION	470	0.408174	1.950907	<0.0001	0.006142
GO ATP DEPENDENT DNA HELICASE ACTIVITY	32	0.690019	1.950762	<0.0001	0.006132
GO REGULATION OF CELL AGING	32	0.566408	1.950722	0.002075	0.006119
GO CHROMATIN BINDING	408	0.455481	1.950214	<0.0001	0.00613
GO MICROTUBULE PLUS END	16	0.749567	1.950093	<0.0001	0.006117
GO CHROMATIN MODIFICATION	490	0.460759	1.945957	0.002096	0.006419
GO PROTEIN DEPOLYMERIZATION	23	0.637516	1.945866	0.009785	0.006402
GO FOUR WAY JUNCTION DNA BINDING	15	0.789724	1.943281	<0.0001	0.006566
GO NUCLEOLAR PART	59	0.67099	1.942796	<0.0001	0.00659
GO POSITIVE REGULATION OF NEURON DEATH	66	0.483996	1.942553	0.00211	0.006588
GO MICROTUBULE ASSOCIATED COMPLEX	141	0.48594	1.941958	<0.0001	0.006616
GO PROTEASOME BINDING	16	0.710134	1.93915	<0.0001	0.006838
GO TRNA BINDING	43	0.601568	1.939055	<0.0001	0.006823
GO POSITIVE REGULATION OF VIRAL GENOME REPLICATION	29	0.565314	1.937777	0.002066	0.006905
GO ENDONUCLEASE ACTIVITY	115	0.477319	1.936932	<0.0001	0.006936
GO POSITIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	58	0.50394	1.936397	<0.0001	0.00695
GO NCRNA METABOLIC PROCESS	499	0.566412	1.932687	<0.0001	0.007279
GO REGULATION OF CELL CYCLE CHECKPOINT	27	0.631019	1.932066	<0.0001	0.007328
GO NEGATIVE REGULATION OF PROTEIN CATABOLIC PROCESS	103	0.441005	1.931086	<0.0001	0.007397
GO RESPONSE TO UV	119	0.446063	1.930994	<0.0001	0.007387
GO REGULATION OF MRNA METABOLIC PROCESS	113	0.524709	1.930349	0.004032	0.007423
GO POSITIVE REGULATION OF CANONICAL WNT SIGNALING PATHWAY	115	0.483245	1.929143	<0.0001	0.007517
GO MITOCHONDRIAL RNA METABOLIC PROCESS	23	0.70645	1.928335	0.001957	0.007557
GO PROTEIN DNA COMPLEX SUBUNIT ORGANIZATION	208	0.567237	1.927983	<0.0001	0.00757
GO SMALL SUBUNIT PROCESSOME	32	0.701533	1.926433	<0.0001	0.007716

GO CELLULAR RESPONSE TO UV	65	0.479396	1.926373	<0.0001	0.007697
GO NUCLEOTIDE EXCISION REPAIR	111	0.529919	1.92591	<0.0001	0.007711
GO SINGLE STRANDED RNA BINDING	63	0.507797	1.92423	<0.0001	0.007818
GO EXONUCLEASE ACTIVITY ACTIVE WITH EITHER RIBO OR DEOXYRIBONUCLEIC ACIDS AND PRODUCING 5 PHOSPHOMONOESTERS	40	0.573445	1.922355	<0.0001	0.00797
GO IMMUNOGLOBULIN PRODUCTION	40	0.54922	1.920782	0.004115	0.008064
GO CELLULAR RESPONSE TO RADIATION	130	0.438634	1.920774	<0.0001	0.008041
GO CELL AGING	66	0.4715	1.920244	<0.0001	0.008086
GO TRANSCRIPTION ELONGATION FROM RNA POLYMERASE II PROMOTER	71	0.570245	1.91935	0.001942	0.008145
GO XY BODY	15	0.70743	1.919339	<0.0001	0.008123
GO CELLULAR RESPONSE TO GAMMA RADIATION	19	0.630048	1.916696	0.003891	0.008373
GO DNA DIRECTED RNA POLYMERASE II HOLOENZYME	93	0.531042	1.916409	<0.0001	0.00838
GO REGULATION OF UBIQUITIN PROTEIN LIGASE ACTIVITY	17	0.654628	1.915393	0.007921	0.008458
GO REGULATION OF HISTONE H3 K9 METHYLATION	17	0.706456	1.915267	0.00409	0.008448
GO PROTEASOME ACCESSORY COMPLEX	23	0.784498	1.91342	0.001934	0.008625
GO TRANSCRIPTION COUPLED NUCLEOTIDE EXCISION REPAIR	72	0.576611	1.911912	<0.0001	0.008723
GO SPLICEOSOMAL SNRNP ASSEMBLY	37	0.671244	1.910732	0.001916	0.008837
GO REGULATION OF MITOPHAGY	40	0.522894	1.909798	<0.0001	0.008894
GO NEGATIVE REGULATION OF DNA DEPENDENT DNA REPLICATION	15	0.742569	1.908885	<0.0001	0.008973
GO CHROMATIN ASSEMBLY OR DISASSEMBLY	155	0.600986	1.906897	0.001898	0.009157
GO NLS BEARING PROTEIN IMPORT INTO NUCLEUS	22	0.677237	1.9055	0.002114	0.009281
GO RNA POLYADENYLATION	29	0.632729	1.905279	0.002049	0.009284
GO CYCLIN DEPENDENT PROTEIN SERINE THREONINE KINASE REGULATOR ACTIVITY	27	0.590407	1.904319	0.001972	0.009365
GO MRNA CLEAVAGE FACTOR COMPLEX	17	0.704436	1.904285	0.004175	0.009344
GO PROTEIN LOCALIZATION TO NUCLEUS	151	0.427168	1.903204	0.006211	0.009409
GO NF KAPPAB BINDING	30	0.566962	1.898048	<0.0001	0.010026
GO ACETYLTRANSFERASE COMPLEX	84	0.51639	1.897359	0.002045	0.010086
GO REGULATION OF CELLULAR AMINE METABOLIC PROCESS	85	0.561863	1.896218	0.001946	0.010178
GO POSITIVE REGULATION OF PROTEOLYSIS	349	0.41401	1.894209	<0.0001	0.010357
GO PROTEIN FOLDING	201	0.482604	1.891141	<0.0001	0.010722
GO UBIQUITIN LIKE PROTEIN BINDING	113	0.457638	1.890835	0.004032	0.010742
GO DNA REPAIR COMPLEX	37	0.559843	1.889806	0.001961	0.01085
GO CYTOPLASMIC EXOSOME RNASE COMPLEX	15	0.721734	1.888195	0.001946	0.011025
GO H4 HISTONE ACETYLTRANSFERASE COMPLEX	17	0.634118	1.886145	0.001869	0.011285
GO MATURATION OF 5 8S RRNA	28	0.701784	1.884435	<0.0001	0.011493
GO ATP GENERATION FROM ADP	35	0.60292	1.884237	0.004016	0.011495
GO FOLIC ACID CONTAINING COMPOUND	27	0.624835	1.883254	0.003984	0.011588

METABOLIC PROCESS					
GO TRNA PROCESSING	106	0.576374	1.882467	0.001996	0.011681
GO FC EPSILON RECEPTOR SIGNALING PATHWAY	123	0.483135	1.879075	0.001988	0.012117
GO NADH METABOLIC PROCESS	33	0.607637	1.877635	0.001992	0.012257
GO NEGATIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	92	0.436219	1.876152	<0.0001	0.012412
GO REGULATION OF CENTROSOME DUPLICATION	31	0.604743	1.873241	<0.0001	0.012852
GO NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS EXONUCLEOLYTIC	30	0.640966	1.872181	0.003945	0.012993
GO RESPONSE TO X RAY	30	0.582953	1.871829	0.003968	0.013016
GO SYNAPTONEMAL COMPLEX	31	0.602429	1.87148	0.006122	0.013031
GO NEGATIVE REGULATION OF RNA SPLICING	24	0.666734	1.869855	0.001898	0.013206
GO ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE ANTIGEN VIA MHC CLASS I	89	0.577135	1.869513	0.004016	0.013226
GO RIBONUCLEOPROTEIN COMPLEX SUBUNIT ORGANIZATION	185	0.529503	1.866915	0.001901	0.013557
GO REGULATION OF GLUCOSE TRANSPORT	93	0.463482	1.866481	0.002075	0.013585
GO UBIQUITIN LIKE PROTEIN CONJUGATING ENZYME ACTIVITY	29	0.625652	1.865029	0.003953	0.013773
GO SPERM EGG RECOGNITION	40	0.525301	1.864832	<0.0001	0.01377
GO POSITIVE REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	126	0.412816	1.864817	0.00202	0.013736
GO MACROMOLECULAR COMPLEX DISASSEMBLY	175	0.544758	1.861033	<0.0001	0.014306
GO ANTIGEN PROCESSING AND PRESENTATION OF EXOGENOUS PEPTIDE ANTIGEN VIA MHC CLASS I	64	0.652445	1.855162	0.008264	0.015237
GO TELOMERASE HOLOENZYME COMPLEX	19	0.657177	1.853749	0.006061	0.015419
GO ERROR FREE TRANSLESION SYNTHESIS	17	0.714489	1.853585	0.003929	0.015395
GO GAMMA TUBULIN COMPLEX	19	0.620028	1.85051	0.004132	0.015806
GO PRERIBOSOME LARGE SUBUNIT PRECURSOR	20	0.773507	1.850055	<0.0001	0.015843
GO PROTEIN LOCALIZATION TO CENTROSOME	15	0.653704	1.849332	0.002045	0.015926
GO SWI SNF SUPERFAMILY TYPE COMPLEX	71	0.530242	1.849134	0.008214	0.015922
GO RNA SECONDARY STRUCTURE UNWINDING	40	0.563401	1.847795	0.007937	0.016138
GO POSITIVE REGULATION OF CELL CYCLE G1 S PHASE TRANSITION	28	0.563727	1.84717	0.002066	0.016193
GO NEGATIVE REGULATION OF CANONICAL WNT SIGNALING PATHWAY	156	0.442693	1.846983	<0.0001	0.016195
GO RIBONUCLEOPROTEIN COMPLEX BIOGENESIS	413	0.567017	1.844167	0.011858	0.016681
GO HISTONE DEACETYLASE BINDING	102	0.445026	1.844106	<0.0001	0.016657
GO PORE COMPLEX ASSEMBLY	15	0.688542	1.843834	0.002041	0.016683
GO DNA LIGATION	16	0.676013	1.843667	<0.0001	0.016673
GO RNA PHOSPHODIESTER BOND HYDROLYSIS	107	0.487643	1.843652	0.001883	0.016633
GO ESC E Z COMPLEX	16	0.700788	1.842375	0.002137	0.016833
GO NUCLEOCYTOPLASMIC TRANSPORTER ACTIVITY	23	0.669362	1.84215	0.002123	0.016843

GO PROTEIN PHOSPHATASE 2A BINDING	27	0.563034	1.841461	0.006024	0.01693
GO POLY PURINE TRACT BINDING	18	0.682015	1.841196	0.008299	0.016925
GO RNA POLYMERASE ACTIVITY	43	0.576239	1.838756	0.003883	0.017338
GO NUCLEAR CHROMATIN	275	0.465706	1.838138	0.002012	0.01741
GO CENTROSOME DUPLICATION	31	0.610027	1.836809	0.010549	0.017624
GO RESPONSE TO HEAT	85	0.447932	1.83321	0.00198	0.018264
GO POSITIVE REGULATION OF NEURON APOPTOTIC PROCESS	46	0.477779	1.831928	0.002088	0.018428
GO POSITIVE REGULATION OF CELLULAR PROTEIN LOCALIZATION	335	0.359166	1.831898	<0.0001	0.018392
GO NUCLEAR EXOSOME RNASE COMPLEX	15	0.731712	1.830979	<0.0001	0.018548
GO REGULATION OF TRANSLATIONAL INITIATION	79	0.506589	1.827255	0.00969	0.019266
GO NUCLEAR INNER MEMBRANE	45	0.480088	1.827133	0.005988	0.019236
GO COVALENT CHROMATIN MODIFICATION	309	0.426947	1.827133	0.002045	0.019192
GO POSITIVE REGULATION OF TELOMERASE ACTIVITY	27	0.544685	1.824107	0.005964	0.019788
GO REGULATION OF PROTEIN EXPORT FROM NUCLEUS	33	0.50935	1.822803	0.009843	0.020058
GO NUCLEAR EUCHROMATIN	23	0.604237	1.822203	0.00202	0.020121
GO REGULATION OF PROTEIN INSERTION INTO MITOCHONDRIAL MEMBRANE INVOLVED IN APOPTOTIC SIGNALING PATHWAY	29	0.563618	1.82211	0.006012	0.020081
GO MRNA BINDING	143	0.466241	1.82181	0.009728	0.020108
GO NAD METABOLIC PROCESS	49	0.535022	1.820286	0.001988	0.020383
GO N ACYLTRANSFERASE ACTIVITY	92	0.45886	1.817552	0.001965	0.020937
GO APOPTOTIC NUCLEAR CHANGES	24	0.572214	1.817411	0.003876	0.02092
GO ACETYLTRANSFERASE ACTIVITY	92	0.455853	1.816179	0.005825	0.021126
GO LRR DOMAIN BINDING	16	0.622011	1.815153	0.003945	0.021319
GO SMALL NUCLEOLAR RIBONUCLEOPROTEIN COMPLEX	18	0.757528	1.814174	<0.0001	0.021468
GO NEGATIVE REGULATION OF HISTONE METHYLATION	16	0.685921	1.813033	0.002114	0.021679
GO MITOCHONDRIAL MEMBRANE ORGANIZATION	90	0.507315	1.811962	0.00396	0.021895
GO RNA STABILIZATION	29	0.56932	1.811077	0.005894	0.022049
GO REGULATION OF PROTEIN IMPORT INTO NUCLEUS TRANSLOCATION	21	0.557225	1.81063	0.008147	0.022114
GO GLUCOSYLTRANSFERASE ACTIVITY	16	0.663743	1.810227	0.005825	0.022185
GO INTRACELLULAR STEROID HORMONE RECEPTOR SIGNALING PATHWAY	66	0.464702	1.80846	0.005882	0.022582
GO PROTEIN N TERMINUS BINDING	101	0.423357	1.807743	<0.0001	0.022707
GO PTERIDINE CONTAINING COMPOUND BIOSYNTHETIC PROCESS	16	0.712559	1.807742	0.003766	0.022657
GO TRNA MODIFICATION	53	0.568414	1.807369	0.005758	0.022687
GO UBIQUITIN LIKE PROTEIN LIGASE BINDING	255	0.389845	1.80564	0.001931	0.023066
GO PRECATALYTIC SPLICEOSOME	21	0.717281	1.804753	0.003922	0.023224
GO MITOCHONDRIAL FUSION	15	0.669528	1.803888	0.001905	0.023411
GO POSITIVE REGULATION OF PROTEASOMAL	95	0.416575	1.80237	0.001957	0.023715

PROTEIN CATABOLIC PROCESS					
GO POSITIVE REGULATION OF WNT SIGNALING PATHWAY	148	0.419547	1.801055	<0.0001	0.023941
GO NEGATIVE REGULATION OF RESPONSE TO DNA DAMAGE STIMULUS	49	0.454304	1.800879	<0.0001	0.023928
GO NCRNA PROCESSING	361	0.559782	1.800783	0.011673	0.023907
GO MATURATION OF 5 8S RRNA FROM TRICISTRONIC RRNA TRANSCRIPT SSU RRNA 5 8S RRNA LSU RRNA	19	0.701754	1.800636	0.005871	0.023886
GO REGULATION OF ANOIKIS	24	0.551068	1.800409	0.007648	0.023883
GO NCRNA 3 END PROCESSING	20	0.701657	1.800391	0.003914	0.023838
GO MALE MEIOSIS	34	0.56026	1.799221	0.004107	0.024052
GO RRNA TRANSCRIPTION	17	0.650274	1.799148	0.004098	0.024034
GO MALE MEIOSIS I	15	0.637796	1.798255	0.00818	0.02421
GO POSITIVE REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	36	0.54146	1.79801	0.009728	0.024206
GO POSITIVE REGULATION OF PEPTIDYL THREONINE PHOSPHORYLATION	24	0.571265	1.796078	0.010081	0.024567
GO PROTEIN ACETYLATION	112	0.441564	1.795415	0.004073	0.024683
GO SUBSTANTIA NIGRA DEVELOPMENT	44	0.519998	1.794092	0.003839	0.024956
GO HISTONE UBIQUITINATION	34	0.555488	1.792955	0.008264	0.025181
GO THREONINE TYPE PEPTIDASE ACTIVITY	20	0.766481	1.79194	0.001965	0.02545
GO NUCLEAR TRANSCRIBED MRNA CATABOLIC PROCESS DEADENYLATION DEPENDENT DECAY	53	0.49926	1.79028	0.005825	0.025816
GO OOCYTE MATURATION	17	0.600612	1.789635	0.003891	0.025908
GO SPLICEOSOMAL TRI SNRNP COMPLEX	26	0.6921	1.785719	0.011152	0.026813
GO PML BODY	93	0.43213	1.785645	0.002045	0.026767
GO NEGATIVE REGULATION OF TRANSFERASE ACTIVITY	338	0.369541	1.785518	<0.0001	0.026743
GO RIBOSOME BINDING	43	0.517325	1.785451	0.007767	0.026704
GO NUCLEOID	39	0.64205	1.785446	0.009862	0.026651
GO ANTIGEN PROCESSING AND PRESENTATION OF PEPTIDE ANTIGEN	168	0.463126	1.784093	0.011696	0.027001
GO NON RECOMBINATIONAL REPAIR	65	0.560959	1.782272	0.001972	0.027433
GO 90S PRERIBOSOME	23	0.699412	1.782138	0.004024	0.027407
GO MODULATION BY VIRUS OF HOST MORPHOLOGY OR PHYSIOLOGY	36	0.498314	1.781727	0.009901	0.027443
GO N ACETYLTRANSFERASE ACTIVITY	76	0.469711	1.781422	0.014113	0.027461
GO COP9 SIGNALOSOME	31	0.516426	1.781354	0.001976	0.027417
GO CELL DIFFERENTIATION INVOLVED IN EMBRYONIC PLACENTA DEVELOPMENT	25	0.574574	1.779166	0.006012	0.027972
GO REGULATION OF CELLULAR SENESCENCE	26	0.536263	1.778809	0.01	0.028033
GO POSITIVE REGULATION OF RNA SPLICING	22	0.60193	1.777157	0.005758	0.028425
GO RESPONSE TO RADIATION	387	0.355978	1.776967	<0.0001	0.028423
GO ADP METABOLIC PROCESS	43	0.527682	1.776176	0.007767	0.028583
GO U4 U6 X U5 TRI SNRNP COMPLEX	21	0.680872	1.776172	0.007463	0.028527
GO ANDROGEN RECEPTOR SIGNALING PATHWAY	40	0.510841	1.775865	0.007952	0.02857

GO SNORNA BINDING	25	0.634217	1.775397	0.011385	0.028657
GO LAMIN BINDING	17	0.563097	1.775094	0.002037	0.028671
GO ANATOMICAL STRUCTURE HOMEOSTASIS	263	0.370103	1.774474	<0.0001	0.028786
GO NEGATIVE REGULATION OF DNA RECOMBINATION	15	0.620471	1.77135	0.017682	0.029598
GO HISTONE MONOUBIQUITINATION	23	0.599946	1.770855	0.01232	0.029688
GO REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	321	0.391898	1.770379	0.003883	0.029744
GO HISTONE H4 ACETYLATION	42	0.510152	1.769717	0.00998	0.029875
GO TRANSCRIPTIONALLY ACTIVE CHROMATIN	16	0.586567	1.769639	0.008065	0.029831
GO NUCLEAR TRANSCRIPTIONAL REPRESSOR COMPLEX	22	0.6081	1.768906	0.014228	0.030008
GO NEGATIVE REGULATION OF WNT SIGNALING PATHWAY	188	0.404768	1.768722	<0.0001	0.030006
GO SMN SM PROTEIN COMPLEX	17	0.760889	1.768103	0.007576	0.030106
GO SPLICEOSOMAL COMPLEX ASSEMBLY	52	0.568863	1.767511	0.019881	0.030203
GO TRANSLATION INITIATION FACTOR ACTIVITY	49	0.592538	1.766117	0.013699	0.030498
GO PROTEIN TRANSPORTER ACTIVITY	96	0.44282	1.766077	0.001869	0.030451
GO ALPHA AMINO ACID BIOSYNTHETIC PROCESS	73	0.507317	1.765848	0.005917	0.030457
GO DNA BINDING BENDING	19	0.593276	1.765707	0.009921	0.030432
GO PRE MRNA BINDING	24	0.589549	1.763815	0.011583	0.030949
GO REGULATION OF HISTONE H3 K4 METHYLATION	24	0.587954	1.762308	0.006061	0.031317
GO INTERCELLULAR BRIDGE	40	0.484845	1.761994	0.003876	0.03133
GO ENDORIBONUCLEASE ACTIVITY	45	0.508261	1.761933	0.011429	0.031288
GO PROTEIN STABILIZATION	125	0.388647	1.761525	<0.0001	0.031345
GO MRNA CLEAVAGE	17	0.610367	1.760144	0.00994	0.031674
GO REGULATION OF DNA BINDING	92	0.421076	1.760069	0.003831	0.031635
GO POSITIVE REGULATION OF VIRAL PROCESS	84	0.443727	1.758816	0.005825	0.031967
GO PYRUVATE METABOLIC PROCESS	59	0.507873	1.758614	0.003992	0.031977
GO REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION TO MITOCHONDRION	120	0.396043	1.758491	0.001942	0.031949
GO DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION RESULTING IN TRANSCRIPTION	15	0.611815	1.757968	0.009881	0.032038
GO INNER MITOCHONDRIAL MEMBRANE ORGANIZATION	16	0.709256	1.756585	0.005769	0.032363
GO OXIDOREDUCTASE ACTIVITY ACTING ON PAIRED DONORS WITH INCORPORATION OR REDUCTION OF MOLECULAR OXYGEN 2 OXOGLUTARATE AS ONE DONOR AND INCORPORATION OF ONE ATOM EACH OF OXYGEN INTO BOTH DONORS	38	0.504523	1.755409	0.00759	0.032635
GO MATURATION OF SSU RRNA	40	0.637143	1.754643	0.011952	0.032814
GO ERROR PRONE TRANSLESION SYNTHESIS	19	0.663224	1.754094	0.01	0.03295
GO RIBOSOME BIOGENESIS	291	0.57683	1.753271	0.027397	0.033169
GO CELLULAR PROTEIN COMPLEX DISASSEMBLY	119	0.581849	1.752879	0.016854	0.033229

GO CELLULAR PROTEIN COMPLEX LOCALIZATION	21	0.556525	1.752391	0.002024	0.033288
GO REGULATION OF MITOCHONDRIAL OUTER MEMBRANE PERMEABILIZATION INVOLVED IN APOPTOTIC SIGNALING PATHWAY	42	0.516347	1.752106	0.011742	0.033303
GO REGULATION OF CHROMATIN ORGANIZATION	146	0.410053	1.749097	0.004149	0.034128
GO REGULATION OF SPINDLE ORGANIZATION	19	0.604458	1.748916	0.005859	0.03412
GO CELLULAR COMPONENT DISASSEMBLY INVOLVED IN EXECUTION PHASE OF APOPTOSIS	41	0.47874	1.748094	0.007843	0.034321
GO CYCLIN DEPENDENT PROTEIN KINASE ACTIVITY	34	0.48956	1.747861	0.008147	0.034328
GO TRANSLATION FACTOR ACTIVITY RNA BINDING	83	0.515768	1.747599	0.013699	0.034332
GO POSITIVE REGULATION OF HISTONE METHYLATION	29	0.563912	1.747438	0.010438	0.034325
GO SAGA TYPE COMPLEX	30	0.548733	1.746721	0.020619	0.03452
GO U12 TYPE SPLICEOSOMAL COMPLEX	25	0.638336	1.743014	0.011257	0.035607
GO MICROTUBULE MOTOR ACTIVITY	75	0.515	1.742868	0.01	0.035583
GO RNA CAPPING	34	0.593204	1.742614	0.011765	0.035599
GO REGULATION OF CELL MATURATION	18	0.579568	1.74233	0.003992	0.035619
GO TELOMERE MAINTENANCE VIA TELOMERE LENGTHENING	24	0.541373	1.741705	0.00956	0.035781
GO NUCLEAR CYCLIN DEPENDENT PROTEIN KINASE HOLOENZYME COMPLEX	15	0.632289	1.74064	0.017176	0.036057
GO RNA MODIFICATION	106	0.478273	1.738686	0.009653	0.036591
GO SYNAPSIS	28	0.566083	1.738236	0.018293	0.036635
GO CENTRIOLE ASSEMBLY	18	0.641218	1.736683	0.026531	0.037114
GO MITOCHONDRIAL TRANSLATION	104	0.643529	1.736309	0.018727	0.037163
GO SERINE FAMILY AMINO ACID METABOLIC PROCESS	38	0.55112	1.735618	0.00996	0.037323
GO CHD TYPE COMPLEX	17	0.634161	1.735196	0.016563	0.0374
GO LEUKOCYTE APOPTOTIC PROCESS	22	0.562818	1.73479	0.013972	0.037485
GO POSITIVE REGULATION OF VIRAL TRANSCRIPTION	35	0.52485	1.733455	0.005964	0.037787
GO NEGATIVE REGULATION OF HISTONE ACETYLATION	15	0.571299	1.733101	0.001946	0.037849
GO U5 SNRNP	16	0.698427	1.729112	0.013258	0.039131
GO 3 5 EXONUCLEASE ACTIVITY	44	0.495525	1.729045	0.009921	0.039076
GO ORGANELLE LOCALIZATION	393	0.358321	1.72892	0.001972	0.03905
GO CELLULAR SENESCENCE	32	0.496093	1.728465	0.007648	0.039148
GO CORE PROMOTER BINDING	146	0.415237	1.727529	<0.0001	0.039366
GO CLEAVAGE INVOLVED IN RRNA PROCESSING	19	0.667942	1.726465	0.020913	0.039667
GO NUCLEAR SPECK	188	0.425684	1.726369	0.010204	0.039648
GO PURINE CONTAINING COMPOUND SALVAGE	15	0.629299	1.723825	0.007921	0.04049
GO NEGATIVE REGULATION OF DNA BIOSYNTHETIC PROCESS	30	0.507658	1.723285	0.003802	0.040628
GO ESTABLISHMENT OF SPINDLE ORIENTATION	24	0.561364	1.723172	0.01006	0.040582
GO MATURATION OF SSU RRNA FROM	33	0.647246	1.722893	0.011811	0.040592

TRICISTRONIC RRNA TRANSCRIPT SSU RRNA 5 8S RRNA LSU RRNA					
GO GENE SILENCING BY RNA	128	0.506453	1.722662	0.005848	0.040615
GO POSITIVE REGULATION OF MRNA METABOLIC PROCESS	42	0.496455	1.722021	0.015595	0.040786
GO NEGATIVE REGULATION OF CELL AGING	16	0.589029	1.72193	0.016327	0.040733
GO RRNA CATABOLIC PROCESS	17	0.592204	1.721746	0.005703	0.040723
GO POSITIVE REGULATION OF G1 S TRANSITION OF MITOTIC CELL CYCLE	24	0.532542	1.720903	0.004107	0.040983
GO TELOMERIC DNA BINDING	28	0.552674	1.720847	0.016194	0.040934
GO CHROMATIN DNA BINDING	76	0.465146	1.720238	0.005952	0.041077
GO SYNAPTONEMAL COMPLEX ORGANIZATION	18	0.605239	1.718469	0.008163	0.041648
GO KINESIN BINDING	30	0.533011	1.716106	0.010638	0.042486
GO REGULATION OF TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	20	0.532314	1.715872	0.01417	0.042494
GO HISTONE DEACETYLASE COMPLEX	60	0.462378	1.714075	0.012146	0.043039
GO NUCLEOSIDE MONOPHOSPHATE BIOSYNTHETIC PROCESS	77	0.527563	1.713836	0.025	0.043073
GO HEXOSE CATABOLIC PROCESS	45	0.499639	1.713806	0.00996	0.043004
GO PHOSPHATASE COMPLEX	43	0.494423	1.712841	0.016032	0.04327
GO NUCLEAR ENVELOPE REASSEMBLY	17	0.635974	1.711194	0.018622	0.043803
GO REGULATION OF DNA METHYLATION	15	0.630775	1.71077	0.024845	0.043885
GO REGULATION OF RNA SPLICING	92	0.468227	1.710524	0.014056	0.04389
GO POLYSOME	38	0.537478	1.710226	0.019685	0.043913
GO POSITIVE REGULATION OF TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER	17	0.56806	1.709138	0.023483	0.04422
GO PYRIMIDINE NUCLEOBASE METABOLIC PROCESS	19	0.540008	1.708514	0.021526	0.044372
GO LIGAND DEPENDENT NUCLEAR RECEPTOR TRANSCRIPTION COACTIVATOR ACTIVITY	51	0.456405	1.708426	0.008282	0.044323
GO POSITIVE REGULATION OF DNA TEMPLATED TRANSCRIPTION INITIATION	24	0.522703	1.702956	0.004065	0.046361
GO FOLIC ACID METABOLIC PROCESS	17	0.60177	1.702791	0.017682	0.046352
GO HISTONE BINDING	164	0.466658	1.701842	0.019763	0.046642
GO DNA CATABOLIC PROCESS	26	0.518235	1.700556	0.013592	0.047046
GO GENE SILENCING	183	0.477833	1.699997	0.009634	0.047162
GO CIS TRANS ISOMERASE ACTIVITY	40	0.503891	1.699777	0.015504	0.047158
GO PROTEIN ACYLATION	142	0.391229	1.699103	0.006098	0.047382
GO METHYL CPG BINDING	15	0.597263	1.698379	0.02008	0.047593
GO CELLULAR RESPONSE TO ESTROGEN STIMULUS	38	0.470614	1.697993	0.010246	0.047639
GO ORGANELLAR RIBOSOME	67	0.681921	1.695575	0.015066	0.048515
GO U2 SNRNP	18	0.683132	1.694866	0.005693	0.048688
GO HSP90 PROTEIN BINDING	27	0.474152	1.694405	0.006198	0.048791
GO TRANSCRIPTION FROM RNA POLYMERASE I PROMOTER	34	0.542907	1.694311	0.025743	0.04874
GO RNA PHOSPHODIESTER BOND HYDROLYSIS ENDONUCLEOLYTIC	54	0.497476	1.693867	0.021236	0.048824

GO TBP CLASS PROTEIN BINDING	20	0.586022	1.693753	0.034156	0.048781
GO TRANSCRIPTION FACTOR TFIID COMPLEX	23	0.561859	1.69373	0.021696	0.04871
GO PEPTIDYL PROLINE MODIFICATION	48	0.485264	1.692788	0.02277	0.049016
GO OXIDOREDUCTION COENZYME METABOLIC PROCESS	96	0.466445	1.692131	0.011583	0.049205
GO WIDE PORE CHANNEL ACTIVITY	22	0.545168	1.691139	0.014141	0.049528
GO REGULATION OF PROTEIN PHOSPHATASE TYPE 2A ACTIVITY	23	0.546205	1.689474	0.011976	0.050173
GO TRANSCRIPTION FROM RNA POLYMERASE III PROMOTER	38	0.513218	1.688685	0.011742	0.050413
GO NUCLEOSIDE PHOSPHATE BIOSYNTHETIC PROCESS	173	0.409357	1.688497	0.011342	0.050411
GO RIBONUCLEASE ACTIVITY	86	0.448288	1.68822	0.015385	0.050443
GO POSITIVE REGULATION OF MRNA PROCESSING	30	0.538175	1.687735	0.013672	0.050552
GO RESPONSE TO PLATELET DERIVED GROWTH FACTOR	18	0.581284	1.687597	0.018987	0.050532
GO REGULATION OF MEMBRANE PERMEABILITY	69	0.455242	1.686723	0.015414	0.050798
GO LYMPHOCYTE APOPTOTIC PROCESS	18	0.581486	1.684565	0.011858	0.051621
GO CELLULAR RESPONSE TO LIGHT STIMULUS	86	0.399763	1.68314	<0.0001	0.052121
GO REGULATION OF GENE SILENCING	50	0.535209	1.682743	0.024	0.052213
GO DNA MODIFICATION	76	0.428374	1.682699	0.006	0.052143
GO CELLULAR RESPONSE TO ESTRADIOL STIMULUS	28	0.512328	1.681776	0.018789	0.052427
GO POSITIVE REGULATION OF CHROMATIN MODIFICATION	81	0.425047	1.681599	0.014228	0.052426
GO OXIDOREDUCTASE ACTIVITY ACTING ON THE CH NH GROUP OF DONORS NAD OR NADP AS ACCEPTOR	16	0.57087	1.680074	0.009416	0.052936
GO HYDROLASE ACTIVITY ACTING ON CARBON NITROGEN BUT NOT PEPTIDE BONDS IN CYCLIC AMIDINES	32	0.513639	1.677474	0.016293	0.054
GO FC RECEPTOR SIGNALING PATHWAY	182	0.411705	1.676753	0.016097	0.054226
GO DEOXYRIBONUCLEOTIDE METABOLIC PROCESS	33	0.564834	1.676717	0.021236	0.054148
GO PTERIDINE CONTAINING COMPOUND METABOLIC PROCESS	34	0.530631	1.675928	0.021154	0.05438
GO GLUCOSE 6 PHOSPHATE METABOLIC PROCESS	21	0.603802	1.675761	0.019531	0.054379
GO TRANSCRIPTION FACTOR COMPLEX	288	0.360187	1.673812	0.008147	0.055176
GO REGULATION OF INCLUSION BODY ASSEMBLY	15	0.596258	1.672564	0.02947	0.055571
GO EXECUTION PHASE OF APOPTOSIS	53	0.428766	1.671464	0.013566	0.055977
GO POSITIVE REGULATION OF TELOMERE CAPPING	15	0.577003	1.67096	0.014344	0.056108
GO PRODUCTION OF MOLECULAR MEDIATOR OF IMMUNE RESPONSE	57	0.435461	1.670808	0.022774	0.056077
GO REGULATION OF MAMMARY GLAND EPITHELIAL CELL PROLIFERATION	16	0.567529	1.670716	0.022541	0.056018

GO TRANSCRIPTION ELONGATION FACTOR COMPLEX	36	0.493055	1.670185	0.015968	0.05619
GO REGULATION OF GENE EXPRESSION EPIGENETIC	202	0.447421	1.669014	0.015385	0.05658
GO PEPTIDE N ACETYLTRANSFERASE ACTIVITY	58	0.465171	1.668373	0.026694	0.056792
GO POSITIVE REGULATION OF MULTI ORGANISM PROCESS	141	0.365866	1.666851	0.001969	0.057374
GO ESTABLISHMENT OF MITOTIC SPINDLE ORIENTATION	19	0.559218	1.666112	0.01996	0.057598
GO METAL CLUSTER BINDING	60	0.491805	1.665482	0.026465	0.057755
GO MYELIN SHEATH	162	0.418921	1.66524	0.024436	0.057762
GO DSRNA FRAGMENTATION	18	0.612578	1.665107	0.018367	0.057739
GO PROTEIN DISULFIDE OXIDOREDUCTASE ACTIVITY	20	0.606465	1.664539	0.017578	0.057921
GO NEURAL NUCLEUS DEVELOPMENT	65	0.446619	1.663791	0.017578	0.058086
GO SPERMATID NUCLEUS DIFFERENTIATION	15	0.573277	1.662565	0.019802	0.058532
GO MITOCHONDRIAL TRANSPORT	161	0.463655	1.662056	0.024715	0.058674
GO NEGATIVE REGULATION OF BINDING	129	0.370602	1.661501	0.007952	0.058702
GO TRANSLATION INITIATION FACTOR BINDING	27	0.540381	1.661247	0.02729	0.058729
GO ALDITOL METABOLIC PROCESS	18	0.608004	1.659982	0.012	0.05916
GO PROTEIN KINASE C BINDING	47	0.438978	1.659957	0.014085	0.059083
GO REGULATION OF RECEPTOR BIOSYNTHETIC PROCESS	21	0.524381	1.659122	0.013158	0.059383
GO INCLUSION BODY	65	0.40347	1.657149	0.004149	0.060225
GO REGULATION OF CELLULAR KETONE METABOLIC PROCESS	165	0.403671	1.657123	0.013359	0.060143
GO LIGASE ACTIVITY FORMING CARBON NITROGEN BONDS	52	0.48172	1.65638	0.028455	0.060397
GO REGULATION OF HISTONE METHYLATION	51	0.491171	1.65499	0.016393	0.060994
GO GMP METABOLIC PROCESS	20	0.51321	1.654619	0.035294	0.061082
GO MONOSACCHARIDE BIOSYNTHETIC PROCESS	53	0.517522	1.654188	0.019417	0.061217
GO ENDORIBONUCLEASE COMPLEX	17	0.616894	1.653271	0.025341	0.06159
GO TUMOR NECROSIS FACTOR MEDIATED SIGNALING PATHWAY	115	0.462006	1.652967	0.042424	0.061642
GO RNA POLYMERASE II CARBOXY TERMINAL DOMAIN KINASE ACTIVITY	16	0.59807	1.652402	0.022267	0.061827
GO POSITIVE REGULATION OF MITOCHONDRION ORGANIZATION	151	0.380845	1.651029	0.004008	0.062374
GO POSITIVE REGULATION OF CATABOLIC PROCESS	383	0.336586	1.650862	<0.0001	0.06235
GO DNA DEMETHYLATION	15	0.590871	1.65064	0.017751	0.062366
GO POSITIVE REGULATION OF ATPASE ACTIVITY	41	0.43714	1.650074	0.014706	0.062524
GO PROTEIN MODIFICATION BY SMALL PROTEIN REMOVAL	107	0.412615	1.649666	0.018405	0.062613
GO BASAL TRANSCRIPTION MACHINERY BINDING	23	0.548269	1.64924	0.03854	0.062735
GO TOR SIGNALING	16	0.553122	1.648578	0.014199	0.062953
GO CEREBRAL CORTEX DEVELOPMENT	103	0.415328	1.64722	0.012146	0.063532

GO IN UTERO EMBRYONIC DEVELOPMENT	301	0.34625	1.646532	<0.0001	0.063782
GO U2 TYPE SPLICEOSOMAL COMPLEX	29	0.560377	1.644315	0.034091	0.064693
GO OOCYTE DIFFERENTIATION	34	0.473364	1.643449	0.016293	0.065006
GO REGULATION OF TELOMERE CAPPING	21	0.527403	1.64276	0.036437	0.065256
GO RESPONSE TO GONADOTROPIN	26	0.508489	1.642164	0.022403	0.065436
GO MITOCHONDRIAL GENOME MAINTENANCE	20	0.53105	1.640402	0.027944	0.066249
GO NEGATIVE REGULATION OF CELLULAR CATABOLIC PROCESS	148	0.353495	1.638954	0.004024	0.066894
GO P53 BINDING	66	0.412291	1.638522	0.028747	0.067
GO MRNA 3 UTR BINDING	47	0.469897	1.6383	0.033597	0.06701
GO LIGASE ACTIVITY	375	0.350899	1.636973	0.006148	0.067521
GO PEPTIDYL SERINE MODIFICATION	146	0.372985	1.634924	0.008316	0.068456
GO DNA CATABOLIC PROCESS ENDONUCLEOLYTIC	18	0.535096	1.630765	0.019608	0.070494
GO WNT SIGNALING PATHWAY	333	0.344627	1.630277	<0.0001	0.070664
GO PYRIMIDINE DEOXYRIBONUCLEOTIDE METABOLIC PROCESS	16	0.6085	1.62951	0.034221	0.070946
GO ANATOMICAL STRUCTURE ARRANGEMENT	17	0.572347	1.628204	0.030181	0.071535
GO RIBONUCLEOSIDE DIPHOSPHATE METABOLIC PROCESS	60	0.436003	1.628064	0.017928	0.071484
GO CYTOPLASMIC TRANSLATION	40	0.649451	1.627425	0.034286	0.071754
GO OOGENESIS	57	0.422513	1.626383	0.010309	0.072198
GO T CELL APOPTOTIC PROCESS	15	0.592985	1.625035	0.019685	0.072826
GO MODULATION BY SYMBIONT OF HOST CELLULAR PROCESS	27	0.487881	1.623172	0.028169	0.073661
GO MICROTUBULE BASED MOVEMENT	192	0.408164	1.622977	0.044177	0.073662
GO PROTEIN C TERMINUS BINDING	182	0.344404	1.620037	<0.0001	0.07512
GO CHAPERONE BINDING	77	0.435938	1.619727	0.016514	0.075193
GO APOPTOTIC DNA FRAGMENTATION	15	0.561805	1.61957	0.02544	0.075158
GO PROTEIN PHOSPHATASE TYPE 2A COMPLEX	19	0.537858	1.619463	0.025591	0.075108
GO RIBOSOMAL LARGE SUBUNIT BIOGENESIS	48	0.61894	1.619308	0.043651	0.075087
GO RNA POLYMERASE II DISTAL ENHANCER SEQUENCE SPECIFIC DNA BINDING	61	0.436756	1.618387	0.018443	0.075505
GO N TERMINAL PROTEIN AMINO ACID MODIFICATION	24	0.489485	1.617354	0.030242	0.075956
GO ORGANELLE DISASSEMBLY	174	0.353527	1.616933	0.00578	0.076098
GO UBIQUITIN LIKE PROTEIN LIGASE ACTIVITY	188	0.369695	1.616615	0.016097	0.076139
GO POSITIVE REGULATION OF TYPE I INTERFERON PRODUCTION	69	0.400754	1.616344	0.01227	0.07619
GO MAGNESIUM ION BINDING	188	0.344687	1.61516	0.002	0.076742
GO ORGANELLAR SMALL RIBOSOMAL SUBUNIT	25	0.684953	1.614828	0.034549	0.076835
GO COPI COATED VESICLE MEMBRANE	16	0.656655	1.613695	0.026616	0.077376
GO MONOSACCHARIDE CATABOLIC PROCESS	54	0.45749	1.611815	0.033138	0.078371
GO TRNA SPECIFIC RIBONUCLEASE ACTIVITY	16	0.649643	1.611021	0.037402	0.078691
GO AGING	256	0.335305	1.610464	<0.0001	0.07891
GO CELLULAR RESPONSE TO NITRIC OXIDE	15	0.525877	1.610183	0.027083	0.078959
GO RNA PHOSPHODIESTER BOND HYDROLYSIS EXONUCLEOLYTIC	33	0.501388	1.610019	0.03301	0.078941
GO PROTEIN TARGETING TO MITOCHONDRION	46	0.559662	1.60927	0.048544	0.079309

GO ANTIGEN PROCESSING AND PRESENTATION	204	0.406144	1.608754	0.033597	0.07949
GO DNA METHYLATION OR DEMETHYLATION	56	0.438784	1.606355	0.028169	0.080671
GO MODIFICATION BY SYMBIONT OF HOST MORPHOLOGY OR PHYSIOLOGY	44	0.451641	1.606206	0.029762	0.08064
GO RIBOSOMAL SMALL SUBUNIT BIOGENESIS	54	0.592499	1.605881	0.049702	0.080732
GO CELLULAR AMINO ACID BIOSYNTHETIC PROCESS	87	0.430164	1.605567	0.023715	0.080776
GO REGULATION OF ATPASE ACTIVITY	61	0.399178	1.603606	0.013359	0.081746
GO ORGANELLE ASSEMBLY	450	0.356074	1.603347	0.01848	0.081789
GO RESPONSE TO TESTOSTERONE	37	0.433258	1.603174	0.011976	0.081781
GO AXON CYTOPLASM	29	0.491822	1.601193	0.043651	0.082844
GO REGULATION OF CANONICAL WNT SIGNALING PATHWAY	226	0.353632	1.601189	0.003976	0.08273
GO NEGATIVE REGULATION OF ANOIKIS	17	0.565864	1.600332	0.036965	0.083124
GO CYTOPLASMIC STRESS GRANULE	31	0.516826	1.600083	0.045267	0.083154
GO VOLTAGE GATED ANION CHANNEL ACTIVITY	17	0.547073	1.59969	0.039448	0.083243
GO CELLULAR METABOLIC COMPOUND SALVAGE	35	0.489086	1.599407	0.031955	0.083265
GO REGULATION OF PROTEIN TARGETING TO MITOCHONDRION	90	0.365941	1.598721	0.004	0.083549
GO CELL SEPARATION AFTER CYTOKINESIS	17	0.593548	1.59795	0.025292	0.083862
GO NEGATIVE REGULATION OF DNA BINDING	46	0.43984	1.597227	0.016129	0.084157
GO DNA REPLICATION FACTOR A COMPLEX	15	0.570212	1.596791	0.03956	0.084288
GO FEMALE GAMETE GENERATION	84	0.378973	1.595978	0.007952	0.084673
GO NEGATIVE REGULATION OF GENE SILENCING	18	0.520446	1.595796	0.038	0.084659
GO REGULATION OF RETINOIC ACID RECEPTOR SIGNALING PATHWAY	16	0.546336	1.593853	0.021696	0.085647
GO REGULATION OF VIRAL TRANSCRIPTION	57	0.419094	1.593598	0.021611	0.085695
GO SINGLE FERTILIZATION	92	0.384302	1.591925	0.01	0.086594
GO NUCLEOTIDE PHOSPHORYLATION	55	0.453622	1.588405	0.038241	0.088515
GO NEGATIVE REGULATION OF PROTEIN BINDING	78	0.377476	1.587577	0.007859	0.08892
GO 4 IRON 4 SULFUR CLUSTER BINDING	40	0.476705	1.587483	0.038986	0.088867
GO REGULATION OF ORGAN MORPHOGENESIS	239	0.357287	1.587285	0.009862	0.088866
GO RNA DEPENDENT DNA BIOSYNTHETIC PROCESS	20	0.507475	1.587176	0.038911	0.088815
GO NCRNA CATABOLIC PROCESS	22	0.54237	1.586006	0.040733	0.089415
GO REGULATION OF MITOCHONDRION ORGANIZATION	197	0.354586	1.585613	0.015717	0.089516
GO FORMATION OF TRANSLATION PREINITIATION COMPLEX	20	0.646662	1.585039	0.048485	0.089749
GO CHROMATIN DISASSEMBLY	16	0.616777	1.584598	0.035294	0.089925
GO IMMUNOGLOBULIN PRODUCTION INVOLVED IN IMMUNOGLOBULIN MEDIATED IMMUNE RESPONSE	22	0.513419	1.583679	0.02863	0.090363
GO MITOCHONDRION MORPHOGENESIS	19	0.528813	1.581946	0.037109	0.091303
GO ORGAN REGENERATION	82	0.385603	1.581233	0.00818	0.091612

GO U1 SNRNP	17	0.651018	1.578656	0.045714	0.093047
GO CELL CYCLE ARREST	142	0.335921	1.577482	0.008	0.093682
GO PROTEIN K48 LINKED UBIQUITINATION	45	0.431925	1.576728	0.043912	0.09393
GO MULTICELLULAR ORGANISM AGING	30	0.430838	1.57631	0.014894	0.094061
GO ISOMERASE ACTIVITY	145	0.399605	1.576192	0.023077	0.094005
GO TOXIN TRANSPORT	36	0.437997	1.574176	0.026769	0.095017
GO ORGANELLE TRANSPORT ALONG MICROTUBULE	54	0.434525	1.571645	0.046122	0.096377
GO ADENYLYLTRANSFERASE ACTIVITY	24	0.487662	1.570051	0.03272	0.097272
GO HORMONE RECEPTOR BINDING	146	0.351538	1.56702	0.012245	0.099135
GO ORGANELLAR LARGE RIBOSOMAL SUBUNIT	30	0.676304	1.566121	0.041276	0.099588
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY	147	0.331058	1.564437	0.003817	0.10045
GO UBIQUITIN LIGASE COMPLEX	247	0.350641	1.560824	0.006186	0.10253
GO MOTOR ACTIVITY	128	0.3998	1.560799	0.029106	0.102407
GO OVARIAN FOLLICLE DEVELOPMENT	55	0.388673	1.560636	0.022267	0.102387
GO PROTEIN COMPLEX LOCALIZATION	50	0.445916	1.5595	0.04918	0.102982
GO TRNA METHYLATION	20	0.539546	1.557408	0.048263	0.104167
GO CELLULAR AMINO ACID METABOLIC PROCESS	313	0.374248	1.5558	0.034615	0.104976
GO REGULATION OF PROTEIN STABILITY	210	0.33289	1.55211	0.007519	0.107229
GO PALLIUM DEVELOPMENT	148	0.37243	1.55177	0.020325	0.10735
GO METHYLATED HISTONE BINDING	46	0.450217	1.551717	0.041667	0.107246
GO PERICENTRIOLAR MATERIAL	18	0.554791	1.550818	0.042463	0.10759
GO NEGATIVE REGULATION OF CATABOLIC PROCESS	193	0.317876	1.550531	0.006073	0.107636
GO GLUTAMINE METABOLIC PROCESS	22	0.510874	1.548629	0.047809	0.10875
GO CELLULAR PROTEIN COMPLEX ASSEMBLY	316	0.344701	1.547526	0.020833	0.109439
GO INTRINSIC APOPTOTIC SIGNALING PATHWAY IN RESPONSE TO DNA DAMAGE	70	0.370668	1.547403	0.013308	0.109238
GO REGULATION OF MEIOTIC CELL CYCLE	38	0.454363	1.546549	0.02459	0.109732
GO GTPASE ACTIVITY	232	0.33265	1.540754	0.015748	0.113565
GO DNA DEALKYLATION	20	0.509693	1.538393	0.043726	0.114972
GO CELLULAR RESPONSE TO ALCOHOL	110	0.36697	1.538208	0.010616	0.114967
GO STRUCTURAL CONSTITUENT OF CYTOSKELETON	94	0.391061	1.537746	0.021739	0.115147
GO ADP BINDING	31	0.445913	1.537035	0.039095	0.115405
GO NEGATIVE REGULATION OF PROTEIN ACETYLATION	20	0.463792	1.533622	0.027076	0.117421
GO CUL4 RING E3 UBIQUITIN LIGASE COMPLEX	25	0.503094	1.533315	0.047619	0.117497
GO REGULATION OF WNT SIGNALING PATHWAY	295	0.323357	1.527464	0.007692	0.121369
GO CELLULAR RESPONSE TO HYDROGEN PEROXIDE	60	0.380988	1.522123	0.030242	0.123712
GO EPHRIN RECEPTOR SIGNALING PATHWAY	84	0.398783	1.521966	0.038911	0.123678
GO SYMPATHETIC NERVOUS SYSTEM DEVELOPMENT	21	0.530393	1.519317	0.040777	0.124965
GO REGULATION OF DNA DAMAGE RESPONSE SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	27	0.460262	1.516521	0.048356	0.126768

GO CHAPERONE MEDIATED PROTEIN FOLDING	44	0.452848	1.515982	0.048507	0.127007
GO REGULATION OF NUCLEOCYTOPLASMIC TRANSPORT	214	0.316107	1.515561	0.010204	0.127185
GO NEGATIVE REGULATION OF SIGNAL TRANSDUCTION BY P53 CLASS MEDIATOR	26	0.46519	1.515073	0.04466	0.127413
GO PROTEIN SERINE THREONINE KINASE ACTIVITY	425	0.313099	1.513725	0.014583	0.128296
GO GLUCOSE METABOLIC PROCESS	113	0.383241	1.511774	0.021912	0.129662
GO RESPONSE TO CAFFEINE	17	0.484744	1.506753	0.03854	0.133458
GO NEURAL PRECURSOR CELL PROLIFERATION	70	0.407592	1.506163	0.027601	0.133811
GO NITROGEN COMPOUND TRANSPORT	476	0.307803	1.50589	0.00994	0.133853
GO PYRIMIDINE CONTAINING COMPOUND METABOLIC PROCESS	71	0.388283	1.505478	0.036822	0.133853
GO MACROMOLECULE METHYLATION	171	0.360051	1.504799	0.031873	0.134234
GO NEGATIVE REGULATION OF CELL CYCLE ARREST	18	0.483197	1.503034	0.045714	0.135353
GO CYTOPLASMIC MRNA PROCESSING BODY	62	0.396273	1.501981	0.029821	0.135858
GO CULLIN RING UBIQUITIN LIGASE COMPLEX	139	0.344329	1.50001	0.025948	0.137292
GO PLACENTA DEVELOPMENT	134	0.338994	1.492943	0.02924	0.142299
GO ENHANCER BINDING	88	0.374882	1.488542	0.030364	0.144964
GO REGULATION OF OXIDATIVE STRESS INDUCED CELL DEATH	42	0.392337	1.487268	0.034483	0.145911
GO MIDBRAIN DEVELOPMENT	86	0.367611	1.485432	0.025194	0.147109
GO FERTILIZATION	122	0.349028	1.485258	0.00625	0.147067
GO PROTEIN PHOSPHATASE BINDING	117	0.332609	1.483928	0.022634	0.148021
GO RESPONSE TO ESTRADIOL	143	0.320967	1.481185	0.016807	0.149502
GO REGULATION OF PROTEIN LOCALIZATION TO NUCLEUS	212	0.305467	1.48024	0.016495	0.150143
GO TRANSCRIPTION INITIATION FROM RNA POLYMERASE II PROMOTER	152	0.317233	1.473564	0.028169	0.155008
GO STEROID HORMONE RECEPTOR BINDING	78	0.358851	1.472436	0.042945	0.155866
GO CELLULAR RESPONSE TO ABIOTIC STIMULUS	248	0.312991	1.472137	0.014113	0.155944
GO DNA TEMPLATED TRANSCRIPTION INITIATION	199	0.330776	1.470671	0.02834	0.156874
GO HISTONE METHYLTRANSFERASE ACTIVITY	47	0.4024	1.469665	0.048682	0.157389
GO POSITIVE REGULATION OF CELLULAR AMIDE METABOLIC PROCESS	100	0.336879	1.467412	0.02549	0.158626
GO RESPONSE TO TEMPERATURE STIMULUS	140	0.32308	1.467324	0.021782	0.158515
GO RESPONSE TO DSRNA	54	0.376507	1.466746	0.046122	0.158828
GO TRANSCRIPTION FACTOR BINDING	498	0.296285	1.466611	0.02	0.158752
GO MULTICELLULAR ORGANISM GROWTH	75	0.372835	1.465618	0.044872	0.159269
GO MALE GAMETE GENERATION	392	0.307269	1.461617	0.014141	0.162046
GO REGULATION OF SYMBIOSIS ENCOMPASSING MUTUALISM THROUGH PARASITISM	190	0.337367	1.460185	0.045455	0.162727
GO FIBROBLAST GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	82	0.36394	1.458055	0.028195	0.164147
GO CELLULAR RESPONSE TO OXIDATIVE STRESS	177	0.307289	1.452635	0.039841	0.168313

GO GAMETE GENERATION	488	0.296253	1.450981	0.008163	0.169159
GO REGENERATION	154	0.320195	1.448667	0.014113	0.17051
GO POSITIVE REGULATION OF APOPTOTIC SIGNALING PATHWAY	165	0.326739	1.44829	0.040153	0.170663
GO MODIFICATION OF MORPHOLOGY OR PHYSIOLOGY OF OTHER ORGANISM	93	0.350985	1.445248	0.04466	0.172447
GO CELL CELL RECOGNITION	55	0.376927	1.444711	0.035433	0.172575
GO POSITIVE REGULATION OF PROTEIN COMPLEX ASSEMBLY	180	0.315865	1.443326	0.022403	0.173563
GO POSITIVE REGULATION OF INTRACELLULAR PROTEIN TRANSPORT	234	0.283669	1.44141	0.006073	0.17518
GO CELLULAR RESPONSE TO ALKALOID	32	0.410123	1.437461	0.047009	0.178375
GO MACROMITOPHAGY	126	0.316175	1.434153	0.02729	0.181027
GO INTRACELLULAR RECEPTOR SIGNALING PATHWAY	160	0.311802	1.42136	0.041322	0.19102
GO TRANSFERASE ACTIVITY TRANSFERRING PENTOSYL GROUPS	51	0.365795	1.419206	0.038076	0.192742
GO RHYTHMIC PROCESS	278	0.304002	1.40876	0.026749	0.200677
GO REGULATION OF APOPTOTIC SIGNALING PATHWAY	345	0.291963	1.407353	0.030303	0.201899
GO TRANSCRIPTION COACTIVATOR ACTIVITY	290	0.296081	1.407209	0.045276	0.201844
GO CELLULAR RESPONSE TO REACTIVE OXYGEN SPECIES	102	0.320337	1.407159	0.043738	0.201686
GO GUANYL NUCLEOTIDE BINDING	354	0.283128	1.406677	0.030181	0.202003
GO TRANSCRIPTION COREPRESSOR ACTIVITY	208	0.304639	1.399538	0.041916	0.208186
GO RESPONSE TO DRUG	422	0.274481	1.397801	0.010101	0.209452
GO POSITIVE REGULATION OF INTRACELLULAR TRANSPORT	344	0.270309	1.397633	0.018219	0.209411
GO REGULATION OF NEURON APOPTOTIC PROCESS	184	0.29975	1.393404	0.031847	0.213397
GO REGULATION OF NEURON DEATH	240	0.289991	1.392277	0.029412	0.214432
GO NEGATIVE REGULATION OF APOPTOTIC SIGNALING PATHWAY	187	0.298141	1.370826	0.032946	0.232941
GO REGULATION OF PROTEIN COMPLEX ASSEMBLY	350	0.27938	1.368159	0.045365	0.234898
GO RESPONSE TO LIGHT STIMULUS	263	0.270883	1.363366	0.029703	0.238373
GO POSITIVE REGULATION OF ESTABLISHMENT OF PROTEIN LOCALIZATION	480	0.262778	1.360569	0.018036	0.240691

ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate; GSEA, gene set enrichment analysis; KIF, kinesin.

Table SVII. GSEA results of c2 reference gene set of high *KIF20A* expression group.

Name	Size	ES	NES	NOM P-value	FDR q-value
SHEPARD BMYB TARGETS	70	0.802631	2.656269	<0.0001	<0.0001
ZHENG GLIOBLASTOMA PLASTICITY UP	240	0.651472	2.615603	<0.0001	<0.0001
LINDGREN BLADDER CANCER CLUSTER 1 DN	356	0.610233	2.613528	<0.0001	<0.0001
SHEPARD BMYB MORPHOLINO DN	193	0.659408	2.581854	<0.0001	<0.0001
WHITFIELD CELL CYCLE G2	169	0.712235	2.573517	<0.0001	<0.0001
SHEPARD CRUSH AND BURN MUTANT DN	174	0.673587	2.568264	<0.0001	<0.0001
AFFAR YY1 TARGETS DN	226	0.639852	2.566641	<0.0001	<0.0001
WANG RESPONSE TO GSK3 INHIBITOR SB216763 DN	332	0.700047	2.554467	<0.0001	<0.0001
BLUM RESPONSE TO SALIRASIB DN	336	0.757989	2.554172	<0.0001	<0.0001
GAVIN FOXP3 TARGETS CLUSTER P6	88	0.841893	2.546011	<0.0001	8.87E-05
WHITFIELD CELL CYCLE G2 M	196	0.678959	2.537096	<0.0001	8.06E-05
CHIANG LIVER CANCER SUBCLASS PROLIFERATION UP	164	0.816784	2.533647	<0.0001	7.39E-05
FURUKAWA DUSP6 TARGETS PCI35 DN	67	0.845559	2.529801	<0.0001	6.82E-05
LINDGREN BLADDER CANCER CLUSTER 3 UP	305	0.754659	2.524941	<0.0001	6.33E-05
CROONQUIST NRAS VS STROMAL STIMULATION DN	98	0.719261	2.516658	<0.0001	1.18E-04
FOURNIER ACINAR DEVELOPMENT LATE 2	265	0.778547	2.515954	<0.0001	1.11E-04
DUTERTRE ESTRADIOL RESPONSE 24HR UP	309	0.844973	2.511946	<0.0001	1.04E-04
RUIZ TNC TARGETS DN	136	0.821116	2.509466	<0.0001	9.85E-05
VECCHI GASTRIC CANCER EARLY UP	384	0.724539	2.508717	<0.0001	9.33E-05
FERREIRA EWINGS SARCOMA UNSTABLE VS STABLE UP	148	0.809669	2.504084	<0.0001	8.87E-05
KEGG CELL CYCLE	124	0.748246	2.501335	<0.0001	8.44E-05
ALCALAY AML BY NPM1 LOCALIZATION DN	180	0.592604	2.501267	<0.0001	8.06E-05
ODONNELL TFRC TARGETS DN	123	0.826077	2.495552	<0.0001	7.71E-05
KAUFFMANN DNA REPLICATION GENES	141	0.707813	2.494323	<0.0001	7.39E-05
TARTE PLASMA CELL VS PLASMABLAST DN	300	0.732544	2.488711	<0.0001	7.09E-05
HORIUCHI WTAP TARGETS DN	293	0.754158	2.488448	<0.0001	6.82E-05
PUJANA BRCA2 PCC NETWORK	401	0.741997	2.481012	<0.0001	6.57E-05
BENPORATH ES 1	356	0.675446	2.479131	<0.0001	6.33E-05
LI WILMS TUMOR VS FETAL KIDNEY 1 DN	159	0.825039	2.474358	<0.0001	6.11E-05
CHEMNITZ RESPONSE TO PROSTAGLANDIN E2 UP	129	0.775623	2.468962	<0.0001	5.91E-05
GOLDRATH ANTIGEN RESPONSE	331	0.649625	2.461392	<0.0001	5.72E-05
LE EGR2 TARGETS UP	104	0.821072	2.457737	<0.0001	5.54E-05
SARRIO EPITHELIAL MESENCHYMAL TRANSITION UP	171	0.802858	2.455491	<0.0001	5.37E-05
FUJII YBX1 TARGETS DN	193	0.784346	2.449808	<0.0001	5.22E-05
FLORIO NEOCORTEX BASAL RADIAL GLIA DN	187	0.859303	2.447377	<0.0001	5.07E-05
REACTOME CELL CYCLE MITOTIC	299	0.768099	2.446904	<0.0001	4.93E-05
TOYOTA TARGETS OF MIR34B AND MIR34C	409	0.651404	2.445212	<0.0001	4.79E-05
KAUFFMANN DNA REPAIR GENES	219	0.67238	2.443899	<0.0001	4.67E-05
GRAHAM CML DIVIDING VS NORMAL	176	0.816467	2.442417	<0.0001	4.55E-05

QUIESCENT UP					
FERRANDO T ALL WITH MLL ENL FUSION DN	83	0.706393	2.441514	<0.0001	4.43E-05
FISCHER G2 M CELL CYCLE	220	0.773016	2.440693	<0.0001	4.32E-05
PENG LEUCINE DEPRIVATION DN	182	0.724565	2.440399	<0.0001	4.22E-05
VILLANUEVA LIVER CANCER KRT19 UP	162	0.745511	2.438866	<0.0001	4.12E-05
WEST ADRENOCORTICAL TUMOR UP	282	0.703868	2.437771	<0.0001	4.03E-05
KOBAYASHI EGFR SIGNALING 24HR DN	242	0.883552	2.431332	<0.0001	5.69E-05
MARKEY RB1 ACUTE LOF UP	223	0.759769	2.427964	<0.0001	5.57E-05
LEE EARLY T LYMPHOCYTE UP	97	0.859455	2.425619	<0.0001	5.45E-05
PENG GLUTAMINE DEPRIVATION DN	324	0.684717	2.42535	<0.0001	5.34E-05
PID FOXM1 PATHWAY	40	0.786062	2.424423	<0.0001	5.23E-05
CHANG CORE SERUM RESPONSE UP	198	0.754768	2.423473	<0.0001	5.12E-05
NADERI BREAST CANCER PROGNOSIS UP	46	0.835304	2.421939	<0.0001	5.02E-05
HOFFMANN LARGE TO SMALL PRE BII LYMPHOCYTE UP	158	0.813413	2.42169	<0.0001	4.92E-05
BASAKI YBX1 TARGETS UP	268	0.755139	2.419762	<0.0001	4.83E-05
BURTON ADIPOGENESIS 3	100	0.885161	2.419248	<0.0001	4.74E-05
SHEDDEN LUNG CANCER POOR SURVIVAL A6	427	0.834268	2.417888	<0.0001	4.66E-05
MORI PRE BI LYMPHOCYTE UP	78	0.792199	2.414612	<0.0001	4.57E-05
DUTERTRE ESTRADIOL RESPONSE 6HR UP	218	0.615295	2.412116	<0.0001	4.49E-05
PAL PRMT5 TARGETS UP	195	0.673493	2.412099	<0.0001	4.42E-05
REACTOME CELL CYCLE	386	0.731138	2.406875	<0.0001	4.34E-05
MITSIADES RESPONSE TO APLIDIN DN	239	0.739487	2.403384	<0.0001	4.27E-05
MORI MATURE B LYMPHOCYTE DN	72	0.698772	2.400354	<0.0001	4.20E-05
ZHANG TLX TARGETS 60HR DN	263	0.822418	2.399016	<0.0001	4.13E-05
PUJANA BREAST CANCER LIT INT NETWORK	97	0.727567	2.395764	<0.0001	4.06E-05
MANALO HYPOXIA DN	271	0.789348	2.393338	<0.0001	4.00E-05
CHIARADONNA NEOPLASTIC TRANSFORMATION KRAS UP	121	0.646252	2.390038	<0.0001	3.94E-05
SUNG METASTASIS STROMA DN	49	0.761507	2.386991	<0.0001	3.88E-05
CHANG CYCLING GENES	138	0.897186	2.380791	<0.0001	3.82E-05
MUELLER PLURINET	296	0.727291	2.375289	<0.0001	3.77E-05
OLSSON E2F3 TARGETS DN	45	0.75663	2.375119	<0.0001	3.71E-05
SENGUPTA NASOPHARYNGEAL CARCINOMA UP	275	0.688554	2.371166	<0.0001	3.66E-05
GRADE COLON AND RECTAL CANCER UP	272	0.689616	2.369742	<0.0001	3.61E-05
RHODES CANCER META SIGNATURE	63	0.824565	2.367783	<0.0001	3.56E-05
YU BAP1 TARGETS	29	0.816978	2.363458	<0.0001	3.51E-05
GARCIA TARGETS OF FLI1 AND DAX1 DN	163	0.685363	2.360428	<0.0001	3.46E-05
STEIN ESR1 TARGETS	82	0.614875	2.356168	<0.0001	3.41E-05
STEIN ESRRA TARGETS RESPONSIVE TO ESTROGEN DN	39	0.838376	2.354901	<0.0001	3.37E-05
LABBE WNT3A TARGETS UP	108	0.564569	2.354374	<0.0001	3.33E-05
MATTIOLI MGUS VS PCL	93	0.670082	2.350928	<0.0001	3.28E-05
WONG EMBRYONIC STEM CELL CORE	330	0.782686	2.349663	<0.0001	3.24E-05
FISCHER G1 S CELL CYCLE	192	0.645141	2.347123	<0.0001	3.20E-05
YAMAZAKI TCEB3 TARGETS DN	204	0.596625	2.346649	<0.0001	3.16E-05
CHICAS RB1 TARGETS GROWING	225	0.660273	2.346521	<0.0001	3.12E-05
PEART HDAC PROLIFERATION CLUSTER DN	73	0.698793	2.345058	<0.0001	3.09E-05
MARTINEZ RESPONSE TO TRABECTEDIN DN	265	0.608323	2.337846	<0.0001	3.05E-05

DANG REGULATED BY MYC UP	71	0.718202	2.337466	<0.0001	3.01E-05
BIDUS METASTASIS UP	204	0.74564	2.336888	<0.0001	2.98E-05
CROONQUIST IL6 DEPRIVATION DN	96	0.926585	2.33466	<0.0001	2.94E-05
NAKAMURA TUMOR ZONE PERIPHERAL VS CENTRAL UP	267	0.62323	2.329402	<0.0001	2.91E-05
WANG CISPLATIN RESPONSE AND XPC UP	190	0.582687	2.327121	<0.0001	3.87E-05
REACTOME MITOTIC PROMETAPHASE	78	0.817117	2.326365	<0.0001	3.83E-05
WU APOPTOSIS BY CDKN1A VIA TP53	54	0.897366	2.319022	<0.0001	3.79E-05
SERVITJA LIVER HNF1A TARGETS UP	132	0.548299	2.318418	<0.0001	3.75E-05
MORI EMU MYC LYMPHOMA BY ONSET TIME UP	99	0.700342	2.317563	<0.0001	3.71E-05
VANTVEER BREAST CANCER METASTASIS DN	111	0.749097	2.313222	<0.0001	5.75E-05
GARY CD5 TARGETS DN	414	0.626669	2.312187	<0.0001	5.69E-05
WINNEPENNINCKX MELANOMA METASTASIS UP	151	0.841519	2.309215	<0.0001	5.63E-05
PID AURORA A PATHWAY	30	0.773165	2.308975	<0.0001	5.58E-05
ZHANG TLX TARGETS 36HR DN	182	0.804029	2.307495	<0.0001	5.52E-05
MORI IMMATURE B LYMPHOCYTE DN	90	0.861128	2.307225	<0.0001	5.46E-05
REACTOME DNA REPLICATION	180	0.815711	2.306703	<0.0001	5.41E-05
MORI LARGE PRE BII LYMPHOCYTE UP	84	0.855263	2.305141	<0.0001	5.36E-05
ZHOU CELL CYCLE GENES IN IR RESPONSE 24HR	119	0.877257	2.304622	<0.0001	5.30E-05
LEE LIVER CANCER SURVIVAL DN	165	0.737533	2.304316	<0.0001	5.25E-05
GRAHAM CML QUIESCENT VS NORMAL QUIESCENT UP	80	0.675598	2.304025	<0.0001	5.20E-05
KIM WT1 TARGETS DN	427	0.548431	2.30239	<0.0001	6.94E-05
NAKAYAMA SOFT TISSUE TUMORS PCA2 UP	86	0.785448	2.301036	<0.0001	6.88E-05
BASSO B LYMPHOCYTE NETWORK	135	0.610607	2.300966	<0.0001	6.81E-05
TANG SENESCENCE TP53 TARGETS DN	54	0.888587	2.296711	<0.0001	7.57E-05
PID E2F PATHWAY	73	0.687721	2.295755	<0.0001	7.50E-05
WHITFIELD CELL CYCLE G1 S	128	0.629731	2.294695	<0.0001	7.43E-05
MISSIAGLIA REGULATED BY METHYLATION DN	115	0.841381	2.293515	<0.0001	7.37E-05
BOYAULT LIVER CANCER SUBCLASS G23 UP	49	0.840838	2.292783	<0.0001	7.30E-05
GAL LEUKEMIC STEM CELL DN	233	0.575006	2.291644	<0.0001	7.23E-05
PUJANA XPRSS INT NETWORK	161	0.79475	2.290809	<0.0001	7.17E-05
SASAKI ADULT T CELL LEUKEMIA	168	0.598799	2.288616	<0.0001	8.44E-05
BIOCARTA G1 PATHWAY	28	0.743284	2.287976	<0.0001	9.51E-05
KOKKINAKIS METHIONINE DEPRIVATION 96HR DN	75	0.622393	2.286718	<0.0001	9.42E-05
REACTOME HIV INFECTION	184	0.646496	2.285704	<0.0001	9.34E-05
REACTOME MITOTIC M M G1 PHASES	160	0.806416	2.284625	<0.0001	9.27E-05
RIZ ERYTHROID DIFFERENTIATION	72	0.66401	2.284129	<0.0001	9.19E-05
BURTON ADIPOGENESIS PEAK AT 24HR	42	0.885326	2.281984	<0.0001	9.11E-05
PETROVA PROX1 TARGETS UP	27	0.833947	2.281804	<0.0001	9.04E-05
REACTOME MITOTIC G1 G1 S PHASES	130	0.772641	2.281422	<0.0001	8.96E-05
KONG E2F3 TARGETS	94	0.892721	2.279917	<0.0001	8.89E-05
VERNELL RETINOBLASTOMA PATHWAY UP	68	0.820238	2.279614	<0.0001	8.82E-05
WILCOX RESPONSE TO PROGESTERONE UP	140	0.633719	2.278736	<0.0001	8.75E-05

PID PLK1 PATHWAY	43	0.82234	2.277788	<0.0001	8.68E-05
REACTOME DNA REPAIR	101	0.66429	2.276695	<0.0001	9.28E-05
LY AGING PREMATURE DN	29	0.857635	2.276457	<0.0001	9.21E-05
PID AURORA B PATHWAY	37	0.835663	2.276183	<0.0001	9.14E-05
HU GENOTOXIC DAMAGE 4HR	35	0.804472	2.27561	<0.0001	9.07E-05
ZHANG TLX TARGETS DN	87	0.903752	2.271087	<0.0001	9.79E-05
KARLSSON TGFB1 TARGETS UP	118	0.68182	2.270156	<0.0001	9.72E-05
BENPORATH PROLIFERATION	136	0.814845	2.267696	<0.0001	9.64E-05
BORCZUK MALIGNANT MESOTHELIOMA UP	291	0.665527	2.267183	<0.0001	9.57E-05
MOLENAAR TARGETS OF CCND1 AND CDK4 DN	51	0.884319	2.267117	<0.0001	9.50E-05
REACTOME MRNA PROCESSING	151	0.690596	2.266044	<0.0001	9.43E-05
VANTVEER BREAST CANCER ESR1 DN	226	0.591236	2.264723	<0.0001	9.36E-05
CROONQUIST NRAS SIGNALING DN	71	0.951107	2.262719	<0.0001	9.92E-05
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS TURQUOISE DN	50	0.750593	2.260403	<0.0001	1.05E-04
HEDENFALK BREAST CANCER BRCA1 VS BRCA2	156	0.566779	2.255127	<0.0001	1.46E-04
JIANG HYPOXIA VIA VHL	33	0.705898	2.254675	<0.0001	1.45E-04
REACTOME PROCESSING OF CAPPED INTRON CONTAINING PRE MRNA	132	0.713803	2.25439	<0.0001	1.44E-04
REACTOME HOST INTERACTIONS OF HIV FACTORS	117	0.68745	2.252121	<0.0001	1.49E-04
BOYAULT LIVER CANCER SUBCLASS G3 UP	181	0.752808	2.250634	<0.0001	1.56E-04
DAIRKEE CANCER PRONE RESPONSE BPA E2	113	0.579432	2.248863	<0.0001	1.62E-04
REN BOUND BY E2F	60	0.899512	2.247448	<0.0001	1.61E-04
PUJANA BRCA CENTERED NETWORK	114	0.8125	2.24344	<0.0001	1.73E-04
BHATTACHARYA EMBRYONIC STEM CELL	86	0.704537	2.241456	<0.0001	1.72E-04
PETROVA ENDOTHELIUM LYMPHATIC VS BLOOD UP	126	0.571703	2.240254	<0.0001	1.70E-04
KEGG OOCYTE MEIOSIS	107	0.575793	2.239956	<0.0001	1.69E-04
REACTOME MITOTIC G2 G2 M PHASES	77	0.682676	2.239458	<0.0001	1.68E-04
HONRADO BREAST CANCER BRCA1 VS BRCA2	18	0.808366	2.237769	<0.0001	1.67E-04
EPPERT PROGENITOR	125	0.654324	2.237695	<0.0001	1.66E-04
NAKAMURA CANCER MICROENVIRONMENT DN	43	0.82616	2.236787	<0.0001	1.65E-04
GENTILE RESPONSE CLUSTER D3	61	0.641656	2.23442	<0.0001	1.83E-04
PID MYC ACTIV PATHWAY	78	0.6856	2.234392	<0.0001	1.82E-04
BHATI G2M ARREST BY 2METHOXYESTRADIOL UP	108	0.580707	2.234217	<0.0001	1.81E-04
CUI TCF21 TARGETS 2 UP	404	0.517304	2.231956	<0.0001	1.88E-04
PUIFFE INVASION INHIBITED BY ASCITES UP	81	0.605884	2.231597	<0.0001	1.86E-04
SONG TARGETS OF IE86 CMV PROTEIN	58	0.883195	2.228269	<0.0001	1.92E-04
GRAHAM NORMAL QUIESCENT VS NORMAL DIVIDING DN	85	0.884784	2.227712	<0.0001	1.99E-04
OUELLET OVARIAN CANCER INVASIVE VS LMP UP	117	0.683375	2.226244	<0.0001	2.03E-04
REACTOME CELL CYCLE CHECKPOINTS	111	0.785429	2.226095	<0.0001	2.02E-04
PENG RAPAMYCIN RESPONSE DN	230	0.658897	2.224966	<0.0001	2.01E-04
XU HGF SIGNALING NOT VIA AKT1 48HR DN	20	0.804219	2.224274	<0.0001	2.07E-04
YAO TEMPORAL RESPONSE TO PROGESTERONE	95	0.638624	2.22407	<0.0001	2.06E-04

CLUSTER 11					
RHEIN ALL GLUCOCORTICOID THERAPY DN	349	0.640348	2.221804	<0.0001	2.15E-04
BIOCARTA G2 PATHWAY	24	0.786952	2.217385	<0.0001	2.25E-04
BOYAULT LIVER CANCER SUBCLASS G123 UP	44	0.786603	2.217216	<0.0001	2.23E-04
OXFORD RALA OR RALB TARGETS UP	45	0.859273	2.216625	<0.0001	2.27E-04
MOHANKUMAR HOXA1 TARGETS UP	384	0.53592	2.216425	<0.0001	2.26E-04
ZHOU CELL CYCLE GENES IN IR RESPONSE 6HR	80	0.898959	2.215656	<0.0001	2.25E-04
BURTON ADIPOGENESIS PEAK AT 16HR	40	0.809052	2.215619	<0.0001	2.23E-04
BENPORATH ES CORE NINE CORRELATED	98	0.626002	2.21552	<0.0001	2.27E-04
SCIBETTA KDM5B TARGETS DN	77	0.634773	2.212216	<0.0001	2.39E-04
GREENBAUM E2A TARGETS UP	32	0.874658	2.211874	<0.0001	2.38E-04
REACTOME MRNA SPLICING	104	0.704787	2.210336	<0.0001	2.42E-04
PID ATR PATHWAY	39	0.827848	2.209876	<0.0001	2.40E-04
LY AGING OLD DN	55	0.817207	2.208008	<0.0001	2.49E-04
KAUFFMANN MELANOMA RELAPSE UP	59	0.89174	2.207599	<0.0001	2.48E-04
ZHANG BREAST CANCER PROGENITORS UP	399	0.623704	2.20744	<0.0001	2.46E-04
REACTOME HIV LIFE CYCLE	105	0.646468	2.206255	<0.0001	2.65E-04
DAIRKEE CANCER PRONE RESPONSE BPA	49	0.641449	2.205406	<0.0001	2.72E-04
WHITEFORD PEDIATRIC CANCER MARKERS	111	0.865998	2.205113	<0.0001	2.71E-04
PID ATM PATHWAY	33	0.747197	2.204631	<0.0001	2.75E-04
JUBAN TARGETS OF SPI1 AND FLI1 DN	84	0.607815	2.204493	<0.0001	2.74E-04
WINTER HYPOXIA UP	88	0.715446	2.204086	<0.0001	2.84E-04
SU TESTIS	67	0.685426	2.202514	<0.0001	2.92E-04
SCHLOSSER MYC TARGETS REPRESSED BY SERUM	153	0.703074	2.201421	<0.0001	2.91E-04
JAEGER METASTASIS UP	43	0.705596	2.198684	<0.0001	3.05E-04
ZAMORA NOS2 TARGETS UP	64	0.688678	2.198016	<0.0001	3.12E-04
PYEON CANCER HEAD AND NECK VS CERVICAL UP	169	0.65919	2.19704	<0.0001	3.29E-04
REACTOME LATE PHASE OF HIV LIFE CYCLE	92	0.656757	2.195408	<0.0001	3.45E-04
MARKEY RB1 CHRONIC LOF UP	111	0.572069	2.195134	<0.0001	3.49E-04
LIAO METASTASIS	495	0.497796	2.194518	<0.0001	3.51E-04
KEGG SPLICEOSOME	123	0.680175	2.193909	<0.0001	3.50E-04
WEST ADRENOCORTICAL TUMOR MARKERS UP	21	0.836116	2.193707	<0.0001	3.48E-04
PID FANCONI PATHWAY	43	0.792264	2.193406	<0.0001	3.46E-04
WHITFIELD CELL CYCLE S	147	0.609519	2.19255	<0.0001	3.49E-04
THILLAINADESAN ZNF217 TARGETS UP	42	0.697736	2.191752	<0.0001	3.47E-04
SHIPP DLBCL VS FOLLICULAR LYMPHOMA UP	44	0.785107	2.191032	<0.0001	3.45E-04
FRASOR RESPONSE TO SERM OR FULVESTRANT DN	50	0.863427	2.187237	<0.0001	3.70E-04
GEORGES CELL CYCLE MIR192 TARGETS	61	0.718211	2.187092	<0.0001	3.68E-04
REACTOME S PHASE	106	0.801519	2.186572	<0.0001	3.74E-04
REACTOME FORMATION OF TUBULIN FOLDING INTERMEDIATES BY CCT TRIC	21	0.826151	2.186182	<0.0001	3.72E-04
KEGG MISMATCH REPAIR	23	0.862493	2.180398	<0.0001	4.24E-04
TURASHVILI BREAST DUCTAL CARCINOMA VS LOBULAR NORMAL UP	71	0.669102	2.178645	<0.0001	4.86E-04
SCHUHMACHER MYC TARGETS UP	77	0.727441	2.178332	<0.0001	4.84E-04
BIOCARTA CELLCYCLE PATHWAY	23	0.783486	2.178084	<0.0001	4.81E-04

REACTOME G1 S TRANSITION	106	0.78687	2.17783	<0.0001	4.79E-04
LE NEURONAL DIFFERENTIATION DN	19	0.862406	2.177309	<0.0001	4.77E-04
REACTOME RNA POL II TRANSCRIPTION	93	0.643004	2.173343	<0.0001	5.37E-04
IWANAGA E2F1 TARGETS INDUCED BY SERUM	29	0.793548	2.172279	<0.0001	5.39E-04
REACTOME DOUBLE STRAND BREAK REPAIR	21	0.81534	2.169414	<0.0001	5.59E-04
SLEBOS HEAD AND NECK CANCER WITH HPV UP	78	0.725707	2.163178	<0.0001	5.92E-04
ODONNELL TARGETS OF MYC AND TFRC DN	43	0.873222	2.159768	<0.0001	6.22E-04
DELPUECH FOXO3 TARGETS DN	39	0.775718	2.15925	<0.0001	6.24E-04
KEGG DNA REPLICATION	36	0.89815	2.159128	<0.0001	6.25E-04
REACTOME CLEAVAGE OF GROWING TRANSCRIPT IN THE TERMINATION REGION	42	0.71992	2.156895	<0.0001	6.62E-04
CHAUHAN RESPONSE TO METHOXYESTRADIOL UP	50	0.652994	2.154467	<0.0001	6.87E-04
REACTOME TRANSPORT OF MATURE TRANSCRIPT TO CYTOPLASM	51	0.722444	2.153955	<0.0001	6.88E-04
MOREAUX MULTIPLE MYELOMA BY TACI DN	154	0.625533	2.151289	<0.0001	7.07E-04
KEGG PROGESTERONE MEDIATED OOCYTE MATURATION	83	0.531597	2.149597	0.001894	7.21E-04
TONKS TARGETS OF RUNX1 RUNX1T1 FUSION MONOCYTE UP	195	0.533094	2.14895	<0.0001	7.26E-04
REACTOME LOSS OF NLP FROM MITOTIC CENTROSOMES	55	0.656564	2.147539	<0.0001	7.49E-04
PYEON HPV POSITIVE TUMORS UP	84	0.673511	2.147419	<0.0001	7.46E-04
SHAFFER IRF4 TARGETS IN ACTIVATED B LYMPHOCYTE	76	0.636532	2.146382	<0.0001	7.60E-04
HERNANDEZ MITOTIC ARREST BY DOCETAXEL 1 DN	36	0.673276	2.14605	<0.0001	7.57E-04
BENPORATH ES 2	39	0.703324	2.14518	<0.0001	7.68E-04
YANG BCL3 TARGETS UP	344	0.458627	2.14427	<0.0001	7.73E-04
GROSS HYPOXIA VIA ELK3 UP	198	0.49746	2.142962	<0.0001	7.88E-04
ENK UV RESPONSE KERATINOCYTE DN	479	0.52216	2.142875	<0.0001	7.85E-04
ABRAMSON INTERACT WITH AIRE	44	0.780777	2.142795	<0.0001	7.81E-04
LI WILMS TUMOR ANAPLASTIC UP	19	0.964552	2.142263	<0.0001	7.95E-04
REICHERT MITOSIS LIN9 TARGETS	27	0.936217	2.141701	<0.0001	8.07E-04
DANG MYC TARGETS UP	138	0.684771	2.140811	<0.0001	8.11E-04
WILLIAMS ESR1 TARGETS UP	26	0.693538	2.14078	<0.0001	8.08E-04
REACTOME PREFOLDIN MEDIATED TRANSFER OF SUBSTRATE TO CCT TRIC	27	0.816855	2.139905	<0.0001	8.17E-04
REACTOME RECRUITMENT OF MITOTIC CENTROSOME PROTEINS AND COMPLEXES	62	0.635064	2.139473	0.001912	8.13E-04
KEGG HOMOLOGOUS RECOMBINATION	26	0.820962	2.137479	<0.0001	8.55E-04
SMIRNOV RESPONSE TO IR 6HR DN	108	0.600225	2.137246	<0.0001	8.51E-04
VANTVEER BREAST CANCER BRCA1 UP	31	0.65899	2.135873	<0.0001	8.59E-04
AMUNDSON GAMMA RADIATION RESPONSE	40	0.880834	2.134877	<0.0001	8.59E-04
SOTIRIOU BREAST CANCER GRADE 1 VS 3 UP	141	0.913044	2.13477	<0.0001	8.55E-04
REACTOME SYNTHESIS OF DNA	90	0.814473	2.134385	<0.0001	8.55E-04
REACTOME ANTIVIRAL MECHANISM BY IFN STIMULATED GENES	64	0.63793	2.132462	<0.0001	8.67E-04

RHODES UNDIFFERENTIATED CANCER	67	0.861496	2.132056	<0.0001	8.70E-04
YANG BREAST CANCER ESR1 LASER DN	49	0.620724	2.130746	<0.0001	8.88E-04
PRAMOONJAGO SOX4 TARGETS DN	50	0.647862	2.129679	<0.0001	9.18E-04
NUNODA RESPONSE TO DASATINIB IMATINIB UP	29	0.674501	2.129547	<0.0001	9.15E-04
REACTOME G2 M CHECKPOINTS	41	0.875112	2.127824	<0.0001	9.34E-04
SIMBULAN PARP1 TARGETS DN	17	0.906684	2.127428	<0.0001	9.31E-04
FOURNIER ACINAR DEVELOPMENT LATE DN	21	0.848796	2.12627	<0.0001	9.34E-04
WONG PROTEASOME GENE MODULE	49	0.72579	2.125879	<0.0001	9.35E-04
JOHANSSON GLIOMAGENESIS BY PDGFB UP	57	0.616287	2.124298	<0.0001	9.52E-04
ROSTY CERVICAL CANCER PROLIFERATION CLUSTER	133	0.904252	2.121761	<0.0001	9.67E-04
WAKASUGI HAVE ZNF143 BINDING SITES	56	0.66893	2.12162	<0.0001	9.63E-04
WANG METASTASIS OF BREAST CANCER ESR1 UP	19	0.868252	2.121269	<0.0001	9.65E-04
KEGG GLYOXYLATE AND DICARBOXYLATE METABOLISM	16	0.79552	2.119847	<0.0001	9.66E-04
REACTOME REGULATION OF MRNA STABILITY BY PROTEINS THAT BIND AU RICH ELEMENTS	81	0.679395	2.116998	<0.0001	0.001002
GROSS HYPOXIA VIA HIF1A UP	75	0.578038	2.113984	<0.0001	0.001046
PID P73PATHWAY	76	0.546559	2.113903	<0.0001	0.001046
VANTVEER BREAST CANCER POOR PROGNOSIS	50	0.620932	2.113634	<0.0001	0.001042
MOREAUX B LYMPHOCYTE MATURATION BY TACI DN	66	0.700655	2.113578	<0.0001	0.001038
SCHLOSSER MYC TARGETS AND SERUM RESPONSE DN	45	0.73432	2.113182	<0.0001	0.001034
WHITFIELD CELL CYCLE LITERATURE	44	0.931355	2.112671	<0.0001	0.001036
PUJANA BREAST CANCER WITH BRCA1 MUTATED UP	54	0.854136	2.112227	<0.0001	0.001033
SAKAI TUMOR INFILTRATING MONOCYTES DN	79	0.618208	2.10654	<0.0001	0.001142
REACTOME M G1 TRANSITION	78	0.812148	2.104081	<0.0001	0.001177
PEART HDAC PROLIFERATION CLUSTER UP	55	0.589599	2.103211	<0.0001	0.001189
UDAYAKUMAR MED1 TARGETS UP	129	0.558246	2.102839	<0.0001	0.001196
REACTOME E2F MEDIATED REGULATION OF DNA REPLICATION	33	0.822152	2.102608	<0.0001	0.001191
BOHN PRIMARY IMMUNODEFICIENCY SYNDROM UP	45	0.643281	2.102323	<0.0001	0.001193
REACTOME REGULATION OF MITOTIC CELL CYCLE	77	0.769912	2.101265	<0.0001	0.001216
CREIGHTON ENDOCRINE THERAPY RESISTANCE 1	483	0.461744	2.100401	<0.0001	0.00124
MENSSEN MYC TARGETS	51	0.734766	2.099857	<0.0001	0.001235
YU MYC TARGETS UP	39	0.873541	2.098673	<0.0001	0.001261
REACTOME DNA STRAND ELONGATION	30	0.936188	2.09486	<0.0001	0.001293
CAIRO PML TARGETS BOUND BY MYC UP	23	0.74116	2.093349	0.001901	0.001323
BROWNE HCMV INFECTION 2HR DN	48	0.638631	2.092457	<0.0001	0.001333
ISHIDA E2F TARGETS	50	0.924752	2.090796	<0.0001	0.001362
PID TELOMERASE PATHWAY	67	0.551803	2.090329	<0.0001	0.001366
TOMIDA METASTASIS UP	26	0.704411	2.089387	<0.0001	0.001391

GENTILE UV HIGH DOSE DN	300	0.495146	2.087322	<0.0001	0.001439
KANG DOXORUBICIN RESISTANCE UP	50	0.969963	2.086468	<0.0001	0.001453
REACTOME EXTENSION OF TELOMERES	27	0.888351	2.086108	<0.0001	0.001452
REACTOME METABOLISM OF NON CODING RNA	47	0.746002	2.085503	<0.0001	0.001459
HESS TARGETS OF HOXA9 AND MEIS1 UP	63	0.611456	2.083679	<0.0001	0.001482
KAMMINGA EZH2 TARGETS	41	0.887804	2.082433	<0.0001	0.00152
BOYLAN MULTIPLE MYELOMA C CLUSTER UP	37	0.603551	2.077402	<0.0001	0.001679
WELCSH BRCA1 TARGETS DN	139	0.60383	2.075231	<0.0001	0.00174
ZUCCHI METASTASIS UP	38	0.633629	2.074429	<0.0001	0.001758
COLLER MYC TARGETS UP	25	0.805873	2.074426	<0.0001	0.001752
MALONEY RESPONSE TO 17AAG DN	76	0.703893	2.071679	<0.0001	0.001831
REACTOME ORC1 REMOVAL FROM CHROMATIN	65	0.789897	2.070334	<0.0001	0.001878
CHEN ETV5 TARGETS TESTIS	21	0.813166	2.070266	<0.0001	0.001872
ELVIDGE HYPOXIA DN	136	0.551501	2.070224	<0.0001	0.001865
REACTOME ANTIGEN PROCESSING UBIQUITINATION PROTEASOME DEGRADATION	192	0.532812	2.069091	<0.0001	0.001873
REACTOME ACTIVATION OF ATR IN RESPONSE TO REPLICATION STRESS	35	0.863226	2.068907	<0.0001	0.001872
REACTOME GLUCOSE TRANSPORT	37	0.685209	2.068649	<0.0001	0.001873
REACTOME INTERACTIONS OF VPR WITH HOST CELLULAR PROTEINS	31	0.726966	2.067803	<0.0001	0.00187
KEGG NUCLEOTIDE EXCISION REPAIR	44	0.669161	2.067488	<0.0001	0.001875
JIANG VHL TARGETS	130	0.517253	2.06359	<0.0001	0.001974
SESTO RESPONSE TO UV C2	53	0.614701	2.062638	<0.0001	0.001993
SMITH TERT TARGETS UP	141	0.521705	2.062025	<0.0001	0.002006
ZHANG RESPONSE TO CANTHARIDIN DN	67	0.692448	2.061692	<0.0001	0.00201
GROSS HYPOXIA VIA ELK3 AND HIF1A DN	100	0.495645	2.059332	<0.0001	0.002081
LAU APOPTOSIS CDKN2A UP	55	0.554561	2.059272	<0.0001	0.00208
BOYLAN MULTIPLE MYELOMA C D UP	129	0.487256	2.059213	0.001869	0.00208
COLINA TARGETS OF 4EBP1 AND 4EBP2	346	0.457786	2.058174	<0.0001	0.002094
SA G1 AND S PHASES	15	0.772091	2.057796	<0.0001	0.002098
REACTOME APC CDC20 MEDIATED DEGRADATION OF NEK2A	21	0.803027	2.057293	<0.0001	0.002107
ZHAN MULTIPLE MYELOMA SUBGROUPS	30	0.812947	2.054572	<0.0001	0.002188
REACTOME ASSEMBLY OF THE PRE REPLICATIVE COMPLEX	63	0.797598	2.053254	<0.0001	0.002203
REACTOME DESTABILIZATION OF MRNA BY KSRP	17	0.723084	2.052988	<0.0001	0.002223
REACTOME PROCESSING OF CAPPED INTRONLESS PRE MRNA	23	0.762658	2.052226	<0.0001	0.002236
CAFFAREL RESPONSE TO THC 24HR 5 DN	55	0.646964	2.051117	<0.0001	0.002257
XU HGF TARGETS INDUCED BY AKT1 48HR DN	24	0.7635	2.050982	<0.0001	0.002253
REACTOME HOMOLOGOUS RECOMBINATION REPAIR OF REPLICATION INDEPENDENT DOUBLE STRAND BREAKS	15	0.849603	2.050763	<0.0001	0.002252
REACTOME G1 S SPECIFIC TRANSCRIPTION	17	0.912568	2.048748	<0.0001	0.002308
REACTOME INHIBITION OF THE PROTEOLYTIC ACTIVITY OF APC C REQUIRED FOR THE ONSET	18	0.810243	2.046922	<0.0001	0.002368

OF ANAPHASE BY MITOTIC SPINDLE CHECKPOINT COMPONENTS					
WHITFIELD CELL CYCLE M G1	140	0.522131	2.046846	<0.0001	0.002361
REACTOME PROTEIN FOLDING	51	0.613705	2.046436	<0.0001	0.002382
WANG RECURRENT LIVER CANCER UP	20	0.689945	2.046239	0.002008	0.002388
WANG SMARCE1 TARGETS DN	348	0.482716	2.045934	<0.0001	0.002388
REACTOME GLOBAL GENOMIC NER GG NER	32	0.689242	2.044657	<0.0001	0.002436
RAMASWAMY METASTASIS UP	64	0.569826	2.043841	<0.0001	0.002466
PID BARD1 PATHWAY	28	0.774452	2.043128	<0.0001	0.002475
GRADE METASTASIS DN	42	0.719103	2.042831	<0.0001	0.00247
REACTOME KINESINS	23	0.797284	2.0425	<0.0001	0.002469
PENG GLUCOSE DEPRIVATION DN	163	0.478019	2.041977	<0.0001	0.002476
SCIAN CELL CYCLE TARGETS OF TP53 AND TP73 DN	22	0.917159	2.041899	<0.0001	0.002468
REACTOME APOPTOSIS	141	0.538101	2.039866	<0.0001	0.002512
LI WILMS TUMOR VS FETAL KIDNEY 2 UP	29	0.689273	2.039436	<0.0001	0.002519
REACTOME CLASS I MHC MEDIATED ANTIGEN PROCESSING PRESENTATION	229	0.503016	2.03856	<0.0001	0.002556
LOCKWOOD AMPLIFIED IN LUNG CANCER	205	0.552248	2.03668	<0.0001	0.002621
SMID BREAST CANCER LUMINAL A DN	18	0.908947	2.035796	<0.0001	0.002651
REACTOME TRANSPORT OF MATURE MRNA DERIVED FROM AN INTRONLESS TRANSCRIPT	31	0.749502	2.03298	<0.0001	0.002761
ZHAN VARIABLE EARLY DIFFERENTIATION GENES DN	30	0.660245	2.028145	<0.0001	0.002932
JI RESPONSE TO FSH DN	57	0.623213	2.028099	<0.0001	0.002924
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 14	134	0.612467	2.02692	<0.0001	0.002937
ONDER CDH1 TARGETS 1 DN	163	0.533362	2.026353	<0.0001	0.002937
OUELLET CULTURED OVARIAN CANCER INVASIVE VS LMP UP	65	0.598103	2.025944	<0.0001	0.002948
DITTMER PTHLH TARGETS UP	110	0.535257	2.023349	<0.0001	0.003051
REACTOME TRANSPORT OF RIBONUCLEOPROTEINS INTO THE HOST NUCLEUS	26	0.770843	2.020681	<0.0001	0.003144
REACTOME FANCONI ANEMIA PATHWAY	19	0.818275	2.020279	<0.0001	0.003147
ZHAN MULTIPLE MYELOMA PR UP	43	0.941423	2.017984	<0.0001	0.003246
REACTOME G0 AND EARLY G1	23	0.785373	2.017868	<0.0001	0.003236
REACTOME PHOSPHORYLATION OF THE APC C	17	0.805142	2.017592	<0.0001	0.003237
MONNIER POSTRADIATION TUMOR ESCAPE UP	374	0.46462	2.015753	<0.0001	0.003323
BROWNE HCMV INFECTION 14HR UP	151	0.469168	2.01557	<0.0001	0.003323
CAFFAREL RESPONSE TO THC 24HR 5 UP	30	0.691348	2.015313	<0.0001	0.003334
REACTOME GLYCOLYSIS	25	0.713664	2.015109	<0.0001	0.003325
MODY HIPPOCAMPUS NEONATAL	35	0.667014	2.012279	<0.0001	0.003439
REACTOME NEP NS2 INTERACTS WITH THE CELLULAR EXPORT MACHINERY	26	0.770374	2.010113	<0.0001	0.003513
JEON SMAD6 TARGETS DN	19	0.766636	2.009998	<0.0001	0.003511
KEGG BASAL TRANSCRIPTION FACTORS	35	0.618564	2.009835	<0.0001	0.003516
BURTON ADIPOGENESIS 4	44	0.604536	2.009718	<0.0001	0.003512
IIZUKA LIVER CANCER PROGRESSION G1 G2 DN	24	0.707872	2.007686	<0.0001	0.003591

REACTOME G1 PHASE	35	0.609747	2.007339	<0.0001	0.003595
REACTOME CYCLIN E ASSOCIATED EVENTS DURING G1 S TRANSITION	62	0.760446	2.003888	<0.0001	0.003722
REACTOME LAGGING STRAND SYNTHESIS	19	0.912678	2.001485	<0.0001	0.003821
LEE METASTASIS AND RNA PROCESSING UP	17	0.800433	2.001459	<0.0001	0.00381
REACTOME TRNA AMINOACYLATION	42	0.711867	2.001071	0.001949	0.003811
REACTOME APC C CDC20 MEDIATED DEGRADATION OF MITOTIC PROTEINS	65	0.769685	2.000939	<0.0001	0.0038
PID MYC PATHWAY	25	0.65387	2.000677	<0.0001	0.003803
KEGG ONE CARBON POOL BY FOLATE	17	0.728533	2.000255	<0.0001	0.003818
REACTOME APC C CDH1 MEDIATED DEGRADATION OF CDC20 AND OTHER APC C CDH1 TARGETED PROTEINS IN LATE MITOSIS EARLY G1	64	0.76339	2.000174	<0.0001	0.003815
SYED ESTRADIOL RESPONSE	19	0.648783	2.000123	<0.0001	0.003805
PELLICCIOTTA HDAC IN ANTIGEN PRESENTATION DN	49	0.698881	1.999564	<0.0001	0.003812
SCHLOSSER MYC TARGETS AND SERUM RESPONSE UP	46	0.667446	1.999523	<0.0001	0.003804
REACTOME REGULATION OF GLUCOKINASE BY GLUCOKINASE REGULATORY PROTEIN	26	0.736698	1.99843	<0.0001	0.003854
REACTOME APC C CDC20 MEDIATED DEGRADATION OF CYCLIN B	19	0.781983	1.997508	<0.0001	0.003898
KORKOLA TERATOMA	39	0.58834	1.997485	<0.0001	0.003888
KEGG BASE EXCISION REPAIR	33	0.677559	1.996618	<0.0001	0.003921
PID P53 REGULATION PATHWAY	57	0.542067	1.996203	<0.0001	0.003925
GENTLES LEUKEMIC STEM CELL DN	18	0.741592	1.994287	<0.0001	0.004038
REACTOME ACTIVATION OF THE PRE REPLICATIVE COMPLEX	30	0.886114	1.993903	<0.0001	0.004046
BENPORATH MYC TARGETS WITH EBOX	219	0.464298	1.992622	<0.0001	0.004141
CONCANNON APOPTOSIS BY EPOXOMICIN DN	159	0.504678	1.992043	<0.0001	0.004163
REACTOME DEADENYLATION DEPENDENT MRNA DECAY	42	0.609905	1.990957	<0.0001	0.004195
CHANDRAN METASTASIS UP	191	0.476314	1.989928	<0.0001	0.004235
GROSS HYPOXIA VIA ELK3 ONLY DN	41	0.542787	1.989453	<0.0001	0.004254
PIONTEK PKD1 TARGETS DN	16	0.734789	1.98645	<0.0001	0.004382
REACTOME RNA POL II PRE TRANSCRIPTION EVENTS	51	0.61407	1.985118	<0.0001	0.004436
BIOCARTA P53 PATHWAY	16	0.689432	1.984748	<0.0001	0.004457
REACTOME CYCLIN A B1 ASSOCIATED EVENTS DURING G2 M TRANSITION	15	0.890008	1.983267	<0.0001	0.00454
CAFFAREL RESPONSE TO THC DN	29	0.72461	1.983187	<0.0001	0.004528
ZHU CMV 24 HR UP	93	0.534773	1.982943	0.003945	0.004527
BILD MYC ONCOGENIC SIGNATURE	187	0.489565	1.982282	<0.0001	0.00457
REACTOME P53 DEPENDENT G1 DNA DAMAGE RESPONSE	53	0.756949	1.982095	<0.0001	0.004573
WATANABE COLON CANCER MSI VS MSS UP	27	0.607195	1.98154	0.002004	0.004596
REACTOME POST CHAPERONIN TUBULIN FOLDING PATHWAY	18	0.726923	1.980388	<0.0001	0.004684

REACTOME DOWNSTREAM SIGNALING EVENTS OF B CELL RECEPTOR BCR	92	0.571358	1.976775	<0.0001	0.004906
MEINHOLD OVARIAN CANCER LOW GRADE DN	20	0.783624	1.976286	<0.0001	0.004933
ACOSTA PROLIFERATION INDEPENDENT MYC TARGETS UP	75	0.542673	1.975191	<0.0001	0.004988
REACTOME CHROMOSOME MAINTENANCE	112	0.708597	1.97397	<0.0001	0.005049
CHIARETTI T ALL RELAPSE PROGNOSIS	19	0.731396	1.973693	<0.0001	0.005061
SANSOM APC TARGETS REQUIRE MYC	192	0.501999	1.971123	0.001957	0.005223
BIOCARTA MCM PATHWAY	18	0.872747	1.970971	<0.0001	0.005226
KOKKINAKIS METHIONINE DEPRIVATION 48HR DN	64	0.497033	1.969555	<0.0001	0.005352
WIERENGA PML INTERACTOME	40	0.599121	1.969317	<0.0001	0.005352
MATZUK MEIOTIC AND DNA REPAIR	35	0.605038	1.968969	<0.0001	0.005362
XU RESPONSE TO TRETINOIN AND NSC682994 DN	15	0.832366	1.968602	<0.0001	0.005369
REACTOME PROCESSIVE SYNTHESIS ON THE LAGGING STRAND	15	0.902101	1.968406	<0.0001	0.005368
REACTOME MRNA SPLICING MINOR PATHWAY	40	0.699261	1.966838	<0.0001	0.005464
BIOCARTA ATRBRCA PATHWAY	19	0.77449	1.966438	0.001972	0.005476
REACTOME TRANSCRIPTION COUPLED NER TC NER	43	0.643506	1.966286	<0.0001	0.005474
BIOCARTA ATM PATHWAY	19	0.666483	1.963068	0.003891	0.005704
WANG TUMOR INVASIVENESS UP	362	0.488607	1.962343	<0.0001	0.005732
REACTOME CDT1 ASSOCIATION WITH THE CDC6 ORC ORIGIN COMPLEX	54	0.776762	1.959886	<0.0001	0.005951
WATANABE RECTAL CANCER RADIOTHERAPY RESPONSIVE DN	89	0.520094	1.959482	<0.0001	0.005965
REACTOME MRNA 3 END PROCESSING	33	0.679651	1.956331	<0.0001	0.00621
REACTOME ER PHAGOSOME PATHWAY	58	0.741241	1.954467	<0.0001	0.00632
JAIN NFKB SIGNALING	71	0.522714	1.954157	<0.0001	0.006335
MATZUK SPERMATOCYTE	68	0.523811	1.953535	0.002045	0.00639
REACTOME ACTIVATION OF NF KAPPAB IN B CELLS	61	0.671809	1.951526	<0.0001	0.006542
KENNY CTNNB1 TARGETS UP	46	0.513427	1.951432	<0.0001	0.006536
KEGG RNA DEGRADATION	56	0.595992	1.950491	0.001946	0.006594
YUAN ZNF143 PARTNERS	21	0.744772	1.949539	<0.0001	0.006656
REACTOME P53 INDEPENDENT G1 S DNA DAMAGE CHECKPOINT	48	0.768678	1.949339	<0.0001	0.006649
VANHARANTA UTERINE FIBROID WITH 7Q DELETION UP	65	0.541866	1.948349	<0.0001	0.006701
GENTILE UV RESPONSE CLUSTER D4	54	0.571648	1.948278	0.003861	0.006693
HU GENOTOXIN ACTION DIRECT VS INDIRECT 24HR	51	0.541123	1.944962	0.001992	0.00694
MORI SMALL PRE BII LYMPHOCYTE DN	74	0.501234	1.944481	<0.0001	0.006965
NEMETH INFLAMMATORY RESPONSE LPS DN	32	0.571956	1.944177	<0.0001	0.006981
REACTOME ACTIVATION OF GENES BY ATF4	23	0.649837	1.944107	0.001942	0.006965
FARMER BREAST CANCER CLUSTER 2	32	0.902986	1.94364	<0.0001	0.00698
SIG REGULATION OF THE ACTIN CYTOSKELETON BY RHO GTPASES	34	0.608855	1.943536	0.001988	0.006971

CHICAS RB1 TARGETS LOW SERUM	84	0.598081	1.942853	0.00396	0.007041
EGUCHI CELL CYCLE RB1 TARGETS	23	0.975887	1.942104	<0.0001	0.007079
REACTOME NUCLEOTIDE EXCISION REPAIR	48	0.604088	1.940962	<0.0001	0.007171
DEN INTERACT WITH LCA5	25	0.718446	1.940296	0.002008	0.007208
REACTOME SCFSKP2 MEDIATED DEGRADATION OF P27 P21	53	0.76694	1.93972	<0.0001	0.007227
RASHI RESPONSE TO IONIZING RADIATION 4	57	0.481413	1.938123	<0.0001	0.007375
KEGG PROTEASOME	42	0.79173	1.937408	<0.0001	0.007424
REACTOME SIGNALING BY WNT	62	0.670359	1.937027	<0.0001	0.007443
FERRANDO HOX11 NEIGHBORS	23	0.696814	1.933924	<0.0001	0.00775
ENK UV RESPONSE EPIDERMIS UP	277	0.457797	1.933273	<0.0001	0.007792
YIH RESPONSE TO ARSENITE C3	35	0.575493	1.932845	<0.0001	0.007816
BROWN MYELOID CELL DEVELOPMENT DN	119	0.469508	1.931227	<0.0001	0.007934
KEGG AMINOACYL TRNA BIOSYNTHESIS	41	0.664378	1.92947	0.001949	0.008054
KUROKAWA LIVER CANCER CHEMOTHERAPY DN	39	0.533797	1.929205	<0.0001	0.008054
REACTOME CROSS PRESENTATION OF SOLUBLE EXOGENOUS ANTIGENS ENDOSOMES	47	0.73592	1.928998	<0.0001	0.008061
MATSUDA NATURAL KILLER DIFFERENTIATION	455	0.391869	1.927797	<0.0001	0.008176
REACTOME CONVERSION FROM APC C CDC20 TO APC C CDH1 IN LATE ANAPHASE	16	0.733423	1.926299	<0.0001	0.008318
REACTOME ANTIGEN PROCESSING CROSS PRESENTATION	72	0.651251	1.926095	0.006	0.008316
REACTOME SCF BETA TRCP MEDIATED DEGRADATION OF EMI1	49	0.759775	1.925905	<0.0001	0.008309
REACTOME CYTOSOLIC TRNA AMINOACYLATION	24	0.785252	1.924682	<0.0001	0.008394
COLDREN GEFITINIB RESISTANCE UP	74	0.543114	1.92393	0.00189	0.008452
REACTOME AUTODEGRADATION OF THE E3 UBIQUITIN LIGASE COP1	47	0.754595	1.923379	<0.0001	0.008487
CHIANG LIVER CANCER SUBCLASS UNANNOTATED DN	182	0.637495	1.922617	0.002053	0.008547
REACTOME REGULATION OF ORNITHINE DECARBOXYLASE ODC	48	0.751893	1.92241	<0.0001	0.008549
SANSOM APC TARGETS UP	113	0.461648	1.919507	<0.0001	0.008791
REACTOME VIF MEDIATED DEGRADATION OF APOBEC3G	47	0.762261	1.917384	<0.0001	0.009031
TSENG IRS1 TARGETS UP	106	0.472892	1.915718	<0.0001	0.009167
REACTOME DESTABILIZATION OF MRNA BY AUF1 HNRNP D0	50	0.752287	1.915214	<0.0001	0.009199
REACTOME INTRINSIC PATHWAY FOR APOPTOSIS	29	0.600553	1.914255	<0.0001	0.009254
SESTO RESPONSE TO UV C1	72	0.566347	1.910846	<0.0001	0.009574
DORMOY ELAVL1 TARGETS	16	0.682283	1.910761	0.001927	0.009561
KOINUMA COLON CANCER MSI UP	16	0.715851	1.908732	<0.0001	0.009769
DOANE BREAST CANCER CLASSES DN	32	0.619728	1.908547	<0.0001	0.009768
REACTOME DESTABILIZATION OF MRNA BY BRF1	17	0.654997	1.907987	0.001848	0.009807
YAO TEMPORAL RESPONSE TO PROGESTERONE	64	0.616165	1.907875	0.004	0.0098

CLUSTER 10					
MULLIGAN NTF3 SIGNALING VIA INSR AND IGF1R UP	23	0.674026	1.907528	0.004073	0.009816
WEIGEL OXIDATIVE STRESS BY HNE AND H2O2	39	0.528866	1.907318	0.001866	0.00981
HEDENFALK BREAST CANCER HEREDITARY VS SPORADIC	46	0.558058	1.906911	0.007752	0.009844
FINETTI BREAST CANCER KINOME RED	16	0.977441	1.905571	<0.0001	0.009981
REACTOME BASE EXCISION REPAIR	19	0.739324	1.905297	0.002049	0.009984
CHANDRAN METASTASIS TOP50 UP	34	0.612386	1.903234	0.005725	0.010219
REACTOME AUTODEGRADATION OF CDH1 BY CDH1 APC C	56	0.736882	1.902159	<0.0001	0.010342
REACTOME CDK MEDIATED PHOSPHORYLATION AND REMOVAL OF CDC6	46	0.772232	1.901237	<0.0001	0.010409
REACTOME FACTORS INVOLVED IN MEGAKARYOCYTE DEVELOPMENT AND PLATELET PRODUCTION	111	0.477751	1.900891	0.001862	0.010433
LIU SOX4 TARGETS DN	293	0.425654	1.899944	<0.0001	0.010537
LY AGING MIDDLE DN	16	0.95546	1.89984	<0.0001	0.010535
VANDESLUIS COMMD1 TARGETS GROUP 2 UP	15	0.700928	1.899336	<0.0001	0.010589
PID RB 1PATHWAY	65	0.495654	1.898447	<0.0001	0.010653
RAMALHO STEMNESS UP	196	0.510455	1.898378	<0.0001	0.010639
IVANOVA HEMATOPOIESIS EARLY PROGENITOR	489	0.413678	1.898225	<0.0001	0.010635
REACTOME PERK REGULATED GENE EXPRESSION	26	0.629411	1.897715	0.003929	0.010675
XU CREBBP TARGETS UP	24	0.619434	1.897401	0.004098	0.010703
KEGG PYRIMIDINE METABOLISM	96	0.530047	1.897114	0.002004	0.010748
ZHANG RESPONSE TO IKK INHIBITOR AND TNF DN	100	0.482826	1.894291	<0.0001	0.011084
REACTOME REGULATION OF APOPTOSIS	56	0.67096	1.892199	<0.0001	0.011324
MARIADASON RESPONSE TO BUTYRATE SULINDAC 4	21	0.626318	1.886468	0.007505	0.01197
BOYLAN MULTIPLE MYELOMA C UP	44	0.525693	1.886409	0.002	0.011955
SPIELMAN LYMPHOBLAST EUROPEAN VS ASIAN UP	467	0.475123	1.886162	0.004008	0.011957
APRELIKOVA BRCA1 TARGETS	48	0.542382	1.884366	<0.0001	0.012183
KEGG P53 SIGNALING PATHWAY	66	0.501395	1.884289	0.002024	0.012186
LI LUNG CANCER	41	0.583701	1.882349	0.00396	0.012429
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS RED UP	16	0.720694	1.878118	<0.0001	0.013061
KEGG PATHOGENIC ESCHERICHIA COLI INFECTION	55	0.532179	1.877661	<0.0001	0.01311
MODY HIPPOCAMPUS PRENATAL	42	0.650805	1.870974	0.007921	0.014078
GENTILE UV RESPONSE CLUSTER D5	37	0.564963	1.868872	0.003953	0.01439
HEIDENBLAD AMPLICON 8Q24 UP	34	0.551487	1.868355	0.005837	0.014466
CUI GLUCOSE DEPRIVATION	58	0.536577	1.86644	0.002008	0.014728
REACTOME METABOLISM OF RNA	252	0.595407	1.866064	0.017613	0.014747
KRASNOSELSKAYA ILF3 TARGETS DN	44	0.532651	1.865432	0.001838	0.014835
BROWNE HCMV INFECTION 48HR UP	174	0.408385	1.864636	<0.0001	0.014952

RIZ ERYTHROID DIFFERENTIATION CCNE1	39	0.527737	1.864409	<0.0001	0.014961
KIM MYC AMPLIFICATION TARGETS UP	186	0.480248	1.863497	0.009671	0.015054
KAN RESPONSE TO ARSENIC TRIOXIDE	118	0.483835	1.863214	0.002	0.015059
ZHU CMV ALL UP	119	0.490735	1.862534	0.009921	0.015126
SHAFFER IRF4 TARGETS IN ACTIVATED DENDRITIC CELL	61	0.532159	1.86247	0.004	0.015104
PEDERSEN METASTASIS BY ERBB2 ISOFORM 7	362	0.399591	1.862343	<0.0001	0.015087
JAZAG TGFB1 SIGNALING UP	104	0.435221	1.858454	<0.0001	0.015694
IRITANI MAD1 TARGETS DN	46	0.674364	1.856611	0.007952	0.015947
BACOLOD RESISTANCE TO ALKYLATING AGENTS DN	57	0.504122	1.856493	<0.0001	0.015935
RAY TUMORIGENESIS BY ERBB2 CDC25A UP	99	0.427637	1.851589	<0.0001	0.016772
NAGY TFTC COMPONENTS HUMAN	18	0.647464	1.851249	0.001876	0.016792
SAKAI CHRONIC HEPATITIS VS LIVER CANCER UP	79	0.544747	1.84924	0.005792	0.017096
KIM TIAL1 TARGETS	31	0.580682	1.847152	<0.0001	0.017428
BIOCARTA TNFR1 PATHWAY	29	0.5413	1.846832	0.003922	0.017443
BILD E2F3 ONCOGENIC SIGNATURE	222	0.414029	1.844264	<0.0001	0.017951
REACTOME RESOLUTION OF AP SITES VIA THE MULTIPLE NUCLEOTIDE PATCH REPLACEMENT PATHWAY	17	0.743707	1.842516	0.002062	0.018255
CHUNG BLISTER CYTOTOXICITY UP	123	0.490669	1.841934	0.006085	0.01834
SILIGAN TARGETS OF EWS FLI1 FUSION DN	17	0.63228	1.840749	0.005792	0.01853
HUANG GATA2 TARGETS DN	67	0.48036	1.83948	<0.0001	0.018738
TOOKER GEMCITABINE RESISTANCE DN	119	0.481571	1.838992	0.003945	0.018795
AMIT EGF RESPONSE 480 MCF10A	40	0.531375	1.837167	0.011905	0.019166
YIH RESPONSE TO ARSENITE C1	23	0.601631	1.836536	0.009488	0.019292
HONMA DOCETAXEL RESISTANCE	30	0.690476	1.835535	<0.0001	0.019472
TIEN INTESTINE PROBIOTICS 2HR DN	85	0.482602	1.835407	<0.0001	0.019456
GOLDRATH HOMEOSTATIC PROLIFERATION	163	0.489531	1.834864	0.003976	0.019503
REACTOME METABOLISM OF NUCLEOTIDES	70	0.53433	1.834687	0.004073	0.019491
PODAR RESPONSE TO ADAPHOSTIN DN	18	0.667153	1.834566	0.007968	0.019468
SHIN B CELL LYMPHOMA CLUSTER 8	36	0.576272	1.834382	0.002016	0.01946
HASLINGER B CLL WITH CHROMOSOME 12 TRISOMY	22	0.64397	1.834308	0.001869	0.019441
CAIRO HEPATOBLASTOMA UP	197	0.446128	1.833735	0.001866	0.019541
WANG TARGETS OF MLL CBP FUSION DN	42	0.546191	1.833113	0.00404	0.01962
IVANOVA HEMATOPOIESIS INTERMEDIATE PROGENITOR	140	0.465495	1.832086	0.011788	0.019779
MACLACHLAN BRCA1 TARGETS UP	21	0.665682	1.831726	0.005871	0.019823
SCHLOSSER MYC AND SERUM RESPONSE SYNERGY	31	0.673333	1.826529	0.01232	0.020812
BANDRES RESPONSE TO CARMUSTIN MGMT 48HR UP	18	0.593765	1.826323	0.003774	0.020816
FARMER BREAST CANCER BASAL VS LULMINAL	317	0.394212	1.825613	<0.0001	0.020906
REACTOME GLUCONEOGENESIS	29	0.634468	1.824592	0.008282	0.021075
REACTOME DESTABILIZATION OF MRNA BY TRISTETRAPROLIN TTP	17	0.646551	1.823261	0.003636	0.021319

REACTOME AMINO ACID SYNTHESIS AND INTERCONVERSION TRANSAMINATION	15	0.701215	1.822876	0.006186	0.021362
REACTOME GLUCOSE METABOLISM	61	0.53118	1.822558	0.004098	0.021381
ALFANO MYC TARGETS	230	0.414119	1.820831	<0.0001	0.021726
SHAFFER IRF4 TARGETS IN MYELOMA VS MATURE B LYMPHOCYTE	99	0.491022	1.819372	0.01002	0.021983
POMEROY MEDULLOBLASTOMA PROGNOSIS DN	43	0.637588	1.818514	0.015656	0.022116
TAYLOR METHYLATED IN ACUTE LYMPHOBLASTIC LEUKEMIA	73	0.485049	1.817824	0.001894	0.022246
BIOCARTA PROTEASOME PATHWAY	28	0.790264	1.817397	0.002045	0.022304
FAELT B CLL WITH VH3 21 UP	42	0.61095	1.815279	0.008197	0.022718
STEIN ESRRA TARGETS RESPONSIVE TO ESTROGEN UP	29	0.545759	1.813202	0.007619	0.023164
KEGG UBIQUITIN MEDIATED PROTEOLYSIS	130	0.44382	1.81142	0.003868	0.023549
REACTOME SIGNALING BY THE B CELL RECEPTOR BCR	121	0.466131	1.811121	0.005894	0.023588
ELVIDGE HIF1A AND HIF2A TARGETS UP	38	0.548682	1.810792	0.009901	0.023621
SESTO RESPONSE TO UV C4	20	0.622422	1.810314	0.001984	0.023691
BRACHAT RESPONSE TO CAMPTOTHECIN DN	43	0.561006	1.810142	0.012397	0.023679
HAHTOLA SEZARY SYNDROM UP	92	0.460854	1.809455	0.002028	0.023782
LOPEZ TRANSLATION VIA FN1 SIGNALING	34	0.543404	1.80931	0.013514	0.023765
REACTOME ASSOCIATION OF TRIC CCT WITH TARGET PROTEINS DURING BIOSYNTHESIS	26	0.576857	1.809084	0.007828	0.023762
CHIN BREAST CANCER COPY NUMBER UP	24	0.626565	1.807274	0.011407	0.024176
ZHAN EARLY DIFFERENTIATION GENES DN	42	0.538012	1.803712	0.012048	0.024962
SANSOM APC MYC TARGETS	198	0.414011	1.802766	<0.0001	0.025115
RICKMAN TUMOR DIFFERENTIATED MODERATELY VS POORLY DN	15	0.720354	1.802597	<0.0001	0.02511
REACTOME RNA POL II TRANSCRIPTION PRE INITIATION AND PROMOTER OPENING	39	0.588001	1.802042	0.005736	0.025206
PID HIF1A PATHWAY	16	0.622846	1.79999	0.005792	0.025662
MARZEC IL2 SIGNALING UP	110	0.450741	1.799554	0.008065	0.025712
PARK HSC VS MULTIPOTENT PROGENITORS DN	18	0.59839	1.796557	0.011673	0.026356
COLLIS PRKDC SUBSTRATES	19	0.649134	1.796201	0.007692	0.026411
REACTOME FORMATION OF RNA POL II ELONGATION COMPLEX	35	0.565006	1.795503	0.003839	0.026537
JAZAERI BREAST CANCER BRCA1 VS BRCA2 UP	47	0.52257	1.794985	0.003976	0.026627
BIOCARTA P53HYPOXIA PATHWAY	22	0.562001	1.794882	0.004107	0.026619
ELVIDGE HIF1A TARGETS UP	63	0.511808	1.793423	0.01002	0.026959
SANSOM APC TARGETS	192	0.385816	1.793128	<0.0001	0.027007
YAGI AML SURVIVAL	119	0.392796	1.793091	<0.0001	0.026971
HOSHIDA LIVER CANCER SUBCLASS S2	113	0.506866	1.792142	0.007605	0.027147
MAYBURD RESPONSE TO L663536 DN	51	0.573153	1.78977	0.006012	0.027691
SMID BREAST CANCER RELAPSE IN BONE DN	293	0.413087	1.789521	<0.0001	0.027712
SARTIPY NORMAL AT INSULIN RESISTANCE UP	33	0.563485	1.788601	0.00813	0.027923
MMS MOUSE LYMPH HIGH 4HRS UP	31	0.612652	1.78594	0.008048	0.028548
MCBRYAN PUBERTAL BREAST 6 7WK DN	76	0.454499	1.785747	0.004008	0.028546
MELLMAN TUT1 TARGETS UP	18	0.620804	1.785377	0.009747	0.028581

BONOME OVARIAN CANCER POOR SURVIVAL DN	20	0.615493	1.784511	0.016	0.02876
REACTOME TRANSCRIPTIONAL ACTIVITY OF SMAD2 SMAD3 SMAD4 HETEROTRIMER	36	0.528308	1.782822	0.009416	0.029187
BLUM RESPONSE TO SALIRASIB UP	236	0.449913	1.782415	0.004057	0.02924
PROVENZANI METASTASIS UP	183	0.430626	1.781555	0.003861	0.029432
DING LUNG CANCER EXPRESSION BY COPY NUMBER	96	0.545864	1.780642	0.00996	0.029619
KARAKAS TGFB1 SIGNALING	18	0.666887	1.78054	0.011952	0.029588
BLALOCK ALZHEIMERS DISEASE INCIPIENT DN	161	0.442609	1.77596	0.003976	0.030702
LIU VMYB TARGETS UP	114	0.414546	1.775587	<0.0001	0.030749
KIM WT1 TARGETS 12HR DN	200	0.420401	1.775088	0.005859	0.030812
ELVIDGE HYPOXIA BY DMOG DN	54	0.470522	1.774423	0.00198	0.030926
HOFMANN CELL LYMPHOMA UP	46	0.496969	1.774181	0.013861	0.030936
PID PRL SIGNALING EVENTS PATHWAY	23	0.577818	1.774123	0.008081	0.030903
BURTON ADIPOGENESIS PEAK AT 8HR	39	0.514567	1.773794	0.011788	0.030946
LEE CALORIE RESTRICTION NEOCORTEX DN	83	0.448359	1.773617	0.004	0.030934
WOOD EBV EBNA1 TARGETS UP	109	0.444139	1.772703	0.007813	0.031136
SANA RESPONSE TO IFNG DN	81	0.539717	1.770497	0.02994	0.031672
GRYDER PAX3FOXO1 TOP ENHANCERS	429	0.391805	1.769585	0.005792	0.031878
DOANE RESPONSE TO ANDROGEN DN	225	0.374168	1.769289	0.004057	0.031899
MILI PSEUDOPODIA HAPTOTAXIS UP	483	0.490231	1.767013	0.035573	0.032574
YANG BREAST CANCER ESR1 BULK DN	22	0.600162	1.766521	0.012097	0.032696
MARKS HDAC TARGETS DN	15	0.645989	1.764346	0.007905	0.033314
SENESE HDAC2 TARGETS UP	107	0.510791	1.762015	0.008	0.033954
BERTUCCI MEDULLARY VS DUCTAL BREAST CANCER UP	187	0.4786	1.759066	0.012	0.034775
REACTOME METABOLISM OF AMINO ACIDS AND DERIVATIVES	190	0.452068	1.758336	0.003906	0.034934
CHOW RASSF1 TARGETS UP	26	0.550912	1.756591	0.019531	0.035417
TIEN INTESTINE PROBIOTICS 6HR DN	158	0.423269	1.756531	0.005859	0.035381
GOTZMANN EPITHELIAL TO MESENCHYMAL TRANSITION UP	68	0.502704	1.755146	0.009728	0.035729
GENTILE UV RESPONSE CLUSTER D8	39	0.544286	1.754054	0.007782	0.036011
GAZDA DIAMOND BLACKFAN ANEMIA PROGENITOR DN	62	0.500077	1.753804	0.021359	0.036039
KRIGE AMINO ACID DEPRIVATION	28	0.58437	1.752743	0.00996	0.036379
KORKOLA YOLK SAC TUMOR UP	19	0.712506	1.751459	0.002008	0.036778
SMID BREAST CANCER RELAPSE IN LUNG UP	20	0.615166	1.750559	0.014523	0.03699
LI DCP2 BOUND MRNA	84	0.57497	1.748359	0.024341	0.037639
POOLA INVASIVE BREAST CANCER UP	266	0.536473	1.747724	0.016529	0.037801
DITTMER PTHLH TARGETS DN	72	0.45498	1.746507	0.007634	0.03813
GHO ATF5 TARGETS DN	16	0.666415	1.746022	0.012048	0.03823
KANNAN TP53 TARGETS DN	21	0.567373	1.744341	0.015296	0.038718
KAMMINGA SENESCENCE	39	0.507797	1.744314	0.00566	0.038664
REACTOME SHC1 EVENTS IN EGFR SIGNALING	15	0.637711	1.743893	0.012	0.038756
APPIERTO RESPONSE TO FENRETINIDE DN	50	0.517017	1.743279	0.01751	0.038901
SESTO RESPONSE TO UV C0	105	0.50052	1.742575	0.018145	0.039076
BENPORATH OCT4 TARGETS	274	0.368796	1.739931	0.001812	0.039918

LEE LIVER CANCER MYC UP	51	0.470873	1.739784	0.015414	0.039899
BRACHAT RESPONSE TO METHOTREXATE DN	26	0.582968	1.738851	0.012685	0.040176
SENGUPTA NASOPHARYNGEAL CARCINOMA WITH LMP1 UP	375	0.426139	1.738469	0.009653	0.040256
GAJATE RESPONSE TO TRABECTEDIN DN	18	0.6074	1.738387	0.020561	0.040212
KORKOLA EMBRYONAL CARCINOMA UP	40	0.601107	1.738059	0.016194	0.040274
REACTOME ELONGATION ARREST AND RECOVERY	24	0.572259	1.735987	0.01006	0.040906
REACTOME RNA POL III TRANSCRIPTION	33	0.554543	1.733553	0.013752	0.041777
SCHAEFFER PROSTATE DEVELOPMENT 6HR DN	482	0.383077	1.732033	<0.0001	0.042289
LIN MELANOMA COPY NUMBER UP	67	0.486542	1.730511	0.009597	0.042759
SATO SILENCED BY METHYLATION IN PANCREATIC CANCER 2	44	0.474967	1.730449	0.006135	0.042709
QI HYPOXIA TARGETS OF HIF1A AND FOXA2	36	0.546909	1.730327	0.021113	0.042674
ZHANG PROLIFERATING VS QUIESCENT	49	0.525785	1.730162	0.017893	0.042681
GRUETZMANN PANCREATIC CANCER UP	345	0.430195	1.728057	0.021782	0.043409
LASTOWSKA NEUROBLASTOMA COPY NUMBER UP	163	0.480287	1.727695	0.02729	0.04348
FIRESTEIN CTNNB1 PATHWAY	32	0.499099	1.724517	0.011429	0.044587
ZHAN MULTIPLE MYELOMA CD2 DN	45	0.486427	1.722374	0.013619	0.045327
STANELLE E2F1 TARGETS	27	0.511908	1.722189	0.005941	0.045334
KEGG PURINE METABOLISM	152	0.402056	1.721215	0.011952	0.045629
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 17	171	0.544585	1.720928	0.038076	0.045644
REACTOME SIGNALING BY TGF BETA RECEPTOR COMPLEX	60	0.466368	1.719172	0.015209	0.046196
BIOCARTA RACCYCD PATHWAY	26	0.536303	1.718753	0.010225	0.046271
PID LIS1 PATHWAY	28	0.540751	1.718078	0.005882	0.046432
CHIBA RESPONSE TO TSA DN	22	0.61224	1.717668	0.017544	0.046521
SHETH LIVER CANCER VS TXNIP LOSS PAM1	221	0.376956	1.717094	0.005988	0.046678
REACTOME METABOLISM OF CARBOHYDRATES	228	0.384737	1.715996	0.001942	0.047008
BHAT ESR1 TARGETS VIA AKT1 UP	267	0.40108	1.715448	0.005952	0.04713
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 15	31	0.495448	1.714906	0.003891	0.047255
AMUNDSON GENOTOXIC SIGNATURE	99	0.39605	1.714298	0.003953	0.047393
PURBEY TARGETS OF CTBP1 AND SATB1 UP	76	0.433125	1.713874	0.009728	0.047484
BYSTRYKH HEMATOPOIESIS STEM CELL AND BRAIN QTL TRANS	175	0.363366	1.713847	0.00189	0.047416
KATSANOU ELAVL1 TARGETS DN	141	0.394473	1.712329	0.003839	0.047959
PANGAS TUMOR SUPPRESSION BY SMAD1 AND SMAD5 DN	142	0.375644	1.712208	0.001927	0.047945
REACTOME TRANSCRIPTION	188	0.532252	1.711974	0.019646	0.047948
HOLLEMAN PREDNISOLONE RESISTANCE B ALL UP	22	0.618822	1.709546	0.015625	0.048829
FERNANDEZ BOUND BY MYC	179	0.387946	1.708552	0.003922	0.049134
SMID BREAST CANCER RELAPSE IN BRAIN UP	39	0.519588	1.708133	0.014286	0.049214
REACTOME PURINE METABOLISM	33	0.523631	1.707014	0.016632	0.049544
ST FAS SIGNALING PATHWAY	63	0.423447	1.704573	0.00969	0.05047

GENTILE UV RESPONSE CLUSTER D7	36	0.481635	1.703185	0.009862	0.050886
BIOCARTA FAS PATHWAY	30	0.518229	1.702645	0.025743	0.051055
PARK HSC AND MULTIPOTENT PROGENITORS	49	0.472364	1.700611	0.017613	0.051796
WANG LMO4 TARGETS DN	326	0.403996	1.699818	0.008	0.052053
REACTOME MICRORNA MIRNA BIOGENESIS	18	0.599508	1.69786	0.00996	0.052754
REACTOME MRNA CAPPING	28	0.571118	1.69714	0.015656	0.052967
DACOSTA UV RESPONSE VIA ERCC3 UP	296	0.423056	1.697077	0.014028	0.052918
YIH RESPONSE TO ARSENITE C4	17	0.561024	1.696625	0.011928	0.053034
DAZARD RESPONSE TO UV SCC DN	119	0.436891	1.696215	0.014953	0.053111
GENTILE UV RESPONSE CLUSTER D1	18	0.557752	1.69553	0.013308	0.053341
REACTOME UNFOLDED PROTEIN RESPONSE	72	0.462362	1.694864	0.019724	0.053535
RAHMAN TP53 TARGETS PHOSPHORYLATED	21	0.683353	1.693765	0.014085	0.053913
KEGG CYSTEINE AND METHIONINE METABOLISM	33	0.523735	1.69293	0.012448	0.05419
AIYAR COBRA1 TARGETS DN	28	0.511169	1.689742	0.004202	0.055541
SCHLOSSER SERUM RESPONSE AUGMENTED BY MYC	101	0.439698	1.689432	0.009804	0.055586
DAZARD UV RESPONSE CLUSTER G6	142	0.489017	1.689368	0.021113	0.055542
STAMBOLSKY BOUND BY MUTATED TP53	17	0.56901	1.689014	0.023211	0.05559
CHEOK RESPONSE TO MERCAPTOPURINE AND HD MTX DN	21	0.533606	1.687393	0.004024	0.05622
PID FOXO PATHWAY	49	0.473654	1.686845	0.009416	0.056377
PID MTOR 4PATHWAY	69	0.429816	1.686695	0.005814	0.056354
BIOCARTA IGF1MTOR PATHWAY	20	0.563866	1.68625	0.021318	0.056472
REACTOME TELOMERE MAINTENANCE	72	0.69233	1.685215	0.021956	0.056833
SENESE HDAC3 TARGETS DN	481	0.342569	1.683217	0.001908	0.057708
REACTOME PROLONGED ERK ACTIVATION EVENTS	19	0.538816	1.682556	0.026585	0.057868
PID BETA CATENIN NUC PATHWAY	74	0.428941	1.68147	0.013514	0.058237
FLECHNER BIOPSY KIDNEY TRANSPLANT OK VS DONOR DN	25	0.500504	1.680263	0.007797	0.05867
ZHOU TNF SIGNALING 4HR	52	0.494397	1.678035	0.026263	0.059537
NGO MALIGNANT GLIOMA 1P LOH	15	0.708102	1.673685	0.007921	0.06137
HU ANGIOGENESIS DN	36	0.573714	1.673117	0.035644	0.06156
REACTOME ACTIVATION OF BH3 ONLY PROTEINS	16	0.597309	1.672686	0.021359	0.061684
NGUYEN NOTCH1 TARGETS DN	84	0.424852	1.66808	0.00789	0.063681
LIAO HAVE SOX4 BINDING SITES	40	0.469765	1.667305	0.020992	0.063968
REACTOME ARMS MEDIATED ACTIVATION	17	0.54707	1.667185	0.032258	0.06394
REACTOME RNA POL I TRANSCRIPTION TERMINATION	19	0.620481	1.666826	0.032075	0.064013
MARIADASON RESPONSE TO CURCUMIN SULINDAC 5	21	0.5335	1.665802	0.028846	0.064369
KEGG PENTOSE PHOSPHATE PATHWAY	25	0.570219	1.665735	0.026749	0.064303
AGUIRRE PANCREATIC CANCER COPY NUMBER UP	271	0.409028	1.665732	0.02549	0.064213
ZHAN V2 LATE DIFFERENTIATION GENES	42	0.51556	1.665591	0.02554	0.064194
BAKKER FOXO3 TARGETS DN	168	0.364676	1.663497	0.001992	0.065118
REACTOME PYRUVATE METABOLISM	18	0.5689	1.662712	0.019881	0.065384

JAERVINEN AMPLIFIED IN LARYNGEAL CANCER	37	0.499937	1.659458	0.021277	0.066918
WANG TUMOR INVASIVENESS DN	200	0.374759	1.657417	0.009747	0.067848
CEBALLOS TARGETS OF TP53 AND MYC DN	37	0.464507	1.657214	0.010438	0.067844
GALE APL WITH FLT3 MUTATED UP	53	0.465663	1.656576	0.013807	0.068089
GEISS RESPONSE TO DSRNA DN	15	0.585713	1.655231	0.021195	0.068673
KYNG ENVIRONMENTAL STRESS RESPONSE DN	19	0.533615	1.653428	0.028056	0.069474
LEI MYB TARGETS	309	0.398878	1.653195	0.017928	0.069514
ZHONG RESPONSE TO AZACITIDINE AND TSA DN	63	0.471926	1.652588	0.022814	0.069717
NAM FXYD5 TARGETS DN	18	0.597997	1.651976	0.034343	0.069894
SESTO RESPONSE TO UV C7	65	0.477195	1.651938	0.023438	0.069821
REACTOME REGULATORY RNA PATHWAYS	21	0.531662	1.650779	0.019685	0.07032
CHEN LUNG CANCER SURVIVAL	26	0.568831	1.650473	0.037109	0.070368
REACTOME SIGNALLING TO RAS	27	0.507797	1.650202	0.03	0.070403
BORLAK LIVER CANCER EGF UP	55	0.452076	1.6502	0.014228	0.070304
BROWNE HCMV INFECTION 18HR UP	171	0.396213	1.64936	0.017143	0.070634
MENSE HYPOXIA UP	93	0.450012	1.648499	0.032922	0.070966
KIM WT1 TARGETS 8HR DN	114	0.365123	1.646874	0.003937	0.071674
YAO TEMPORAL RESPONSE TO PROGESTERONE CLUSTER 7	72	0.451079	1.646841	0.019569	0.071588
BURTON ADIPOGENESIS 2	72	0.438126	1.646385	0.029412	0.071699
AMUNDSON POOR SURVIVAL AFTER GAMMA RADIATION 2G	161	0.361826	1.646234	0.005769	0.071669
BURTON ADIPOGENESIS 12	31	0.611127	1.64571	0.028	0.071817
BRUINS UVC RESPONSE EARLY LATE	292	0.339721	1.64524	0.003795	0.071917
BIOCARTA CASPASE PATHWAY	23	0.538726	1.64446	0.035928	0.072236
DARWICHE PAPILLOMA RISK LOW UP	149	0.398128	1.644139	0.010288	0.072318
POMEROY MEDULLOBLASTOMA DESMOPLASIC VS CLASSIC UP	58	0.407074	1.643405	0.005837	0.072511
CREIGHTON ENDOCRINE THERAPY RESISTANCE 4	278	0.347047	1.642436	0.002012	0.072976
KUMAR PATHOGEN LOAD BY MACROPHAGES	245	0.324788	1.640057	0.001938	0.074045
HELLER HDAC TARGETS DN	275	0.365715	1.64001	0.005929	0.073962
AMIT SERUM RESPONSE 480 MCF10A	34	0.552532	1.636711	0.033797	0.075511
AMUNDSON RESPONSE TO ARSENITE	211	0.34884	1.63541	0.007634	0.076051
FLECHNER PBL KIDNEY TRANSPLANT OK VS DONOR UP	145	0.385983	1.634868	0.021782	0.076204
DEBIASI APOPTOSIS BY REOVIRUS INFECTION UP	303	0.416946	1.634465	0.024194	0.076303
BIOCARTA MPR PATHWAY	33	0.507954	1.633851	0.026423	0.076506
YEGNASUBRAMANIAN PROSTATE CANCER	117	0.412479	1.633661	0.002066	0.076502
SMIRNOV RESPONSE TO IR 2HR DN	52	0.446206	1.63262	0.017408	0.076967
IVANOVA HEMATOPOIESIS LATE PROGENITOR	499	0.369651	1.632608	0.016327	0.076869
PID DELTA NP63 PATHWAY	45	0.4617	1.63256	0.023121	0.076782
KEGG PANCREATIC CANCER	69	0.418428	1.632359	0.010101	0.076793
JACKSON DNMT1 TARGETS UP	74	0.436081	1.631741	0.010204	0.077025
FARMER BREAST CANCER APOCRINE VS BASAL	316	0.35774	1.63033	0.002053	0.077661
FARMER BREAST CANCER CLUSTER 5	18	0.675713	1.625719	0.043977	0.080083

KOKKINAKIS METHIONINE DEPRIVATION 48HR UP	124	0.390954	1.6245	0.019305	0.080626
KAPOSI LIVER CANCER MET UP	17	0.599186	1.623897	0.041667	0.080847
SENESE HDAC1 TARGETS UP	425	0.403055	1.622724	0.023301	0.081412
LU EZH2 TARGETS DN	356	0.369337	1.622484	0.011407	0.081458
REACTOME ADAPTIVE IMMUNE SYSTEM	497	0.366093	1.622	0.016194	0.081652
DIRMEIER LMP1 RESPONSE LATE UP	55	0.474896	1.621838	0.038986	0.081638
BIOCARTA ACTINY PATHWAY	20	0.580583	1.620578	0.041502	0.082166
ZHENG IL22 SIGNALING DN	37	0.451594	1.619909	0.015595	0.082455
FLECHNER PBL KIDNEY TRANSPLANT REJECTED VS OK UP	62	0.4115	1.619786	0.011881	0.082414
MA MYELOID DIFFERENTIATION UP	38	0.460089	1.619698	0.031189	0.082364
KAYO AGING MUSCLE DN	118	0.413931	1.618078	0.040984	0.083196
ZHOU TNF SIGNALING 30MIN	51	0.499099	1.615697	0.045908	0.084461
BIOCARTA CHEMICAL PATHWAY	22	0.502849	1.615101	0.024742	0.08469
DARWICHE PAPILLOMA RISK HIGH UP	136	0.391127	1.614209	0.014	0.085031
REACTOME SMAD2 SMAD3 SMAD4 HETEROTRIMER REGULATES TRANSCRIPTION	25	0.51567	1.611986	0.019802	0.086053
AUNG GASTRIC CANCER	53	0.44126	1.611559	0.01417	0.086187
YAGI AML RELAPSE PROGNOSIS	34	0.490241	1.611135	0.034816	0.086352
JOHNSTONE PARVB TARGETS 2 DN	315	0.422626	1.610181	0.037182	0.086691
KIM MYCL1 AMPLIFICATION TARGETS DN	19	0.538227	1.606744	0.03876	0.088531
CHOI ATL STAGE PREDICTOR	38	0.501418	1.605912	0.048	0.088932
VANOEVELEN MYOGENESIS SIN3A TARGETS	209	0.355476	1.60589	0.007648	0.088826
RIZ ERYTHROID DIFFERENTIATION HBZ	40	0.452344	1.60548	0.019841	0.088966
HIRSCH CELLULAR TRANSFORMATION SIGNATURE DN	95	0.384764	1.604487	0.011583	0.089275
REACTOME DOWNREGULATION OF SMAD2 3 SMAD4 TRANSCRIPTIONAL ACTIVITY	19	0.55709	1.603846	0.036609	0.089289
GOLUB ALL VS AML UP	24	0.539396	1.603475	0.027668	0.089387
DEURIG T CELL PROLYMPHOCYTIC LEUKEMIA UP	340	0.334938	1.60289	0.001988	0.089634
LEE TARGETS OF PTCH1 AND SUFU UP	48	0.456557	1.602207	0.03006	0.089917
PID PI3KCI AKT PATHWAY	35	0.486655	1.602135	0.032323	0.089845
SEIDEN ONCOGENESIS BY MET	84	0.503572	1.600871	0.048387	0.090497
BILANGES SERUM SENSITIVE VIA TSC2	37	0.536964	1.600165	0.047259	0.090839
ALCALA APOPTOSIS	85	0.449618	1.597359	0.044534	0.092377
PID ILK PATHWAY	45	0.465464	1.596905	0.032389	0.092574
REACTOME SHC MEDIATED SIGNALLING	15	0.566816	1.595817	0.030426	0.0931
BIOCARTA MITOCHONDRIA PATHWAY	21	0.54933	1.594292	0.031056	0.09392
KYNG ENVIRONMENTAL STRESS RESPONSE NOT BY 4NQO IN WS	39	0.419614	1.5942	0.015842	0.093868
CAIRO HEPATOBLASTOMA POOR SURVIVAL	15	0.606056	1.59265	0.02988	0.094675
WANG RESPONSE TO FORSKOLIN UP	22	0.532073	1.592173	0.033663	0.094853
VERHAAK GLIOBLASTOMA PRONEURAL	167	0.44146	1.591357	0.02621	0.095217
BHAT ESR1 TARGETS NOT VIA AKT1 UP	204	0.370554	1.589123	0.014113	0.096474
BAKER HEMATOPOIESIS STAT3 TARGETS	16	0.570944	1.588886	0.024809	0.096491
BENPORATH NOS TARGETS	167	0.359405	1.587503	0.009225	0.097254
HOLLMANN APOPTOSIS VIA CD40 UP	189	0.367514	1.586191	0.010438	0.097944

REACTOME GRB2 EVENTS IN ERBB2 SIGNALING	22	0.503936	1.585609	0.027833	0.098181
REACTOME PYRIMIDINE METABOLISM	23	0.521913	1.584481	0.037549	0.09884
WANG ADIPOGENIC GENES REPRESSED BY SIRT1	26	0.548806	1.58247	0.039526	0.100008
BIOCARTA ARF PATHWAY	17	0.532239	1.582089	0.049808	0.100119
HU GENOTOXIC DAMAGE 24HR	32	0.506298	1.581691	0.046653	0.10025
KYNG DNA DAMAGE BY 4NQO OR UV	63	0.394732	1.581533	0.009881	0.100238
DOANE BREAST CANCER ESR1 DN	47	0.477376	1.581199	0.028747	0.100211
REACTOME SHC RELATED EVENTS	17	0.542609	1.580058	0.032129	0.100837
KRIEG HYPOXIA VIA KDM3A	50	0.470908	1.579343	0.044807	0.101024
WU HBX TARGETS 2 UP	22	0.516771	1.578107	0.035433	0.101707
RICKMAN TUMOR DIFFERENTIATED MODERATELY VS POORLY UP	114	0.379773	1.577521	0.026369	0.101961
REACTOME ABORTIVE ELONGATION OF HIV1 TRANSCRIPT IN THE ABSENCE OF TAT	19	0.575448	1.575224	0.040816	0.103384
MARTORIATI MDM4 TARGETS FETAL LIVER DN	495	0.369638	1.574268	0.020992	0.10396
OUYANG PROSTATE CANCER MARKERS	19	0.516968	1.574154	0.045726	0.103916
ZEMBUTSU SENSITIVITY TO METHOTREXATE	16	0.53489	1.573963	0.024482	0.103897
GRESHOCK CANCER COPY NUMBER UP	313	0.360443	1.57383	0.011561	0.103879
SIG PIP3 SIGNALING IN CARDIAC MYOCTES	66	0.400808	1.573734	0.031873	0.103818
KEGG BLADDER CANCER	40	0.426503	1.573104	0.015873	0.104107
REACTOME SHC1 EVENTS IN ERBB4 SIGNALING	20	0.510957	1.57302	0.022901	0.104028
GROSS HIF1A TARGETS DN	23	0.552367	1.572917	0.039749	0.103973
WEI MIR34A TARGETS	141	0.366197	1.572348	0.022901	0.104227
TAKAO RESPONSE TO UVB RADIATION DN	95	0.416768	1.571543	0.036329	0.104627
HOLLEMAN PREDNISOLONE RESISTANCE ALL UP	19	0.56107	1.570808	0.046748	0.104985
KYNG WERNER SYNDROM AND NORMAL AGING UP	87	0.375606	1.568077	0.009728	0.106292
JIANG AGING CEREBRAL CORTEX DN	53	0.438811	1.565642	0.031185	0.107457
CEBALLOS TARGETS OF TP53 AND MYC UP	21	0.508984	1.564147	0.027184	0.107872
SEMENZA HIF1 TARGETS	35	0.524358	1.563799	0.04829	0.10799
SWEET KRAS TARGETS DN	61	0.412861	1.563619	0.020534	0.107964
BOYAULT LIVER CANCER SUBCLASS G2	27	0.47087	1.56339	0.027027	0.108013
REACTOME RNA POL III TRANSCRIPTION INITIATION FROM TYPE 2 PROMOTER	23	0.539026	1.563213	0.047525	0.108015
KYNG RESPONSE TO H2O2 VIA ERCC6 DN	44	0.441741	1.561874	0.037624	0.108848
JACKSON DNMT1 TARGETS DN	24	0.545188	1.561622	0.039033	0.10889
STONER ESOPHAGEAL CARCINOGENESIS UP	36	0.457234	1.561434	0.04817	0.108752
SMITH LIVER CANCER	43	0.498756	1.561043	0.041152	0.108909
SANSOM WNT PATHWAY REQUIRE MYC	57	0.422715	1.560403	0.028846	0.109191
MOOTHA GLUCONEOGENESIS	31	0.496544	1.558225	0.041916	0.110478
CHENG IMPRINTED BY ESTRADIOL	100	0.361582	1.557951	0.014463	0.110533
GARGALOVIC RESPONSE TO OXIDIZED PHOSPHOLIPIDS GREEN DN	22	0.499176	1.551441	0.023576	0.114696
TERAO AOX4 TARGETS SKIN UP	35	0.451873	1.550985	0.028112	0.114862
BROWNE HCMV INFECTION 24HR UP	139	0.352274	1.550466	0.014493	0.115131
REACTOME MHC CLASS II ANTIGEN PRESENTATION	87	0.39917	1.549929	0.037773	0.115366

SHETH LIVER CANCER VS TXNIP LOSS PAM3	67	0.403894	1.549401	0.027613	0.115624
SHIPP DLBCL CURED VS FATAL DN	42	0.407602	1.547219	0.015905	0.11693
ROESSLER LIVER CANCER METASTASIS UP	102	0.35375	1.546567	0.00616	0.116987
JIANG HYPOXIA CANCER	76	0.434074	1.545477	0.042	0.117314
SHETH LIVER CANCER VS TXNIP LOSS PAM2	144	0.34491	1.539279	0.032454	0.121628
HOFFMANN IMMATURE TO MATURE B LYMPHOCYTE DN	50	0.433968	1.539225	0.036017	0.121518
PID NOTCH PATHWAY	58	0.408909	1.538972	0.017241	0.121559
GALLUZZI PERMEABILIZE MITOCHONDRIA	43	0.427044	1.538971	0.038536	0.121418
PID ATF2 PATHWAY	58	0.410909	1.53888	0.026316	0.121342
NOUZOVA TRETINOIN AND H4 ACETYLATION	130	0.3784	1.53758	0.031128	0.122224
CHNG MULTIPLE MYELOMA HYPERPLOID DN	28	0.529976	1.535975	0.049485	0.123068
PID LKB1 PATHWAY	46	0.418381	1.535684	0.044316	0.12314
MARTIN INTERACT WITH HDAC	43	0.410289	1.533477	0.026365	0.12449
WEST ADRENOCORTICAL CARCINOMA VS ADENOMA UP	18	0.515806	1.531735	0.049213	0.125589
KOYAMA SEMA3B TARGETS DN	370	0.314341	1.531156	0.005882	0.125873
HAHTOLA MYCOSIS FUNGOIDES CD4 DN	109	0.386874	1.531013	0.044574	0.125692
BECKER TAMOXIFEN RESISTANCE DN	50	0.430428	1.53085	0.028846	0.125657
RICKMAN TUMOR DIFFERENTIATED WELL VS MODERATELY DN	107	0.466784	1.52963	0.047817	0.126294
BAE BRCA1 TARGETS DN	32	0.433241	1.528747	0.042308	0.126765
DACOSTA UV RESPONSE VIA ERCC3 COMMON UP	70	0.387219	1.5286	0.029528	0.126712
FLECHNER PBL KIDNEY TRANSPLANT REJECTED VS OK DN	50	0.417441	1.527244	0.035225	0.127564
BIOCARTA CARM ER PATHWAY	35	0.442014	1.526328	0.030948	0.127953
PURBEY TARGETS OF CTBP1 AND SATB1 DN	174	0.328326	1.525377	0.01006	0.12847
FORTSCHEGGER PHF8 TARGETS UP	248	0.335887	1.523701	0.026923	0.129436
WINTER HYPOXIA METAGENE	229	0.381003	1.522935	0.045082	0.129756
REACTOME SIGNALLING TO ERKS	35	0.431755	1.521357	0.038618	0.130815
CHEN HOXA5 TARGETS 9HR DN	36	0.448273	1.520952	0.048733	0.130995
IWANAGA CARCINOGENESIS BY KRAS PTEN UP	163	0.329468	1.519181	0.011494	0.131768
MULLIGHAN NPM1 MUTATED SIGNATURE 2 UP	127	0.356497	1.519016	0.028112	0.131765
PID CDC42 PATHWAY	69	0.400509	1.514054	0.045276	0.134319
BIOCARTA VEGF PATHWAY	29	0.458892	1.512633	0.036965	0.134938
KUNINGER IGF1 VS PDGFB TARGETS DN	43	0.432276	1.510486	0.046784	0.136213
PID HDAC CLASSI PATHWAY	65	0.392029	1.508864	0.032381	0.13671
TSAI RESPONSE TO IONIZING RADIATION	144	0.364818	1.505166	0.046784	0.13902
YANG BREAST CANCER ESR1 DN	24	0.472833	1.504519	0.031873	0.13937
LINSLEY MIR16 TARGETS	190	0.341199	1.503248	0.045098	0.139914
SHEPARD BMYB MORPHOLINO UP	201	0.331275	1.501624	0.012024	0.140947
REACTOME BASIGIN INTERACTIONS	24	0.479126	1.501503	0.037182	0.140895
OUILLETTE CLL 13Q14 DELETION UP	69	0.395825	1.500209	0.033962	0.141724
QI HYPOXIA	136	0.356963	1.4983	0.03252	0.14278
JIANG TIP30 TARGETS UP	44	0.424957	1.495697	0.048356	0.144561
GRAESSMANN RESPONSE TO MC AND SERUM DEPRIVATION DN	78	0.363386	1.493716	0.018036	0.145737
YOSHIMURA MAPK8 TARGETS DN	350	0.324904	1.484714	0.014028	0.151977

POS HISTAMINE RESPONSE NETWORK	32	0.442072	1.48223	0.042802	0.153474
PID CASPASE PATHWAY	51	0.384227	1.47734	0.043651	0.156388
HOFFMANN SMALL PRE BII TO IMMATURE B LYMPHOCYTE DN	45	0.372562	1.473417	0.041502	0.158456
HOFFMANN PRE BI TO LARGE PRE BII LYMPHOCYTE UP	35	0.396877	1.472927	0.039761	0.158727
PID P53 DOWNSTREAM PATHWAY	133	0.334232	1.466732	0.042169	0.162927
WANG CLIM2 TARGETS UP	217	0.315482	1.465924	0.028195	0.163489
DARWICHE SKIN TUMOR PROMOTER UP	127	0.349238	1.456778	0.040161	0.168139
STAMBOLSKY TARGETS OF MUTATED TP53 UP	46	0.400182	1.455109	0.048638	0.168721
MULLIGHAN NPM1 SIGNATURE 3 UP	311	0.296923	1.453482	0.028958	0.170023
LIU COMMON CANCER GENES	67	0.362628	1.452871	0.046729	0.170426
ROSS AML OF FAB M7 TYPE	64	0.373503	1.451377	0.036437	0.171608
GRYDER PAX3FOXO1 ENHANCERS KO DOWN	426	0.320877	1.451109	0.046296	0.171667
RIZKI TUMOR INVASIVENESS 3D DN	259	0.297978	1.450605	0.009785	0.171602
RAO BOUND BY SALL4 ISOFORM B	480	0.299963	1.44362	0.032692	0.177022
PENG LEUCINE DEPRIVATION UP	134	0.322544	1.437752	0.035225	0.181856
GARY CD5 TARGETS UP	444	0.29384	1.436339	0.034836	0.182804
BROWNE HCMV INFECTION 30MIN DN	136	0.317756	1.43474	0.027397	0.18395
WANG LMO4 TARGETS UP	330	0.302702	1.432158	0.042636	0.185472
BILANGES SERUM SENSITIVE GENES	86	0.32838	1.417551	0.045635	0.196246
FIGUEROA AML METHYLATION CLUSTER 4 UP	97	0.316713	1.411657	0.037849	0.201317
KYNG WERNER SYNDROM AND NORMAL AGING DN	211	0.295641	1.404526	0.018036	0.207186
LEE CALORIE RESTRICTION NEOCORTEX UP	81	0.333622	1.400835	0.039216	0.209193
BROWNE HCMV INFECTION 20HR UP	230	0.303127	1.391798	0.043393	0.215266
OKUMURA INFLAMMATORY RESPONSE LPS	171	0.304923	1.387206	0.035088	0.217712
BROWNE HCMV INFECTION 1HR DN	208	0.277264	1.386098	0.013861	0.218114
TANAKA METHYLATED IN ESOPHAGEAL CARCINOMA	97	0.332809	1.376805	0.04023	0.223842
BROWNE HCMV INFECTION 4HR DN	241	0.270784	1.374737	0.027944	0.225098

ES, enrichment score; NES, normalized enrichment score; FDR, false discovery rate; GSEA, gene set enrichment analysis; KIF, kinesin.