```
# Supplementary Note 3
# Names and sizes of founder gene sets, grouped by clusters
# Total number of clusters in this report: 163
# Total number of founder sets in this report: 3274
################################################################################

cluster ID = 2
cluster size = 7
      gene set name    size (number of genes in the set)
1     chr16q24   123
2     NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON   53
3     GRATIAS_RETINOBLASTOMA_16Q24 17
4     KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER_CORR_DN    36
5     KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DENSITY_CORR_DN     88
6     KIM_ALL_DISORDERS_CALB1_CORR_DN   37
7     KIM_ALL_DISORDERS_DURATION_CORR_UP 9


cluster ID = 5
cluster size = 10
      gene set name    size (number of genes in the set)
1     chr7p21    57
2     KONDO_HYPOXIA    8
3     GROSS_HYPOXIA_VIA_ELK3_ONLY_UP    33
4     SHIN_B_CELL_LYMPHOMA_CLUSTER_5    18
5     WU_HBX_TARGETS_2_DN    16
6     WU_HBX_TARGETS_1_DN    23
7     WU_HBX_TARGETS_3_DN    13
8     CHEN_ETV5_TARGETS_SERTOLI    20
9     WU_HBX_TARGETS_1_UP    16
10    WU_HBX_TARGETS_2_UP    23


cluster ID = 11
cluster size = 14
      gene set name    size (number of genes in the set)
1     chr4q12    57
2     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_DN     16
3     GRAHAM_CML_QUIESCENT_VS_CML_DIVIDING_DN 11
4     GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_UP     13
5     NAKAJIMA_EOSINOPHIL    30
6     HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_DN  20
7     HOFMANN_MYELODYSPLASTIC_SYNDROM_RISK_DN 23
8     IRITANI_MAD1_TARGETS_UP     13
9     GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_2   13
10    KASLER_HDAC7_TARGETS_2_UP    6
11    SCHMIDT_POR_TARGETS_IN_LIMB_BUD_DN 8
12    GENTLES_LEUKEMIC_STEM_CELL_DN     19
13    MODULE_470  16
14    MODULE_557  11


cluster ID = 13
cluster size = 10
      gene set name    size (number of genes in the set)
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1     chr2p22     56
2     chr4p11     9
3     DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN      20
4     DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_DN     68
5     DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_DN      15
6     DASU_IL6_SIGNALING_SCAR_UP   30
7     GENTILE_UV_RESPONSE_CLUSTER_D5    39
8     MATZUK_MATERNAL_EFFECT 9
9     DASU_IL6_SIGNALING_UP  59
10    WANG_METASTASIS_OF_BREAST_CANCER_ESR1_DN      30


cluster ID = 15
cluster size = 6
      gene set name    size (number of genes in the set)
1     chr8p11     55
2     chr8p12     50
3     chr3q27     83
4     JAERVINEN_AMPLIFIED_IN_LARYNGEAL_CANCER 40
5     NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON      57
6     DING_LUNG_CANCER_EXPRESSION_BY_COPY_NUMBER    100


cluster ID = 19
cluster size = 22
      gene set name    size (number of genes in the set)
1     chr7p13     54
2
      REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_IGF_ACTIVITY_BY_INSULIN_
LIKE_GROWTH_FACTOR_BINDING_PROTEINS_IGFBPS    16
3     BERENJENO_TRANSFORMED_BY_RHOA_REVERSIBLY_DN   29
4     TSUNODA_CISPLATIN_RESISTANCE_UP    15
5     FRIDMAN_SENESCENCE_UP  77
6     FRIDMAN_IMMORTALIZATION_DN   34
7     HALMOS_CEBPA_TARGETS_DN      46
8     GERHOLD_ADIPOGENESIS_DN      64
9     PAL_PRMT5_TARGETS_DN   29
10    VERRECCHIA_RESPONSE_TO_TGFB1_C3    14
11    WANG_LSD1_TARGETS_UP   24
12    MASRI_RESISTANCE_TO_TAMOXIFEN_AND_AROMATASE_INHIBITORS_DN20
13    LABBE_WNT3A_TARGETS_UP 112
14    LABBE_TGFB1_TARGETS_UP 102
15    LABBE_TARGETS_OF_TGFB1_AND_WNT3A_UP     111
16    JIANG_TIP30_TARGETS_UP 46
17    LIU_VAV3_PROSTATE_CARCINOGENESIS_DN     17
18    BOYAULT_LIVER_CANCER_SUBCLASS_G56_DN    17
19    COULOUARN_TEMPORAL_TGFB1_SIGNATURE_UP   109
20    MODULE_190  12
21    MODULE_474  17
22    CORDENONSI_YAP_CONSERVED_SIGNATURE 57


cluster ID = 21
cluster size = 6
      gene set name    size (number of genes in the set)
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1     chr8q22     102
2     chr8q12     57
3     chr8q21     94
4     chr8q13     56
5     NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON      132
6     NIKOLSKY_MUTATED_AND_AMPLIFIED_IN_BREAST_CANCER     94


cluster ID = 23
cluster size = 6
      gene set name    size (number of genes in the set)
1     chryp11     82
2     chryq11     204
3     RUNNE_GENDER_EFFECT_UP 9
4     RICKMAN_HEAD_AND_NECK_CANCER_B     48
5     LEE_NAIVE_T_LYMPHOCYTE 19
6     PYEON_CANCER_HEAD_AND_NECK_VS_CERVICAL_DN     29


cluster ID = 31
cluster size = 6
      gene set name    size (number of genes in the set)
1     chr2q22     27
2     chr2p 11
3     chr4q33     12
4     REACTOME_TRYPTOPHAN_CATABOLISM     11
5     FREDERICK_PRKCI_TARGETS      10
6     BERNARD_PPAPDC1B_TARGETS_UP  40


cluster ID = 32
cluster size = 10
      gene set name    size (number of genes in the set)
1     chr9q33     82
2     chr9q22     133
3     chr9q32     45
4     chr9q34     267
5     chr9q21     92
6     chr9q31     80
7     LINDGREN_BLADDER_CANCER_CLUSTER_1_UP    121
8     LINDGREN_BLADDER_CANCER_CLUSTER_2A_DN   141
9     LINDGREN_BLADDER_CANCER_WITH_LOH_IN_CHR9Q     116
10    MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_8    18


cluster ID = 34
cluster size = 6
      gene set name    size (number of genes in the set)
1     chr3q28     25
2     LUND_SILENCED_BY_METHYLATION 16
3     SHIPP_DLBCL_VS_FOLLICULAR_LYMPHOMA_DN   45
4     BUCKANOVICH_T_LYMPHOCYTE_HOMING_ON_TUMOR_DN   24
5     BOYAULT_LIVER_CANCER_SUBCLASS_G6_DN     19
6     CCAATNNSNNNGCG_UNKNOWN 59
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cluster ID = 38
cluster size = 6
      gene set name    size (number of genes in the set)
1     chr6p11    13
2     GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_UP      30
3     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_UP   23
4     STREICHER_LSM1_TARGETS_DN    19
5     GALI_TP53_TARGETS_APOPTOTIC_DN     6
6     NOUSHMEHR_GBM_SOMATIC_MUTATED      9


cluster ID = 43
cluster size = 7
      gene set name    size (number of genes in the set)
1     chr22q     6
2     ABDULRAHMAN_KIDNEY_CANCER_VHL_DN   14
3     PALOMERO_GSI_SENSITIVITY_DN  6
4     KYNG_NORMAL_AGING_UP   19
5     KYNG_NORMAL_AGING_DN   30
6     KYNG_WERNER_SYNDROM_UP 20
7     KYNG_WERNER_SYNDROM_DN 29


cluster ID = 48
cluster size = 15
      gene set name    size (number of genes in the set)
1     chr7p 6
2     chr5q15    32
3     KEGG_RENIN_ANGIOTENSIN_SYSTEM      17
4     HAEGERSTRAND_RESPONSE_TO_IMATINIB  9
5     YAMASHITA_SILENCED_BY_METHYLATION  7
6     YAMASHITA_METHYLATED_IN_PROSTATE_CANCER 57
7     NICK_RESPONSE_TO_PROC_TREATMENT_DN 27
8     ZHAN_VARIABLE_EARLY_DIFFERENTIATION_GENES_UP  15
9     MODULE_402  12
10    MODULE_492  17
11    REGULATION_OF_BLOOD_PRESSURE 22
12    EXOPEPTIDASE_ACTIVITY  32
13    METALLOEXOPEPTIDASE_ACTIVITY 13
14    CARBOXYPEPTIDASE_ACTIVITY    12
15    AMINOPEPTIDASE_ACTIVITY      14


cluster ID = 51
cluster size = 18
      gene set name    size (number of genes in the set)
1     chr16q22   168
2     chr16q23   47
3     KEGG_AMINOACYL_TRNA_BIOSYNTHESIS   41
4     REACTOME_MITOCHONDRIAL_TRNA_AMINOACYLATION    21
5     REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION  24
6     REACTOME_TRNA_AMINOACYLATION 42
7     MAYBURD_RESPONSE_TO_L663536_UP    29
8     PROVENZANI_METASTASIS_UP     194
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9     TOMIDA_METASTASIS_DN   18
10    CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_UP 51
11    MODULE_35   16
12    MODULE_110  16
13    MODULE_133  15
14    MODULE_160  15
15    MODULE_322  59
16    TRNA_PROCESSING  10
17    TRNA_METABOLIC_PROCESS 19
18    LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS   14


cluster ID = 52
cluster size = 6
      gene set name    size (number of genes in the set)
1     chr11q24   122
2     LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_UP    44
3     LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_LARGE_VS_TINY_DN    45
4     LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_UP    38
5     LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_SMALL_VS_HUGE_DN    33
6     LIANG_HEMATOPOIESIS_STEM_CELL_NUMBER_QTL      17


cluster ID = 55
cluster size = 9
      gene set name    size (number of genes in the set)
1     chr5q21    48
2     TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_DN 7
3     LIU_CMYB_TARGETS_DN    7
4     SILIGAN_TARGETS_OF_EWS_FLI1_FUSION_UP   15
5     VETTER_TARGETS_OF_PRKCA_AND_ETS1_UP     16
6     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_3    5
7     YANAGIHARA_ESX1_TARGETS      30
8     KIM_MYCL1_AMPLIFICATION_TARGETS_UP 13
9     YIH_RESPONSE_TO_ARSENITE_C2  18


cluster ID = 58
cluster size = 548
      gene set name    size (number of genes in the set)
1     chr1p35    116
2     chr1p34    195
3     chr1p36    504
4     LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_DN  800
5     SERVITJA_ISLET_HNF1A_TARGETS_DN   109
6     AAANWWTGC_UNKNOWN 193
7     AAAYRNCTG_UNKNOWN 374
8     V$MYOD_01   265
9     V$E47_01    253
10    V$CMYB_01   249
11    V$AP4_01    262
12    AACTTT_UNKNOWN    1890
13    V$MEF2_01   144
14    V$ELK1_01   269
15    V$SP1_01    237
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16	V$EVI1_06	22
17	V$ATF_01	259
18	V$ELK1_02	248
19	V$RSRFC4_01	245
20	V$CETS1P54_01	258
21	AACWWCAANK_UNKNOWN	142
22	V$P300_01	249
23	V$NFE2_01	272
24	V$CREB_01	262
25	V$CREBP1_01	179
26	V$CREBP1CJUN_01	259
27	V$SOX5_01	265
28	V$E4BP4_01	223
29	V$NFKAPPAB65_01	237
30	V$CREL_01	256
31	AACYNNNNTTCCS_UNKNOWN	95
32	V$NFKAPPAB_01	251
33	V$NMYC_01	271
34	V$MYOGNF1_01	48
35	V$COMP1_01	115
36	V$HEN1_02	198
37	V$YY1_01	246
38	V$IRF1_01	250
39	V$IRF2_01	125
40	V$TAL1BETAE47_01	248
41	V$TAL1ALPHAE47_01	252
42	AAGWWRNYGGC_UNKNOWN	119
43	V$HEN1_01	196
44	V$YY1_02	242
45	V$TAL1BETAITF2_01	256
46	V$E47_02	250
47	V$CP2_01	260
48	V$GATA1_01	244
49	V$GATA2_01	104
50	V$GATA3_01	242
51	V$EVI1_01	16
52	V$EVI1_02	132
53	ACAWNRNSRCGG_UNKNOWN	63
54	V$EVI1_03	57
55	V$EVI1_04	238
56	V$EVI1_05	172
57	V$MZF1_01	236
58	V$MZF1_02	232
59	V$ZID_01	259
60	V$IK1_01	278
61	V$IK2_01	267
62	V$IK3_01	225
63	V$CDP_01	92
64	ACAWYAAAG_UNKNOWN	103
65	V$PBX1_01	252
66	V$PAX6_01	101
67	V$PAX2_01	58
68	V$S8_01	245
69	V$CDP_02	108
70	V$CDPCR1_01	130

71	V$CDPCR3HD_01	236
72	V$NRF2_01	270
73	V$CEBPB_01	262
74	ACCTGTTG_UNKNOWN	154
75	V$CREB_02	254
76	V$TAXCREB_01	137
77	V$CEBPA_01	244
78	V$CEBPB_02	258
79	V$MYCMAX_01	255
80	V$MAX_01	262
81	V$USF_01	256
82	V$USF_02	272
83	V$MYCMAX_02	268
84	ACTAYRNNNCCCR_UNKNOWN	449
85	V$PBX1_02	128
86	V$GATA1_02	244
87	V$GATA1_03	245
88	V$GATA1_04	245
89	V$HFH1_01	243
90	V$FOXD3_01	199
91	V$HNF3B_01	221
92	V$HNF1_01	245
93	V$TST1_01	262
94	V$HNF4_01	269
95	ACTWSNACTNY_UNKNOWN	103
96	V$OCT1_01	266
97	V$OCT1_02	214
98	V$OCT1_03	230
99	V$OCT1_04	241
100	V$LYF1_01	264
101	V$PAX5_01	154
102	V$BRN2_01	237
103	V$HSF1_01	267
104	AGCYRWTTC_UNKNOWN	122
105	V$HSF2_01	250
106	V$SRY_01	224
107	V$SRF_01	50
108	V$ARP1_01	165
109	V$RORA1_01	242
110	V$RORA2_01	151
111	V$COUP_01	263
112	V$CEBP_01	272
113	V$SRY_02	255
114	V$OCT1_05	254
115	ARGGGTTAA_UNKNOWN	121
116	V$OCT1_06	266
117	V$AP1FJ_Q2	268
118	V$AP1_Q2	265
119	V$AP1_Q6	259
120	V$AP4_Q5	273
121	V$AP4_Q6	226
122	V$CREB_Q2	263
123	V$CREB_Q4	268
124	V$CREBP1_Q2	254
125	V$MYB_Q6	255

126	V$MYOD_Q6	245
127	V$NFY_Q6	262
128	V$SRF_Q6	241
129	V$USF_Q6	259
130	V$AP1_Q4	271
131	V$AP2_Q6	258
132	V$CEBP_Q2	234
133	V$ER_Q6	276
134	V$GR_Q6	271
135	V$NF1_Q6	261
136	ATGGYGGA_UNKNOWN	102
137	V$NFKB_Q6	254
138	V$OCT1_Q6	270
139	V$SP1_Q6	256
140	V$AP1_C	275
141	V$CEBP_C	200
142	V$GATA_C	266
143	V$GRE_C	126
144	V$HNF1_C	243
145	V$NFKB_C	263
146	V$NFY_C	245
147	V$OCT_C	268
148	V$SRF_C	211
149	V$TATA_C	283
150	V$USF_C	279
151	V$SREBP1_01	168
152	V$SREBP1_02	88
153	V$HAND1E47_01	277
154	V$STAT_01	253
155	V$STAT1_01	68
156	V$STAT3_01	22
157	V$MEF2_02	228
158	V$MEF2_03	238
159	V$AHRARNT_01	140
160	V$ARNT_01	261
161	V$NKX25_01	125
162	V$NKX25_02	262
163	V$PPARA_01	37
164	CATRRAGC_UNKNOWN	138
165	V$EGR1_01	269
166	V$NGFIC_01	255
167	V$EGR3_01	86
168	V$EGR2_01	199
169	V$OCT1_07	162
170	V$CHOP_01	238
171	V$GFI1_01	262
172	V$XBP1_01	133
173	V$TATA_01	255
174	V$RREB1_01	207
175	V$ISRE_01	247
176	V$HLF_01	254
177	V$OLF1_01	272
178	V$AML1_01	263
179	V$P53_02	254
180	V$LMO2COM_01	264

181	V$LMO2COM_02	246
182	V$TCF11MAFG_01	207
183	V$TCF11_01	253
184	V$NFY_01	254
185	V$HFH3_01	191
186	V$FREAC2_01	260
187	V$FREAC3_01	251
188	V$FREAC4_01	150
189	V$FREAC7_01	195
190	V$HFH8_01	203
191	CCAWNWWNNNGGC_UNKNOWN	84
192	V$NFAT_Q6	246
193	V$MYCMAX_B	268
194	V$PAX3_B	90
195	V$PAX8_B	106
196	V$WHN_B	254
197	V$ZF5_B	239
198	V$ATF_B	187
199	V$ETS1_B	259
200	V$ETS2_B	274
201	V$GABP_B	259
202	CCAWYNNGAAR_UNKNOWN	145
203	V$OCT1_B	267
204	V$GATA1_05	283
205	V$PAX4_01	262
206	V$PAX4_02	237
207	V$PAX4_03	253
208	V$PAX4_04	218
209	V$MSX1_01	174
210	V$EN1_01	109
211	CCCNNNNNNAAGWT_UNKNOWN	102
212	V$AMEF2_Q6	259
213	V$MMEF2_Q6	272
214	V$HMEF2_Q6	138
215	V$RSRFC4_Q2	214
216	V$SOX9_B1	237
217	V$HNF4_01_B	253
218	V$AREB6_01	271
219	V$AREB6_02	254
220	V$AREB6_03	258
221	V$AREB6_04	252
222	CCGNMNNTNACG_UNKNOWN	77
223	V$CART1_01	226
224	V$TGIF_01	247
225	V$MEIS1_01	239
226	V$MEIS1AHOXA9_01	117
227	V$MEIS1BHOXA9_01	145
228	V$FOXJ2_01	184
229	V$FOXJ2_02	237
230	V$NKX61_01	236
231	CCTNTMAGA_UNKNOWN	127
232	V$TITF1_Q3	239
233	V$IPF1_Q4	260
234	V$CHX10_01	225
235	V$VDR_Q3	225

236	V$SPZ1_01	231
237	V$AR_Q2	125
238	V$ZIC1_01	261
239	V$ZIC2_01	247
240	V$ZIC3_01	255
241	V$NKX3A_01	237
242	V$IRF7_01	252
243	V$FAC1_01	222
244	V$STAT5A_01	251
245	V$STAT5B_01	247
246	V$STAT5A_02	141
247	V$GATA6_01	265
248	V$POU3F2_01	100
249	V$POU3F2_02	260
250	V$POU6F1_01	240
251	V$HIF1_Q5	244
252	V$AP2REP_01	178
253	V$AP2ALPHA_01	241
254	V$AP2GAMMA_01	250
255	V$TBP_01	245
256	CTCNANGTGNY_UNKNOWN	91
257	V$FOXO4_01	243
258	V$FOXO1_01	245
259	V$FOXO1_02	240
260	V$FOXO4_02	255
261	V$FOXO3_01	245
262	V$CDC5_01	256
263	V$AR_01	157
264	V$PITX2_Q2	255
265	V$ATF6_01	123
266	V$NCX_01	171
267	CTGCAGY_UNKNOWN	765
268	V$NKX22_01	190
269	V$PAX2_02	258
270	V$NKX62_Q2	241
271	V$BACH2_01	271
272	V$MAZR_01	220
273	V$STAT1_02	252
274	V$STAT5A_03	265
275	V$STAT6_01	264
276	V$BACH1_01	263
277	V$STAT1_03	248
278	CTGRYYYNATT_UNKNOWN	72
279	V$STAT3_02	147
280	V$STAT4_01	266
281	V$STAT5A_04	213
282	V$STAT6_02	258
283	V$LHX3_01	224
284	V$ERR1_Q2	259
285	V$PPARG_01	46
286	V$ATF3_Q6	248
287	V$ATF4_Q2	258
288	CTGYNNCTYTAA_UNKNOWN	84
289	V$AP1_01	267
290	V$PPARA_02	129

291	V$GNCF_01	78
292	V$NERF_Q2	247
293	V$RP58_01	207
294	V$HTF_01	72
295	V$ARNT_02	248
296	V$MYCMAX_03	252
297	V$AFP1_Q6	264
298	CTTTAAR_UNKNOWN	972
299	V$CEBPDELTA_Q6	240
300	V$CEBPGAMMA_Q6	257
301	V$CRX_Q4	269
302	V$DBP_Q6	257
303	V$FOXM1_01	246
304	V$FXR_Q3	116
305	V$GATA4_Q3	249
306	V$GCM_Q2	242
307	V$HNF4ALPHA_Q6	271
308	V$HNF6_Q6	234
309	V$HOXA4_Q2	267
310	V$HSF_Q6	201
311	V$LBP1_Q6	224
312	V$LFA1_Q6	246
313	V$LXR_Q3	77
314	V$MAF_Q6	259
315	V$MAZ_Q6	193
316	V$MTF1_Q4	252
317	V$NFMUE1_Q6	245
318	GAANYNYGACNY_UNKNOWN	75
319	V$NRF1_Q6	252
320	V$PEA3_Q6	255
321	V$PTF1BETA_Q6	244
322	V$PU1_Q6	234
323	V$SP3_Q3	245
324	V$TCF1P_Q6	266
325	V$TCF4_Q5	242
326	V$TEF_Q6	255
327	V$TEL2_Q6	233
328	V$ALPHACP1_01	260
329	GATGKMRGCG_UNKNOWN	65
330	V$AP3_Q6	247
331	V$ATF1_Q6	231
332	V$E12_Q6	262
333	V$E4F1_Q6	289
334	V$ETF_Q6	117
335	V$HEB_Q6	265
336	V$ICSBP_Q6	248
337	V$SMAD3_Q6	239
338	V$TEF1_Q6	226
339	V$TFIII_Q6	205
340	GCCNNNWTAAR_UNKNOWN	149
341	V$TFIIA_Q6	251
342	V$MYOGENIN_Q6	255
343	V$ZF5_01	238
344	V$PAX8_01	38
345	V$CACBINDINGPROTEIN_Q6	242

346	V$CACCCBINDINGFACTOR_Q6	268
347	V$COREBINDINGFACTOR_Q6	273
348	V$HNF3ALPHA_Q6	208
349	V$HP1SITEFACTOR_Q6	230
350	V$USF2_Q6	251
351	GCGNNANTTCC_UNKNOWN	123
352	V$SF1_Q6	257
353	V$CDX2_Q5	254
354	V$OSF2_Q6	264
355	V$SMAD4_Q6	241
356	V$CIZ_01	246
357	GCGSCMNTTT_UNKNOWN	69
358	V$HFH4_01	200
359	V$POU1F1_Q6	238
360	V$LEF1_Q6	261
361	V$ELF1_Q6	244
362	V$IRF1_Q6	258
363	V$SREBP1_Q6	245
364	V$HMGIY_Q6	248
365	V$AML1_Q6	263
366	V$P53_DECAMER_Q2	256
367	V$DR1_Q3	257
368	GCTNWTTGK_UNKNOWN	306
369	V$PPAR_DR1_Q2	259
370	V$HNF4_DR1_Q3	261
371	V$COUP_DR1_Q6	247
372	V$LXR_DR4_Q3	92
373	V$FXR_IR1_Q6	112
374	V$AML_Q6	266
375	V$CEBP_Q3	251
376	V$ETS_Q4	247
377	V$IRF_Q6	242
378	V$MYB_Q3	250
379	GGAANCGGAANY_UNKNOWN	106
380	V$NFKB_Q6_01	232
381	V$NFY_Q6_01	264
382	V$SREBP_Q3	258
383	V$STAT_Q6	260
384	V$AHR_Q5	215
385	V$GATA_Q6	198
386	V$HNF1_Q6	253
387	V$HNF3_Q6	189
388	V$SMAD_Q6	255
389	V$YY1_Q6	245
390	GGAMTNNNNNTCCY_UNKNOWN	117
391	V$TTF1_Q6	262
392	V$OCT_Q6	265
393	V$USF_Q6_01	239
394	V$HIF1_Q3	230
395	V$MYC_Q2	185
396	V$AP2_Q3	251
397	V$CREB_Q3	252
398	V$PIT1_Q6	236
399	V$E2F_Q2	176
400	V$E2A_Q2	243

401	GGARNTKYCCA_UNKNOWN	78
402	V$LEF1_Q2	226
403	V$NF1_Q6_01	268
404	V$EGR_Q6	275
405	V$PAX_Q6	259
406	V$FOX_Q2	213
407	V$SRF_Q4	221
408	V$NRF2_Q4	255
409	V$CEBP_Q2_01	267
410	V$MYB_Q5_01	267
411	V$ER_Q6_01	269
412	V$AP2_Q6_01	272
413	V$CREB_Q2_01	220
414	V$CREB_Q4_01	211
415	V$GR_Q6_01	279
416	V$SRF_Q5_01	220
417	V$AP1_Q2_01	275
418	V$AP1_Q6_01	264
419	GGCNKCCATNK_UNKNOWN	118
420	V$AP1_Q4_01	261
421	V$AP4_Q6_01	255
422	V$MYOD_Q6_01	257
423	V$OCT1_Q5_01	273
424	V$SP1_Q6_01	243
425	V$SP1_Q4_01	258
426	V$SP1_Q2_01	245
427	V$NFAT_Q4_01	266
428	GGCNNMSMYNTTG_UNKNOWN	75
429	V$MEF2_Q6_01	244
430	V$CP2_02	253
431	V$AR_02	40
432	V$PR_01	148
433	V$GR_01	204
434	V$AR_03	59
435	V$PR_02	136
436	V$ER_Q6_02	252
437	V$PR_Q2	266
438	GGCNRNWCTTYS_UNKNOWN	83
439	V$VDR_Q6	269
440	V$AR_Q6	259
441	V$T3R_Q6	251
442	V$PXR_Q2	256
443	V$DR4_Q2	260
444	V$DR3_Q4	145
445	V$HNF4_Q6	263
446	GGGYGTGNY_UNKNOWN	664
447	GTGGGTGK_UNKNOWN	293
448	KCCGNSWTTT_UNKNOWN	105
449	KMCATNNWGGA_UNKNOWN	90
450	MCAATNNNNNGCG_UNKNOWN	81
451	MYAATNNNNNNNGGC_UNKNOWN	111
452	RAAGNYNNCTTY_UNKNOWN	145
453	RACTNNRTTTNC_UNKNOWN	123
454	RNCTGNYNRNCTGNY_UNKNOWN	86
455	RNGTGGGC_UNKNOWN	766

456	RRAGTTGT_UNKNOWN	251
457	RTTTNNNYTGGM_UNKNOWN	153
458	RYAAAKNNNNNNTTGW_UNKNOWN	84
459	RYTAAWNNNTGAY_UNKNOWN	62
460	SMTTTTGT_UNKNOWN	402
461	SNACANNNYSYAGA_UNKNOWN	90
462	SYATTGTG_UNKNOWN	235
463	TAANNYSGCG_UNKNOWN	80
464	TAAYNRNNTCC_UNKNOWN	172
465	TCCATTKW_UNKNOWN	239
466	TCCCRNNRTGC_UNKNOWN	213
467	TGACATY_UNKNOWN	665
468	TGCGCANK_UNKNOWN	545
469	TGCTGAY_UNKNOWN	538
470	TGGNNNNNNKCCAR_UNKNOWN	424
471	TNCATNTCCYR_UNKNOWN	131
472	TTANTCA_UNKNOWN	952
473	TTANWNANTGGM_UNKNOWN	65
474	TTCYRGAA_UNKNOWN	326
475	WCAANNNYCAG_UNKNOWN	254
476	WGTTNNNNNAAA_UNKNOWN	547
477	WTGAAAT_UNKNOWN	616
478	WTTGKCTG_UNKNOWN	516
479	WWTAAGGC_UNKNOWN	142
480	WYAAANNRNNNGCG_UNKNOWN	65
481	YAATNRNNNYNATT_UNKNOWN	104
482	YATTNATC_UNKNOWN	377
483	YCATTAA_UNKNOWN	556
484	YGACNNYACAR_UNKNOWN	96
485	YGCANTGCR_UNKNOWN	126
486	YGCGYRCGC_UNKNOWN	319
487	YGTCCTTGR_UNKNOWN	98
488	YKACATTT_UNKNOWN	276
489	YNGTTNNNATT_UNKNOWN	365
490	YNTTTNNNANGCARM_UNKNOWN	70
491	YRTCANNRCGC_UNKNOWN	65
492	YTAAYNGCT_UNKNOWN	151
493	YTCCCRNNAGGY_UNKNOWN	72
494	YWATTWNNRGCT_UNKNOWN	70
495	YYCATTCAWW_UNKNOWN	191
496	RACCACAR_V$AML_Q6	261
497	TGANTCA_V$AP1_C	1121
498	CAGCTG_V$AP4_Q5	1524
499	CAGGTA_V$AREB6_01	792
500	TGACGTCA_V$ATF3_Q6	231
501	TGAYRTCA_V$ATF3_Q6	538
502	TTGCWCAAY_V$CEBPB_02	63
503	TAATTA_V$CHX10_01	810
504	TTAYRTAA_V$E4BP4_01	265
505	GTGACGY_V$E4F1_Q6	658
506	SCGGAAGY_V$ELK1_02	1199
507	TGACCTY_V$ERR1_Q2	1043
508	RYTTCCTG_V$ETS2_B	1085
509	RTAAACA_V$FREAC2_01	919
510	MGGAAGTG_V$GABP_B	757

511	GATAAGR_V$GATA_C	295
512	TGATTTRY_V$GFI1_01	294
513	AAAYWAACM_V$HFH4_01	254
514	RGTTAMWNATT_V$HNF1_01	75
515	TGTTTGY_V$HNF3_Q6	738
516	TTCNRGNNNNTTC_V$HSF_Q6	152
517	RGAANNTTC_V$HSF1_01	446
518	STTTCRNTTT_V$IRF_Q6	188
519	CTTTGA_V$LEF1_Q2	1232
520	CTTTGT_V$LEF1_Q2	1972
521	YTAATTAA_V$LHX3_01	184
522	YTATTTTNR_V$MEF2_02	697
523	TGACAGNY_V$MEIS1_01	827
524	CACGTG_V$MYC_Q2	1032
525	GCANCTGNY_V$MYOD_Q6	924
526	TGCCAAR_V$NF1_Q6	722
527	TGGAAA_V$NFAT_Q4_01	1896
528	TGASTMAGC_V$NFE2_01	195
529	GGGNNTTTCC_V$NFKB_Q6_01	134
530	GATTGGY_V$NFY_Q6_01	1160
531	RCGCANGCGY_V$NRF1_Q6	918
532	YATGNWAAT_V$OCT_C	360
533	CCCNNGGGAR_V$OLF1_01	320
534	CGTSACG_V$PAX3_B	148
535	GGGTGGRR_V$PAX4_03	1294
536	GGATTA_V$PITX2_Q2	587
537	RGAGGAARY_V$PU1_Q6	502
538	CTAWWWATA_V$RSRFC4_Q2	361
539	TAAWWATAG_V$RSRFC4_Q2	165
540	TGACCTTG_V$SF1_Q6	249
541	CATTGTYY_V$SOX9_B1	358
542	TCANNTGAY_V$SREBP1_01	475
543	CCAWWNAAGG_V$SRF_Q4	87
544	TTCYNRGAA_V$STAT5B_01	335
545	TATAAA_V$TATA_01	1296
546	TGANNYRGCA_V$TCF11MAFG_01	301
547	WGGAATGY_V$TEF1_Q6	378
548	GCCATNTTG_V$YY1_Q6	427

cluster ID = 62
cluster size = 7

	gene set name	size (number of genes in the set)
1	chr18q21	128
2	chr20p11	86
3	MODULE_164	61
4	PROTEASE_INHIBITOR_ACTIVITY	41
5	ENZYME_REGULATOR_ACTIVITY	323
6	ENZYME_INHIBITOR_ACTIVITY	119
7	SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	25

cluster ID = 65
cluster size = 10

	gene set name	size (number of genes in the set)

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1     chr17q22   41
2     chr17q23   96
3     chr17q     16
4     chr17q25   218
5     chr17q21   339
6     chr17q24   56
7     LASTOWSKA_NEUROBLASTOMA_COPY_NUMBER_UP  181
8     FARMER_BREAST_CANCER_CLUSTER_6     16
9     NIKOLSKY_BREAST_CANCER_17Q21_Q25_AMPLICON     335
10    AGUIRRE_PANCREATIC_CANCER_COPY_NUMBER_UP      298


cluster ID = 67
cluster size = 7
      gene set name    size (number of genes in the set)
1     chr10p13   36
2     CALVET_IRINOTECAN_SENSITIVE_VS_REVERTED_UP    5
3     MATTHEWS_AP1_TARGETS   17
4     LEE_LIVER_CANCER_HEPATOBLAST 16
5     MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA_VHL_UP     7
6     HOLLEMAN_VINCRISTINE_RESISTANCE_B_ALL_DN      15
7     HOLLEMAN_VINCRISTINE_RESISTANCE_ALL_DN  19


cluster ID = 73
cluster size = 37
      gene set name    size (number of genes in the set)
1     chr19p     8
2     chr6q12    28
3     KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT      38
4     REACTOME_BOTULINUM_NEUROTOXICITY  19
5     REACTOME_PROTEOLYTIC_CLEAVAGE_OF_SNARE_COMPLEX_PROTEINS  17
6     REACTOME_GLUTAMATE_NEUROTRANSMITTER_RELEASE_CYCLE  15
7     REACTOME_NEUROTRANSMITTER_RELEASE_CYCLE 34
8     REACTOME_DOPAMINE_NEUROTRANSMITTER_RELEASE_CYCLE    11
9     REACTOME_ACETYLCHOLINE_NEUROTRANSMITTER_RELEASE_CYCLE     10
10    REACTOME_NOREPINEPHRINE_NEUROTRANSMITTER_RELEASE_CYCLE    10
11    REACTOME_GABA_SYNTHESIS_RELEASE_REUPTAKE_AND_DEGRADATION 17
12    OUELLET_OVARIAN_CANCER_INVASIVE_VS_LMP_DN     11
13    LEE_TARGETS_OF_PTCH1_AND_SUFU_DN  83
14    MODY_HIPPOCAMPUS_POSTNATAL  63
15    LU_AGING_BRAIN_DN153
16    JIANG_AGING_HYPOTHALAMUS_DN  40
17    MCCLUNG_COCAINE_REWARD_5D    79
18    JIANG_AGING_CEREBRAL_CORTEX_DN    54
19    LEIN_NEURON_MARKERS    69
20    WANG_LSD1_TARGETS_DN   39
21    GNF2_AF1Q  25
22    GNF2_DNM1  73
23    GNF2_MAPT  41
24    GNF2_RAB3A 37
25    GNF2_RTN1  52
26    GNF2_TM4SF2 26
27    MODULE_381 12
28    MODULE_563 15
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29    SYNAPSE_PART     13
30    SYNAPSE    27
31    REGULATION_OF_NEUROTRANSMITTER_LEVELS   24
32    ESTABLISHMENT_OF_ORGANELLE_LOCALIZATION 18
33    ESTABLISHMENT_OF_VESICLE_LOCALIZATION   10
34    REGULATED_SECRETORY_PATHWAY  15
35    VESICLE_LOCALIZATION   11
36    NEUROTRANSMITTER_SECRETION   13
37    ORGANELLE_LOCALIZATION 25


cluster ID = 76
cluster size = 26
      gene set name    size (number of genes in the set)
1     chr7p11    60
2     chr5q14    72
3     chr2p15    28
4     KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION    59
5     REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS
      27
6     REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_CCT_TRIC  28
7     REACTOME_PROTEIN_FOLDING     53
8     REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES_BY_CCT_TRIC      22
9     REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY    19
10    LAIHO_COLORECTAL_CANCER_SERRATED_UP     112
11    HUMMEL_BURKITTS_LYMPHOMA_UP  43
12    MODY_HIPPOCAMPUS_NEONATAL    35
13    ALONSO_METASTASIS_EMT_UP     36
14    ALONSO_METASTASIS_NEURAL_UP  18
15    ALONSO_METASTASIS_UP   198
16    PUJANA_BREAST_CANCER_WITH_BRCA1_MUTATED_DN    9
17    PURBEY_TARGETS_OF_CTBP1_AND_SATB1_UP    87
18    FU_INTERACT_WITH_ALKBH8      13
19    MODULE_155  25
20    MODULE_245  26
21    MODULE_299  35
22    MODULE_355  29
23    PROTEIN_FOLDING  58
24    CHAPERONE_BINDING12
25    SIGNAL_SEQUENCE_BINDING      15
26    UNFOLDED_PROTEIN_BINDING     42


cluster ID = 77
cluster size = 7
      gene set name    size (number of genes in the set)
1     chr16q13   50
2     chr16q12   65
3     chr16q11   13
4     ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_UP     63
5     ROYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_DN     26
6     CHNG_MULTIPLE_MYELOMA_HYPERPLOID_DN     28
7     NAKAYAMA_FGF2_TARGETS  29
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cluster ID = 83
cluster size = 11
        gene set name     size (number of genes in the set)
1       chr2q34     29
2       SAMOLS_TARGETS_OF_KHSV_MIRNAS_DN   62
3       RODRIGUES_THYROID_CARCINOMA_DN     77
4       OZANNE_AP1_TARGETS_DN  5
5       BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_AND_PAX3   7
6       KARAKAS_TGFB1_SIGNALING      18
7       GUENTHER_GROWTH_SPHERICAL_VS_ADHERENT_DN      26
8       IIZUKA_LIVER_CANCER_PROGRESSION_L0_L1_UP      17
9       IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_DN      12
10      KENNY_CTNNB1_TARGETS_DN      52
11      OUYANG_PROSTATE_CANCER_MARKERS     19


cluster ID = 92
cluster size = 6
        gene set name     size (number of genes in the set)
1       chr6p21     544
2       chr17p13    293
3       GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_DN   335
4       GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN      180
5       SENGUPTA_EBNA1_ANTICORRELATED      173
6       VERHAAK_GLIOBLASTOMA_MESENCHYMAL   210


cluster ID = 97
cluster size = 187
        gene set name     size (number of genes in the set)
1       chr5q31     247
2       WEI_MIR34A_TARGETS      148
3       BONCI_TARGETS_OF_MIR15A_AND_MIR16_1      91
4       GABRIELY_MIR21_TARGETS 289
5       CARD_MIR302A_TARGETS   77
6       IVANOVSKA_MIR106B_TARGETS    90
7       LINSLEY_MIR16_TARGETS  206
8       IKEDA_MIR1_TARGETS_UP  53
9       IKEDA_MIR30_TARGETS_UP 116
10      AGCACTT,MIR-93,MIR-302A,MIR-302B,MIR-302C,MIR-302D,MIR-372,MIR-373,MIR-
520E,MIR-520A,MIR-526B,MIR-520B,MIR-520C,MIR-520D   343
11      CTACCTC,LET-7A,LET-7B,LET-7C,LET-7D,LET-7E,LET-7F,MIR-98,LET-7G,LET-7I
        391
12      GCACTTT,MIR-17-5P,MIR-20A,MIR-106A,MIR-106B,MIR-20B,MIR-519D   595
13      TGCTGCT,MIR-15A,MIR-16,MIR-15B,MIR-195,MIR-424,MIR-497    601
14      TGTTTAC,MIR-30A-5P,MIR-30C,MIR-30D,MIR-30B,MIR-30E-5P     579
15      GTGCAAT,MIR-25,MIR-32,MIR-92,MIR-363,MIR-367  311
16      TGAATGT,MIR-181A,MIR-181B,MIR-181C,MIR-181D   484
17      TGGTGCT,MIR-29A,MIR-29B,MIR-29C    521
18      TGCACTG,MIR-148A,MIR-152,MIR-148B  304
19      CACTGCC,MIR-34A,MIR-34C,MIR-449    280
20      TTGCACT,MIR-130A,MIR-301,MIR-130B  403
21      TGCACTT,MIR-519C,MIR-519B,MIR-519A 448
22      CAGTATT,MIR-200B,MIR-200C,MIR-429  469
23      ACATTCC,MIR-1,MIR-206  300
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24	AAGTCCA,MIR-422B,MIR-422A	71
25	AAAGGGA,MIR-204,MIR-211	224
26	AATGTGA,MIR-23A,MIR-23B	419
27	CACTGTG,MIR-128A,MIR-128B	337
28	ACTGAAA,MIR-30A-3P,MIR-30E-3P	201
29	CTCAGGG,MIR-125B,MIR-125A	329
30	TACTTGA,MIR-26A,MIR-26B	300
31	GTATGAT,MIR-154,MIR-487	70
32	CAGTGTT,MIR-141,MIR-200A	310
33	TAGGTCA,MIR-192,MIR-215	47
34	ATGTAGC,MIR-221,MIR-222	140
35	ACTGTGA,MIR-27A,MIR-27B	474
36	TTTGCAC,MIR-19A,MIR-19B	516
37	ACTACCT,MIR-196A,MIR-196B	145
38	TTGGAGA,MIR-515-5P,MIR-519E	149
39	CACTTTG,MIR-520G,MIR-520H	237
40	GGGACCA,MIR-133A,MIR-133B	201
41	GACTGTT,MIR-212,MIR-132	161
42	AAGCCAT,MIR-135A,MIR-135B	335
43	ATGCTGC,MIR-103,MIR-107	221
44	ACAGGGT,MIR-10A,MIR-10B	123
45	CTCTGGA,MIR-520A,MIR-525	158
46	ACACTGG,MIR-199A,MIR-199B	157
47	GCACCTT,MIR-18A,MIR-18B	117
48	GGCCAGT,MIR-193A,MIR-193B	89
49	GTGCCTT,MIR-506	727
50	ACAACTT,MIR-382	72
51	ATGTTAA,MIR-302C	243
52	CATTTCA,MIR-203	287
53	TCCAGAT,MIR-516-5P	109
54	ACACTCC,MIR-122A	75
55	GTGTGAG,MIR-342	68
56	CTATGCA,MIR-153	216
57	AGGGCAG,MIR-18A	136
58	GTGCCAT,MIR-183	175
59	ACTGCAG,MIR-17-3P	110
60	GTTTGTT,MIR-495	257
61	TATTATA,MIR-374	284
62	CTTGTAT,MIR-381	206
63	AAAGGAT,MIR-501	126
64	GGGGCCC,MIR-296	74
65	CTACTGT,MIR-199A	183
66	CAAGGAT,MIR-362	66
67	GTGTTGA,MIR-505	105
68	ATACTGT,MIR-144	199
69	TGTATGA,MIR-485-3P	153
70	GTATTAT,MIR-369-3P	207
71	TCCCCAC,MIR-491	57
72	GCTTGAA,MIR-498	114
73	GTGGTGA,MIR-197	72
74	GGGCATT,MIR-365	108
75	TGAGATT,MIR-216	107
76	GGTGAAG,MIR-412	61
77	AGGGCCA,MIR-328	80
78	GTGACTT,MIR-224	158

79	GAGACTG,MIR-452	94
80	CAGGGTC,MIR-504	85
81	GCTCTTG,MIR-335	86
82	GTCTTCC,MIR-7	169
83	AGGCACT,MIR-515-3P	89
84	ATAGGAA,MIR-202	102
85	CCAGGTT,MIR-490	67
86	TTGCCAA,MIR-182	327
87	TAGCTTT,MIR-9	236
88	CTGAGCC,MIR-24	231
89	TTGGGAG,MIR-150	90
90	AAACCAC,MIR-140	111
91	CCCACAT,MIR-299-3P	54
92	ATGTTTC,MIR-494	162
93	GTACTGT,MIR-101	257
94	CAGGTCC,MIR-492	63
95	GAGCCTG,MIR-484	108
96	GTAAGAT,MIR-200A	54
97	TATCTGG,MIR-488	62
98	AGGAAGC,MIR-516-3P	123
99	ATATGCA,MIR-448	212
100	AATGGAG,MIR-136	80
101	CCTGTGA,MIR-513	125
102	ATGAAGG,MIR-205	157
103	CTCAAGA,MIR-526B	75
104	GGCAGCT,MIR-22	232
105	TCTGGAC,MIR-198	84
106	CAGCTTT,MIR-320	256
107	CCATCCA,MIR-432	60
108	CATGTAA,MIR-496	176
109	AAGCACA,MIR-218	398
110	ATGTCAC,MIR-489	88
111	CCTGCTG,MIR-214	240
112	GACAGGG,MIR-339	67
113	ATACCTC,MIR-202	179
114	GGCAGTG,MIR-324-3P	97
115	GAGCCAG,MIR-149	145
116	TCTCTCC,MIR-185	124
117	AGCATTA,MIR-155	134
118	GCAAAAA,MIR-129	183
119	GGCACAT,MIR-455	58
120	CTTTGTA,MIR-524	433
121	CTGTTAC,MIR-194	107
122	ATGCAGT,MIR-217	115
123	ATGCTGG,MIR-338	115
124	ACATATC,MIR-190	60
125	CTCCAAG,MIR-432	83
126	AAGCAAT,MIR-137	223
127	ACCAAAG,MIR-9	499
128	TTTGTAG,MIR-520D	336
129	TGCCTTA,MIR-124A	552
130	AACTGAC,MIR-223	96
131	AAAGACA,MIR-511	202
132	ATAAGCT,MIR-21	116
133	TCTGATA,MIR-361	91

134	TACAATC,MIR-508	65
135	ACTTTAT,MIR-142-5P	288
136	TTTGCAG,MIR-518A-2	210
137	AACATTC,MIR-409-3P	142
138	ACAACCT,MIR-453	43
139	GTGCCAA,MIR-96	303
140	TCATCTC,MIR-143	149
141	GAGCTGG,MIR-337	159
142	AGTCTTA,MIR-499	76
143	CCCAGAG,MIR-326	155
144	ACCATTT,MIR-522	160
145	AGCTCCT,MIR-28	95
146	ACTGCCT,MIR-34B	219
147	GTTAAAG,MIR-302B	69
148	GACAATC,MIR-219	143
149	AACTGGA,MIR-145	234
150	AAGCACT,MIR-520F	238
151	AGGAGTG,MIR-483	66
152	GTGTCAA,MIR-514	61
153	GCAAGGA,MIR-502	71
154	AGGTGCA,MIR-500	99
155	ACTGTAG,MIR-139	123
156	GTGCAAA,MIR-507	131
157	TGCTTTG,MIR-330	335
158	TTTTGAG,MIR-373	225
159	TAGAACC,MIR-182	38
160	GGGATGC,MIR-324-5P	50
161	CCAGGGG,MIR-331	97
162	ACCAATC,MIR-509	47
163	GGCACTT,MIR-519E	124
164	ATGTACA,MIR-493	314
165	GCATTTG,MIR-105	175
166	TCCAGAG,MIR-518C	148
167	CACCAGC,MIR-138	226
168	CAGCACT,MIR-512-3P	158
169	GTTATAT,MIR-410	93
170	ACACTAC,MIR-142-3P	130
171	ATTCTTT,MIR-186	272
172	TGTGTGA,MIR-377	200
173	ATCATGA,MIR-433	115
174	CAGCAGG,MIR-370	155
175	CTTTGCA,MIR-527	235
176	GGTGTGT,MIR-329	113
177	ATTACAT,MIR-380-3P	102
178	ATCTTGC,MIR-31	77
179	AAGGGAT,MIR-188	75
180	TGCAAAC,MIR-452	111
181	CAGCCTC,MIR-485-5P	145
182	GTAAACC,MIR-299-5P	52
183	GGTAACC,MIR-409-5P	33
184	TAATAAT,MIR-126	222
185	CCACACA,MIR-147	63
186	TAATGTG,MIR-323	160
187	CAATGCA,MIR-33	92

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cluster ID = 104
cluster size = 8
      gene set name    size (number of genes in the set)
1     chr6p23    25
2     chr6p24    45
3     LU_TUMOR_VASCULATURE_DN      13
4     GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION      14
5     PETRETTO_HEART_MASS_QTL_CIS_UP     28
6     PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_UP 6
7     NIKOLSKY_BREAST_CANCER_6P24_P22_AMPLICON      21
8     LU_TUMOR_ENDOTHELIAL_MARKERS_DN    5


cluster ID = 106
cluster size = 43
      gene set name    size (number of genes in the set)
1     chr5q35    179
2     BIOCARTA_CARM_ER_PATHWAY     35
3     PID_HDAC_CLASSII_PATHWAY     34
4     PID_HDAC_CLASSI_PATHWAY      66
5     MARTIN_INTERACT_WITH_HDAC    44
6     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_27   15
7     PETRETTO_LEFT_VENTRICLE_MASS_QTL_CIS_DN 7
8     SAKAI_TUMOR_INFILTRATING_MONOCYTES_UP   27
9     GAZIN_EPIGENETIC_SILENCING_BY_KRAS 26
10    AGCGCAG,MIR-191  13
11    CHROMATIN_REMODELING_COMPLEX 17
12    HISTONE_DEACETYLASE_COMPLEX  20
13    ONE_CARBON_COMPOUND_METABOLIC_PROCESS   26
14    CHROMATIN_REMODELING   25
15    CHROMATIN_ASSEMBLY     16
16    NUCLEOSOME_ASSEMBLY    10
17    CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY    13
18    PROTEIN_COMPLEX_DISASSEMBLY  14
19    COVALENT_CHROMATIN_MODIFICATION   25
20    REGULATION_OF_GENE_EXPRESSION_EPIGENETIC      30
21    PROTEIN_AMINO_ACID_ADP_RIBOSYLATION     10
22    HISTONE_MODIFICATION   24
23    MACROMOLECULAR_COMPLEX_DISASSEMBLY 15
24    DNA_MODIFICATION 11
25    CHROMOSOME_ORGANIZATION_AND_BIOGENESIS  124
26    CHROMATIN_MODIFICATION 55
27    ESTABLISHMENT_AND_OR_MAINTENANCE_OF_CHROMATIN_ARCHITECTURE     77
28    DNA_PACKAGING    35
29    GENE_SILENCING   10
30    CHROMATIN_ASSEMBLY_OR_DISASSEMBLY  26
31    HISTONE_METHYLTRANSFERASE_ACTIVITY 11
32    HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_NOT_PEPTIDEBONDS  46
33    PROTEIN_METHYLTRANSFERASE_ACTIVITY 14
34    HISTONE_DEACETYLASE_BINDING  10
35    S_ADENOSYLMETHIONINE_DEPENDENT_METHYLTRANSFERASE_ACTIVITY 23
36    SPECIFIC_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY   12
37    N_METHYLTRANSFERASE_ACTIVITY 13
38    METHYLTRANSFERASE_ACTIVITY   36
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39    PROTEIN_DEACETYLASE_ACTIVITY 10
40    DEACETYLASE_ACTIVITY   11
41    TRANSFERASE_ACTIVITY_TRANSFERRING_ONE_CARBON_GROUPS 37
42    TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS   20
43
      HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_NOT_PEPTIDEBONDSIN_LINEAR_AMI
DES   21


cluster ID = 109
cluster size = 16
      gene set name    size (number of genes in the set)
1     chr3p24    69
2     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELLOW_DN   11
3     ZIRN_TRETINOIN_RESPONSE_WT1_UP     23
4     ZIRN_TRETINOIN_RESPONSE_UP   21
5     XU_AKT1_TARGETS_48HR   9
6     SCHLESINGER_METHYLATED_IN_COLON_CANCER  10
7     SCHLESINGER_METHYLATED_DE_NOVO_IN_CANCER      88
8     OHM_METHYLATED_IN_ADULT_CANCERS    27
9     OHM_EMBRYONIC_CARCINOMA_UP   6
10    OHM_EMBRYONIC_CARCINOMA_DN   8
11    LOPES_METHYLATED_IN_COLON_CANCER_UP      27
12    LOPES_METHYLATED_IN_COLON_CANCER_DN      28
13    KONDO_COLON_CANCER_HCP_WITH_H3K27ME3    7
14    HOQUE_METHYLATED_IN_CANCER   56
15    MCGARVEY_SILENCED_BY_METHYLATION_IN_COLON_CANCER    42
16    LI_PROSTATE_CANCER_EPIGENETIC      30


cluster ID = 110
cluster size = 13
      gene set name    size (number of genes in the set)
1     chr7q33    37
2     CASTELLANO_HRAS_TARGETS_UP   5
3     BYSTRYKH_HEMATOPOIESIS_STEM_CELL_QTL_CIS      128
4     CHESLER_BRAIN_QTL_CIS  75
5     BYSTRYKH_HEMATOPOIESIS_STEM_CELL_AND_BRAIN_QTL_CIS  65
6     CHESLER_BRAIN_HIGHEST_GENETIC_VARIANCE  37
7     CHESLER_BRAIN_HIGHEST_EXPRESSION  40
8     COATES_MACROPHAGE_M1_VS_M2_UP      81
9     COATES_MACROPHAGE_M1_VS_M2_DN      78
10    SAGIV_CD24_TARGETS_UP  23
11    SAGIV_CD24_TARGETS_DN  46
12    ELLWOOD_MYC_TARGETS_UP 13
13    BAUS_TFF2_TARGETS_DN   11


cluster ID = 111
cluster size = 11
      gene set name    size (number of genes in the set)
1     chr12p12   81
2     chr12p11   58
3     KORKOLA_EMBRYONAL_CARCINOMA_DN     13
4     KORKOLA_CHORIOCARCINOMA_DN   11
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5     KORKOLA_SEMINOMA_DN    13
6     BARRIER_COLON_CANCER_RECURRENCE_UP 42
7     HEIDENBLAD_AMPLIFIED_IN_PANCREATIC_CANCER     31
8     HEIDENBLAD_AMPLICON_12P11_12_UP    33
9     KUUSELO_PANCREATIC_CANCER_19Q13_AMPLIFICATION 35
10    WEBER_METHYLATED_LCP_IN_FIBROBLAST_DN    10
11    WEBER_METHYLATED_LCP_IN_SPERM_DN    7


cluster ID = 112
cluster size = 15
      gene set name    size (number of genes in the set)
1     chr9p23    12
2     REACTOME_GAP_JUNCTION_DEGRADATION  10
3     REACTOME_GAP_JUNCTION_TRAFFICKING  27
4     REACTOME_GAP_JUNCTION_ASSEMBLY     18
5     LI_CISPLATIN_RESISTANCE_UP   28
6     BAFNA_MUC4_TARGETS_DN  5
7     WALLACE_PROSTATE_CANCER_DN   6
8     SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP 6
9     KORKOLA_EMBRYONIC_CARCINOMA_VS_SEMINOMA_UP    22
10    ZEMBUTSU_SENSITIVITY_TO_DOXORUBICIN     17
11    ZWANG_EGF_PERSISTENTLY_DN    61
12    INTERCALATED_DISC 9
13    CYTOPLASM_ORGANIZATION_AND_BIOGENESIS   15
14    INTERCELLULAR_JUNCTION_ASSEMBLY    11
15    INTERCELLULAR_JUNCTION_ASSEMBLY_AND_MAINTENANCE     13


cluster ID = 113
cluster size = 8
      gene set name    size (number of genes in the set)
1     chr7p14    89
2     REACTOME_PASSIVE_TRANSPORT_BY_AQUAPORINS      11
3     ZIRN_TRETINOIN_RESPONSE_WT1_DN    6
4     HOEGERKORP_CD44_TARGETS_DIRECT_UP  27
5     JOSEPH_RESPONSE_TO_SODIUM_BUTYRATE_DN   64
6     MODULE_416  23
7     MODULE_571  15
8     EXCRETION   36


cluster ID = 118
cluster size = 35
      gene set name    size (number of genes in the set)
1     chr4q31    104
2     chr4q 8
3     KEGG_TASTE_TRANSDUCTION      52
4     PID_CONE_PATHWAY 23
5     PID_RHODOPSIN_PATHWAY  24
6     REACTOME_ELEVATION_OF_CYTOSOLIC_CA2_LEVELS    10
7     REACTOME_OPSINS  10
8     REACTOME_EFFECTS_OF_PIP2_HYDROLYSIS     25
9     REACTOME_ROLE_OF_SECOND_MESSENGERS_IN_NETRIN1_SIGNALING  11
10    REACTOME_PLATELET_CALCIUM_HOMEOSTASIS   18
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11     EHRLICH_ICF_SYNDROM_UP 13
12     LEE_INTRATHYMIC_T_PROGENITOR 21
13     MODULE_65   10
14     MODULE_248  129
15     MODULE_287  50
16     MODULE_445  15
17     DETECTION_OF_ABIOTIC_STIMULUS      19
18     DETECTION_OF_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION      21
19     SENSORY_PERCEPTION_OF_TASTE  11
20     PHOTOTRANSDUCTION 13
21     RESPONSE_TO_LIGHT_STIMULUS   46
22     DETECTION_OF_STIMULUS  47
23     DETECTION_OF_CHEMICAL_STIMULUS     18
24     PROTEIN_TARGETING_TO_MEMBRANE      12
25     RESPONSE_TO_ABIOTIC_STIMULUS 89
26     SENSORY_PERCEPTION_OF_CHEMICAL_STIMULUS 20
27     RESPONSE_TO_UV   26
28     RESPONSE_TO_RADIATION  60
29     DETECTION_OF_EXTERNAL_STIMULUS     23
30     PHOSPHORUS_OXYGEN_LYASE_ACTIVITY   10
31     TASTE_RECEPTOR_ACTIVITY      15
32     CYCLASE_ACTIVITY 11
33     CRX_DN.V1_UP     136
34     CRX_NRL_DN.V1_UP 140
35     NRL_DN.V1_UP     136


cluster ID = 123
cluster size = 12
       gene set name    size (number of genes in the set)
1      chr11p12    18
2      SHIRAISHI_PLZF_TARGETS_UP    10
3      DER_IFN_BETA_RESPONSE_DN     8
4      DER_IFN_GAMMA_RESPONSE_DN    11
5      BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_24HR_UP  14
6      BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_48HR_UP  18
7      BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_48HR_UP    18
8      DER_IFN_ALPHA_RESPONSE_DN    7
9      HOFMANN_MYELODYSPLASTIC_SYNDROM_LOW_RISK_UP   22
10     HOFMANN_MYELODYSPLASTIC_SYNDROM_HIGH_RISK_UP  10
11     SETLUR_PROSTATE_CANCER_TMPRSS2_ERG_FUSION_UP  67
12     BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_24HR_UP    9


cluster ID = 126
cluster size = 7
       gene set name    size (number of genes in the set)
1      chrxq21     78
2      JIANG_HYPOXIA_CANCER   83
3      DAVIES_MULTIPLE_MYELOMA_VS_MGUS_DN 28
4      YANAGISAWA_LUNG_CANCER_RECURRENCE  9
5      MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_1   10
6      VISALA_AGING_LYMPHOCYTE_UP   10
7      GUILLAUMOND_KLF10_TARGETS_DN 30
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cluster ID = 127
cluster size = 191

	gene set name	size (number of genes in the set)
1	chr19q13	948
2	KEGG_BASAL_TRANSCRIPTION_FACTORS	36
3	BIOCARTA_VDR_PATHWAY	12
4	BIOCARTA_EGFR_SMRTE_PATHWAY	11
5	BIOCARTA_RARRXR_PATHWAY	15
6	BIOCARTA_NUCLEARRS_PATHWAY	15
7	PID_ERB_GENOMIC_PATHWAY	15
8	PID_MYC_PATHWAY	25
9	PID_AR_TF_PATHWAY	53
10	PID_RXR_VDR_PATHWAY	26
11	PID_ERA_GENOMIC_PATHWAY	65
12	PID_RETINOIC_ACID_PATHWAY	30
13	PID_HNF3APATHWAY	44
14	REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	36
15	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	104
16	REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	24
17	REACTOME_YAP1_AND_WWTR1_TAZ_STIMULATED_GENE_EXPRESSION	24
18	REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	23
19	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	352
20	REACTOME_NUCLEAR_RECEPTOR_TRANSCRIPTION_PATHWAY	49
21	REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	168
22	REACTOME_CIRCADIAN_CLOCK	53
23	REACTOME_TRANSCRIPTIONAL_REGULATION_OF_WHITE_ADIPOCYTE_DIFFERENTIATION	72
24	NAGY_TFTC_COMPONENTS_HUMAN	19
25	NAGY_STAGA_COMPONENTS_HUMAN	15
26	NAGY_PCAF_COMPONENTS_HUMAN	9
27	FIRESTEIN_PROLIFERATION	175
28	GRESHOCK_CANCER_COPY_NUMBER_UP	323
29	LIU_IL13_MEMORY_MODEL_UP	17
30	MODULE_249	22
31	MODULE_377	11
32	NUCLEOPLASM	279
33	ORGANELLE_PART	1197
34	CYTOPLASMIC_PART	1383
35	NUCLEAR_PART	579
36	ORGANELLE_LUMEN	458
37	NUCLEAR_LUMEN	387
38	NUCLEUS	1430
39	CYTOSOL	205
40	MEDIATOR_COMPLEX	18
41	INTEGRATOR_COMPLEX	13
42	MEMBRANE_ENCLOSED_LUMEN	458
43	DNA_DIRECTED_RNA_POLYMERASEII_HOLOENZYME	67
44	NUCLEOPLASM_PART	211
45	INTRACELLULAR_ORGANELLE_PART	1192
46	MACROMOLECULAR_COMPLEX	945
47	TRANSCRIPTION_FACTOR_TFIID_COMPLEX	14
48	TRANSCRIPTION_FACTOR_COMPLEX	89
49	PROTEIN_COMPLEX	816
50	NUCLEOLUS	126

51	RNA_METABOLIC_PROCESS	841
52	PROTEIN_OLIGOMERIZATION	40
53	NEGATIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	211
54	NEGATIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS	259
55	PROTEIN_AUTOPROCESSING	32
56	POSITIVE_REGULATION_OF_SIGNAL_TRANSDUCTION	126
57	POSITIVE_REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT	118
58	CELL_DEVELOPMENT	577
59	NEGATIVE_REGULATION_OF_APOPTOSIS	150
60	REGULATION_OF_KINASE_ACTIVITY	157
61	REGULATION_OF_PROTEIN_KINASE_ACTIVITY	155
62	N_TERMINAL_PROTEIN_AMINO_ACID_MODIFICATION	11
63	BIOPOLYMER_METABOLIC_PROCESS	1684
64	POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	65
65	MACROMOLECULAR_COMPLEX_ASSEMBLY	280
66	PROTEIN_TETRAMERIZATION	14
67	REGULATION_OF_MOLECULAR_FUNCTION	324
68	SIGNAL_TRANSDUCTION	1634
69	NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	1244
70	ACTIVATION_OF_JNK_ACTIVITY	16
71	TRANSCRIPTION_DNA_DEPENDENT	636
72	REGULATION_OF_TRANSFERASE_ACTIVITY	161
73	PROGRAMMED_CELL_DEATH	432
74	POSITIVE_REGULATION_OF_CATALYTIC_ACTIVITY	165
75	POSITIVE_REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	154
76	POSITIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	120
77	NEGATIVE_REGULATION_OF_TRANSCRIPTION_DNA_DEPENDENT	130
78	REGULATION_OF_MAPKKK_CASCADE	20
79	PROTEIN_AMINO_ACID_AUTOPHOSPHORYLATION	31
80	I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	114
81	REGULATION_OF_SIGNAL_TRANSDUCTION	222
82	TRANSCRIPTION_INITIATION	35
83	NEGATIVE_REGULATION_OF_CELLULAR_PROCESS	646
84	REGULATION_OF_DEVELOPMENTAL_PROCESS	440
85	ACTIVATION_OF_MAPK_ACTIVITY	41
86	PROTEIN_DNA_COMPLEX_ASSEMBLY	49
87	RNA_BIOSYNTHETIC_PROCESS	638
88	CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	33
89	JNK_CASCADE	47
90	POSITIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	87
91	POSITIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	47
92	REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	289
93	REGULATION_OF_CELLULAR_METABOLIC_PROCESS	787
94	REGULATION_OF_GENE_EXPRESSION	673
95	POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	218
96	POST_TRANSLATIONAL_PROTEIN_MODIFICATION	476
97	CELLULAR_COMPONENT_ASSEMBLY	298
98	REGULATION_OF_JNK_CASCADE	12
99	POSITIVE_REGULATION_OF_METABOLIC_PROCESS	236
100	CELLULAR_PROTEIN_METABOLIC_PROCESS	1117
101	PROTEIN_KINASE_CASCADE	293

102	REGULATION_OF_TRANSCRIPTIONDNA_DEPENDENT	461
103	STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	20
104	BIOPOLYMER_MODIFICATION	650
105	REGULATION_OF_MAP_KINASE_ACTIVITY	67
106	NEGATIVE_REGULATION_OF_TRANSCRIPTION	188
107	NEGATIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	84
108	REGULATION_OF_CATALYTIC_ACTIVITY	276
109	ANTI_APOPTOSIS	118
110	INTRACELLULAR_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	21
111	PROTEIN_PROCESSING	49
112	PROTEIN_COMPLEX_ASSEMBLY	167
113	PROTEIN_METABOLIC_PROCESS	1231
114	NEGATIVE_REGULATION_OF_RNA_METABOLIC_PROCESS	132
115	TRANSCRIPTION	753
116	POSITIVE_REGULATION_OF_CELLULAR_METABOLIC_PROCESS	229
117	POSITIVE_REGULATION_OF_BIOLOGICAL_PROCESS	709
118	TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER	29
119	NEGATIVE_REGULATION_OF_METABOLIC_PROCESS	262
120	POSITIVE_REGULATION_OF_JNK_ACTIVITY	18
121	REGULATION_OF_METABOLIC_PROCESS	799
122	PROTEIN_HOMOOLIGOMERIZATION	22
123	POSITIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	86
124	MAPKKK_CASCADE_GO_0000165	104
125	ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	12
126	REGULATION_OF_JNK_ACTIVITY	20
127	REGULATION_OF_NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_METABOLIC_PROCESS	618
128	PROTEIN_MODIFICATION_PROCESS	631
129	PROTEIN_AMINO_ACID_PHOSPHORYLATION	279
130	NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION	37
131	REGULATION_OF_RNA_METABOLIC_PROCESS	471
132	CELLULAR_MACROMOLECULE_METABOLIC_PROCESS	1131
133	NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	197
134	POSITIVE_REGULATION_OF_CELLULAR_PROCESS	668
135	TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER	457
136	POSITIVE_REGULATION_OF_MAPKKK_CASCADE	11
137	PHOSPHORYLATION	313
138	NEGATIVE_REGULATION_OF_BIOLOGICAL_PROCESS	677
139	REGULATION_OF_APOPTOSIS	341
140	NEGATIVE_REGULATION_OF_PROGRAMMED_CELL_DEATH	151
141	REGULATION_OF_PROGRAMMED_CELL_DEATH	342
142	INTRACELLULAR_SIGNALING_CASCADE	667
143	REGULATION_OF_TRANSCRIPTION	566
144	STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_PATHWAY	49
145	ACTIVATION_OF_PROTEIN_KINASE_ACTIVITY	28
146	POSITIVE_REGULATION_OF_TRANSCRIPTION	144
147	APOPTOSIS_GO	431
148	REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_CASCADE	93
149	NUCLEOTIDE_BINDING	224
150	TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	59
151	PHOSPHOTRANSFERASE_ACTIVITY_ALCOHOL_GROUP_AS_ACCEPTOR	334
152	SPECIFIC_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	35
153	PROTEIN_HOMODIMERIZATION_ACTIVITY	121
154	RNA_POLYMERASE_II_TRANSCRIPTION_MEDIATOR_ACTIVITY	13

155	RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	182
156	PURINE_NUCLEOTIDE_BINDING	211
157	LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_ACTIVITY	25
158	N_ACETYLTRANSFERASE_ACTIVITY	21
159	IDENTICAL_PROTEIN_BINDING	304
160	PROTEIN_KINASE_ACTIVITY	285
161	ADENYL_RIBONUCLEOTIDE_BINDING	163
162	ADENYL_NUCLEOTIDE_BINDING	169
163	KINASE_ACTIVITY	369
164	PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	205
165	HISTONE_ACETYLTRANSFERASE_ACTIVITY	16
166	STEROID_HORMONE_RECEPTOR_ACTIVITY	13
167	N_ACYLTRANSFERASE_ACTIVITY	24
168	TRANSCRIPTION_COACTIVATOR_ACTIVITY	123
169	ACETYLTRANSFERASE_ACTIVITY	25
170	TRANSCRIPTION_COREPRESSOR_ACTIVITY	94
171	TRANSCRIPTION_ACTIVATOR_ACTIVITY	173
172	TRANSCRIPTION_REPRESSOR_ACTIVITY	152
173	NUCLEAR_HORMONE_RECEPTOR_BINDING	28
174	MAGNESIUM_ION_BINDING	62
175	TRANSCRIPTION_FACTOR_ACTIVITY	354
176	STEROID_HORMONE_RECEPTOR_BINDING	10
177	TRANSCRIPTION_FACTOR_BINDING	307
178	PROTEIN_HETERODIMERIZATION_ACTIVITY	77
179	TRANSFERASE_ACTIVITY_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	424
180	PROTEIN_DIMERIZATION_ACTIVITY	182
181	PURINE_RIBONUCLEOTIDE_BINDING	205
182	THYROID_HORMONE_RECEPTOR_BINDING	17
183	RIBONUCLEOPROTEIN_BINDING	12
184	GENERAL_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITY	32
185	TRANSFERASE_ACTIVITY_TRANSFERRING_GROUPS_OTHER_THAN_AMINO_ACYL_GROUPS	49
186	DNA_BINDING	602
187	HORMONE_RECEPTOR_BINDING	29
188	ATP_BINDING	156
189	MAP_KINASE_KINASE_KINASE_ACTIVITY	10
190	CASPASE_REGULATOR_ACTIVITY	14
191	TRANSCRIPTION_COFACTOR_ACTIVITY	228

cluster ID = 132
cluster size = 7

	gene set name	size (number of genes in the set)
1	chr11p14	39
2	chr1p	14
3	VANHARANTA_UTERINE_FIBROID_WITH_7Q_DELETION_DN	36
4	KANG_DOXORUBICIN_RESISTANCE_DN	19
5	WANG_RECURRENT_LIVER_CANCER_UP	20
6	MICROVILLUS	11
7	PHOTORECEPTOR_CELL_MAINTENANCE	10

cluster ID = 133
cluster size = 67

	gene set name	size (number of genes in the set)

1	chr1q	6
2	chr5q34	33
3	KEGG_CARDIAC_MUSCLE_CONTRACTION	80
4	KEGG_HYPERTROPHIC_CARDIOMYOPATHY_HCM	85
5	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	76
6	KEGG_DILATED_CARDIOMYOPATHY	92
7	BIOCARTA_GABA_PATHWAY	10
8	REACTOME_ACETYLCHOLINE_BINDING_AND_DOWNSTREAM_EVENTS	16
9	REACTOME_HIGHLY_CALCIUM_PERMEABLE_POSTSYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	13
10	REACTOME_PRESYNAPTIC_NICOTINIC_ACETYLCHOLINE_RECEPTORS	12
11	REACTOME_GABA_A_RECEPTOR_ACTIVATION	12
12	REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT	21
13	REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNELS	43
14	REACTOME_TANDEM_PORE_DOMAIN_POTASSIUM_CHANNELS	12
15	REACTOME_POTASSIUM_CHANNELS	98
16	LEIN_MIDBRAIN_MARKERS	82
17	LEIN_PONS_MARKERS	89
18	LEIN_MEDULLA_MARKERS	81
19	MODULE_141	16
20	MODULE_214	27
21	MODULE_215	15
22	MODULE_267	15
23	MODULE_316	70
24	MODULE_328	14
25	MODULE_396	12
26	VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	15
27	VOLTAGE_GATED_POTASSIUM_CHANNEL_COMPLEX	40
28	NICOTINIC_ACETYLCHOLINE_GATED_RECEPTOR_CHANNEL_COMPLEX	11
29	DI___TRI_VALENT_INORGANIC_CATION_TRANSPORT	32
30	CALCIUM_ION_TRANSPORT	27
31	METAL_ION_TRANSPORT	117
32	REGULATION_OF_HEART_CONTRACTION	25
33	SODIUM_ION_TRANSPORT	22
34	CATION_TRANSPORT	147
35	MONOVALENT_INORGANIC_CATION_TRANSPORT	94
36	POTASSIUM_ION_TRANSPORT	58
37	ION_TRANSPORT	185
38	CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	213
39	INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	12
40	CATION_CHANNEL_ACTIVITY	119
41	SODIUM_CHANNEL_ACTIVITY	17
42	VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	36
43	EXCITATORY_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	21
44	VOLTAGE_GATED_CHANNEL_ACTIVITY	73
45	GATED_CHANNEL_ACTIVITY	122
46	VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	18
47	SUBSTRATE_SPECIFIC_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	344
48	SUBSTRATE_SPECIFIC_CHANNEL_ACTIVITY	156
49	DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	12
50	SUBSTRATE_SPECIFIC_TRANSPORTER_ACTIVITY	392
51	GABA_RECEPTOR_ACTIVITY	11
52	POTASSIUM_CHANNEL_ACTIVITY	50
53	VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	66

54	VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	11
55	LIGAND_GATED_CHANNEL_ACTIVITY	40
56	CALCIUM_CHANNEL_ACTIVITY	33
57	ACETYLCHOLINE_BINDING	17
58	AUXILIARY_TRANSPORT_PROTEIN_ACTIVITY	26
59	POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	14
60	EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	22
61	METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	147
62	ION_CHANNEL_ACTIVITY	149
63	CHANNEL_REGULATOR_ACTIVITY	24
64	AMINE_BINDING	23
65	NICOTINIC_ACETYLCHOLINE_ACTIVATED_CATION_SELECTIVE_CHANNEL_ACTIVITY	11
66	TRANSMEMBRANE_TRANSPORTER_ACTIVITY	375
67	ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	278

cluster ID = 134
cluster size = 42

	gene set name	size (number of genes in the set)
1	chr20q12	51
2	chr6p22	180
3	KEGG_SYSTEMIC_LUPUS_ERYTHEMATOSUS	140
4	REACTOME_MEIOSIS	116
5	REACTOME_RNA_POL_I_TRANSCRIPTION	89
6	REACTOME_TRANSCRIPTION	210
7	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	122
8	REACTOME_CHROMOSOME_MAINTENANCE	122
9	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	64
10	REACTOME_RNA_POL_I_PROMOTER_OPENING	62
11	REACTOME_MEIOTIC_RECOMBINATION	86
12	REACTOME_MEIOTIC_SYNAPSIS	73
13	REACTOME_AMYLOIDS	83
14	REACTOME_PACKAGING_OF_TELOMERE_ENDS	48
15	REACTOME_TELOMERE_MAINTENANCE	75
16	HAHTOLA_SEZARY_SYNDROM_UP	98
17	HAHTOLA_MYCOSIS_FUNGOIDES_UP	19
18	PARK_HSC_VS_MULTIPOTENT_PROGENITORS_DN	18
19	GNATENKO_PLATELET_SIGNATURE	48
20	ZHAN_MULTIPLE_MYELOMA_UP	64
21	HASLINGER_B_CLL_WITH_6Q21_DELETION	20
22	ACEVEDO_LIVER_CANCER_WITH_H3K27ME3_DN	228
23	ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN	120
24	CHUNG_BLISTER_CYTOTOXICITY_DN	44
25	RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP	18
26	HAHTOLA_CTCL_CUTANEOUS	26
27	DAZARD_UV_RESPONSE_CLUSTER_G24	28
28	RAGHAVACHARI_PLATELET_SPECIFIC_GENES	70
29	KRCTCNNNNMANAGC_UNKNOWN	66
30	TTTNNANAGCYR_UNKNOWN	133
31	MODULE_89	14
32	MODULE_90	17
33	MODULE_127	26
34	MODULE_168	22
35	MODULE_189	23

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36    MODULE_203  16
37    MODULE_222  22
38    MODULE_392  18
39    MODULE_421  28
40    MODULE_457  10
41    MODULE_534  18
42    MODULE_552  18


cluster ID = 137
cluster size = 27
      gene set name    size (number of genes in the set)
1     chr5q 6
2     HOEBEKE_LYMPHOID_STEM_CELL_DN      86
3     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_GRANULOCYTE_UP    15
4     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_HSC_UP  185
5     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_UP      55
6     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_UP   204
7     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_ERYTHROCYTE_UP      157
8     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_UP 21
9     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINDED_IN_ERYTHROCYTE_UP   44
10    JAATINEN_HEMATOPOIETIC_STEM_CELL_UP     316
11    GRAHAM_CML_QUIESCENT_VS_NORMAL_QUIESCENT_DN   47
12    GRAHAM_CML_DIVIDING_VS_NORMAL_QUIESCENT_DN    95
13    GRAHAM_NORMAL_QUIESCENT_VS_NORMAL_DIVIDING_UP 66
14    ROSS_AML_OF_FAB_M7_TYPE      68
15    HADDAD_T_LYMPHOCYTE_AND_NK_PROGENITOR_UP      78
16    YAGI_AML_FAB_MARKERS   191
17    GEORGANTAS_HSC_MARKERS 71
18    OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_DN     6
19    FIGUEROA_AML_METHYLATION_CLUSTER_1_UP   125
20    FIGUEROA_AML_METHYLATION_CLUSTER_2_UP   54
21    FIGUEROA_AML_METHYLATION_CLUSTER_3_UP   170
22    FIGUEROA_AML_METHYLATION_CLUSTER_4_UP   112
23    FIGUEROA_AML_METHYLATION_CLUSTER_5_UP   12
24    FIGUEROA_AML_METHYLATION_CLUSTER_6_UP   140
25    FIGUEROA_AML_METHYLATION_CLUSTER_7_UP   118
26    GENTLES_LEUKEMIC_STEM_CELL_UP     29
27    PEPTIDE_METABOLIC_PROCESS    10


cluster ID = 143
cluster size = 46
      gene set name    size (number of genes in the set)
1     chr15q22   118
2     GCM_BAG5   38
3     GCM_BCL2L1  35
4     GCM_ERBB2IP 64
5     GCM_GSTA4   67
6     GCM_SIRT2   43
7     GCM_TINF2   40
8     GCM_AQP4    45
9     GCM_BMPR2   84
10    GCM_CALM1   109
11    GCM_CASP2   27
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12	GCM_CHUK	72
13	GCM_CRKL	64
14	GCM_CSNK1A1	36
15	GCM_CSNK1D	32
16	GCM_DDX11	44
17	GCM_DEAF1	28
18	GCM_DENR	49
19	GCM_DFFA	129
20	GCM_DLG1	78
21	GCM_FANCL	24
22	GCM_GSPT1	167
23	GCM_HBP1	69
24	GCM_IL6ST	54
25	GCM_ING1	66
26	GCM_MAP1B	65
27	GCM_MAP4K4	171
28	GCM_MAPK10	82
29	GCM_MAX	30
30	GCM_MLL	173
31	GCM_MYST2	173
32	GCM_NCAM1	128
33	GCM_NF2	301
34	GCM_NUMA1	56
35	GCM_PPM1D	26
36	GCM_PTK2	145
37	GCM_PTPRD	58
38	GCM_RAB10	176
39	GCM_RAN	197
40	GCM_RAP2A	34
41	GCM_RBM8A	81
42	GCM_SMO	60
43	GCM_SUFU	77
44	GCM_UBE2N	155
45	GCM_USP6	69
46	GCM_ZNF198	118

cluster ID = 150
cluster size = 6

	gene set name	size (number of genes in the set)
1	chr2q23	33
2	RASHI_RESPONSE_TO_IONIZING_RADIATION_3	48
3	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX1_UP	15
4	SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX4_DN	32
5	IIZUKA_LIVER_CANCER_PROGRESSION_G1_G2_DN	25
6	CTAGGAA,MIR-384	64

cluster ID = 152
cluster size = 7

	gene set name	size (number of genes in the set)
1	chr9q13	23
2	INAMURA_LUNG_CANCER_SCC_DN	14
3	SCHMAHL_PDGF_SIGNALING	9
4	PETRETTO_BLOOD_PRESSURE_UP	12

5	AMIT_SERUM_RESPONSE_20_MCF10A	21
6	PARK_HSC_MARKERS	44
7	CHEN_PDGF_TARGETS	19

cluster ID = 166
cluster size = 9

	gene set name	size (number of genes in the set)
1	chr4p13	23
2	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_UP	18
3	WALLACE_PROSTATE_CANCER_RACE_DN	88
4	NIELSEN_LEIOMYOSARCOMA_DN	18
5	MODULE_147	107
6	MODULE_195	147
7	MODULE_356	150
8	MODULE_503	112
9	MODULE_576	110

cluster ID = 168
cluster size = 8

	gene set name	size (number of genes in the set)
1	chr21q22	261
2	chr21q11	45
3	chr20q13	244
4	GINESTIER_BREAST_CANCER_ZNF217_AMPLIFIED_UP	78
5	GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_UP	119
6	NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICON	149
7	CERIBELLI_PROMOTERS_INACTIVE_AND_BOUND_BY_NFY	44
8	CERIBELLI_GENES_INACTIVE_AND_BOUND_BY_NFY	45

cluster ID = 171
cluster size = 6

	gene set name	size (number of genes in the set)
1	chr11q23	163
2	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_SMAD4_DN	8
3	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_23	24
4	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_11	5
5	CALVET_IRINOTECAN_SENSITIVE_VS_RESISTANT_UP	5
6	HASLINGER_B_CLL_WITH_11Q23_DELETION	23

cluster ID = 173
cluster size = 12

	gene set name	size (number of genes in the set)
1	chr7q	13
2	CHANG_POU5F1_TARGETS_DN	8
3	IGLESIAS_E2F_TARGETS_DN	16
4	DAZARD_UV_RESPONSE_CLUSTER_G3	15
5	SU_PANCREAS	54
6	ZHENG_FOXP3_TARGETS_IN_THYMUS_DN	12
7	HANN_RESISTANCE_TO_BCL2_INHIBITOR_DN	48
8	WALLACE_JAK2_TARGETS_UP	26
9	BERGER_MBD2_TARGETS	7

10	GNF2_SERPINI2	25
11	GNF2_SPINK1	27
12	DIGESTION	44

cluster ID = 177
cluster size = 7

	gene set name	size (number of genes in the set)
1	chr9p	8
2	PASTURAL_RIZ1_TARGETS_UP	11
3	YANG_BREAST_CANCER_ESR1_BULK_DN	23
4	SCHUHMACHER_MYC_TARGETS_DN	7
5	VISALA_RESPONSE_TO_HEAT_SHOCK_AND_AGING_UP	15
6	VISALA_AGING_LYMPHOCYTE_DN	19
7	MARSON_FOXP3_TARGETS_STIMULATED_DN	11

cluster ID = 187
cluster size = 8

	gene set name	size (number of genes in the set)
1	chr2p23	102
2	chr2p25	91
3	LASTOWSKA_COAMPLIFIED_WITH_MYCN	43
4	CHEN_NEUROBLASTOMA_COPY_NUMBER_GAINS	50
5	BOYAULT_LIVER_CANCER_SUBCLASS_G6_UP	65
6	CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP	176
7	CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN	52
8	CAGNYGKNAAA_UNKNOWN	75

cluster ID = 189
cluster size = 9

	gene set name	size (number of genes in the set)
1	chr2q	9
2	GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_DN	8
3	RAMJAUN_APOPTOSIS_BY_TGFB1_VIA_MAPK1_DN	8
4	CAFFAREL_RESPONSE_TO_THC_24HR_3_DN	13
5	SARTIPY_BLUNTED_BY_INSULIN_RESISTANCE_DN	18
6	ISHIDA_TARGETS_OF_SYT_SSX_FUSIONS	6
7	VANLOO_SP3_TARGETS_UP	9
8	PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_5	11
9	PARK_OSTEOBLAST_DIFFERENTIATION_BY_PHENYLAMIL_UP	13

cluster ID = 192
cluster size = 6

	gene set name	size (number of genes in the set)
1	chr13q33	29
2	KOBAYASHI_RESPONSE_TO_ROMIDEPSIN	19
3	DACOSTA_ERCC3_ALLELE_XPCS_VS_TTD_UP	28
4	TSENG_IRS1_TARGETS_UP	113
5	TSENG_ADIPOGENIC_POTENTIAL_UP	30
6	THILLAINADESAN_ZNF217_TARGETS_DN	9

cluster ID = 193
cluster size = 26

	gene set name	size (number of genes in the set)
1	chr1p21	73
2	KEGG_OTHER_GLYCAN_DEGRADATION	16
3	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	21
4	KEGG_SPHINGOLIPID_METABOLISM	40
5	KEGG_LYSOSOME	121
6	REACTOME_PTM_GAMMA_CARBOXYLATION_HYPUSINE_FORMATION_AND_ARYLSULFATASE_ACTIVATION	27
7	REACTOME_SPHINGOLIPID_DE_NOVO_BIOSYNTHESIS	31
8	REACTOME_GLYCOSPHINGOLIPID_METABOLISM	38
9	REACTOME_CS_DS_DEGRADATION	12
10	REACTOME_HYALURONAN_UPTAKE_AND_DEGRADATION	10
11	REACTOME_THE_ACTIVATION_OF_ARYLSULFATASES	12
12	REACTOME_HYALURONAN_METABOLISM	14
13	REACTOME_SPHINGOLIPID_METABOLISM	69
14	REACTOME_DIGESTION_OF_DIETARY_CARBOHYDRATE	12
15	PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP	52
16	APPEL_IMATINIB_RESPONSE	33
17	GLYCOLIPID_METABOLIC_PROCESS	16
18	SPHINGOLIPID_METABOLIC_PROCESS	29
19	GLYCOSPHINGOLIPID_METABOLIC_PROCESS	12
20	CERAMIDE_METABOLIC_PROCESS	11
21	SPHINGOID_METABOLIC_PROCESS	12
22	SPHINGOLIPID_BIOSYNTHETIC_PROCESS	10
23	ARYLSULFATASE_ACTIVITY	12
24	HYDROLASE_ACTIVITY_ACTING_ON_GLYCOSYL_BONDS	47
25	HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	37
26	SULFURIC_ESTER_HYDROLASE_ACTIVITY	16

cluster ID = 195
cluster size = 7

	gene set name	size (number of genes in the set)
1	chr5p13	77
2	RASHI_RESPONSE_TO_IONIZING_RADIATION_4	61
3	BREDEMEYER_RAG_SIGNALING_NOT_VIA_ATM_DN	57
4	BOYLAN_MULTIPLE_MYELOMA_D_CLUSTER_DN	40
5	BOYLAN_MULTIPLE_MYELOMA_D_DN	78
6	VANASSE_BCL2_TARGETS_UP	40
7	BOYLAN_MULTIPLE_MYELOMA_PCA3_DN	69

cluster ID = 196
cluster size = 8

	gene set name	size (number of genes in the set)
1	chr14q22	85
2	REACTOME_EICOSANOID_LIGAND_BINDING_RECEPTORS	16
3	REACTOME_PROSTANOID_LIGAND_RECEPTORS	10
4	SABATES_COLORECTAL_ADENOMA_SIZE_DN	14
5	WATANABE_ULCERATIVE_COLITIS_WITH_CANCER_DN	14
6	ROVERSI_GLIOMA_LOH_REGIONS	44
7	NIKOLSKY_BREAST_CANCER_14Q22_AMPLICON	14

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8     RESPIRATORY_GASEOUS_EXCHANGE 14


cluster ID = 207
cluster size = 10
      gene set name    size (number of genes in the set)
1     chr6q26    16
2     REACTOME_ABACAVIR_TRANSPORT_AND_METABOLISM    10
3     REACTOME_ORGANIC_CATION_ANION_ZWITTERION_TRANSPORT  13
4     SU_KIDNEY   15
5     AMUNDSON_GAMMA_RADIATION_RESISTANCE     20
6     VITAMIN_TRANSPORT13
7     COFACTOR_TRANSPORT     11
8     BODY_FLUID_SECRETION   10
9     VITAMIN_BINDING  12
10    COFACTOR_TRANSPORTER_ACTIVITY     10


cluster ID = 211
cluster size = 6
      gene set name    size (number of genes in the set)
1     chrxq26    95
2     TONG_INTERACT_WITH_PTTG1     57
3     ROSS_AML_WITH_PML_RARA_FUSION     77
4     ZHENG_IL22_SIGNALING_DN      42
5     VALK_AML_CLUSTER_12    30
6     VALK_AML_WITH_T_8_21_TRANSLOCATION 5


cluster ID = 212
cluster size = 16
      gene set name    size (number of genes in the set)
1     chr3q23    32
2     MIKKELSEN_MCV6_LCP_WITH_H3K4ME3   162
3     MIKKELSEN_MEF_LCP_WITH_H3K4ME3    128
4     MIKKELSEN_IPS_LCP_WITH_H3K4ME3    174
5     MIKKELSEN_ES_LCP_WITH_H3K4ME3     142
6     MIKKELSEN_NPC_LCP_WITH_H3K4ME3    58
7     LI_DCP2_BOUND_MRNA     89
8     ORGANELLAR_RIBOSOME    22
9     ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT 11
10    MITOCHONDRIAL_SMALL_RIBOSOMAL_SUBUNIT   11
11    MITOCHONDRIAL_MATRIX   46
12    MITOCHONDRIAL_LUMEN    46
13    RIBOSOME   39
14    SMALL_RIBOSOMAL_SUBUNIT      11
15    MITOCHONDRIAL_RIBOSOME 22
16    RIBOSOMAL_SUBUNIT20


cluster ID = 222
cluster size = 20
      gene set name    size (number of genes in the set)
1     chr12p13   270
2     REACTOME_FACILITATIVE_NA_INDEPENDENT_GLUCOSE_TRANSPORTERS12
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3     KORKOLA_EMBRYONAL_CARCINOMA_UP     41
4     KORKOLA_TERATOMA_UP    16
5     KORKOLA_YOLK_SAC_TUMOR_UP    20
6     KORKOLA_CHORIOCARCINOMA_UP   6
7     KORKOLA_SEMINOMA_UP    44
8     BERTUCCI_MEDULLARY_VS_DUCTAL_BREAST_CANCER_UP 206
9     GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_UP   39
10    RODRIGUES_DCC_TARGETS_UP     5
11    ITO_PTTG1_TARGETS_UP   12
12    YAMANAKA_GLIOBLASTOMA_SURVIVAL_UP  11
13    VANDESLUIS_COMMD1_TARGETS_GROUP_4_UP    19
14    KASLER_HDAC7_TARGETS_1_DN    17
15    MODULE_311  18
16    MODULE_573  25
17    CARBOHYDRATE_TRANSPORT 19
18    SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY      11
19    MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY   10
20    CARBOHYDRATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY     16


cluster ID = 223
cluster size = 22
      gene set name    size (number of genes in the set)
1     chr7p15    110
2     MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_UP   276
3     MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_UP   139
4     MULLIGHAN_MLL_SIGNATURE_1_UP 380
5     MULLIGHAN_MLL_SIGNATURE_2_UP 418
6     MULLIGHAN_NPM1_SIGNATURE_3_UP      341
7     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_29   11
8     NIKOLSKY_BREAST_CANCER_7P15_AMPLICON    11
9     ROSS_AML_WITH_MLL_FUSIONS    78
10    ALCALAY_AML_BY_NPM1_LOCALIZATION_UP     140
11    VERHAAK_AML_WITH_NPM1_MUTATED_UP   183
12    YAO_HOXA10_TARGETS_VIA_PROGESTERONE_DN  19
13    MATZUK_IMPLANTATION_AND_UTERINE   22
14    ROSS_LEUKEMIA_WITH_MLL_FUSIONS     78
15    VALK_AML_CLUSTER_2     29
16    VALK_AML_CLUSTER_3     33
17    VALK_AML_CLUSTER_6     33
18    VALK_AML_CLUSTER_16    26
19    VALK_AML_WITH_11Q23_REARRANGED     22
20    VALK_AML_WITH_FLT3_ITD 40
21    YAGI_AML_WITH_T_9_11_TRANSLOCATION 130
22    YAGI_AML_WITH_11Q23_REARRANGED     351


cluster ID = 226
cluster size = 59
      gene set name    size (number of genes in the set)
1     chr12q11   9
2     SENGUPTA_NASOPHARYNGEAL_CARCINOMA_WITH_LMP1_DN      175
3     TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_DUCTAL_NORMAL_DN    198
4     TURASHVILI_BREAST_DUCTAL_CARCINOMA_VS_LOBULAR_NORMAL_DN   69
5     TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORMAL_DN   91
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6	TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_LOBULAR_NORMAL_UP	94
7	DOANE_BREAST_CANCER_ESR1_DN	48
8	SABATES_COLORECTAL_ADENOMA_UP	141
9	LIU_CDX2_TARGETS_DN	8
10	WANG_BARRETTS_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN	37
11	WANG_ESOPHAGUS_CANCER_VS_NORMAL_DN	101
12	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_UP	69
13	YANG_BREAST_CANCER_ESR1_DN	25
14	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_POORLY_DN	382
15	RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DN	110
16	RICKMAN_HEAD_AND_NECK_CANCER_C	113
17	RICKMAN_HEAD_AND_NECK_CANCER_E	89
18	LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT	108
19	ONDER_CDH1_TARGETS_1_DN	169
20	ONDER_CDH1_TARGETS_3_DN	59
21	GILDEA_METASTASIS	30
22	CROMER_METASTASIS_DN	81
23	LIANG_SILENCED_BY_METHYLATION_UP	32
24	JI_CARCINOGENESIS_BY_KRAS_AND_STK11_UP	12
25	SMID_BREAST_CANCER_RELAPSE_IN_BRAIN_UP	39
26	SMID_BREAST_CANCER_RELAPSE_IN_BONE_DN	315
27	SMID_BREAST_CANCER_LUMINAL_B_DN	564
28	SMID_BREAST_CANCER_NORMAL_LIKE_UP	476
29	SMID_BREAST_CANCER_BASAL_UP	648
30	MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_DN	24
31	BERNARD_PPAPDC1B_TARGETS_DN	58
32	HUPER_BREAST_BASAL_VS_LUMINAL_UP	54
33	CROMER_TUMORIGENESIS_DN	51
34	GU_PDEF_TARGETS_DN	39
35	VANTVEER_BREAST_CANCER_ESR1_DN	240
36	POOLA_INVASIVE_BREAST_CANCER_DN	134
37	BOSCO_EPITHELIAL_DIFFERENTIATION_MODULE	69
38	GNF2_CDH3	27
39	GNF2_SERPINB5	28
40	GNF2_SPRR1B	25
41	MODULE_68	26
42	MODULE_153	34
43	MODULE_154	75
44	MODULE_297	80
45	MODULE_298	26
46	MODULE_357	80
47	MODULE_418	60
48	MODULE_438	68
49	MODULE_455	39
50	MODULE_533	45
51	INTERMEDIATE_FILAMENT_CYTOSKELETON	24
52	CORNIFIED_ENVELOPE	13
53	INTERMEDIATE_FILAMENT	24
54	TISSUE_DEVELOPMENT	138
55	KERATINOCYTE_DIFFERENTIATION	15
56	EPIDERMIS_DEVELOPMENT	71
57	ECTODERM_DEVELOPMENT	80
58	STRUCTURAL_MOLECULE_ACTIVITY	244
59	STRUCTURAL_CONSTITUENT_OF_CYTOSKELETON	57

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cluster ID = 240
cluster size = 6
      gene set name     size (number of genes in the set)
1     chr2p14     50
2     GAUSSMANN_MLL_AF4_FUSION_TARGETS_B_UP    26
3     NIELSEN_SCHWANNOMA_UP  18
4     ZHENG_FOXP3_TARGETS_IN_T_LYMPHOCYTE_UP  12
5     GCGCTTT,MIR-518B,MIR-518C,MIR-518D 20
6     AGCGCTT,MIR-518F,MIR-518E,MIR-518A 18


cluster ID = 243
cluster size = 70
      gene set name     size (number of genes in the set)
1     KEGG_N_GLYCAN_BIOSYNTHESIS   46
2     KEGG_O_GLYCAN_BIOSYNTHESIS   30
3     KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_KERATAN_SULFATE 15
4     KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS 25
5     KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES  26
6     KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GLOBO_SERIES    14
7     KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES  15
8     REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS     59
9     REACTOME_TERMINATION_OF_O_GLYCAN_BIOSYNTHESIS 24
10    REACTOME_KERATAN_SULFATE_BIOSYNTHESIS   26
11    REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM   30
12    REACTOME_KERATAN_SULFATE_DEGRADATION    11
13    REACTOME_METABOLISM_OF_PROTEINS   518
14
      REACTOME_POST_TRANSLATIONAL_MODIFICATION_SYNTHESIS_OF_GPI_ANCHORED_PROTEIN
S     26
15    REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION    188
16    REACTOME_SYNTHESIS_OF_SUBSTRATES_IN_N_GLYCAN_BIOSYTHESIS  14
17    REACTOME_ASPARAGINE_N_LINKED_GLYCOSYLATION    81
18
      REACTOME_BIOSYNTHESIS_OF_THE_N_GLYCAN_PRECURSOR_DOLICHOL_LIPID_LINKED_OLIG
OSACCHARIDE_LLO_AND_TRANSFER_TO_A_NASCENT_PROTEIN   29
19    REACTOME_TRANSPORT_TO_THE_GOLGI_AND_SUBSEQUENT_MODIFICATION    33
20    REACTOME_N_GLYCAN_ANTENNAE_ELONGATION   14
21    REACTOME_N_GLYCAN_ANTENNAE_ELONGATION_IN_THE_MEDIAL_TRANS_GOLGI      18
22    REACTOME_SYNTHESIS_OF_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI    17
23    LOPEZ_MESOTELIOMA_SURVIVAL_TIME_DN 7
24    LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_DN  7
25    MATZUK_POST-IMPLANTATION_AND_POST-PARTUM      14
26    WAGNER_APO2_SENSITIVITY      25
27    LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_UP  7
28    LOPEZ_MESOTHELIOMA_SURVIVAL_UP     11
29    ZHAN_MULTIPLE_MYELOMA_CD1_DN 45
30    INTRINSIC_TO_ENDOPLASMIC_RETICULUM_MEMBRANE   24
31    INTEGRAL_TO_ENDOPLASMIC_RETICULUM_MEMBRANE    24
32    ENDOPLASMIC_RETICULUM_MEMBRANE     85
33    ENDOPLASMIC_RETICULUM  294
34    ORGANELLE_MEMBRANE     299
35    NUCLEAR_ENVELOPE_ENDOPLASMIC_RETICULUM_NETWORK      94
36    ENDOMEMBRANE_SYSTEM    220
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37    INTEGRAL_TO_ORGANELLE_MEMBRANE    50
38    GOLGI_STACK 13
39    INTRINSIC_TO_ORGANELLE_MEMBRANE   52
40    ENDOPLASMIC_RETICULUM_PART   97
41    PHOSPHOLIPID_BIOSYNTHETIC_PROCESS 39
42    GLYCEROPHOSPHOLIPID_BIOSYNTHETIC_PROCESS      30
43    GLYCOPROTEIN_METABOLIC_PROCESS    90
44    PROTEIN_AMINO_ACID_N_LINKED_GLYCOSYLATION     30
45    MEMBRANE_LIPID_METABOLIC_PROCESS  101
46    MEMBRANE_LIPID_BIOSYNTHETIC_PROCESS     49
47    LIPOPROTEIN_METABOLIC_PROCESS     33
48    LIPID_METABOLIC_PROCESS      325
49    LIPID_BIOSYNTHETIC_PROCESS   97
50    OLIGOSACCHARIDE_METABOLIC_PROCESS 11
51    UNFOLDED_PROTEIN_RESPONSE    10
52    PROTEIN_AMINO_ACID_LIPIDATION     24
53    GLYCOPROTEIN_BIOSYNTHETIC_PROCESS 74
54    PHOSPHOINOSITIDE_BIOSYNTHETIC_PROCESS   24
55    LIPOPROTEIN_BIOSYNTHETIC_PROCESS  26
56    CELLULAR_LIPID_METABOLIC_PROCESS  255
57    GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS   46
58    PROTEIN_AMINO_ACID_O_LINKED_GLYCOSYLATION     18
59    PHOSPHOLIPID_METABOLIC_PROCESS    74
60    ER_NUCLEAR_SIGNALING_PATHWAY 16
61    PHOSPHOINOSITIDE_METABOLIC_PROCESS 31
62    TRANSFERASE_ACTIVITY_TRANSFERRING_HEXOSYL_GROUPS    81
63    MANNOSYLTRANSFERASE_ACTIVITY 10
64    UDP_GLYCOSYLTRANSFERASE_ACTIVITY  42
65    FUCOSYLTRANSFERASE_ACTIVITY  10
66    TRANSFERASE_ACTIVITY_TRANSFERRING_GLYCOSYL_GROUPS   112
67    ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY      12
68    SIALYLTRANSFERASE_ACTIVITY   10
69    ACETYLGLUCOSAMINYLTRANSFERASE_ACTIVITY  16
70    GALACTOSYLTRANSFERASE_ACTIVITY    16


cluster ID = 244
cluster size = 27
      gene set name    size (number of genes in the set)
1     KEGG_GLYCEROLIPID_METABOLISM 49
2     KEGG_GLYCEROPHOSPHOLIPID_METABOLISM     77
3     KEGG_ETHER_LIPID_METABOLISM  33
4     KEGG_ARACHIDONIC_ACID_METABOLISM  58
5     KEGG_LINOLEIC_ACID_METABOLISM     29
6     KEGG_ALPHA_LINOLENIC_ACID_METABOLISM    19
7     REACTOME_ACYL_CHAIN_REMODELLING_OF_PI   15
8     REACTOME_ACYL_CHAIN_REMODELLING_OF_PC   22
9     REACTOME_PHOSPHOLIPID_METABOLISM  198
10    REACTOME_SYNTHESIS_OF_PA     27
11    REACTOME_ACYL_CHAIN_REMODELLING_OF_PG   16
12    REACTOME_ACYL_CHAIN_REMODELLING_OF_PE   21
13    REACTOME_ACYL_CHAIN_REMODELLING_OF_PS   15
14    REACTOME_GLYCEROPHOSPHOLIPID_BIOSYNTHESIS     82
15    REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS      478
16    YANG_MUC2_TARGETS_DUODENUM_6MO_UP 10
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17	MODULE_346	17
18	MODULE_401	16
19	MODULE_408	18
20	MODULE_417	22
21	LIPASE_ACTIVITY	50
22	INOSITOL_OR_PHOSPHATIDYLINOSITOL_PHOSPHODIESTERASE_ACTIVITY	13
23	PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	40
24	PHOSPHOLIPASE_C_ACTIVITY	15
25	PHOSPHOLIPASE_A2_ACTIVITY	13
26	CARBOXYLESTERASE_ACTIVITY	33
27	PHOSPHOLIPASE_ACTIVITY	42

cluster ID = 246
cluster size = 32

	gene set name	size (number of genes in the set)
1	KEGG_NICOTINATE_AND_NICOTINAMIDE_METABOLISM	24
2	REACTOME_PYRIMIDINE_CATABOLISM	12
3	REACTOME_METABOLISM_OF_NUCLEOTIDES	72
4	REACTOME_PURINE_RIBONUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHESIS	11
5	REACTOME_PURINE_SALVAGE	13
6	REACTOME_PURINE_CATABOLISM	10
7	REACTOME_SYNTHESIS_AND_INTERCONVERSION_OF_NUCLEOTIDE_DI_AND_TRIPHOSPHATES	19
8	REACTOME_PURINE_METABOLISM	33
9	REACTOME_PYRIMIDINE_METABOLISM	24
10	LI_CYTIDINE_ANALOG_PATHWAY	17
11	FERRANDO_HOX11_NEIGHBORS	23
12	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_UP	20
13	TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_UP	271
14	MODULE_21	10
15	MODULE_56	12
16	MODULE_61	50
17	MODULE_102	19
18	MODULE_126	183
19	MODULE_219	27
20	NUCLEOBASENUCLEOSIDE_AND_NUCLEOTIDE_METABOLIC_PROCESS	52
21	CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	11
22	PURINE_NUCLEOTIDE_METABOLIC_PROCESS	12
23	PURINE_RIBONUCLEOTIDE_METABOLIC_PROCESS	10
24	PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	10
25	RIBONUCLEOTIDE_METABOLIC_PROCESS	16
26	NUCLEOTIDE_BIOSYNTHETIC_PROCESS	20
27	NUCLEOTIDE_METABOLIC_PROCESS	42
28	PHOSPHOTRANSFERASE_ACTIVITY_PHOSPHATE_GROUP_AS_ACCEPTOR	18
29	HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_NOT_PEPTIDEBONDSIN_CYCLIC_AMIDINES	16
30	DEAMINASE_ACTIVITY	14
31	NUCLEOTIDE_KINASE_ACTIVITY	13
32	NUCLEOBASENUCLEOSIDENUCLEOTIDE_KINASE_ACTIVITY	25

cluster ID = 250
cluster size = 40

	gene set name	size (number of genes in the set)
1	KEGG_NON_HOMOLOGOUS_END_JOINING	14
2	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	23
3	PID_DNAPK_PATHWAY	16
4	REACTOME_CELL_SURFACE_INTERACTIONS_AT_THE_VASCULAR_WALL	91
5	REACTOME_BASIGIN_INTERACTIONS	30
6	REACTOME_ION_TRANSPORT_BY_P_TYPE_ATPASES	34
7	REACTOME_ION_CHANNEL_TRANSPORT	55
8	REACTOME_EARLY_PHASE_OF_HIV_LIFE_CYCLE	21
9	REACTOME_BINDING_AND_ENTRY_OF_HIV_VIRION	10
10	REACTOME_INTEGRATION_OF_PROVIRUS	16
11	REACTOME_APOBEC3G_MEDIATED_RESISTANCE_TO_HIV1_INFECTION	12
12	PETRETTO_BLOOD_PRESSURE_DN	7
13	COLLIS_PRKDC_SUBSTRATES	20
14	COLLIS_PRKDC_REGULATORS	15
15	ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_DN	19
16	MODULE_229	31
17	MODULE_318	28
18	RESPONSE_TO_IONIZING_RADIATION	10
19	HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDES	228
20	DI___TRI_VALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	22
21	DNA_HELICASE_ACTIVITY	25
22	RNA_HELICASE_ACTIVITY	24
23	ATP_DEPENDENT_HELICASE_ACTIVITY	27
24	CATION_TRANSPORTING_ATPASE_ACTIVITY	11
25	ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS_PHOSPHORYLATIVE_MECHANISM	20
26	CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	11
27	HYDROLASE_ACTIVITY_ACTING_ON_ACID_ANHYDRIDESCATALYZING_TRANSMEMBRANE_MOVEMENT_OF_SUBSTANCES	39
28	HELICASE_ACTIVITY	51
29	NUCLEOSIDE_TRIPHOSPHATASE_ACTIVITY	212
30	ATPASE_ACTIVITY_COUPLED_TO_TRANSMEMBRANE_MOVEMENT_OF_IONS	24
31	ATP_DEPENDENT_RNA_HELICASE_ACTIVITY	17
32	ATPASE_ACTIVITY_COUPLED	93
33	PRIMARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	40
34	RNA_DEPENDENT_ATPASE_ACTIVITY	18
35	ATP_DEPENDENT_DNA_HELICASE_ACTIVITY	11
36	DNA_DEPENDENT_ATPASE_ACTIVITY	22
37	ATPASE_ACTIVITY	112
38	GTPASE_ACTIVITY	99
39	PYROPHOSPHATASE_ACTIVITY	226
40	ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	40

cluster ID = 257
cluster size = 8

	gene set name	size (number of genes in the set)
1	KEGG_CIRCADIAN_RHYTHM_MAMMAL	13
2	PID_CIRCADIANPATHWAY	16
3	WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_LIVER_DAMAGE_UP	8
4	TUOMISTO_TUMOR_SUPPRESSION_BY_COL13A1_UP	18
5	MATZUK_STEROIDOGENESIS	7

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6     MARIADASON_RESPONSE_TO_BUTYRATE_CURCUMIN_SULINDAC_TSA_2  8
7     MODULE_340  26
8     CIRCADIAN_RHYTHM 14


cluster ID = 258
cluster size = 18
      gene set name    size (number of genes in the set)
1     KEGG_PRIMARY_IMMUNODEFICIENCY     35
2     KLEIN_TARGETS_OF_BCR_ABL1_FUSION  45
3     SHIN_B_CELL_LYMPHOMA_CLUSTER_9    19
4     MORI_PRE_BI_LYMPHOCYTE_DN   77
5     MORI_LARGE_PRE_BII_LYMPHOCYTE_DN  58
6     MORI_IMMATURE_B_LYMPHOCYTE_UP     53
7     MORI_MATURE_B_LYMPHOCYTE_UP 90
8     MORI_PLASMA_CELL_DN   33
9     KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN58
10    TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN    38
11    HOFMANN_CELL_LYMPHOMA_UP    50
12    YU_MYC_TARGETS_DN55
13    ZHAN_MULTIPLE_MYELOMA_CD2_UP 45
14    BASSO_CD40_SIGNALING_DN     68
15    ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_DN     52
16    HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_UP  70
17    ZHAN_EARLY_DIFFERENTIATION_GENES_DN     42
18    ZHAN_MULTIPLE_MYELOMA_MF_DN  41


cluster ID = 259
cluster size = 23
      gene set name    size (number of genes in the set)
1     BIOCARTA_GRANULOCYTES_PATHWAY     14
2     BIOCARTA_LYM_PATHWAY   11
3     BIOCARTA_BLYMPHOCYTE_PATHWAY 11
4     BIOCARTA_LAIR_PATHWAY  17
5     BIOCARTA_MONOCYTE_PATHWAY    11
6     PID_INTEGRIN_CS_PATHWAY     26
7     PID_ARF6_TRAFFICKINGPATHWAY  49
8     PID_INTEGRIN2_PATHWAY  29
9     PID_INTEGRIN5_PATHWAY  17
10    REACTOME_INSULIN_SYNTHESIS_AND_PROCESSING     21
11    DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_UP  6
12    AMIT_EGF_RESPONSE_20_MCF10A  14
13    VERRECCHIA_RESPONSE_TO_TGFB1_C5   21
14    VERRECCHIA_DELAYED_RESPONSE_TO_TGFB1    39
15    VERRECCHIA_RESPONSE_TO_TGFB1_C4   13
16    YAMANAKA_GLIOBLASTOMA_SURVIVAL_DN  9
17    OKAMOTO_LIVER_CANCER_MULTICENTRIC_OCCURRENCE_UP     25
18    MODULE_275  16
19    MODULE_412  13
20    RECEPTOR_COMPLEX 56
21    INTEGRIN_COMPLEX 19
22    LEUKOCYTE_CHEMOTAXIS   13
23    LEUKOCYTE_MIGRATION    16
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cluster ID = 260
cluster size = 9
      gene set name    size (number of genes in the set)
1     BIOCARTA_NEUROTRANSMITTERS_PATHWAY 6
2     REACTOME_AMINE_DERIVED_HORMONES   15
3     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_GRANULOCYTE_DN    7
4     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_GRANULOCYTE_DN     17
5     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_MONOCYTE_DN  54
6     TONKS_TARGETS_OF_RUNX1_RUNX1T1_FUSION_SUSTAINED_IN_MONOCYTE_DN 8
7     NAKAJIMA_MAST_CELL     46
8     CARBOXY_LYASE_ACTIVITY 14
9     CARBON_CARBON_LYASE_ACTIVITY 18


cluster ID = 265
cluster size = 25
      gene set name    size (number of genes in the set)
1     BIOCARTA_CHREBP2_PATHWAY     42
2     REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE 16
3     REACTOME_CTLA4_INHIBITORY_SIGNALING     21
4     REACTOME_PLATELET_SENSITIZATION_BY_LDL  16
5     MODULE_173  16
6     MODULE_407  13
7     PROTEIN_SERINE_THREONINE_PHOSPHATASE_COMPLEX  10
8     DEPHOSPHORYLATION 70
9     NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY    17
10    INACTIVATION_OF_MAPK_ACTIVITY     14
11    NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY   35
12    NEGATIVE_REGULATION_OF_CATALYTIC_ACTIVITY     69
13    PROTEIN_AMINO_ACID_DEPHOSPHORYLATION    63
14    PROTEIN_PHOSPHATASE_TYPE_2A_REGULATOR_ACTIVITY      14
15    PROTEIN_TYROSINE_PHOSPHATASE_ACTIVITY   53
16    PHOSPHORIC_MONOESTER_HYDROLASE_ACTIVITY 112
17    PHOSPHATASE_INHIBITOR_ACTIVITY     11
18    HYDROLASE_ACTIVITY_ACTING_ON_ESTER_BONDS      269
19    PHOSPHORIC_ESTER_HYDROLASE_ACTIVITY     153
20    PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY 24
21    TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY 19
22    PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY     81
23    PROTEIN_PHOSPHATASE_BINDING  10
24    PHOSPHATASE_BINDING    13
25    PHOSPHATASE_REGULATOR_ACTIVITY    26


cluster ID = 266
cluster size = 58
      gene set name    size (number of genes in the set)
1     BIOCARTA_RANMS_PATHWAY 10
2     PID_RANBP2PATHWAY 11
3     REACTOME_METABOLISM_OF_NON_CODING_RNA   49
4     REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES      66
5     REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM      54
6     REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT
      33
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7     REACTOME_GLUCOSE_TRANSPORT   38
8     REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY  27
9     REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS 27
10    REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS 33
11    REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN 27
12    LIU_BREAST_CANCER30
13    WANG_TARGETS_OF_MLL_CBP_FUSION_DN  45
14    LEE_CALORIE_RESTRICTION_MUSCLE_DN  51
15    KAPOSI_LIVER_CANCER_MET_UP   18
16    KAMMINGA_SENESCENCE    41
17    GKCGCNNNNNNNTGAYG_UNKNOWN    59
18    MODULE_352  17
19    PORE_COMPLEX      36
20    NUCLEAR_ENVELOPE 73
21    NUCLEAR_MEMBRANE 50
22    NUCLEAR_PORE      31
23    NUCLEAR_MEMBRANE_PART  42
24    NUCLEAR_IMPORT    50
25    ESTABLISHMENT_OF_PROTEIN_LOCALIZATION    190
26    ESTABLISHMENT_OF_LOCALIZATION      870
27    NEGATIVE_REGULATION_OF_TRANSPORT   20
28    NUCLEOBASENUCLEOSIDENUCLEOTIDE_AND_NUCLEIC_ACID_TRANSPORT31
29    INTRACELLULAR_TRANSPORT      280
30    INTRACELLULAR_PROTEIN_TRANSPORT    145
31    ESTABLISHMENT_OF_CELLULAR_LOCALIZATION  353
32    NUCLEAR_TRANSPORT88
33    PROTEIN_TARGETING109
34    MAINTENANCE_OF_CELLULAR_LOCALIZATION    12
35    PROTEIN_IMPORT    62
36    POSITIVE_REGULATION_OF_TRANSPORT   23
37    PHAGOCYTOSIS      17
38    REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT     22
39    NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT      11
40    PROTEIN_EXPORT_FROM_NUCLEUS  12
41    PROTEIN_IMPORT_INTO_NUCLEUS  48
42    NUCLEAR_EXPORT    33
43    MAINTENANCE_OF_LOCALIZATION  22
44    MACROMOLECULE_LOCALIZATION   235
45    RNA_EXPORT_FROM_NUCLEUS      20
46    TRANSPORT   795
47    NLS_BEARING_SUBSTRATE_IMPORT_INTO_NUCLEUS     13
48    MAINTENANCE_OF_CELLULAR_PROTEIN_LOCALIZATION  11
49    REGULATION_OF_INTRACELLULAR_TRANSPORT   25
50    REGULATION_OF_ENDOCYTOSIS    16
51    CELLULAR_LOCALIZATION  371
52    REGULATION_OF_TRANSPORT      67
53    PROTEIN_TRANSPORT157
54    PROTEIN_IMPORT_INTO_NUCLEUS_TRANSLOCATION     11
55    PROTEIN_LOCALIZATION   214
56    REGULATION_OF_PROTEIN_IMPORT_INTO_NUCLEUS     16
57    MAINTENANCE_OF_PROTEIN_LOCALIZATION     13
58    NUCLEOCYTOPLASMIC_TRANSPORT  87


cluster ID = 267
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cluster size = 31
      gene set name    size (number of genes in the set)
1     BIOCARTA_TEL_PATHWAY   18
2     MARKS_ACETYLATED_NON_HISTONE_PROTEINS   15
3     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_6    6
4     SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP  9
5     SCIAN_INVERSED_TARGETS_OF_TP53_AND_TP73_UP    11
6     HE_PTEN_TARGETS_UP     16
7     DING_LUNG_CANCER_MUTATED_SIGNIFICANTLY  26
8     DING_LUNG_CANCER_MUTATED_FREQUENTLY     12
9     CHEOK_RESPONSE_TO_MERCAPTOPURINE_UP     13
10    HASLINGER_B_CLL_WITH_17P13_DELETION     21
11    WEIGEL_OXIDATIVE_STRESS_BY_TBH_AND_H2O2 36
12    MARIADASON_RESPONSE_TO_CURCUMIN_SULINDAC_7    19
13    GEISS_RESPONSE_TO_DSRNA_DN   16
14    MACLACHLAN_BRCA1_TARGETS_DN  16
15    MOREIRA_RESPONSE_TO_TSA_UP   28
16    JIANG_TIP30_TARGETS_DN 24
17    DING_LUNG_CANCER_MUTATED_RECURRENTLY    6
18    DING_LUNG_CANCER_BY_MUTATION_RATE  20
19    TCGA_GLIOBLASTOMA_MUTATED    8
20    CGGAARNGGCNG_UNKNOWN   51
21    MODULE_458  38
22    INSOLUBLE_FRACTION     15
23    NUCLEAR_MATRIX   12
24    RESPONSE_TO_NUTRIENT   17
25    RESPONSE_TO_EXTRACELLULAR_STIMULUS 33
26    CELLULAR_RESPONSE_TO_STRESS  10
27    RESPONSE_TO_NUTRIENT_LEVELS  29
28    AGING 13
29    CELLULAR_RESPONSE_TO_STIMULUS      19
30    CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS   12
31    CELLULAR_RESPONSE_TO_NUTRIENT_LEVELS    10


cluster ID = 271
cluster size = 7
      gene set name    size (number of genes in the set)
1     PID_VEGF_VEGFR_PATHWAY 10
2     REACTOME_VEGF_LIGAND_RECEPTOR_INTERACTIONS    10
3     AGARWAL_AKT_PATHWAY_TARGETS  10
4     HE_PTEN_TARGETS_DN     7
5     KANG_AR_TARGETS_DN     19
6     ZHU_SKIL_TARGETS_UP    20
7     KASLER_HDAC7_TARGETS_2_DN    32


cluster ID = 273
cluster size = 54
      gene set name    size (number of genes in the set)
1     REACTOME_RECYCLING_OF_BILE_ACIDS_AND_SALTS    11
2     REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE  31
3     REACTOME_TRANSMEMBRANE_TRANSPORT_OF_SMALL_MOLECULES 413
4     REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT 241
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5	REACTOME_TRANSPORT_OF_GLUCOSE_AND_OTHER_SUGARS_BILE_SALTS_AND_ORGANIC_ACIDS_METAL_IONS_AND_AMINE_COMPOUNDS	89
6	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	94
7	REACTOME_AMINO_ACID_AND_OLIGOPEPTIDE_SLC_TRANSPORTERS	49
8	REACTOME_NA_CL_DEPENDENT_NEUROTRANSMITTER_TRANSPORTERS	17
9	REACTOME_ZINC_TRANSPORTERS	15
10	REACTOME_METAL_ION_SLC_TRANSPORTERS	22
11	REACTOME_BILE_SALT_AND_ORGANIC_ANION_SLC_TRANSPORTERS	11
12	REACTOME_AMINE_COMPOUND_SLC_TRANSPORTERS	27
13	REACTOME_TRANSPORT_OF_VITAMINS_NUCLEOSIDES_AND_RELATED_MOLECULES	31
14	REACTOME_TRANSPORT_OF_ORGANIC_ANIONS	11
15	CASTELLANO_HRAS_TARGETS_DN	6
16	FARMER_BREAST_CANCER_CLUSTER_4	16
17	SASAI_TARGETS_OF_CXCR6_AND_PTCH1_UP	13
18	MIKKELSEN_IPS_LCP_WITH_H3K4ME3_AND_H3K27ME3	5
19	MIKKELSEN_ES_LCP_WITH_H3K4ME3_AND_H3K27ME3	6
20	MAEKAWA_ATF2_TARGETS	24
21	MODULE_71	22
22	MODULE_162	19
23	MODULE_186	20
24	MODULE_218	20
25	MODULE_368	18
26	MODULE_415	13
27	INORGANIC_ANION_TRANSPORT	18
28	AMINO_ACID_TRANSPORT	26
29	ORGANIC_ACID_TRANSPORT	42
30	MONOCARBOXYLIC_ACID_TRANSPORT	10
31	ANION_TRANSPORT	31
32	NEUTRAL_AMINO_ACID_TRANSPORT	10
33	CARBOXYLIC_ACID_TRANSPORT	41
34	TRANSITION_METAL_ION_TRANSPORT	12
35	AMINE_TRANSPORT	38
36	ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	122
37	INORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	19
38	SYMPORTER_ACTIVITY	31
39	PHOSPHATE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	13
40	SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	47
41	SOLUTE_SODIUM_SYMPORTER_ACTIVITY	13
42	ANION_CATION_SYMPORTER_ACTIVITY	16
43	ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	10
44	AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	29
45	NEUTRAL_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	12
46	ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	59
47	AMINE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	41
48	MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	11
49	ANION_CHANNEL_ACTIVITY	20
50	CHLORIDE_CHANNEL_ACTIVITY	19
51	L_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	17
52	ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	45
53	CARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	44
54	TRANSITION_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	10

cluster ID = 274
cluster size = 22

	gene set name	size (number of genes in the set)
1	REACTOME_METABOLISM_OF_STEROID_HORMONES_AND_VITAMINS_A_AND_D	35
2	REACTOME_ANDROGEN_BIOSYNTHESIS	10
3	REACTOME_GLYCOPROTEIN_HORMONES	12
4	REACTOME_PEPTIDE_HORMONE_BIOSYNTHESIS	14
5	REACTOME_STEROID_HORMONES	29
6	REACTOME_HORMONE_LIGAND_BINDING_RECEPTORS	10
7	KORKOLA_CHORIOCARCINOMA	6
8	ABBUD_LIF_SIGNALING_2_DN	7
9	SU_PLACENTA	30
10	MATZUK_CENTRAL_FOR_FEMALE_FERTILITY	29
11	GYORFFY_DOXORUBICIN_RESISTANCE	56
12	GNF2_CDKN1C	27
13	GNF2_EGFR	32
14	GNF2_IGFBP1	35
15	GNF2_KISS1	49
16	GNF2_MMP11	42
17	GNF2_TIMP2	46
18	MODULE_382	28
19	DEVELOPMENT_OF_PRIMARY_SEXUAL_CHARACTERISTICS	26
20	MALE_GONAD_DEVELOPMENT	12
21	NEUROPEPTIDE_HORMONE_ACTIVITY	12
22	HORMONE_ACTIVITY	44

cluster ID = 275
cluster size = 20

	gene set name	size (number of genes in the set)
1	REACTOME_SIGNALING_BY_NODAL	18
2	KERLEY_RESPONSE_TO_CISPLATIN_DN	5
3	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_9	8
4	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_16	14
5	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_14	6
6	KORKOLA_EMBRYONAL_CARCINOMA	13
7	FUNG_IL2_SIGNALING_2	12
8	FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES_T1	9
9	BENPORATH_ES_2	40
10	TESAR_ALK_TARGETS_HUMAN_ES_4D_DN	6
11	TESAR_ALK_TARGETS_HUMAN_ES_5D_DN	7
12	NELSON_RESPONSE_TO_ANDROGEN_DN	19
13	TESAR_ALK_AND_JAK_TARGETS_MOUSE_ES_D4_DN	6
14	BIERIE_INFLAMMATORY_RESPONSE_TGFB1	5
15	CONRAD_STEM_CELL	39
16	MIKKELSEN_PLURIPOTENT_STATE_UP	11
17	KORKOLA_CORRELATED_WITH_POU5F1	34
18	KOHOUTEK_CCNT2_TARGETS	58
19	EXTRINSIC_TO_PLASMA_MEMBRANE	13
20	EXTRINSIC_TO_MEMBRANE	25

cluster ID = 276
cluster size = 21

	gene set name	size (number of genes in the set)
1	REACTOME_HDL_MEDIATED_LIPID_TRANSPORT	15
2	REACTOME_LIPID_DIGESTION_MOBILIZATION_AND_TRANSPORT	46
3	REACTOME_LIPOPROTEIN_METABOLISM	28
4	REACTOME_CHYLOMICRON_MEDIATED_LIPID_TRANSPORT	16
5	NIELSEN_LIPOSARCOMA_UP	18
6	MODULE_236	18
7	ENDOCYTIC_VESICLE	14
8	REGULATION_OF_LIPID_METABOLIC_PROCESS	12
9	LIPID_TRANSPORT	28
10	PROTEIN_STABILIZATION	11
11	REGULATION_OF_CATABOLIC_PROCESS	16
12	LIPID_HOMEOSTASIS	16
13	TRIACYLGLYCEROL_METABOLIC_PROCESS	10
14	REGULATION_OF_PROTEIN_STABILITY	19
15	LIPID_BINDING	87
16	STEROL_BINDING	11
17	PHOSPHOLIPID_BINDING	47
18	PHOSPHOINOSITIDE_BINDING	20
19	STEROID_BINDING	18
20	LIPID_TRANSPORTER_ACTIVITY	28
21	PHOSPHOLIPID_TRANSPORTER_ACTIVITY	12

cluster ID = 277
cluster size = 10

	gene set name	size (number of genes in the set)
1	REACTOME_CGMP_EFFECTS	19
2	REACTOME_NITRIC_OXIDE_STIMULATES_GUANYLATE_CYCLASE	25
3	REACTOME_PLATELET_HOMEOSTASIS	78
4	ZHENG_FOXP3_TARGETS_DN	5
5	WU_ALZHEIMER_DISEASE_DN	19
6	MODULE_465	16
7	MODULE_560	12
8	PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	12
9	3_5_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	13
10	CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	14

cluster ID = 278
cluster size = 20

	gene set name	size (number of genes in the set)
1	REACTOME_CALNEXIN_CALRETICULIN_CYCLE	11
2	REACTOME_N_GLYCAN_TRIMMING_IN_THE_ER_AND_CALNEXIN_CALRETICULIN_CYCLE	13
3	PRAMOONJAGO_SOX4_TARGETS_DN	51
4	TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_UP	78
5	FLECHNER_PBL_KIDNEY_TRANSPLANT_OK_VS_DONOR_DN	41
6	KLEIN_PRIMARY_EFFUSION_LYMPHOMA_UP	51
7	FLECHNER_PBL_KIDNEY_TRANSPLANT_REJECTED_VS_OK_UP	63
8	JIANG_VHL_TARGETS	138
9	GRADE_COLON_VS_RECTAL_CANCER_UP	38
10	CUI_GLUCOSE_DEPRIVATION	60
11	SHAFFER_IRF4_MULTIPLE_MYELOMA_PROGRAM	36
12	SHAFFER_IRF4_TARGETS_IN_MYELOMA_VS_MATURE_B_LYMPHOCYTE	101
13	SHAFFER_IRF4_TARGETS_IN_PLASMA_CELL_VS_MATURE_B_LYMPHOCYTE	67

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14     SHAFFER_IRF4_TARGETS_IN_ACTIVATED_B_LYMPHOCYTE      81
15     SHAFFER_IRF4_TARGETS_IN_ACTIVATED_DENDRITIC_CELL    65
16     ZHAN_LATE_DIFFERENTIATION_GENES_UP 33
17     JIANG_HYPOXIA_VIA_VHL  34
18     TCGATGG,MIR-213  7
19     ER_GOLGI_INTERMEDIATE_COMPARTMENT  24
20     ENDOPLASMIC_RETICULUM_LUMEN  14


cluster ID = 281
cluster size = 10
      gene set name    size (number of genes in the set)
1     WEST_ADRENOCORTICAL_TUMOR_MARKERS_DN    20
2     NADERI_BREAST_CANCER_PROGNOSIS_DN  18
3     SHI_SPARC_TARGETS_DN   13
4     TERAMOTO_OPN_TARGETS_CLUSTER_6    27
5     GROSS_HIF1A_TARGETS_UP 8
6     SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX2_UP   6
7     SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX5_UP   11
8     SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX6_UP   8
9     MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN     10
10    NIELSEN_SCHWANNOMA_DN  18


cluster ID = 285
cluster size = 15
      gene set name    size (number of genes in the set)
1     PYEON_HPV_POSITIVE_TUMORS_DN 10
2     LOPEZ_MESOTELIOMA_SURVIVAL_TIME_UP 14
3     LOPEZ_MESOTHELIOMA_SURVIVAL_WORST_VS_BEST_UP  14
4     CHIN_BREAST_CANCER_COPY_NUMBER_UP  27
5     SUZUKI_AMPLIFIED_IN_ORAL_CANCER    16
6     SNIJDERS_AMPLIFIED_IN_HEAD_AND_NECK_TUMORS    37
7     WILLERT_WNT_SIGNALING  24
8     VERNELL_RETINOBLASTOMA_PATHWAY_DN  22
9     ZHAN_MULTIPLE_MYELOMA_SPIKED 22
10    SIMBULAN_PARP1_TARGETS_UP    31
11    BURTON_ADIPOGENESIS_7  51
12    CLIMENT_BREAST_CANCER_COPY_NUMBER_UP    23
13    SYED_ESTRADIOL_RESPONSE      19
14    LOPEZ_MESOTHELIOMA_SURVIVAL_OVERALL_DN  16
15    LOPEZ_MESOTHELIOMA_SURVIVAL_DN    12


cluster ID = 292
cluster size = 9
      gene set name    size (number of genes in the set)
1     DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_UP      59
2     DAVICIONI_MOLECULAR_ARMS_VS_ERMS_UP     332
3     DAVICIONI_TARGETS_OF_PAX_FOXO1_FUSIONS_UP     255
4     DAVICIONI_RHABDOMYOSARCOMA_PAX_FOXO1_FUSION_UP      64
5     LIU_CMYB_TARGETS_UP    165
6     LIU_VMYB_TARGETS_UP    127
7     EBAUER_TARGETS_OF_PAX3_FOXO1_FUSION_DN  48
8     REN_ALVEOLAR_RHABDOMYOSARCOMA_UP  98
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9     IZADPANAH_STEM_CELL_ADIPOSE_VS_BONE_UP  126


cluster ID = 294
cluster size = 13
      gene set name    size (number of genes in the set)
1     FOURNIER_ACINAR_DEVELOPMENT_LATE_UP     11
2     AKL_HTLV1_INFECTION_UP 27
3     AIYAR_COBRA1_TARGETS_DN      29
4     SANSOM_APC_TARGETS_UP  126
5     SANSOM_APC_TARGETS     212
6     SANSOM_APC_MYC_TARGETS 217
7     SANSOM_APC_TARGETS_REQUIRE_MYC    210
8     SANSOM_WNT_PATHWAY_REQUIRE_MYC    58
9     CLAUS_PGR_POSITIVE_MENINGIOMA_DN  12
10    ASGHARZADEH_NEUROBLASTOMA_POOR_SURVIVAL_DN    46
11    GERHOLD_RESPONSE_TO_TZD_DN   13
12    TORCHIA_TARGETS_OF_EWSR1_FLI1_FUSION_TOP20_DN 18
13    TTCCGTT,MIR-191  29


cluster ID = 295
cluster size = 11
      gene set name    size (number of genes in the set)
1     NAM_FXYD5_TARGETS_DN   18
2     CHOW_RASSF1_TARGETS_DN 29
3     XU_HGF_TARGETS_REPRESSED_BY_AKT1_UP     10
4     MANTOVANI_NFKB_TARGETS_UP    43
5     MANTOVANI_VIRAL_GPCR_SIGNALING_UP 86
6     WOTTON_RUNX_TARGETS_UP 21
7     LEI_HOXC8_TARGETS_UP   12
8     NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_UP      18
9     NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_DN    20
10    MISHRA_CARCINOMA_ASSOCIATED_FIBROBLAST_UP     24
11    YIH_RESPONSE_TO_ARSENITE_C5  10


cluster ID = 297
cluster size = 31
      gene set name    size (number of genes in the set)
1     FRASOR_TAMOXIFEN_RESPONSE_DN 11
2     ROY_WOUND_BLOOD_VESSEL_DN    22
3     TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_6HR_DN   41
4     CALVET_IRINOTECAN_SENSITIVE_VS_REVERTED_DN    5
5     FALVELLA_SMOKERS_WITH_LUNG_CANCER 80
6     CAFFAREL_RESPONSE_TO_THC_8HR_3_UP 5
7     RANKIN_ANGIOGENIC_TARGETS_OF_VHL_HIF2A_DN     8
8     SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX2_DN   7
9     SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX5_DN   8
10    SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX6_DN   5
11    SCHAEFFER_PROSTATE_DEVELOPMENT_AND_CANCER_BOX3      5
12    BALDWIN_PRKCI_TARGETS_UP     35
13    KYNG_DNA_DAMAGE_BY_GAMMA_RADIATION 81
14    KYNG_DNA_DAMAGE_BY_UV  62
15    KYNG_DNA_DAMAGE_BY_4NQO_OR_UV     63
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16    KYNG_DNA_DAMAGE_BY_GAMMA_AND_UV_RADIATION     88
17    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_OLD    13
18    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_4NQO_IN_WS     40
19    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_OLD   31
20    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_GAMMA_IN_WS    33
21    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_OLD 25
22    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_NOT_BY_UV_IN_WS  12
23    KYNG_DNA_DAMAGE_DN     195
24    KYNG_DNA_DAMAGE_UP     226
25    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_UP   56
26    KYNG_ENVIRONMENTAL_STRESS_RESPONSE_DN   21
27    SPIRA_SMOKERS_LUNG_CANCER_UP 38
28    KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_UP 93
29    VACUOLAR_TRANSPORT     13
30    LYSOSOMAL_TRANSPORT    10
31    ENDOSOME_TRANSPORT     23


cluster ID = 298
cluster size = 9
      gene set name    size (number of genes in the set)
1     WATANABE_COLON_CANCER_MSI_VS_MSS_UP     29
2     GAUSSMANN_MLL_AF4_FUSION_TARGETS_D_DN   9
3     SCHRAMM_INHBA_TARGETS_UP     7
4     NAKAYAMA_FRA2_TARGETS  43
5     HASEGAWA_TUMORIGENESIS_BY_RET_C634R     11
6     SWEET_KRAS_TARGETS_DN  66
7     HINATA_NFKB_TARGETS_KERATINOCYTE_DN     23
8     LEE_SP4_THYMOCYTE 14
9     LIU_IL13_MEMORY_MODEL_DN     5


cluster ID = 300
cluster size = 9
      gene set name    size (number of genes in the set)
1     KOBAYASHI_EGFR_SIGNALING_6HR_UP   7
2     CHEOK_RESPONSE_TO_HD_MTX_DN  24
3     SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_DN 21
4     HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_UP     22
5     HOLLEMAN_ASPARAGINASE_RESISTANCE_B_ALL_DN     15
6     HOLLEMAN_DAUNORUBICIN_B_ALL_DN    12
7     HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_DN 19
8     HOLLEMAN_DAUNORUBICIN_ALL_DN 8
9     HOLLEMAN_ASPARAGINASE_RESISTANCE_ALL_DN 25


cluster ID = 302
cluster size = 6
      gene set name    size (number of genes in the set)
1     GAZDA_DIAMOND_BLACKFAN_ANEMIA_MYELOID_DN      38
2     GAZDA_DIAMOND_BLACKFAN_ANEMIA_PROGENITOR_DN   66
3     DITTMER_PTHLH_TARGETS_UP     112
4     HEDENFALK_BREAST_CANCER_HEREDITARY_VS_SPORADIC     50
5     HEDENFALK_BREAST_CANCER_BRCA1_VS_BRCA2  163
6     MODULE_243  81
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cluster ID = 303
cluster size = 11
      gene set name    size (number of genes in the set)
1     IGARASHI_ATF4_TARGETS_UP      6
2     YEMELYANOV_GR_TARGETS_DN      10
3     HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_2NM_DN      25
4     HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_2_DN    19
5     WIEMANN_TELOMERE_SHORTENING_AND_CHRONIC_LIVER_DAMAGE_DN   6
6     FRIDMAN_SENESCENCE_DN  13
7     MURAKAMI_UV_RESPONSE_6HR_DN  21
8     MURAKAMI_UV_RESPONSE_24HR    20
9     TSAI_RESPONSE_TO_RADIATION_THERAPY 32
10    MURAKAMI_UV_RESPONSE_1HR_DN  10
11    TERAO_AOX4_TARGETS_HG_DN      6


cluster ID = 304
cluster size = 6
      gene set name    size (number of genes in the set)
1     IGARASHI_ATF4_TARGETS_DN      90
2     ONDER_CDH1_TARGETS_1_UP       140
3     ONDER_CDH1_TARGETS_3_UP       17
4     YAO_HOXA10_TARGETS_VIA_PROGESTERONE_UP  79
5     YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_1     68
6     YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_6     75


cluster ID = 306
cluster size = 12
      gene set name    size (number of genes in the set)
1     TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBULAR_UP 68
2     RIZ_ERYTHROID_DIFFERENTIATION_HBZ  41
3     RIZ_ERYTHROID_DIFFERENTIATION_HEMGN     31
4     RIZ_ERYTHROID_DIFFERENTIATION_6HR  40
5     KYNG_RESPONSE_TO_H2O2_VIA_ERCC6    17
6     KYNG_RESPONSE_TO_H2O2  71
7     GUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_DN      9
8     KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_DN 46
9     V$MEF2_04   25
10    MODULE_284  45
11    MODULE_285  49
12    MODULE_366  33


cluster ID = 310
cluster size = 6
      gene set name    size (number of genes in the set)
1     CHANDRAN_METASTASIS_TOP50_DN 45
2     GAUSSMANN_MLL_AF4_FUSION_TARGETS_E_UP   97
3     INGRAM_SHH_TARGETS_DN  64
4     LINDVALL_IMMORTALIZED_BY_TERT_UP   78
5     MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_DN    67
6     CHANDRAN_METASTASIS_DN 306
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cluster ID = 314
cluster size = 7
      gene set name    size (number of genes in the set)
1     PIEPOLI_LGI1_TARGETS_UP     15
2     HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_UP     23
3     HERNANDEZ_MITOTIC_ARREST_BY_DOCETAXEL_1_UP   36
4     GRANDVAUX_IRF3_TARGETS_DN   19
5     STEGER_ADIPOGENESIS_DN 25
6     DELACROIX_RAR_TARGETS_DN    24
7     YAP1_DN    48


cluster ID = 315
cluster size = 10
      gene set name    size (number of genes in the set)
1     PIEPOLI_LGI1_TARGETS_DN     14
2     MOROSETTI_FACIOSCAPULOHUMERAL_MUSCULAR_DISTROPHY_UP 20
3     CHOW_RASSF1_TARGETS_UP 27
4     DACOSTA_LOW_DOSE_UV_RESPONSE_VIA_ERCC3_XPCS_DN     9
5     WOTTON_RUNX_TARGETS_DN 29
6     MARIADASON_REGULATED_BY_HISTONE_ACETYLATION_UP     83
7     CHIBA_RESPONSE_TO_TSA  50
8     GENTILE_UV_RESPONSE_CLUSTER_D2    41
9     GAUTSCHI_SRC_SIGNALING 8
10    EHLERS_ANEUPLOIDY_UP   41


cluster ID = 320
cluster size = 6
      gene set name    size (number of genes in the set)
1     DEURIG_T_CELL_PROLYMPHOCYTIC_LEUKEMIA_UP     368
2     XU_HGF_TARGETS_REPRESSED_BY_AKT1_DN     95
3     SHEN_SMARCA2_TARGETS_DN     357
4     MOREAUX_MULTIPLE_MYELOMA_BY_TACI_UP     412
5     MOREAUX_B_LYMPHOCYTE_MATURATION_BY_TACI_UP   92
6     SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A12   317


cluster ID = 328
cluster size = 50
      gene set name    size (number of genes in the set)
1     GRABARCZYK_BCL11B_TARGETS_UP 81
2     HAHTOLA_SEZARY_SYNDROM_DN   42
3     DIRMEIER_LMP1_RESPONSE_LATE_DN    32
4     PARK_HSC_VS_MULTIPOTENT_PROGENITORS_UP  19
5     THEILGAARD_NEUTROPHIL_AT_SKIN_WOUND_DN  225
6     XU_RESPONSE_TO_TRETINOIN_UP 16
7     GAVIN_IL2_RESPONSIVE_FOXP3_TARGETS_DN   5
8     AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_8G    95
9     AMUNDSON_POOR_SURVIVAL_AFTER_GAMMA_RADIATION_2G    171
10    MARSHALL_VIRAL_INFECTION_RESPONSE_DN    29
11    CHAN_INTERFERON_PRODUCING_DENDRITIC_CELL     12
12    LEE_EARLY_T_LYMPHOCYTE_DN   57
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13	FINAK_BREAST_CANCER_SDPP_SIGNATURE	26
14	HAHTOLA_CTCL_PATHOGENESIS	16
15	KYNG_WERNER_SYNDROM_AND_NORMAL_AGING_DN	225
16	KIM_GLIS2_TARGETS_DN	6
17	GNF2_ATM	30
18	GNF2_BNIP2	34
19	GNF2_CASP4	24
20	GNF2_CASP8	27
21	GNF2_CD48	32
22	GNF2_CD53	58
23	GNF2_CD7	40
24	GNF2_CD97	38
25	GNF2_HLA-C	47
26	GNF2_ICAM3	39
27	GNF2_IL2RB	47
28	GNF2_INPP5D	43
29	GNF2_ITGAL	55
30	GNF2_JAK1	32
31	GNF2_LYN	27
32	GNF2_MATK	25
33	GNF2_MSN	24
34	GNF2_MYD88	60
35	GNF2_PAK2	28
36	GNF2_PTPN4	51
37	GNF2_PTPN6	47
38	GNF2_PTPRC	68
39	GNF2_RAB7L1	34
40	GNF2_RAP1B	36
41	GNF2_SELL	47
42	GNF2_SNRK	28
43	GNF2_STAT6	79
44	GNF2_TYK2	33
45	GNF2_VAV1	36
46	GNF2_ZAP70	27
47	MODULE_430	55
48	MODULE_484	42
49	MODULE_575	12
50	IMMUNOLOGICAL_SYNAPSE	11

cluster ID = 331
cluster size = 8

	gene set name	size (number of genes in the set)
1	NOJIMA_SFRP2_TARGETS_UP	31
2	BARRIER_CANCER_RELAPSE_NORMAL_SAMPLE_DN	31
3	MAHADEVAN_RESPONSE_TO_MP470_DN	19
4	SHI_SPARC_TARGETS_UP	24
5	SUH_COEXPRESSED_WITH_ID1_AND_ID2_UP	19
6	MARCINIAK_ER_STRESS_RESPONSE_VIA_CHOP	25
7	XU_CREBBP_TARGETS_UP	26
8	CHO_NR4A1_TARGETS	33

cluster ID = 335
cluster size = 12

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      gene set name    size (number of genes in the set)
1     VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_DN    138
2     WANG_BARRETTS_ESOPHAGUS_UP   51
3     TSUNODA_CISPLATIN_RESISTANCE_DN    51
4     WOOD_EBV_EBNA1_TARGETS_DN    47
5     MOHANKUMAR_TLX1_TARGETS_DN   193
6     WANG_HCP_PROSTATE_CANCER     111
7     AMIT_SERUM_RESPONSE_480_MCF10A     39
8     ENGELMANN_CANCER_PROGENITORS_DN    70
9     KYNG_RESPONSE_TO_H2O2_VIA_ERCC6_UP 40
10    GHANDHI_DIRECT_IRRADIATION_DN      33
11    GHANDHI_BYSTANDER_IRRADIATION_DN   12
12    MODULE_426  88


cluster ID = 338
cluster size = 8
      gene set name    size (number of genes in the set)
1     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_UP   32
2     SHIN_B_CELL_LYMPHOMA_CLUSTER_6     11
3     HALMOS_CEBPA_TARGETS_UP      52
4     TAVOR_CEBPA_TARGETS_UP 48
5     EHRLICH_ICF_SYNDROM_DN 15
6     JEPSEN_SMRT_TARGETS    33
7     MELLMAN_TUT1_TARGETS_DN      47
8     KUWANO_RNA_STABILIZED_BY_NO  7


cluster ID = 339
cluster size = 7
      gene set name    size (number of genes in the set)
1     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_YELLOW_DN   23
2     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREEN_DN    25
3     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_BLUE_DN     61
4     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_22   13
5     RAY_TARGETS_OF_P210_BCR_ABL_FUSION_DN   16
6     CAGTCAC,MIR-134  52
7     YRCCAKNNGNCGC_UNKNOWN  65


cluster ID = 341
cluster size = 8
      gene set name    size (number of genes in the set)
1     GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_LIGHTYELLOW_UP    11
2     LI_WILMS_TUMOR_ANAPLASTIC_DN 5
3     CALVET_IRINOTECAN_SENSITIVE_VS_RESISTANT_DN   5
4     STONER_ESOPHAGEAL_CARCINOGENESIS_DN      7
5     MURAKAMI_UV_RESPONSE_6HR_UP  37
6     ZHAN_EARLY_DIFFERENTIATION_GENES_UP      7
7     MURAKAMI_UV_RESPONSE_1HR_UP  17
8     GGATCCG,MIR-127  11


cluster ID = 344
cluster size = 9
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	gene set name	size (number of genes in the set)
1	TAKEDA_TARGETS_OF_NUP98_HOXA9_FUSION_3D_DN	31
2	PEPPER_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	33
3	HUMMERICH_BENIGN_SKIN_TUMOR_UP	18
4	HUMMERICH_MALIGNANT_SKIN_TUMOR_UP	16
5	KENNY_CTNNB1_TARGETS_UP	50
6	ROSS_AML_WITH_CBFB_MYH11_FUSION	52
7	SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_DN	27
8	ZHENG_IL22_SIGNALING_UP	56
9	VALK_AML_CLUSTER_9	35

cluster ID = 346
cluster size = 6

	gene set name	size (number of genes in the set)
1	BILBAN_B_CLL_LPL_UP	63
2	CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_DN	25
3	CROONQUIST_IL6_DEPRIVATION_UP	20
4	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_DN	56
5	MODULE_424	18
6	MODULE_478	19

cluster ID = 347
cluster size = 6

	gene set name	size (number of genes in the set)
1	HOEBEKE_LYMPHOID_STEM_CELL_UP	95
2	HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN	116
3	ZHAN_LATE_DIFFERENTIATION_GENES_DN	16
4	CHIARETTI_T_ALL_REFRACTORY_TO_THERAPY	30
5	MODULE_169	97
6	MODULE_456	113

cluster ID = 350
cluster size = 16

	gene set name	size (number of genes in the set)
1	MULLIGHAN_NPM1_MUTATED_SIGNATURE_1_DN	126
2	MULLIGHAN_NPM1_MUTATED_SIGNATURE_2_DN	77
3	MULLIGHAN_MLL_SIGNATURE_1_DN	242
4	MULLIGHAN_MLL_SIGNATURE_2_DN	281
5	MULLIGHAN_NPM1_SIGNATURE_3_DN	162
6	DUNNE_TARGETS_OF_AML1_MTG8_FUSION_DN	19
7	ROSS_ACUTE_MYELOID_LEUKEMIA_CBF	82
8	ROSS_AML_WITH_AML1_ETO_FUSION	76
9	ALCALAY_AML_BY_NPM1_LOCALIZATION_DN	184
10	VERHAAK_AML_WITH_NPM1_MUTATED_DN	246
11	BONOME_OVARIAN_CANCER_POOR_SURVIVAL_UP	31
12	WANG_NEOPLASTIC_TRANSFORMATION_BY_CCND1_MYC	21
13	SCHRAETS_MLL_TARGETS_UP	35
14	VALK_AML_CLUSTER_11	36
15	VALK_AML_CLUSTER_13	30
16	YAGI_AML_WITH_T_8_21_TRANSLOCATION	368

cluster ID = 351
cluster size = 12

	gene set name	size (number of genes in the set)
1	DITTMER_PTHLH_TARGETS_DN	73
2	SASAKI_TARGETS_OF_TP73_AND_TP63	11
3	SUNG_METASTASIS_STROMA_DN	54
4	IIZUKA_LIVER_CANCER_PROGRESSION_L1_G1_UP	25
5	CHUANG_OXIDATIVE_STRESS_RESPONSE_UP	28
6	CHEN_LVAD_SUPPORT_OF_FAILING_HEART_UP	103
7	ZHENG_RESPONSE_TO_ARSENITE_UP	18
8	BACOLOD_RESISTANCE_TO_ALKYLATING_AGENTS_UP	26
9	NAKAMURA_ADIPOGENESIS_EARLY_UP	66
10	NAKAMURA_ADIPOGENESIS_LATE_UP	104
11	CHICAS_RB1_TARGETS_LOW_SERUM	100
12	KIM_TIAL1_TARGETS	32

cluster ID = 357
cluster size = 17

	gene set name	size (number of genes in the set)
1	GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN	12
2	GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN	10
3	HAHTOLA_MYCOSIS_FUNGOIDES_SKIN_DN	27
4	HAHTOLA_MYCOSIS_FUNGOIDES_DN	16
5	WONG_ENDOMETRIAL_CANCER_LATE	10
6	RICKMAN_HEAD_AND_NECK_CANCER_D	37
7	PETRETTO_HEART_MASS_QTL_CIS_DN	24
8	CHIARETTI_ACUTE_LYMPHOBLASTIC_LEUKEMIA_ZAP70	67
9	WU_SILENCED_BY_METHYLATION_IN_BLADDER_CANCER	55
10	WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_DN	12
11	CROONQUIST_STROMAL_STIMULATION_DN	13
12	CROONQUIST_NRAS_SIGNALING_UP	41
13	CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP	41
14	GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP	12
15	YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_3	15
16	LIM_MAMMARY_LUMINAL_PROGENITOR_UP	58
17	GLI1_UP.V1_UP	27

cluster ID = 361
cluster size = 10

	gene set name	size (number of genes in the set)
1	PACHER_TARGETS_OF_IGF1_AND_IGF2_UP	35
2	PENG_LEUCINE_DEPRIVATION_UP	142
3	PENG_GLUCOSE_DEPRIVATION_UP	48
4	PENG_RAPAMYCIN_RESPONSE_UP	203
5	ZHAN_MULTIPLE_MYELOMA_CD1_UP	45
6	ZHAN_MULTIPLE_MYELOMA_CD1_VS_CD2_UP	66
7	KRIGE_AMINO_ACID_DEPRIVATION	29
8	BHATI_G2M_ARREST_BY_2METHOXYESTRADIOL_DN	127
9	FORTSCHEGGER_PHF8_TARGETS_UP	279
10	NFE2L2.V2	481

cluster ID = 362

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cluster size = 9
      gene set name    size (number of genes in the set)
1     PASTURAL_RIZ1_TARGETS_DN     5
2     PATTERSON_DOCETAXEL_RESISTANCE    29
3     MAINA_HYPOXIA_VHL_TARGETS_UP 6
4     MAINA_VHL_TARGETS_UP   10
5     DAZARD_UV_RESPONSE_CLUSTER_G4     21
6     NIELSEN_GIST_AND_SYNOVIAL_SARCOMA_UP    20
7     DE_YY1_TARGETS_UP20
8     NIELSEN_MALIGNAT_FIBROUS_HISTIOCYTOMA_DN      18
9     SUBTIL_PROGESTIN_TARGETS     36


cluster ID = 363
cluster size = 7
      gene set name    size (number of genes in the set)
1     LANDIS_BREAST_CANCER_PROGRESSION_UP     44
2     LANDIS_ERBB2_BREAST_TUMORS_65_UP  22
3     LANDIS_ERBB2_BREAST_PRENEOPLASTIC_UP    20
4     LANDIS_ERBB2_BREAST_TUMORS_324_UP 150
5     CAFFAREL_RESPONSE_TO_THC_8HR_3_DN 10
6     HOLLEMAN_DAUNORUBICIN_B_ALL_UP    10
7     HOLLEMAN_DAUNORUBICIN_ALL_UP 7


cluster ID = 364
cluster size = 7
      gene set name    size (number of genes in the set)
1     LAU_APOPTOSIS_CDKN2A_DN     5
2     KREPPEL_CD99_TARGETS_UP     6
3     GOLUB_ALL_VS_AML_DN    24
4     PARK_APL_PATHOGENESIS_DN     50
5     HOLLEMAN_PREDNISOLONE_RESISTANCE_B_ALL_DN     12
6     HOLLEMAN_PREDNISOLONE_RESISTANCE_ALL_UP 11
7     PROTEIN_TRANSPORTER_ACTIVITY 14


cluster ID = 365
cluster size = 11
      gene set name    size (number of genes in the set)
1     CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_UP 58
2     CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_CDC25_DN 51
3     CHIARADONNA_NEOPLASTIC_TRANSFORMATION_KRAS_UP 126
4     CHIARADONNA_NEOPLASTIC_TRANSFORMATION_CDC25_UP     120
5     HOWLIN_PUBERTAL_MAMMARY_GLAND     69
6     BURTON_ADIPOGENESIS_2  72
7     SARTIPY_NORMAL_AT_INSULIN_RESISTANCE_UP 34
8     MULLIGAN_NTF3_SIGNALING_VIA_INSR_AND_IGF1R_UP 23
9     BURTON_ADIPOGENESIS_PEAK_AT_8HR   39
10    YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_0     76
11    KATSANOU_ELAVL1_TARGETS_DN   148


cluster ID = 368
cluster size = 6
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      gene set name    size (number of genes in the set)
1     BERENJENO_ROCK_SIGNALING_NOT_VIA_RHOA_UP      29
2     VANHARANTA_UTERINE_FIBROID_DN     67
3     BILANGES_SERUM_SENSITIVE_VIA_TSC1 23
4     PLASARI_NFIC_TARGETS_BASAL_DN     18
5     PLASARI_TGFB1_SIGNALING_VIA_NFIC_1HR_UP 33
6     PLASARI_TGFB1_SIGNALING_VIA_NFIC_10HR_DN      30


cluster ID = 376
cluster size = 10
      gene set name    size (number of genes in the set)
1     GAUSSMANN_MLL_AF4_FUSION_TARGETS_C_DN   19
2     FUJIWARA_PARK2_HEPATOCYTE_PROLIFERATION_UP    10
3     FUJIWARA_PARK2_IN_LIVER_CANCER_UP 8
4     FUJIWARA_PARK2_IN_LIVER_CANCER_DN 5
5     POS_RESPONSE_TO_HISTAMINE_DN 11
6     HUANG_FOXA2_TARGETS_UP 45
7     SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_DN      7
8     BOYAULT_LIVER_CANCER_SUBCLASS_G1_DN     40
9     MODULE_471  10
10    MODULE_528  11


cluster ID = 383
cluster size = 11
      gene set name    size (number of genes in the set)
1     TAKADA_GASTRIC_CANCER_COPY_NUMBER_UP    7
2     CHOI_ATL_ACUTE_STAGE   6
3     TAKAYAMA_BOUND_BY_AR   10
4     HASINA_NOL7_TARGETS_DN 13
5     RADAEVA_RESPONSE_TO_IFNA1_DN 10
6     SHARMA_PILOCYTIC_ASTROCYTOMA_LOCATION_UP      25
7     TSUDA_ALVEOLAR_SOFT_PART_SARCOMA  10
8     POTTI_PACLITAXEL_SENSITIVITY 39
9     BOYLAN_MULTIPLE_MYELOMA_PCA1_DN   8
10    TRACEY_RESISTANCE_TO_IFNA2_UP     6
11    CGGTGTG,MIR-220  6


cluster ID = 388
cluster size = 10
      gene set name    size (number of genes in the set)
1     DUNNE_TARGETS_OF_AML1_MTG8_FUSION_UP    52
2     GOERING_BLOOD_HDL_CHOLESTEROL_QTL_TRANS 14
3     CHEOK_RESPONSE_TO_HD_MTX_UP  23
4     WANG_IMMORTALIZED_BY_HOXA9_AND_MEIS1_UP 31
5     LIAN_NEUTROPHIL_GRANULE_CONSTITUENTS    25
6     SCHURINGA_STAT5A_TARGETS_DN  18
7     VILIMAS_NOTCH1_TARGETS_DN    20
8     MARTINELLI_IMMATURE_NEUTROPHIL_UP 11
9     KAMIKUBO_MYELOID_CEBPA_NETWORK    28
10    MODULE_247  37
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cluster ID = 389
cluster size = 127

	gene set name	size (number of genes in the set)
1	OUELLET_CULTURED_OVARIAN_CANCER_INVASIVE_VS_LMP_DN	35
2	KONG_E2F1_TARGETS	10
3	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_21	9
4	TARTE_PLASMA_CELL_VS_PLASMABLAST_UP	398
5	MARTINEZ_RESPONSE_TO_TRABECTEDIN	50
6	KAYO_AGING_MUSCLE_UP	244
7	GENTILE_UV_LOW_DOSE_DN	67
8	MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN	7
9	BOYERINAS_ONCOFETAL_TARGETS_OF_LET7A1	12
10	NADELLA_PRKAR1A_TARGETS_DN	8
11	LE_SKI_TARGETS_UP	17
12	TSAI_DNAJB4_TARGETS_DN	6
13	MORF_ATRX	211
14	MORF_BCL2	222
15	MORF_BNIP1	190
16	MORF_BCL2L11	188
17	MORF_BRCA1	264
18	MORF_CCNF	77
19	MORF_ERCC2	102
20	MORF_FDXR	226
21	MORF_MDM2	282
22	MORF_MT4	246
23	MORF_MSH3	245
24	MORF_NF1	169
25	MORF_PSMF1	164
26	MORF_RAD51L3	392
27	MORF_RFC1	110
28	MORF_RFC5	76
29	MORF_STK17A	171
30	MORF_TFDP2	231
31	MORF_MYC	79
32	MORF_ARAF1	78
33	MORF_ARL3	307
34	MORF_ATF2	332
35	MORF_CAMK4	294
36	MORF_CASP10	117
37	MORF_CASP2	103
38	MORF_CD8A	127
39	MORF_CDC2L5	140
40	MORF_CDH4	140
41	MORF_CNTN1	108
42	MORF_CTSB	190
43	MORF_DDX11	156
44	MORF_DMPK	176
45	MORF_EIF4E	84
46	MORF_ERCC4	326
47	MORF_ESR1	172
48	MORF_ETV3	64
49	MORF_FANCG	166
50	MORF_FLT1	126
51	MORF_FOSL1	409
52	MORF_FSHR	282

53	MORF_HEAB	81
54	MORF_IFNA1	207
55	MORF_IKBKG	137
56	MORF_IL13	233
57	MORF_IL16	242
58	MORF_IL4	196
59	MORF_ITGA2	57
60	MORF_JAG1	94
61	MORF_JAK3	96
62	MORF_KDR	95
63	MORF_LMO1	50
64	MORF_LTK	147
65	MORF_MAGEA8	263
66	MORF_MAGEA9	428
67	MORF_MAP2K7	185
68	MORF_MLLT10	305
69	MORF_MYL3	71
70	MORF_MYST2	68
71	MORF_NOS2A	291
72	MORF_ORC1L	69
73	MORF_PAX7	269
74	MORF_PDCD1	73
75	MORF_PDPK1	74
76	MORF_PML	145
77	MORF_PPP2R5B	175
78	MORF_PPP5C	90
79	MORF_PRKACA	111
80	MORF_PRKCA	183
81	MORF_PTEN	85
82	MORF_PTPN9	61
83	MORF_PTPRB	257
84	MORF_PTPRR	103
85	MORF_RAGE	148
86	MORF_RAP1A	139
87	MORF_RBBP8	213
88	MORF_RBM8A	85
89	MORF_REV3L	57
90	MORF_RUNX1	150
91	MORF_SS18	61
92	MORF_SUPT3H	332
93	MORF_THPO	129
94	MORF_THRA	54
95	MORF_TNFRSF25	268
96	MORF_TNFRSF6	169
97	MORF_TPR	144
98	MORF_TTN	51
99	GCM_ATM	27
100	GCM_BNIP1	78
101	GCM_BECN1	68
102	GCM_AIP	40
103	GCM_CDH5	35
104	GCM_DPF2	32
105	GCM_ERCC4	29
106	GCM_FANCC	124
107	GCM_FCGR2B	38

108	GCM_HMGA2	122
109	GCM_LTK	46
110	GCM_MYCL1	25
111	GCM_PRKAG1	50
112	GCM_PRKCG	62
113	GCM_PTPRU	54
114	GCM_RING1	110
115	GCM_SMARCC1	37
116	GCM_SMARCD1	104
117	GCM_SUPT4H1	58
118	GCM_TEC	32
119	GCM_VAV1	47
120	CAR_MLANA	43
121	CAR_MYST2	27
122	CAR_TNFRSF25	30
123	CAR_WBSCR22	36
124	MODULE_20	83
125	MODULE_111	153
126	MODULE_113	107
127	MODULE_157	108

cluster ID = 390
cluster size = 7

	gene set name	size (number of genes in the set)
1	LUCAS_HNF4A_TARGETS_DN	8
2	MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_30	9
3	BRUNEAU_SEPTATION_ATRIAL	5
4	BRUNEAU_SEPTATION_VENTRICULAR	10
5	BRUNEAU_HEART_GREAT_VESSELS_AND_VALVULOGENESIS	8
6	RAFFEL_VEGFA_TARGETS_DN	5
7	PHONG_TNF_TARGETS_DN	8

cluster ID = 392
cluster size = 10

	gene set name	size (number of genes in the set)
1	DARWICHE_SKIN_TUMOR_PROMOTER_UP	142
2	DARWICHE_SKIN_TUMOR_PROMOTER_DN	185
3	DARWICHE_PAPILLOMA_RISK_LOW_UP	162
4	DARWICHE_PAPILLOMA_RISK_LOW_DN	165
5	DARWICHE_PAPILLOMA_RISK_HIGH_UP	147
6	DARWICHE_PAPILLOMA_RISK_HIGH_DN	180
7	DARWICHE_SQUAMOUS_CELL_CARCINOMA_UP	146
8	DARWICHE_SQUAMOUS_CELL_CARCINOMA_DN	181
9	DARWICHE_PAPILLOMA_PROGRESSION_RISK	74
10	DARWICHE_PAPILLOMA_RISK_HIGH_VS_LOW_DN	32

cluster ID = 394
cluster size = 6

	gene set name	size (number of genes in the set)
1	TOMIDA_METASTASIS_UP	26
2	MORI_PLASMA_CELL_UP	51
3	TOMIDA_LUNG_CANCER_POOR_SURVIVAL	5

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4     BYSTRYKH_HEMATOPOIESIS_STEM_CELL_RUNX1  9
5     TRACEY_RESISTANCE_TO_IFNA2_DN      32
6     OLIGOSACCHARYL_TRANSFERASE_COMPLEX 10


cluster ID = 395
cluster size = 7
      gene set name     size (number of genes in the set)
1     HWANG_PROSTATE_CANCER_MARKERS      28
2     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_15   13
3     PARK_TRETINOIN_RESPONSE      12
4     PARK_TRETINOIN_RESPONSE_AND_PML_RARA_FUSION   30
5     PARK_TRETINOIN_RESPONSE_AND_RARA_PLZF_FUSION  22
6     MUELLER_COMMON_TARGETS_OF_AML_FUSIONS_DN      31
7     V$PAX5_02   17


cluster ID = 404
cluster size = 7
      gene set name     size (number of genes in the set)
1     RIZ_ERYTHROID_DIFFERENTIATION_APOBEC2   27
2     RIZ_ERYTHROID_DIFFERENTIATION_12HR 43
3     MA_MYELOID_DIFFERENTIATION_DN      44
4     NIKOLSKY_OVERCONNECTED_IN_BREAST_CANCER 22
5     YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_4     15
6     MODULE_500  30
7     RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_ACTIVITYENHANCER_BINDING      14


cluster ID = 405
cluster size = 27
      gene set name     size (number of genes in the set)
1     PEREZ_TP53_TARGETS     1174
2     PEREZ_TP63_TARGETS     355
3     PEREZ_TP53_AND_TP63_TARGETS  205
4     HATADA_METHYLATED_IN_LUNG_CANCER_UP     390
5     BENPORATH_SUZ12_TARGETS      1038
6     BENPORATH_EED_TARGETS  1062
7     BENPORATH_ES_WITH_H3K27ME3   1118
8     BENPORATH_PRC2_TARGETS 652
9     ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION 88
10    BILD_E2F3_ONCOGENIC_SIGNATURE      246
11    RIGGI_EWING_SARCOMA_PROGENITOR_UP  430
12    MEISSNER_NPC_HCP_WITH_H3K27ME3     79
13    MEISSNER_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3    142
14    MEISSNER_NPC_HCP_WITH_H3_UNMETHYLATED   536
15    MEISSNER_BRAIN_HCP_WITH_H3K27ME3   269
16    MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3  1069
17    MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27ME3    349
18    MEISSNER_NPC_HCP_WITH_H3K4ME2      491
19    MIKKELSEN_MCV6_HCP_WITH_H3K27ME3   435
20    MIKKELSEN_NPC_HCP_WITH_H3K27ME3    341
21    MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27ME3   210
22    MIKKELSEN_MEF_HCP_WITH_H3K27ME3    590
23    MARTENS_TRETINOIN_RESPONSE_UP      857
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24    BRUINS_UVC_RESPONSE_VIA_TP53_GROUP_A    898
25    MIYAGAWA_TARGETS_OF_EWSR1_ETS_FUSIONS_UP      259
26    ZWANG_TRANSIENTLY_UP_BY_2ND_EGF_PULSE_ONLY    1725
27    E2F3_UP.V1_UP    196


cluster ID = 410
cluster size = 20
      gene set name    size (number of genes in the set)
1     NAKAMURA_LUNG_CANCER   8
2     JAZAG_TGFB1_SIGNALING_DN     35
3     INAMURA_LUNG_CANCER_SCC_UP   14
4     YIH_RESPONSE_TO_ARSENITE_C1  24
5     MATZUK_CUMULUS_EXPANSION     9
6     VIRAL_GENOME_REPLICATION     21
7     FEMALE_PREGNANCY 53
8     FEMALE_GAMETE_GENERATION     17
9     REPRODUCTIVE_PROCESS   162
10    GAMETE_GENERATION114
11    VIRAL_INFECTIOUS_CYCLE 32
12    VIRAL_REPRODUCTIVE_PROCESS   36
13    SEXUAL_REPRODUCTION    139
14    VIRAL_REPRODUCTION     41
15    INTERACTION_WITH_HOST  17
16    REPRODUCTION     265
17    REGULATION_OF_VIRAL_REPRODUCTION   12
18    DRUG_BINDING     16
19    SMALL_CONJUGATING_PROTEIN_BINDING  12
20    UBIQUITIN_BINDING11


cluster ID = 412
cluster size = 7
      gene set name    size (number of genes in the set)
1     HUMMERICH_SKIN_CANCER_PROGRESSION_UP    88
2     SCHLINGEMANN_SKIN_CARCINOGENESIS_TPA_UP 42
3     LABBE_WNT3A_TARGETS_DN 97
4     LABBE_TGFB1_TARGETS_DN 108
5     LABBE_TARGETS_OF_TGFB1_AND_WNT3A_DN     108
6     PIONTEK_PKD1_TARGETS_UP      38
7     GUILLAUMOND_KLF10_TARGETS_UP 51


cluster ID = 414
cluster size = 13
      gene set name    size (number of genes in the set)
1     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_7    8
2     HERNANDEZ_ABERRANT_MITOSIS_BY_DOCETACEL_4NM_DN      7
3     TERAMOTO_OPN_TARGETS_CLUSTER_1     13
4     CAFFAREL_RESPONSE_TO_THC_24HR_5_UP 34
5     COLIN_PILOCYTIC_ASTROCYTOMA_VS_GLIOBLASTOMA_DN      28
6     KEEN_RESPONSE_TO_ROSIGLITAZONE_UP  38
7     LUDWICZEK_TREATING_IRON_OVERLOAD   7
8     YAO_TEMPORAL_RESPONSE_TO_PROGESTERONE_CLUSTER_8     49
9     DEMAGALHAES_AGING_DN   16
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10    HUANG_GATA2_TARGETS_DN 72
11    MODULE_191  19
12    MODULE_262  19
13    MODULE_540  10


cluster ID = 415
cluster size = 13
      gene set name    size (number of genes in the set)
1     MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_2    5
2     FUNG_IL2_SIGNALING_1   11
3     FUNG_IL2_TARGETS_WITH_STAT5_BINDING_SITES     7
4     SHIN_B_CELL_LYMPHOMA_CLUSTER_2     30
5     MORI_SMALL_PRE_BII_LYMPHOCYTE_DN   76
6     IIZUKA_LIVER_CANCER_EARLY_RECURRENCE    11
7     HOFFMANN_PRE_BI_TO_LARGE_PRE_BII_LYMPHOCYTE_DN      75
8     HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_UP   43
9     MIKKELSEN_PLURIPOTENT_STATE_DN     8
10    MILI_PSEUDOPODIA 43
11    MILI_PSEUDOPODIA_CHEMOTAXIS_UP     74
12    GERHOLD_RESPONSE_TO_TZD_UP   6
13    CGCTGCT,MIR-503  24


cluster ID = 420
cluster size = 6
      gene set name    size (number of genes in the set)
1     LA_MEN1_TARGETS  24
2     COWLING_MYCN_TARGETS   43
3     LEI_HOXC8_TARGETS_DN   17
4     RAMASWAMY_METASTASIS_DN      61
5     KUMAR_PATHOGEN_LOAD_BY_MACROPHAGES 275
6     KUMAR_AUTOPHAGY_NETWORK      71


cluster ID = 421
cluster size = 7
      gene set name    size (number of genes in the set)
1     LI_CISPLATIN_RESISTANCE_DN   35
2     KORKOLA_YOLK_SAC_TUMOR 62
3     AMIT_EGF_RESPONSE_240_HELA   60
4     AMIT_EGF_RESPONSE_240_MCF10A 20
5     AMIT_SERUM_RESPONSE_240_MCF10A    57
6     AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_DN   121
7     AZARE_STAT3_TARGETS    24


cluster ID = 424
cluster size = 8
      gene set name    size (number of genes in the set)
1     NAISHIRO_CTNNB1_TARGETS_WITH_LEF1_MOTIF 8
2     SIMBULAN_UV_RESPONSE_NORMAL_DN     33
3     SIMBULAN_UV_RESPONSE_IMMORTALIZED_DN    31
4     ABBUD_LIF_SIGNALING_1_DN     26
5     TRAYNOR_RETT_SYNDROM_DN      19
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6     JI_RESPONSE_TO_FSH_DN  58
7     DE_YY1_TARGETS_DN92
8     ZHAN_V1_LATE_DIFFERENTIATION_GENES_UP   32


cluster ID = 426
cluster size = 6
      gene set name    size (number of genes in the set)
1     TERAMOTO_OPN_TARGETS_CLUSTER_7    19
2     TERAMOTO_OPN_TARGETS_CLUSTER_8    8
3     YE_METASTATIC_LIVER_CANCER   27
4     VIETOR_IFRD1_TARGETS   23
5     MATTHEWS_SKIN_CARCINOGENESIS_VIA_JUN    17
6     ROESSLER_LIVER_CANCER_METASTASIS_UP     107


cluster ID = 431
cluster size = 15
      gene set name    size (number of genes in the set)
1     BORLAK_LIVER_CANCER_EGF_UP   57
2     SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM2   153
3     SHETH_LIVER_CANCER_VS_TXNIP_LOSS_PAM3   70
4     KHETCHOUMIAN_TRIM24_TARGETS_UP    47
5     LEE_LIVER_CANCER_MYC_UP      54
6     LEE_LIVER_CANCER_MYC_TGFA_UP 61
7     LEE_LIVER_CANCER_ACOX1_UP    64
8     LEE_LIVER_CANCER_MYC_E2F1_UP 56
9     CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_LD_MTX_DN     21
10    LEE_LIVER_CANCER_CIPROFIBRATE_UP  60
11    LEE_LIVER_CANCER_DENA_UP     60
12    LEE_LIVER_CANCER_E2F1_UP     62
13    ZHAN_MULTIPLE_MYELOMA_DN     41
14    OHGUCHI_LIVER_HNF4A_TARGETS_UP    44
15    SERVITJA_LIVER_HNF1A_TARGETS_UP   135


cluster ID = 432
cluster size = 6
      gene set name    size (number of genes in the set)
1     JOHANSSON_BRAIN_CANCER_EARLY_VS_LATE_DN 45
2     XU_GH1_EXOGENOUS_TARGETS_UP  85
3     TSENG_IRS1_TARGETS_DN  135
4     XU_GH1_AUTOCRINE_TARGETS_UP  268
5     TSENG_ADIPOGENIC_POTENTIAL_DN     46
6     LEIN_ASTROCYTE_MARKERS 42


cluster ID = 440
cluster size = 7
      gene set name    size (number of genes in the set)
1     WANG_RESPONSE_TO_PACLITAXEL_VIA_MAPK8_DN     5
2     KAUFFMANN_MELANOMA_RELAPSE_DN     6
3     HOEGERKORP_CD44_TARGETS_TEMPORAL_DN     25
4     CHEOK_RESPONSE_TO_MERCAPTOPURINE_AND_HD_MTX_UP     5
5     REGULATION_OF_CHROMOSOME_ORGANIZATION_AND_BIOGENESIS     10
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6     TELOMERIC_DNA_BINDING  10
7     SEQUENCE_SPECIFIC_DNA_BINDING      58


cluster ID = 445
cluster size = 9
      gene set name    size (number of genes in the set)
1     SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_2FC_UP 14
2     MORI_EMU_MYC_LYMPHOMA_BY_ONSET_TIME_DN  17
3     BOYAULT_LIVER_CANCER_SUBCLASS_G2   27
4     PLASARI_TGFB1_TARGETS_1HR_DN 6
5     V$SEF1_C    6
6     V$AHRARNT_02     15
7     CACGTTT,MIR-302A 31
8     CGCAAAA,MIR-450  9
9     ATGCACG,MIR-517B 20


cluster ID = 447
cluster size = 6
      gene set name    size (number of genes in the set)
1     HUI_MAPK14_TARGETS_UP  21
2     HASLINGER_B_CLL_WITH_MUTATED_VH_GENES   18
3     ALONSO_METASTASIS_EMT_DN     5
4     ALONSO_METASTASIS_DN   26
5     WU_ALZHEIMER_DISEASE_UP      14
6     VALK_AML_CLUSTER_1     28


cluster ID = 454
cluster size = 6
      gene set name    size (number of genes in the set)
1     ROPERO_HDAC2_TARGETS   114
2     SHEDDEN_LUNG_CANCER_GOOD_SURVIVAL_A4    196
3     RAPA_EARLY_UP.V1_UP    183
4     PIGF_UP.V1_DN     194
5     VEGF_A_UP.V1_UP  196
6     JNK_DN.V1_DN     191


cluster ID = 457
cluster size = 6
      gene set name    size (number of genes in the set)
1     FUJIWARA_PARK2_HEPATOCYTE_PROLIFERATION_DN    8
2     GOLUB_ALL_VS_AML_UP    24
3     HOEGERKORP_CD44_TARGETS_TEMPORAL_UP     13
4     MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_UP     10
5     HOWLIN_CITED1_TARGETS_1_UP   35
6     HOWLIN_CITED1_TARGETS_2_UP   17


cluster ID = 461
cluster size = 8
      gene set name    size (number of genes in the set)
1     SCHAEFFER_PROSTATE_DEVELOPMENT_12HR_DN  57
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2     SCHAEFFER_SOX9_TARGETS_IN_PROSTATE_DEVELOPMENT_DN   45
3     RORIE_TARGETS_OF_EWSR1_FLI1_FUSION_DN   30
4     MCCLUNG_DELTA_FOSB_TARGETS_2WK    48
5     MCCLUNG_CREB1_TARGETS_UP     100
6     CAGNWMCNNNGAC_UNKNOWN  85
7     V$NRSF_01   97
8     CAHOY_NEURONAL   100


cluster ID = 467
cluster size = 8
      gene set name    size (number of genes in the set)
1     MORI_SMALL_PRE_BII_LYMPHOCYTE_UP   86
2     MORI_MATURE_B_LYMPHOCYTE_DN  75
3     BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_UP    38
4     BOYLAN_MULTIPLE_MYELOMA_C_UP 47
5     VANASSE_BCL2_TARGETS_DN      74
6     HOFFMANN_LARGE_TO_SMALL_PRE_BII_LYMPHOCYTE_DN 72
7     HOFFMANN_SMALL_PRE_BII_TO_IMMATURE_B_LYMPHOCYTE_DN  50
8     HOFFMANN_IMMATURE_TO_MATURE_B_LYMPHOCYTE_DN   50


cluster ID = 468
cluster size = 20
      gene set name    size (number of genes in the set)
1     NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON 7
2     CHEN_HOXA5_TARGETS_6HR_DN    6
3     MEISSNER_ES_ICP_WITH_H3K4ME3 34
4     MEISSNER_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3     14
5     MEISSNER_NPC_ICP_WITH_H3K4ME3      20
6     MEISSNER_NPC_ICP_WITH_H3_UNMETHYLATED   24
7     MEISSNER_BRAIN_ICP_WITH_H3K4ME3   32
8     MIKKELSEN_MCV6_ICP_WITH_H3K4ME3_AND_H3K27ME3  34
9     MIKKELSEN_MCV6_ICP_WITH_H3K27ME3  74
10    MIKKELSEN_MEF_ICP_WITH_H3K4ME3_AND_H3K27ME3   38
11    MIKKELSEN_MEF_ICP_WITH_H3K27ME3   206
12    MIKKELSEN_IPS_ICP_WITH_H3K4ME3_AND_H327ME3    126
13    MIKKELSEN_IPS_ICP_WITH_H3K27ME3   54
14    MIKKELSEN_ES_ICP_WITH_H3K27ME3    42
15    MIKKELSEN_ES_ICP_WITH_H3K4ME3     718
16    MIKKELSEN_ES_ICP_WITH_H3K4ME3_AND_H3K27ME3    137
17    MIKKELSEN_NPC_ICP_WITH_H3K4ME3    445
18    NUCLEAR_BODY     33
19    NUCLEAR_SPECK    11
20    PML_BODY   14


cluster ID = 469
cluster size = 6
      gene set name    size (number of genes in the set)
1     JI_METASTASIS_REPRESSED_BY_STK11  27
2     HASLINGER_B_CLL_WITH_13Q14_DELETION     24
3     LE_SKI_TARGETS_DN8
4     POTTI_5FU_SENSITIVITY  43
5     LOPEZ_EPITHELIOID_MESOTHELIOMA    17
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6     GTCGATC,MIR-369-5P     5


cluster ID = 471
cluster size = 7
      gene set name    size (number of genes in the set)
1     ZEILSTRA_CD44_TARGETS_UP     7
2     LY_AGING_MIDDLE_UP     14
3     LIN_TUMOR_ESCAPE_FROM_IMMUNE_ATTACK     18
4     MCMURRAY_TP53_HRAS_COOPERATION_RESPONSE_UP    26
5     LY_AGING_OLD_UP  7
6     MODULE_481 89
7     MODULE_544 88


cluster ID = 491
cluster size = 6
      gene set name    size (number of genes in the set)
1     FAELT_B_CLL_WITH_VH_REARRANGEMENTS_UP   48
2     FAELT_B_CLL_WITH_VH_REARRANGEMENTS_DN   48
3     FAELT_B_CLL_WITH_VH3_21_DN  49
4     SESTO_RESPONSE_TO_UV_C2     54
5     GENTILE_UV_RESPONSE_CLUSTER_D7    40
6     ZEMBUTSU_SENSITIVITY_TO_FLUOROURACIL    17


cluster ID = 494
cluster size = 9
      gene set name    size (number of genes in the set)
1     ASTIER_INTEGRIN_SIGNALING   59
2     MODULE_166 54
3     MODULE_192 112
4     MODULE_256 62
5     MODULE_279 141
6     MODULE_333 29
7     MODULE_334 166
8     MODULE_427 116
9     MODULE_480 98


cluster ID = 507
cluster size = 11
      gene set name    size (number of genes in the set)
1     MCCLUNG_CREB1_TARGETS_DN     57
2     MCCLUNG_COCAIN_REWARD_4WK    75
3     TACGGGT,MIR-99A,MIR-100,MIR-99B   23
4     GGCAGAC,MIR-346  43
5     TCCGTCC,MIR-184  13
6     MODULE_97  99
7     MODULE_182 101
8     MODULE_261 101
9     MODULE_277 55
10    MODULE_358 81
11    MODULE_525 67
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cluster ID = 509
cluster size = 6
      gene set name    size (number of genes in the set)
1     YAMAZAKI_TCEB3_TARGETS_UP    175
2     DURAND_STROMA_MAX_DN   153
3     ESC_J1_UP_EARLY.V1_UP  183
4     ESC_J1_UP_LATE.V1_UP   191
5     ESC_V6.5_UP_EARLY.V1_UP      170
6     ESC_V6.5_UP_LATE.V1_UP 190


cluster ID = 511
cluster size = 7
      gene set name    size (number of genes in the set)
1     KANG_FLUOROURACIL_RESISTANCE_DN    16
2     GENTILE_UV_RESPONSE_CLUSTER_D1     18
3     MARSHALL_VIRAL_INFECTION_RESPONSE_UP    7
4     ONGUSAHA_BRCA1_TARGETS_UP    13
5     RB_DN.V1_DN 126
6     RB_P107_DN.V1_DN 128
7     RB_P130_DN.V1_DN 139


cluster ID = 513
cluster size = 6
      gene set name    size (number of genes in the set)
1     KANG_FLUOROURACIL_RESISTANCE_UP    22
2     KANG_CISPLATIN_RESISTANCE_UP 19
3     SASAI_TARGETS_OF_CXCR6_AND_PTCH1_DN     8
4     AZARE_NEOPLASTIC_TRANSFORMATION_BY_STAT3_UP   17
5     CCANNAGRKGGC_UNKNOWN   117
6     RYCACNNRNNRNCAG_UNKNOWN      76


cluster ID = 522
cluster size = 7
      gene set name    size (number of genes in the set)
1     ABE_INNER_EAR    48
2     MATZUK_PREOVULATORY_FOLLICLE 10
3     POTTI_DOCETAXEL_SENSITIVITY  47
4     SUPEROXIDE_METABOLIC_PROCESS 10
5     OXYGEN_AND_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS     20
6     SENSORY_ORGAN_DEVELOPMENT    14
7     COPPER_ION_BINDING     15


cluster ID = 528
cluster size = 7
      gene set name    size (number of genes in the set)
1     CHEN_ETV5_TARGETS_TESTIS     23
2     TESAR_JAK_TARGETS_MOUSE_ES_D3_DN   9
3     MATZUK_EMBRYONIC_GERM_CELL   19
4     MATZUK_MALE_REPRODUCTION_SERTOLI   28
5     MATZUK_SPERMATOGONIA   24
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6     CONRAD_GERMLINE_STEM_CELL    13
7     WANG_THOC1_TARGETS_DN  20


cluster ID = 537
cluster size = 15
      gene set name    size (number of genes in the set)
1     MCGOWAN_RSP6_TARGETS_UP      18
2     YANG_BCL3_TARGETS_DN   8
3     MODULE_148  13
4     MODULE_156  22
5     MODULE_240  20
6     MODULE_313  19
7     MODULE_326  13
8     MODULE_327  21
9     MODULE_431  15
10    MODULE_462  15
11    MODULE_547  16
12    FATTY_ACID_BIOSYNTHETIC_PROCESS    14
13    ICOSANOID_METABOLIC_PROCESS  17
14    INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY  19
15    ISOMERASE_ACTIVITY     35


cluster ID = 539
cluster size = 6
      gene set name    size (number of genes in the set)
1     CLAUS_PGR_POSITIVE_MENINGIOMA_UP   10
2     BOYLAN_MULTIPLE_MYELOMA_C_CLUSTER_DN    32
3     BOYLAN_MULTIPLE_MYELOMA_C_DN 59
4     CHIANG_LIVER_CANCER_SUBCLASS_POLYSOMY7_DN     24
5     BOYLAN_MULTIPLE_MYELOMA_PCA3_UP    80
6     PARK_OSTEOBLAST_DIFFERENTIATION_BY_PHENYLAMIL_DN    6


cluster ID = 540
cluster size = 7
      gene set name    size (number of genes in the set)
1     LEE_METASTASIS_AND_RNA_PROCESSING_UP    17
2     TGCACGA,MIR-517A,MIR-517C    18
3     ACCGAGC,MIR-423  8
4     AGTGCGT,MIR-521  6
5     HETEROGENEOUS_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX     14
6     MRNA_BINDING     23
7     SINGLE_STRANDED_RNA_BINDING  13


cluster ID = 565
cluster size = 6
      gene set name    size (number of genes in the set)
1     FONTAINE_FOLLICULAR_THYROID_ADENOMA_UP  75
2     FONTAINE_FOLLICULAR_THYROID_ADENOMA_DN  68
3     FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_UP      36
4     FONTAINE_THYROID_TUMOR_UNCERTAIN_MALIGNANCY_DN      26
5     FONTAINE_PAPILLARY_THYROID_CARCINOMA_UP 66
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6     FONTAINE_PAPILLARY_THYROID_CARCINOMA_DN 80


cluster ID = 572
cluster size = 7
      gene set name    size (number of genes in the set)
1     FIGUEROA_AML_METHYLATION_CLUSTER_1_DN   48
2     FIGUEROA_AML_METHYLATION_CLUSTER_2_DN   9
3     FIGUEROA_AML_METHYLATION_CLUSTER_3_DN   42
4     FIGUEROA_AML_METHYLATION_CLUSTER_4_DN   15
5     FIGUEROA_AML_METHYLATION_CLUSTER_5_DN   50
6     FIGUEROA_AML_METHYLATION_CLUSTER_6_DN   38
7     FIGUEROA_AML_METHYLATION_CLUSTER_7_DN   5


cluster ID = 584
cluster size = 13
      gene set name    size (number of genes in the set)
1     V$MIF1_01  181
2     V$RFX1_01  256
3     V$RFX1_02  278
4     V$EFC_Q6   268
5     CYTAGCAAY_UNKNOWN147
6     GTCNYYATGR_UNKNOWN     111
7     GTTGNYNNRGNAAC_UNKNOWN 108
8     GTTNYYNNGGTNA_UNKNOWN  88
9     GTTRYCATRR_UNKNOWN     172
10    RYTGCNWTGGNR_UNKNOWN   116
11    TGTYNNNNNRGCARM_UNKNOWN     86
12    WCTCNATGGY_UNKNOWN     82
13    RYTGCNNRGNAAC_V$MIF1_01     86


cluster ID = 587
cluster size = 12
      gene set name    size (number of genes in the set)
1     MORF_BMPR2 53
2     MORF_DCC   113
3     MORF_EPHA7 140
4     MORF_FRK   111
5     MORF_IL9   94
6     MORF_LCAT  134
7     MORF_MAP3K14     121
8     MORF_RAB3A 89
9     MORF_WNT1  107
10    MORF_ZNF10 54
11    MODULE_59  28
12    MODULE_489 32


cluster ID = 588
cluster size = 20
      gene set name    size (number of genes in the set)
1     MODULE_9   125
2     MODULE_26  207
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3     MODULE_37  477
4     MODULE_48  338
5     MODULE_49  294
6     MODULE_67  230
7     MODULE_69  532
8     MODULE_95  566
9     MODULE_136 497
10    MODULE_163 572
11    MODULE_179 474
12    MODULE_205 307
13    MODULE_206 154
14    MODULE_207 227
15    MODULE_255 456
16    MODULE_317 446
17    MODULE_378 441
18    MODULE_389 218
19    MODULE_459 437
20    MODULE_532 413


cluster ID = 590
cluster size = 11
      gene set name     size (number of genes in the set)
1     MODULE_105 200
2     MODULE_120 72
3     MODULE_138 87
4     MODULE_174 95
5     MODULE_175 54
6     MODULE_241 73
7     MODULE_291 65
8     MODULE_522 34
9     ANTIGEN_BINDING  28
10    CYCLIN_D1_KE_.V1_UP    190
11    CYCLIN_D1_UP.V1_UP     188


cluster ID = 596
cluster size = 21
      gene set name     size (number of genes in the set)
1     ATF2_S_UP.V1_UP  193
2     ATF2_UP.V1_UP    192
3     ATM_DN.V1_DN     149
4     ATM_DN.V1_UP     146
5     P53_DN.V2_DN     145
6     RELA_DN.V1_DN    141
7     PRC1_BMI_UP.V1_UP190
8     PRC2_EDD_UP.V1_UP193
9     PRC2_EZH2_UP.V1_UP     195
10    PRC2_SUZ12_UP.V1_UP    194
11    JNK_DN.V1_UP     192
12    BRCA1_DN.V1_UP   141
13    CTIP_DN.V1_UP    138
14    PTEN_DN.V2_UP    143
15    DCA_UP.V1_UP     191
16    PTEN_DN.V1_DN    187
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17	NOTCH_DN.V1_DN	189
18	IL15_UP.V1_DN	190
19	IL2_UP.V1_DN	196
20	IL21_UP.V1_DN	187
21	JAK2_DN.V1_UP	188