

| Gene Set | SIZE | ES | NES | NOM | | FWER p- | | RANK | LEADING EDGE |
|--|------|-------|-------|-------|-----------|---------|--------|---------------------------------|--------------|
| | | | | p-val | FDR q-val | val | AT MAX | | |
| GO_AXONEME_PART | 31 | 0.869 | 2.806 | 0 | 0 | 0 | 630 | tags=90%, list=9%, signal=98% | |
| GO_CELL_PROJECTION_ASSEMBLY | 236 | 0.639 | 2.793 | 0 | 0 | 0 | 960 | tags=50%, list=13%, signal=56% | |
| GO_AXONEMAL_DYNEIN_COMPLEX_ASSEMBLY | 22 | 0.917 | 2.735 | 0 | 0 | 0 | 630 | tags=100%, list=9%, signal=109% | |
| GO_CILIUM_OR_FLAGELLUM_DEPENDENT_CELL_MOTILITY | 24 | 0.885 | 2.703 | 0 | 0 | 0 | 544 | tags=92%, list=7%, signal=99% | |
| GO_MICROTUBULE_BASED_PROCESS | 295 | 0.595 | 2.664 | 0 | 0 | 0 | 765 | tags=41%, list=10%, signal=44% | |
| GO_DYNEIN_COMPLEX | 30 | 0.828 | 2.663 | 0 | 0 | 0 | 630 | tags=73%, list=9%, signal=80% | |
| GO_ORGANELLE_ASSEMBLY | 291 | 0.567 | 2.555 | 0 | 0 | 0 | 1027 | tags=43%, list=14%, signal=48% | |
| GO_INTRACILIARY_TRANSPORT_INVOLVED_IN_CILIUM_ASSEMBLY | 22 | 0.837 | 2.535 | 0 | 0 | 0 | 765 | tags=82%, list=10%, signal=91% | |
| GO_CILIARY_TRANSITION_ZONE | 20 | 0.850 | 2.495 | 0 | 0 | 0 | 765 | tags=85%, list=10%, signal=95% | |
| GO_SPERM_PART | 75 | 0.654 | 2.493 | 0 | 0 | 0 | 1357 | tags=64%, list=19%, signal=78% | |
| GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION | 206 | 0.554 | 2.418 | 0 | 0 | 0 | 1027 | tags=41%, list=14%, signal=47% | |
| GO_SPERM_MOTILITY | 35 | 0.722 | 2.385 | 0 | 0 | 0 | 630 | tags=57%, list=9%, signal=62% | |
| GO_MICROTUBULE_ASSOCIATED_COMPLEX | 71 | 0.625 | 2.360 | 0 | 0 | 0 | 630 | tags=41%, list=9%, signal=44% | |
| GO_DYNEIN_LIGHT_CHAIN_BINDING | 16 | 0.854 | 2.320 | 0 | 0 | 0 | 630 | tags=81%, list=9%, signal=89% | |
| GO_MICROTUBULE_CYTOSKELETON | 398 | 0.498 | 2.290 | 0 | 0 | 0 | 1027 | tags=37%, list=14%, signal=41% | |
| GO_MICROTUBULE_ORGANIZING_CENTER | 238 | 0.511 | 2.255 | 0 | 1.06E-05 | 0.001 | 1047 | tags=40%, list=14%, signal=46% | |
| GO_NON_MOTILE_CILIUM | 43 | 0.631 | 2.178 | 0 | 1.15E-04 | 0.012 | 1134 | tags=47%, list=15%, signal=55% | |
| GO_SPERMATID_DIFFERENTIATION | 40 | 0.624 | 2.133 | 0 | 3.51E-04 | 0.039 | 763 | tags=48%, list=10%, signal=53% | |
| GO_MALE_GAMETE_GENERATION | 161 | 0.494 | 2.103 | 0 | 5.29E-04 | 0.059 | 1256 | tags=39%, list=17%, signal=45% | |
| GO_9PLUS0_NON_MOTILE_CILIUM | 32 | 0.638 | 2.070 | 0 | 8.99E-04 | 0.102 | 1134 | tags=44%, list=15%, signal=52% | |
| GO_CYTOSKELETON_DEPENDENT_INTRACELLULAR_TRANSPORT | 72 | 0.536 | 2.039 | 0 | 1.69E-03 | 0.19 | 805 | tags=36%, list=11%, signal=40% | |
| GO_GAMETE_GENERATION | 197 | 0.449 | 1.947 | 0 | 0.008 | 0.638 | 1399 | tags=37%, list=19%, signal=44% | |
| SPIRA_SMOKERS_LUNG_CANCER_UP | 22 | 0.646 | 1.935 | 0 | 0.009 | 0.708 | 1085 | tags=50%, list=15%, signal=59% | |
| GO_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION | 42 | 0.554 | 1.920 | 0 | 0.011 | 0.793 | 1080 | tags=43%, list=15%, signal=50% | |
| GO_PROTEIN_CONTAINING_COMPLEX_LOCALIZATION | 94 | 0.485 | 1.916 | 0 | 0.012 | 0.816 | 765 | tags=29%, list=10%, signal=32% | |
| DOANE_BREAST_CANCER_ESR1_UP | 63 | 0.516 | 1.890 | 0 | 0.016 | 0.907 | 1346 | tags=43%, list=18%, signal=52% | |
| GO_SEXUAL_REPRODUCTION | 237 | 0.428 | 1.886 | 0 | 0.017 | 0.91 | 1399 | tags=34%, list=19%, signal=41% | |
| GO_SMOOTHENED_SIGNALING_PATHWAY | 66 | 0.508 | 1.872 | 0 | 0.019 | 0.94 | 740 | tags=35%, list=10%, signal=38% | |
| REACTOME_CARGO_TRAFFICKING_TO_THE_PERICILIARY_MEMBRANE | 18 | 0.656 | 1.870 | 0.002 | 0.020 | 0.947 | 1176 | tags=44%, list=16%, signal=53% | |
| GO_TUBULIN_BINDING | 128 | 0.446 | 1.849 | 0 | 0.026 | 0.983 | 924 | tags=32%, list=13%, signal=36% | |
| SMID_BREAST_CANCER_RELAPSE_IN_BONE_UP | 54 | 0.518 | 1.847 | 0 | 0.026 | 0.984 | 1265 | tags=44%, list=17%, signal=53% | |

| Gene Set | SIZE | ES | NES | NOM p-val | FDR q-val | FWER p-val | RANK AT MAX | LEADING EDGE |
|--|------|-------|-------|-----------|-----------|------------|-------------|--------------------------------|
| GO_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS | 16 | 0.672 | 1.846 | 0.002 | 0.026 | 0.985 | 633 | tags=44%, list=9%, signal=48% |
| GO_ATPASE_ACTIVITY | 124 | 0.447 | 1.839 | 0 | 0.029 | 0.989 | 1389 | tags=37%, list=19%, signal=45% |
| GO_GERM_CELL_DEVELOPMENT | 65 | 0.494 | 1.839 | 0 | 0.028 | 0.989 | 1350 | tags=42%, list=18%, signal=50% |
| GSE5542_IFNG_VS_IFNA_TREATED_EPITHELIAL_CELLS_24H_UP | 60 | 0.480 | 1.773 | 0 | 0.055 | 1 | 1097 | tags=28%, list=15%, signal=33% |
| RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_UP | 47 | 0.505 | 1.771 | 0 | 0.055 | 1 | 1572 | tags=43%, list=21%, signal=54% |
| GO_CELLULAR_PROCESS_INVOLVED_IN_REPRODUCTION_IN_MULTICELLULAR_ORGANISM | 95 | 0.439 | 1.752 | 0.001 | 0.066 | 1 | 1350 | tags=35%, list=18%, signal=42% |
| KIM_MYC_AMPLIFICATION_TARGETS_DN | 39 | 0.513 | 1.742 | 0.003 | 0.072 | 1 | 1840 | tags=51%, list=25%, signal=68% |
| GO_MULTICELLULAR_ORGANISM_REPRODUCTION | 262 | 0.382 | 1.710 | 0 | 0.092 | 1 | 1399 | tags=31%, list=19%, signal=36% |
| HALLMARK_SPERMATOGENESIS | 34 | 0.515 | 1.701 | 0.006 | 0.100 | 1 | 1438 | tags=41%, list=20%, signal=51% |
| GSE21670_UNTREATED_VS_TGFB_TREATED_CD4_TCELL_UP | 86 | 0.428 | 1.683 | 0.004 | 0.117 | 1 | 1016 | tags=26%, list=14%, signal=29% |
| GSE5542_IFNG_VS_IFNA_TREATED_EPITHELIAL_CELLS_6H_UP | 60 | 0.453 | 1.674 | 0.01 | 0.125 | 1 | 985 | tags=32%, list=13%, signal=36% |
| WUNDER_INFLAMMATORY_RESPONSE_AND_CHOLESTEROL_UP | 20 | 0.571 | 1.653 | 0.003 | 0.146 | 1 | 1152 | tags=30%, list=16%, signal=35% |
| GO_SINGLE_STRANDED_DNA_BINDING | 21 | 0.550 | 1.630 | 0.017 | 0.172 | 1 | 785 | tags=33%, list=11%, signal=37% |
| GO_MULTI_ORGANISM_REPRODUCTIVE_PROCESS | 312 | 0.361 | 1.626 | 0 | 0.175 | 1 | 1440 | tags=29%, list=20%, signal=35% |
| GO_REGULATION_OF_CILIUM_ASSEMBLY | 17 | 0.567 | 1.616 | 0.019 | 0.188 | 1 | 865 | tags=53%, list=12%, signal=60% |
| RODRIGUES_THYROID_CARINOMA_ANAPLASTIC_UP | 218 | 0.369 | 1.605 | 0 | 0.207 | 1 | 1764 | tags=34%, list=24%, signal=43% |
| GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY | 23 | 0.527 | 1.600 | 0.021 | 0.216 | 1 | 1425 | tags=57%, list=19%, signal=70% |
| GO_FERTILIZATION | 39 | 0.470 | 1.592 | 0.016 | 0.225 | 1 | 1522 | tags=36%, list=21%, signal=45% |
| HAMAI_APOPTOSIS_VIA_TRAIL_UP | 214 | 0.362 | 1.587 | 0.002 | 0.228 | 1 | 1706 | tags=34%, list=23%, signal=43% |
| GO_MITOTIC_SPINDLE_ASSEMBLY | 15 | 0.581 | 1.581 | 0.028 | 0.239 | 1 | 1014 | tags=40%, list=14%, signal=46% |

Supplementary file 6, part 1, most related gene sets the expression of which enriched along with the expression of IL7.

Columns: Size: Number of genes in the gene set that included in the expression matrix; ES: enrichment score; NES: Normalized enrichment score; NOM p-value: Nominal p-value; FDR q-value: False discovery rate; FWER p-value: Familywise-error rate; RANK AT MAX: The position in the ranked list at which the maximum enrichment score occurred; LEADING EDGE: three statistics used to define the leading-edge subsets (<https://www.gsea-msigdb.org/gsea/doc/GSEASUserGuideFrame.html>).

| Gene Set | SIZE | ES | NES | NOM | | FWER p- val | RANK AT MAX | LEADING EDGE |
|--|------|--------|--------|-------|-----------|----------------|----------------|---------------------------------|
| | | | | p-val | FDR q-val | | | |
| GO_ENDOTHELIAL_CELL_MIGRATION | 99 | -0.503 | -2.384 | 0 | 0 | 0 | 1809 | tags=46%, list=25%, signal=61% |
| GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION | 52 | -0.559 | -2.286 | 0 | 5.27E-04 | 0.01 | 1745 | tags=52%, list=24%, signal=68% |
| GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION | 78 | -0.496 | -2.229 | 0 | 1.15E-03 | 0.032 | 1809 | tags=47%, list=25%, signal=62% |
| BENPORATH_MYC_TARGETS_WITH_EBOX | 74 | -0.484 | -2.139 | 0 | 0.003 | 0.135 | 1247 | tags=39%, list=17%, signal=47% |
| GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS | 111 | -0.440 | -2.085 | 0 | 0.005 | 0.249 | 2350 | tags=54%, list=32%, signal=78% |
| GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION | 219 | -0.396 | -2.067 | 0 | 0.006 | 0.303 | 2082 | tags=44%, list=28%, signal=60% |
| GSE1432_6H_VS_24H_IFNG_MICROGLIA_UP | 79 | -0.467 | -2.067 | 0 | 0.006 | 0.305 | 1502 | tags=41%, list=20%, signal=50% |
| GO_TISSUE_MIGRATION | 145 | -0.408 | -2.026 | 0 | 0.008 | 0.449 | 1828 | tags=41%, list=25%, signal=54% |
| GO_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX | 197 | -0.391 | -2.012 | 0 | 0.008 | 0.505 | 1934 | tags=43%, list=26%, signal=56% |
| GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION | 16 | -0.667 | -2.000 | 0.002 | 0.009 | 0.554 | 580 | tags=50%, list=8%, signal=54% |
| HAMAI_APOPTOSIS_VIA_TRAIL_DN | 81 | -0.446 | -1.999 | 0 | 0.009 | 0.557 | 1798 | tags=42%, list=25%, signal=55% |
| REACTOME_EXTRACELLULAR_MATRIX_ORGANIZATION | 162 | -0.395 | -1.980 | 0 | 0.010 | 0.655 | 2349 | tags=52%, list=32%, signal=76% |
| GO_AMEBOIDAL_TYPE_CELL_MIGRATION | 191 | -0.379 | -1.973 | 0 | 0.010 | 0.687 | 2006 | tags=42%, list=27%, signal=57% |
| ROY_WOUND_BLOOD_VESSEL_UP | 30 | -0.542 | -1.972 | 0 | 0.010 | 0.689 | 2337 | tags=60%, list=32%, signal=88% |
| GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS | 31 | -0.535 | -1.933 | 0 | 0.013 | 0.826 | 1619 | tags=45%, list=22%, signal=58% |
| GO_REGULATION_OF_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS | 22 | -0.580 | -1.932 | 0.003 | 0.014 | 0.834 | 1619 | tags=55%, list=22%, signal=70% |
| GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION | 21 | -0.590 | -1.929 | 0 | 0.014 | 0.84 | 2279 | tags=67%, list=31%, signal=96% |
| KEGG_ECM_RECEPTOR_INTERACTION | 48 | -0.474 | -1.929 | 0 | 0.014 | 0.84 | 2316 | tags=60%, list=32%, signal=88% |
| GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT | 89 | -0.420 | -1.927 | 0 | 0.014 | 0.847 | 2645 | tags=64%, list=36%, signal=99% |
| GO_ROUGH_ENDOPLASMIC_RETICULUM | 26 | -0.554 | -1.919 | 0.006 | 0.014 | 0.866 | 1651 | tags=58%, list=23%, signal=74% |
| GO_T_CELL_MEDIATED_IMMUNITY | 34 | -0.519 | -1.899 | 0 | 0.016 | 0.922 | 1455 | tags=41%, list=20%, signal=51% |
| GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION | 18 | -0.600 | -1.889 | 0 | 0.017 | 0.946 | 1518 | tags=50%, list=21%, signal=63% |
| GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY | 16 | -0.614 | -1.884 | 0.003 | 0.017 | 0.95 | 2350 | tags=69%, list=32%, signal=101% |
| GO_ENDOTHELIUM_DEVELOPMENT | 54 | -0.450 | -1.853 | 0 | 0.021 | 0.983 | 957 | tags=33%, list=13%, signal=38% |
| GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS | 37 | -0.492 | -1.852 | 0.003 | 0.021 | 0.983 | 1805 | tags=51%, list=25%, signal=68% |
| GO_LATE_ENDOSOME_MEMBRANE | 44 | -0.478 | -1.852 | 0 | 0.021 | 0.983 | 971 | tags=34%, list=13%, signal=39% |
| GO_EXTRACELLULAR_MATRIX_COMPONENT | 29 | -0.521 | -1.847 | 0 | 0.022 | 0.984 | 2645 | tags=79%, list=36%, signal=124% |
| GO_EXTRACELLULAR_MATRIX | 254 | -0.345 | -1.844 | 0 | 0.022 | 0.986 | 1934 | tags=38%, list=26%, signal=50% |
| GO_EXTRACELLULAR_MATRIX_BINDING | 31 | -0.505 | -1.831 | 0 | 0.024 | 0.99 | 2341 | tags=61%, list=32%, signal=90% |
| GO_ACTIVATION_OF_MAPKK_ACTIVITY | 21 | -0.560 | -1.819 | 0.003 | 0.026 | 0.998 | 2304 | tags=62%, list=31%, signal=90% |

| Gene Set | SIZE | ES | NES | NOM p-val | FDR q-val | FWER p- val | RANK AT MAX | LEADING EDGE |
|--|------|--------|--------|--------------|-----------|----------------|----------------|---------------------------------|
| SWEET_LUNG_CANCER_KRAS_DN | 227 | -0.342 | -1.787 | 0 | 0.031 | 1 | 2099 | tags=47%, list=29%, signal=63% |
| GO_T_CELL_MEDIATED_CYTOTOXICITY | 17 | -0.544 | -1.682 | 0.016 | 0.050 | 1 | 1437 | tags=47%, list=20%, signal=58% |
| REACTOME_INTERLEUKIN_1_SIGNALING | 18 | -0.541 | -1.668 | 0.018 | 0.053 | 1 | 779 | tags=33%, list=11%, signal=37% |
| JECHLINGER_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_UP | 30 | -0.464 | -1.668 | 0.011 | 0.053 | 1 | 2316 | tags=60%, list=32%, signal=87% |
| GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION | 16 | -0.555 | -1.663 | 0.013 | 0.054 | 1 | 1113 | tags=38%, list=15%, signal=44% |
| GO_WOUND_HEALING | 217 | -0.323 | -1.646 | 0 | 0.060 | 1 | 2040 | tags=41%, list=28%, signal=55% |
| GO_EPITHELIAL_CELL_APOPTOTIC_PROCESS | 42 | -0.425 | -1.637 | 0.003 | 0.062 | 1 | 1626 | tags=45%, list=22%, signal=58% |
| GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION | 49 | -0.396 | -1.583 | 0.007 | 0.076 | 1 | 2651 | tags=53%, list=36%, signal=83% |
| GO_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY | 22 | -0.476 | -1.583 | 0.016 | 0.076 | 1 | 1455 | tags=36%, list=20%, signal=45% |
| GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY | 174 | -0.314 | -1.580 | 0 | 0.077 | 1 | 1825 | tags=37%, list=25%, signal=48% |
| GO_POSITIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION | 20 | -0.475 | -1.543 | 0.035 | 0.090 | 1 | 633 | tags=20%, list=9%, signal=22% |
| GO_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS | 28 | -0.430 | -1.523 | 0.043 | 0.098 | 1 | 1626 | tags=46%, list=22%, signal=59% |
| REACTOME_INTERLEUKIN_1_FAMILY_SIGNALING | 28 | -0.413 | -1.475 | 0.028 | 0.121 | 1 | 1437 | tags=29%, list=20%, signal=35% |
| GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_SIGNALING_PATHWAY | 21 | -0.446 | -1.466 | 0.034 | 0.125 | 1 | 2634 | tags=67%, list=36%, signal=104% |
| GO_POSITIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCION | 27 | -0.416 | -1.451 | 0.037 | 0.132 | 1 | 1437 | tags=33%, list=20%, signal=41% |
| GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS | 28 | -0.420 | -1.450 | 0.043 | 0.132 | 1 | 2267 | tags=57%, list=31%, signal=82% |
| GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS | 18 | -0.463 | -1.450 | 0.08 | 0.132 | 1 | 2252 | tags=56%, list=31%, signal=80% |
| GO_VASCULOGENESIS | 35 | -0.386 | -1.449 | 0.038 | 0.132 | 1 | 1944 | tags=46%, list=27%, signal=62% |
| GO_APOPTOTIC_CELL_CLEARANCE | 17 | -0.457 | -1.402 | 0.084 | 0.157 | 1 | 1670 | tags=41%, list=23%, signal=53% |
| REACTOME_SIGNALING_BY_NON_RECEPTOR_TYROSINE_KINASES | 20 | -0.437 | -1.400 | 0.081 | 0.158 | 1 | 1725 | tags=45%, list=24%, signal=59% |
| GSE8678_IL7R_LOW_VS_HIGH_EFF_CD8_TCELL_UP | 81 | -0.314 | -1.388 | 0.035 | 0.166 | 1 | 1102 | tags=30%, list=15%, signal=34% |
| GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE | 28 | -0.387 | -1.359 | 0.1 | 0.185 | 1 | 2122 | tags=43%, list=29%, signal=60% |
| REACTOME_CELL_DEATH_SIGNALLING_VIA_NRAGE_NRIF_AND_NADE | 29 | -0.378 | -1.357 | 0.087 | 0.186 | 1 | 2134 | tags=55%, list=29%, signal=78% |
| GO_LEUKOCYTE_MEDIATED_IMMUNITY | 344 | -0.251 | -1.357 | 0.011 | 0.186 | 1 | 1648 | tags=24%, list=22%, signal=29% |
| KEGG_SMALL_CELL_LUNG_CANCER | 27 | -0.380 | -1.355 | 0.067 | 0.188 | 1 | 2320 | tags=48%, list=32%, signal=70% |
| REACTOME_PROGRAMMED_CELL_DEATH | 40 | -0.355 | -1.355 | 0.09 | 0.188 | 1 | 1900 | tags=45%, list=26%, signal=60% |
| GO_POSITIVE_REGULATION_OF_CELL_DEATH | 266 | -0.256 | -1.352 | 0 | 0.190 | 1 | 2052 | tags=37%, list=28%, signal=49% |
| GO_POSITIVE_REGULATION_OF_T_CELL_MEDIATED_IMMUNITY | 15 | -0.460 | -1.348 | 0.112 | 0.193 | 1 | 2122 | tags=47%, list=29%, signal=66% |
| ZWANG_EGF_INTERVAL_DN | 97 | -0.287 | -1.342 | 0.02 | 0.198 | 1 | 2152 | tags=42%, list=29%, signal=59% |
| GSE2197_IMMUNOSUPPRESSIVE_DNA_VS_UNTREATEDIN_DC_DN | 67 | -0.310 | -1.339 | 0.055 | 0.200 | 1 | 1435 | tags=31%, list=20%, signal=39% |

| Gene Set | SIZE | ES | NES | NOM p-val | FDR q-val | FWER p-val | RANK AT MAX | LEADING EDGE |
|--|------|--------|--------|-----------|-----------|------------|-------------|---------------------------------|
| GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_TENSILE_STRENGTH | 29 | -0.381 | -1.332 | 0.095 | 0.206 | 1 | 2034 | tags=52%, list=28%, signal=71% |
| REACTOME_DEATH_RECEPTOR_SIGNALLING | 51 | -0.329 | -1.329 | 0.077 | 0.208 | 1 | 2134 | tags=49%, list=29%, signal=69% |
| GSE44955_MCSF_VS_MCSF_AND_IL27_STIM_MACROPHAGE_UP | 76 | -0.300 | -1.327 | 0.032 | 0.210 | 1 | 1859 | tags=38%, list=25%, signal=51% |
| GSE13229_IMM_VS_MATURE_NKCELL_DN | 71 | -0.312 | -1.327 | 0.049 | 0.210 | 1 | 851 | tags=24%, list=12%, signal=27% |
| GO_LEUKOCYTE_MEDIATED_CYTOTOXICITY | 41 | -0.339 | -1.323 | 0.079 | 0.213 | 1 | 2224 | tags=44%, list=30%, signal=63% |
| GSE43955_TH0_VS_TGFB_IL6_TH17_ACT_CD4_TCELL_52H_UP | 78 | -0.298 | -1.321 | 0.033 | 0.215 | 1 | 1564 | tags=31%, list=21%, signal=39% |
| GO_POSITIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION | 31 | -0.369 | -1.317 | 0.101 | 0.218 | 1 | 1853 | tags=35%, list=25%, signal=47% |
| YU_MYC_TARGETS_DN | 29 | -0.370 | -1.311 | 0.105 | 0.223 | 1 | 1313 | tags=28%, list=18%, signal=33% |
| GO_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE | 45 | -0.323 | -1.302 | 0.085 | 0.231 | 1 | 1825 | tags=33%, list=25%, signal=44% |
| PID_TGFBR_PATHWAY | 22 | -0.398 | -1.293 | 0.16 | 0.238 | 1 | 2651 | tags=50%, list=36%, signal=78% |
| GSE43955_TH0_VS_TGFB_IL6_TH17_ACT_CD4_TCELL_1H_DN | 70 | -0.297 | -1.293 | 0.063 | 0.238 | 1 | 1585 | tags=34%, list=22%, signal=43% |
| GSE3920_IFNA_VS_IFNG_TREATED_FIBROBLAST_DN | 82 | -0.289 | -1.291 | 0.08 | 0.239 | 1 | 2077 | tags=45%, list=28%, signal=62% |
| GO_POSITIVE_REGULATION_OF_WOUND_HEALING | 22 | -0.385 | -1.291 | 0.134 | 0.240 | 1 | 2012 | tags=50%, list=27%, signal=69% |
| GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY | 95 | -0.277 | -1.285 | 0.045 | 0.245 | 1 | 1410 | tags=28%, list=19%, signal=35% |
| GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION | 26 | -0.377 | -1.285 | 0.141 | 0.245 | 1 | 2681 | tags=65%, list=37%, signal=103% |
| GSE9601_NFKB_INHIBITOR_VS_PI3K_INHIBITOR_TREATED_HCMV_INF_MONOCYTE_UP | 80 | -0.289 | -1.285 | 0.062 | 0.245 | 1 | 1672 | tags=34%, list=23%, signal=43% |
| GSE27786_BCELL_VS_MONO_MAC_DN | 80 | -0.296 | -1.285 | 0.077 | 0.245 | 1 | 2025 | tags=43%, list=28%, signal=58% |
| GSE22601_DOUBLE_NEGATIVE_VS_DOUBLE_POSITIVE_THYMOCYTE_DN | 71 | -0.294 | -1.285 | 0.073 | 0.245 | 1 | 1437 | tags=25%, list=20%, signal=31% |
| GSE27786_CD8_TCELL_VS_NKCELL_DN | 76 | -0.298 | -1.285 | 0.058 | 0.245 | 1 | 2278 | tags=51%, list=31%, signal=74% |
| GSE22025_UNTREATED_VS_TGFB1_AND_PROGESTERONE_TREATED_CD4_TCELL_UP | 87 | -0.278 | -1.284 | 0.058 | 0.246 | 1 | 1987 | tags=39%, list=27%, signal=53% |
| GSE1925_CTRL_VS_3H_IFNG_STIM_MACROPHAGE_UP | 61 | -0.304 | -1.284 | 0.108 | 0.246 | 1 | 1695 | tags=31%, list=23%, signal=40% |
| GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION | 43 | -0.326 | -1.283 | 0.103 | 0.247 | 1 | 1388 | tags=30%, list=19%, signal=37% |

Supplementary file 6, part 2, most related gene sets expression of which reduced along with the expression of IL7.

Columns: Size: Number of genes in the gene set that included in the expression matrix; ES: enrichment score; NES: Normalized enrichment score; NOM p-value: Nominal p-value; FDR q-value: False discovery rate; FWER p-value: Familywise-error rate; RANK AT MAX: The position in the ranked list at which the maximum enrichment score occurred; LEADING EDGE: three statistics used to define the leading-edge subsets (<https://www.gsea-msigdb.org/gsea/doc/GSEAUUserGuideFrame.html>).