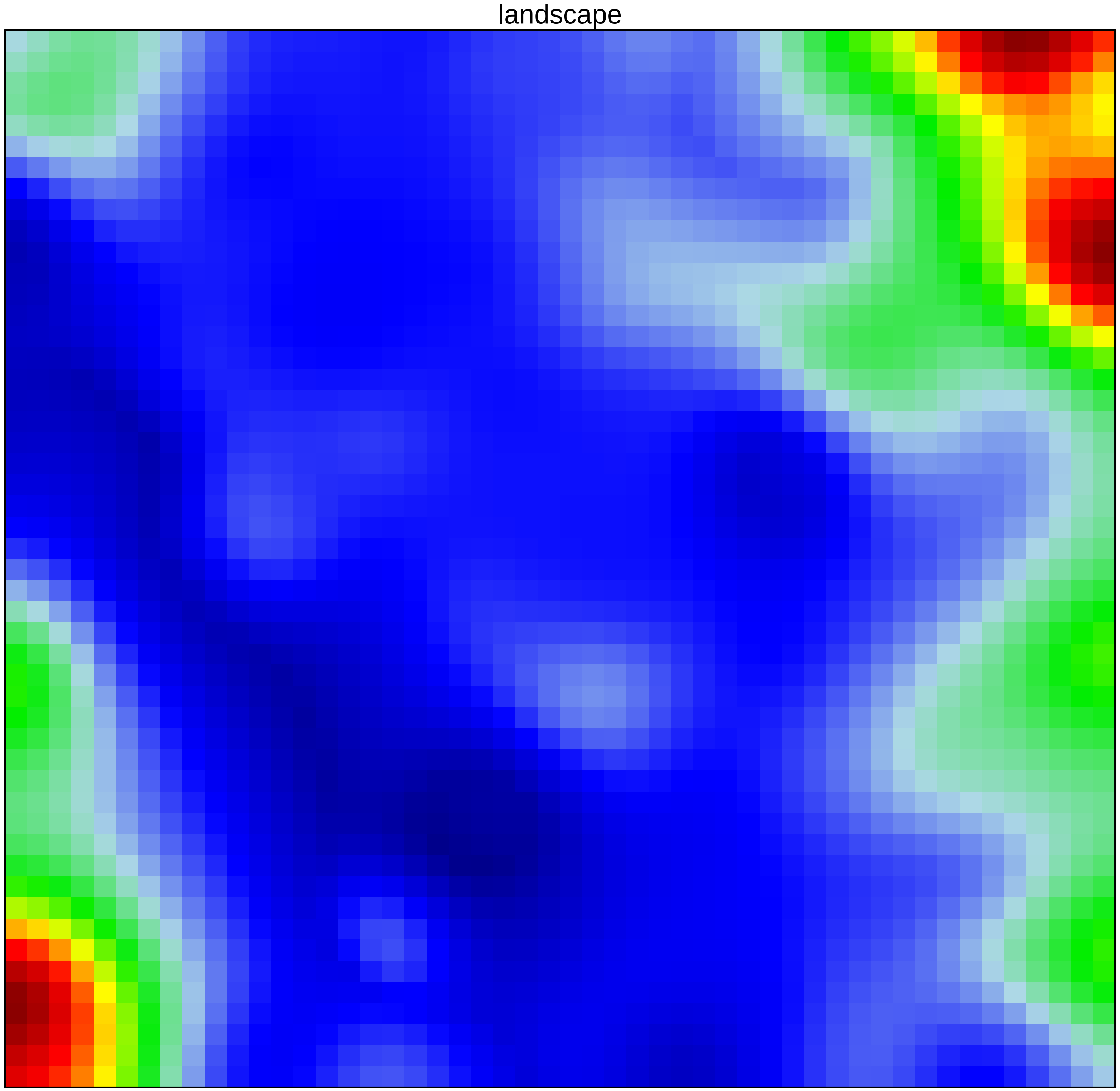
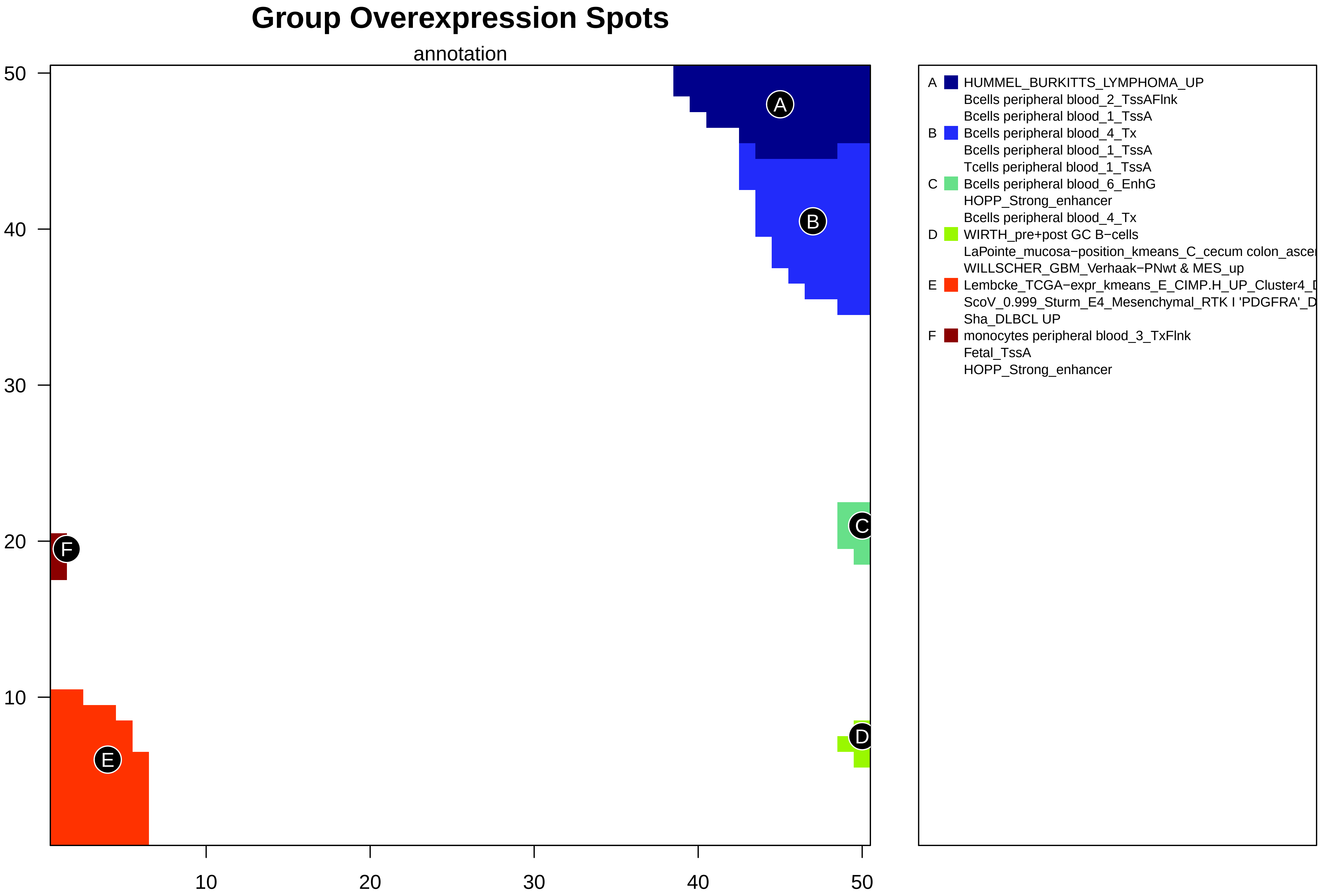
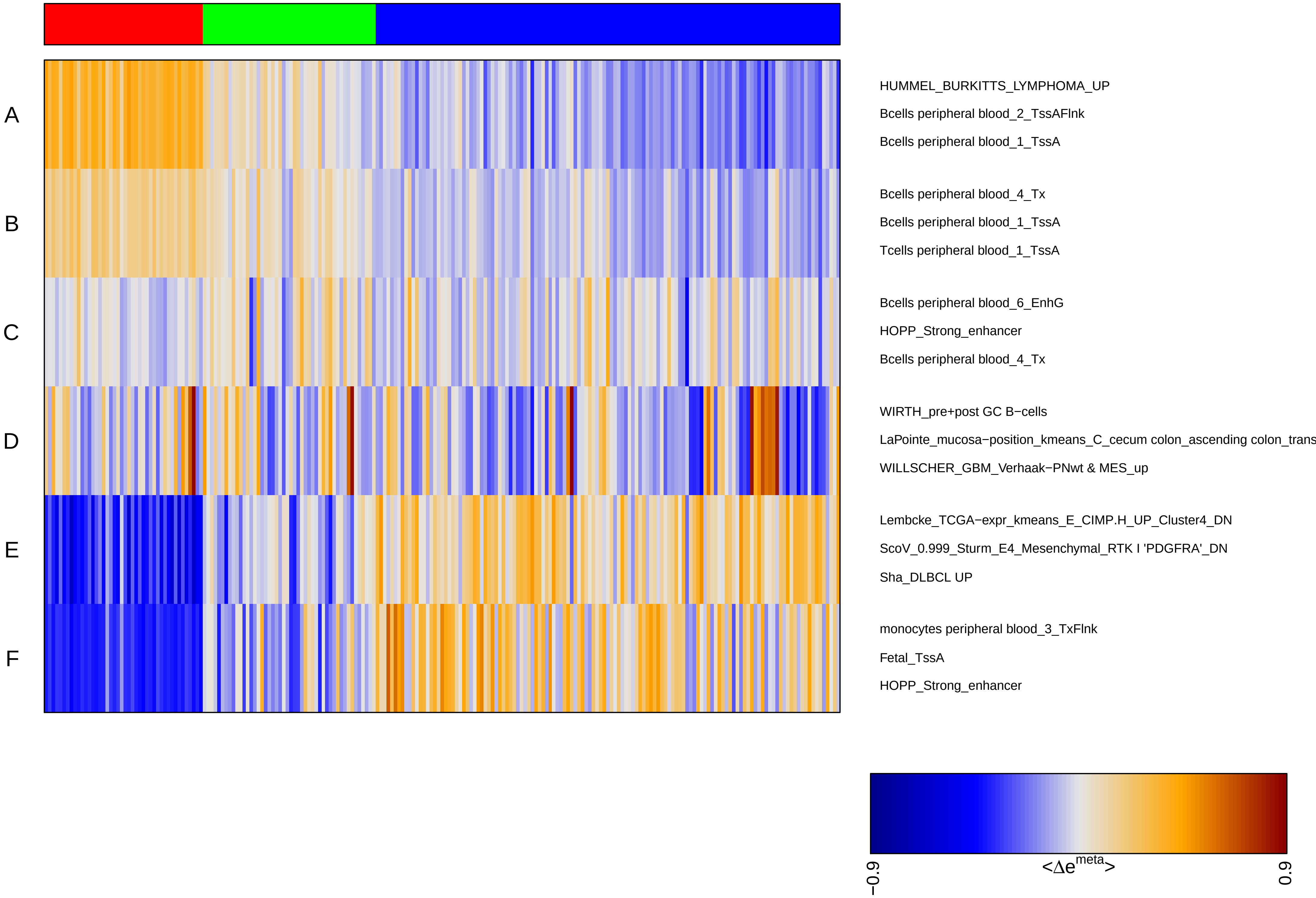
# Group Overexpression Spots




Group Overexpression Spots
annotation
50
40
30
20
10
10
20
30
40
50
A
B
C
D
E
F
A 🟦 HUMMEL_BURKITTS_LYMPHOMA_UP
Bcells peripheral blood_2_TssAFlnk
Bcells peripheral blood_1_TssA
B 🟦 Bcells peripheral blood_4_Tx
Bcells peripheral blood_1_TssA
Tcells peripheral blood_1_TssA
C 🟩 Bcells peripheral blood_6_EnhG
HOPP_Strong_enhancer
Bcells peripheral blood_4_Tx
D 🟩 WIRTH_pre+post GC B−cells
LaPointe_mucosa−position_kmeans_C_cecum colon_ascen
WILLSCHER_GBM_Verhaak−PNwt & MES_up
E 🟥 Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_D
ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_D
Sha_DLBCL UP
F 🟥 monocytes peripheral blood_3_TxFlnk
Fetal_TssA
HOPP_Strong_enhancer


A
B
C
D
E
F
HUMMEL_BURKITTS_LYMPHOMA_UP
Bcells peripheral blood_2_TssAFlnk
Bcells peripheral blood_1_TssA
Bcells peripheral blood_4_Tx
Bcells peripheral blood_1_TssA
Tcells peripheral blood_1_TssA
Bcells peripheral blood_6_EnhG
HOPP_Strong_enhancer
Bcells peripheral blood_4_Tx
WIRTH_pre+post GC B−cells
LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans
WILLSCHER_GBM_Verhaak−PNwt & MES_up
Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN
ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN
Sha_DLBCL UP
monocytes peripheral blood_3_TxFlnk
Fetal_TssA
HOPP_Strong_enhancer
−0.9
<Δe^meta>
0.9

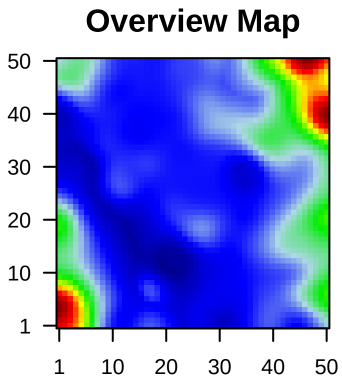
# Group Overexpression Spo

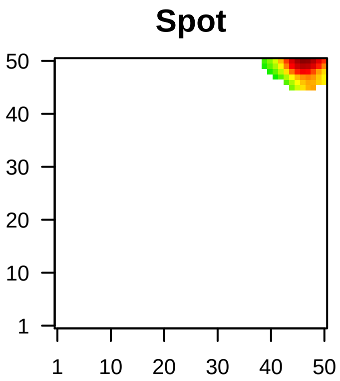
## Spot Summary: A

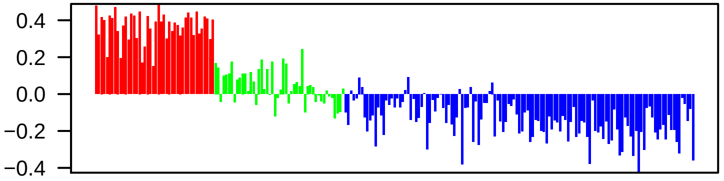
# metagenes = 58
# genes = 853

<r> metagenes = 0.9
<r> genes = 0.27
beta: r2= 12.2  /  log p= −Inf

# samples with spot = 41 ( 18.6 %)
mBL : 40 ( 90.9 %)
intermediate : 1 ( 2.1 %)





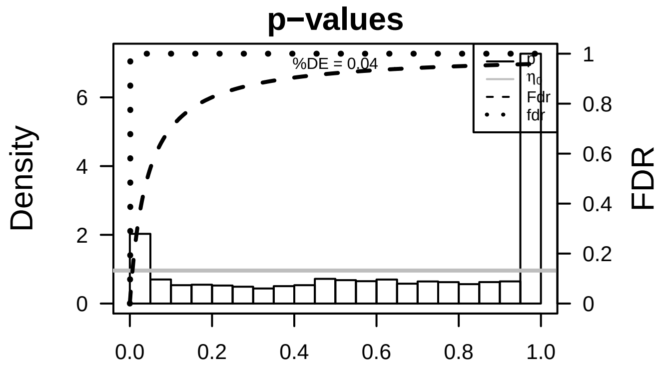


## Spot Genelist

| Rank | ID | max e | min e | r | Symbol | Description |
|---|---|---|---|---|---|---|
| 1 | AFFX−r2−Hs1 | 3.22 | −1.13 | 0.3 | | |
| 2 | AFFX−r2−Hs1 | 3.07 | −1.49 | 0.23 | | |
| 3 | AFFX−HUMR | 2.91 | −0.94 | 0.31 | | microRNA 3687−2 [Source:HGNC Symbol;Acc:HGNC:50835 |
| 4 | AFFX−HUMR | 2.85 | −1.18 | 0.21 | | |
| 5 | 206660_at | 2.83 | −0.99 | 0.46 | IGLL1 | immunoglobulin lambda like polypeptide 1 [Source:HGNC Sy |
| 6 | 221349_at | 2.76 | −0.89 | 0.69 | VPREB1 | V−set pre−B cell surrogate light chain 1 [Source:HGNC Sym |
| 7 | 206413_s_at | 2.76 | −1.22 | 0.37 | TCL1B | T cell leukemia/lymphoma 1B [Source:HGNC Symbol;Acc:HG |
| 8 | AFFX−r2−Hs1 | 2.71 | −1.22 | 0.37 | | |
| 9 | AFFX−r2−Hs2 | 2.62 | −0.97 | 0.32 | | |
| 10 | AFFX−M2783 | 2.6 | −1.58 | 0.35 | | |
| 11 | AFFX−HUMR | 2.6 | −1.04 | 0.31 | | |
| 12 | 203980_at | 2.41 | −1.55 | 0.28 | FABP4 | fatty acid binding protein 4 [Source:HGNC Symbol;Acc:HGN |
| 13 | 204914_s_at | 2.24 | −0.89 | 0.61 | SOX11 | SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191] |
| 14 | AFFX−r2−Hs2 | 2.21 | −1.56 | 0.32 | | |
| 15 | 213920_at | 2.19 | −1.02 | 0.46 | CUX2 | cut like homeobox 2 [Source:HGNC Symbol;Acc:HGNC:1934 |
| 16 | 219855_at | 2.18 | −0.78 | 0.43 | NUDT11 | nudix hydrolase 11 [Source:HGNC Symbol;Acc:HGNC:18011 |
| 17 | 213674_x_at | 2.16 | −1.9 | 0.3 | | immunoglobulin heavy constant delta [Source:HGNC Symbol |
| 18 | 38037_at | 2.16 | −1.11 | 0.52 | HBEGF | heparin binding EGF like growth factor [Source:HGNC Symbo |
| 19 | 204915_s_at | 2.16 | −0.86 | 0.53 | SOX11 | SRY−box 11 [Source:HGNC Symbol;Acc:HGNC:11191] |
| 20 | 209598_at | 2.13 | −0.99 | 0.18 | PNMA2 | PNMA family member 2 [Source:HGNC Symbol;Acc:HGNC:9 |

## Geneset Overrepresentation

| Rank | p−value | #in/all | Geneset | |
|---|---|---|---|---|
| 1 | 2e−44 | 38 / 42 | GSEA | HUMMEL_BURKITTS_LYMPHOMA_UP |
| 2 | 3e−41 | 53 / 99 | Lympl | Sha_BL UP |
| 3 | 2e−37 | 155 / 966 | GSEA | KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 4 | 5e−37 | 80 / 280 | GSEA | MANALO_HYPOXIA_DN |
| 5 | 4e−34 | 93 / 409 | Canc | Lembcke_Normal vs Adenoma |
| 6 | 1e−32 | 80 / 319 | Melar | Gerber_wt/wt_melanoma−cells−SpotA |
| 7 | 4e−32 | 62 / 192 | Lympl | Victora_Dark zone signature |
| 8 | 2e−31 | 92 / 431 | GSEA | GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| 9 | 1e−29 | 149 / 1052 | GSEA | DODD_NASOPHARYNGEAL_CARCINOMA_DN |
| 10 | 3e−29 | 140 / 955 | Lympl | SPANG_BCR UP |
| 11 | 4e−29 | 119 / 728 | GSEA | KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN |
| 12 | 6e−29 | 85 / 400 | GSEA | PUJANA_BRCA2_PCC_NETWORK |
| 13 | 2e−28 | 98 / 526 | GSEA | MARSON_BOUND_BY_E2F4_UNSTIMULATED |
| 14 | 7e−28 | 184 / 1527 | GSEA | PUJANA_BRCA1_PCC_NETWORK |
| 15 | 2e−27 | 116 / 726 | GSEA | PUJANA_CHEK2_PCC_NETWORK |
| 16 | 2e−25 | 98 / 575 | GSEA | CAIRO_HEPATOBLASTOMA_CLASSES_UP |
| 17 | 1e−24 | 83 / 439 | GSEA | SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 |
| 18 | 7e−23 | 101 / 651 | GSEA | KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN |
| 19 | 6e−22 | 96 / 615 | GSEA | BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN |
| 20 | 6e−22 | 104 / 703 | GSEA | LEE_BMP2_TARGETS_DN |
| 21 | 4e−21 | 418 / 5529 | Lympl | HOPP_Txn_elongation |
| 22 | 5e−21 | 239 / 2541 | CC | nucleoplasm |
| 23 | 6e−21 | 107 / 758 | GSEA | NUYTTEN_EZH2_TARGETS_DN |
| 24 | 4e−20 | 56 / 254 | GSEA | DUTERTRE_ESTRADIOL_RESPONSE_24HR_UP |
| 25 | 9e−19 | 431 / 5908 | Lympl | HOPP_Active_promoter |
| 26 | 2e−18 | 52 / 240 | GSEA | MITSIADES_RESPONSE_TO_APLIDIN_DN |
| 27 | 3e−17 | 92 / 669 | GSEA | JOHNSTONE_PARVB_TARGETS_3_DN |
| 28 | 3e−17 | 352 / 4579 | CC | nucleus |
| 29 | 4e−17 | 44 / 187 | HM | HALLMARK_E2F_TARGETS |
| 30 | 1e−16 | 50 / 244 | GSEA | KOBAYASHI_EGFR_SIGNALING_24HR_DN |
| 31 | 2e−16 | 58 / 321 | GSEA | BLUM_RESPONSE_TO_SALIRASIB_DN |
| 32 | 6e−16 | 33 / 115 | Gliom | WILLSCHER_GBM_Verhaak−CL_up ( C) |
| 33 | 1e−15 | 43 / 195 | HM | HALLMARK_G2M_CHECKPOINT |
| 34 | 3e−15 | 46 / 226 | GSEA | ZHANG_TLX_TARGETS_60HR_DN |
| 35 | 3e−15 | 13 / 15 | Lympl | BENTINK_mBL UP |
| 36 | 9e−15 | 52 / 290 | GSEA | WANG_RESPONSE_TO_GSK3_INHIBITOR_SB216763_DN |
| 37 | 1e−14 | 55 / 321 | GSEA | TOYOTA_TARGETS_OF_MIR34B_AND_MIR34C |
| 38 | 2e−14 | 34 / 135 | Lympl | DAVE_BL−vs−DLBCL |
| 39 | 2e−14 | 56 / 335 | GSEA | BENPORATH_ES_1 |
| 40 | 2e−14 | 37 / 160 | GSEA | PUJANA_XPRSS_INT_NETWORK |



## Aging

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.03 | 11 / 107 | HORVATH_aging_genes meth UP |
| 2 | 0.37 | 6 / 92 | HORVATH_aging_genes meth DOWN |
| 3 | 0.93 | 1 / 47 | TESCHENDORFF_age_hypermethylated |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## BP

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−12 | 47 / 281 | DNA repair |
| 2 | 5e−11 | 64 / 497 | cell cycle |
| 3 | 3e−09 | 27 / 137 | DNA replication |
| 4 | 2e−08 | 46 / 351 | cellular response to DNA damage stimulus |
| 5 | 2e−07 | 40 / 307 | cell division |
| 6 | 6e−07 | 27 / 174 | rRNA processing |
| 7 | 4e−06 | 10 / 32 | centrosome cycle |
| 8 | 4e−06 | 15 / 71 | regulation of G2/M transition of mitotic cell cycle |
| 9 | 6e−06 | 19 / 110 | regulation of cell cycle |
| 10 | 6e−05 | 8 / 27 | DNA biosynthetic process |
| 11 | 9e−05 | 15 / 91 | G1/S transition of mitotic cell cycle |
| 12 | 1e−04 | 9 / 37 | interstrand cross−link repair |
| 13 | 2e−04 | 13 / 76 | DNA recombination |
| 14 | 2e−04 | 17 / 119 | G2/M transition of mitotic cell cycle |
| 15 | 3e−04 | 5 / 12 | centriole replication |

## Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−34 | 93 / 409 | Lembcke_Normal vs Adenoma |
| 2 | 1e−11 | 10 / 12 | BENTINK_e2f3.2 |
| 3 | 3e−08 | 8 / 12 | BENTINK_ras.1 |
| 4 | 2e−07 | 2 / 14 | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP |
| 5 | 2e−05 | 20 / 130 | PanCan_CC+Apop_geneset_nanostring |
| 6 | 5e−05 | 10 / 41 | PanCan_DNARepair_geneset_nanostring |
| 7 | 9e−05 | 5 / 10 | GENTLES_modul3 |
| 8 | 6e−04 | 5 / 14 | BENTINK_myc.1 |
| 9 | 2e−03 | 8 / 45 | KUIPER_MM poor survival |
| 10 | 5e−03 | 4 / 14 | LIU_COMMON_CANCER_GENES |
| 11 | 5e−03 | 4 / 14 | BENTINK_src.10 |
| 12 | 7e−03 | 4 / 15 | RHODES_UNDIFFERENTIATED_CANCER |
| 13 | 7e−03 | 4 / 15 | GENTLES_modul2 |
| 14 | 3e−02 | 3 / 13 | GENTLES_modul1 |
| 15 | 4e−02 | 3 / 15 | GENTLES_modul7 |

## CC

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−21 | 239 / 2541 | nucleoplasm |
| 2 | 3e−17 | 352 / 4579 | nucleus |
| 3 | 8e−09 | 71 / 653 | nucleolus |
| 4 | 2e−07 | 44 / 354 | centrosome |
| 5 | 4e−06 | 18 / 98 | spindle pole |
| 6 | 5e−06 | 38 / 324 | chromosome |
| 7 | 7e−06 | 35 / 292 | microtubule organizing center |
| 8 | 6e−05 | 18 / 118 | chromosome, centromeric region |
| 9 | 2e−04 | 5 / 11 | Fanconi anaemia nuclear complex |
| 10 | 3e−04 | 33 / 326 | nuclear speck |
| 11 | 5e−04 | 27 / 251 | microtubule |
| 12 | 5e−04 | 74 / 936 | cytoskeleton |
| 13 | 5e−04 | 6 / 20 | centriolar satellite |
| 14 | 1e−03 | 28 / 277 | mitochondrial matrix |
| 15 | 1e−03 | 18 / 149 | nuclear envelope |

## Chr

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−04 | 50 / 548 | Chr 16 |
| 2 | 3e−04 | 27 / 242 | Chr 13 |
| 3 | 4e−03 | 30 / 333 | Chr 22 |
| 4 | 3e−02 | 33 / 437 | Chr 8 |
| 5 | 9e−02 | 82 / 1325 | Chr 1 |
| 6 | 2e−01 | 31 / 480 | Chr 4 |
| 7 | 2e−01 | 4 / 41 | Chr Y |
| 8 | 2e−01 | 25 / 382 | Chr 15 |
| 9 | 3e−01 | 41 / 700 | Chr 12 |
| 10 | 3e−01 | 48 / 833 | Chr 19 |
| 11 | 3e−01 | 29 / 492 | Chr 9 |
| 12 | 5e−01 | 37 / 669 | Chr 6 |
| 13 | 5e−01 | 22 / 403 | Chr 14 |
| 14 | 6e−01 | 41 / 776 | Chr 17 |
| 15 | 7e−01 | 24 / 490 | Chr 10 |

## Chromatin states

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−44 | 613 / 8406 | Bcells peripheral blood_2_TssAFlnk |
| 2 | 9e−43 | 586 / 7833 | Bcells peripheral blood_1_TssA |
| 3 | 1e−41 | 605 / 8322 | T CD8+ naive cells peripheral blood_1_TssA |
| 4 | 7e−39 | 589 / 8068 | Thelper cells peripheral blood_1_TssA |
| 5 | 4e−34 | 565 / 7751 | natural killer cells peripheral blood_1_TssA |
| 6 | 9e−34 | 592 / 8370 | natural killer cells peripheral blood_2_TssAFlnk |
| 7 | 1e−33 | 625 / 9160 | 2_TssA_Neuronal_Progenitor |
| 8 | 3e−33 | 608 / 8766 | 2_TssA_Melanocytes |
| 9 | 4e−33 | 571 / 7930 | Tregulatory cells peripheral blood_1_TssA |
| 10 | 5e−33 | 572 / 7957 | Tcells peripheral blood_2_TssAFlnk |
| 11 | 1e−32 | 609 / 8816 | Thelper cells peripheral blood_2_TssAFlnk |
| 12 | 1e−32 | 446 / 5456 | 5_Tx_Neuronal_Progenitor |
| 13 | 4e−32 | 583 / 8245 | Tregulatory cells peripheral blood_2_TssAFlnk |
| 14 | 6e−32 | 584 / 8275 | 2_TssA_Fibroblasts |
| 15 | 5e−31 | 533 / 7225 | Overlap_fetal_midbrain_ReprPC |

## Colon Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−12 | 75 / 602 | Pentrack_CRC_TCGA_corr_R_normal_DN |
| 2 | 1e−07 | 61 / 561 | Pentrack_CRC_TCGA_group.over_C_normal_DN |
| 3 | 6e−07 | 138 / 1729 | LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t |
| 4 | 2e−05 | 25 / 184 | Kosinski_lower−crypt−long−list |
| 5 | 6e−04 | 75 / 958 | LaPointe_mucosa−position_kmeans_D_transverse colon_UP_ |
| 6 | 8e−04 | 88 / 1174 | LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo |
| 7 | 2e−02 | 60 / 848 | LaPointe_mucosa−position_kmeans_O_transverse colon_UP_ |
| 8 | 4e−02 | 58 / 854 | LaPointe_mucosa−position_kmeans_A_ascending colon_UP_ |
| 9 | 5e−02 | 3 / 16 | Budinska_B_Lower crypt−like_UP |
| 10 | 7e−02 | 2 / 8 | KIM_MSI−in−EC |
| 11 | 9e−02 | 36 / 532 | LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U |
| 12 | 1e−01 | 1 / 2 | Hewish_dMMR−secondary−mutations_Damage_signaling |
| 13 | 1e−01 | 2 / 12 | Juehling−MSI−enriched−in−6 |
| 14 | 2e−01 | 1 / 3 | Budinska_C_CIMP−H−like_DOWN |
| 15 | 2e−01 | 355 / 6368 | LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_ |

## Glioma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−16 | 33 / 115 | WILLSCHER_GBM_Verhaak−CL_up ( C) |
| 2 | 5e−06 | 121 / 1523 | Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN |
| 3 | 3e−05 | 106 / 1343 | Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP |
| 4 | 3e−03 | 8 / 47 | developing astrocytes |
| 5 | 9e−02 | 4 / 32 | WIRTH_PN subtype |
| 6 | 1e−01 | 6 / 59 | GIEZELT_GBM_STS_up_VS_LTS |
| 7 | 1e−01 | 1 / 2 | Phillips Prolif up vs PN & MES |
| 8 | 1e−01 | 3 / 23 | Christensen_hypomethylated_in_grade3_astrocytoma |
| 9 | 1e−01 | 2 / 12 | Mukasa_UP_in_Oligodendroglioma_with_1intact |
| 10 | 1e−01 | 28 / 421 | Down_b |
| 11 | 2e−01 | 5 / 59 | WILLSCHER_GBM_Verhaak−PNwt & MES_up |
| 12 | 2e−01 | 2 / 16 | VERHAAK_CL subtype |
| 13 | 2e−01 | 2 / 16 | VERHAAK_PN subtype |
| 14 | 3e−01 | 3 / 34 | WILLSCHER_GBM_proteomics_wtOnly_SpotH |
| 15 | 3e−01 | 9 / 132 | Christensen_hypermethylated_in_grade3_oligoastrocytoma |

## GSEA C2

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−44 | 38 / 42 | HUMMEL_BURKITTS_LYMPHOMA_UP |
| 2 | 2e−37 | 155 / 966 | KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP |
| 3 | 5e−37 | 80 / 280 | MANALO_HYPOXIA_DN |
| 4 | 2e−31 | 92 / 431 | GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP |
| 5 | 1e−29 | 149 / 1052 | DODD_NASOPHARYNGEAL_CARCINOMA_DN |
| 6 | 4e−29 | 119 / 728 | KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN |
| 7 | 6e−29 | 85 / 400 | PUJANA_BRCA2_PCC_NETWORK |
| 8 | 2e−28 | 98 / 526 | MARSON_BOUND_BY_E2F4_UNSTIMULATED |
| 9 | 7e−28 | 184 / 1527 | PUJANA_BRCA1_PCC_NETWORK |
| 10 | 2e−27 | 116 / 726 | PUJANA_CHEK2_PCC_NETWORK |
| 11 | 2e−25 | 98 / 575 | CAIRO_HEPATOBLASTOMA_CLASSES_UP |
| 12 | 1e−24 | 83 / 439 | SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 |
| 13 | 7e−23 | 101 / 651 | KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN |
| 14 | 6e−22 | 96 / 615 | BUYTAERT_PHOTODYNAMIC_THERAPY_STRESS_DN |
| 15 | 6e−22 | 104 / 703 | LEE_BMP2_TARGETS_DN |

## HM

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−17 | 44 / 187 | HALLMARK_E2F_TARGETS |
| 2 | 1e−15 | 43 / 195 | HALLMARK_G2M_CHECKPOINT |
| 3 | 8e−07 | 14 / 55 | HALLMARK_MYC_TARGETS_V2 |
| 4 | 1e−03 | 20 / 173 | HALLMARK_MITOTIC_SPINDLE |
| 5 | 1e−03 | 21 / 190 | HALLMARK_MYC_TARGETS_V1 |
| 6 | 3e−02 | 17 / 192 | HALLMARK_MTORC1_SIGNALING |
| 7 | 1e−01 | 15 / 194 | HALLMARK_ESTROGEN_RESPONSE_EARLY |
| 8 | 1e−01 | 4 / 38 | HALLMARK_WNT_BETA_CATENIN_SIGNALING |
| 9 | 2e−01 | 14 / 193 | HALLMARK_ESTROGEN_RESPONSE_LATE |
| 10 | 2e−01 | 8 / 106 | HALLMARK_UNFOLDED_PROTEIN_RESPONSE |
| 11 | 3e−01 | 9 / 133 | HALLMARK_DNA_REPAIR |
| 12 | 3e−01 | 4 / 51 | HALLMARK_TGF_BETA_SIGNALING |
| 13 | 5e−01 | 2 / 29 | HALLMARK_NOTCH_SIGNALING |
| 14 | 5e−01 | 8 / 141 | HALLMARK_UV_RESPONSE_DN |
| 15 | 6e−01 | 9 / 174 | HALLMARK_ADIPOGENESIS |

## Immunome

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.01 | 5 / 26 | Angelova_immune−metagene−activated_CD4 |
| 2 | 0.20 | 1 / 4 | Angelova_CRC_MSS−neoantigens |
| 3 | 0.24 | 1 / 5 | Angelova_immune−metagene−NK56_bright |
| 4 | 0.27 | 2 / 19 | Angelova_immune−metagene−activated_CD8 |
| 5 | 0.32 | 1 / 7 | Angelova_CRC_MSI−neoantigens |
| 6 | 0.39 | 2 / 25 | Angelova_immune−metagene−DC |
| 7 | 0.42 | 1 / 10 | Angelova_immune−metagene−neutrophils |
| 8 | 0.48 | 1 / 12 | Angelova_immune−metagene−memory_B−cells |
| 9 | 0.51 | 1 / 13 | Angelova_immune−metagene−activated_B−cells |
| 10 | 0.51 | 1 / 13 | Angelova_immune−metagene−immature_B−cells |
| 11 | 0.51 | 1 / 13 | Angelova_CRC_MSS^−neoantigens |
| 12 | 0.61 | 1 / 17 | Angelova_immune−metagene−central_memory_CD8 |
| 13 | 0.63 | 1 / 18 | Angelova_immune−metagene−pDC |
| 14 | 0.63 | 1 / 18 | Angelova_CRC_immunostimulators |
| 15 | 0.69 | 1 / 21 | Angelova_immune−metagene−central_memory_CD4 |

## Lifestyle

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.09 | 4 / 32 | Marjolein_ageing−genes_DN |
| 2 | 0.29 | 10 / 150 | Homuth_BMI−associated−genes_UP |
| 3 | 0.70 | 10 / 210 | Homuth_BMI−associated−genes_DN |
| 4 | 0.70 | 1 / 22 | DUMEAUX_Fasting enriched genes |
| 5 | 0.85 | 2 / 62 | DUMEAUX_Smoking enriched genes |
| 6 | 1.00 | 0 / 10 | DUMEAUX_Smoking literature genes up |
| 7 | 1.00 | 0 / 4 | DUMEAUX_Exercising non smoker literature enriched genes |
| 8 | 1.00 | 0 / 5 | DUMEAUX_Estrogen related in smokers literature genes up |
| 9 | 1.00 | 0 / 7 | DUMEAUX_Estrogen related in non smokers literature genes up |
| 10 | 1.00 | 0 / 7 | DUMEAUX_Hormon therapy  in non smokers literature genes up |
| 11 | 1.00 | 0 / 9 | DUMEAUX_Monocytes in smokers literature genes up |
| 12 | 1.00 | 0 / 16 | DUMEAUX_Red blood cells in non smokers literature genes up |
| 13 | 1.00 | 0 / 12 | DUMEAUX_Women normal BMI literature genes up |
| 14 | 1.00 | 0 / 22 | DUMEAUX_High bmi enriched genes |
| 15 | 1.00 | 0 / 14 | Huan_blood−pressure_SBP−signature |

## Lymphoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−41 | 53 / 99 | Sha_BL UP |
| 2 | 4e−32 | 62 / 192 | Victora_Dark zone signature |
| 3 | 3e−29 | 140 / 955 | SPANG_BCR UP |
| 4 | 4e−21 | 418 / 5529 | HOPP_Txn_elongation |
| 5 | 9e−19 | 431 / 5908 | HOPP_Active_promoter |
| 6 | 3e−15 | 13 / 15 | BENTINK_mBL UP |
| 7 | 2e−14 | 34 / 135 | DAVE_BL−vs−DLBCL |
| 8 | 5e−12 | 41 / 227 | SPANG_IL21 UP |
| 9 | 1e−10 | 308 / 4261 | HOPP_Txn_transition |
| 10 | 2e−08 | 6 / 6 | MASCQUE_mBL UP |
| 11 | 7e−08 | 37 / 263 | SPANG_CD40 6hrs UP |
| 12 | 7e−07 | 368 / 5682 | HOPP_Weak_promoter |
| 13 | 7e−06 | 36 / 305 | TARTE_Plasmablast signature |
| 14 | 2e−05 | 7 / 17 | DAVE_c−myc BL UP |
| 15 | 5e−05 | 5 / 9 | DAVE_BL UP |

## Melanoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−32 | 80 / 319 | Gerber_wt/wt_melanoma−cells−SpotA |
| 2 | 4e−09 | 20 / 79 | Tirosh_core cycling genes in low− and high−proliferation melanoma |
| 3 | 1e−05 | 11 / 44 | Tirosh_top50 correlated genes PC2 |
| 4 | 2e−05 | 10 / 38 | Tirosh_G1/S phase specific genes |
| 5 | 8e−04 | 9 / 47 | Tirosh_G2/M phase specific genes |
| 6 | 8e−03 | 9 / 65 | Harbst_melanoma_highgrade_up |
| 7 | 2e−02 | 2 / 4 | Melanoma Epi−Enzyme Cluster 5 |
| 8 | 1e−01 | 1 / 2 | Melanoma Epi−Enzyme Cluster 6 |
| 9 | 1e−01 | 20 / 276 | Gerber_wt/wt_melanoma−cells−SpotB |
| 10 | 2e−01 | 6 / 68 | Tirosh_housekeeping_genes |
| 11 | 2e−01 | 1 / 4 | Melanoma Epi−Enzyme Cluster 3 |
| 12 | 2e−01 | 4 / 46 | Tirosh_top50 correlated genes PC5 |
| 13 | 3e−01 | 6 / 83 | TCGA_melanoma_immune_high |
| 14 | 4e−01 | 2 / 24 | Tirosh_B−cell specific genes−melanoma |
| 15 | 5e−01 | 13 / 230 | Gerber_wt/wt_melanoma−cells−SpotC |

## MF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−11 | 116 / 1161 | RNA binding |
| 2 | 1e−08 | 133 / 1541 | DNA binding |
| 3 | 9e−05 | 14 / 81 | single−stranded DNA binding |
| 4 | 2e−04 | 468 / 7864 | protein binding |
| 5 | 4e−04 | 69 / 852 | nucleic acid binding |
| 6 | 2e−03 | 14 / 106 | ligase activity |
| 7 | 2e−03 | 16 / 132 | methyltransferase activity |
| 8 | 2e−03 | 13 / 97 | double−stranded DNA binding |
| 9 | 3e−03 | 4 / 12 | S−adenosylmethionine−dependent methyltransferase activity |
| 10 | 3e−03 | 6 / 28 | Ran GTPase binding |
| 11 | 3e−03 | 5 / 20 | dynein complex binding |
| 12 | 4e−03 | 5 / 21 | gamma−tubulin binding |
| 13 | 5e−03 | 6 / 30 | repressing transcription factor binding |
| 14 | 5e−03 | 5 / 22 | translation factor activity, RNA binding |
| 15 | 6e−03 | 29 / 328 | chromatin binding |

## miRNA target

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−04 | 8 / 31 | hsa−miR−661 |
| 2 | 2e−03 | 12 / 87 | hsa−miR−449b |
| 3 | 3e−03 | 25 / 260 | hsa−let−7e |
| 4 | 4e−03 | 23 / 236 | hsa−miR−34a |
| 5 | 6e−03 | 17 / 160 | hsa−miR−330−3p |
| 6 | 6e−03 | 16 / 148 | hsa−miR−196b |
| 7 | 7e−03 | 7 / 42 | hsa−miR−411 |
| 8 | 8e−03 | 9 / 65 | hsa−miR−557 |
| 9 | 8e−03 | 12 / 101 | hsa−miR−515−3p |
| 10 | 8e−03 | 25 / 278 | hsa−let−7d |
| 11 | 9e−03 | 11 / 90 | hsa−miR−507 |
| 12 | 1e−02 | 6 / 35 | hsa−miR−1224−5p |
| 13 | 1e−02 | 4 / 17 | hsa−miR−609 |
| 14 | 1e−02 | 5 / 26 | hsa−miR−934 |
| 15 | 1e−02 | 8 / 58 | hsa−miR−331−3p |

## Pneumonia

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.03 | 7 / 57 | Burnham_day1_vs_5_UP |
| 2 | 0.07 | 5 / 41 | Scicluna_DN |
| 3 | 0.16 | 5 / 54 | Burnham_timecourse |
| 4 | 0.37 | 4 / 57 | Burnham_viral_UP |
| 5 | 0.63 | 9 / 179 | Terre_MSV_multiple_respiratory_viruses_dn |
| 6 | 0.63 | 1 / 18 | Scicluna_UP |
| 7 | 0.71 | 3 / 68 | Burnham_sep_vs_con_UP |
| 8 | 0.74 | 6 / 135 | Terre_MSV_multiple_respiratory_viruses_up |
| 9 | 0.81 | 2 / 56 | Burnham_sep_vs_con_DN |
| 10 | 0.84 | 1 / 33 | Sweeney_viral_dn |
| 11 | 0.90 | 2 / 71 | Burnham_cap_fp_vs_con_UP |
| 12 | 0.93 | 1 / 48 | Burnham_cap_fp_vs_con_DN |
| 13 | 0.93 | 1 / 48 | Burnham_viral_DN |
| 14 | 0.94 | 1 / 52 | Burnham_day1_vs_5_DN |
| 15 | 0.96 | 3 / 122 | Terre_IMS_influenza_meta_signature |

## Reference Signatures

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−09 | 36 / 219 | WIRTH_GC B−cells |
| 2 | 8e−04 | 56 / 677 | PROTEINATLAS_esophagus |
| 3 | 2e−03 | 49 / 595 | PROTEINATLAS_breast |
| 4 | 2e−03 | 54 / 678 | PROTEINATLAS_lymph node |
| 5 | 3e−03 | 79 / 1081 | PROTEINATLAS_testis |
| 6 | 3e−03 | 35 / 399 | PROTEINATLAS_soft tissue |
| 7 | 4e−03 | 34 / 390 | PROTEINATLAS_ovary |
| 8 | 6e−03 | 45 / 569 | PROTEINATLAS_salivary gland |
| 9 | 6e−03 | 6 / 32 | VAQUERIZAS_Liver_TF |
| 10 | 7e−03 | 7 / 42 | Chaussabel_1,3_B−cells |
| 11 | 8e−03 | 60 / 819 | PROTEINATLAS_bronchus |
| 12 | 9e−03 | 4 / 16 | VAQUERIZAS_Fetal liver_TF |
| 13 | 1e−02 | 57 / 776 | PROTEINATLAS_skin |
| 14 | 1e−02 | 50 / 671 | PROTEINATLAS_cervix, uterine |
| 15 | 1e−02 | 45 / 593 | PROTEINATLAS_lateral ventricle |

## Telomeres

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.004 | 4 / 13 | Alternative lengthening of telomeres |
| 2 | 0.054 | 4 / 27 | Nabetani_alt len telomeres_genes_ko |
| 3 | NA | 0 / 0 | |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## TF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−10 | 118 / 1241 | KIM_MYC targets |
| 2 | 6e−07 | 93 / 1044 | ICGC_Six5_targets |
| 3 | 1e−06 | 96 / 1107 | ICGC_Myc_targets |
| 4 | 2e−06 | 246 / 3564 | ICGC_Taf1_targets |
| 5 | 1e−05 | 217 / 3150 | ICGC_Creb1_targets |
| 6 | 2e−05 | 90 / 1089 | ICGC_Ets1_targets |
| 7 | 1e−04 | 121 / 1630 | ICGC_SrfV0416101_targets |
| 8 | 2e−04 | 50 / 549 | ICGC_Atf3_targets |
| 9 | 2e−04 | 201 / 2994 | ICGC_Zeb1_targets |
| 10 | 5e−04 | 289 / 4602 | ICGC_Elf1_targets |
| 11 | 5e−04 | 273 / 4319 | ICGC_Pou2_targets |
| 12 | 5e−04 | 234 / 3630 | ICGC_Sp1_targets |
| 13 | 6e−04 | 243 / 3796 | ICGC_Nficsc81335_targets |
| 14 | 7e−04 | 243 / 3804 | ICGC_Stat5_targets |
| 15 | 1e−03 | 236 / 3703 | ICGC_Foxm1_targets |

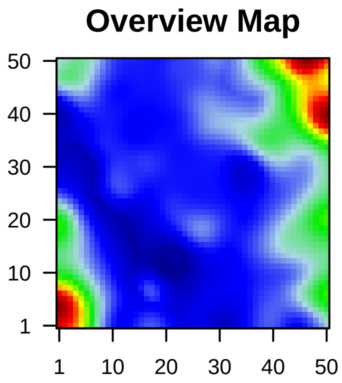
# Group Overexpression Spo

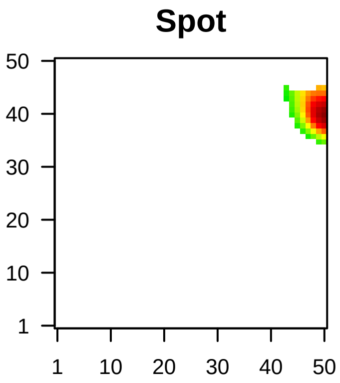
## Spot Summary: B

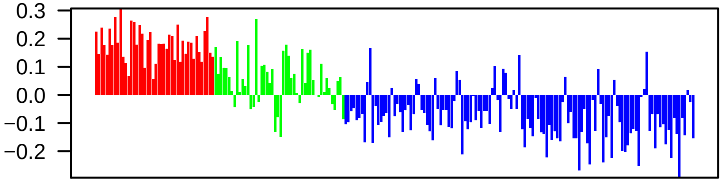
# metagenes = 63
# genes = 749

<r> metagenes = 0.84
<r> genes = 0.17
beta: r2= 5.08  /  log p= −Inf

# samples with spot = 10 ( 4.5 %)
mBL : 9 ( 20.5 %)
intermediate : 1 ( 2.1 %)


**Overview Map**


**Spot**

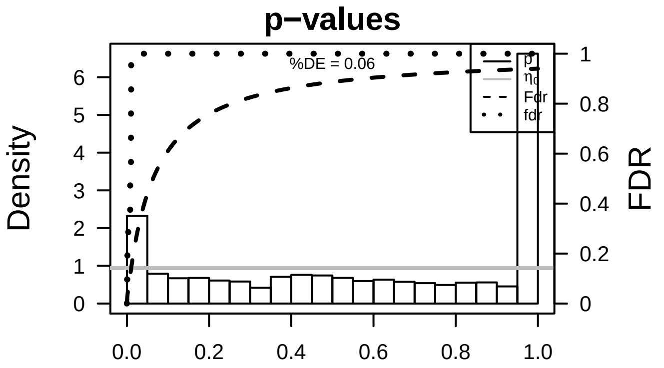


## Spot Genelist

| Rank | ID | max e | min e | r | Symbol | Description |
|---|---|---|---|---|---|---|
| 1 | 219655_at | 2.48 | −0.74 | 0.52 | SUGCT | succinyl−CoA:glutarate−CoA transferase [Source:HGNC Sym |
| 2 | 221933_at | 2.43 | −0.83 | 0.25 | NLGN4X | neuroligin 4, X−linked [Source:HGNC Symbol;Acc:HGNC:142 |
| 3 | 205123_s_at | 2.4 | −0.7 | 0.41 | TMEFF1 | transmembrane protein with EGF like and two follistatin like d |
| 4 | 220448_at | 2.35 | −0.95 | 0.47 | KCNK12 | potassium two pore domain channel subfamily K member 12 |
| 5 | 203865_s_at | 2.33 | −1.02 | 0.36 | ADARB1 | adenosine deaminase, RNA specific B1 [Source:HGNC Symb |
| 6 | 221879_at | 2.18 | −0.84 | 0.25 | | |
| 7 | 205902_at | 2.03 | −0.94 | 0.46 | KCNN3 | potassium calcium−activated channel subfamily N member 3 |
| 8 | 208719_s_at | 2 | −1.36 | 0.14 | DDX17 | DEAD−box helicase 17 [Source:HGNC Symbol;Acc:HGNC:2 |
| 9 | 210640_s_at | 1.98 | −0.91 | 0.41 | GPER1 | G protein−coupled estrogen receptor 1 [Source:HGNC Symb |
| 10 | 220432_s_at | 1.97 | −0.86 | 0.54 | CYP39A1 | cytochrome P450 family 39 subfamily A member 1 [Source:H |
| 11 | 211998_at | 1.94 | −0.89 | 0.26 | H3F3B | H3 histone family member 3B [Source:HGNC Symbol;Acc:HG |
| 12 | 217373_x_at | 1.92 | −1.07 | 0.43 | MDM2 | MDM2 proto−oncogene [Source:HGNC Symbol;Acc:HGNC:6 |
| 13 | 213436_at | 1.92 | −1.49 | 0.4 | CNR1 | cannabinoid receptor 1 [Source:HGNC Symbol;Acc:HGNC:21 |
| 14 | 212186_at | 1.91 | −1.42 | 0.35 | ACACA | acetyl−CoA carboxylase alpha [Source:HGNC Symbol;Acc:H |
| 15 | 219743_at | 1.91 | −0.7 | 0.52 | HEY2 | hes related family bHLH transcription factor with YRPW motif |
| 16 | 218980_at | 1.88 | −0.67 | 0.51 | FHOD3 | formin homology 2 domain containing 3 [Source:HGNC Symb |
| 17 | 209493_at | 1.88 | −1.38 | 0.38 | PDZD2 | PDZ domain containing 2 [Source:HGNC Symbol;Acc:HGNC |
| 18 | 205340_at | 1.82 | −0.76 | 0.3 | ZBTB24 | zinc finger and BTB domain containing 24 [Source:HGNC Sy |
| 19 | 210461_s_at | 1.78 | −0.98 | 0.47 | ABLIM1 | actin binding LIM protein 1 [Source:HGNC Symbol;Acc:HGNC |
| 20 | 211363_s_at | 1.76 | −1.12 | 0.36 | MTAP | methylthioadenosine phosphorylase [Source:HGNC Symbol; |

## Geneset Overrepresentation

| Rank | p−value | #in/all | Geneset | |
|---|---|---|---|---|
| 1 | 2e−45 | 452 / 5908 | Lymph | HOPP_Active_promoter |
| 2 | 3e−45 | 434 / 5529 | Lymph | HOPP_Txn_elongation |
| 3 | 2e−32 | 414 / 5682 | Lymph | HOPP_Weak_promoter |
| 4 | 1e−28 | 334 / 4261 | Lymph | HOPP_Txn_transition |
| 5 | 2e−25 | 123 / 955 | Lymph | SPANG_BCR UP |
| 6 | 4e−23 | 377 / 5404 | Lymph | HOPP_Strong_enhancer |
| 7 | 5e−22 | 107 / 830 | GSEA | DACOSTA_UV_RESPONSE_VIA_ERCC3_DN |
| 8 | 7e−22 | 56 / 263 | Lymph | SPANG_CD40 6hrs UP |
| 9 | 3e−21 | 319 / 4357 | Lymph | HOPP_Weak_txn |
| 10 | 2e−20 | 327 / 4559 | Lymph | HOPP_Weak_enhancer |
| 11 | 2e−19 | 151 / 1527 | GSEA | PUJANA_BRCA1_PCC_NETWORK |
| 12 | 2e−18 | 56 / 310 | Refer | Chaussabel_3,4_Protein phosphatases |
| 13 | 5e−16 | 119 / 1174 | Colon | LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c |
| 14 | 9e−16 | 313 / 4579 | CC | nucleus |
| 15 | 4e−15 | 65 / 469 | GSEA | DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN |
| 16 | 7e−15 | 29 / 106 | Refer | Chaussabel_2,11_Replication |
| 17 | 1e−14 | 140 / 1550 | GSEA | PILON_KLF1_TARGETS_DN |
| 18 | 2e−14 | 50 / 309 | GSEA | DAZARD_RESPONSE_TO_UV_NHEK_DN |
| 19 | 3e−14 | 59 / 417 | GSEA | SHEN_SMARCA2_TARGETS_UP |
| 20 | 1e−13 | 196 / 2541 | CC | nucleoplasm |
| 21 | 2e−13 | 45 / 275 | GSEA | HADDAD_B_LYMPHOCYTE_PROGENITOR |
| 22 | 4e−13 | 37 / 195 | GSEA | HOLLMANN_APOPTOSIS_VIA_CD40_UP |
| 23 | 4e−11 | 115 / 1312 | GSEA | PUJANA_ATM_PCC_NETWORK |
| 24 | 2e−10 | 71 / 673 | GSEA | SCHLOSSER_SERUM_RESPONSE_DN |
| 25 | 2e−10 | 115 / 1343 | Gliom | Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP |
| 26 | 2e−10 | 240 / 3564 | TF | ICGC_Taf1_targets |
| 27 | 2e−10 | 18 / 61 | GSEA | BASSO_CD40_SIGNALING_DN |
| 28 | 3e−10 | 125 / 1523 | Gliom | Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN |
| 29 | 4e−10 | 82 / 848 | Colon | LaPointe_mucosa−position_kmeans_O_transverse colon_UP_ |
| 30 | 7e−09 | 36 / 260 | BP | chromatin organization |
| 31 | 7e−09 | 210 / 3121 | TF | ICGC_Egr1_targets |
| 32 | 1e−08 | 70 / 726 | GSEA | PUJANA_CHEK2_PCC_NETWORK |
| 33 | 1e−08 | 66 / 669 | GSEA | JOHNSTONE_PARVB_TARGETS_3_DN |
| 34 | 2e−08 | 111 / 1390 | GSEA | GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN |
| 35 | 3e−08 | 49 / 442 | GSEA | KIM_WT1_TARGETS_DN |
| 36 | 7e−08 | 23 / 133 | GSEA | PENG_LEUCINE_DEPRIVATION_UP |
| 37 | 7e−08 | 15 / 59 | GSEA | HUTTMANN_B_CLL_POOR_SURVIVAL_DN |
| 38 | 7e−08 | 12 / 37 | GSEA | ZHAN_MULTIPLE_MYELOMA_CD2_UP |
| 39 | 9e−08 | 85 / 1001 | Colon | LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP |
| 40 | 1e−07 | 124 / 1655 | BP | transcription, DNA−templated |


**p−values**

### Aging

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.8 | 4 / 107 | HORVATH_aging_genes meth UP |
| 2 | 0.9 | 1 / 47 | TESCHENDORFF_age_hypermethylated |
| 3 | 1.0 | 1 / 92 | HORVATH_aging_genes meth DOWN |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

### BP

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 7e−09 | 36 / 260 | chromatin organization |
| 2 | 1e−07 | 124 / 1655 | transcription, DNA−templated |
| 3 | 2e−07 | 129 / 1764 | regulation of transcription, DNA−templated |
| 4 | 8e−05 | 12 / 68 | protein sumoylation |
| 5 | 2e−04 | 50 / 621 | negative regulation of transcription from RNA polymerase II promoter |
| 6 | 4e−04 | 17 / 141 | protein dephosphorylation |
| 7 | 5e−04 | 35 / 407 | viral process |
| 8 | 7e−04 | 11 / 74 | regulation of mitotic cell cycle |
| 9 | 8e−04 | 9 / 53 | circadian regulation of gene expression |
| 10 | 9e−04 | 26 / 281 | DNA repair |
| 11 | 9e−04 | 5 / 17 | T cell proliferation |
| 12 | 1e−03 | 33 / 391 | protein ubiquitination |
| 13 | 2e−03 | 9 / 59 | cellular response to hydrogen peroxide |
| 14 | 2e−03 | 4 / 12 | negative regulation of actin filament polymerization |
| 15 | 2e−03 | 7 / 38 | negative regulation of fat cell differentiation |

### Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.002 | 10 / 72 | PanCan_Wnt_geneset_nanostring |
| 2 | 0.003 | 4 / 14 | BENTINK_src.2 |
| 3 | 0.007 | 12 / 113 | PanCan_Driver_Gene_geneset_nanostring |
| 4 | 0.011 | 1 / 12 | LIU_BREAST_CANCER |
| 5 | 0.021 | 12 / 130 | PanCan_CC+Apop_geneset_nanostring |
| 6 | 0.030 | 2 / 6 | ZHANG_MGUS up |
| 7 | 0.042 | 4 / 28 | PanCan_HK_geneset_nanostring |
| 8 | 0.079 | 2 / 10 | GENTLES_modul3 |
| 9 | 0.094 | 2 / 11 | LIU_PROSTATE_CANCER_UP |
| 10 | 0.109 | 2 / 12 | GENTLES_modul12 |
| 11 | 0.124 | 1 / 16 | LIU_LIVER_CANCER |
| 12 | 0.141 | 5 / 58 | SHAUGHNESSY_MM high risk |
| 13 | 0.141 | 2 / 14 | GENTLES_modul10 |
| 14 | 0.141 | 2 / 14 | BENTINK_myc.1 |
| 15 | 0.141 | 2 / 14 | BENTINK_ras.6 |

### CC

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 9e−16 | 313 / 4579 | nucleus |
| 2 | 1e−13 | 196 / 2541 | nucleoplasm |
| 3 | 1e−05 | 274 / 4701 | cytoplasm |
| 4 | 1e−05 | 229 / 3805 | cytosol |
| 5 | 2e−04 | 13 / 86 | PML body |
| 6 | 7e−04 | 6 / 24 | heterochromatin |
| 7 | 7e−04 | 23 / 233 | nuclear body |
| 8 | 1e−03 | 20 / 196 | nuclear membrane |
| 9 | 1e−03 | 5 / 18 | replication fork |
| 10 | 1e−03 | 4 / 11 | pericentric heterochromatin |
| 11 | 2e−03 | 16 / 149 | nuclear envelope |
| 12 | 2e−03 | 6 / 29 | histone deacetylase complex |
| 13 | 3e−03 | 47 / 653 | nucleolus |
| 14 | 3e−03 | 7 / 42 | transcriptional repressor complex |
| 15 | 4e−03 | 27 / 326 | nuclear speck |

### Chr

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−04 | 52 / 669 | Chr 6 |
| 2 | 3e−03 | 57 / 832 | Chr 2 |
| 3 | 6e−03 | 33 / 437 | Chr 8 |
| 4 | 7e−02 | 36 / 585 | Chr 7 |
| 5 | 7e−02 | 42 / 700 | Chr 12 |
| 6 | 2e−01 | 71 / 1325 | Chr 1 |
| 7 | 2e−01 | 28 / 490 | Chr 10 |
| 8 | 2e−01 | 9 / 139 | Chr 21 |
| 9 | 3e−01 | 30 / 554 | Chr 5 |
| 10 | 3e−01 | 25 / 480 | Chr 4 |
| 11 | 5e−01 | 33 / 689 | Chr 3 |
| 12 | 6e−01 | 17 / 369 | Chr 20 |
| 13 | 7e−01 | 14 / 333 | Chr 22 |
| 14 | 8e−01 | 33 / 776 | Chr 17 |
| 15 | 8e−01 | 16 / 403 | Chr 14 |

### Chromatin states

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−62 | 473 / 5716 | Bcells peripheral blood_4_Tx |
| 2 | 2e−58 | 552 / 7833 | Bcells peripheral blood_1_TssA |
| 3 | 9e−58 | 536 / 7420 | Tcells peripheral blood_1_TssA |
| 4 | 1e−57 | 548 / 7751 | natural killer cells peripheral blood_1_TssA |
| 5 | 2e−55 | 463 / 5753 | Tcells peripheral blood_4_Tx |
| 6 | 4e−55 | 452 / 5527 | Tregulatory cells peripheral blood_4_Tx |
| 7 | 1e−54 | 462 / 5766 | natural killer cells peripheral blood_4_Tx |
| 8 | 3e−54 | 566 / 8406 | Bcells peripheral blood_2_TssAFlnk |
| 9 | 2e−53 | 475 / 6099 | HSC_4_Tx |
| 10 | 1e−52 | 451 / 5601 | Thelper cells peripheral blood_4_Tx |
| 11 | 2e−52 | 548 / 7957 | Tcells peripheral blood_2_TssAFlnk |
| 12 | 5e−52 | 560 / 8322 | T CD8+ naive cells peripheral blood_1_TssA |
| 13 | 1e−49 | 554 / 8245 | Tregulatory cells peripheral blood_2_TssAFlnk |
| 14 | 3e−49 | 531 / 7635 | monocytes peripheral blood_1_TssA |
| 15 | 3e−49 | 542 / 7930 | Tregulatory cells peripheral blood_1_TssA |

### Colon Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−16 | 119 / 1174 | LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo |
| 2 | 4e−10 | 82 / 848 | LaPointe_mucosa−position_kmeans_O_transverse colon_UP_ |
| 3 | 9e−08 | 85 / 1001 | LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_ |
| 4 | 4e−05 | 117 / 1729 | LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t |
| 5 | 1e−03 | 46 / 602 | Pentrack_CRC_TCGA_corr_R_normal_DN |
| 6 | 2e−03 | 87 / 1354 | LaPointe_mucosa−position_kmeans_N_cecum colon_ascending colon_UP_a |
| 7 | 3e−03 | 4 / 14 | Hewish_dMMR−secondary−mutations_DNA−repair |
| 8 | 5e−03 | 3 / 8 | Boland_CRC−MMR−system |
| 9 | 8e−03 | 7 / 49 | Pentrack_CRC_TCGA_corr_N_msi−h_DN |
| 10 | 9e−03 | 56 / 854 | LaPointe_mucosa−position_kmeans_A_ascending colon_UP_ |
| 11 | 1e−02 | 39 / 561 | Pentrack_CRC_TCGA_group.over_C_normal_DN |
| 12 | 1e−02 | 72 / 1166 | LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a |
| 13 | 2e−02 | 36 / 532 | LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U |
| 14 | 4e−02 | 2 / 7 | TCGA_Mutated−in−CRC_mismatch−repair−genes |
| 15 | 8e−02 | 321 / 6368 | LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_ |

### Glioma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−10 | 115 / 1343 | Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP |
| 2 | 3e−10 | 125 / 1523 | Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN |
| 3 | 7e−05 | 51 / 614 | Sturm_GBM_Meth_overexpression_E_G34_UP |
| 4 | 2e−03 | 28 / 330 | Up |
| 5 | 7e−03 | 8 / 59 | WILLSCHER_GBM_Verhaak−PNwt & MES_up |
| 6 | 8e−03 | 23 / 282 | WILLSCHER_GBM_Verhaak−PNwt & CL_up |
| 7 | 1e−02 | 7 / 55 | WILLSCHER_GBM_proteomics_wtOnly_SpotJ |
| 8 | 3e−02 | 2 / 6 | WILLSCHER_GBM_Verhaak−PNmut_up (M) |
| 9 | 3e−02 | 7 / 64 | Weller_LGG_A_vs_O_DOWN |
| 10 | 4e−02 | 6 / 52 | GIEZELT_GBM_WT_down_VS_mut |
| 11 | 5e−02 | 2 / 8 | WILLSCHER_GBM_LTSmut_proteomics−A_UP |
| 12 | 7e−02 | 27 / 421 | Down_b |
| 13 | 8e−02 | 3 / 22 | Sturm_GBM_Meth_overexpression_H_K27_UP |
| 14 | 2e−01 | 3 / 30 | Shaw_responders_down_in_oligo_glioma |
| 15 | 2e−01 | 2 / 16 | VERHAAK_PN subtype |

### GSEA C2

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−22 | 107 / 830 | DACOSTA_UV_RESPONSE_VIA_ERCC3_DN |
| 2 | 2e−19 | 151 / 1527 | PUJANA_BRCA1_PCC_NETWORK |
| 3 | 4e−15 | 65 / 469 | DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN |
| 4 | 1e−14 | 140 / 1550 | PILON_KLF1_TARGETS_DN |
| 5 | 2e−14 | 50 / 309 | DAZARD_RESPONSE_TO_UV_NHEK_DN |
| 6 | 3e−14 | 59 / 417 | SHEN_SMARCA2_TARGETS_UP |
| 7 | 2e−13 | 45 / 275 | HADDAD_B_LYMPHOCYTE_PROGENITOR |
| 8 | 4e−13 | 37 / 195 | HOLLMANN_APOPTOSIS_VIA_CD40_UP |
| 9 | 4e−11 | 115 / 1312 | PUJANA_ATM_PCC_NETWORK |
| 10 | 2e−10 | 71 / 673 | SCHLOSSER_SERUM_RESPONSE_DN |
| 11 | 2e−10 | 18 / 61 | BASSO_CD40_SIGNALING_DN |
| 12 | 1e−08 | 70 / 726 | PUJANA_CHEK2_PCC_NETWORK |
| 13 | 1e−08 | 66 / 669 | JOHNSTONE_PARVB_TARGETS_3_DN |
| 14 | 2e−08 | 111 / 1390 | GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN |
| 15 | 3e−08 | 49 / 442 | KIM_WT1_TARGETS_DN |

### HM

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−04 | 21 / 187 | HALLMARK_E2F_TARGETS |
| 2 | 6e−04 | 13 / 96 | HALLMARK_ANDROGEN_RESPONSE |
| 3 | 2e−03 | 19 / 195 | HALLMARK_G2M_CHECKPOINT |
| 4 | 2e−02 | 13 / 141 | HALLMARK_UV_RESPONSE_DN |
| 5 | 2e−02 | 16 / 190 | HALLMARK_MYC_TARGETS_V1 |
| 6 | 3e−02 | 5 / 38 | HALLMARK_WNT_BETA_CATENIN_SIGNALING |
| 7 | 7e−02 | 14 / 192 | HALLMARK_MTORC1_SIGNALING |
| 8 | 1e−01 | 5 / 55 | HALLMARK_MYC_TARGETS_V2 |
| 9 | 2e−01 | 7 / 94 | HALLMARK_PROTEIN_SECRETION |
| 10 | 2e−01 | 11 / 170 | HALLMARK_IL2_STAT5_SIGNALING |
| 11 | 2e−01 | 11 / 173 | HALLMARK_MITOTIC_SPINDLE |
| 12 | 2e−01 | 4 / 51 | HALLMARK_TGF_BETA_SIGNALING |
| 13 | 3e−01 | 11 / 191 | HALLMARK_P53_PATHWAY |
| 14 | 3e−01 | 8 / 139 | HALLMARK_FATTY_ACID_METABOLISM |
| 15 | 4e−01 | 6 / 106 | HALLMARK_UNFOLDED_PROTEIN_RESPONSE |

### Immunome

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.003 | 4 / 13 | Angelova_immune−metagene−immature_B−cells |
| 2 | 0.052 | 2 / 8 | Angelova_immune−metagene−mDC |
| 3 | 0.125 | 2 / 13 | Angelova_immune−metagene−activated_B−cells |
| 4 | 0.175 | 2 / 16 | Angelova_immune−metagene−Th17 |
| 5 | 0.177 | 1 / 4 | Angelova_CRC_MSS−neoantigens |
| 6 | 0.289 | 1 / 7 | Angelova_CRC_MSI−neoantigens |
| 7 | 0.386 | 1 / 10 | Angelova_immune−metagene−neutrophils |
| 8 | 0.386 | 1 / 10 | Angelova_immune−metagene−TFH |
| 9 | 0.415 | 1 / 11 | Angelova_immune−metagene−macrophages |
| 10 | 0.443 | 1 / 12 | Angelova_immune−metagene−effector_memory_CD4 |
| 11 | 0.443 | 1 / 12 | Angelova_immune−metagene−memory_B−cells |
| 12 | 0.469 | 1 / 13 | Angelova_CRC_MSS^−neoantigens |
| 13 | 0.495 | 1 / 14 | Angelova_immune−metagene−eosinophil |
| 14 | 0.519 | 1 / 15 | Angelova_immune−metagene−NK |
| 15 | 0.584 | 1 / 18 | Angelova_immune−metagene−pDC |

### Lifestyle

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−04 | 22 / 210 | Homuth_BMI−associated−genes_DN |
| 2 | 2e−01 | 2 / 16 | DUMEAUX_Red blood cells in non smokers literature genes up |
| 3 | 2e−01 | 10 / 150 | Homuth_BMI−associated−genes_UP |
| 4 | 2e−01 | 3 / 32 | Marjolein_ageing−genes_DN |
| 5 | 2e−01 | 1 / 5 | DUMEAUX_Estrogen related in smokers literature genes up |
| 6 | 3e−01 | 2 / 22 | DUMEAUX_Fasting enriched genes |
| 7 | 3e−01 | 1 / 8 | Marjolein_ageing−genes_UP |
| 8 | 4e−01 | 1 / 9 | DUMEAUX_Monocytes in smokers literature genes up |
| 9 | 7e−01 | 1 / 22 | DUMEAUX_High bmi enriched genes |
| 10 | 1e+00 | 0 / 62 | DUMEAUX_Smoking enriched genes |
| 11 | 1e+00 | 0 / 10 | DUMEAUX_Smoking literature genes up |
| 12 | 1e+00 | 0 / 4 | DUMEAUX_Exercising non smoker literature enriched genes |
| 13 | 1e+00 | 0 / 7 | DUMEAUX_Estrogen related in non smokers literature genes up |
| 14 | 1e+00 | 0 / 7 | DUMEAUX_Hormon therapy  in non smokers literature genes up |
| 15 | 1e+00 | 0 / 12 | DUMEAUX_Women normal BMI literature genes up |

### Lymphoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−45 | 452 / 5908 | HOPP_Active_promoter |
| 2 | 3e−45 | 434 / 5529 | HOPP_Txn_elongation |
| 3 | 2e−32 | 414 / 5682 | HOPP_Weak_promoter |
| 4 | 1e−28 | 334 / 4261 | HOPP_Txn_transition |
| 5 | 2e−25 | 123 / 955 | SPANG_BCR UP |
| 6 | 4e−23 | 377 / 5404 | HOPP_Strong_enhancer |
| 7 | 7e−22 | 56 / 263 | SPANG_CD40 6hrs UP |
| 8 | 3e−21 | 319 / 4357 | HOPP_Weak_txn |
| 9 | 2e−20 | 327 / 4559 | HOPP_Weak_enhancer |
| 10 | 3e−07 | 6 / 8 | MASCQUE_GCB UP |
| 11 | 5e−07 | 18 / 96 | SPANG_LPS 6hrs UP |
| 12 | 1e−06 | 26 / 192 | Victora_Dark zone signature |
| 13 | 4e−06 | 17 / 99 | Sha_BL UP |
| 14 | 6e−06 | 11 / 45 | Monti_BCR_cluster |
| 15 | 1e−05 | 27 / 227 | SPANG_IL21 UP |

### Melanoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.03 | 4 / 24 | Tirosh_B−cell specific genes−melanoma |
| 2 | 0.03 | 6 / 51 | Tirosh_genes from CD8 T−cells in Mel79−melanoma |
| 3 | 0.05 | 17 / 230 | Gerber_wt/wt_melanoma−cells−SpotC |
| 4 | 0.09 | 1 / 2 | Melanoma Epi−Enzyme Cluster 2 |
| 5 | 0.09 | 3 / 23 | Melanoma Epi−Enzyme Cluster 7 |
| 6 | 0.11 | 15 / 222 | Gerber_wt/wt_melanoma−cells−SpotF |
| 7 | 0.13 | 20 / 319 | Gerber_wt/wt_melanoma−cells−SpotA |
| 8 | 0.14 | 8 / 107 | Tirosh_Exhaustion program in Mel75 |
| 9 | 0.17 | 12 / 185 | Tirosh_genes from malignant cells in Mel79−melanoma |
| 10 | 0.18 | 1 / 4 | Melanoma Epi−Enzyme Cluster 3 |
| 11 | 0.22 | 1 / 5 | Joensson_Melanoma Proliferative subtype |
| 12 | 0.23 | 14 / 236 | Gerber_wt/wt_group3−specific |
| 13 | 0.24 | 16 / 276 | Gerber_wt/wt_melanoma−cells−SpotB |
| 14 | 0.27 | 3 / 38 | Hugo_melanoma−BRAFmut−MET_UP |
| 15 | 0.27 | 3 / 38 | Tirosh_top50 correlated genes PC1 |

### MF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−07 | 92 / 1161 | RNA binding |
| 2 | 6e−07 | 432 / 7864 | protein binding |
| 3 | 6e−07 | 12 / 44 | methylated histone binding |
| 4 | 1e−06 | 113 / 1541 | DNA binding |
| 5 | 4e−06 | 70 / 852 | nucleic acid binding |
| 6 | 5e−05 | 94 / 1329 | transferase activity |
| 7 | 6e−05 | 9 / 38 | core promoter sequence−specific DNA binding |
| 8 | 2e−04 | 25 / 237 | ubiquitin−protein transferase activity |
| 9 | 2e−04 | 31 / 331 | protein serine/threonine kinase activity |
| 10 | 3e−04 | 5 / 14 | SUMO transferase activity |
| 11 | 8e−04 | 24 / 249 | ubiquitin protein ligase binding |
| 12 | 1e−03 | 8 / 44 | protein serine/threonine phosphatase activity |
| 13 | 1e−03 | 79 / 1185 | ATP binding |
| 14 | 2e−03 | 5 / 20 | ubiquitin conjugating enzyme activity |
| 15 | 2e−03 | 24 / 268 | transcription factor binding |

### miRNA target

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 8e−06 | 21 / 150 | hsa−miR−300 |
| 2 | 2e−05 | 35 / 344 | hsa−miR−19b |
| 3 | 2e−05 | 16 / 101 | hsa−miR−199b−5p |
| 4 | 3e−05 | 36 / 364 | hsa−miR−548n |
| 5 | 3e−05 | 11 / 53 | hsa−miR−606 |
| 6 | 3e−05 | 12 / 63 | hsa−miR−657 |
| 7 | 4e−05 | 21 / 165 | hsa−miR−520d−5p |
| 8 | 4e−05 | 30 / 285 | hsa−miR−548b−5p |
| 9 | 4e−05 | 27 / 244 | hsa−miR−34c−5p |
| 10 | 5e−05 | 20 / 155 | hsa−miR−381 |
| 11 | 5e−05 | 16 / 108 | hsa−miR−380 |
| 12 | 8e−05 | 17 / 124 | hsa−miR−450b−5p |
| 13 | 9e−05 | 29 / 284 | hsa−miR−548d−5p |
| 14 | 1e−04 | 24 / 216 | hsa−miR−524−5p |
| 15 | 1e−04 | 33 / 344 | hsa−miR−19a |

### Pneumonia

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.002 | 18 / 179 | Terre_MSV_multiple_respiratory_viruses_dn |
| 2 | 0.044 | 5 / 41 | Scicluna_DN |
| 3 | 0.735 | 2 / 54 | Burnham_timecourse |
| 4 | 0.800 | 1 / 33 | Sweeney_viral_dn |
| 5 | 0.836 | 1 / 37 | Sweeney_viral_up |
| 6 | 0.838 | 4 / 122 | Terre_IMS_influenza_meta_signature |
| 7 | 0.904 | 1 / 48 | Burnham_viral_DN |
| 8 | 0.935 | 1 / 56 | Burnham_sep_vs_con_DN |
| 9 | 0.938 | 1 / 57 | Burnham_viral_UP |
| 10 | 0.938 | 1 / 57 | Burnham_day1_vs_5_UP |
| 11 | 0.999 | 1 / 135 | Terre_MSV_multiple_respiratory_viruses_up |
| 12 | 1.000 | 0 / 68 | Burnham_sep_vs_con_UP |
| 13 | 1.000 | 0 / 48 | Burnham_cap_fp_vs_con_DN |
| 14 | 1.000 | 0 / 71 | Burnham_cap_fp_vs_con_UP |
| 15 | 1.000 | 0 / 52 | Burnham_day1_vs_5_DN |

### Reference Signatures

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−18 | 56 / 310 | Chaussabel_3,4_Protein phosphatases |
| 2 | 7e−15 | 29 / 106 | Chaussabel_2,11_Replication |
| 3 | 3e−07 | 27 / 188 | Chaussabel_3,8_Enzymes |
| 4 | 4e−07 | 82 / 989 | PROTEINATLAS_tonsil |
| 5 | 5e−07 | 62 / 678 | PROTEINATLAS_lymph node |
| 6 | 2e−06 | 71 / 848 | PROTEINATLAS_adrenal gland |
| 7 | 4e−06 | 57 / 645 | PROTEINATLAS_bone marrow |
| 8 | 5e−06 | 54 / 604 | PROTEINATLAS_hippocampus |
| 9 | 2e−05 | 72 / 923 | PROTEINATLAS_cerebral cortex |
| 10 | 2e−05 | 10 / 42 | Chaussabel_1,3_B−cells |
| 11 | 2e−05 | 68 / 861 | PROTEINATLAS_nasopharynx |
| 12 | 2e−05 | 79 / 1048 | PROTEINATLAS_rectum |
| 13 | 5e−05 | 37 / 390 | PROTEINATLAS_ovary |
| 14 | 7e−05 | 77 / 1048 | PROTEINATLAS_gallbladder |
| 15 | 9e−05 | 16 / 113 | Chaussabel_1,8_Metabolism Biosynthesis |

### Telomeres

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.1 | 2 / 13 | Alternative lengthening of telomeres |
| 2 | 0.4 | 2 / 27 | Nabetani_alt len telomeres_genes_ko |
| 3 | NA | 0 / 0 | |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

### TF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−10 | 240 / 3564 | ICGC_Taf1_targets |
| 2 | 7e−09 | 210 / 3121 | ICGC_Egr1_targets |
| 3 | 1e−07 | 240 / 3796 | ICGC_Nficsc81335_targets |
| 4 | 5e−07 | 155 / 2254 | ICGC_BatfPcr1_targets |
| 5 | 5e−07 | 235 / 3769 | ICGC_Pmlsc71910_targets |
| 6 | 1e−06 | 217 / 3451 | ICGC_Atf2_targets |
| 7 | 1e−06 | 235 / 3804 | ICGC_Stat5_targets |
| 8 | 4e−06 | 227 / 3703 | ICGC_Foxm1_targets |
| 9 | 4e−06 | 222 / 3608 | ICGC_Tcf12_targets |
| 10 | 4e−06 | 223 / 3630 | ICGC_Sp1_targets |
| 11 | 4e−06 | 128 / 1848 | ICGC_Pbx3_targets |
| 12 | 6e−06 | 84 / 1089 | ICGC_Ets1_targets |
| 13 | 6e−06 | 85 / 1107 | ICGC_Myc_targets |
| 14 | 8e−06 | 107 / 1494 | ICGC_Cebpbsc150_targets |
| 15 | 1e−05 | 107 / 1508 | ICGC_Mef2_targets |

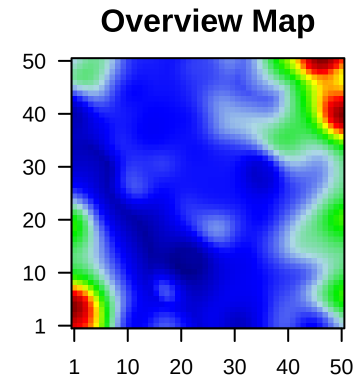
# Group Overexpression Sp

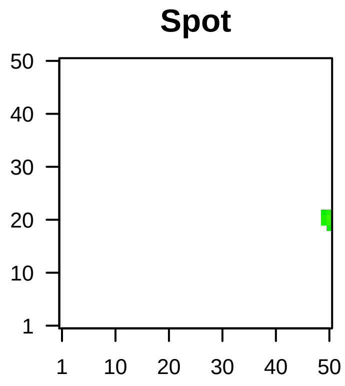
## Spot Summary: C

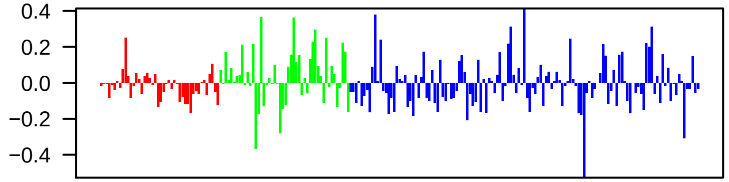
# metagenes = 7
# genes = 152

<r> metagenes = 0.97
<r> genes = 0.16
beta: r2= 1.84  /  log p= −Inf

# samples with spot = 11 ( 5 %)
mBL : 1 ( 2.3 %)
intermediate : 4 ( 8.3 %)
non−mBL : 6 ( 4.7 %)


**Overview Map**


**Spot**

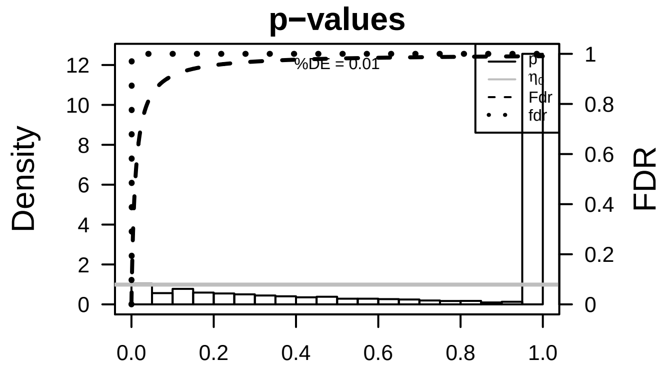


## Spot Genelist

| Rank | ID | max e | min e | r | Symbol | Description |
|---|---|---|---|---|---|---|
| 1 | 217469_at | 2.61 | −1.06 | 0.38 | | immunoglobulin heavy constant epsilon [Source:HGNC Symb |
| 2 | 205593_s_at | 2.17 | −0.78 | 0.42 | PDE9A | phosphodiesterase 9A [Source:HGNC Symbol;Acc:HGNC:87 |
| 3 | 211010_s_at | 2.09 | −0.89 | 0.18 | NCR3 | natural cytotoxicity triggering receptor 3 [Source:HGNC Symb |
| 4 | 218692_at | 2.03 | −1.04 | 0.38 | SYBU | syntabulin [Source:HGNC Symbol;Acc:HGNC:26011] |
| 5 | 207819_s_at | 1.84 | −1.12 | 0.29 | ABCB4 | ATP binding cassette subfamily B member 4 [Source:HGNC |
| 6 | 209739_s_at | 1.82 | −1.43 | 0.36 | PNPLA4 | patatin like phospholipase domain containing 4 [Source:HGN |
| 7 | 219820_at | 1.81 | −0.83 | 0.51 | SLC6A16 | solute carrier family 6 member 16 [Source:HGNC Symbol;Ac |
| 8 | 205551_at | 1.79 | −0.79 | 0.31 | SV2B | synaptic vesicle glycoprotein 2B [Source:HGNC Symbol;Acc: |
| 9 | 204465_s_at | 1.68 | −0.74 | 0.31 | INA | internexin neuronal intermediate filament protein alpha [Sour |
| 10 | 215967_s_at | 1.63 | −1.03 | 0.46 | LY9 | lymphocyte antigen 9 [Source:HGNC Symbol;Acc:HGNC:673 |
| 11 | 214772_at | 1.61 | −0.73 | 0.39 | KIAA1549L | KIAA1549 like [Source:HGNC Symbol;Acc:HGNC:24836] |
| 12 | 205389_s_at | 1.6 | −0.71 | 0.47 | ANK1 | ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492] |
| 13 | 210370_s_at | 1.59 | −0.95 | 0.49 | LY9 | lymphocyte antigen 9 [Source:HGNC Symbol;Acc:HGNC:673 |
| 14 | 212448_at | 1.56 | −1.11 | 0.31 | NEDD4L | neural precursor cell expressed, developmentally down−regul |
| 15 | 209498_at | 1.52 | −1.4 | 0.36 | CEACAM1 | carcinoembryonic antigen related cell adhesion molecule 1 [S |
| 16 | 209917_s_at | 1.5 | −1.09 | 0.42 | | TP53 target 1 (non−protein coding) [Source:HGNC Symbol;A |
| 17 | 207087_x_at | 1.47 | −0.81 | 0.41 | ANK1 | ankyrin 1 [Source:HGNC Symbol;Acc:HGNC:492] |
| 18 | 204530_s_at | 1.47 | −1.01 | 0.35 | TOX | thymocyte selection associated high mobility group box [Sour |
| 19 | 214564_s_at | 1.44 | −0.79 | 0.39 | PCDHGC3 | protocadherin gamma subfamily C, 3 [Source:HGNC Symbol; |
| 20 | 218144_s_at | 1.42 | −0.72 | 0.36 | INF2 | inverted formin, FH2 and WH2 domain containing [Source:H |

## Geneset Overrepresentation

| Rank | p−value | #in/all | | Geneset |
|---|---|---|---|---|
| 1 | 1e−14 | 98 / 5404 | Lymp | HOPP_Strong_enhancer |
| 2 | 8e−08 | 8 / 56 | GSE | KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN |
| 3 | 1e−07 | 6 / 24 | Mela | Tirosh_B−cell specific genes−melanoma |
| 4 | 3e−07 | 7 / 45 | Lymp | Monti_BCR_cluster |
| 5 | 5e−07 | 88 / 5908 | Lymp | HOPP_Active_promoter |
| 6 | 7e−07 | 7 / 51 | GSE | MORI_LARGE_PRE_BII_LYMPHOCYTE_DN |
| 7 | 9e−07 | 71 / 4357 | Lymp | HOPP_Weak_txn |
| 8 | 1e−06 | 6 / 34 | Lymp | TARTE_B−cell signature |
| 9 | 1e−06 | 5 / 19 | GSE | SHIN_B_CELL_LYMPHOMA_CLUSTER_9 |
| 10 | 1e−06 | 6 / 35 | GSE | TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN |
| 11 | 1e−06 | 17 / 429 | GSE | SMID_BREAST_CANCER_NORMAL_LIKE_UP |
| 12 | 3e−06 | 82 / 5529 | Lymp | HOPP_Txn_elongation |
| 13 | 4e−06 | 6 / 42 | Refe | Chaussabel_1,3_B−cells |
| 14 | 6e−06 | 10 / 163 | GSE | ZHENG_FOXP3_TARGETS_IN_THYMUS_UP |
| 15 | 1e−05 | 12 / 263 | Lymp | SPANG_CD40 6hrs UP |
| 16 | 2e−05 | 14 / 368 | GSE | ZHENG_BOUND_BY_FOXP3 |
| 17 | 3e−05 | 27 / 1166 | Colon | LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon |
| 18 | 5e−05 | 65 / 4261 | Lymp | HOPP_Txn_transition |
| 19 | 5e−05 | 80 / 5682 | Lymp | HOPP_Weak_promoter |
| 20 | 5e−05 | 18 / 621 | BP | negative regulation of transcription from RNA polymerase II promoter |
| 21 | 6e−05 | 33 / 1636 | TF | ICGC_Bcl11_targets |
| 22 | 7e−05 | 31 / 1508 | TF | ICGC_Mef2_targets |
| 23 | 1e−04 | 10 / 227 | Lymp | SPANG_IL21 UP |
| 24 | 1e−04 | 10 / 229 | GSE | QI_PLASMACYTOMA_UP |
| 25 | 1e−04 | 3 / 10 | BP | respiratory burst |
| 26 | 2e−04 | 9 / 195 | GSE | HOLLMANN_APOPTOSIS_VIA_CD40_UP |
| 27 | 2e−04 | 16 / 560 | GSE | KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP |
| 28 | 2e−04 | 5 / 52 | GSE | SMIRNOV_RESPONSE_TO_IR_2HR_DN |
| 29 | 2e−04 | 18 / 694 | GSE | KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP |
| 30 | 2e−04 | 7 / 121 | GSE | PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN |
| 31 | 3e−04 | 16 / 589 | Colon | Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 32 | 3e−04 | 30 / 1550 | GSE | PILON_KLF1_TARGETS_DN |
| 33 | 3e−04 | 5 / 59 | GSE | PID_BCR_5PATHWAY |
| 34 | 4e−04 | 5 / 61 | GSE | BASSO_CD40_SIGNALING_DN |
| 35 | 4e−04 | 6 / 96 | Lymp | SPANG_LPS 6hrs UP |
| 36 | 4e−04 | 3 / 15 | GSE | XU_RESPONSE_TO_TRETINOIN_UP |
| 37 | 5e−04 | 4 / 36 | GSE | NAKAYAMA_FRA2_TARGETS |
| 38 | 5e−04 | 8 / 179 | Pneu | Terre_MSV_multiple_respiratory_viruses_dn |
| 39 | 5e−04 | 10 / 275 | GSE | HADDAD_B_LYMPHOCYTE_PROGENITOR |
| 40 | 5e−04 | 3 / 16 | Glio | VERHAAK_MES subtype |


**p−values**

## Aging

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.4 | 1 / 47 | TESCHENDORFF_age_hypermethylated |
| 2 | 0.7 | 1 / 107 | HORVATH_aging_genes meth UP |
| 3 | 1.0 | 0 / 92 | HORVATH_aging_genes meth DOWN |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## CC

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−04 | 3 / 17 | T cell receptor complex |
| 2 | 2e−03 | 54 / 3805 | cytosol |
| 3 | 6e−03 | 2 / 12 | HOPS complex |
| 4 | 1e−02 | 6 / 196 | nuclear membrane |
| 5 | 1e−02 | 3 / 51 | clathrin−coated vesicle |
| 6 | 2e−02 | 3 / 56 | lipid droplet |
| 7 | 3e−02 | 2 / 25 | basal plasma membrane |
| 8 | 3e−02 | 10 / 494 | endosome |
| 9 | 6e−02 | 4 / 146 | lamellipodium |
| 10 | 7e−02 | 2 / 42 | Cul3−RING ubiquitin ligase complex |
| 11 | 7e−02 | 2 / 42 | sarcoplasmic reticulum |
| 12 | 7e−02 | 7 / 354 | centrosome |
| 13 | 7e−02 | 2 / 43 | myosin complex |
| 14 | 9e−02 | 15 / 1016 | intracellular |
| 15 | 9e−02 | 2 / 51 | endoplasmic reticulum−Golgi intermediate compartment |

## Colon Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−05 | 27 / 1166 | LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a |
| 2 | 3e−04 | 16 / 589 | Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 3 | 4e−03 | 29 / 1729 | LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t |
| 4 | 3e−02 | 2 / 25 | Ang_CRC−CIMPH−vs−L_hypo |
| 5 | 4e−02 | 6 / 255 | Kosinski_top−crypt−long−list |
| 6 | 5e−02 | 14 / 848 | LaPointe_mucosa−position_kmeans_O_transverse colon_UP_ |
| 7 | 5e−02 | 2 / 35 | Ang_CRC_Hypomethylated |
| 8 | 7e−02 | 73 / 6368 | LaPointe_mucosa−position_kmeans_F_cecum colon_transverse colon_UP_ |
| 9 | 1e−01 | 11 / 738 | Lembcke_TCGA−expr_kmeans_N_CIMP.H_DN |
| 10 | 1e−01 | 14 / 1001 | LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_ |
| 11 | 1e−01 | 1 / 15 | TCGA−CRC_less−agressive−disease−markers |
| 12 | 2e−01 | 12 / 854 | LaPointe_mucosa−position_kmeans_A_ascending colon_UP_ |
| 13 | 2e−01 | 5 / 290 | Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN |
| 14 | 2e−01 | 3 / 164 | Lembcke_TCGA_meth_kmeans_B_Cluster4_DN |
| 15 | 2e−01 | 2 / 92 | Marisa_CRC−cluster−h |

## HM

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.007 | 6 / 170 | HALLMARK_IL2_STAT5_SIGNALING |
| 2 | 0.026 | 5 / 166 | HALLMARK_INTERFERON_GAMMA_RESPONSE |
| 3 | 0.170 | 3 / 141 | HALLMARK_UV_RESPONSE_DN |
| 4 | 0.256 | 2 / 97 | HALLMARK_PEROXISOME |
| 5 | 0.256 | 3 / 174 | HALLMARK_APICAL_JUNCTION |
| 6 | 0.275 | 3 / 181 | HALLMARK_XENOBIOTIC_METABOLISM |
| 7 | 0.292 | 1 / 34 | HALLMARK_APICAL_SURFACE |
| 8 | 0.292 | 1 / 34 | HALLMARK_ANGIOGENESIS |
| 9 | 0.294 | 3 / 188 | HALLMARK_HYPOXIA |
| 10 | 0.300 | 3 / 190 | HALLMARK_TNFA_SIGNALING_VIA_NFKB |
| 11 | 0.303 | 3 / 191 | HALLMARK_P53_PATHWAY |
| 12 | 0.305 | 3 / 192 | HALLMARK_MTORC1_SIGNALING |
| 13 | 0.308 | 3 / 193 | HALLMARK_HEME_METABOLISM |
| 14 | 0.311 | 3 / 194 | HALLMARK_KRAS_SIGNALING_UP |
| 15 | 0.320 | 1 / 38 | HALLMARK_WNT_BETA_CATENIN_SIGNALING |

## Lymphoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−14 | 98 / 5404 | HOPP_Strong_enhancer |
| 2 | 3e−07 | 7 / 45 | Monti_BCR_cluster |
| 3 | 5e−07 | 88 / 5908 | HOPP_Active_promoter |
| 4 | 9e−07 | 71 / 4357 | HOPP_Weak_txn |
| 5 | 1e−06 | 6 / 34 | TARTE_B−cell signature |
| 6 | 3e−06 | 82 / 5529 | HOPP_Txn_elongation |
| 7 | 1e−05 | 12 / 263 | SPANG_CD40 6hrs UP |
| 8 | 5e−05 | 65 / 4261 | HOPP_Txn_transition |
| 9 | 5e−05 | 80 / 5682 | HOPP_Weak_promoter |
| 10 | 1e−04 | 10 / 227 | SPANG_IL21 UP |
| 11 | 4e−04 | 6 / 96 | SPANG_LPS 6hrs UP |
| 12 | 6e−04 | 21 / 955 | SPANG_BCR UP |
| 13 | 6e−04 | 3 / 17 | Aukema_BCL2 UP_BCL6 DN |
| 14 | 2e−03 | 19 / 906 | SPANG_BCR DN |
| 15 | 1e−02 | 9 / 378 | TARTE_Mature plasma cell signature |

## miRNA target

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.003 | 7 / 194 | hsa−miR−124 |
| 2 | 0.004 | 3 / 31 | hsa−miR−34c−3p |
| 3 | 0.004 | 6 / 148 | hsa−miR−1 |
| 4 | 0.004 | 4 / 64 | hsa−miR−562 |
| 5 | 0.005 | 5 / 109 | hsa−miR−194 |
| 6 | 0.007 | 6 / 166 | hsa−miR−29b |
| 7 | 0.010 | 3 / 45 | hsa−miR−891b |
| 8 | 0.018 | 6 / 205 | hsa−miR−548p |
| 9 | 0.019 | 3 / 56 | hsa−miR−618 |
| 10 | 0.019 | 4 / 101 | hsa−miR−155 |
| 11 | 0.021 | 5 / 157 | hsa−miR−206 |
| 12 | 0.022 | 3 / 59 | hsa−miR−643 |
| 13 | 0.023 | 5 / 160 | hsa−miR−545 |
| 14 | 0.023 | 8 / 344 | hsa−miR−19b |
| 15 | 0.025 | 3 / 62 | hsa−miR−578 |

## Telomeres

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1 | 0 / 13 | Alternative lengthening of telomeres |
| 2 | 1 | 0 / 27 | Nabetani_alt len telomeres_genes_ko |
| 3 | NA | 0 / 0 | |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## BP

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−05 | 18 / 621 | negative regulation of transcription from RNA polymerase II promoter |
| 2 | 1e−04 | 3 / 10 | respiratory burst |
| 3 | 7e−04 | 6 / 106 | regulation of small GTPase mediated signal transduction |
| 4 | 2e−03 | 3 / 26 | cellular response to dexamethasone stimulus |
| 5 | 2e−03 | 4 / 56 | regulation of Rho protein signal transduction |
| 6 | 3e−03 | 9 / 288 | positive regulation of apoptotic process |
| 7 | 4e−03 | 3 / 31 | cellular response to estradiol stimulus |
| 8 | 5e−03 | 2 / 11 | leukotriene biosynthetic process |
| 9 | 6e−03 | 5 / 115 | actin cytoskeleton organization |
| 10 | 6e−03 | 2 / 12 | actin polymerization or depolymerization |
| 11 | 6e−03 | 2 / 12 | negative regulation of fatty acid biosynthetic process |
| 12 | 7e−03 | 3 / 39 | B cell receptor signaling pathway |
| 13 | 1e−02 | 2 / 15 | negative regulation of cell−matrix adhesion |
| 14 | 1e−02 | 2 / 15 | oogenesis |
| 15 | 1e−02 | 9 / 361 | intracellular signal transduction |

## Chr

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.001 | 14 / 556 | Chr X |
| 2 | 0.015 | 12 / 585 | Chr 7 |
| 3 | 0.217 | 11 / 832 | Chr 2 |
| 4 | 0.221 | 6 / 403 | Chr 14 |
| 5 | 0.228 | 4 / 242 | Chr 13 |
| 6 | 0.315 | 7 / 548 | Chr 16 |
| 7 | 0.410 | 2 / 139 | Chr 21 |
| 8 | 0.488 | 6 / 554 | Chr 5 |
| 9 | 0.540 | 4 / 382 | Chr 15 |
| 10 | 0.546 | 7 / 689 | Chr 3 |
| 11 | 0.552 | 5 / 490 | Chr 10 |
| 12 | 0.556 | 5 / 492 | Chr 9 |
| 13 | 0.646 | 4 / 437 | Chr 8 |
| 14 | 0.656 | 3 / 333 | Chr 22 |
| 15 | 0.718 | 4 / 480 | Chr 4 |

## Glioma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−04 | 3 / 16 | VERHAAK_MES subtype |
| 2 | 6e−04 | 5 / 67 | Sturm_GBM_Meth_overexpression_I_RTK I 'PDGFRA'_UP |
| 3 | 2e−03 | 9 / 268 | ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN |
| 4 | 6e−03 | 4 / 71 | Weller_LGG_1p19qDel−vs−intact_DOWN |
| 5 | 8e−03 | 4 / 78 | Weller_LGG_A_vs_O_UP |
| 6 | 1e−02 | 3 / 45 | Donson−innate immunity−associated with LTS in HGA |
| 7 | 1e−02 | 10 / 447 | ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN |
| 8 | 2e−02 | 3 / 55 | Hopp_Sturm_GBM_Epi3_C2_adult_fetus_DN |
| 9 | 2e−02 | 7 / 269 | ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 10 | 3e−02 | 6 / 239 | ScoV_0.001_Sturm_M3_RTK II 'Classic'_DN |
| 11 | 4e−02 | 2 / 30 | Shaw_responders_down_in_oligo_glioma |
| 12 | 4e−02 | 5 / 191 | ScoV_0.5_Sturm_C2_RTK I 'PDGFRA'_DN |
| 13 | 5e−02 | 6 / 264 | Hopp_Sturm_GBM_Epi3_no_zentr_3_RTK II_UP_adult_fetus_K27_DN |
| 14 | 5e−02 | 4 / 139 | WILLSCHER_GBM_proteomics_wtOnly_Differencelist |
| 15 | 6e−02 | 1 / 6 | WILLSCHER_GBM_Verhaak−PNmut_up (M) |

## Immunome

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.004 | 2 / 10 | Angelova_immune−metagene−TFH |
| 2 | 0.007 | 2 / 13 | Angelova_immune−metagene−activated_B−cells |
| 3 | 0.007 | 2 / 13 | Angelova_immune−metagene−immature_B−cells |
| 4 | 0.040 | 1 / 4 | Angelova_CRC_MHC_class_II |
| 5 | 0.078 | 1 / 8 | Immunity_HLA−class−II |
| 6 | 0.167 | 1 / 18 | Angelova_immune−metagene−pDC |
| 7 | 0.208 | 1 / 23 | Angelova_immune−metagene−Treg |
| 8 | 0.255 | 1 / 29 | Angelova_immune−metagene−Th1 |
| 9 | 0.277 | 1 / 32 | Angelova_immune−metagene−effector_memory_CD8 |
| 10 | 0.493 | 1 / 67 | Angelova_immune−metagene−T−cells |
| 11 | 1.000 | 0 / 26 | Angelova_immune−metagene−activated_CD4 |
| 12 | 1.000 | 0 / 19 | Angelova_immune−metagene−activated_CD8 |
| 13 | 1.000 | 0 / 21 | Angelova_immune−metagene−central_memory_CD4 |
| 14 | 1.000 | 0 / 17 | Angelova_immune−metagene−central_memory_CD8 |
| 15 | 1.000 | 0 / 7 | Angelova_immune−metagene−cytotoxic_cells |

## Melanoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−07 | 6 / 24 | Tirosh_B−cell specific genes−melanoma |
| 2 | 2e−02 | 2 / 23 | Melanoma Epi−Enzyme Cluster 7 |
| 3 | 2e−02 | 4 / 107 | Tirosh_Exhaustion program in Mel75 |
| 4 | 6e−02 | 9 / 497 | Gerber_wt/wt_melanoma−cells−SpotD |
| 5 | 9e−02 | 5 / 236 | Gerber_wt/wt_group3−specific |
| 6 | 9e−02 | 2 / 51 | Tirosh_genes from CD8 T−cells in Mel79−melanoma |
| 7 | 9e−02 | 4 / 171 | Landsberg_dedifferentiation_up |
| 8 | 2e−01 | 2 / 83 | TCGA_melanoma_immune_high |
| 9 | 3e−01 | 1 / 33 | Tirosh_T−cell specific genes−melanoma |
| 10 | 4e−01 | 3 / 222 | Gerber_wt/wt_melanoma−cells−SpotF |
| 11 | 4e−01 | 3 / 230 | Gerber_wt/wt_melanoma−cells−SpotC |
| 12 | 5e−01 | 1 / 64 | Harbst_melanoma_lowgrade_up |
| 13 | 6e−01 | 2 / 185 | Tirosh_genes from malignant cells in Mel79−melanoma |
| 14 | 6e−01 | 1 / 81 | Tirosh_Genes in the MITF program |
| 15 | 6e−01 | 2 / 189 | Tirosh_genes preferentially expressed by Tregs |

## Pneumonia

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−04 | 8 / 179 | Terre_MSV_multiple_respiratory_viruses_dn |
| 2 | 3e−01 | 1 / 41 | Scicluna_DN |
| 3 | 4e−01 | 1 / 48 | Burnham_cap_fp_vs_con_DN |
| 4 | 4e−01 | 1 / 48 | Burnham_viral_DN |
| 5 | 4e−01 | 2 / 135 | Terre_MSV_multiple_respiratory_viruses_up |
| 6 | 4e−01 | 1 / 52 | Burnham_day1_vs_5_DN |
| 7 | 4e−01 | 1 / 54 | Burnham_timecourse |
| 8 | 4e−01 | 1 / 56 | Burnham_sep_vs_con_DN |
| 9 | 5e−01 | 1 / 68 | Burnham_sep_vs_con_UP |
| 10 | 5e−01 | 1 / 71 | Burnham_cap_fp_vs_con_UP |
| 11 | 1e+00 | 0 / 57 | Burnham_viral_UP |
| 12 | 1e+00 | 0 / 57 | Burnham_day1_vs_5_UP |
| 13 | 1e+00 | 0 / 18 | Scicluna_UP |
| 14 | 1e+00 | 0 / 37 | Sweeney_viral_up |
| 15 | 1e+00 | 0 / 33 | Sweeney_viral_dn |

## TF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−05 | 33 / 1636 | ICGC_Bcl11_targets |
| 2 | 7e−05 | 31 / 1508 | ICGC_Mef2_targets |
| 3 | 6e−04 | 39 / 2321 | ICGC_Rad21_targets |
| 4 | 6e−04 | 38 / 2254 | ICGC_BatfPcr1_targets |
| 5 | 7e−04 | 34 / 1941 | ICGC_Bcl3_targets |
| 6 | 8e−04 | 49 / 3213 | ICGC_Pu1_targets |
| 7 | 1e−03 | 36 / 2150 | ICGC_Irf4_targets |
| 8 | 2e−03 | 27 / 1494 | ICGC_Cebpbsc150_targets |
| 9 | 3e−03 | 46 / 3121 | ICGC_Egr1_targets |
| 10 | 4e−03 | 49 / 3435 | ICGC_Ebfsc137065_targets |
| 11 | 5e−03 | 30 / 1848 | ICGC_Pbx3_targets |
| 12 | 6e−03 | 52 / 3796 | ICGC_Nficsc81335_targets |
| 13 | 7e−03 | 19 / 1032 | ICGC_Usf1_targets |
| 14 | 1e−02 | 47 / 3420 | ICGC_Bclaf101388_targets |
| 15 | 1e−02 | 49 / 3630 | ICGC_Sp1_targets |

## Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.001 | 2 / 6 | ZHANG_MGUS up |
| 2 | 0.023 | 10 / 480 | Lembcke_Colonic Inflammation |
| 3 | 0.114 | 1 / 12 | GENTLES_modul12 |
| 4 | 0.114 | 1 / 12 | HLA2_signature |
| 5 | 0.123 | 1 / 13 | GENTLES_modul11 |
| 6 | 0.123 | 1 / 13 | GENTLES_modul18 |
| 7 | 0.123 | 1 / 13 | BENTINK_e2f3.1 |
| 8 | 0.150 | 1 / 16 | LIU_LIVER_CANCER |
| 9 | 0.224 | 1 / 25 | PanCan_HH_geneset_nanostring |
| 10 | 0.366 | 1 / 45 | KUIPER_MM poor survival |
| 11 | 0.445 | 1 / 58 | SHAUGHNESSY_MM high risk |
| 12 | 0.519 | 1 / 72 | PanCan_Wnt_geneset_nanostring |
| 13 | 0.565 | 2 / 187 | PanCan_PI3K_geneset_nanostring |
| 14 | 0.594 | 4 / 409 | Lembcke_Normal vs Adenoma |
| 15 | 0.623 | 1 / 96 | PanCan_TXmisReg_geneset_nanostring |

## Chromatin states

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−15 | 82 / 3767 | Bcells peripheral blood_6_EnhG |
| 2 | 4e−11 | 95 / 5716 | Bcells peripheral blood_4_Tx |
| 3 | 4e−09 | 89 / 5527 | Tregulatory cells peripheral blood_4_Tx |
| 4 | 3e−08 | 105 / 7407 | natural killer cells peripheral blood_5_TxWk |
| 5 | 7e−08 | 87 / 5601 | Thelper cells peripheral blood_4_Tx |
| 6 | 9e−08 | 24 / 693 | Bcells peripheral blood_3_TxFlnk |
| 7 | 2e−07 | 65 / 3682 | natural killer cells peripheral blood_6_EnhG |
| 8 | 4e−07 | 111 / 8406 | Bcells peripheral blood_2_TssAFlnk |
| 9 | 4e−07 | 103 / 7489 | monocytes peripheral blood_5_TxWk |
| 10 | 4e−07 | 106 / 7833 | Bcells peripheral blood_1_TssA |
| 11 | 5e−07 | 95 / 6637 | Tcells peripheral blood_5_TxWk |
| 12 | 1e−06 | 85 / 5738 | monocytes peripheral blood_4_Tx |
| 13 | 2e−06 | 104 / 7751 | natural killer cells peripheral blood_1_TssA |
| 14 | 2e−06 | 85 / 5766 | natural killer cells peripheral blood_4_Tx |
| 15 | 2e−06 | 27 / 1009 | Tcells peripheral blood_8_ZNF_Rpts |

## GSEA C2

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 8e−08 | 8 / 56 | KLEIN_PRIMARY_EFFUSION_LYMPHOMA_DN |
| 2 | 7e−07 | 7 / 51 | MORI_LARGE_PRE_BII_LYMPHOCYTE_DN |
| 3 | 1e−06 | 5 / 19 | SHIN_B_CELL_LYMPHOMA_CLUSTER_9 |
| 4 | 1e−06 | 6 / 35 | TARTE_PLASMA_CELL_VS_B_LYMPHOCYTE_DN |
| 5 | 1e−06 | 17 / 429 | SMID_BREAST_CANCER_NORMAL_LIKE_UP |
| 6 | 6e−06 | 10 / 163 | ZHENG_FOXP3_TARGETS_IN_THYMUS_UP |
| 7 | 2e−05 | 14 / 368 | ZHENG_BOUND_BY_FOXP3 |
| 8 | 1e−04 | 10 / 229 | QI_PLASMACYTOMA_UP |
| 9 | 2e−04 | 9 / 195 | HOLLMANN_APOPTOSIS_VIA_CD40_UP |
| 10 | 2e−04 | 16 / 560 | KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_UP |
| 11 | 2e−04 | 5 / 52 | SMIRNOV_RESPONSE_TO_IR_2HR_DN |
| 12 | 2e−04 | 18 / 694 | KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_UP |
| 13 | 2e−04 | 7 / 121 | PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN |
| 14 | 3e−04 | 30 / 1550 | PILON_KLF1_TARGETS_DN |
| 15 | 3e−04 | 5 / 59 | PID_BCR_5PATHWAY |

## Lifestyle

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.001 | 8 / 210 | Homuth_BMI−associated−genes_DN |
| 2 | 0.004 | 3 / 32 | Marjolein_ageing−genes_DN |
| 3 | 0.114 | 1 / 12 | DUMEAUX_Women normal BMI literature genes up |
| 4 | 0.150 | 1 / 16 | DUMEAUX_Red blood cells in non smokers literature genes up |
| 5 | 0.467 | 1 / 62 | DUMEAUX_Smoking enriched genes |
| 6 | 0.783 | 1 / 150 | Homuth_BMI−associated−genes_UP |
| 7 | 1.000 | 0 / 10 | DUMEAUX_Smoking literature genes up |
| 8 | 1.000 | 0 / 4 | DUMEAUX_Exercising non smoker literature enriched genes |
| 9 | 1.000 | 0 / 5 | DUMEAUX_Estrogen related in smokers literature genes up |
| 10 | 1.000 | 0 / 7 | DUMEAUX_Estrogen related in non smokers literature genes up |
| 11 | 1.000 | 0 / 7 | DUMEAUX_Hormon therapy  in non smokers literature genes up |
| 12 | 1.000 | 0 / 9 | DUMEAUX_Monocytes in smokers literature genes up |
| 13 | 1.000 | 0 / 22 | DUMEAUX_High bmi enriched genes |
| 14 | 1.000 | 0 / 22 | DUMEAUX_Fasting enriched genes |
| 15 | 1.000 | 0 / 14 | Huan_blood−pressure_SBP−signature |

## MF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.002 | 4 / 54 | Rho guanyl−nucleotide exchange factor activity |
| 2 | 0.003 | 5 / 96 | SH3 domain binding |
| 3 | 0.004 | 5 / 104 | transcriptional repressor activity, RNA polymerase II proximal promoter seque |
| 4 | 0.004 | 2 / 10 | profilin binding |
| 5 | 0.006 | 9 / 331 | protein serine/threonine kinase activity |
| 6 | 0.007 | 3 / 38 | signal transducer activity, downstream of receptor |
| 7 | 0.010 | 5 / 130 | guanyl−nucleotide exchange factor activity |
| 8 | 0.011 | 2 / 16 | phospholipid transporter activity |
| 9 | 0.015 | 2 / 19 | RNA polymerase II core binding |
| 10 | 0.015 | 2 / 19 | steroid binding |
| 11 | 0.016 | 6 / 202 | GTPase activator activity |
| 12 | 0.017 | 2 / 20 | phosphatidylinositol−3,4−bisphosphate binding |
| 13 | 0.020 | 2 / 22 | histone demethylase activity |
| 14 | 0.020 | 2 / 22 | protein phosphatase 2A binding |
| 15 | 0.022 | 91 / 7864 | protein binding |

## Reference Signatures

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−06 | 6 / 42 | Chaussabel_1,3_B−cells |
| 2 | 6e−04 | 8 / 188 | Chaussabel_3,8_Enzymes |
| 3 | 9e−04 | 11 / 355 | WIRTH_Immune system |
| 4 | 1e−03 | 3 / 21 | VAQUERIZAS_Tonsil_TF |
| 5 | 1e−03 | 13 / 496 | PROTEINATLAS_spleen |
| 6 | 7e−03 | 2 / 13 | WIRTH_B−cells |
| 7 | 1e−02 | 2 / 16 | VAQUERIZAS_Ovary_TF |
| 8 | 1e−02 | 3 / 49 | VAQUERIZAS_Uterus_TF |
| 9 | 2e−02 | 17 / 989 | PROTEINATLAS_tonsil |
| 10 | 2e−02 | 2 / 24 | VAQUERIZAS_Pituitary_TF |
| 11 | 3e−02 | 3 / 66 | VAQUERIZAS_Whole blood_TF |
| 12 | 4e−02 | 2 / 30 | VAQUERIZAS_Smooth muscle_TF |
| 13 | 4e−02 | 15 / 905 | PROTEINATLAS_appendix |
| 14 | 4e−02 | 12 / 678 | PROTEINATLAS_lymph node |
| 15 | 4e−02 | 2 / 32 | VAQUERIZAS_Liver_TF |

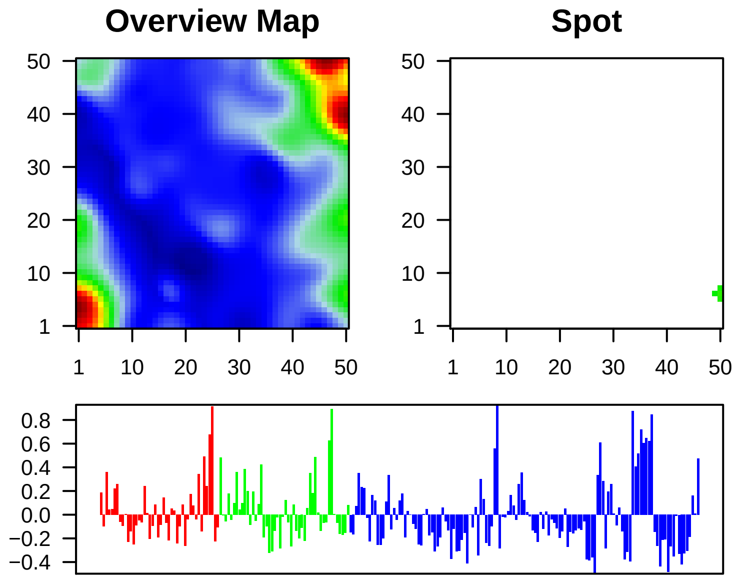
# Group Overexpression Sp

## Spot Summary: D

# metagenes = 4
# genes = 188

<r> metagenes = 1
<r> genes = 0.48
beta: r2= 9.65  /  log p= −Inf

# samples with spot = 37 ( 16.7 %)
mBL : 8 ( 18.2 %)
intermediate : 8 ( 16.7 %)
non−mBL : 21 ( 16.3 %)

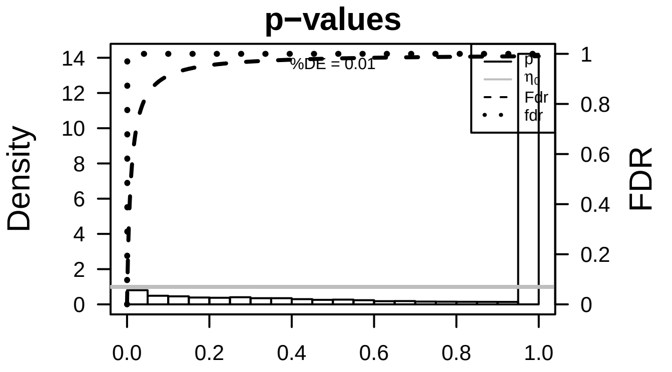


## Spot Genelist

| Rank | ID | max e | min e | r | Symbol | Description |
|---|---|---|---|---|---|---|
| 1 | 214753_at | 2.14 | −1.23 | 0.73 | | |
| 2 | 207492_at | 2.1 | −1.01 | 0.76 | | |
| 3 | 220918_at | 2.03 | −0.81 | 0.79 | | |
| 4 | 220940_at | 1.83 | −1.2 | 0.77 | | |
| 5 | 215768_at | 1.81 | −0.79 | 0.44 | | |
| 6 | 217534_at | 1.8 | −0.88 | 0.76 | FAM49B | family with sequence similarity 49 member B [Source:HGNC |
| 7 | 216197_at | 1.78 | −0.87 | 0.76 | | |
| 8 | 221616_s_at | 1.78 | −0.7 | 0.75 | | |
| 9 | 222358_x_at | 1.78 | −0.81 | 0.84 | | |
| 10 | 216614_at | 1.77 | −0.95 | 0.75 | | |
| 11 | 220704_at | 1.76 | −1.2 | 0.8 | IKZF1 | IKAROS family zinc finger 1 [Source:HGNC Symbol;Acc:HG |
| 12 | 210230_at | 1.75 | −1.07 | 0.64 | | |
| 13 | 213089_at | 1.75 | −1.37 | 0.89 | | |
| 14 | 215599_at | 1.73 | −0.9 | 0.84 | | glucuronidase, beta pseudogene 3 [Source:HGNC Symbol;A |
| 15 | 215024_at | 1.72 | −0.92 | 0.78 | CCZ1 | CCZ1 homolog, vacuolar protein trafficking and biogenesis a |
| 16 | 222284_at | 1.72 | −0.83 | 0.74 | | |
| 17 | 220338_at | 1.71 | −1.05 | 0.66 | RALGPS2 | Ral GEF with PH domain and SH3 binding motif 2 [Source:H |
| 18 | 216310_at | 1.7 | −0.75 | 0.78 | TAOK1 | TAO kinase 1 [Source:HGNC Symbol;Acc:HGNC:29259] |
| 19 | 216109_at | 1.67 | −0.76 | 0.7 | | |
| 20 | 217671_at | 1.67 | −0.75 | 0.79 | | |

## Geneset Overrepresentation

| Rank | p−value | #in/all | Geneset | |
|---|---|---|---|---|
| 1 | 1e−23 | 26 / 218 | Refer | WIRTH_pre+post GC B−cells |
| 2 | 7e−15 | 26 / 492 | Colon | LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_tra |
| 3 | 3e−14 | 12 / 59 | Gliom | WILLSCHER_GBM_Verhaak−PNwt & MES_up |
| 4 | 6e−14 | 5 / 14 | Cance | LIU_COMMON_CANCER_GENES |
| 5 | 6e−14 | 5 / 14 | Cance | LIU_COMMON_CANCER_GENES |
| 6 | 4e−13 | 36 / 1174 | Colon | LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse c |
| 7 | 1e−12 | 8 / 20 | Refer | Chaussabel_2,7_Unknown function |
| 8 | 6e−12 | 14 / 143 | GSEA | LEE_DIFFERENTIATING_T_LYMPHOCYTE |
| 9 | 3e−11 | 67 / 4261 | Lymph | HOPP_Txn_transition |
| 10 | 3e−10 | 14 / 188 | Refer | Chaussabel_3,8_Enzymes |
| 11 | 3e−09 | 6 / 17 | GSEA | SPIRA_SMOKERS_LUNG_CANCER_DN |
| 12 | 8e−09 | 10 / 102 | Lymph | ROSOLOWSKI_blue total |
| 13 | 7e−07 | 5 / 22 | Refer | Chaussabel_1,6_Signaling molecules |
| 14 | 1e−06 | 16 / 477 | GSEA | NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN |
| 15 | 1e−06 | 9 / 136 | GSEA | REACTOME_MRNA_PROCESSING |
| 16 | 3e−06 | 25 / 1161 | MF | RNA binding |
| 17 | 4e−06 | 10 / 198 | BP | mRNA splicing, via spliceosome |
| 18 | 4e−06 | 19 / 730 | GSEA | ONKEN_UVEAL_MELANOMA_UP |
| 19 | 5e−06 | 67 / 5529 | Lymph | HOPP_Txn_elongation |
| 20 | 5e−06 | 8 / 120 | GSEA | REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE |
| 21 | 1e−05 | 20 / 852 | MF | nucleic acid binding |
| 22 | 1e−05 | 5 / 39 | GSEA | BILBAN_B_CLL_LPL_DN |
| 23 | 1e−05 | 11 / 281 | BP | mRNA processing |
| 24 | 2e−05 | 16 / 600 | GSEA | RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN |
| 25 | 3e−05 | 20 / 906 | Lymph | SPANG_BCR DN |
| 26 | 3e−05 | 3 / 8 | Gliom | WILLSCHER_GBM_LTSmut_proteomics−A_UP |
| 27 | 7e−05 | 7 / 127 | GSEA | GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN |
| 28 | 9e−05 | 6 / 92 | GSEA | REACTOME_MRNA_SPLICING |
| 29 | 1e−04 | 9 / 233 | BP | RNA splicing |
| 30 | 1e−04 | 26 / 1527 | GSEA | PUJANA_BRCA1_PCC_NETWORK |
| 31 | 1e−04 | 10 / 297 | GSEA | BASAKI_YBX1_TARGETS_DN |
| 32 | 2e−04 | 13 / 496 | Refer | PROTEINATLAS_spleen |
| 33 | 2e−04 | 3 / 14 | Cance | GUSTAFSON_PI3K_DN |
| 34 | 2e−04 | 6 / 106 | Refer | Chaussabel_2,11_Replication |
| 35 | 3e−04 | 26 / 1602 | GSEA | BLALOCK_ALZHEIMERS_DISEASE_UP |
| 36 | 3e−04 | 6 / 112 | GSEA | HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN |
| 37 | 3e−04 | 19 / 989 | Refer | PROTEINATLAS_tonsil |
| 38 | 3e−04 | 54 / 4579 | CC | nucleus |
| 39 | 3e−04 | 5 / 75 | GSEA | REACTOME_3_UTR_MEDIATED_TRANSLATIONAL_REGULATION |
| 40 | 3e−04 | 4 / 42 | BP | RNA metabolic process |



### Aging

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1 | 0 / 92 | HORVATH_aging_genes meth DOWN |
| 2 | 1 | 0 / 107 | HORVATH_aging_genes meth UP |
| 3 | 1 | 0 / 47 | TESCHENDORFF_age_hypermethylated |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

### BP

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−06 | 10 / 198 | mRNA splicing, via spliceosome |
| 2 | 1e−05 | 11 / 281 | mRNA processing |
| 3 | 1e−04 | 9 / 233 | RNA splicing |
| 4 | 3e−04 | 4 / 42 | RNA metabolic process |
| 5 | 5e−04 | 8 / 232 | translation |
| 6 | 2e−03 | 5 / 110 | translational initiation |
| 7 | 2e−03 | 5 / 113 | rhythmic process |
| 8 | 4e−03 | 4 / 83 | viral transcription |
| 9 | 5e−03 | 2 / 14 | regulation of establishment of cell polarity |
| 10 | 6e−03 | 4 / 91 | mRNA transport |
| 11 | 6e−03 | 2 / 15 | positive regulation of telomere capping |
| 12 | 7e−03 | 3 / 49 | RNA export from nucleus |
| 13 | 7e−03 | 7 / 281 | DNA repair |
| 14 | 8e−03 | 2 / 17 | negative regulation of mRNA splicing, via spliceosome |
| 15 | 8e−03 | 2 / 17 | skeletal muscle tissue regeneration |

### Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−14 | 5 / 14 | LIU_COMMON_CANCER_GENES |
| 2 | 2e−04 | 3 / 14 | GUSTAFSON_PI3K_DN |
| 3 | 9e−02 | 1 / 12 | LIU_BREAST_CANCER |
| 4 | 1e−01 | 1 / 14 | GENTLES_modul10 |
| 5 | 1e−01 | 1 / 14 | BENTINK_myc.1 |
| 6 | 3e−01 | 1 / 41 | PanCan_DNARepair_geneset_nanostring |
| 7 | 3e−01 | 2 / 134 | PanCan_RAS_geneset_nanostring |
| 8 | 3e−01 | 1 / 45 | KUIPER_MM poor survival |
| 9 | 3e−01 | 5 / 480 | Lembcke_Colonic Inflammation |
| 10 | 3e−01 | 0 / 14 | LIU_PROSTATE_CANCER_DN |
| 11 | 4e−01 | 2 / 187 | PanCan_PI3K_geneset_nanostring |
| 12 | 5e−01 | 0 / 11 | LIU_PROSTATE_CANCER_UP |
| 13 | 6e−01 | 3 / 409 | Lembcke_Normal vs Adenoma |
| 14 | 7e−01 | 1 / 147 | PanCan_MAPK_geneset_nanostring |
| 15 | 8e−01 | 1 / 186 | SPANG_LPS−index2 |

### CC

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−04 | 54 / 4579 | nucleus |
| 2 | 9e−04 | 34 / 2541 | nucleoplasm |
| 3 | 3e−03 | 2 / 11 | holo TFIIH complex |
| 4 | 4e−03 | 3 / 41 | cytosolic large ribosomal subunit |
| 5 | 5e−03 | 5 / 139 | ribosome |
| 6 | 6e−03 | 7 / 268 | intracellular ribonucleoprotein complex |
| 7 | 2e−02 | 7 / 326 | nuclear speck |
| 8 | 2e−02 | 2 / 24 | stereocilium |
| 9 | 2e−02 | 4 / 128 | spliceosomal complex |
| 10 | 2e−02 | 3 / 77 | catalytic step 2 spliceosome |
| 11 | 2e−02 | 2 / 30 | aggresome |
| 12 | 4e−02 | 4 / 157 | spindle |
| 13 | 4e−02 | 2 / 42 | cleavage furrow |
| 14 | 4e−02 | 2 / 42 | transcriptional repressor complex |
| 15 | 5e−02 | 3 / 100 | chromatin |

### Chr

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.07 | 11 / 833 | Chr 19 |
| 2 | 0.09 | 8 / 585 | Chr 7 |
| 3 | 0.15 | 7 / 548 | Chr 16 |
| 4 | 0.27 | 5 / 437 | Chr 8 |
| 5 | 0.30 | 3 / 242 | Chr 13 |
| 6 | 0.34 | 8 / 832 | Chr 2 |
| 7 | 0.36 | 4 / 382 | Chr 15 |
| 8 | 0.42 | 7 / 776 | Chr 17 |
| 9 | 0.43 | 2 / 184 | Chr 18 |
| 10 | 0.49 | 6 / 700 | Chr 12 |
| 11 | 0.50 | 3 / 333 | Chr 22 |
| 12 | 0.62 | 5 / 669 | Chr 6 |
| 13 | 0.63 | 3 / 403 | Chr 14 |
| 14 | 0.65 | 4 / 554 | Chr 5 |
| 15 | 0.67 | 1 / 139 | Chr 21 |

### Chromatin states

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−09 | 59 / 3767 | Bcells peripheral blood_6_EnhG |
| 2 | 1e−08 | 57 / 3682 | natural killer cells peripheral blood_6_EnhG |
| 3 | 5e−08 | 88 / 7833 | Bcells peripheral blood_1_TssA |
| 4 | 5e−08 | 40 / 2144 | T CD8+ naive cells peripheral blood_6_EnhG |
| 5 | 6e−08 | 54 / 3524 | Tregulatory cells peripheral blood_6_EnhG |
| 6 | 1e−07 | 21 / 693 | Bcells peripheral blood_3_TxFlnk |
| 7 | 1e−07 | 57 / 3938 | Thelper cells peripheral blood_6_EnhG |
| 8 | 2e−07 | 42 / 2450 | HSC_6_EnhG |
| 9 | 1e−06 | 70 / 5716 | Bcells peripheral blood_4_Tx |
| 10 | 3e−06 | 68 / 5601 | Thelper cells peripheral blood_4_Tx |
| 11 | 3e−06 | 59 / 4528 | T CD8+ naive cells peripheral blood_4_Tx |
| 12 | 5e−06 | 54 / 4009 | 6_EnhG_ESC_Mesoderm |
| 13 | 6e−06 | 81 / 7420 | Tcells peripheral blood_1_TssA |
| 14 | 6e−06 | 11 / 258 | T CD8+ naive cells peripheral blood_3_TxFlnk |
| 15 | 7e−06 | 66 / 5456 | 5_Tx_Neuronal_Progenitor |

### Colon Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 7e−15 | 26 / 492 | LaPointe_mucosa−position_kmeans_C_cecum colon_ascending colon_trans |
| 2 | 4e−13 | 36 / 1174 | LaPointe_mucosa−position_kmeans_E_transverse colon_UP_transverse colo |
| 3 | 4e−03 | 24 / 1729 | LaPointe_mucosa−position_kmeans_G_cecum colon_ascending colon_UP_t |
| 4 | 1e−02 | 10 / 561 | Pentrack_CRC_TCGA_group.over_C_normal_DN |
| 5 | 2e−02 | 13 / 854 | LaPointe_mucosa−position_kmeans_A_ascending colon_UP_ |
| 6 | 4e−02 | 12 / 848 | LaPointe_mucosa−position_kmeans_O_transverse colon_UP_ |
| 7 | 6e−02 | 1 / 8 | KIM_MSI−in−EC |
| 8 | 8e−02 | 1 / 10 | KIM_CRC−MSI−regulated_DN |
| 9 | 8e−02 | 2 / 60 | Marisa_CRC−cluster−g |
| 10 | 9e−02 | 1 / 12 | Juehling_HNPCC−mutated−in−4 |
| 11 | 1e−01 | 1 / 14 | Hewish_dMMR−secondary−mutations_DNA−repair |
| 12 | 1e−01 | 1 / 16 | Vilar_mutated−in−CRC−CamP |
| 13 | 1e−01 | 7 / 532 | LaPointe_mucosa−position_kmeans_B_ascending colon_transverse colon_U |
| 14 | 1e−01 | 7 / 539 | Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN |
| 15 | 2e−01 | 7 / 602 | Pentrack_CRC_TCGA_corr_R_normal_DN |

### Glioma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−14 | 12 / 59 | WILLSCHER_GBM_Verhaak−PNwt & MES_up |
| 2 | 3e−05 | 3 / 8 | WILLSCHER_GBM_LTSmut_proteomics−A_UP |
| 3 | 2e−02 | 1 / 2 | WILLSCHER_GBM_Verhaak−PN (mut&wt)_up (L) |
| 4 | 5e−02 | 18 / 1523 | Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN |
| 5 | 7e−02 | 2 / 55 | WILLSCHER_GBM_proteomics_wtOnly_SpotJ |
| 6 | 8e−02 | 1 / 10 | Phillips PN up vs MES & Prolif |
| 7 | 1e−01 | 1 / 15 | Donson−chemokine/cytokine−receptors−associated with LTS in HGA |
| 8 | 1e−01 | 1 / 16 | VERHAAK_PN subtype |
| 9 | 1e−01 | 2 / 78 | Weller_LGG_A_vs_O_UP |
| 10 | 2e−01 | 1 / 22 | Sturm_GBM_Meth_overexpression_H_K27_UP |
| 11 | 2e−01 | 4 / 282 | WILLSCHER_GBM_Verhaak−PNwt & CL_up |
| 12 | 2e−01 | 1 / 32 | WIRTH_PN subtype |
| 13 | 2e−01 | 1 / 35 | Gorovets_LGG_EPL_subclass |
| 14 | 3e−01 | 13 / 1343 | Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP |
| 15 | 3e−01 | 1 / 42 | Sturm_GBM_Meth_overexpression_D_G34_UP |

### GSEA C2

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−14 | 5 / 14 | LIU_COMMON_CANCER_GENES |
| 2 | 6e−12 | 14 / 143 | LEE_DIFFERENTIATING_T_LYMPHOCYTE |
| 3 | 3e−09 | 6 / 17 | SPIRA_SMOKERS_LUNG_CANCER_DN |
| 4 | 1e−06 | 16 / 477 | NAKAMURA_TUMOR_ZONE_PERIPHERAL_VS_CENTRAL_DN |
| 5 | 1e−06 | 9 / 136 | REACTOME_MRNA_PROCESSING |
| 6 | 4e−06 | 19 / 730 | ONKEN_UVEAL_MELANOMA_UP |
| 7 | 5e−06 | 8 / 120 | REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_ |
| 8 | 1e−05 | 5 / 39 | BILBAN_B_CLL_LPL_DN |
| 9 | 2e−05 | 16 / 600 | RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFERENTIATED_DN |
| 10 | 7e−05 | 7 / 127 | GINESTIER_BREAST_CANCER_20Q13_AMPLIFICATION_DN |
| 11 | 9e−05 | 6 / 92 | REACTOME_MRNA_SPLICING |
| 12 | 1e−04 | 26 / 1527 | PUJANA_BRCA1_PCC_NETWORK |
| 13 | 1e−04 | 10 / 297 | BASAKI_YBX1_TARGETS_DN |
| 14 | 3e−04 | 26 / 1602 | BLALOCK_ALZHEIMERS_DISEASE_UP |
| 15 | 3e−04 | 6 / 112 | HAHTOLA_MYCOSIS_FUNGOIDES_CD4_DN |

### HM

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.02 | 5 / 190 | HALLMARK_MYC_TARGETS_V1 |
| 2 | 0.05 | 2 / 44 | HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY |
| 3 | 0.07 | 4 / 195 | HALLMARK_G2M_CHECKPOINT |
| 4 | 0.20 | 3 / 193 | HALLMARK_HEME_METABOLISM |
| 5 | 0.24 | 1 / 34 | HALLMARK_APICAL_SURFACE |
| 6 | 0.24 | 1 / 34 | HALLMARK_ANGIOGENESIS |
| 7 | 0.29 | 2 / 133 | HALLMARK_DNA_REPAIR |
| 8 | 0.39 | 2 / 170 | HALLMARK_IL2_STAT5_SIGNALING |
| 9 | 0.44 | 2 / 187 | HALLMARK_E2F_TARGETS |
| 10 | 0.44 | 2 / 188 | HALLMARK_HYPOXIA |
| 11 | 0.46 | 2 / 194 | HALLMARK_KRAS_SIGNALING_UP |
| 12 | 0.54 | 1 / 97 | HALLMARK_BILE_ACID_METABOLISM |
| 13 | 0.54 | 1 / 97 | HALLMARK_PEROXISOME |
| 14 | 0.57 | 1 / 106 | HALLMARK_UNFOLDED_PROTEIN_RESPONSE |
| 15 | 0.75 | 1 / 173 | HALLMARK_MITOTIC_SPINDLE |

### Immunome

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.05 | 1 / 7 | Angelova_immune−metagene−cytotoxic_cells |
| 2 | 0.08 | 1 / 10 | Angelova_immune−metagene−neutrophils |
| 3 | 0.10 | 1 / 13 | Angelova_immune−metagene−immature_B−cells |
| 4 | 0.17 | 1 / 23 | Angelova_immune−metagene−monocytes |
| 5 | 0.30 | 1 / 45 | Angelova_immune−metagene−MDSC |
| 6 | 1.00 | 0 / 13 | Angelova_immune−metagene−activated_B−cells |
| 7 | 1.00 | 0 / 26 | Angelova_immune−metagene−activated_CD4 |
| 8 | 1.00 | 0 / 19 | Angelova_immune−metagene−activated_CD8 |
| 9 | 1.00 | 0 / 21 | Angelova_immune−metagene−central_memory_CD4 |
| 10 | 1.00 | 0 / 17 | Angelova_immune−metagene−central_memory_CD8 |
| 11 | 1.00 | 0 / 25 | Angelova_immune−metagene−DC |
| 12 | 1.00 | 0 / 12 | Angelova_immune−metagene−effector_memory_CD4 |
| 13 | 1.00 | 0 / 32 | Angelova_immune−metagene−effector_memory_CD8 |
| 14 | 1.00 | 0 / 14 | Angelova_immune−metagene−eosinophil |
| 15 | 1.00 | 0 / 19 | Angelova_immune−metagene−iDC |

### Lifestyle

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.2 | 1 / 22 | DUMEAUX_Fasting enriched genes |
| 2 | 0.3 | 2 / 150 | Homuth_BMI−associated−genes_UP |
| 3 | 0.5 | 2 / 210 | Homuth_BMI−associated−genes_DN |
| 4 | 1.0 | 0 / 62 | DUMEAUX_Smoking enriched genes |
| 5 | 1.0 | 0 / 10 | DUMEAUX_Smoking literature genes up |
| 6 | 1.0 | 0 / 4 | DUMEAUX_Exercising non smoker literature enriched genes |
| 7 | 1.0 | 0 / 5 | DUMEAUX_Estrogen related in smokers literature genes up |
| 8 | 1.0 | 0 / 7 | DUMEAUX_Estrogen related in non smokers literature genes up |
| 9 | 1.0 | 0 / 7 | DUMEAUX_Hormon therapy  in non smokers literature genes up |
| 10 | 1.0 | 0 / 9 | DUMEAUX_Monocytes in smokers literature genes up |
| 11 | 1.0 | 0 / 16 | DUMEAUX_Red blood cells in non smokers literature genes up |
| 12 | 1.0 | 0 / 12 | DUMEAUX_Women normal BMI literature genes up |
| 13 | 1.0 | 0 / 22 | DUMEAUX_High bmi enriched genes |
| 14 | 1.0 | 0 / 14 | Huan_blood−pressure_SBP−signature |
| 15 | 1.0 | 0 / 13 | Huan_blood−pressure_DBP−signature |

### Lymphoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−11 | 67 / 4261 | HOPP_Txn_transition |
| 2 | 8e−09 | 10 / 102 | ROSOLOWSKI_blue total |
| 3 | 5e−06 | 67 / 5529 | HOPP_Txn_elongation |
| 4 | 3e−05 | 20 / 906 | SPANG_BCR DN |
| 5 | 1e−03 | 2 / 7 | Shaknovich_ABC_hypo_meth |
| 6 | 4e−03 | 61 / 5908 | HOPP_Active_promoter |
| 7 | 5e−03 | 3 / 45 | Monti_BCR_cluster |
| 8 | 7e−03 | 56 / 5404 | HOPP_Strong_enhancer |
| 9 | 1e−02 | 2 / 19 | Subero_MCL_hypo_meth |
| 10 | 4e−02 | 3 / 99 | Sha_BL UP |
| 11 | 5e−02 | 1 / 6 | MASCQUE_mBL UP |
| 12 | 1e−01 | 1 / 14 | Subero_B−ALL_hypo_meth |
| 13 | 1e−01 | 1 / 17 | DAVE_c−myc BL UP |
| 14 | 2e−01 | 1 / 33 | Subero_T−PLL_hypo_meth |
| 15 | 3e−01 | 49 / 5682 | HOPP_Weak_promoter |

### Melanoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.02 | 2 / 24 | Tirosh_B−cell specific genes−melanoma |
| 2 | 0.02 | 1 / 2 | Melanoma Epi−Enzyme Cluster 6 |
| 3 | 0.07 | 5 / 276 | Gerber_wt/wt_melanoma−cells−SpotB |
| 4 | 0.10 | 2 / 68 | Tirosh_housekeeping_genes |
| 5 | 0.12 | 1 / 16 | Hugo_melanoma−all−LEF1_UP |
| 6 | 0.14 | 4 / 249 | Gerber_wt/wt_melanoma−cells−SpotE |
| 7 | 0.17 | 1 / 23 | Melanoma Epi−Enzyme Cluster 7 |
| 8 | 0.26 | 3 / 222 | Gerber_wt/wt_melanoma−cells−SpotF |
| 9 | 0.26 | 1 / 38 | Tirosh_top50 correlated genes PC1 |
| 10 | 0.27 | 1 / 39 | Tirosh_top50 correlated genes PC4 |
| 11 | 0.28 | 1 / 41 | Tirosh_top50 correlated genes PC3 |
| 12 | 0.40 | 2 / 171 | Landsberg_dedifferentiation_up |
| 13 | 0.43 | 2 / 185 | Tirosh_genes from malignant cells in Mel79−melanoma |
| 14 | 0.45 | 2 / 189 | Tirosh_genes preferentially expressed by Tregs |
| 15 | 0.47 | 3 / 319 | Gerber_wt/wt_melanoma−cells−SpotA |

### MF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−06 | 25 / 1161 | RNA binding |
| 2 | 1e−05 | 20 / 852 | nucleic acid binding |
| 3 | 1e−02 | 2 / 19 | miRNA binding |
| 4 | 1e−02 | 2 / 20 | RNA polymerase II transcription corepressor activity |
| 5 | 1e−02 | 2 / 22 | translation factor activity, RNA binding |
| 6 | 2e−02 | 2 / 29 | SH2 domain binding |
| 7 | 2e−02 | 2 / 30 | histone−lysine N−methyltransferase activity |
| 8 | 3e−02 | 2 / 33 | DNA−dependent ATPase activity |
| 9 | 3e−02 | 2 / 37 | ribosome binding |
| 10 | 4e−02 | 3 / 93 | protein N−terminus binding |
| 11 | 5e−02 | 3 / 107 | mRNA binding |
| 12 | 6e−02 | 2 / 48 | translation initiation factor activity |
| 13 | 6e−02 | 3 / 109 | structural constituent of ribosome |
| 14 | 7e−02 | 2 / 55 | damaged DNA binding |
| 15 | 7e−02 | 2 / 55 | double−stranded RNA binding |

### miRNA target

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−04 | 8 / 234 | hsa−miR−101 |
| 2 | 7e−04 | 6 / 136 | hsa−miR−511 |
| 3 | 2e−03 | 5 / 111 | hsa−miR−656 |
| 4 | 2e−03 | 3 / 33 | hsa−miR−654−3p |
| 5 | 3e−03 | 4 / 72 | hsa−miR−339−5p |
| 6 | 5e−03 | 3 / 44 | hsa−miR−455−5p |
| 7 | 9e−03 | 2 / 18 | hsa−miR−668 |
| 8 | 1e−02 | 8 / 378 | hsa−miR−16 |
| 9 | 1e−02 | 2 / 20 | hsa−miR−662 |
| 10 | 1e−02 | 3 / 59 | hsa−miR−499−3p |
| 11 | 1e−02 | 4 / 114 | hsa−miR−494 |
| 12 | 1e−02 | 3 / 62 | hsa−miR−489 |
| 13 | 2e−02 | 4 / 121 | hsa−miR−922 |
| 14 | 2e−02 | 4 / 124 | hsa−miR−655 |
| 15 | 2e−02 | 2 / 27 | hsa−miR−770−5p |

### Pneumonia

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−04 | 7 / 179 | Terre_MSV_multiple_respiratory_viruses_dn |
| 2 | 3e−01 | 1 / 41 | Scicluna_DN |
| 3 | 1e+00 | 0 / 68 | Burnham_sep_vs_con_UP |
| 4 | 1e+00 | 0 / 56 | Burnham_sep_vs_con_DN |
| 5 | 1e+00 | 0 / 48 | Burnham_cap_fp_vs_con_DN |
| 6 | 1e+00 | 0 / 71 | Burnham_cap_fp_vs_con_UP |
| 7 | 1e+00 | 0 / 48 | Burnham_viral_DN |
| 8 | 1e+00 | 0 / 57 | Burnham_viral_UP |
| 9 | 1e+00 | 0 / 57 | Burnham_day1_vs_5_UP |
| 10 | 1e+00 | 0 / 52 | Burnham_day1_vs_5_DN |
| 11 | 1e+00 | 0 / 54 | Burnham_timecourse |
| 12 | 1e+00 | 0 / 18 | Scicluna_UP |
| 13 | 1e+00 | 0 / 37 | Sweeney_viral_up |
| 14 | 1e+00 | 0 / 33 | Sweeney_viral_dn |
| 15 | 1e+00 | 0 / 122 | Terre_IMS_influenza_meta_signature |

### Reference Signatures

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−23 | 26 / 218 | WIRTH_pre+post GC B−cells |
| 2 | 1e−12 | 8 / 20 | Chaussabel_2,7_Unknown function |
| 3 | 3e−10 | 14 / 188 | Chaussabel_3,8_Enzymes |
| 4 | 7e−07 | 5 / 22 | Chaussabel_1,6_Signaling molecules |
| 5 | 2e−04 | 13 / 496 | PROTEINATLAS_spleen |
| 6 | 2e−04 | 6 / 106 | Chaussabel_2,11_Replication |
| 7 | 3e−04 | 19 / 989 | PROTEINATLAS_tonsil |
| 8 | 8e−04 | 13 / 593 | PROTEINATLAS_lateral ventricle |
| 9 | 9e−04 | 14 / 678 | PROTEINATLAS_lymph node |
| 10 | 1e−03 | 16 / 866 | PROTEINATLAS_cerebellum |
| 11 | 2e−03 | 13 / 642 | PROTEINATLAS_lung |
| 12 | 2e−03 | 18 / 1076 | PROTEINATLAS_stomach |
| 13 | 3e−03 | 13 / 671 | PROTEINATLAS_cervix, uterine |
| 14 | 3e−03 | 15 / 840 | PROTEINATLAS_urinary bladder |
| 15 | 4e−03 | 4 / 83 | Chaussabel_1,7_MHC Ribosomal proteins |

### Telomeres

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1 | 0 / 13 | Alternative lengthening of telomeres |
| 2 | 1 | 0 / 27 | Nabetani_alt len telomeres_genes_ko |
| 3 | NA | 0 / 0 | |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

### TF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.08 | 1 / 10 | MYC_RNA processing binding UP |
| 2 | 0.09 | 2 / 62 | MYC_Targets UP |
| 3 | 0.09 | 7 / 485 | ICGC_NrsfPcr2_targets |
| 4 | 0.12 | 17 / 1578 | ICGC_GabpPcr2_targets |
| 5 | 0.12 | 1 / 16 | MYC_Protein synthesis degradation UP |
| 6 | 0.15 | 30 / 3150 | ICGC_Creb1_targets |
| 7 | 0.18 | 33 / 3564 | ICGC_Taf1_targets |
| 8 | 0.22 | 16 / 1630 | ICGC_SrfV0416101_targets |
| 9 | 0.25 | 33 / 3703 | ICGC_Foxm1_targets |
| 10 | 0.25 | 38 / 4319 | ICGC_Pou2_targets |
| 11 | 0.30 | 10 / 1025 | ICGC_NrsfPcr1_targets |
| 12 | 0.30 | 33 / 3796 | ICGC_Nficsc81335_targets |
| 13 | 0.31 | 14 / 1508 | ICGC_Mef2_targets |
| 14 | 0.33 | 20 / 2254 | ICGC_BatfPcr1_targets |
| 15 | 0.35 | 39 / 4602 | ICGC_Elf1_targets |

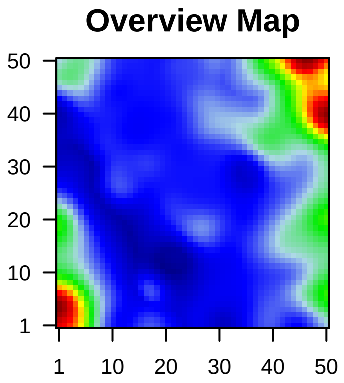
# Group Overexpression Sp

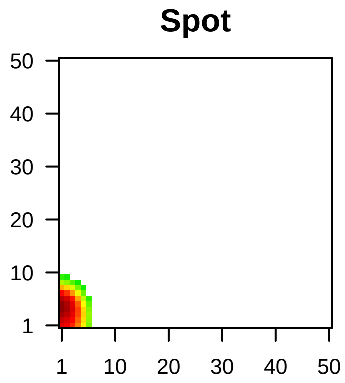
## Spot Summary: E

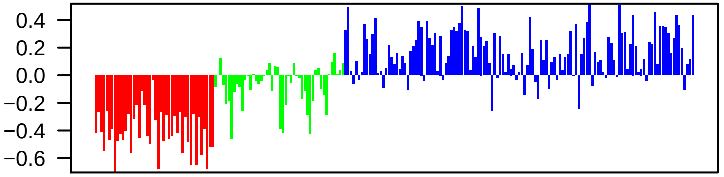
# metagenes = 52
# genes = 795

<r> metagenes = 0.93
<r> genes = 0.34
beta: r2= 19.61 / log p= −Inf

# samples with spot = 49 ( 22.2 %)
non−mBL : 49 ( 38 %)





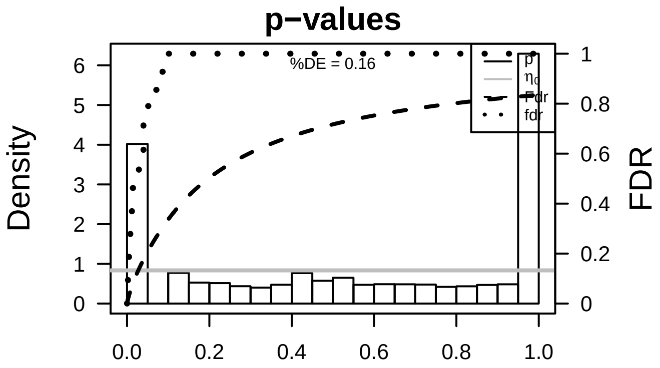


## Spot Genelist

| Rank | ID | max e | min e | r | Symbol | Description |
|---|---|---|---|---|---|---|
| 1 | 205040_at | 2.98 | −1.17 | 0.45 | ORM1 | orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498] |
| 2 | 207900_at | 2.93 | −0.94 | 0.32 | CCL17 | C−C motif chemokine ligand 17 [Source:HGNC Symbol;Acc: |
| 3 | 205041_s_at | 2.9 | −1.48 | 0.51 | ORM1 | orosomucoid 1 [Source:HGNC Symbol;Acc:HGNC:8498] |
| 4 | 217002_s_at | 2.74 | −1.28 | 0.31 | HTR3A | 5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Ac |
| 5 | 211644_x_at | 2.59 | −1.77 | 0.32 |  | immunoglobulin kappa variable 3−20 [Source:HGNC Symbol; |
| 6 | 221185_s_at | 2.57 | −1.49 | 0.57 | IQCG | IQ motif containing G [Source:HGNC Symbol;Acc:HGNC:252 |
| 7 | 214551_s_at | 2.53 | −1.11 | 0.6 | CD7 | CD7 molecule [Source:HGNC Symbol;Acc:HGNC:1695] |
| 8 | 216615_s_at | 2.49 | −1.56 | 0.38 | HTR3A | 5−hydroxytryptamine receptor 3A [Source:HGNC Symbol;Ac |
| 9 | 219316_s_at | 2.46 | −0.79 | 0.64 | FLVCR2 | feline leukemia virus subgroup C cellular receptor family me |
| 10 | 208451_s_at | 2.38 | −1.57 | 0.56 | C4A | complement C4A (Rodgers blood group) [Source:HGNC Sym |
| 11 | 203535_at | 2.34 | −1.86 | 0.56 | S100A9 | S100 calcium binding protein A9 [Source:HGNC Symbol;Acc: |
| 12 | 217022_s_at | 2.33 | −2.54 | 0.46 |  | immunoglobulin heavy constant alpha 2 (A2m marker) [Sourc |
| 13 | 217546_at | 2.25 | −0.88 | 0.47 |  | metallothionein 1M [Source:HGNC Symbol;Acc:HGNC:14296 |
| 14 | 208168_s_at | 2.22 | −1.13 | 0.5 | CHIT1 | chitinase 1 [Source:HGNC Symbol;Acc:HGNC:1936] |
| 15 | 207245_at | 2.21 | −1.2 | 0.38 | UGT2B17 | UDP glucuronosyltransferase family 2 member B17 [Source: |
| 16 | 204561_x_at | 2.19 | −1.95 | 0.33 |  | APOC4−APOC2 readthrough (NMD candidate) [Source:HGN |
| 17 | 205819_at | 2.09 | −0.95 | 0.49 | MARCO | macrophage receptor with collagenous structure [Source:HG |
| 18 | 221841_s_at | 2.08 | −1.17 | 0.44 | KLF4 | Kruppel like factor 4 [Source:HGNC Symbol;Acc:HGNC:6348 |
| 19 | 202833_s_at | 2.04 | −2.04 | 0.76 | SERPINA1 | serpin family A member 1 [Source:HGNC Symbol;Acc:HGNC |
| 20 | 202357_s_at | 1.99 | −1.29 | 0.57 | CFB | complement factor B [Source:HGNC Symbol;Acc:HGNC:103 |

## Geneset Overrepresentation

| Rank | p−value | #in/all | Geneset | |
|---|---|---|---|---|
| 1 | 1e−99 | 182 / 589 | Colon | Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 2 | 3e−91 | 149 / 447 | Gliom | ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN |
| 3 | 1e−61 | 60 / 85 | Lymp | Sha_DLBCL UP |
| 4 | 2e−60 | 64 / 102 | Refer | WIRTH_EBV B−cells |
| 5 | 2e−55 | 98 / 317 | Canc | SPANG_BCL6−index2 |
| 6 | 3e−53 | 107 / 404 | GSE | RUTELLA_RESPONSE_TO_HGF_UP |
| 7 | 4e−52 | 88 / 269 | Gliom | ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 8 | 2e−49 | 80 / 231 | Gliom | WILLSCHER_GBM_Verhaak−CL & MES_up |
| 9 | 1e−48 | 100 / 386 | GSE | RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP |
| 10 | 4e−47 | 109 / 480 | Canc | Lembcke_Colonic Inflammation |
| 11 | 3e−45 | 75 / 223 | GSE | MCLACHLAN_DENTAL_CARIES_UP |
| 12 | 8e−44 | 68 / 186 | Canc | SPANG_LPS−index2 |
| 13 | 5e−43 | 45 / 71 | Mela | Tirosh_Macrophage specific genes−melanoma |
| 14 | 2e−42 | 68 / 194 | GSE | JAATINEN_HEMATOPOIETIC_STEM_CELL_DN |
| 15 | 1e−39 | 69 / 219 | GSE | MCLACHLAN_DENTAL_CARIES_DN |
| 16 | 7e−39 | 44 / 78 | Mela | Tirosh_expression higher in CAFs than in T−cells |
| 17 | 1e−36 | 71 / 255 | GSE | HELLER_SILENCED_BY_METHYLATION_UP |
| 18 | 2e−36 | 72 / 265 | GSE | WALLACE_PROSTATE_CANCER_RACE_UP |
| 19 | 4e−36 | 58 / 166 | HM | HALLMARK_INTERFERON_GAMMA_RESPONSE |
| 20 | 3e−34 | 46 / 104 | GSE | ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION |
| 21 | 3e−34 | 78 / 336 | BP | immune response |
| 22 | 6e−33 | 72 / 297 | GSE | RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN |
| 23 | 2e−32 | 86 / 431 | BP | immune system process |
| 24 | 7e−32 | 54 / 166 | GSE | VERHAAK_AML_WITH_NPM1_MUTATED_UP |
| 25 | 9e−32 | 77 / 354 | GSE | FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN |
| 26 | 2e−31 | 66 / 261 | GSE | POOLA_INVASIVE_BREAST_CANCER_UP |
| 27 | 2e−30 | 61 / 229 | GSE | QI_PLASMACYTOMA_UP |
| 28 | 2e−29 | 67 / 288 | Colon | Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN |
| 29 | 7e−29 | 52 / 173 | Lymp | Victora_Light zone signature |
| 30 | 8e−29 | 39 / 90 | GSE | BASSO_CD40_SIGNALING_UP |
| 31 | 1e−28 | 73 / 354 | GSE | RODWELL_AGING_KIDNEY_UP |
| 32 | 2e−28 | 70 / 327 | GSE | RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_UP |
| 33 | 3e−28 | 46 / 135 | Lymp | DAVE_BL−vs−DLBCL |
| 34 | 5e−28 | 55 / 202 | GSE | VERHAAK_GLIOBLASTOMA_MESENCHYMAL |
| 35 | 6e−28 | 69 / 323 | BP | inflammatory response |
| 36 | 1e−27 | 53 / 190 | HM | HALLMARK_TNFA_SIGNALING_VIA_NFKB |
| 37 | 3e−27 | 119 / 902 | GSE | CHEN_METABOLIC_SYNDROM_NETWORK |
| 38 | 1e−26 | 36 / 83 | Mela | TCGA_melanoma_immune_high |
| 39 | 4e−26 | 51 / 187 | HM | HALLMARK_INFLAMMATORY_RESPONSE |
| 40 | 1e−25 | 49 / 176 | HM | HALLMARK_ALLOGRAFT_REJECTION |



## Aging

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.1 | 7 / 92 | HORVATH_aging_genes meth DOWN |
| 2 | 0.4 | 3 / 47 | TESCHENDORFF_age_hypermethylated |
| 3 | 0.9 | 3 / 107 | HORVATH_aging_genes meth UP |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## BP

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−34 | 78 / 336 | immune response |
| 2 | 2e−32 | 86 / 431 | immune system process |
| 3 | 6e−28 | 69 / 323 | inflammatory response |
| 4 | 4e−18 | 51 / 274 | cytokine−mediated signaling pathway |
| 5 | 1e−17 | 59 / 367 | innate immune response |
| 6 | 3e−16 | 60 / 403 | neutrophil degranulation |
| 7 | 4e−16 | 33 / 131 | chemotaxis |
| 8 | 1e−14 | 29 / 113 | regulation of immune response |
| 9 | 6e−13 | 21 / 66 | interferon−gamma−mediated signaling pathway |
| 10 | 2e−12 | 20 / 63 | chemokine−mediated signaling pathway |
| 11 | 5e−12 | 32 / 169 | response to lipopolysaccharide |
| 12 | 4e−11 | 62 / 553 | apoptotic process |
| 13 | 2e−10 | 29 / 161 | adaptive immune response |
| 14 | 4e−10 | 35 / 232 | cell surface receptor signaling pathway |
| 15 | 5e−10 | 111 / 1361 | signal transduction |

## Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−55 | 98 / 317 | SPANG_BCL6−index2 |
| 2 | 4e−47 | 109 / 480 | Lembcke_Colonic Inflammation |
| 3 | 8e−44 | 68 / 186 | SPANG_LPS−index2 |
| 4 | 2e−08 | 8 / 13 | GENTLES_modul18 |
| 5 | 3e−07 | 18 / 96 | PanCan_TXmisReg_geneset_nanostring |
| 6 | 2e−06 | 6 / 10 | BENTINK_ras.4 |
| 7 | 4e−05 | 2 / 14 | LIU_PROSTATE_CANCER_DN |
| 8 | 1e−04 | 5 / 12 | HLA2_signature |
| 9 | 3e−04 | 12 / 80 | PanCan_JAK−ST_geneset_nanostring |
| 10 | 4e−04 | 5 / 15 | WANG_ER_UP |
| 11 | 2e−03 | 4 / 13 | GENTLES_modul11 |
| 12 | 3e−03 | 15 / 147 | PanCan_MAPK_geneset_nanostring |
| 13 | 3e−03 | 4 / 14 | BENTINK_src.10 |
| 14 | 2e−02 | 3 / 14 | GUSTAFSON_PI3K_UP |
| 15 | 4e−02 | 11 / 130 | PanCan_CC+Apop_geneset_nanostring |

## CC

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−14 | 228 / 3210 | plasma membrane |
| 2 | 5e−13 | 135 / 1611 | extracellular region |
| 3 | 5e−12 | 33 / 179 | external side of plasma membrane |
| 4 | 6e−12 | 100 / 1090 | extracellular space |
| 5 | 6e−11 | 20 / 74 | secretory granule membrane |
| 6 | 1e−10 | 218 / 3270 | integral component of membrane |
| 7 | 1e−09 | 52 / 462 | cell surface |
| 8 | 3e−09 | 313 / 5339 | membrane |
| 9 | 4e−08 | 91 / 1128 | integral component of plasma membrane |
| 10 | 5e−08 | 15 / 60 | tertiary granule membrane |
| 11 | 9e−08 | 152 / 2239 | extracellular exosome |
| 12 | 1e−07 | 13 / 48 | ficolin−1−rich granule membrane |
| 13 | 3e−07 | 8 / 17 | T cell receptor complex |
| 14 | 6e−07 | 33 / 281 | lysosome |
| 15 | 1e−06 | 50 / 537 | perinuclear region of cytoplasm |

## Chr

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.04 | 49 / 832 | Chr 2 |
| 2 | 0.13 | 28 / 490 | Chr 10 |
| 3 | 0.14 | 31 / 556 | Chr X |
| 4 | 0.22 | 35 / 669 | Chr 6 |
| 5 | 0.24 | 66 / 1325 | Chr 1 |
| 6 | 0.38 | 34 / 700 | Chr 12 |
| 7 | 0.42 | 36 / 756 | Chr 11 |
| 8 | 0.42 | 18 / 369 | Chr 20 |
| 9 | 0.48 | 23 / 492 | Chr 9 |
| 10 | 0.58 | 26 / 585 | Chr 7 |
| 11 | 0.61 | 6 / 139 | Chr 21 |
| 12 | 0.62 | 34 / 776 | Chr 17 |
| 13 | 0.63 | 30 / 689 | Chr 3 |
| 14 | 0.71 | 18 / 437 | Chr 8 |
| 15 | 0.74 | 7 / 184 | Chr 18 |

## Chromatin states

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−25 | 76 / 432 | monocytes peripheral blood_3_TxFlnk |
| 2 | 4e−20 | 207 / 2507 | Mid_Frontal_Lobe_ReprPC |
| 3 | 6e−18 | 81 / 626 | natural killer cells peripheral blood_3_TxFlnk |
| 4 | 7e−18 | 152 / 1676 | Fetal_TxTrans |
| 5 | 6e−16 | 234 / 3223 | monocytes peripheral blood_6_EnhG |
| 6 | 1e−14 | 121 / 1308 | Mid_Frontal_Lobe_K9K27me3 |
| 7 | 7e−12 | 84 / 847 | Fetal_TssP |
| 8 | 1e−11 | 450 / 8200 | monocytes peripheral blood_2_TssAFlnk |
| 9 | 1e−11 | 149 / 1930 | Fetal_TssA |
| 10 | 2e−09 | 125 / 1639 | Fetal_TssF |
| 11 | 1e−08 | 44 / 383 | K9acLow_Colon |
| 12 | 5e−08 | 79 / 932 | Tcells peripheral blood_3_TxFlnk |
| 13 | 1e−07 | 74 / 867 | Mid_Frontal_Lobe_Quies |
| 14 | 2e−07 | 120 / 1684 | 1_TssP_Neuronal_Progenitor |
| 15 | 3e−07 | 32 / 258 | T CD8+ naive cells peripheral blood_3_TxFlnk |

## Colon Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−99 | 182 / 589 | Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 2 | 2e−29 | 67 / 288 | Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN |
| 3 | 4e−23 | 60 / 297 | Pentrack_CRC_TCGA_group.over_B_msi−h_UP |
| 4 | 2e−10 | 26 / 132 | Marisa_CRC−cluster−a |
| 5 | 2e−08 | 8 / 13 | Budinska_B_Lower crypt−like_DOWN |
| 6 | 3e−08 | 13 / 43 | Marisa_CRC−cluster−f |
| 7 | 2e−06 | 71 / 883 | LaPointe_mucosa−position_kmeans_L_transverse colon_cecum colon_DN |
| 8 | 3e−06 | 82 / 1083 | LaPointe_mucosa−position_kmeans_J_cecum colon_ascending colon_transv |
| 9 | 9e−06 | 31 / 290 | Lembcke_TCGA_meth_kmeans_O_CIMP.H_DN |
| 10 | 3e−05 | 37 / 397 | Pentrack_CRC_TCGA_corr_C_normal_UP |
| 11 | 7e−05 | 11 / 60 | Marisa_CRC−cluster−g |
| 12 | 2e−04 | 70 / 1001 | LaPointe_mucosa−position_kmeans_H_cecum colon_ascending colon_UP_ |
| 13 | 3e−04 | 43 / 539 | Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN |
| 14 | 3e−04 | 19 / 172 | Pentrack_CRC_TCGA_corr_U_msi−h_UP |
| 15 | 6e−04 | 30 / 349 | Lembcke_TCGA_meth_kmeans_F_CIMP.H_UP_ |

## Glioma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−91 | 149 / 447 | ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN |
| 2 | 4e−52 | 88 / 269 | ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 3 | 2e−49 | 80 / 231 | WILLSCHER_GBM_Verhaak−CL & MES_up |
| 4 | 8e−24 | 55 / 242 | ScoV_0.5_Sturm_C1_IDH_DN |
| 5 | 1e−18 | 51 / 268 | ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN |
| 6 | 9e−14 | 42 / 246 | ScoV_0.001_Sturm_M1_IDH_RTK I 'PDGFRA'_DN |
| 7 | 3e−11 | 10 / 14 | Donson−chemokines/cytokines−associated with LTS in HGA |
| 8 | 5e−11 | 16 / 45 | Donson−innate immunity−associated with LTS in HGA |
| 9 | 8e−11 | 21 / 83 | ScoV_0.999_Sturm_E3_RTK I 'PDGFRA'_DN |
| 10 | 9e−11 | 24 / 109 | Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP |
| 11 | 9e−08 | 16 / 71 | Weller_LGG_1p19qDel−vs−intact_DOWN |
| 12 | 2e−07 | 10 / 27 | Donson−Misc immune function−associated with LTS in HGA |
| 13 | 2e−07 | 80 / 979 | Hopp_Sturm_GBM_Epi3_no_zentr_5_IDH_UP_fetus_adult_DN |
| 14 | 2e−06 | 7 / 15 | Donson−chemokine/cytokine−receptors−associated with LTS in HGA |
| 15 | 6e−06 | 6 / 12 | Donson−immune cell intra signaling−associated with LTS in HGA |

## GSEA C2

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−53 | 107 / 404 | RUTELLA_RESPONSE_TO_HGF_UP |
| 2 | 1e−48 | 100 / 386 | RUTELLA_RESPONSE_TO_HGF_VS_CSF2RB_AND_IL4_UP |
| 3 | 3e−45 | 75 / 223 | MCLACHLAN_DENTAL_CARIES_UP |
| 4 | 2e−42 | 68 / 194 | JAATINEN_HEMATOPOIETIC_STEM_CELL_DN |
| 5 | 1e−39 | 69 / 219 | MCLACHLAN_DENTAL_CARIES_DN |
| 6 | 1e−36 | 71 / 255 | HELLER_SILENCED_BY_METHYLATION_UP |
| 7 | 2e−36 | 72 / 265 | WALLACE_PROSTATE_CANCER_RACE_UP |
| 8 | 3e−34 | 46 / 104 | ALTEMEIER_RESPONSE_TO_LPS_WITH_MECHANICAL_VENTILATION |
| 9 | 6e−33 | 72 / 297 | RUTELLA_RESPONSE_TO_CSF2RB_AND_IL4_DN |
| 10 | 7e−32 | 54 / 166 | VERHAAK_AML_WITH_NPM1_MUTATED_UP |
| 11 | 9e−32 | 77 / 354 | FULCHER_INFLAMMATORY_RESPONSE_LECTIN_VS_LPS_DN |
| 12 | 2e−31 | 66 / 261 | POOLA_INVASIVE_BREAST_CANCER_UP |
| 13 | 2e−30 | 61 / 229 | QI_PLASMACYTOMA_UP |
| 14 | 8e−29 | 39 / 90 | BASSO_CD40_SIGNALING_UP |
| 15 | 1e−28 | 73 / 354 | RODWELL_AGING_KIDNEY_UP |

## HM

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−36 | 58 / 166 | HALLMARK_INTERFERON_GAMMA_RESPONSE |
| 2 | 1e−27 | 53 / 190 | HALLMARK_TNFA_SIGNALING_VIA_NFKB |
| 3 | 4e−26 | 51 / 187 | HALLMARK_INFLAMMATORY_RESPONSE |
| 4 | 1e−25 | 49 / 176 | HALLMARK_ALLOGRAFT_REJECTION |
| 5 | 2e−17 | 40 / 178 | HALLMARK_COMPLEMENT |
| 6 | 2e−17 | 39 / 170 | HALLMARK_IL2_STAT5_SIGNALING |
| 7 | 3e−17 | 28 / 85 | HALLMARK_IL6_JAK_STAT3_SIGNALING |
| 8 | 8e−10 | 19 / 76 | HALLMARK_INTERFERON_ALPHA_RESPONSE |
| 9 | 9e−10 | 31 / 194 | HALLMARK_KRAS_SIGNALING_UP |
| 10 | 4e−09 | 26 / 150 | HALLMARK_APOPTOSIS |
| 11 | 1e−07 | 27 / 188 | HALLMARK_HYPOXIA |
| 12 | 4e−07 | 21 / 130 | HALLMARK_COAGULATION |
| 13 | 2e−05 | 23 / 191 | HALLMARK_P53_PATHWAY |
| 14 | 1e−03 | 9 / 59 | HALLMARK_CHOLESTEROL_HOMEOSTASIS |
| 15 | 6e−03 | 16 / 174 | HALLMARK_APICAL_JUNCTION |

## Immunome

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−10 | 13 / 32 | Angelova_immune−metagene−effector_memory_CD8 |
| 2 | 7e−10 | 18 / 67 | Angelova_immune−metagene−T−cells |
| 3 | 2e−09 | 12 / 29 | Angelova_immune−metagene−Th1 |
| 4 | 2e−08 | 13 / 42 | Angelova_immune−metagene−TGD |
| 5 | 5e−07 | 12 / 45 | Angelova_immune−metagene−MDSC |
| 6 | 9e−07 | 8 / 19 | Angelova_immune−metagene−iDC |
| 7 | 6e−05 | 4 / 6 | Immunity_immune−checkpoint−inhibitors |
| 8 | 9e−05 | 7 / 25 | Angelova_immune−metagene−DC |
| 9 | 1e−04 | 6 / 18 | Angelova_CRC_immunostimulators |
| 10 | 1e−04 | 4 / 7 | Angelova_immune−metagene−cytotoxic_cells |
| 11 | 7e−04 | 4 / 10 | Angelova_immune−metagene−TFH |
| 12 | 8e−04 | 5 / 17 | Angelova_immune−metagene−central_memory_CD8 |
| 13 | 2e−03 | 5 / 21 | Angelova_immune−metagene−central_memory_CD4 |
| 14 | 2e−03 | 4 / 13 | Angelova_immune−metagene−activated_B−cells |
| 15 | 3e−03 | 5 / 23 | Angelova_immune−metagene−Treg |

## Lifestyle

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 6e−06 | 6 / 12 | DUMEAUX_Women normal BMI literature genes up |
| 2 | 2e−05 | 6 / 14 | Huan_blood−pressure_SBP−signature |
| 3 | 4e−05 | 7 / 22 | DUMEAUX_High bmi enriched genes |
| 4 | 4e−04 | 4 / 9 | DUMEAUX_Monocytes in smokers literature genes up |
| 5 | 2e−03 | 4 / 13 | Huan_blood−pressure_DBP−signature |
| 6 | 4e−03 | 3 / 8 | Marjolein_ageing−genes_UP |
| 7 | 6e−03 | 2 / 3 | Huan_blood−pressure_HTN−signature |
| 8 | 2e−02 | 2 / 5 | DUMEAUX_Estrogen related in smokers literature genes up |
| 9 | 3e−02 | 16 / 210 | Homuth_BMI−associated−genes_DN |
| 10 | 7e−02 | 2 / 10 | DUMEAUX_Smoking literature genes up |
| 11 | 2e−01 | 3 / 32 | Marjolein_ageing−genes_DN |
| 12 | 3e−01 | 4 / 62 | DUMEAUX_Smoking enriched genes |
| 13 | 4e−01 | 8 / 150 | Homuth_BMI−associated−genes_UP |
| 14 | 1e+00 | 0 / 4 | DUMEAUX_Exercising non smoker literature enriched genes |
| 15 | 1e+00 | 0 / 7 | DUMEAUX_Estrogen related in non smokers literature genes up |

## Lymphoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−61 | 60 / 85 | Sha_DLBCL UP |
| 2 | 7e−29 | 52 / 173 | Victora_Light zone signature |
| 3 | 3e−28 | 46 / 135 | DAVE_BL−vs−DLBCL |
| 4 | 2e−25 | 31 / 62 | Monti_Host_response_cluster |
| 5 | 3e−23 | 51 / 213 | SPANG_IL21 DN |
| 6 | 8e−20 | 61 / 353 | SPANG_CD40 6hrs DN |
| 7 | 9e−17 | 345 / 5404 | HOPP_Strong_enhancer |
| 8 | 1e−16 | 99 / 906 | SPANG_BCR DN |
| 9 | 3e−14 | 14 / 22 | DAVE_NFkB BL DN |
| 10 | 2e−12 | 10 / 12 | BENTINK_mBL DOWN |
| 11 | 9e−12 | 50 / 378 | TARTE_Mature plasma cell signature |
| 12 | 4e−11 | 22 / 88 | ROSOLOWSKI_green UP |
| 13 | 2e−10 | 34 / 214 | LENZ_Stromal signature 1 |
| 14 | 8e−10 | 13 / 33 | Care_Extended T−cell |
| 15 | 2e−09 | 14 / 41 | ROSOLOWSKI_blue DOWN |

## Melanoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 5e−43 | 45 / 71 | Tirosh_Macrophage specific genes−melanoma |
| 2 | 7e−39 | 44 / 78 | Tirosh_expression higher in CAFs than in T−cells |
| 3 | 1e−26 | 36 / 83 | TCGA_melanoma_immune_high |
| 4 | 1e−17 | 19 / 33 | Tirosh_T−cell specific genes−melanoma |
| 5 | 1e−15 | 39 / 189 | Tirosh_genes preferentially expressed by Tregs |
| 6 | 4e−14 | 35 / 171 | Landsberg_dedifferentiation_up |
| 7 | 4e−10 | 23 / 107 | Tirosh_Exhaustion program in Mel75 |
| 8 | 1e−06 | 16 / 85 | Tirosh_AXL−signature |
| 9 | 2e−06 | 12 / 51 | Tirosh_genes from CD8 T−cells in Mel79−melanoma |
| 10 | 1e−05 | 23 / 185 | Tirosh_genes from malignant cells in Mel79−melanoma |
| 11 | 2e−05 | 4 / 5 | Joensson_Melanoma Proliferative subtype |
| 12 | 6e−05 | 23 / 204 | Landsberg_dedifferentiation_down |
| 13 | 7e−05 | 7 / 24 | Tirosh_exhuastion−associated genes consitent across tumors |
| 14 | 2e−03 | 21 / 230 | Gerber_wt/wt_melanoma−cells−SpotC |
| 15 | 4e−03 | 36 / 497 | Gerber_wt/wt_melanoma−cells−SpotD |

## MF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 9e−08 | 12 / 39 | chemokine activity |
| 2 | 3e−07 | 25 / 173 | cytokine activity |
| 3 | 6e−07 | 11 / 38 | cytokine receptor activity |
| 4 | 1e−06 | 8 / 20 | chemokine receptor activity |
| 5 | 2e−06 | 26 / 205 | receptor activity |
| 6 | 5e−06 | 9 / 30 | tumor necrosis factor receptor binding |
| 7 | 2e−05 | 53 / 644 | protein homodimerization activity |
| 8 | 5e−05 | 6 / 16 | CCR chemokine receptor binding |
| 9 | 7e−05 | 5 / 11 | MAP kinase tyrosine/serine/threonine phosphatase activity |
| 10 | 1e−04 | 6 / 19 | tumor necrosis factor−activated receptor activity |
| 11 | 2e−04 | 41 / 500 | signal transducer activity |
| 12 | 2e−04 | 18 / 154 | serine−type endopeptidase activity |
| 13 | 3e−04 | 7 / 29 | coreceptor activity |
| 14 | 3e−04 | 6 / 22 | peptide antigen binding |
| 15 | 4e−04 | 9 / 50 | amyloid−beta binding |

## miRNA target

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.002 | 6 / 29 | hsa−miR−647 |
| 2 | 0.016 | 4 / 22 | hsa−miR−941 |
| 3 | 0.019 | 8 / 74 | hsa−miR−595 |
| 4 | 0.042 | 7 / 71 | hsa−miR−188−3p |
| 5 | 0.046 | 3 / 18 | hsa−miR−1228 |
| 6 | 0.046 | 3 / 18 | hsa−miR−591 |
| 7 | 0.052 | 10 / 122 | hsa−miR−506 |
| 8 | 0.060 | 2 / 9 | hsa−miR−604 |
| 9 | 0.068 | 10 / 128 | hsa−miR−200b |
| 10 | 0.076 | 3 / 22 | hsa−miR−24−1* |
| 11 | 0.076 | 5 / 50 | hsa−miR−384 |
| 12 | 0.076 | 5 / 50 | hsa−miR−892a |
| 13 | 0.080 | 4 / 36 | hsa−miR−146b−3p |
| 14 | 0.101 | 2 / 12 | hsa−miR−191* |
| 15 | 0.109 | 9 / 123 | hsa−miR−429 |

## Pneumonia

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−14 | 21 / 56 | Burnham_sep_vs_con_DN |
| 2 | 1e−11 | 17 / 48 | Burnham_cap_fp_vs_con_DN |
| 3 | 2e−10 | 25 / 122 | Terre_IMS_influenza_meta_signature |
| 4 | 6e−09 | 15 / 52 | Burnham_day1_vs_5_DN |
| 5 | 2e−08 | 15 / 57 | Burnham_viral_UP |
| 6 | 3e−06 | 20 / 135 | Terre_MSV_multiple_respiratory_viruses_up |
| 7 | 8e−06 | 11 / 48 | Burnham_viral_DN |
| 8 | 3e−05 | 9 / 37 | Sweeney_viral_up |
| 9 | 1e−03 | 5 / 18 | Scicluna_UP |
| 10 | 4e−03 | 9 / 68 | Burnham_sep_vs_con_UP |
| 11 | 5e−03 | 9 / 71 | Burnham_cap_fp_vs_con_UP |
| 12 | 2e−02 | 5 / 33 | Sweeney_viral_dn |
| 13 | 4e−02 | 5 / 41 | Scicluna_DN |
| 14 | 1e−01 | 12 / 179 | Terre_MSV_multiple_respiratory_viruses_dn |
| 15 | 4e−01 | 3 / 54 | Burnham_timecourse |

## Reference Signatures

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−60 | 64 / 102 | WIRTH_EBV B−cells |
| 2 | 3e−19 | 32 / 99 | Chaussabel_1,5_Myeloid lineage |
| 3 | 5e−19 | 60 / 355 | WIRTH_Immune system |
| 4 | 6e−15 | 39 / 198 | Chaussabel_3,3_Inflammation II |
| 5 | 2e−14 | 39 / 204 | Chaussabel_3,2_Inflammation I |
| 6 | 4e−14 | 28 / 109 | Chaussabel_2,6_Myeloid lineage |
| 7 | 8e−12 | 33 / 182 | WIRTH_post GC B−cells |
| 8 | 1e−10 | 19 / 68 | Chaussabel_2,1_Cytotoxic cells |
| 9 | 2e−09 | 18 / 72 | Chaussabel_3,1_Interferon−inducible |
| 10 | 5e−09 | 16 / 59 | Chaussabel_2,10_Immune related cell surface molecules |
| 11 | 8e−06 | 45 / 496 | PROTEINATLAS_spleen |
| 12 | 1e−03 | 21 / 219 | WIRTH_GC B−cells |
| 13 | 7e−03 | 8 / 62 | VAQUERIZAS_Lung_TF |
| 14 | 1e−02 | 10 / 93 | Chaussabel_1,4_Replication |
| 15 | 2e−02 | 6 / 45 | VAQUERIZAS_Placenta_TF |

## Telomeres

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.4 | 2 / 27 | Nabetani_alt len telomeres_genes_ko |
| 2 | 1.0 | 0 / 13 | Alternative lengthening of telomeres |
| 3 | NA | 0 / 0 | |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## TF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−07 | 150 / 2254 | ICGC_BatfPcr1_targets |
| 2 | 5e−06 | 194 / 3213 | ICGC_Pu1_targets |
| 3 | 5e−06 | 112 / 1636 | ICGC_Bcl11_targets |
| 4 | 2e−05 | 201 / 3435 | ICGC_Ebfsc137065_targets |
| 5 | 6e−05 | 100 / 1508 | ICGC_Mef2_targets |
| 6 | 7e−04 | 117 / 1941 | ICGC_Bcl3_targets |
| 7 | 9e−04 | 127 / 2150 | ICGC_Irf4_targets |
| 8 | 3e−03 | 254 / 4851 | ICGC_Runx3_targets |
| 9 | 4e−03 | 66 / 1041 | ICGC_P300_targets |
| 10 | 4e−03 | 131 / 2321 | ICGC_Rad21_targets |
| 11 | 5e−03 | 89 / 1494 | ICGC_Cebpbsc150_targets |
| 12 | 7e−03 | 200 / 3778 | ICGC_Pol24_targets |
| 13 | 2e−02 | 153 / 2899 | ICGC_Nfatc1_targets |
| 14 | 4e−02 | 206 / 4072 | ICGC_Mta3_targets |
| 15 | 4e−02 | 193 / 3796 | ICGC_Nficsc81335_targets |

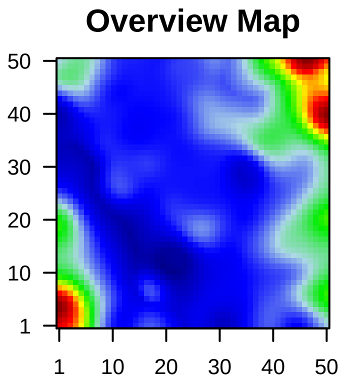
# Group Overexpression Sp

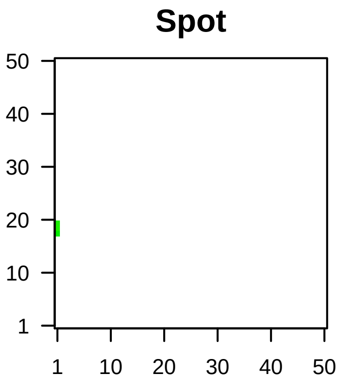
## Spot Summary: F

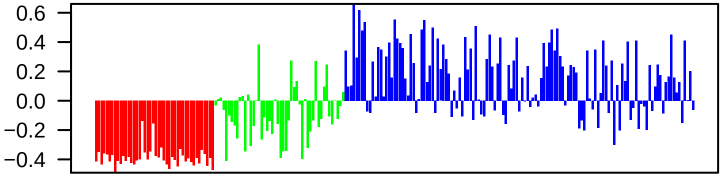
# metagenes = 3
# genes = 85

<r> metagenes = 0.99
<r> genes = 0.3
beta: r2= 9.25  /  log p= −Inf

# samples with spot = 62 ( 28.1 %)
intermediate : 4 ( 8.3 %)
non−mBL : 58 ( 45 %)


**Overview Map**


**Spot**

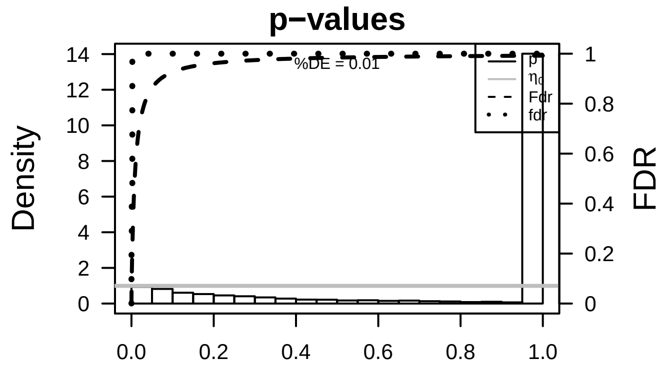


## Spot Genelist

| Rank | ID | max e | min e | r | Symbol | Description |
|---|---|---|---|---|---|---|
| 1 | 219836_at | 2.38 | −1.24 | 0.61 | ZBED2 | zinc finger BED−type containing 2 [Source:HGNC Symbol;Ac |
| 2 | 218186_at | 2.28 | −1.29 | 0.4 | RAB25 | RAB25, member RAS oncogene family [Source:HGNC Symb |
| 3 | 217523_at | 2.2 | −1.4 | 0.73 | CD44 | CD44 molecule (Indian blood group) [Source:HGNC Symbol; |
| 4 | 219255_x_at | 2.16 | −1.57 | 0.45 | IL17RB | interleukin 17 receptor B [Source:HGNC Symbol;Acc:HGNC: |
| 5 | 204086_at | 2.11 | −1.29 | 0.5 | PRAME | preferentially expressed antigen in melanoma [Source:HGNC |
| 6 | 204724_s_at | 2.01 | −1.6 | 0.37 | COL9A3 | collagen type IX alpha 3 chain [Source:HGNC Symbol;Acc:H |
| 7 | 202986_at | 1.95 | −0.86 | 0.63 | ARNT2 | aryl hydrocarbon receptor nuclear translocator 2 [Source:HG |
| 8 | 205987_at | 1.93 | −1.33 | 0.37 | CD1C | CD1c molecule [Source:HGNC Symbol;Acc:HGNC:1636] |
| 9 | 33197_at | 1.89 | −0.9 | 0.52 | MYO7A | myosin VIIA [Source:HGNC Symbol;Acc:HGNC:7606] |
| 10 | 219959_at | 1.84 | −0.95 | 0.59 | MOCOS | molybdenum cofactor sulfurase [Source:HGNC Symbol;Acc: |
| 11 | 205542_at | 1.83 | −1.05 | 0.48 | STEAP1 | STEAP family member 1 [Source:HGNC Symbol;Acc:HGNC: |
| 12 | 210753_s_at | 1.81 | −1.19 | 0.62 | EPHB1 | EPH receptor B1 [Source:HGNC Symbol;Acc:HGNC:3392] |
| 13 | 213385_at | 1.76 | −1.42 | 0.5 | CHN2 | chimerin 2 [Source:HGNC Symbol;Acc:HGNC:1944] |
| 14 | 222281_s_at | 1.76 | −1.97 | 0.73 | | |
| 15 | 206698_at | 1.73 | −1.34 | 0.64 | XK | X−linked Kx blood group [Source:HGNC Symbol;Acc:HGNC: |
| 16 | 220565_at | 1.72 | −1.38 | 0.64 | CCR10 | C−C motif chemokine receptor 10 [Source:HGNC Symbol;Ac |
| 17 | 217553_at | 1.7 | −0.92 | 0.48 | STEAP1B | STEAP family member 1B [Source:HGNC Symbol;Acc:HGN |
| 18 | 209094_at | 1.63 | −1.37 | 0.48 | DDAH1 | dimethylarginine dimethylaminohydrolase 1 [Source:HGNC S |
| 19 | 207433_at | 1.6 | −0.83 | 0.67 | IL10 | interleukin 10 [Source:HGNC Symbol;Acc:HGNC:5962] |
| 20 | 208189_s_at | 1.54 | −0.68 | 0.39 | MYO7A | myosin VIIA [Source:HGNC Symbol;Acc:HGNC:7606] |

## Geneset Overrepresentation

| Rank | p−value | #in/all | Geneset | |
|---|---|---|---|---|
| 1 | 7e−07 | 53 / 5404 | Lymp | HOPP_Strong_enhancer |
| 2 | 1e−06 | 9 / 182 | Refer | WIRTH_post GC B−cells |
| 3 | 2e−06 | 11 / 317 | Canc | SPANG_BCL6−index2 |
| 4 | 7e−06 | 8 / 173 | Lymp | Victora_Light zone signature |
| 5 | 1e−05 | 6 / 85 | Lymp | Aukema_BCL2 DN_BCL6 UP |
| 6 | 1e−05 | 6 / 87 | GSE | BOSCO_TH1_CYTOTOXIC_MODULE |
| 7 | 2e−05 | 7 / 139 | GSE | BROCKE_APOPTOSIS_REVERSED_BY_IL6 |
| 8 | 3e−05 | 5 / 63 | GSE | BOYLAN_MULTIPLE_MYELOMA_D_DN |
| 9 | 3e−05 | 8 / 213 | Lymp | SPANG_IL21 DN |
| 10 | 4e−05 | 3 / 12 | BP | leukocyte chemotaxis |
| 11 | 4e−05 | 3 / 12 | GSE | GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP |
| 12 | 4e−05 | 5 / 67 | Immu | Angelova_immune−metagene−T−cells |
| 13 | 7e−05 | 4 / 38 | GSE | CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP |
| 14 | 1e−04 | 8 / 249 | GSE | HUTTMANN_B_CLL_POOR_SURVIVAL_UP |
| 15 | 1e−04 | 5 / 85 | Lymp | Sha_DLBCL UP |
| 16 | 1e−04 | 3 / 18 | Lymp | WRIGHT_ABC UP |
| 17 | 2e−04 | 4 / 49 | GSE | GAURNIER_PSMD4_TARGETS |
| 18 | 2e−04 | 7 / 206 | GSE | KOYAMA_SEMA3B_TARGETS_UP |
| 19 | 5e−04 | 4 / 63 | GSE | RICKMAN_HEAD_AND_NECK_CANCER_A |
| 20 | 5e−04 | 8 / 321 | GSE | PHONG_TNF_RESPONSE_NOT_VIA_P38 |
| 21 | 8e−04 | 11 / 608 | GSE | SMID_BREAST_CANCER_BASAL_UP |
| 22 | 9e−04 | 4 / 73 | GSE | VANDESLUIS_COMMD1_TARGETS_GROUP_3_UP |
| 23 | 9e−04 | 9 / 434 | BP | negative regulation of apoptotic process |
| 24 | 1e−03 | 4 / 77 | GSE | KEGG_HEMATOPOIETIC_CELL_LINEAGE |
| 25 | 1e−03 | 9 / 447 | Gliom | ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN |
| 26 | 1e−03 | 4 / 80 | GSE | ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION |
| 27 | 1e−03 | 9 / 453 | GSE | ONDER_CDH1_TARGETS_2_DN |
| 28 | 1e−03 | 4 / 82 | Gliom | laffaire_hypermeth_LGG_vs_control |
| 29 | 1e−03 | 38 / 4261 | Lymp | HOPP_Txn_transition |
| 30 | 1e−03 | 7 / 290 | GSE | ODONNELL_TFRC_TARGETS_UP |
| 31 | 2e−03 | 4 / 85 | HM | HALLMARK_IL6_JAK_STAT3_SIGNALING |
| 32 | 2e−03 | 3 / 40 | GSE | WINTER_HYPOXIA_DN |
| 33 | 2e−03 | 2 / 11 | BP | negative regulation of nitric oxide biosynthetic process |
| 34 | 2e−03 | 9 / 480 | Canc | Lembcke_Colonic Inflammation |
| 35 | 2e−03 | 3 / 42 | GSE | PENG_GLUCOSE_DEPRIVATION_UP |
| 36 | 2e−03 | 4 / 90 | GSE | BASSO_CD40_SIGNALING_UP |
| 37 | 2e−03 | 13 / 902 | GSE | CHEN_METABOLIC_SYNDROM_NETWORK |
| 38 | 2e−03 | 13 / 906 | Lymp | SPANG_BCR DN |
| 39 | 2e−03 | 2 / 12 | BP | positive regulation of heterotypic cell−cell adhesion |
| 40 | 2e−03 | 2 / 12 | Lymp | BENTINK_mBL DOWN |


**p−values**

## Aging

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.2 | 1 / 47 | TESCHENDORFF_age_hypermethylated |
| 2 | 0.4 | 1 / 92 | HORVATH_aging_genes meth DOWN |
| 3 | 0.5 | 1 / 107 | HORVATH_aging_genes meth UP |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## BP

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−05 | 3 / 12 | leukocyte chemotaxis |
| 2 | 9e−04 | 9 / 434 | negative regulation of apoptotic process |
| 3 | 2e−03 | 2 / 11 | negative regulation of nitric oxide biosynthetic process |
| 4 | 2e−03 | 2 / 12 | positive regulation of heterotypic cell−cell adhesion |
| 5 | 3e−03 | 5 / 168 | regulation of gene expression |
| 6 | 3e−03 | 9 / 520 | positive regulation of transcription, DNA−templated |
| 7 | 3e−03 | 2 / 15 | skeletal muscle fiber development |
| 8 | 3e−03 | 3 / 52 | positive regulation of signal transduction |
| 9 | 4e−03 | 2 / 16 | defense response to protozoan |
| 10 | 4e−03 | 2 / 16 | N−glycan processing |
| 11 | 4e−03 | 2 / 16 | positive regulation of T cell differentiation |
| 12 | 4e−03 | 3 / 54 | phagocytosis |
| 13 | 4e−03 | 4 / 112 | regulation of cell shape |
| 14 | 6e−03 | 3 / 64 | negative regulation of inflammatory response |
| 15 | 7e−03 | 2 / 21 | negative regulation of interleukin−6 production |

## Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 2e−06 | 11 / 317 | SPANG_BCL6−index2 |
| 2 | 2e−03 | 9 / 480 | Lembcke_Colonic Inflammation |
| 3 | 5e−03 | 5 / 186 | SPANG_LPS−index2 |
| 4 | 1e−02 | 3 / 80 | PanCan_JAK−ST_geneset_nanostring |
| 5 | 7e−02 | 1 / 13 | BENTINK_e2f3.1 |
| 6 | 8e−02 | 1 / 14 | LIU_COMMON_CANCER_GENES |
| 7 | 2e−01 | 1 / 45 | KUIPER_MM poor survival |
| 8 | 3e−01 | 2 / 187 | PanCan_PI3K_geneset_nanostring |
| 9 | 4e−01 | 0 / 11 | LIU_PROSTATE_CANCER_UP |
| 10 | 4e−01 | 0 / 14 | LIU_PROSTATE_CANCER_DN |
| 11 | 4e−01 | 3 / 409 | Lembcke_Normal vs Adenoma |
| 12 | 4e−01 | 1 / 96 | PanCan_TXmisReg_geneset_nanostring |
| 13 | 1e+00 | 0 / 15 | RHODES_CANCER_META_SIGNATURE |
| 14 | 1e+00 | 0 / 15 | RHODES_UNDIFFERENTIATED_CANCER |
| 15 | 1e+00 | 0 / 16 | SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN |

## CC

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.003 | 3 / 48 | ficolin−1−rich granule membrane |
| 2 | 0.005 | 2 / 18 | phagocytic cup |
| 3 | 0.008 | 8 / 494 | endosome |
| 4 | 0.009 | 2 / 24 | stereocilium |
| 5 | 0.013 | 13 / 1128 | integral component of plasma membrane |
| 6 | 0.015 | 28 / 3270 | integral component of membrane |
| 7 | 0.015 | 41 / 5339 | membrane |
| 8 | 0.022 | 27 / 3210 | plasma membrane |
| 9 | 0.024 | 4 / 188 | endosome membrane |
| 10 | 0.032 | 3 / 118 | cytoplasmic vesicle membrane |
| 11 | 0.032 | 2 / 48 | microvillus |
| 12 | 0.038 | 2 / 53 | rough endoplasmic reticulum |
| 13 | 0.045 | 10 / 938 | Golgi apparatus |
| 14 | 0.046 | 4 / 231 | apical plasma membrane |
| 15 | 0.048 | 2 / 60 | tertiary granule membrane |

## Chr

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.007 | 7 / 382 | Chr 15 |
| 2 | 0.082 | 12 / 1325 | Chr 1 |
| 3 | 0.126 | 6 / 585 | Chr 7 |
| 4 | 0.278 | 6 / 756 | Chr 11 |
| 5 | 0.358 | 6 / 833 | Chr 19 |
| 6 | 0.375 | 5 / 689 | Chr 3 |
| 7 | 0.552 | 4 / 669 | Chr 6 |
| 8 | 0.558 | 1 / 139 | Chr 21 |
| 9 | 0.582 | 2 / 333 | Chr 22 |
| 10 | 0.635 | 3 / 556 | Chr X |
| 11 | 0.639 | 2 / 369 | Chr 20 |
| 12 | 0.662 | 1 / 184 | Chr 18 |
| 13 | 0.671 | 4 / 776 | Chr 17 |
| 14 | 0.686 | 2 / 403 | Chr 14 |
| 15 | 0.723 | 4 / 832 | Chr 2 |

## Chromatin states

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 3e−09 | 16 / 432 | monocytes peripheral blood_3_TxFlnk |
| 2 | 3e−08 | 31 / 1930 | Fetal_TssA |
| 3 | 2e−06 | 16 / 693 | Bcells peripheral blood_3_TxFlnk |
| 4 | 2e−06 | 37 / 3110 | 14_ReprPCWk_ESC_Endoderm |
| 5 | 2e−06 | 31 / 2327 | 14_ReprPCWk_ESC_Mesoderm |
| 6 | 3e−06 | 34 / 2724 | Tcells peripheral blood_11_BivFlnk |
| 7 | 3e−06 | 15 / 626 | natural killer cells peripheral blood_3_TxFlnk |
| 8 | 4e−06 | 25 / 1649 | 13_ReprPC_ESC_Mesoderm |
| 9 | 4e−06 | 32 / 2507 | Mid_Frontal_Lobe_ReprPC |
| 10 | 7e−06 | 35 / 2972 | 13_ReprPC_ESC_Endoderm |
| 11 | 7e−06 | 20 / 1161 | Overlap_fetal_midbrain_TssF |
| 12 | 9e−06 | 24 / 1611 | natural killer cells peripheral blood_11_BivFlnk |
| 13 | 1e−05 | 64 / 7943 | Enh_Colon |
| 14 | 1e−05 | 40 / 3767 | Bcells peripheral blood_6_EnhG |
| 15 | 1e−05 | 29 / 2269 | 9_ReprPCWk_Neuronal_Progenitor |

## Colon Cancer

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.007 | 9 / 589 | Lembcke_TCGA−expr_kmeans_E_CIMP.H_UP_Cluster4_DN |
| 2 | 0.010 | 11 / 848 | LaPointe_mucosa−position_kmeans_O_transverse colon_UP_ |
| 3 | 0.013 | 8 / 539 | Lembcke_TCGA_meth_kmeans_L_CIMP.H_DN |
| 4 | 0.016 | 7 / 452 | Lembcke_TCGA−expr_kmeans_L_CIMP.H_UP_Cluster4_DN |
| 5 | 0.018 | 4 / 172 | Pentrack_CRC_TCGA_corr_U_msi−h_UP |
| 6 | 0.046 | 1 / 8 | Marisa_CRC−C3 |
| 7 | 0.062 | 6 / 483 | Lembcke_TCGA−expr_kmeans_H_CIMP.H_UP_Cluster3_DN |
| 8 | 0.087 | 4 / 288 | Pentrack_CRC_TCGA_corr_J_msi−h_UP_mss_DN |
| 9 | 0.095 | 4 / 297 | Pentrack_CRC_TCGA_group.over_B_msi−h_UP |
| 10 | 0.166 | 1 / 31 | Kosinski_lower−crypt−short−list |
| 11 | 0.200 | 1 / 38 | Marisa_CRC−cluster−e |
| 12 | 0.230 | 7 / 854 | LaPointe_mucosa−position_kmeans_A_ascending colon_UP_ |
| 13 | 0.238 | 9 / 1166 | LaPointe_mucosa−position_kmeans_K_transverse colon_UP_cecum colon_a |
| 14 | 0.283 | 3 / 318 | Lembcke_TCGA_meth_kmeans_E_CIMP.H_UP_ |
| 15 | 0.291 | 2 / 184 | Kosinski_lower−crypt−long−list |

## Glioma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.001 | 9 / 447 | ScoV_0.999_Sturm_E4_Mesenchymal_RTK I 'PDGFRA'_DN |
| 2 | 0.001 | 4 / 82 | laffaire_hypermeth_LGG_vs_control |
| 3 | 0.003 | 2 / 14 | Donson−chemokines/cytokines−associated with LTS in HGA |
| 4 | 0.017 | 1 / 3 | laffaire_hypometh_LGG_vs_control |
| 5 | 0.020 | 5 / 269 | ScoV_0.5_Sturm_C3_Mesenchymal_DN |
| 6 | 0.028 | 2 / 45 | Donson−innate immunity−associated with LTS in HGA |
| 7 | 0.029 | 3 / 114 | Christensen_hypermethylated_in_grade2_oligoastrocytoma |
| 8 | 0.033 | 2 / 49 | OPC |
| 9 | 0.034 | 2 / 50 | Christensen_hypomethylated_in_primary_glioblastoma |
| 10 | 0.040 | 1 / 7 | KIM_epithelial−mesenchymal−transition related genes_decreased expression |
| 11 | 0.040 | 1 / 7 | oligodendrocytes_glio |
| 12 | 0.042 | 3 / 132 | Christensen_hypermethylated_in_grade3_oligoastrocytoma |
| 13 | 0.049 | 2 / 61 | Christensen_hypomethylated_in_secondary_glioblastoma |
| 14 | 0.052 | 3 / 144 | Christensen_hypermethylated_in_grade2_oligodendroglioma |
| 15 | 0.071 | 4 / 268 | ScoV_0.001_Sturm_M2_Mesenchymal_RTK I 'PDGFRA'_DN |

## GSEA C2

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−05 | 6 / 87 | BOSCO_TH1_CYTOTOXIC_MODULE |
| 2 | 2e−05 | 7 / 139 | BROCKE_APOPTOSIS_REVERSED_BY_IL6 |
| 3 | 3e−05 | 5 / 63 | BOYLAN_MULTIPLE_MYELOMA_D_DN |
| 4 | 4e−05 | 3 / 12 | GUTIERREZ_CHRONIC_LYMPHOCYTIC_LEUKEMIA_UP |
| 5 | 7e−05 | 4 / 38 | CROONQUIST_NRAS_VS_STROMAL_STIMULATION_UP |
| 6 | 1e−04 | 8 / 249 | HUTTMANN_B_CLL_POOR_SURVIVAL_UP |
| 7 | 2e−04 | 4 / 49 | GAURNIER_PSMD4_TARGETS |
| 8 | 2e−04 | 7 / 206 | KOYAMA_SEMA3B_TARGETS_UP |
| 9 | 5e−04 | 4 / 63 | RICKMAN_HEAD_AND_NECK_CANCER_A |
| 10 | 5e−04 | 8 / 321 | PHONG_TNF_RESPONSE_NOT_VIA_P38 |
| 11 | 8e−04 | 11 / 608 | SMID_BREAST_CANCER_BASAL_UP |
| 12 | 9e−04 | 4 / 73 | VANDESLUIS_COMMD1_TARGETS_GROUP_3_UP |
| 13 | 1e−03 | 4 / 77 | KEGG_HEMATOPOIETIC_CELL_LINEAGE |
| 14 | 1e−03 | 4 / 80 | ZHANG_TARGETS_OF_EWSR1_FLI1_FUSION |
| 15 | 1e−03 | 9 / 453 | ONDER_CDH1_TARGETS_2_DN |

## HM

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.002 | 4 / 85 | HALLMARK_IL6_JAK_STAT3_SIGNALING |
| 2 | 0.004 | 5 / 176 | HALLMARK_ALLOGRAFT_REJECTION |
| 3 | 0.026 | 4 / 193 | HALLMARK_HEME_METABOLISM |
| 4 | 0.027 | 4 / 194 | HALLMARK_ESTROGEN_RESPONSE_EARLY |
| 5 | 0.027 | 2 / 44 | HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY |
| 6 | 0.073 | 2 / 76 | HALLMARK_INTERFERON_ALPHA_RESPONSE |
| 7 | 0.077 | 3 / 170 | HALLMARK_IL2_STAT5_SIGNALING |
| 8 | 0.099 | 3 / 190 | HALLMARK_TNFA_SIGNALING_VIA_NFKB |
| 9 | 0.103 | 3 / 193 | HALLMARK_ESTROGEN_RESPONSE_LATE |
| 10 | 0.104 | 3 / 194 | HALLMARK_KRAS_SIGNALING_UP |
| 11 | 0.252 | 2 / 166 | HALLMARK_INTERFERON_GAMMA_RESPONSE |
| 12 | 0.292 | 1 / 59 | HALLMARK_CHOLESTEROL_HOMEOSTASIS |
| 13 | 0.315 | 2 / 195 | HALLMARK_G2M_CHECKPOINT |
| 14 | 0.512 | 1 / 122 | HALLMARK_SPERMATOGENESIS |
| 15 | 0.558 | 1 / 139 | HALLMARK_FATTY_ACID_METABOLISM |

## Immunome

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 4e−05 | 5 / 67 | Angelova_immune−metagene−T−cells |
| 2 | 1e−02 | 2 / 29 | Angelova_immune−metagene−Th1 |
| 3 | 6e−02 | 1 / 10 | Angelova_CRC_immonoinhibitors |
| 4 | 6e−02 | 1 / 11 | Angelova_immune−metagene−macrophages |
| 5 | 7e−02 | 1 / 13 | Angelova_immune−metagene−activated_B−cells |
| 6 | 9e−02 | 1 / 16 | Angelova_immune−metagene−Th17 |
| 7 | 2e−01 | 1 / 45 | Angelova_immune−metagene−MDSC |
| 8 | 1e+00 | 0 / 26 | Angelova_immune−metagene−activated_CD4 |
| 9 | 1e+00 | 0 / 19 | Angelova_immune−metagene−activated_CD8 |
| 10 | 1e+00 | 0 / 21 | Angelova_immune−metagene−central_memory_CD4 |
| 11 | 1e+00 | 0 / 17 | Angelova_immune−metagene−central_memory_CD8 |
| 12 | 1e+00 | 0 / 7 | Angelova_immune−metagene−cytotoxic_cells |
| 13 | 1e+00 | 0 / 25 | Angelova_immune−metagene−DC |
| 14 | 1e+00 | 0 / 12 | Angelova_immune−metagene−effector_memory_CD4 |
| 15 | 1e+00 | 0 / 32 | Angelova_immune−metagene−effector_memory_CD8 |

## Lifestyle

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.1 | 1 / 22 | DUMEAUX_High bmi enriched genes |
| 2 | 1.0 | 0 / 62 | DUMEAUX_Smoking enriched genes |
| 3 | 1.0 | 0 / 10 | DUMEAUX_Smoking literature genes up |
| 4 | 1.0 | 0 / 4 | DUMEAUX_Exercising non smoker literature enriched genes |
| 5 | 1.0 | 0 / 5 | DUMEAUX_Estrogen related in smokers literature genes up |
| 6 | 1.0 | 0 / 7 | DUMEAUX_Estrogen related in non smokers literature genes up |
| 7 | 1.0 | 0 / 7 | DUMEAUX_Hormon therapy  in non smokers literature genes up |
| 8 | 1.0 | 0 / 9 | DUMEAUX_Monocytes in smokers literature genes up |
| 9 | 1.0 | 0 / 16 | DUMEAUX_Red blood cells in non smokers literature genes up |
| 10 | 1.0 | 0 / 12 | DUMEAUX_Women normal BMI literature genes up |
| 11 | 1.0 | 0 / 22 | DUMEAUX_Fasting enriched genes |
| 12 | 1.0 | 0 / 150 | Homuth_BMI−associated−genes_UP |
| 13 | 1.0 | 0 / 210 | Homuth_BMI−associated−genes_DN |
| 14 | 1.0 | 0 / 14 | Huan_blood−pressure_SBP−signature |
| 15 | 1.0 | 0 / 13 | Huan_blood−pressure_DBP−signature |

## Lymphnoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 7e−07 | 53 / 5404 | HOPP_Strong_enhancer |
| 2 | 7e−06 | 8 / 173 | Victora_Light zone signature |
| 3 | 1e−05 | 6 / 85 | Aukema_BCL2 DN_BCL6 UP |
| 4 | 3e−05 | 8 / 213 | SPANG_IL21 DN |
| 5 | 1e−04 | 5 / 85 | Sha_DLBCL UP |
| 6 | 1e−04 | 3 / 18 | WRIGHT_ABC UP |
| 7 | 1e−03 | 38 / 4261 | HOPP_Txn_transition |
| 8 | 2e−03 | 13 / 906 | SPANG_BCR DN |
| 9 | 2e−03 | 2 / 12 | BENTINK_mBL DOWN |
| 10 | 2e−03 | 6 / 234 | Hopp_Lymphoma_Epi1_no_zentr_6_MCL_DN |
| 11 | 3e−03 | 2 / 15 | Subero_T−ALL_hypo_meth |
| 12 | 4e−03 | 7 / 353 | SPANG_CD40 6hrs DN |
| 13 | 8e−03 | 4 / 135 | DAVE_BL−vs−DLBCL |
| 14 | 2e−02 | 18 / 1894 | HOPP_Poised_promoter |
| 15 | 2e−02 | 1 / 4 | MASCQUE_mBL DOWN |

## Melanoma

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.009 | 2 / 24 | Tirosh_B−cell specific genes−melanoma |
| 2 | 0.022 | 2 / 39 | Tirosh_melanoma specific genes |
| 3 | 0.055 | 2 / 65 | Harbst_melanoma_highgrade_up |
| 4 | 0.089 | 1 / 16 | Hugo_melanoma−all−LEF1_UP |
| 5 | 0.098 | 3 / 189 | Tirosh_genes preferentially expressed by Tregs |
| 6 | 0.131 | 1 / 24 | Tirosh_exhuastion−associated genes consitent across tumors |
| 7 | 0.151 | 3 / 230 | Gerber_wt/wt_melanoma−cells−SpotC |
| 8 | 0.195 | 1 / 37 | Hugo_melanoma−all−MET_DN |
| 9 | 0.204 | 1 / 39 | Tirosh_top50 correlated genes PC4 |
| 10 | 0.214 | 1 / 41 | Tirosh_top50 correlated genes PC3 |
| 11 | 0.236 | 1 / 46 | Tirosh_top50 correlated genes PC5 |
| 12 | 0.263 | 2 / 171 | Landsberg_dedifferentiation_up |
| 13 | 0.313 | 1 / 64 | Harbst_melanoma_lowgrade_up |
| 14 | 0.334 | 2 / 204 | Landsberg_dedifferentiation_down |
| 15 | 0.367 | 1 / 78 | Tirosh_expression higher in CAFs than in T−cells |

## MF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.002 | 3 / 46 | SH3/SH2 adaptor activity |
| 2 | 0.006 | 4 / 125 | transcriptional activator activity, RNA polymerase II transcription regulatory re |
| 3 | 0.008 | 3 / 69 | ATPase binding |
| 4 | 0.018 | 4 / 173 | cytokine activity |
| 5 | 0.019 | 3 / 96 | SH3 domain binding |
| 6 | 0.021 | 2 / 38 | cytokine receptor activity |
| 7 | 0.022 | 4 / 182 | RNA polymerase II regulatory region sequence−specific DNA binding |
| 8 | 0.030 | 4 / 202 | GTPase activator activity |
| 9 | 0.035 | 3 / 123 | transporter activity |
| 10 | 0.049 | 3 / 141 | growth factor activity |
| 11 | 0.051 | 2 / 62 | transcription factor activity, RNA polymerase II distal enhancer sequence−spe |
| 12 | 0.057 | 1 / 10 | lipopeptide binding |
| 13 | 0.057 | 1 / 10 | monocarboxylic acid transmembrane transporter activity |
| 14 | 0.058 | 2 / 67 | drug binding |
| 15 | 0.062 | 1 / 11 | C−C chemokine receptor activity |

## miRNA target

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.004 | 3 / 55 | hsa−miR−140−3p |
| 2 | 0.010 | 2 / 26 | hsa−miR−1292 |
| 3 | 0.018 | 2 / 35 | hsa−miR−331−5p |
| 4 | 0.021 | 2 / 38 | hsa−miR−658 |
| 5 | 0.027 | 2 / 44 | hsa−miR−552 |
| 6 | 0.034 | 2 / 50 | hsa−miR−219−5p |
| 7 | 0.034 | 1 / 6 | hsa−miR−523 |
| 8 | 0.046 | 2 / 59 | hsa−miR−643 |
| 9 | 0.051 | 2 / 62 | hsa−miR−578 |
| 10 | 0.051 | 2 / 62 | hsa−miR−205 |
| 11 | 0.051 | 1 / 9 | hsa−miR−887 |
| 12 | 0.062 | 1 / 11 | hsa−miR−744 |
| 13 | 0.074 | 2 / 77 | hsa−miR−362−5p |
| 14 | 0.076 | 2 / 78 | hsa−miR−125a−3p |
| 15 | 0.084 | 1 / 15 | hsa−miR−542−5p |

## Pneumonia

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.2 | 2 / 135 | Terre_MSV_multiple_respiratory_viruses_up |
| 2 | 0.2 | 1 / 41 | Scicluna_DN |
| 3 | 0.3 | 1 / 52 | Burnham_day1_vs_5_DN |
| 4 | 0.3 | 1 / 54 | Burnham_timecourse |
| 5 | 0.3 | 1 / 57 | Burnham_viral_UP |
| 6 | 0.5 | 1 / 122 | Terre_IMS_influenza_meta_signature |
| 7 | 1.0 | 0 / 68 | Burnham_sep_vs_con_UP |
| 8 | 1.0 | 0 / 56 | Burnham_sep_vs_con_DN |
| 9 | 1.0 | 0 / 48 | Burnham_cap_fp_vs_con_DN |
| 10 | 1.0 | 0 / 71 | Burnham_cap_fp_vs_con_UP |
| 11 | 1.0 | 0 / 48 | Burnham_viral_DN |
| 12 | 1.0 | 0 / 57 | Burnham_day1_vs_5_UP |
| 13 | 1.0 | 0 / 18 | Scicluna_UP |
| 14 | 1.0 | 0 / 37 | Sweeney_viral_up |
| 15 | 1.0 | 0 / 33 | Sweeney_viral_dn |

## Reference Signatures

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1e−06 | 9 / 182 | WIRTH_post GC B−cells |
| 2 | 2e−02 | 6 / 352 | WIRTH_Nervous System |
| 3 | 2e−02 | 6 / 355 | WIRTH_Immune system |
| 4 | 2e−02 | 2 / 42 | Chaussabel_1,3_B−cells |
| 5 | 4e−02 | 4 / 218 | WIRTH_pre+post GC B−cells |
| 6 | 7e−02 | 1 / 12 | VAQUERIZAS_Kidney_TF |
| 7 | 9e−02 | 1 / 16 | VAQUERIZAS_Fetal liver_TF |
| 8 | 9e−02 | 1 / 16 | VAQUERIZAS_Salivary gland_TF |
| 9 | 1e−01 | 1 / 21 | VAQUERIZAS_Tonsil_TF |
| 10 | 1e−01 | 3 / 204 | Chaussabel_3,2_Inflammation I |
| 11 | 1e−01 | 1 / 22 | VAQUERIZAS_Trachea_TF |
| 12 | 1e−01 | 1 / 24 | VAQUERIZAS_Spinal cord_TF |
| 13 | 1e−01 | 2 / 109 | Chaussabel_2,6_Myeloid lineage |
| 14 | 1e−01 | 3 / 219 | WIRTH_GC B−cells |
| 15 | 2e−01 | 1 / 30 | VAQUERIZAS_Smooth muscle_TF |

## Telomeres

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 1 | 0 / 13 | Alternative lengthening of telomeres |
| 2 | 1 | 0 / 27 | Nabetani_alt len telomeres_genes_ko |
| 3 | NA | 0 / 0 | |
| 4 | NA | 0 / 0 | |
| 5 | NA | 0 / 0 | |
| 6 | NA | 0 / 0 | |
| 7 | NA | 0 / 0 | |
| 8 | NA | 0 / 0 | |
| 9 | NA | 0 / 0 | |
| 10 | NA | 0 / 0 | |
| 11 | NA | 0 / 0 | |
| 12 | NA | 0 / 0 | |
| 13 | NA | 0 / 0 | |
| 14 | NA | 0 / 0 | |
| 15 | NA | 0 / 0 | |

## TF

| Rank | p−value | #in/all | Geneset |
|---|---|---|---|
| 1 | 0.05 | 17 / 1941 | ICGC_Bcl3_targets |
| 2 | 0.08 | 10 / 1041 | ICGC_P300_targets |
| 3 | 0.10 | 18 / 2254 | ICGC_BatfPcr1_targets |
| 4 | 0.11 | 12 / 1387 | HEBENSTREIT_high expression TF |
| 5 | 0.24 | 12 / 1636 | ICGC_Bcl11_targets |
| 6 | 0.26 | 11 / 1508 | ICGC_Mef2_targets |
| 7 | 0.36 | 4 / 522 | ICGC_SrfPcr2_targets |
| 8 | 0.43 | 18 / 2899 | ICGC_Nfatc1_targets |
| 9 | 0.49 | 18 / 2994 | ICGC_Zeb1_targets |
| 10 | 0.51 | 9 / 1494 | ICGC_Cebpbsc150_targets |
| 11 | 0.61 | 13 / 2321 | ICGC_Rad21_targets |
| 12 | 0.62 | 9 / 1630 | ICGC_SrfV0416101_targets |
| 13 | 0.66 | 21 / 3796 | ICGC_Nficsc81335_targets |
| 14 | 0.66 | 24 / 4319 | ICGC_Pou2_targets |
| 15 | 0.66 | 19 / 3451 | ICGC_Atf2_targets |