

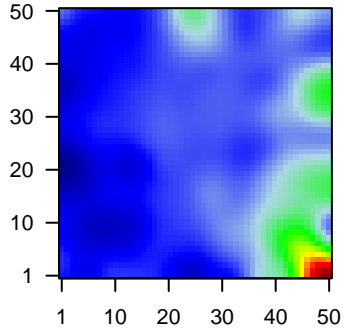
# GW\_062

## Global Summary

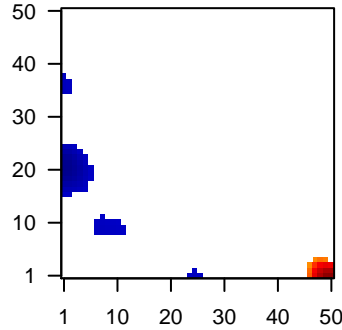
%DE = 0.14  
 # genes with fdr < 0.2 = 1747 ( 1036 + / 711 - )  
 # genes with fdr < 0.1 = 1428 ( 879 + / 549 - )  
 # genes with fdr < 0.05 = 1062 ( 691 + / 371 - )  
 # genes with fdr < 0.01 = 802 ( 558 + / 244 - )  
 # genes in genesets = 16332

<FC> = 0  
 <shrinkage-t> = 0  
 <p-value> = 0.11  
 <fdr> = 0.86

Profile



Regulated Spots



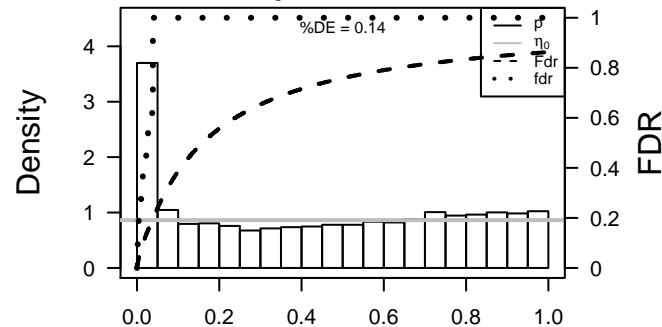
## Global Genelist

| Rank | ID     | log(FC) | fdr p-value | Description | Metagene   |
|------|--------|---------|-------------|-------------|--|
| 1    | 25890  | 1.19    | 2e-16 4e-14 | 50 x 4      | ABI family, member 3 (NESH) binding protein [Source:HGNC     |
| 2    | 31     | 1.18    | 2e-16 4e-14 | 12 x 50     | acetyl-CoA carboxylase alpha [Source:HGNC Symbol;Acc:84      |
| 3    | 27299  | 1.25    | 2e-16 4e-14 | 49 x 1      | ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]          |
| 4    | 8644   | 2.07    | 2e-16 4e-14 | 1 x 50      | aldo-keto reductase family 1, member C3 [Source:HGNC Sym     |
| 5    | 1109   | 1.4     | 2e-16 4e-14 | 13 x 50     | aldo-keto reductase family 1, member C4 [Source:HGNC Sym     |
| 6    | 216    | 1.21    | 2e-16 4e-14 | 50 x 50     | aldehyde dehydrogenase 1 family, member A1 [Source:HGNC      |
| 7    | 401138 | 2.13    | 2e-16 4e-14 | 1 x 5       | amelotin [Source:HGNC Symbol;Acc:33188]                      |
| 8    | 55107  | 1.87    | 2e-16 4e-14 | 1 x 5       | anoctamin 1, calcium activated chloride channel [Source:HG   |
| 9    | 9459   | 1.24    | 2e-16 4e-14 | 50 x 1      | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou    |
| 10   | 25805  | 1.15    | 2e-16 4e-14 | 8 x 1       | BMP and activin membrane-bound inhibitor [Source:HGNC S      |
| 11   | 144809 | 1.15    | 2e-16 4e-14 | 45 x 8      | family with sequence similarity 216, member B [Source:HGNC   |
| 12   | 92747  | -1.23   | 2e-16 4e-14 | 50 x 10     | BPI fold containing family B, member 1 [Source:HGNC Symb     |
| 13   | 260436 | 2.71    | 2e-16 4e-14 | 50 x 1      | follicular dendritic cell secreted protein [Source:HGNC Symb |
| 14   | 79783  | 1.45    | 2e-16 4e-14 | 1 x 5       | succinyl-CoA:glutarate-CoA transferase [Source:HGNC Symb     |
| 15   | 57172  | 1.57    | 2e-16 4e-14 | 49 x 1      | calcium/calmodulin-dependent protein kinase IG [Source:HG    |
| 16   | 55832  | 1.39    | 2e-16 4e-14 | 47 x 50     | cullin-associated and neddylation-dissociated 1 [Source:HGI  |
| 17   | 131076 | 1.19    | 2e-16 4e-14 | 1 x 16      | coiled-coil domain containing 58 [Source:HGNC Symbol;Acc     |
| 18   | 6363   | 1.82    | 2e-16 4e-14 | 50 x 1      | chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc      |
| 19   | 6366   | 1.69    | 2e-16 4e-14 | 50 x 2      | chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc      |
| 20   | 1236   | 1.3     | 2e-16 4e-14 | 50 x 1      | chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac      |

## Global Geneset Analysis

| Rank                  | GSZ   | p-value | #all | Geneset  |
|-----------------------|-------|---------|------|--|
| <i>Overexpressed</i>  |       |         |      |  |
| 1                     | 23.07 | NULL    | 417  | H.Tiss WIRTH_Immune system                             |
| 2                     | 19.15 | NULL    | 553  | Cancer Lembcke_Colonc Inflammation                     |
| 3                     | 9.98  | NULL    | 6    | GSEA C27ARMER_BREAST_CANCER_CLUSTER_8                  |
| 4                     | 9.82  | NULL    | 316  | Cancer SPANG_BCL6-index2                               |
| 5                     | 8.9   | NULL    | 327  | Lymphoma SPANG_CD40 6hrs UP                            |
| 6                     | 8.71  | NULL    | 28   | BP B cell receptor signaling pathway                   |
| 7                     | 8.64  | NULL    | 312  | BP immune response                                     |
| 8                     | 8.41  | NULL    | 13   | Cancer GENTLES_modul18                                 |
| 9                     | 8.26  | NULL    | 16   | GSEA C25U_THYMUS                                       |
| 10                    | 8.13  | NULL    | 162  | CC external side of plasma membrane                    |
| 11                    | 7.81  | NULL    | 60   | BP T cell costimulation                                |
| 12                    | 7.72  | NULL    | 5    | GSEA C2WONG_ENDOMETRIAL_CANCER_LATE                    |
| 13                    | 7.68  | NULL    | 28   | BP B cell activation                                   |
| 14                    | 7.65  | NULL    | 265  | Glio wilscher_GBM_Verhaak-CL_expression_B_up           |
| 15                    | 7.65  | NULL    | 265  | Glio wilscher_GBM_Verhaak-MES_expression_B_up          |
| 16                    | 7.65  | NULL    | 265  | Glio wilscher_GBM_Verhaak-PNwt_expression_B_down       |
| 17                    | 7.65  | NULL    | 265  | Glio wilscher_GBM_Verhaak-PNmut_expression_B_down      |
| 18                    | 7.47  | NULL    | 12   | BP dendritic cell chemotaxis                           |
| 19                    | 7.4   | NULL    | 11   | GSEA C2BIOCARTA_THELPER_PATHWAY                        |
| 20                    | 7.3   | NULL    | 15   | CC MHC class II protein complex                        |
| <i>Underexpressed</i> |       |         |      |  |
| 1                     | -7.13 | NULL    | 1135 | Chr Chr 19   |
| 2                     | -6.25 | NULL    | 127  | H.Tiss WIRTH_Muscle                                    |
| 3                     | -5.55 | NULL    | 633  | Chr Chr 9  |
| 4                     | -4.9  | NULL    | 36   | BP muscle filament sliding                             |
| 5                     | -4.77 | NULL    | 84   | BP muscle contraction                                  |
| 6                     | -4.76 | NULL    | 16   | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F                  |
| 7                     | -4.7  | NULL    | 1318 | CC mitochondrion                                       |
| 8                     | -4.7  | NULL    | 16   | GSEA C2HARRIS_HYPOXIA                                  |
| 9                     | -4.67 | NULL    | 59   | Lymphoma ENZ_Stromal signature 2                       |
| 10                    | -4.49 | NULL    | 15   | GSEA C2BECKER_TAMOXIFEN_RESISTANCE_UP                  |
| 11                    | -4.34 | NULL    | 13   | GSEA C2REACTOME_REGULATION_OF_INSULIN_LIKE_GROWTH_FACT |
| 12                    | -4.33 | NULL    | 10   | GSEA C2BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX          |
| 13                    | -4.28 | NULL    | 15   | GSEA C2KRIGE_AMINO_ACID_DEPRIVATION                    |
| 14                    | -4.19 | NULL    | 9    | GSEA C2SATO_SILENCED_BY_METHYLATION_IN_PANCREATIC_CANC |
| 15                    | -4.12 | NULL    | 16   | GSEA C2JROSEVIC_RESPONSE_TO_IMIQUMOD                   |
| 16                    | -4.11 | NULL    | 44   | MF structural constituent of muscle                    |
| 17                    | -3.98 | NULL    | 13   | GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN            |
| 18                    | -3.95 | NULL    | 957  | Chr Chr 11   |
| 19                    | -3.93 | NULL    | 13   | GSEA C2BIOCARTA_AMI_PATHWAY                            |
| 20                    | -3.92 | NULL    | 16   | GSEA C2AMIT_EGF_RESPONSE_480_MCF10A                    |

p-values



# GW\_062

## Local Summary

%DE = 0.93  
 # metagenes = 18  
 # genes = 276  
 # genes in genesets = 274

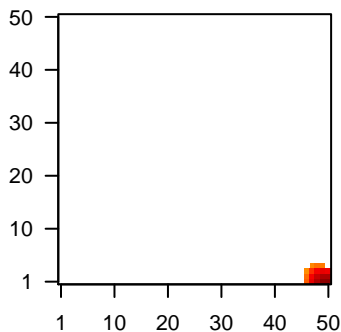
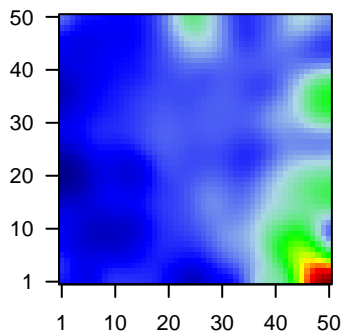
# genes with  $fdr < 0.1 = 250$  ( 250 + / 0 - )  
 # genes with  $fdr < 0.05 = 250$  ( 250 + / 0 - )  
 # genes with  $fdr < 0.01 = 220$  ( 220 + / 0 - )

<r> metagenes = 0.99  
 <r> genes = 0.61

<FC> = 0.7  
 <shrinkage-t> = 24.52  
 <p-value> = 0  
 <fdr> = 0.17

Profile

Spot



## Local Genelist

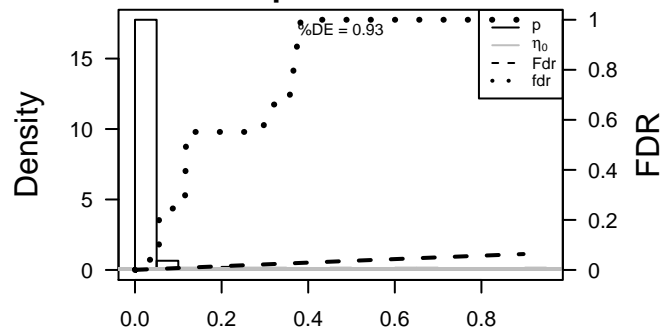
| Rank | ID     | log(FC) | fdr   | p-value | Description   |
|------|--------|---------|-------|---------|---|
| 1    | 27299  | 1.25    | 2e-16 | 1e-16   | 49 x 1 ADAM-like, decysin 1 [Source:HGNC Symbol;Acc:16299]            |
| 2    | 9459   | 1.24    | 2e-16 | 1e-16   | 50 x 1 Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 [Sou      |
| 3    | 260436 | 2.71    | 2e-16 | 1e-16   | 50 x 1 follicular dendritic cell secreted protein [Source:HGNC Symbc  |
| 4    | 57172  | 1.57    | 2e-16 | 1e-16   | 49 x 1 calcium/calmodulin-dependent protein kinase IG [Source:HG      |
| 5    | 6363   | 1.82    | 2e-16 | 1e-16   | 50 x 1 chemokine (C-C motif) ligand 19 [Source:HGNC Symbol;Acc        |
| 6    | 6366   | 1.69    | 2e-16 | 1e-16   | 50 x 2 chemokine (C-C motif) ligand 21 [Source:HGNC Symbol;Acc        |
| 7    | 1236   | 1.3     | 2e-16 | 1e-16   | 50 x 1 chemokine (C-C motif) receptor 7 [Source:HGNC Symbol;Ac        |
| 8    | 930    | 1.58    | 2e-16 | 1e-16   | 49 x 1 CD19 molecule [Source:HGNC Symbol;Acc:1633]                    |
| 9    | 919    | 1.17    | 2e-16 | 1e-16   | 50 x 1 CD247 molecule [Source:HGNC Symbol;Acc:1677]                   |
| 10   | 962    | 1.75    | 2e-16 | 1e-16   | 50 x 1 CD48 molecule [Source:HGNC Symbol;Acc:1683]                    |
| 11   | 1043   | 1.26    | 2e-16 | 1e-16   | 50 x 1 CD52 molecule [Source:HGNC Symbol;Acc:1804]                    |
| 12   | 51755  | 1.36    | 2e-16 | 1e-16   | 49 x 1 cyclin-dependent kinase 12 [Source:HGNC Symbol;Acc:242         |
| 13   | 10563  | 1.23    | 2e-16 | 1e-16   | 50 x 1 chemokine (C-X-C motif) ligand 13 [Source:HGNC Symbol;#        |
| 14   | 55619  | 1.31    | 2e-16 | 1e-16   | 50 x 1 dedicator of cytokinesis 10 [Source:HGNC Symbol;Acc:2347#      |
| 15   | 9214   | 1.36    | 2e-16 | 1e-16   | 49 x 1 Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;A#     |
| 16   | 54855  | 1.56    | 2e-16 | 1e-16   | 49 x 1 family with sequence similarity 46, member C [Source:HGNC      |
| 17   | 55303  | 1.16    | 2e-16 | 1e-16   | 50 x 1 GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:          |
| 18   | 3059   | 1.16    | 2e-16 | 1e-16   | 50 x 1 hematopoietic cell-specific Lyn substrate 1 [Source:HGNC S     |
| 19   | 3113   | 1.42    | 2e-16 | 1e-16   | 50 x 1 major histocompatibility complex, class II, DP alpha 1 [Source |
| 20   | 3119   | 1.15    | 2e-16 | 1e-16   | 49 x 1 major histocompatibility complex, class II, DQ beta 1 [Source: |

## Local Geneset Analysis

Overexpression

| Rank | GSZ   | p-value | #in/all   | Geneset  |
|------|-------|---------|-----------|--|
| 1    | 34.27 | NULL    | 99 / 417  | H.Tiss WIRTH_Immune system   |
| 2    | 30.49 | NULL    | 101 / 553 | Cancer Lembecke_Colonc Inflammation                                    |
| 3    | 24.36 | NULL    | 12 / 15   | CC MHC class II protein complex  |
| 4    | 23.12 | NULL    | 9 / 16    | GSEA C2FARMER_BREAST_CANCER_CLUSTER_1                                  |
| 5    | 21.35 | NULL    | 3 / 5     | GSEA C2WONG_ENDOMETRIAL_CANCER_LATE                                    |
| 6    | 20.73 | NULL    | 53 / 312  | BP immune response   |
| 7    | 19.3  | NULL    | 5 / 12    | BP dendritic cell chemotaxis   |
| 8    | 19.13 | NULL    | 8 / 16    | GSEA C2SU_THYMUS   |
| 9    | 19.02 | NULL    | 7 / 11    | GSEA C2BIOCARTA_THelper_PATHWAY  |
| 10   | 18.53 | NULL    | 8 / 13    | Cancer GENTLES_modul18   |
| 11   | 18.51 | NULL    | 7 / 15    | GSEA C2FINAK_BREAST_CANCER_SDDP_SIGNATURE                              |
| 12   | 18.34 | NULL    | 7 / 11    | GSEA C2BIOCARTA_TCYTOTOXIC_PATHWAY                                     |
| 13   | 17.08 | NULL    | 18 / 60   | BP T cell costimulation  |
| 14   | 16.54 | NULL    | 3 / 9     | GSEA C2MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN                       |
| 15   | 16.13 | NULL    | 5 / 10    | GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE                                |
| 16   | 16.02 | NULL    | 3 / 7     | GSEA C2GRAHAM_CML_DIVIDING_VS_NORMAL_DIVIDING_DN                       |
| 17   | 15.52 | NULL    | 11 / 28   | BP B cell receptor signaling pathway                                   |
| 18   | 15.44 | NULL    | 45 / 265  | Glio willscher_GBM_Verhaak-CL_expression_B_up                          |
| 19   | 15.44 | NULL    | 45 / 265  | Glio willscher_GBM_Verhaak-MES_expression_B_up                         |
| 20   | 15.44 | NULL    | 45 / 265  | Glio willscher_GBM_Verhaak-PNwt_expression_B_down                      |
| 21   | 15.44 | NULL    | 45 / 265  | Glio willscher_GBM_Verhaak-PNmut_expression_B_down                     |
| 22   | 15.16 | NULL    | 5 / 17    | BP positive regulation of neutrophil chemotaxis                        |
| 23   | 14.65 | NULL    | 27 / 162  | CC external side of plasma membrane                                    |
| 24   | 14.36 | NULL    | 14 / 47   | BP antigen processing and presentation                                 |
| 25   | 14.27 | NULL    | 6 / 12    | GSEA C2BIOCARTA_CTL_PATHWAY  |
| 26   | 14.02 | NULL    | 4 / 8     | Glio Donson-migration tethering and rolling-associated with LTS in HGA |
| 27   | 13.64 | NULL    | 5 / 8     | GSEA C2BIOCARTA_TCRA_PATHWAY   |
| 28   | 13.45 | NULL    | 17 / 74   | BP regulation of immune response                                       |
| 29   | 13.36 | NULL    | 6 / 14    | GSEA C2BIOCARTA_NO2IL12_PATHWAY  |
| 30   | 13.3  | NULL    | 4 / 10    | GSEA C2FLECHNER_BIOPSY_KIDNEY_TRANSPLANT_REJECTED_VS_                  |
| 31   | 13.18 | NULL    | 5 / 12    | GSEA C2ZHAN_MULTIPLE_MYELOMA_DN  |
| 32   | 13.05 | NULL    | 4 / 8     | GSEA C2GRAHAM_CML_QUIESCENT_VS_NORMAL_DIVIDING_DN                      |
| 33   | 12.86 | NULL    | 17 / 84   | BP T cell receptor signaling pathway                                   |
| 34   | 12.8  | NULL    | 6 / 13    | GSEA C2BIOCARTA_IL17_PATHWAY   |
| 35   | 12.56 | NULL    | 4 / 10    | GSEA C2BIOCARTA_LYM_PATHWAY  |
| 36   | 12.2  | NULL    | 5 / 15    | Glio Donson-chemokines/cytokines-associated with LTS in HGA            |
| 37   | 11.94 | NULL    | 10 / 45   | BP T cell activation   |
| 38   | 11.82 | NULL    | 4 / 8     | GSEA C2REACTOME_IMMUNOREGULATORY_INTERACTIONS_BETWE                    |
| 39   | 11.78 | NULL    | 4 / 9     | GSEA C2SUTIERREZ_WALDENSTROEMS_MACROGLOBULINEMIA_1_D                   |
| 40   | 11.7  | NULL    | 6 / 14    | GSEA C2FINETTI_BREAST_CANCER_KINOME_GREEN                              |

p-values



# GW\_062

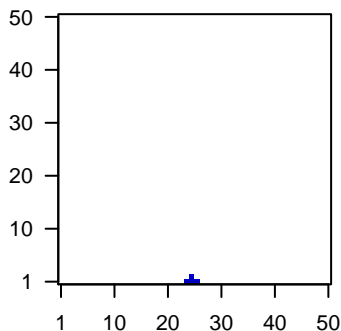
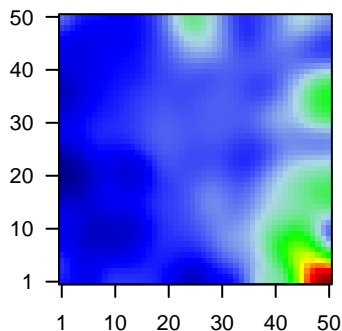
## Local Summary

%DE = 0.83  
 # metagenes = 4  
 # genes = 83  
 # genes in genesets = 83  
 # genes with  $fdr < 0.1 = 55$  ( 2 + / 53 - )  
 # genes with  $fdr < 0.05 = 34$  ( 1 + / 33 - )  
 # genes with  $fdr < 0.01 = 23$  ( 0 + / 23 - )

<r> metagenes = 1  
 <r> genes = 0.67  
 <FC> = -0.3  
 <shrinkage-t> = -10.66  
 <p-value> = 0.01  
 <fdr> = 0.66

Profile

Spot



## Local Genelist

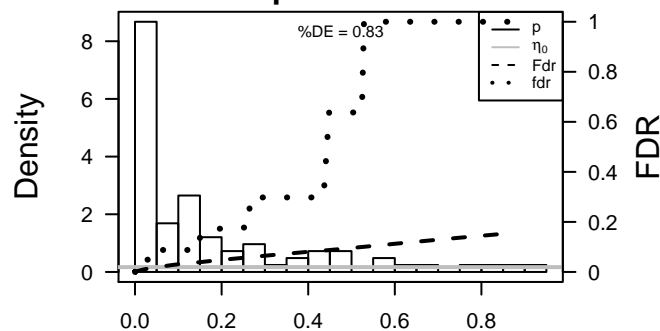
| Rank | ID     | log(FC) | fdr   | p-value | Description  |
|------|--------|---------|-------|---------|--|
| 1    | 1410   | -1.4    | 2e-16 | 2e-15   | 25 x 1 crystallin, alpha B [Source:HGNC Symbol;Acc:2389]   |
| 2    | 1917   | -1.15   | 2e-16 | 2e-15   | 25 x 1 eukaryotic translation elongation factor 1 alpha 2 [Source:HGNC Symbol;Acc:2389]                    |
| 3    | 2318   | -1.11   | 2e-15 | 8e-12   | 25 x 1 filamin C, gamma [Source:HGNC Symbol;Acc:3756]  |
| 4    | 58     | -1.01   | 6e-13 | 1e-09   | 25 x 1 actin, alpha 1, skeletal muscle [Source:HGNC Symbol;Acc:12]   |
| 5    | 6588   | -0.91   | 8e-11 | 8e-07   | 25 x 1 sarcolipin [Source:HGNC Symbol;Acc:11089]   |
| 6    | 7060   | -0.76   | 5e-08 | 4e-06   | 25 x 1 thrombospondin 4 [Source:HGNC Symbol;Acc:11788]   |
| 7    | 70     | -0.72   | 3e-07 | 4e-05   | 25 x 1 actin, alpha, cardiac muscle 1 [Source:HGNC Symbol;Acc:14]  |
| 8    | 283120 | -0.65   | 3e-06 | 3e-04   | 25 x 1 H19, imprinted maternally expressed transcript (non-protein coding) [Source:HGNC Symbol;Acc:283120] |
| 9    | 4151   | -0.59   | 2e-05 | 6e-04   | 25 x 1 myoglobin [Source:HGNC Symbol;Acc:6915]   |
| 10   | 1158   | -0.56   | 8e-05 | 6e-04   | 25 x 1 creatine kinase, muscle [Source:HGNC Symbol;Acc:1994]   |
| 11   | 4608   | -0.53   | 2e-04 | 6e-04   | 25 x 1 myosin binding protein H [Source:HGNC Symbol;Acc:7552]  |
| 12   | 222166 | -0.52   | 2e-04 | 6e-04   | 24 x 1 maturin, neural progenitor differentiation regulator homolog 1 [Source:HGNC Symbol;Acc:222166]      |
| 13   | 115265 | -0.52   | 2e-04 | 3e-03   | 25 x 1 DNA-damage-inducible transcript 4-like [Source:HGNC Symbol;Acc:115265]                              |
| 14   | 6236   | -0.49   | 4e-04 | 5e-03   | 26 x 1 Ras-related associated with diabetes [Source:HGNC Symbol;Acc:6236]                                  |
| 15   | 7136   | -0.44   | 2e-03 | 5e-03   | 25 x 1 troponin I type 2 (skeletal, fast) [Source:HGNC Symbol;Acc:7136]                                    |
| 16   | 8736   | -0.44   | 2e-03 | 5e-03   | 25 x 1 myomesin 1 [Source:HGNC Symbol;Acc:7613]  |
| 17   | 4633   | -0.43   | 2e-03 | 5e-03   | 25 x 1 myosin, light chain 2, regulatory, cardiac, slow [Source:HGNC Symbol;Acc:4633]                      |
| 18   | 10324  | -0.43   | 2e-03 | 5e-03   | 25 x 1 kelch-like family member 41 [Source:HGNC Symbol;Acc:10324]  |
| 19   | 7134   | -0.43   | 2e-03 | 7e-03   | 25 x 1 troponin C type 1 (slow) [Source:HGNC Symbol;Acc:11943]   |
| 20   | 4620   | -0.42   | 3e-03 | 7e-03   | 25 x 1 myosin, heavy chain 2, skeletal muscle, adult [Source:HGNC Symbol;Acc:4620]                         |

## Local Geneset Analysis

Underexpression

| Rank | GSZ    | p-value | #in/all  | Geneset                                    |
|------|--------|---------|----------|--|
| 1    | -46.53 | NULL    | 11 / 16  | GSEA C2RICKMAN_HEAD_AND_NECK_CANCER_F      |
| 2    | -39.9  | NULL    | 21 / 36  | BP muscle filament sliding                 |
| 3    | -39.29 | NULL    | 46 / 127 | H.Tiss WIRTH_Muscle                        |
| 4    | -35.99 | NULL    | 9 / 16   | H.Tiss WIRTH_Hippocampus                   |
| 5    | -31.3  | NULL    | 7 / 14   | CC contractile fiber                       |
| 6    | -27    | NULL    | 19 / 44  | MF structural constituent of muscle        |
| 7    | -26.57 | NULL    | 8 / 12   | CC myosin filament                         |
| 8    | -25.69 | NULL    | 9 / 20   | CC I band                                  |
| 9    | -24.54 | NULL    | 19 / 84  | BP muscle contraction                      |
| 10   | -23.22 | NULL    | 11 / 37  | CC sarcomere                               |
| 11   | -22.64 | NULL    | 1 / 6    | GSEA C2Y_AGING_OLD_UP                      |
| 12   | -20.4  | NULL    | 17 / 88  | CC Z disc                                  |
| 13   | -19.88 | NULL    | 7 / 16   | CC M band                                  |
| 14   | -19.13 | NULL    | 2 / 6    | GSEA C2BIOCARTA_HSP27_PATHWAY              |
| 15   | -17.89 | NULL    | 2 / 14   | MF structural constituent of eye lens      |
| 16   | -17.52 | NULL    | 3 / 15   | Cancer BEN-PORATH_UP                       |
| 17   | -17.37 | NULL    | 5 / 11   | BP cardiac muscle tissue morphogenesis     |
| 18   | -17.02 | NULL    | 6 / 12   | BP skeletal muscle contraction             |
| 19   | -16.77 | NULL    | 1 / 10   | GSEA C2FOURNIER_ACINAR_DEVELOPMENT_LATE_UP |
| 20   | -16.77 | NULL    | 1 / 10   | GSEA C2LUI_THYROID_CANCER_CLUSTER_5        |
| 21   | -16.76 | NULL    | 2 / 12   | BP muscle fiber development                |
| 22   | -16.1  | NULL    | 11 / 34  | CC myofibril                               |
| 23   | -15.89 | NULL    | 6 / 13   | CC muscle myosin complex                   |
| 24   | -15.84 | NULL    | 9 / 37   | BP cardiac muscle contraction              |
| 25   | -15.1  | NULL    | 1 / 12   | BP cellular response to gamma radiation    |
| 26   | -14.27 | NULL    | 6 / 53   | MF cytoskeletal protein binding            |
| 27   | -14.09 | NULL    | 3 / 18   | CC costamere                               |
| 28   | -14.03 | NULL    | 2 / 20   | MF myosin binding                          |
| 29   | -13.82 | NULL    | 1 / 14   | GSEA C2DORSEY_GAB2_TARGETS                 |
| 30   | -13.78 | NULL    | 2 / 10   | BP heart contraction                       |
| 31   | -13.59 | NULL    | 6 / 18   | BP regulation of muscle contraction        |
| 32   | -12.89 | NULL    | 1 / 5    | GSEA C2LUI_VAV3_PROSTATE_CARCINOGENESIS_UP |
| 33   | -12.87 | NULL    | 1 / 9    | GSEA C2PENG_GLUCCOSE_DEPRIVATION_UP        |
| 34   | -12.87 | NULL    | 1 / 9    | GSEA C2PENG_GLUCCOSE_DEPRIVATION_DN        |
| 35   | -12.81 | NULL    | 1 / 16   | GSEA C2RUGO_UV_RESPONSE                    |
| 36   | -12.81 | NULL    | 1 / 16   | GSEA C2KYNG_DNA_DAMAGE_BY_UV               |
| 37   | -12.61 | NULL    | 1 / 11   | GSEA C2TAGHAVI_NEOPLASTIC_TRANSFORMATION   |
| 38   | -12.47 | NULL    | 5 / 12   | MF titin binding                           |
| 39   | -12.1  | NULL    | 1 / 10   | GSEA C2BIOCARTA_EPHA4_PATHWAY              |
| 40   | -11.96 | NULL    | 4 / 36   | CC sarcoplasmic reticulum                  |

p-values



# GW\_062

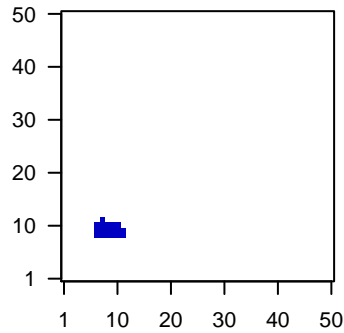
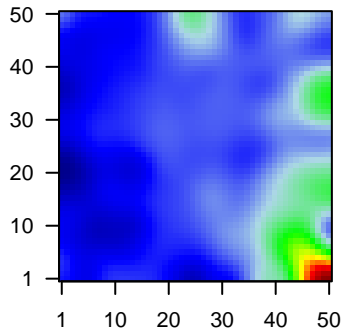
## Local Summary

%DE = 0.57  
 # metagenes = 18  
 # genes = 190  
 # genes in genesets = 190  
 # genes with fdr < 0.1 = 38 ( 4 + / 34 - )  
 # genes with fdr < 0.05 = 27 ( 4 + / 23 - )  
 # genes with fdr < 0.01 = 10 ( 3 + / 7 - )

<r> metagenes = 0.93  
 <r> genes = 0.32  
 <FC> = -0.16  
 <shrinkage-t> = -5.74  
 <p-value> = 0.07  
 <fdr> = 0.79

Profile

Spot



## Local Genelist

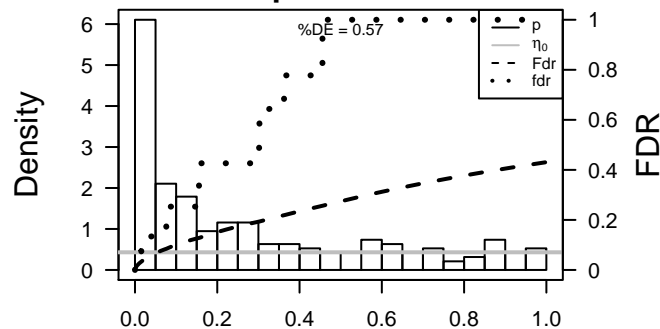
| Rank | ID        | log(FC) | fdr   | p-value | Description  |
|------|-----------|---------|-------|---------|--|
| 1    | 9862      | 1.04    | 1e-13 | 1e-05   | 8 x 12 mediator complex subunit 24 [Source:HGNC Symbol;Acc:229             |
| 2    | 57176     | -0.74   | 1e-07 | 3e-05   | 9 x 11 Valine--tRNA ligase, mitochondrial [Source:UniProtKB/TrEM           |
| 3    | 10948     | 0.71    | 5e-07 | 3e-03   | 7 x 11 StAR--related lipid transfer (START) domain containing 3 [So        |
| 4    | 57106     | -0.58   | 4e-05 | 5e-03   | 10 x 9 N-acetyltransferase 14 (GCN5--related, putative) [Source:HG         |
| 5    | 100170841 | 0.52    | 2e-04 | 5e-03   | 10 x 10 chromosome 17 open reading frame 96 [Source:HGNC Synt              |
| 6    | 79414     | -0.52   | 2e-04 | 5e-03   | 7 x 9 leucine rich repeat and fibronectin type III domain containi         |
| 7    | 100128927 | -0.52   | 2e-04 | 5e-03   | 11 x 11 zinc finger and BTB domain containing 42 [Source:HGNC Sy           |
| 8    | 692227    | -0.51   | 3e-04 | 5e-03   | 8 x 11 small nucleolar RNA, C/D box 104 [Source:HGNC Symbol;Ac             |
| 9    | 10078     | -0.5    | 3e-04 | 7e-03   | 7 x 10 tumor suppressing subtransferable candidate 4 [Source:HGN           |
| 10   | 6526      | -0.49   | 4e-04 | 1e-02   | 8 x 10 sodium/myo--inositol cotransporter [Source:RefSeq peptide;f         |
| 11   | 54764     | -0.49   | 5e-04 | 1e-02   | 8 x 9 zinc finger, RAN--binding domain containing 1 [Source:HGNC           |
| 12   | 23203     | -0.47   | 7e-04 | 1e-02   | 7 x 11 peptidase (mitochondrial processing) alpha [Source:HGNC S           |
| 13   | 537       | -0.47   | 8e-04 | 1e-02   | 8 x 9 ATPase, H+ transporting, lysosomal accessory protein 1 [Sou          |
| 14   | 147912    | -0.46   | 1e-03 | 2e-02   | 8 x 9 SIX homeobox 5 [Source:HGNC Symbol;Acc:10891]                        |
| 15   | 126208    | -0.45   | 1e-03 | 2e-02   | 7 x 10 zinc finger protein 787 [Source:HGNC Symbol;Acc:26998]              |
| 16   | 26262     | -0.45   | 1e-03 | 2e-02   | 8 x 10 tetraspanin 17 [Source:HGNC Symbol;Acc:13594]                       |
| 17   | 27043     | -0.44   | 2e-03 | 4e-02   | 9 x 11 proline, glutamate and leucine rich protein 1 [Source:HGNC S        |
| 18   | 55810     | 0.42    | 3e-03 | 4e-02   | 9 x 10 forkhead box J2 [Source:HGNC Symbol;Acc:24818]                      |
| 19   | 54758     | -0.42   | 3e-03 | 4e-02   | 8 x 11 kelch domain containing 4 [Source:HGNC Symbol;Acc:25272             |
| 20   | 6499      | -0.41   | 3e-03 | 4e-02   | 7 x 11 superkiller viralicidic activity 2--like (S. cerevisiae) [Source:HC |

## Local Geneset Analysis

Underexpression

| Rank | GSZ   | p-value | #in/all   | Geneset   |
|------|-------|---------|-----------|---|
| 1    | -7.74 | NULL    | 2 / 12    | GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP                           |
| 2    | -6.94 | NULL    | 2 / 23    | Chr Chr HSCHR6_MHC_DBB  |
| 3    | -6.72 | NULL    | 2 / 10    | MF K63--linked polyubiquitin binding                                  |
| 4    | -6.67 | NULL    | 39 / 1135 | Chr Chr 19  |
| 5    | -6.44 | NULL    | 2 / 14    | Cancer LIU_COMMON_CANCER_GENES  |
| 6    | -6.38 | NULL    | 3 / 19    | MF hydrolase activity, acting on acid anhydrides, in phosphorus-conta |
| 7    | -5.66 | NULL    | 2 / 9     | miRNA target set 3187-184   |
| 8    | -5.65 | NULL    | 3 / 35    | miRNA target set 3187-3p  |
| 9    | -5.54 | NULL    | 2 / 22    | MF N--acetyltransferase activity                                      |
| 10   | -5.47 | NULL    | 1 / 5     | miRNA target set 3187-205   |
| 11   | -5.21 | NULL    | 2 / 27    | BP DNA--dependent transcription, initiation                           |
| 12   | -5.12 | NULL    | 1 / 5     | miRNA target set 3187-196a  |
| 13   | -5.11 | NULL    | 2 / 5     | GSEA C2NIKOLSKY_BREAST_CANCER_19Q13.4_AMPLICON                        |
| 14   | -5.08 | NULL    | 2 / 15    | BP intracellular estrogen receptor signaling pathway                  |
| 15   | -4.98 | NULL    | 1 / 4     | GSEA C2WEBER_METHYLATED_ICP_IN_SPERM_UP                               |
| 16   | -4.94 | NULL    | 2 / 29    | BP ATP hydrolysis coupled proton transport                            |
| 17   | -4.87 | NULL    | 1 / 11    | Glio willscher_GBM_Verhaak--CL_expression_M_down                      |
| 18   | -4.87 | NULL    | 1 / 11    | Glio willscher_GBM_Verhaak--MES_expression_M_down                     |
| 19   | -4.87 | NULL    | 1 / 11    | Glio willscher_GBM_Verhaak--PNmut_expression_M_up                     |
| 20   | -4.87 | NULL    | 1 / 7     | miRNA target set 3187-39a   |
| 21   | -4.72 | NULL    | 2 / 11    | BP maintenance of protein location in nucleus                         |
| 22   | -4.69 | NULL    | 3 / 24    | BP centrosome organization  |
| 23   | -4.67 | NULL    | 3 / 42    | BP inositol phosphate metabolic process                               |
| 24   | -4.57 | NULL    | 2 / 15    | MF acetylglucosaminyltransferase activity                             |
| 25   | -4.56 | NULL    | 1 / 7     | GSEA C2BANDRES_RESPONSE_TO_CARMUSTIN_WITHOUT_MGMT_2                   |
| 26   | -4.47 | NULL    | 2 / 12    | GSEA C2BROWNE_HCMV_INFECTION_14HR_UP                                  |
| 27   | -4.35 | NULL    | 2 / 11    | GSEA C2BIOCARTA_AHSP_PATHWAY  |
| 28   | -4.3  | NULL    | 2 / 13    | CC STAGA complex  |
| 29   | -4.26 | NULL    | 1 / 14    | BP protein K63--linked deubiquitination                               |
| 30   | -4.15 | NULL    | 2 / 12    | BP porphyrin--containing compound biosynthetic process                |
| 31   | -4.15 | NULL    | 2 / 27    | CC MLL1 complex   |
| 32   | -3.97 | NULL    | 1 / 35    | MF aminoacyl--tRNA ligase activity                                    |
| 33   | -3.95 | NULL    | 1 / 16    | BP regulation of cell morphogenesis                                   |
| 34   | -3.89 | NULL    | 1 / 15    | GSEA C2GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_E                |
| 35   | -3.85 | NULL    | 1 / 5     | GSEA C2NAGY_PCAF_COMPONENTS_HUMAN                                     |
| 36   | -3.83 | NULL    | 2 / 15    | GSEA C2OLSSON_E2F3_TARGETS_DN   |
| 37   | -3.83 | NULL    | 1 / 13    | GSEA C2NIKOLSKY_BREAST_CANCER_16Q24_AMPLICON                          |
| 38   | -3.82 | NULL    | 2 / 16    | CC NuRD complex   |
| 39   | -3.8  | NULL    | 1 / 16    | MF proton--transporting ATPase activity, rotational mechanism         |
| 40   | -3.8  | NULL    | 1 / 11    | BP positive regulation of protein dephosphorylation                   |

p-values



# GW\_062

## Local Summary

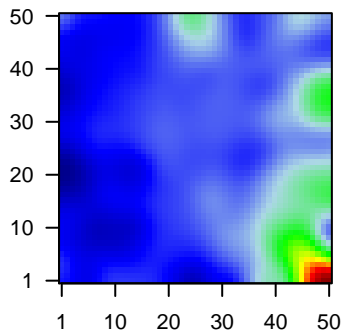
%DE = 0.58  
 # metagenes = 47  
 # genes = 449  
 # genes in genesets = 444

# genes with  $fdr < 0.1 = 132$  ( 9 + / 123 - )  
 # genes with  $fdr < 0.05 = 108$  ( 6 + / 102 - )  
 # genes with  $fdr < 0.01 = 34$  ( 3 + / 31 - )

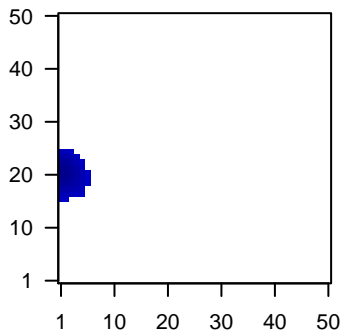
$\langle r \rangle$  metagenes = 0.93  
 $\langle r \rangle$  genes = 0.25

$\langle FC \rangle = -0.2$   
 $\langle \text{shrinkage-t} \rangle = -6.93$   
 $\langle p\text{-value} \rangle = 0.04$   
 $\langle fdr \rangle = 0.74$

Profile



Spot



## Local Genelist

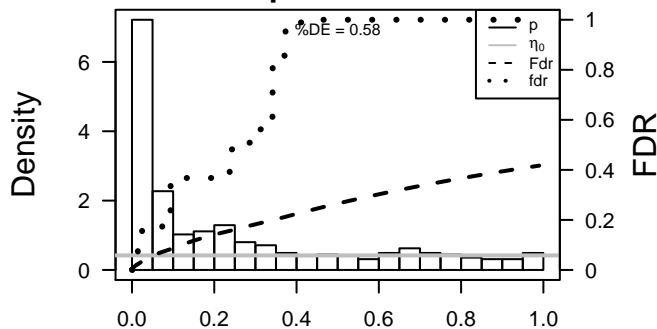
| Rank | ID     | log(FC) | fdr   | p-value | Description   |
|------|--------|---------|-------|---------|---|
| 1    | 131076 | 1.19    | 2e-16 | 2e-14   | 1 x 16 coiled-coil domain containing 58 [Source:HGNC Symbol;Acc:131076]   |
| 2    | 80154  | -1.21   | 2e-16 | 2e-14   | 1 x 23  |
| 3    | 283869 | 1.1     | 6e-15 | 1e-09   | 1 x 17 neuropeptide W [Source:HGNC Symbol;Acc:30509]  |
| 4    | 5691   | 0.95    | 6e-12 | 9e-08   | 3 x 18 proteasome (prosome, macropain) subunit, beta type, 3 [Source:HGNC Symbol;Acc:5691]                        |
| 5    | 6884   | -0.87   | 5e-10 | 5e-06   | 1 x 22 TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor 13 [Source:HGNC Symbol;Acc:6884] |
| 6    | 23423  | -0.78   | 3e-08 | 5e-06   | 1 x 24 transmembrane emp24 protein transport domain containing 3 [Source:HGNC Symbol;Acc:23423]                   |
| 7    | 284085 | -0.77   | 5e-08 | 2e-04   | 3 x 18 keratin 18 pseudogene 55 [Source:HGNC Symbol;Acc:26874]  |
| 8    | 51367  | -0.69   | 1e-06 | 6e-04   | 1 x 17 processing of precursor 5, ribonuclease P/MRP subunit (S. cerevisiae) [Source:HGNC Symbol;Acc:51367]       |
| 9    | 7988   | -0.62   | 1e-05 | 6e-04   | 2 x 24 zinc finger protein 212 [Source:HGNC Symbol;Acc:13004]   |
| 10   | 10134  | -0.62   | 1e-05 | 6e-04   | 1 x 21 B-cell receptor-associated protein 31 [Source:HGNC Symbol;Acc:10134]                                       |
| 11   | 55210  | -0.61   | 2e-05 | 6e-04   | 1 x 18 ATPase family, AAA domain containing 3A [Source:HGNC Symbol;Acc:55210]                                     |
| 12   | 118881 | -0.6    | 2e-05 | 6e-04   | 1 x 22 catechol-O-methyltransferase domain containing 1 [Source:HGNC Symbol;Acc:118881]                           |
| 13   | 29988  | -0.59   | 2e-05 | 6e-04   | 2 x 21 solute carrier family 2 (facilitated glucose transporter), member 1 [Source:HGNC Symbol;Acc:29988]         |
| 14   | 128240 | -0.59   | 2e-05 | 6e-04   | 4 x 18 apolipoprotein A-I binding protein [Source:HGNC Symbol;Acc:128240]   |
| 15   | 8427   | -0.59   | 2e-05 | 8e-04   | 1 x 25 zinc finger protein 282 [Source:HGNC Symbol;Acc:13076]   |
| 16   | 5702   | -0.59   | 3e-05 | 1e-03   | 1 x 19 proteasome (prosome, macropain) 26S subunit, ATPase, 3 [Source:HGNC Symbol;Acc:5702]                       |
| 17   | 164091 | -0.57   | 4e-05 | 1e-03   | 1 x 23 progesterin and adiponectin receptor family member VII [Source:HGNC Symbol;Acc:164091]                     |
| 18   | 2194   | -0.57   | 4e-05 | 1e-03   | 1 x 17 fatty acid synthase [Source:HGNC Symbol;Acc:3594]  |
| 19   | 85019  | -0.57   | 4e-05 | 1e-03   | 1 x 22 transmembrane protein 241 [Source:HGNC Symbol;Acc:3172]  |
| 20   | 57761  | -0.57   | 5e-05 | 1e-03   | 1 x 17 tribbles pseudokinase 3 [Source:HGNC Symbol;Acc:16228]   |

## Local Geneset Analysis

Underexpression

| Rank | GSZ   | p-value | #in/all   | Geneset  |
|------|-------|---------|-----------|--|
| 1    | -8.77 | NULL    | 3 / 10    | GSEA C2REACTOME_HIV1_TRANSCRIPTION_INITIATION                    |
| 2    | -8.64 | NULL    | 2 / 4     | TF MYC_Cell growth and proliferation UP                          |
| 3    | -8.38 | NULL    | 4 / 16    | GSEA C2MOOHA_HUMAN_MITODB_6_2002                                 |
| 4    | -8.38 | NULL    | 4 / 16    | GSEA C2MOOHA_MITOCHONDRIA  |
| 5    | -8.38 | NULL    | 5 / 10    | MF NADH dehydrogenase activity                                   |
| 6    | -7.69 | NULL    | 2 / 7     | GSEA C2REACTOME_P53_INDEPENDENT_DNA_DAMAGE_RESPONSE              |
| 7    | -7.69 | NULL    | 2 / 7     | GSEA C2REACTOME_SCF_BETA_TRCP_MEDIATED_DEGRADATION_OF_P27        |
| 8    | -7.69 | NULL    | 2 / 7     | GSEA C2REACTOME_SCF_SKP2_MEDIATED_DEGRADATION_OF_P27             |
| 9    | -7.69 | NULL    | 2 / 7     | GSEA C2REACTOME_STABILIZATION_OF_P53                             |
| 10   | -7.55 | NULL    | 3 / 10    | MF monosaccharide binding  |
| 11   | -7.15 | NULL    | 2 / 12    | GSEA C2CAMPS_COLON_CANCER_COPY_NUMBER_DN                         |
| 12   | -7.04 | NULL    | 99 / 1318 | CC mitochondrion   |
| 13   | -6.74 | NULL    | 2 / 7     | GSEA C2REACTOME_SIGNALING_BY_WNT                                 |
| 14   | -6.63 | NULL    | 2 / 11    | GSEA C2KEGG_BASAL_TRANSCRIPTION_FACTORS                          |
| 15   | -6.37 | NULL    | 4 / 14    | GSEA C2REACTOME_PI3K_AKT_SIGNALING                               |
| 16   | -6.17 | NULL    | 4 / 15    | GSEA C2ANTVEER_BREAST_CANCER_BRCA1_UP                            |
| 17   | -6.14 | NULL    | 2 / 10    | BP pantothenate metabolic process                                |
| 18   | -6.14 | NULL    | 2 / 10    | GSEA C2REACTOME_VITAMIN_B5_(PANTOTHENATE)_METABOLISM             |
| 19   | -6.02 | NULL    | 39 / 579  | CC nucleolus   |
| 20   | -6    | NULL    | 3 / 15    | GSEA C2KEGG_PENTOSE_PHOSPHATE_PATHWAY                            |
| 21   | -5.97 | NULL    | 2 / 11    | GSEA C2WONG_PROTEASOME_GENE_MODULE                               |
| 22   | -5.96 | NULL    | 3 / 17    | CC proteasome accessory complex                                  |
| 23   | -5.95 | NULL    | 3 / 9     | GSEA C2REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE                     |
| 24   | -5.88 | NULL    | 4 / 14    | GSEA C2ZHANG_CORE_SERUM_RESPONSE_UP                              |
| 25   | -5.63 | NULL    | 8 / 64    | BP tRNA processing   |
| 26   | -5.61 | NULL    | 3 / 10    | GSEA C2REACTOME_HIV_LIFE_CYCLE                                   |
| 27   | -5.44 | NULL    | 1 / 3     | TF MYC_Tumor suppressor genes UP                                 |
| 28   | -5.35 | NULL    | 2 / 24    | CC endoplasmic reticulum-Golgi intermediate compartment membrane |
| 29   | -5.23 | NULL    | 3 / 15    | GSEA C2KEGG_PROPANOATE_METABOLISM                                |
| 30   | -5.21 | NULL    | 32 / 304  | CC mitochondrial inner membrane                                  |
| 31   | -5.18 | NULL    | 1 / 3     | GSEA C2KEGG_OXIDATIVE_PHOSPHORYLATION                            |
| 32   | -5.18 | NULL    | 1 / 3     | GSEA C2KEGG_PARKINSONS_DISEASE                                   |
| 33   | -5.17 | NULL    | 5 / 16    | GSEA C2BIOCARTA_PTDINS_PATHWAY                                   |
| 34   | -5.07 | NULL    | 1 / 9     | miRNA target site B202*  |
| 35   | -5.05 | NULL    | 3 / 12    | BP apoptotic nuclear changes                                     |
| 36   | -5.04 | NULL    | 3 / 13    | GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN                      |
| 37   | -5.04 | NULL    | 3 / 15    | GSEA C2BASAKI_YBX1_TARGETS_UP                                    |
| 38   | -5.02 | NULL    | 3 / 16    | GSEA C2REACTOME_TRKA_SIGNALING_FROM_THE_PLASMA_MEMBRANE          |
| 39   | -5.02 | NULL    | 2 / 16    | GSEA C2AMIT_EGF_RESPONSE_480_MCF10A                              |
| 40   | -4.94 | NULL    | 2 / 10    | GSEA C2KEGG_LIMONENE_AND_PINENE_DEGRADATION                      |

p-values



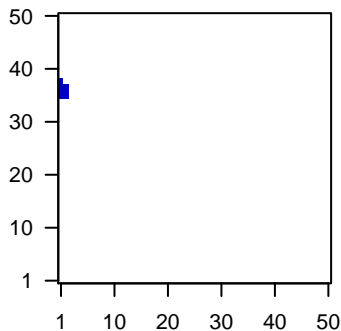
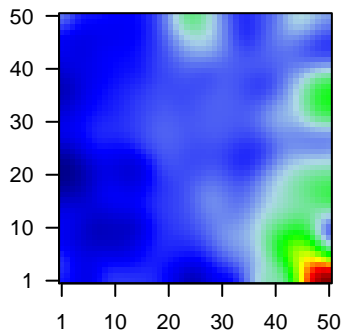
# GW\_062

## Local Summary

%DE = 0.61  
 # metagenes = 7  
 # genes = 118  
 # genes in genesets = 116  
  
 # genes with  $fdr < 0.1$  = 38 ( 5 + / 33 - )  
 # genes with  $fdr < 0.05$  = 22 ( 5 + / 17 - )  
 # genes with  $fdr < 0.01$  = 13 ( 4 + / 9 - )  
  
 $\langle r \rangle$  metagenes = 0.99  
 $\langle r \rangle$  genes = 0.29  
  
 $\langle FC \rangle = -0.18$   
 $\langle \text{shrinkage-t} \rangle = -6.34$   
 $\langle p\text{-value} \rangle = 0.03$   
 $\langle fdr \rangle = 0.72$

Profile

Spot



## Local Genelist

| Rank | ID     | log(FC) | fdr p-value | Description Metagene  |
|------|--------|---------|-------------|---|
| 1    | 414059 | 0.95    | 1e-11 4e-08 | 1 x 35 TBC1 domain family, member 3B [Source:HGNC Symbol;Acc:654341]                                    |
| 2    | 654341 | 0.86    | 9e-10 9e-08 | 2 x 35 TBC1 domain family, member 3 [Source:HGNC Symbol;Acc:18338]                                      |
| 3    | 8338   | -0.83   | 3e-09 3e-04 | 2 x 37 histone cluster 2, H2ac [Source:HGNC Symbol;Acc:4738]  |
| 4    | 2582   | -0.63   | 6e-06 4e-04 | 1 x 35 UDP-galactose-4-epimerase [Source:HGNC Symbol;Acc:418608]  |
| 5    | 8608   | 0.6     | 2e-05 4e-04 | 1 x 38 retinol dehydrogenase 16 (all-trans) [Source:HGNC Symbol;Acc:30851]                              |
| 6    | 30851  | 0.59    | 3e-05 1e-03 | 1 x 38 Tax1 (human T-cell leukemia virus type 1) binding protein 3 [Source:HGNC Symbol;Acc:79670]       |
| 7    | 79670  | -0.57   | 5e-05 1e-03 | 1 x 36 zinc finger, CCHC domain containing 6 [Source:HGNC Symbol;Acc:10383]                             |
| 8    | 10383  | -0.55   | 9e-05 1e-03 | 1 x 38 tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:20771]  |
| 9    | 54795  | -0.55   | 9e-05 3e-03 | 1 x 36 transient receptor potential cation channel, subfamily M, member 1 [Source:HGNC Symbol;Acc:6924] |
| 10   | 6924   | -0.52   | 2e-04 3e-03 | 1 x 35 transcription elongation factor B (SIII), polypeptide 3 (110kDa) [Source:HGNC Symbol;Acc:85450]  |
| 11   | 85450  | -0.51   | 2e-04 3e-03 | 1 x 38 inositol 1,4,5-trisphosphate receptor interacting protein [Source:HGNC Symbol;Acc:645]           |
| 12   | 645    | -0.51   | 3e-04 4e-03 | 1 x 36 biliverdin reductase B (flavin reductase (NADPH)) [Source:HGNC Symbol;Acc:1984]                  |
| 13   | 1984   | -0.5    | 4e-04 4e-03 | 1 x 37 eukaryotic translation initiation factor 5A [Source:HGNC Symbol;Acc:134285]                      |
| 14   | 134285 | -0.49   | 4e-04 1e-02 | 1 x 37 transmembrane protein 171 [Source:HGNC Symbol;Acc:7262]  |
| 15   | 7262   | -0.46   | 9e-04 1e-02 | 1 x 38 pleckstrin homology-like domain, family A, member 2 [Source:HGNC Symbol;Acc:79369]               |
| 16   | 79369  | -0.46   | 1e-03 1e-02 | 1 x 36 UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1 [Source:HGNC Symbol;Acc:7415]      |
| 17   | 7415   | -0.44   | 2e-03 1e-02 | 1 x 36 valosin containing protein [Source:HGNC Symbol;Acc:5355]   |
| 18   | 5355   | -0.44   | 2e-03 1e-02 | 1 x 37 proteolipid protein 2 (colonial epithelium-enriched) [Source:HGNC Symbol;Acc:2731]               |
| 19   | 2731   | 0.43    | 2e-03 1e-02 | 1 x 38 glycine dehydrogenase (decarboxylating) [Source:HGNC Symbol;Acc:54741]                           |
| 20   | 54741  | -0.43   | 2e-03 1e-02 | 1 x 37 leptin receptor [Source:HGNC Symbol;Acc:6554]  |

## Local Geneset Analysis

Underexpression

| Rank | GSZ    | p-value | #in/all | Geneset  |
|------|--------|---------|---------|--|
| 1    | -15    | NULL    | 1 / 2   | MMML C65CIEJ_MMML_43   |
| 2    | -14.31 | NULL    | 2 / 10  | MF 3-beta-hydroxy-delta5-steroid dehydrogenase activity                          |
| 3    | -13.03 | NULL    | 2 / 11  | GSEA C2SU_PLACENTA   |
| 4    | -12.8  | NULL    | 2 / 7   | GSEA C2DACAOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_UP                                  |
| 5    | -9.49  | NULL    | 1 / 2   | Disease BCHETNIA_EBM down  |
| 6    | -9.18  | NULL    | 2 / 12  | BP extracellular polysaccharide biosynthetic process                             |
| 7    | -8.99  | NULL    | 1 / 13  | GSEA C2REACTOME_PACKAGING_OF_TELOMERE_ENDS                                       |
| 8    | -8.33  | NULL    | 3 / 36  | MF coenzyme binding  |
| 9    | -7.99  | NULL    | 2 / 13  | GSEA C2CREIGHTON_AKT1_SIGNALING_VIA_MTOR_DN                                      |
| 10   | -7.77  | NULL    | 2 / 31  | BP steroid biosynthetic process  |
| 11   | -7.45  | NULL    | 1 / 11  | GSEA C2PAPASPYRIDONOS_UNSTABLE_ATEROSCLEROTIC_PLAQUE_UP                          |
| 12   | -6.8   | NULL    | 1 / 13  | GSEA C2KEGG_GALACTOSE_METABOLISM   |
| 13   | -6.77  | NULL    | 1 / 10  | GSEA C2WEBER_METHYLATED_HCP_IN_SPERM_UP  |
| 14   | -6.66  | NULL    | 2 / 41  | MF oxidoreductase activity, acting on the CH-OH group of donors, NADPH dependent |
| 15   | -6.64  | NULL    | 2 / 14  | GSEA C2AZARD_UV_RESPONSE_CLUSTER_G2  |
| 16   | -6.45  | NULL    | 1 / 11  | GSEA C2REACTOME_CHAPERONIN_MEDIATED_PROTEIN_FOLDING                              |
| 17   | -6.43  | NULL    | 1 / 11  | GSEA C2WEBER_METHYLATED_HCP_IN_FIBROBLAST_DN                                     |
| 18   | -6.3   | NULL    | 1 / 10  | GSEA C2LUI_THYROID_CANCER_CLUSTER_5  |
| 19   | -6.3   | NULL    | 1 / 10  | GSEA C2BIOCARTA_IL10_PATHWAY   |
| 20   | -6.15  | NULL    | 1 / 12  | MF MHC class I protein binding   |
| 21   | -6.15  | NULL    | 1 / 12  | GSEA C2REACTOME_PREFOLDIN_MEDIATED_TRANSFER_OF_SUBSTRATE_TO_PROTEIN_COMPLEXES    |
| 22   | -6.13  | NULL    | 1 / 12  | BP dendritic cell chemotaxis   |
| 23   | -5.88  | NULL    | 1 / 13  | GSEA C2KEGG_GAP_JUNCTION   |
| 24   | -5.88  | NULL    | 1 / 13  | GSEA C2KEGG_PATHOGENIC_ESCHERICHIA_COLL_INFECTIO                                 |
| 25   | -5.71  | NULL    | 1 / 10  | GSEA C2ETTER_TARGETS_OF_PRKCA_AND_ETS1_DN  |
| 26   | -5.71  | NULL    | 1 / 10  | GSEA C2SHIRAIISHI_PLZF_TARGETS_UP  |
| 27   | -5.7   | NULL    | 1 / 12  | H.Tiss WIRTH_Prim.Lymphoid organs  |
| 28   | -5.64  | NULL    | 1 / 14  | GSEA C2REACTOME_CENTROSOME_MATURATION  |
| 29   | -5.64  | NULL    | 1 / 14  | GSEA C2REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES                             |
| 30   | -5.63  | NULL    | 1 / 5   | GSEA C2RADAIEVA_RESPONSE_TO_IFNA1_DN   |
| 31   | -5.63  | NULL    | 1 / 14  | GSEA C2WALK_AML_WITH_11Q23_REARRANGED  |
| 32   | -5.55  | NULL    | 1 / 12  | GSEA C2L_LUNG_CANCER   |
| 33   | -5.55  | NULL    | 1 / 12  | miRNA target-mir339  |
| 34   | -5.51  | NULL    | 1 / 13  | GSEA C2WALLACE_JAK2_TARGETS_UP   |
| 35   | -5.51  | NULL    | 1 / 13  | GSEA C2REACTOME_TAT_MEDIATED_HIV1_ELONGATION_ARREST_AND_TAT_REPRESSION           |
| 36   | -5.49  | NULL    | 2 / 9   | GSEA C2SCIAN_CELL_CYCLE_TARGETS_OF_TP53_AND_TP73_UP                              |
| 37   | -5.43  | NULL    | 1 / 15  | GSEA C2ACEVEDO_LIVER_CANCER_WITH_H3K9ME3_DN                                      |
| 38   | -5.43  | NULL    | 1 / 15  | GSEA C2REACTOME_FORMATION_OF_TUBULIN_FOLDING_INTERMEDIATES                       |
| 39   | -5.43  | NULL    | 1 / 15  | GSEA C2REACTOME_POST_CHAPERONIN_TUBULIN_FOLDING_PATHWAY                          |
| 40   | -5.41  | NULL    | 1 / 15  | GSEA C2WALK_AML_CLUSTER_16   |

p-values

