

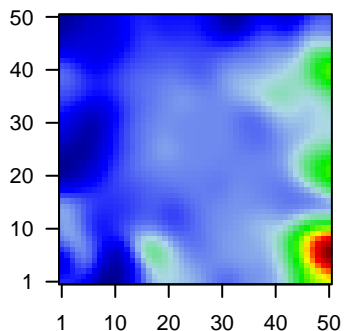
# MPI-229

## Global Summary

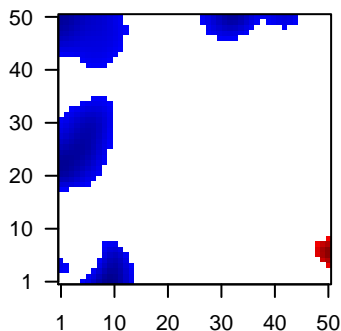
%DE = 0.05  
 # genes with  $fdr < 0.2 = 749$  ( 418 + / 331 -)  
 # genes with  $fdr < 0.1 = 484$  ( 277 + / 207 -)  
 # genes with  $fdr < 0.05 = 378$  ( 220 + / 158 -)  
 # genes with  $fdr < 0.01 = 235$  ( 141 + / 94 -)  
  
 # genes in genesets = 13152

<FC> = 0  
 <t-score> = -0.02  
 <p-value> = 0.25  
 <fdr> = 0.95

### Portrait



### Regulated Metagenes



## Global Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	44790_s_at	-2.05	2e-16	5e-13	42 x 49 RUN and cysteine rich domain containing beclin 1 interacting
2	205861_at	-1.16	2e-16	5e-13	0 x 23 Spi-B transcription factor [Source:HGNC Symbol;Acc:HGNC:205861]
3	209374_s_at	-1.94	2e-16	5e-13	0 x 22 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:209374]
4	212827_at	-1.73	2e-16	5e-13	41 x 44 immunoglobulin heavy constant mu [Source:HGNC Symbol;Acc:HGNC:212827]
5	214669_x_at	-1.78	2e-16	5e-13	0 x 3
6	215176_x_at	-1.79	2e-16	5e-13	10 x 5 immunoglobulin kappa variable 1-39 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:215176]
7	219471_at	-2.21	2e-16	5e-13	42 x 49 RUN and cysteine rich domain containing beclin 1 interacting
8	221651_x_at	-3.22	2e-16	5e-13	0 x 3 immunoglobulin kappa constant [Source:HGNC Symbol;Acc:HGNC:221651]
9	221671_x_at	-3.14	2e-16	5e-13	0 x 3 immunoglobulin kappa constant [Source:HGNC Symbol;Acc:HGNC:221671]
10	216766_at	2.26	2e-15	3e-11	46 x 8
11	39318_at	-1.18	3e-15	4e-11	46 x 49 T cell leukemia/lymphoma 1A [Source:HGNC Symbol;Acc:HGNC:39318]
12	215049_x_at	-1.52	5e-15	5e-11	8 x 10 CD163 molecule [Source:HGNC Symbol;Acc:HGNC:1631]
13	201162_at	-1.02	7e-15	3e-10	10 x 3 insulin like growth factor binding protein 7 [Source:HGNC Symbol;Acc:HGNC:201162]
14	215200_x_at	2.17	3e-14	3e-10	45 x 8
15	206310_at	2.16	4e-14	3e-09	17 x 6 serine peptidase inhibitor, Kazal type 2 [Source:HGNC Symbol;Acc:HGNC:206310]
16	201909_at	-1.35	2e-13	3e-09	43 x 49 ribosomal protein S4, Y-linked 1 [Source:HGNC Symbol;Acc:HGNC:201909]
17	208791_at	-1.41	5e-13	3e-09	0 x 3 clusterin [Source:HGNC Symbol;Acc:HGNC:2095]
18	214836_x_at	-1.05	5e-13	1e-08	0 x 3
19	200648_s_at	-1.26	9e-13	1e-08	2 x 0 glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGNC:200648]
20	203645_s_at	-1.35	1e-12	2e-08	8 x 10 CD163 molecule [Source:HGNC Symbol;Acc:HGNC:1631]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	10.44	NULL	188	Reference:GSEA:3,8_Enzymes
2	8.85	NULL	1174	Colon Cancer:pointe_mucosa-position_kmeans_E_transverse_colon_UP_transcriptome
3	8.39	NULL	14	Lymphoma:WRIGHT_GCB_UP
4	8.08	NULL	59	Glioma:WILLSCHER_GBM_Verhaak-PNwt & MES_up
5	7.63	NULL	6	Lymphoma:Rare_GCB_UP
6	7.23	NULL	4	Lymphoma:WRIGHT_custom_GCB-DLBCL_UP
7	6.98	NULL	8	Lymphoma:WASCQUE_GCB_UP
8	6.96	NULL	554	Chr Chr 5
9	6.95	NULL	17	Lymphoma:leukemia_BCL2_UP_BCL6_DN
10	6.95	NULL	17	BP antigen processing and presentation of peptide or polysaccharide antigen fragments
11	6.93	NULL	18	CC MHC class II protein complex
12	6.93	NULL	6368	Colon Cancer:pointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_UP
13	6.89	NULL	143	GSEA:ZEE_DIFFERENTIATING_T_LYMPHOCYTE
14	6.82	NULL	12	MF MHC class II receptor activity
15	5.99	NULL	3682	Chromatin:transcription_factor_killer_cells_peripheral_blood_6_EnhG
16	5.73	NULL	68	Reference:GSEA:2,1_Cytotoxic_cells
17	5.59	NULL	159	GSEA:ZELSON_SICKLE_CELL_DISEASE_DN
18	5.38	NULL	492	Colon Cancer:pointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_UP
19	5.34	NULL	309	GSEA:ZAZARD_RESPONSE_TO_UV_NHEK_DN
20	5.21	NULL	5527	Chromatin:transcription_factor_killer_cells_peripheral_blood_4_Tx
<i>Underexpressed</i>				
1	-13.81	NULL	32	Reference:GSEA:1,1_Plasma_Cells
2	-11.98	NULL	52	BP complement activation, classical pathway
3	-10.76	NULL	44	MF antigen binding
4	-10.01	NULL	82	Colon Cancer:retrack_CRC_TCGA_group.over_A_normal_UP
5	-10	NULL	16	MF immunoglobulin receptor binding
6	-9.54	NULL	85	Lymphoma:leukemia_BCL2_DN_BCL6_UP
7	-9.42	NULL	116	CC blood microparticle
8	-9.33	NULL	18	Lymphoma:WRIGHT_ABC_UP
9	-8.8	NULL	77	Lymphoma:WARTES_Plasma_cell_signature
10	-8.62	NULL	196	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
11	-8.46	NULL	19	BP positive regulation of B cell activation
12	-8.29	NULL	53	BP regulation of complement activation
13	-8.01	NULL	234	GSEA:ZHOLLMANN_APOPTOSIS_VIA_CD40_DN
14	-7.79	NULL	397	Colon Cancer:retrack_CRC_TCGA_corr_C_normal_UP
15	-7.72	NULL	39	BP complement activation
16	-7.68	NULL	397	GSEA:ZREN_ALVEOLAR_RHABDOMYOSARCOMA_DN
17	-7.46	NULL	21	BP phagocytosis, recognition
18	-7.35	NULL	11	MF peptidoglycan binding
19	-7.27	NULL	3	Colon Cancer:Batistina_C_CIMP-H-like_DOWN
20	-7.26	NULL	36	BP phagocytosis, engulfment

### p-values

