

MLH1_normHNPC vs

Global Summary

%DE = 0.31
 # genes with fdr < 0.2 = 3 (1 + / 2 -)
 # genes with fdr < 0.1 = 3 (1 + / 2 -)
 # genes with fdr < 0.05 = 0 (0 + / 0 -)
 # genes with fdr < 0.01 = 0 (0 + / 0 -)
 # genes in genesets = 18990

<FC> = 0
 <t-score> = 0.04
 <p-value> = 0.28
 <fdr> = 0.69

Global Genelist

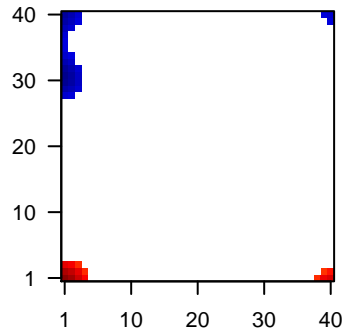
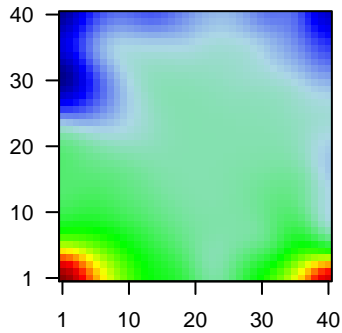
Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG00000001	0	9e-06	0.07 19 x 25 G protein-coupled receptor 83 [Source:HGNC Symbol;Acc:HGNC:10001]
2	ENSG00000001	-0.06	1e-05	0.07 40 x 24 SEC11 homolog A, signal peptidase complex subunit [Source:HGNC Symbol;Acc:HGNC:10001]
3	ENSG00000001	-0.04	2e-05	0.08 28 x 37 proteasome (prosome, macropain) 26S subunit, non-ATPase [Source:HGNC Symbol;Acc:HGNC:10001]
4	ENSG00000002	-0.04	2e-05	0.38 30 x 40 tripartite motif containing 16 [Source:HGNC Symbol;Acc:HGNC:10001]
5	ENSG00000001	-0.07	7e-05	0.38 12 x 39 kinesin family member 13A [Source:HGNC Symbol;Acc:HGNC:10001]
6	ENSG00000002	-0.03	1e-04	0.38 35 x 25 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F61001]
7	ENSG00000000	0.06	2e-04	0.38 16 x 1 cyclin-dependent kinase 11A [Source:HGNC Symbol;Acc:HGNC:10001]
8	ENSG00000000	0.09	2e-04	0.38 14 x 1 diacylglycerol kinase, delta 130kDa [Source:HGNC Symbol;Acc:HGNC:10001]
9	ENSG00000001	0	2e-04	0.38 30 x 25 dynein, axonemal, heavy chain 14 [Source:HGNC Symbol;Acc:HGNC:10001]
10	ENSG00000000	-0.12	3e-04	0.38 27 x 40 solute carrier family 9, subfamily A (NHE3, cation proton antiporter) [Source:HGNC Symbol;Acc:HGNC:10001]
11	ENSG00000001	0.25	3e-04	0.38 4 x 1 pleckstrin homology domain containing, family F (with FYVE domain) [Source:HGNC Symbol;Acc:HGNC:10001]
12	ENSG00000000	0.09	3e-04	0.38 18 x 1 microtubule associated serine/threonine kinase 3 [Source:HGNC Symbol;Acc:HGNC:10001]
13	ENSG00000001	0.07	3e-04	0.38 12 x 2 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H71001]
14	ENSG00000001	0.06	3e-04	0.38 14 x 2 zinc finger protein 439 [Source:HGNC Symbol;Acc:HGNC:20001]
15	ENSG00000001	-0.13	4e-04	0.38 28 x 40 phosphorylase, glycogen, liver [Source:HGNC Symbol;Acc:HGNC:10001]
16	ENSG00000001	-0.03	4e-04	0.38 22 x 35 UDP-glucose glycoprotein glucosyltransferase 2 [Source:HGNC Symbol;Acc:HGNC:10001]
17	ENSG00000001	-0.05	4e-04	0.38 19 x 40 NAD kinase 2, mitochondrial [Source:HGNC Symbol;Acc:HGNC:10001]
18	ENSG00000001	-0.01	5e-04	0.38 32 x 27 microfibrillar-associated protein 3-like [Source:HGNC Symbol;Acc:HGNC:10001]
19	ENSG00000001	-0.07	5e-04	0.38 22 x 40 ribulose-5-phosphate-3-epimerase [Source:HGNC Symbol;Acc:HGNC:10001]
20	ENSG00000001	-0.03	5e-04	0.38 21 x 38 zinc finger, BED-type containing 3 [Source:HGNC Symbol;Acc:HGNC:10001]

Global Geneset Analysis

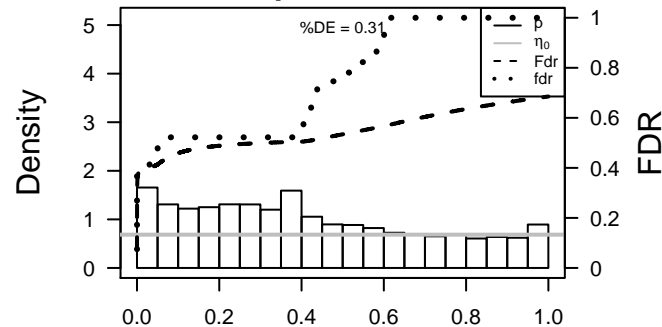
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	24.16	0e+00	427	Tissue WIRTH_Immune system
2	21.4	0e+00	844	Colon Cancer Lembecke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
3	15.7	2e-05	175	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
4	14.79	3e-05	336	LymphomaHopp_June14_MMML937_tumors+controls_group.overexpression_DN
5	14.71	3e-05	347	LymphomaWIRTH_lymphoma937_spot H
6	14.45	3e-05	484	LymphomaHopp_June14_MMML937_tumors+controls_group.overexpression_DN
7	14.39	3e-05	500	LymphomaWIRTH_lymphoma937_spot J
8	14.16	4e-05	7592	LymphomaHOPP_Strong_enhancer
9	13.27	4e-05	208	Tissue PALMER_B-Cell signature up
10	12.89	5e-05	1340	GSEA C2PUJANA_ATM_PCC_NETWORK
11	11.64	7e-05	246	GSEA C2QI_PLASMACYTOMA_UP
12	11.01	9e-05	5643	LymphomaHOPP_Txn_transition
13	10.96	9e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
14	10.49	1e-04	3064	Glio Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
15	9.61	2e-04	51	GSEA C2MORI_LARGE_PRE_BII_LYMPHOCYTE_DN
16	9.4	2e-04	163	GSEA C2PASQUALUCCI_LYMPHOMA_BY_GC_STAGE_DN
17	9.33	2e-04	507	Colon CancerTrack_CRC_TCGA_corr_C_normal_UP
18	9.13	2e-04	473	GSEA C2ZHENG_BOUND_BY_FOXP3
19	9.09	2e-04	781	Glio Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
20	9.07	3e-04	122	BP adaptive immune response
<i>Underexpressed</i>				
1	-14.54	3e-05	830	Colon CancerTrack_CRC_TCGA_corr_R_normal_DN
2	-14.09	4e-05	713	Colon CancerTrack_CRC_TCGA_group.over_C_normal_DN
3	-13.88	4e-05	550	Cancer Lembecke_Normal vs Adenoma
4	-13.64	4e-05	1441	CC mitochondrion
5	-13.61	4e-05	1298	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_DN
6	-13.49	4e-05	10239	Brain Overlap_fetal_midbrain_ReprPC
7	-12.69	5e-05	1197	GSEA C2BLALOCK_ALZHEIMERS_DISEASE_DN
8	-12.61	6e-05	2838	LymphomaHOPP_Poised_promoter
9	-12.15	6e-05	944	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_24HR_DN
10	-11.64	7e-05	9923	Brain Overlap_fetal_midbrain_K9K27me3
11	-11.37	8e-05	811	LymphomaWIRTH_lymphoma937_spot D
12	-11.27	8e-05	807	LymphomaHopp_June14_MMML937_tumors+controls_group.overexpression_DN
13	-10.67	1e-04	850	GSEA C2KRIGE_RESPONSE_TO_TOSEDOSTAT_6HR_DN
14	-10.64	1e-04	5039	LymphomaHOPP_Repressed
15	-10.44	1e-04	1105	GSEA C2BRUINS_UVC_RESPONSE_LATE
16	-10.24	2e-04	775	GSEA C2WEL_MYCN_TARGETS_WITH_E_BOX
17	-10.21	2e-04	499	GSEA C2STARK_PREFRONTAL_CORTEX_22Q11_DELETION_DN
18	-9.98	2e-04	401	GSEA C2REN_ALVEOLAR_RHABDOMYOSARCOMA_DN
19	-9.86	2e-04	350	GSEA C2ZHEIN_ALL_GLUCCORTICOID_THERAPY_DN
20	-9.71	2e-04	198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION

Profile

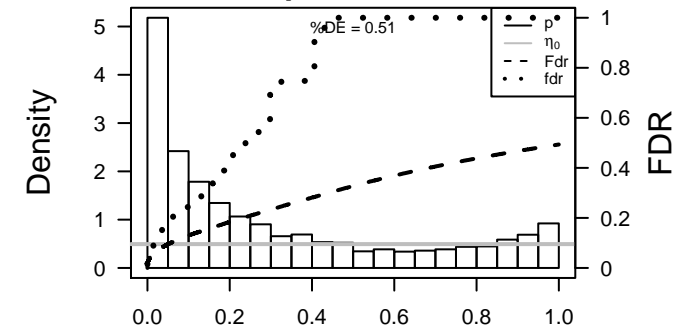
Regulated Spots



p-values



p-values



MLH1_normHNPC vs

Local Summary

%DE = 0.9
 # metagenes = 11
 # genes = 238
 # genes in genesets = 233

 # genes with $fdr < 0.1$ = 195 (195 + / 0 -)
 # genes with $fdr < 0.05$ = 184 (184 + / 0 -)
 # genes with $fdr < 0.01$ = 126 (126 + / 0 -)

<r> metagenes = 1
 <r> genes = 0.89

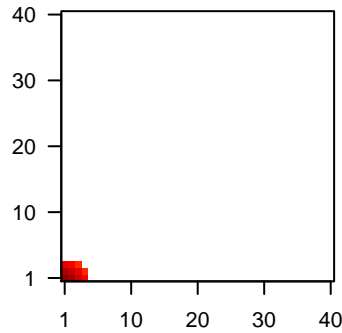
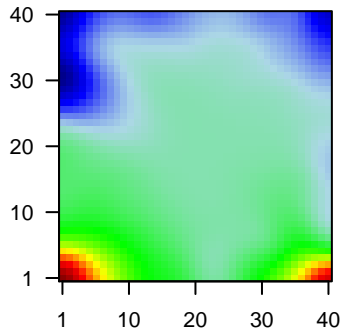
 <FC> = 0.25
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 <p-value> = 0.04
 <fdr> = 0.48

Local Genelist

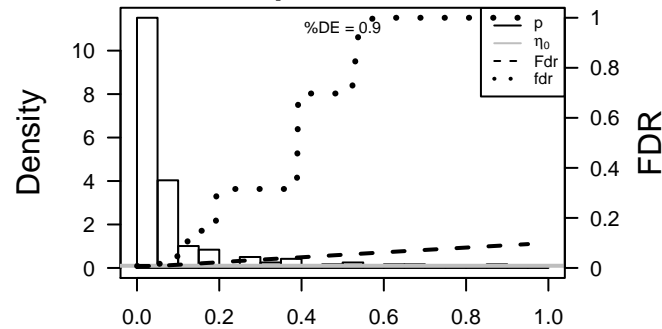
Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.25	3e-04	0.008	4 x 1 pleckstrin homology domain containing, family F (with FYVE c
2	ENSG0000001	0.25	2e-03	0.008	2 x 1 lymphocyte antigen 86 [Source:HGNC Symbol;Acc:HGNC:16
3	ENSG0000001	0.32	2e-03	0.008	1 x 1 Fc receptor-like A [Source:HGNC Symbol;Acc:HGNC:18504]
4	ENSG0000000	0.47	2e-03	0.008	1 x 1 CD79b molecule, immunoglobulin-associated beta [Source:H
5	ENSG0000001	0.59	2e-03	0.008	1 x 1 pre-B lymphocyte 3 [Source:HGNC Symbol;Acc:HGNC:1271
6	ENSG0000001	0.29	3e-03	0.008	3 x 1 family with sequence similarity 102, member A [Source:HGN
7	ENSG0000001	0.25	3e-03	0.008	4 x 1 deoxyribonuclease I-like 3 [Source:HGNC Symbol;Acc:HGNC
8	ENSG0000002	0.4	3e-03	0.008	1 x 1 protein tyrosine phosphatase, receptor type, C-associated pr
9	ENSG0000001	0.21	4e-03	0.008	4 x 2 tumor protein p53 inducible nuclear protein 1 [Source:HGNC
10	ENSG0000001	0.67	4e-03	0.008	1 x 1 CD79a molecule, immunoglobulin-associated alpha [Source:
11	ENSG0000002	0.35	5e-03	0.008	1 x 1 major histocompatibility complex, class II, DO beta [Source:H
12	ENSG0000001	0.31	5e-03	0.008	1 x 1 CD1c molecule [Source:HGNC Symbol;Acc:HGNC:1636]
13	ENSG0000001	0.22	5e-03	0.008	4 x 1 histocompatibility (minor) HA-1 [Source:HGNC Symbol;Acc:t
14	ENSG0000000	0.31	6e-03	0.008	2 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Av
15	ENSG0000001	0.4	7e-03	0.008	1 x 1 CD19 molecule [Source:HGNC Symbol;Acc:HGNC:1633]
16	ENSG0000002	0.21	7e-03	0.008	3 x 3 apolipoprotein B mRNA editing enzyme, catalytic polypeptide
17	ENSG0000002	0.3	8e-03	0.008	3 x 1 Spi-B transcription factor (Spi-1/PU.1 related) [Source:HGN
18	ENSG0000001	0.2	8e-03	0.008	4 x 1 neutrophil cytosolic factor 1 [Source:HGNC Symbol;Acc:HGNC
19	ENSG0000001	0.23	8e-03	0.008	3 x 1 POU class 2 associating factor 1 [Source:HGNC Symbol;Acc:
20	ENSG0000001	0.51	9e-03	0.008	1 x 1 Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGNC

Profile

Spot



p-values



MLH1_normHNPC vs

Local Summary

%DE = 0.69
 # metagenes = 5
 # genes = 140
 # genes in genesets = 139

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

<r> metagenes = 0.98
 <r> genes = 0.42

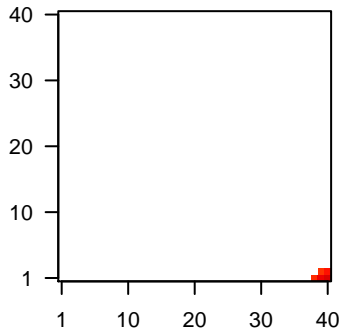
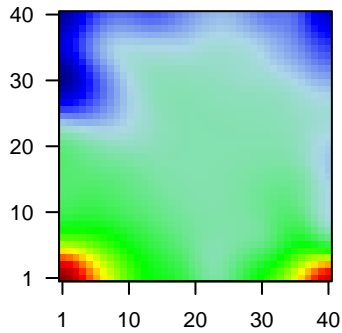
 <FC> = 0.27
 <t-score> = 1.15
 <p-value> = 0.27
 <fdr> = 0.67

Local Genelist

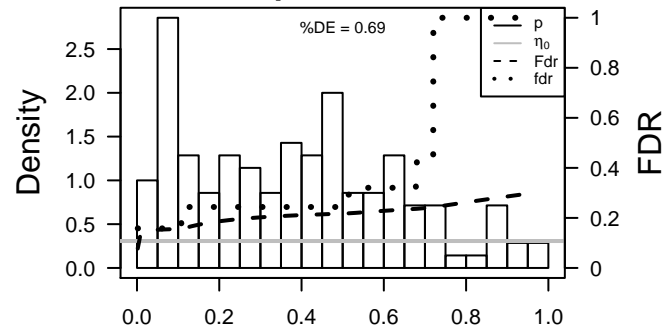
Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	0.63	0.002	0.2	39 x 1 uncharacterized LOC25845 [Source:EntrezGene;Acc:25845]
2	ENSG0000001	1.03	0.008	0.2	40 x 1 aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
3	ENSG0000000	0.95	0.020	0.2	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HGNC:642]
4	ENSG0000001	0.6	0.028	0.2	40 x 1 alanyl (membrane) aminopeptidase [Source:HGNC Symbol;Acc:HGNC:642]
5	ENSG0000001	0.41	0.036	0.2	39 x 1 placenta-specific 8 [Source:HGNC Symbol;Acc:HGNC:19254]
6	ENSG0000001	0.51	0.044	0.2	40 x 1 chromosome 11 open reading frame 86 [Source:HGNC Symbol;Acc:HGNC:19254]
7	ENSG0000001	0.33	0.046	0.2	38 x 1 protein kinase (cAMP-dependent, catalytic) inhibitor beta [Source:HGNC Symbol;Acc:HGNC:19254]
8	ENSG0000001	0.36	0.052	0.2	40 x 1 solute carrier family 9, subfamily A (NHE3, cation proton antiporter) member 1 [Source:HGNC Symbol;Acc:HGNC:19254]
9	ENSG0000000	0.27	0.059	0.2	39 x 1 interleukin 32 [Source:HGNC Symbol;Acc:HGNC:16830]
10	ENSG0000001	0.51	0.062	0.2	40 x 1 proline-rich acidic protein 1 [Source:HGNC Symbol;Acc:HGNC:19254]
11	ENSG0000001	0.39	0.063	0.2	40 x 1 ADP-ribosylation factor-like 14 [Source:HGNC Symbol;Acc:HGNC:19254]
12	ENSG0000002	0.44	0.072	0.2	40 x 1 tripartite motif containing 31 [Source:HGNC Symbol;Acc:HGNC:19254]
13	ENSG0000001	0.27	0.074	0.2	39 x 1 polymerase (DNA-directed), delta 4, accessory subunit [Source:HGNC Symbol;Acc:HGNC:19254]
14	ENSG0000000	0.28	0.078	0.2	38 x 1 cadherin-related family member 2 [Source:HGNC Symbol;Acc:HGNC:19254]
15	ENSG0000000	0.36	0.080	0.2	40 x 1 hydroxysteroid (17-beta) dehydrogenase 2 [Source:HGNC Symbol;Acc:HGNC:19254]
16	ENSG0000001	0.25	0.081	0.2	38 x 1 cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
17	ENSG0000000	0.39	0.082	0.2	39 x 1 ezrin [Source:HGNC Symbol;Acc:HGNC:12691]
18	ENSG0000000	0.67	0.082	0.2	40 x 1 guanylate cyclase activator 2B (uroguanylin) [Source:HGNC Symbol;Acc:HGNC:19254]
19	ENSG0000002	0.24	0.089	0.2	39 x 2 UDP glucuronosyltransferase 1 family, polypeptide A7 [Source:HGNC Symbol;Acc:HGNC:19254]
20	ENSG0000002	0.33	0.091	0.2	40 x 1 UDP glucuronosyltransferase 1 family, polypeptide A8 [Source:HGNC Symbol;Acc:HGNC:19254]

Profile

Spot



p-values



MLH1_normHNPC vs

Local Summary

%DE = 0.75
 # metagenes = 29
 # genes = 497
 # genes in genesets = 494

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

<r> metagenes = 0.91
 <r> genes = 0.71

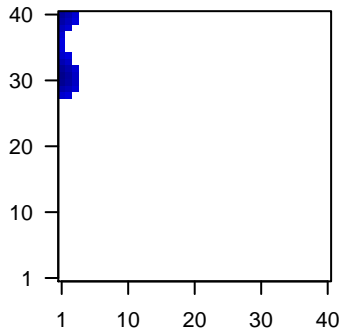
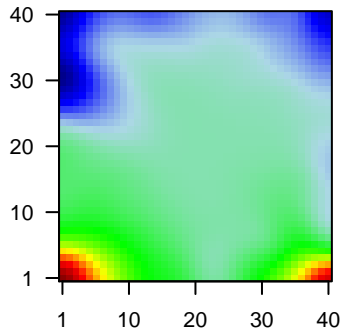
<FC> = -0.15
 <t-score> = -1.12
 <p-value> = 0.31
 <fdr> = 0.64

Local Genelist

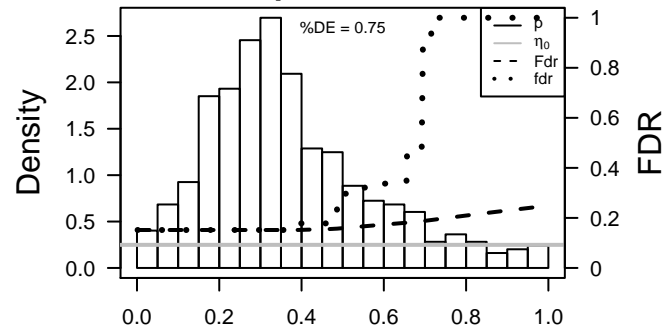
Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.38	0.001	0.2	1 x 31 jun B proto-oncogene [Source:HGNC Symbol;Acc:HGNC:62]
2	ENSG0000001	-0.29	0.008	0.2	2 x 32 lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
3	ENSG0000001	-0.52	0.010	0.2	1 x 31 FBJ murine osteosarcoma viral oncogene homolog [Source:H
4	ENSG0000002	-0.21	0.016	0.2	3 x 29 metallothionein 1A [Source:HGNC Symbol;Acc:HGNC:7393]
5	ENSG0000001	-0.22	0.020	0.2	2 x 33 jun proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6204]
6	ENSG0000001	-0.19	0.025	0.2	2 x 28 sulfatase 2 [Source:HGNC Symbol;Acc:HGNC:20392]
7	ENSG0000001	0.26	0.026	0.2	1 x 38
8	ENSG0000002	-0.19	0.032	0.2	1 x 34 DNAJC25-GNG10 readthrough [Source:HGNC Symbol;Acc:I
9	ENSG0000002	-0.19	0.033	0.2	1 x 34 guanine nucleotide binding protein (G protein), gamma 10 [S
10	ENSG0000001	-0.21	0.043	0.2	1 x 34 WW domain binding protein 5 [Source:HGNC Symbol;Acc:HC
11	ENSG0000001	-0.2	0.050	0.2	1 x 32 tropomyosin 4 [Source:HGNC Symbol;Acc:HGNC:12013]
12	ENSG0000001	-0.45	0.055	0.2	1 x 31 metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
13	ENSG0000001	-0.27	0.057	0.2	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
14	ENSG0000001	-0.18	0.061	0.2	3 x 29 protein S (alpha) [Source:HGNC Symbol;Acc:HGNC:9456]
15	ENSG0000001	-0.23	0.062	0.2	1 x 35 annexin A5 [Source:HGNC Symbol;Acc:HGNC:543]
16	ENSG0000001	-0.13	0.066	0.2	3 x 39 melanoma antigen family D2 [Source:HGNC Symbol;Acc:HGI
17	ENSG0000001	-0.49	0.069	0.2	1 x 32 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:H
18	ENSG0000001	-0.28	0.077	0.2	1 x 40 integrin, beta 1 (fibronectin receptor, beta polypeptide, antige
19	ENSG0000001	-0.42	0.078	0.2	1 x 31 nuclear receptor subfamily 4, group A, member 1 [Source:HG
20	ENSG0000001	-0.45	0.081	0.2	1 x 31 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2

Profile

Spot



p-values



MLH1_normHNPC vs

Local Summary

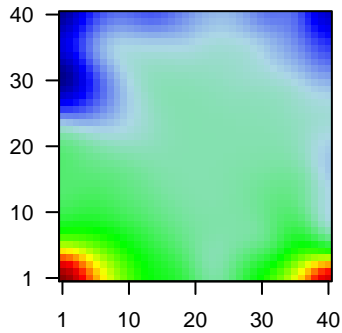
%DE = 0.78
 # metagenes = 3
 # genes = 128
 # genes in genesets = 127

 # genes with $fdr < 0.1 = 14$ (0 + / 14 -)
 # genes with $fdr < 0.05 = 0$ (0 + / 0 -)
 # genes with $fdr < 0.01 = 0$ (0 + / 0 -)

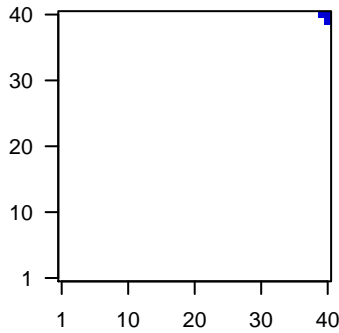
$\langle r \rangle$ metagenes = 1
 $\langle r \rangle$ genes = 0.86

 $\langle FC \rangle = -0.14$
 $\langle t\text{-score} \rangle = -1.48$
 $\langle p\text{-value} \rangle = 0.19$
 $\langle fdr \rangle = 0.61$

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.18	0.001	0.06	39 x 40 cytoskeleton-associated protein 4 [Source:HGNC Symbol;Acc:HGNC:11879]
2	ENSG0000000	-0.18	0.004	0.06	40 x 39 gamma-glutamylcyclotransferase [Source:HGNC Symbol;Acc:HGNC:11879]
3	ENSG0000001	-0.46	0.005	0.06	40 x 40 S100 calcium binding protein A11 [Source:HGNC Symbol;Acc:HGNC:11879]
4	ENSG0000001	-0.18	0.008	0.06	40 x 40 CDC42 effector protein (Rho GTPase binding) 1 [Source:HGNC Symbol;Acc:HGNC:11879]
5	ENSG0000000	-0.29	0.012	0.06	40 x 40 thymosin beta 10 [Source:HGNC Symbol;Acc:HGNC:11879]
6	ENSG0000001	-0.2	0.013	0.06	40 x 40 eukaryotic translation initiation factor 4E binding protein 1 [Source:HGNC Symbol;Acc:HGNC:11879]
7	ENSG0000001	-1.13	0.016	0.06	40 x 40 phospholipase A2, group IIA (platelets, synovial fluid) [Source:HGNC Symbol;Acc:HGNC:11879]
8	ENSG0000001	-0.21	0.016	0.07	39 x 40 proteasome (prosome, macropain) subunit, beta type, 5 [Source:HGNC Symbol;Acc:HGNC:11879]
9	ENSG0000001	-0.14	0.022	0.07	39 x 40 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:FGS0000001]
10	ENSG0000002	-0.19	0.024	0.07	40 x 40 NME1-NME2 readthrough [Source:HGNC Symbol;Acc:HGNC:11879]
11	ENSG0000000	-0.24	0.028	0.07	40 x 40 NME/NM23 nucleoside diphosphate kinase 2 [Source:HGNC Symbol;Acc:HGNC:11879]
12	ENSG0000001	-0.16	0.030	0.07	40 x 40 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein ret1 [Source:HGNC Symbol;Acc:HGNC:11879]
13	ENSG0000001	-0.23	0.030	0.07	40 x 40 KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein ret2 [Source:HGNC Symbol;Acc:HGNC:11879]
14	ENSG0000001	-0.19	0.032	0.07	40 x 39 pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor [Source:HGNC Symbol;Acc:HGNC:11879]
15	ENSG0000001	-0.2	0.033	0.11	40 x 40 peroxiredoxin 4 [Source:HGNC Symbol;Acc:HGNC:17169]
16	ENSG0000001	-0.19	0.043	0.11	40 x 40 pyrroline-5-carboxylate reductase 1 [Source:HGNC Symbol;Acc:HGNC:17169]
17	ENSG0000001	-0.2	0.045	0.11	40 x 40 transmembrane emp24 protein transport domain containing 3 [Source:HGNC Symbol;Acc:HGNC:17169]
18	ENSG0000001	-0.14	0.050	0.11	39 x 40 transmembrane emp24 protein transport domain containing 9 [Source:HGNC Symbol;Acc:HGNC:17169]
19	ENSG0000000	-0.14	0.068	0.11	40 x 40 myeloid-derived growth factor [Source:HGNC Symbol;Acc:HGNC:17169]
20	ENSG0000002	-0.16	0.072	0.11	40 x 39 centromere protein W [Source:HGNC Symbol;Acc:HGNC:214]

p-values

