

MLH1_normHNPC vs

Global Summary

%DE = 0.33
 # genes with fdr < 0.2 = 0 (0 + / 0 -)
 # genes with fdr < 0.1 = 0 (0 + / 0 -)
 # genes with fdr < 0.05 = 0 (0 + / 0 -)
 # genes with fdr < 0.01 = 0 (0 + / 0 -)

 # genes in genesets = 18990

 <FC> = 0
 <t-score> = -0.13
 <p-value> = 0.28
 <fdr> = 0.67

Global Genelist

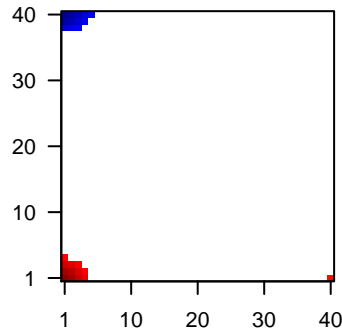
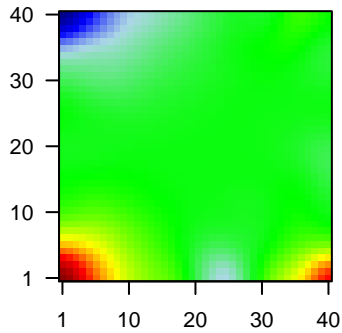
Rank	ID	log(FC)	fdr p-value	Description Metagene	
1	ENSG00000002	0.01	5e-05	0.4	20 x 16
2	ENSG00000001	-0.02	6e-05	0.4	35 x 22 REM2 and RAB-like small GTPase 1 [Source:HGNC Symbol]
3	ENSG00000002	-0.05	1e-04	0.4	30 x 40 tripartite motif containing 16 [Source:HGNC Symbol;Acc:HGNC]
4	ENSG00000002	0	1e-04	0.4	18 x 14 chromosome 12 open reading frame 74 [Source:HGNC Symt]
5	ENSG00000001	0.07	2e-04	0.4	9 x 10 transient receptor potential cation channel, subfamily C, mem
6	ENSG00000001	-0.04	2e-04	0.4	14 x 29 UBX domain protein 2A [Source:HGNC Symbol;Acc:HGNC:2]
7	ENSG00000000	-0.14	2e-04	0.4	40 x 33 myeloid leukemia factor 2 [Source:HGNC Symbol;Acc:HGNC]
8	ENSG00000001	-0.01	3e-04	0.4	36 x 23 FGGY carbohydrate kinase domain containing [Source:HGNC]
9	ENSG00000001	-0.09	3e-04	0.4	39 x 31 mitochondrial ribosomal protein L40 [Source:HGNC Symbol;A
10	ENSG00000001	-0.09	3e-04	0.4	10 x 33 diphthamide biosynthesis 3 [Source:HGNC Symbol;Acc:HGNC]
11	ENSG00000001	0.03	4e-04	0.4	14 x 11 proline rich 14-like [Source:HGNC Symbol;Acc:HGNC:28738]
12	ENSG00000001	-0.04	5e-04	0.4	32 x 21 dynein, cytoplasmic 2, light intermediate chain 1 [Source:HG]
13	ENSG00000001	0	5e-04	0.4	28 x 20 transducin-like enhancer of split 6 [Source:HGNC Symbol;Ac
14	ENSG00000001	0.03	5e-04	0.4	28 x 33 ADP-ribosylation factor-like 6 interacting protein 6 [Source:H
15	ENSG00000001	-0.06	6e-04	0.4	29 x 33 COX11 cytochrome c oxidase copper chaperone [Source:HG]
16	ENSG00000001	-0.11	6e-04	0.4	40 x 34 spermine synthase [Source:HGNC Symbol;Acc:HGNC:11123]
17	ENSG00000001	0.22	6e-04	0.4	4 x 1 pleckstrin homology domain containing, family F (with FYVE c
18	ENSG00000001	0.06	7e-04	0.4	34 x 35 CCR4-NOT transcription complex, subunit 11 [Source:HGNC]
19	ENSG00000001	-0.02	8e-04	0.4	36 x 24 histone deacetylase 8 [Source:HGNC Symbol;Acc:HGNC:133]
20	ENSG00000001	0.24	8e-04	0.4	5 x 3 solute carrier family 44 (choline transporter), member 2 [Sour

Global Geneset Analysis

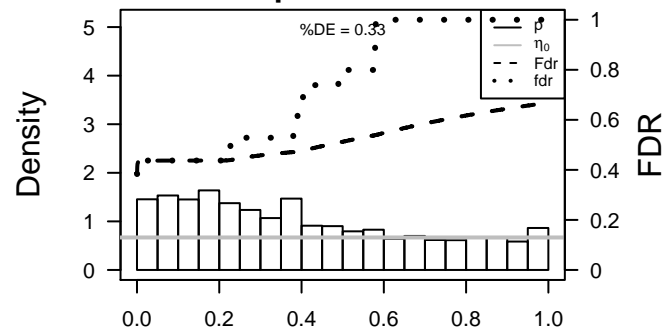
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	29.82	0e+00	844	Colon Cancer_Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
2	29.22	0e+00	427	Tissue WIRTH_Immune system
3	23.81	0e+00	5643	Lymphoma_OPP_Txn_transition
4	20.28	0e+00	7592	Lymphoma_OPP_Strong_enhancer
5	19.49	3e-06	1340	GSEA C2P_UJANA_ATM_PCC_NETWORK
6	17.22	2e-05	175	GSEA C2LEE_DIFFERENTIATING_T_LYMPHOCYTE
7	16.93	2e-05	3122	Colon Cancer_Lembcke_H1_Colon
8	15.75	2e-05	500	Lymphoma_WIRTH_lymphoma937_spot J
9	15.68	2e-05	484	Lymphoma_Opp_June14_MMML937_tumors+controls_group.overexpression
10	14.54	3e-05	574	Cancer_Lembcke_Colonc_Inflammation
11	14.54	3e-05	1215	Lymphoma_OPPANG_BCR_DN
12	14.02	4e-05	7491	Lymphoma_OPP_Txn_elongation
13	13.86	4e-05	246	GSEA C2O1_PLASMACYTOMA_UP
14	13.85	4e-05	347	Lymphoma_WIRTH_lymphoma937_spot H
15	13.8	4e-05	343	BP immune response
16	13.54	4e-05	336	Lymphoma_Opp_June14_MMML937_tumors+controls_group.overexpression
17	13.41	4e-05	220	GSEA C2MCLACHLAN_DENTAL_CARIES_UP
18	13.25	4e-05	186	HM HALLMARK_INTERFERON_GAMMA_RESPONSE
19	13.24	4e-05	259	GSEA C2POOLA_INVASIVE_BREAST_CANCER_UP
20	13.08	4e-05	1914	GSEA C2PILON_KLF1_TARGETS_DN
<i>Underexpressed</i>				
1	-19.16	3e-06	5039	Lymphoma_OPP_Repressed
2	-15.69	2e-05	2838	Lymphoma_OPP_Poised_promoter
3	-14.18	4e-05	1197	GSEA C2BLALOCK_ALZHEIMERS_DISEASE_DN
4	-12.66	6e-05	3109	Colon Cancer_P_Colon
5	-12.6	6e-05	476	Tissue WIRTH_Nervous System
6	-12.06	6e-05	10239	Brain Overlap_fetal_midbrain_ReprPC
7	-12.03	6e-05	1441	CC mitochondrion
8	-11.77	7e-05	4879	Colon Cancer_S1_Colon
9	-11.51	8e-05	198	HM HALLMARK_OXIDATIVE_PHOSPHORYLATION
10	-11.28	8e-05	5285	Toxic LU_BPDE_0.005_DN
11	-11.24	8e-05	10278	Brain Overlap_fetal_midbrain_ReprPCWk
12	-11.18	6e-02	16	Cancer LIU_PROSTATE_CANCER_DN
13	-11.11	9e-05	425	CC mitochondrial inner membrane
14	-10.53	1e-04	83	GSEA C2MOOHA_VOXPHOS
15	-10.45	1e-04	132	Colon Cancer_Metastasis_CRC-cluster-b
16	-10.33	2e-04	136	BP cellular metabolic process
17	-10.32	2e-04	3406	Colon Cancer_ReprPC_Colon
18	-10.23	2e-04	76	GSEA C2REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_ATP_S
19	-10.19	2e-04	96	BP respiratory electron transport chain
20	-10.16	2e-04	111	GSEA C2REACTOME_TCA_CYCLE_AND_RESPIRATORY_ELECTRON_T

Profile

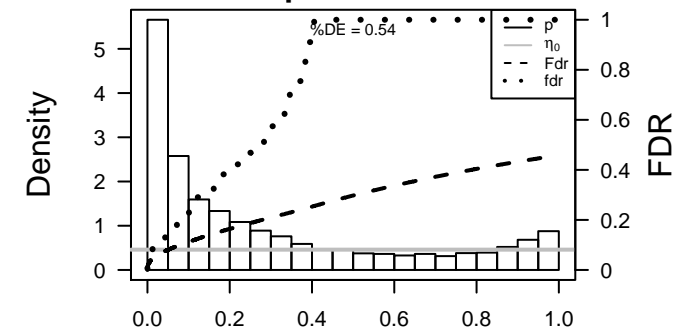
Regulated Spots



p-values



p-values



MLH1_normHNPC vs

Local Summary

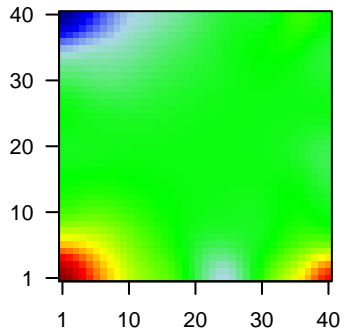
%DE = 0.98
 # metagenes = 12
 # genes = 258
 # genes in genesets = 253

 # genes with $fdr < 0.1$ = 249 (249 + / 0 -)
 # genes with $fdr < 0.05$ = 249 (249 + / 0 -)
 # genes with $fdr < 0.01$ = 232 (232 + / 0 -)

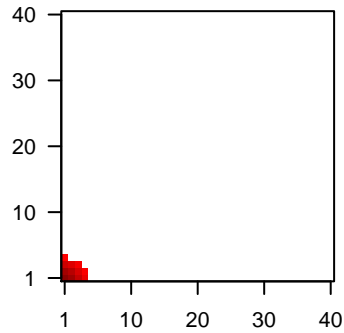
<r> metagenes = 1
 <r> genes = 0.88

 <FC> = 0.28
 <t-score> = 2.44
 <p-value> = 0.04
 <fdr> = 0.45

Profile



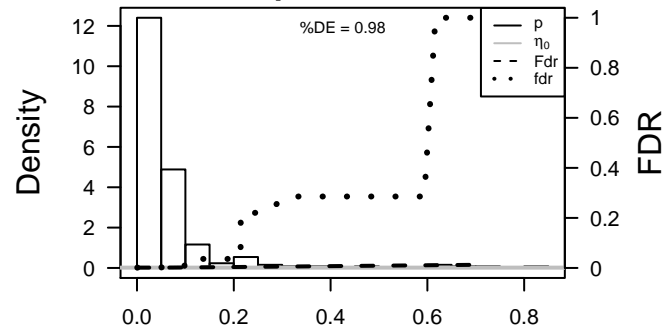
Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.22	6e-04	0.001	4 x 1 pleckstrin homology domain containing, family F (with FYVE c
2	ENSG0000001	0.43	3e-03	0.001	1 x 1 major histocompatibility complex, class II, DQ beta 1 [Source:
3	ENSG0000001	0.76	4e-03	0.001	1 x 1 chemokine (C-X-C motif) receptor 4 [Source:HGNC Symbol;
4	ENSG0000000	0.31	5e-03	0.001	2 x 1 baculoviral IAP repeat containing 3 [Source:HGNC Symbol;A
5	ENSG0000001	0.2	6e-03	0.001	4 x 2 tumor protein p53 inducible nuclear protein 1 [Source:HGNC
6	ENSG0000001	0.32	7e-03	0.001	1 x 1 ribonuclease, RNase A family, k6 [Source:HGNC Symbol;Acc
7	ENSG0000001	0.29	7e-03	0.001	2 x 1 matrix metalloproteinase 9 [Source:HGNC Symbol;Acc:HGNC
8	ENSG0000001	0.25	7e-03	0.001	4 x 1 CDC42 small effector 2 [Source:HGNC Symbol;Acc:HGNC:11
9	ENSG0000001	0.37	9e-03	0.001	1 x 1 B-cell translocation gene 1, anti-proliferative [Source:HGNC
10	ENSG0000001	0.21	9e-03	0.001	3 x 1 family with sequence similarity 102, member A [Source:HGNC
11	ENSG0000000	0.57	9e-03	0.001	1 x 1 lysozyme [Source:HGNC Symbol;Acc:HGNC:6740]
12	ENSG0000000	0.36	1e-02	0.001	1 x 1 serine/threonine kinase 17b [Source:HGNC Symbol;Acc:HGNC
13	ENSG0000001	0.51	1e-02	0.001	1 x 1 Fc fragment of IgM receptor [Source:HGNC Symbol;Acc:HGNC
14	ENSG0000001	0.27	1e-02	0.001	1 x 1 CD1c molecule [Source:HGNC Symbol;Acc:HGNC:1636]
15	ENSG0000001	0.22	1e-02	0.001	4 x 1 histocompatibility (minor) HA-1 [Source:HGNC Symbol;Acc:H
16	ENSG0000001	0.34	1e-02	0.001	1 x 1 macrophage expressed 1 [Source:HGNC Symbol;Acc:HGNC
17	ENSG0000002	0.27	1e-02	0.001	4 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E71
18	ENSG0000001	0.51	1e-02	0.001	1 x 1 selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
19	ENSG0000001	0.24	1e-02	0.001	4 x 1 c-src tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:244
20	ENSG0000000	0.29	2e-02	0.001	2 x 1 tumor necrosis factor receptor superfamily, member 1B [Sour

p-values



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%DE = 0.41
 # metagenes = 1
 # genes = 92
 # genes in genesets = 91

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

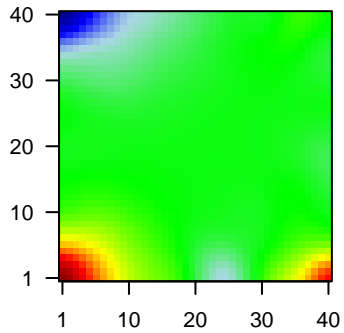
<r> metagenes = NA
 <r> genes = 0.46

 <FC> = 0.29
 <t-score> = 0.94
 <p-value> = 0.36
 <fdr> = 0.7

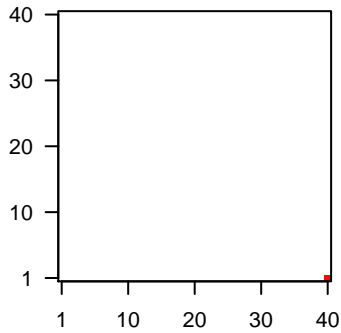
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000000	0.88	0.04	0.4	40 x 1 chloride channel accessory 4 [Source:HGNC Symbol;Acc:HG
2	ENSG000001	0.89	0.04	0.4	40 x 1 aquaporin 8 [Source:HGNC Symbol;Acc:HGNC:642]
3	ENSG000001	0.48	0.07	0.4	40 x 1 solute carrier family 26 (anion exchanger), member 2 [Source
4	ENSG000001	0.82	0.08	0.4	40 x 1 carcinoembryonic antigen-related cell adhesion molecule 5 [
5	ENSG000000	0.88	0.10	0.4	40 x 1 carcinoembryonic antigen-related cell adhesion molecule 7 [
6	ENSG000000	0.34	0.10	0.4	40 x 1 carbonic anhydrase XII [Source:HGNC Symbol;Acc:HGNC:1
7	ENSG000002	0.55	0.10	0.4	40 x 1 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:M0
8	ENSG000001	0.44	0.11	0.4	40 x 1 carbonic anhydrase IV [Source:HGNC Symbol;Acc:HGNC:13
9	ENSG000002	0.62	0.11	0.4	40 x 1
10	ENSG000002	0.38	0.12	0.4	40 x 1 tripartite motif containing 31 [Source:HGNC Symbol;Acc:HG
11	ENSG000000	0.5	0.13	0.4	40 x 1 carcinoembryonic antigen-related cell adhesion molecule 6 (l
12	ENSG000001	0.5	0.13	0.4	40 x 1 chromosome 10 open reading frame 99 [Source:HGNC Synt
13	ENSG000001	0.38	0.13	0.4	40 x 1 selenium binding protein 1 [Source:HGNC Symbol;Acc:HGNC
14	ENSG000000	0.68	0.14	0.4	40 x 1 solute carrier family 26 (anion exchanger), member 3 [Source
15	ENSG000000	0.46	0.17	0.4	40 x 1 carcinoembryonic antigen-related cell adhesion molecule 1 (l
16	ENSG000001	0.76	0.20	0.4	40 x 1 guanylate cyclase activator 2A (guanylin) [Source:HGNC Syn
17	ENSG000001	0.48	0.20	0.4	40 x 1 stratifin [Source:HGNC Symbol;Acc:HGNC:10773]
18	ENSG000001	0.34	0.21	0.4	40 x 1 transmembrane and immunoglobulin domain containing 1 [Sc
19	ENSG000001	0.57	0.22	0.4	40 x 1 tetraspanin 1 [Source:HGNC Symbol;Acc:HGNC:20657]
20	ENSG000001	0.29	0.25	0.4	40 x 1 hydroxysteroid (11-beta) dehydrogenase 2 [Source:HGNC S

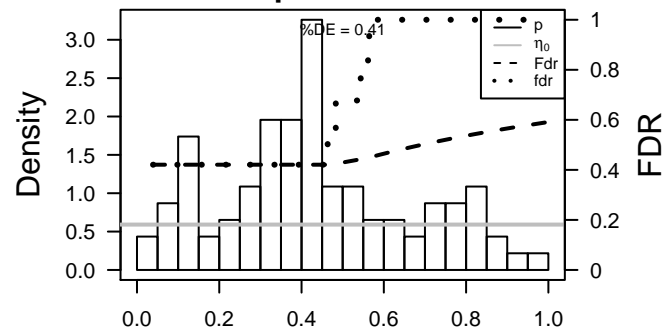
Profile



Spot



p-values



MLH1_normHNPC vs

Local Summary

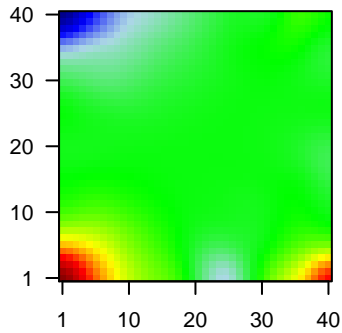
%DE = 0.96
 # metagenes = 12
 # genes = 286
 # genes in genesets = 283

 # genes with $fdr < 0.1$ = 275 (0 + / 275 -)
 # genes with $fdr < 0.05$ = 263 (0 + / 263 -)
 # genes with $fdr < 0.01$ = 0 (0 + / 0 -)

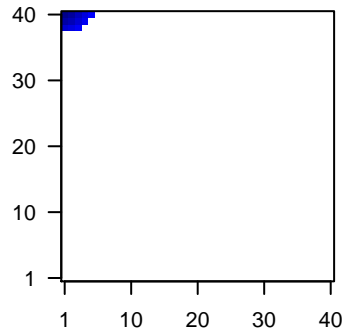
<r> metagenes = 1
 <r> genes = 0.91

 <FC> = -0.26
 <t-score> = -1.56
 <p-value> = 0.18
 <fdr> = 0.48

Profile



Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.27	0.009	0.01	3 x 38 Shwachman-Bodian-Diamond syndrome [Source:HGNC Syr
2	ENSG0000001	-0.57	0.031	0.01	2 x 40 aldehyde dehydrogenase 1 family, member A1 [Source:HGNC
3	ENSG0000001	-0.24	0.033	0.01	5 x 40 acyl-CoA thioesterase 1 [Source:HGNC Symbol;Acc:HGNC::
4	ENSG0000001	-0.33	0.039	0.01	3 x 40 related RAS viral (r-ras) oncogene homolog [Source:HGNC
5	ENSG0000001	-0.54	0.040	0.01	1 x 40 regulator of G-protein signaling 2 [Source:HGNC Symbol;Acc
6	ENSG0000001	-0.36	0.040	0.01	1 x 39 peripheral myelin protein 22 [Source:HGNC Symbol;Acc:HGNC
7	ENSG0000001	-0.35	0.044	0.01	1 x 40 receptor (G protein-coupled) activity modifying protein 1 [Sou
8	ENSG0000000	-0.33	0.048	0.01	3 x 40 monoamine oxidase B [Source:HGNC Symbol;Acc:HGNC:68
9	ENSG0000001	-0.33	0.051	0.01	3 x 40 tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:HGNC::
10	ENSG0000001	-0.28	0.054	0.01	4 x 40 BCL2-associated athanogene 3 [Source:HGNC Symbol;Acc:
11	ENSG0000001	-0.33	0.067	0.01	3 x 40 chemokine (C-C motif) ligand 11 [Source:HGNC Symbol;Acc
12	ENSG0000002	-0.35	0.069	0.01	1 x 40 aquaporin 1 (Colton blood group) [Source:HGNC Symbol;Acc
13	ENSG0000001	-0.34	0.070	0.01	5 x 40 nuclear protein, transcriptional regulator, 1 [Source:HGNC Sy
14	ENSG0000001	-0.15	0.073	0.01	5 x 40 selenoprotein M [Source:EntrezGene;Acc:140606]
15	ENSG0000001	-0.23	0.074	0.01	5 x 40 tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:HGNC::
16	ENSG0000001	-0.29	0.082	0.01	3 x 40 dual specificity phosphatase 3 [Source:HGNC Symbol;Acc:Hi
17	ENSG0000001	-0.25	0.088	0.01	2 x 40 cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) [Sc
18	ENSG0000000	-0.27	0.090	0.01	4 x 40 TEA domain family member 3 [Source:HGNC Symbol;Acc:HC
19	ENSG0000001	-0.24	0.104	0.01	4 x 40 nerve growth factor receptor (TNFRSF16) associated protein
20	ENSG0000001	-0.37	0.105	0.01	1 x 40 A kinase (PRKA) anchor protein 12 [Source:HGNC Symbol;A

p-values

