

MLH1_cancerHNPCC

Global Summary

%DE = 0.39
 # genes with fdr < 0.2 = 5 (3 + / 2 -)
 # 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> = 0.23
 <p-value> = 0.26
 <fdr> = 0.61

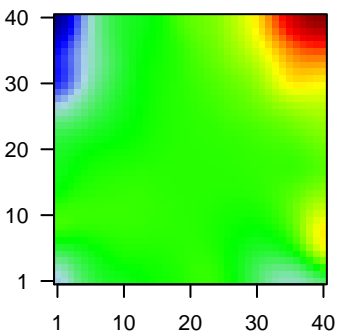
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG000000	0.05	3e-05	29 x 35 spindle apparatus coiled-coil protein 1 [Source:HGNC Symb
2	ENSG000000	0.03	4e-05	11 x 10 zinc finger protein 317 [Source:HGNC Symbol;Acc:HGNC:13
3	ENSG000000	-0.05	6e-05	18 x 1 Sin3A-associated protein, 25kDa [Source:HGNC Symbol;Acc
4	ENSG000000	-0.1	6e-05	7 x 1 actin related protein 2/3 complex, subunit 2, 34kDa [Source:H
5	ENSG000000	0.09	6e-05	36 x 34 mitochondrial ribosome recycling factor [Source:HGNC Symb
6	ENSG000000	0.01	7e-05	24 x 30 mediator complex subunit 17 [Source:HGNC Symbol;Acc:HG
7	ENSG000000	0.03	1e-04	27 x 35 UTP15, U3 small nucleolar ribonucleoprotein, homolog (S. ce
8	ENSG000000	0.04	1e-04	28 x 35 HAU5 augmin-like complex, subunit 6 [Source:HGNC Symbc
9	ENSG000000	0.08	2e-04	35 x 33 pro-melanin-concentrating hormone [Source:HGNC Symbol;
10	ENSG000000	0.02	2e-04	22 x 34 cadherin, EGF LAG seven-pass G-type receptor 2 [Source:f
11	ENSG000000	0.02	3e-04	30 x 26 ATPase family, AAA domain containing 5 [Source:HGNC Sym
12	ENSG000000	0.07	3e-04	40 x 31 ribosomal protein S6 kinase, 90kDa, polypeptide 4 [Source:H
13	ENSG000000	0.13	3e-04	34 x 40 basic transcription factor 3 [Source:HGNC Symbol;Acc:HGNC
14	ENSG000000	0.03	4e-04	37 x 25 coiled-coil domain containing 77 [Source:HGNC Symbol;Acc
15	ENSG000000	-0.06	4e-04	11 x 1 ankyrin repeat domain 12 [Source:HGNC Symbol;Acc:HGNC
16	ENSG000000	-0.08	4e-04	6 x 1 interleukin 6 receptor [Source:HGNC Symbol;Acc:HGNC:601
17	ENSG000000	0.08	5e-04	29 x 37 endothelial cell-specific molecule 1 [Source:HGNC Symbol;A
18	ENSG000000	0.02	5e-04	32 x 25 zinc finger protein 695 [Source:HGNC Symbol;Acc:HGNC:30
19	ENSG000000	0.03	5e-04	35 x 25 ligand dependent nuclear receptor corepressor-like [Source:l
20	ENSG000000	0.07	5e-04	34 x 33 SCL/TAL1 interrupting locus [Source:HGNC Symbol;Acc:HG

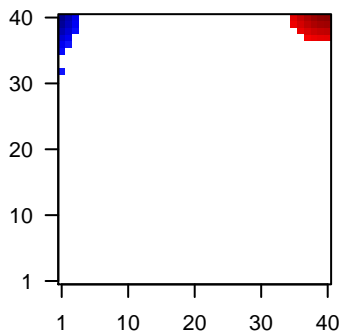
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	31.29	0	807	Lymphom10pp_June14_MMML937 tumors+controls_group.overexpression
2	31.19	0	811	Lymphom10IRTH_lymphoma937_spot D
3	29.03	0	550	Cancer_Lembcke_Normal vs Adenoma
4	27.76	0	1298	GSEA C2DODD_NASOPHARYNGEAL_CARINOMA_DN
5	27.64	0	582	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
6	25.14	0	830	Colon CaReTrack_CRC_TCGA_corr_R_normal_DN
7	24.53	0	713	Colon CaReTrack_CRC_TCGA_group.over_C_normal_DN
8	24.38	0	546	GSEA C2BOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
9	23.85	0	316	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
10	23.67	0	145	Glio_WILLSCHER_GBM_Verhaak-CL_up (C)
11	23.18	0	668	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
12	22.33	0	747	GSEA C2PUJANA_CHEK2_PCC_NETWORK
13	22.28	0	282	GSEA C2MANALO_HYPOXIA_DN
14	22.16	0	1228	GSEA C2KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP
15	22.06	0	859	GSEA C2LEE_BMP2_TARGETS_DN
16	21.7	0	138	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
17	21.59	0	1563	GSEA C2PUJANA_BRCA1_PCC_NETWORK
18	21.38	0	248	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
19	21.36	0	446	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
20	20.82	0	400	GSEA C2VECHI_GASTRIC_CANCER_EARLY_UP
<i>Underexpressed</i>				
1	-19.74	3e-06	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
2	-19.44	3e-06	507	Colon CaReTrack_CRC_TCGA_corr_C_normal_UP
3	-18.22	1e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
4	-18.19	1e-05	262	GSEA C2SABATES_COLORECTAL_ADENOMA_DN
5	-15.95	2e-05	5039	Lymphom10PP_Repressed
6	-15.79	2e-05	368	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_2B
7	-15.58	2e-05	844	Colon CaLembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
8	-15.44	3e-05	3507	CC_plasma membrane
9	-15.35	3e-05	692	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
10	-14.98	3e-05	3109	Colon CaReTrack_P_Colon
11	-14.82	1e-02	16	Cancer_LIU_PROSTATE_CANCER_DN
12	-14.74	3e-05	4879	Colon CaGoes1_Colon
13	-14.4	3e-05	4327	Colon CaLombWk2_Colon
14	-14.12	4e-05	347	Lymphom10IRTH_lymphoma937_spot H
15	-14.09	4e-05	336	GSEA C2VECHI_GASTRIC_CANCER_EARLY_DN
16	-14.04	4e-05	132	Colon CaLombisa_CRC-cluster-b
17	-13.79	4e-05	336	Lymphom10pp_June14_MMML937 tumors+controls_group.overexpression
18	-13.74	4e-05	1210	Brain_Fetal_TssP
19	-13.67	4e-05	478	GSEA C2JIM_MAMMARY_STEM_CELL_UP
20	-13.43	4e-05	418	GSEA C2SWEET_LUNG_CANCER_KRAS_DN

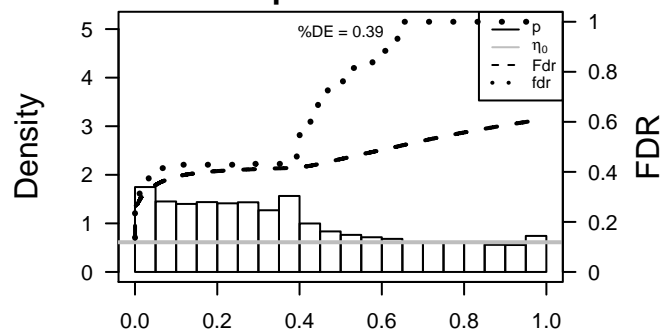
Profile



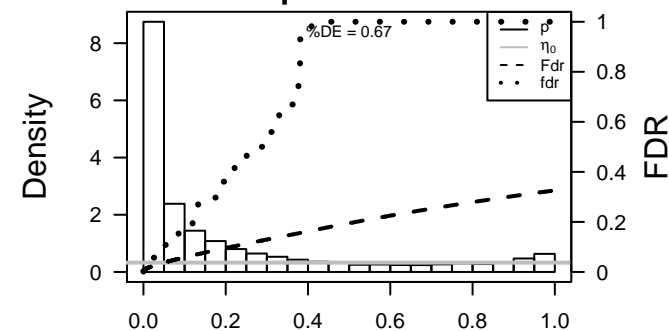
Regulated Spots



p-values



p-values



MLH1_cancerHNPCC

Local Summary

%DE = 0.9
 # metagenes = 21
 # genes = 423
 # genes in genesets = 417

 # genes with $fdr < 0.1$ = 350 (349 + / 1 -)
 # genes with $fdr < 0.05$ = 338 (337 + / 1 -)
 # genes with $fdr < 0.01$ = 115 (115 + / 0 -)

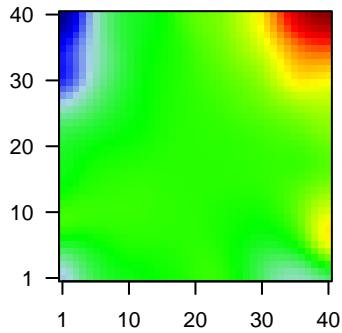
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.84

 $\langle FC \rangle$ = 0.19
 $\langle t\text{-score} \rangle$ = 2.48
 $\langle p\text{-value} \rangle$ = 0.05
 $\langle fdr \rangle$ = 0.42

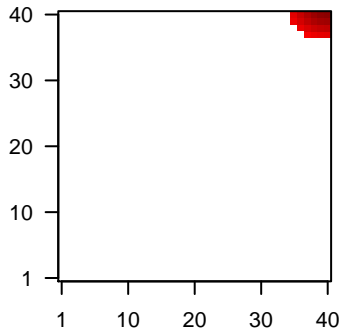
Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	0.21	0.001	0.008	36 x 40 ribosomal protein L27a [Source:HGNC Symbol;Acc:HGNC:10
2	ENSG0000000	0.31	0.002	0.008	38 x 40 ribosomal protein, large, P0 [Source:HGNC Symbol;Acc:HGNC
3	ENSG0000001	0.21	0.002	0.008	37 x 39 nucleolar and spindle associated protein 1 [Source:HGNC Sy
4	ENSG0000001	0.15	0.002	0.008	36 x 40 guanine nucleotide binding protein-like 3 (nucleolar) [Source:
5	ENSG0000001	0.21	0.002	0.008	39 x 38 suppressor APC domain containing 2 [Source:HGNC Symbol
6	ENSG0000001	0.3	0.002	0.008	37 x 40 phosphoribosylaminoimidazole carboxylase, phosphoribosyla
7	ENSG0000000	0.34	0.003	0.008	37 x 40 ribosomal protein L18 [Source:HGNC Symbol;Acc:HGNC:10
8	ENSG0000001	0.13	0.003	0.008	35 x 40 chromobox homolog 3 [Source:HGNC Symbol;Acc:HGNC:15
9	ENSG0000002	0.18	0.003	0.008	37 x 38 phosphoglycerate mutase family member 5 [Source:HGNC S
10	ENSG0000001	0.39	0.003	0.008	40 x 40 chromosome 19 open reading frame 48 [Source:HGNC Synt
11	ENSG0000001	0.22	0.003	0.008	40 x 38 pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:H
12	ENSG0000001	0.21	0.003	0.008	38 x 38 transmembrane protein 97 [Source:HGNC Symbol;Acc:HGNC
13	ENSG0000002	0.25	0.004	0.008	36 x 40 guanine nucleotide binding protein (G protein), beta polypepti
14	ENSG0000001	0.27	0.004	0.008	35 x 40 ribosomal protein S3 [Source:HGNC Symbol;Acc:HGNC:104
15	ENSG0000001	0.32	0.004	0.008	37 x 40 ribosomal protein L29 [Source:HGNC Symbol;Acc:HGNC:10
16	ENSG0000001	0.21	0.004	0.008	40 x 38 leucine rich repeat containing 75A [Source:HGNC Symbol;Ac
17	ENSG0000001	0.25	0.004	0.008	35 x 40 neurobeachin-like 1 [Source:HGNC Symbol;Acc:HGNC:2068
18	ENSG0000002	0.31	0.004	0.008	36 x 40 ribosomal protein S18 [Source:HGNC Symbol;Acc:HGNC:10
19	ENSG0000002	0.22	0.005	0.008	40 x 38 pituitary tumor-transforming 2 [Source:HGNC Symbol;Acc:H
20	ENSG0000001	0.2	0.005	0.008	36 x 40 NIN1/RPN12 binding protein 1 homolog [Source:HGNC Synt

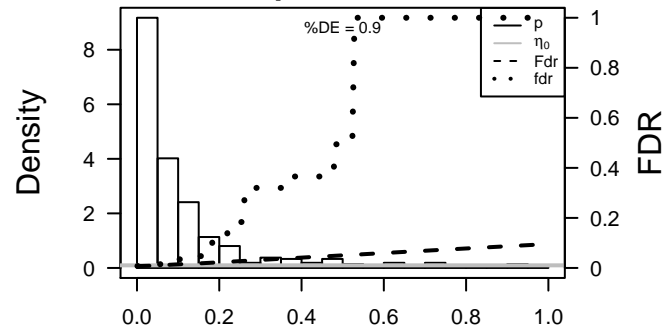
Profile



Spot



p-values



MLH1_cancerHNPCC

Local Summary

%DE = 0.56
 # metagenes = 1
 # genes = 18
 # genes in genesets = 18

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

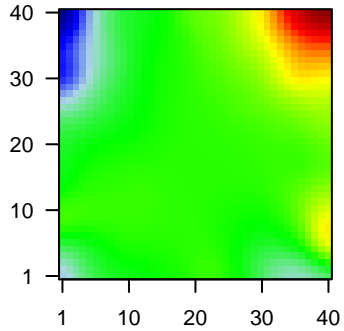
<r> metagenes = NA
 <r> genes = 0.81

 <FC> = -0.2
 <t-score> = -1.36
 <p-value> = 0.25
 <fdr> = 0.57

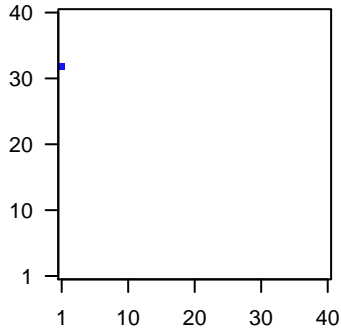
Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG0000001	-0.78	0.02	0.2	1 x 32 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:10000]
2	ENSG0000001	-0.24	0.13	0.2	1 x 32 cysteine-serine-rich nuclear protein 1 [Source:HGNC Symbol;Acc:HGNC:10000]
3	ENSG0000001	-0.19	0.13	0.2	1 x 32 regulator of calcineurin 2 [Source:HGNC Symbol;Acc:HGNC:10000]
4	ENSG0000002	-0.33	0.13	0.2	1 x 32 complement component 4A (Rodgers blood group) [Source:HGNC Symbol;Acc:HGNC:10000]
5	ENSG0000002	-0.36	0.14	0.2	1 x 32 complement component 4B (Chido blood group) [Source:HGNC Symbol;Acc:HGNC:10000]
6	ENSG0000001	-0.13	0.14	0.2	1 x 32 tropomyosin 4 [Source:HGNC Symbol;Acc:HGNC:12013]
7	ENSG0000000	-0.26	0.19	0.2	1 x 32 growth arrest and DNA-damage-inducible, beta [Source:HGNC Symbol;Acc:HGNC:10000]
8	ENSG0000001	-0.15	0.23	0.2	1 x 32 cysteine rich transmembrane BMP regulator 1 (chordin-like) [Source:HGNC Symbol;Acc:HGNC:10000]
9	ENSG0000001	-0.14	0.27	0.2	1 x 32 B-cell CLL/lymphoma 6 [Source:HGNC Symbol;Acc:HGNC:10000]
10	ENSG0000001	-0.23	0.27	0.2	1 x 32 Kruppel-like factor 2 [Source:HGNC Symbol;Acc:HGNC:6347]
11	ENSG0000001	-0.21	0.29	0.2	1 x 32 annexin A1 [Source:HGNC Symbol;Acc:HGNC:533]
12	ENSG0000001	-0.13	0.31	0.7	1 x 32 aspirin [Source:HGNC Symbol;Acc:HGNC:14872]
13	ENSG0000001	-0.14	0.39	0.7	1 x 32 transglutaminase 2 [Source:HGNC Symbol;Acc:HGNC:11778]
14	ENSG0000001	-0.1	0.48	1.0	1 x 32 immunoglobulin superfamily containing leucine-rich repeat [Source:HGNC Symbol;Acc:HGNC:10000]
15	ENSG0000001	-0.07	0.61	1.0	1 x 32 zinc finger, AN1-type domain 5 [Source:HGNC Symbol;Acc:HGNC:10000]
16	ENSG0000001	-0.13	0.65	1.0	1 x 32 S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:HGNC:10000]
17	ENSG0000001	0.06	0.76	1.0	1 x 32 periostin, osteoblast specific factor [Source:HGNC Symbol;Acc:HGNC:10000]
18	ENSG0000001	-0.01	0.96	1.0	1 x 32 collagen, type I, alpha 2 [Source:HGNC Symbol;Acc:HGNC:20000]

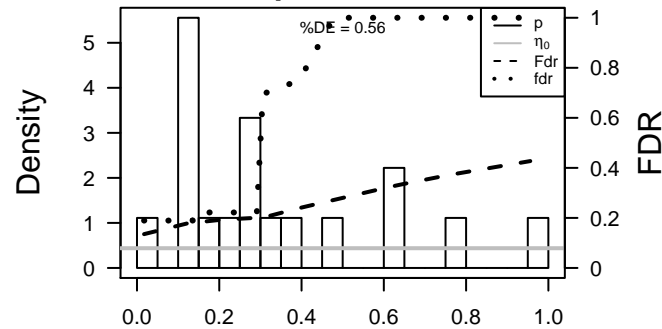
Profile



Spot



p-values



MLH1_cancerHNPCC

Local Summary

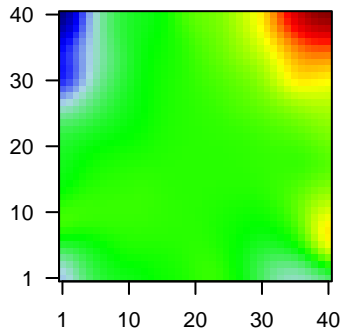
%DE = 0.91
 # metagenes = 14
 # genes = 247
 # genes in genesets = 244

 # genes with $fdr < 0.1$ = 205 (0 + / 205 -)
 # genes with $fdr < 0.05$ = 198 (0 + / 198 -)
 # genes with $fdr < 0.01$ = 0 (0 + / 0 -)

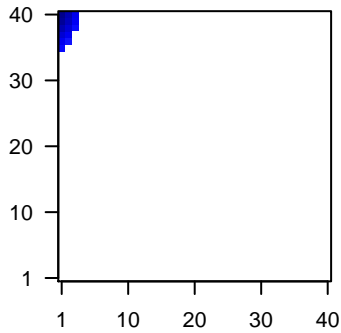
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.9

 $\langle FC \rangle$ = -0.24
 $\langle t\text{-score} \rangle$ = -1.77
 $\langle p\text{-value} \rangle$ = 0.16
 $\langle fdr \rangle$ = 0.46

Profile



Spot



Local Genelist

Rank	ID	log(FC)	p-value	fdr	Description
1	ENSG00000000	-0.22	0.001	0.02	1 x 35 actin, beta [Source:HGNC Symbol;Acc:HGNC:132]
2	ENSG00000001	-0.16	0.002	0.02	3 x 40 calmodulin 1 (phosphorylase kinase, delta) [Source:HGNC S]
3	ENSG00000001	-0.39	0.003	0.03	1 x 38
4	ENSG00000001	-0.17	0.005	0.03	2 x 38 praja ring finger 2, E3 ubiquitin protein ligase [Source:HGNC
5	ENSG00000001	-0.26	0.010	0.03	1 x 40 AHNAK nucleoprotein [Source:HGNC Symbol;Acc:HGNC:34]
6	ENSG00000001	-0.45	0.011	0.03	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
7	ENSG00000002	-0.22	0.015	0.03	2 x 36 SNRPN upstream reading frame [Source:HGNC Symbol;Acc:
8	ENSG00000001	-0.31	0.015	0.03	2 x 39 gelsolin [Source:HGNC Symbol;Acc:HGNC:4620]
9	ENSG00000001	-0.26	0.015	0.03	3 x 38 Shwachman-Bodian-Diamond syndrome [Source:HGNC Syr
10	ENSG00000001	-0.16	0.017	0.03	2 x 37 fibrinogen-like 2 [Source:HGNC Symbol;Acc:HGNC:3696]
11	ENSG00000001	-0.27	0.019	0.03	1 x 38 brain expressed, X-linked 4 [Source:HGNC Symbol;Acc:HGNC
12	ENSG00000001	-0.16	0.020	0.03	2 x 38 POTE ankyrin domain family, member E [Source:HGNC Syml
13	ENSG00000001	-0.23	0.021	0.03	1 x 36 yippee-like 5 [Source:HGNC Symbol;Acc:HGNC:18329]
14	ENSG00000002	-0.15	0.023	0.03	2 x 38 POTE ankyrin domain family, member J [Source:HGNC Syml
15	ENSG00000000	-0.39	0.024	0.03	1 x 37 phosphatidic acid phosphatase type 2A [Source:HGNC Syml
16	ENSG00000001	-0.2	0.028	0.03	1 x 37 serine incorporator 1 [Source:HGNC Symbol;Acc:HGNC:134]
17	ENSG00000001	-0.34	0.028	0.03	1 x 38 chromosome 8 open reading frame 4 [Source:HGNC Symbol
18	ENSG00000000	-0.15	0.029	0.03	2 x 38 cold shock domain containing E1, RNA-binding [Source:HGNC
19	ENSG00000001	-0.2	0.033	0.03	1 x 36 muscleblind-like splicing regulator 1 [Source:HGNC Symbol;
20	ENSG00000001	-0.32	0.036	0.03	1 x 40 SH3 domain binding glutamate-rich protein like [Source:HGNC

p-values

