

MLH1_adenomaHNPC

Global Summary

%DE = 0.29
 # genes with $fdr < 0.2 = 4$ (4 + / 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> = 0.09
 <p-value> = 0.34
 <fdr> = 0.71

Global Genelist

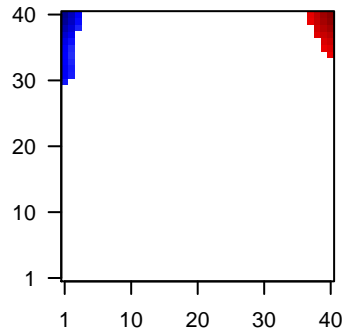
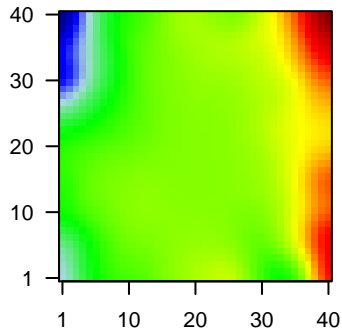
Rank	ID	log(FC)	fdr p-value	Description Metagene	
1	ENSG00000001	0	1e-06	0.2	23 x 18 chromosome 8 open reading frame 74 [Source:HGNC Symbc
2	ENSG00000001	0.01	2e-05	0.2	28 x 16 hes family bHLH transcription factor 5 [Source:HGNC Symbol
3	ENSG00000001	0	4e-05	0.2	23 x 23 hephaestin-like 1 [Source:HGNC Symbol;Acc:HGNC:30477]
4	ENSG00000001	0.01	5e-05	0.2	24 x 30 spermatogenesis associated 5 [Source:HGNC Symbol;Acc:H
5	ENSG00000001	0.07	6e-05	0.3	38 x 36 tumor-associated calcium signal transducer 2 [Source:HGNC
6	ENSG00000002	0	9e-05	0.3	21 x 19 methyltransferase like 11B [Source:HGNC Symbol;Acc:HGNC
7	ENSG00000001	0	9e-05	0.5	23 x 22 myosin XVIIIIB [Source:HGNC Symbol;Acc:HGNC:18150]
8	ENSG00000001	0.02	1e-04	0.6	32 x 26 zinc finger protein 607 [Source:HGNC Symbol;Acc:HGNC:28
9	ENSG00000001	0.08	2e-04	0.6	38 x 23 solute carrier family 29 (equilibrative nucleoside transporter),
10	ENSG00000001	0.01	2e-04	0.6	27 x 27 dynein, axonemal, assembly factor 3 [Source:HGNC Symbol;
11	ENSG00000001	0.03	4e-04	0.6	25 x 32 meiosis-specific nuclear structural 1 [Source:HGNC Symbol;
12	ENSG00000001	-0.52	4e-04	0.6	1 x 31 jun B proto-oncogene [Source:HGNC Symbol;Acc:HGNC:62
13	ENSG00000000	0.01	4e-04	0.6	30 x 20 transglutaminase 1 [Source:HGNC Symbol;Acc:HGNC:11777
14	ENSG00000000	-0.3	4e-04	0.6	1 x 35 actin, beta [Source:HGNC Symbol;Acc:HGNC:132]
15	ENSG00000000	0.08	5e-04	0.6	28 x 35 breast cancer 1, early onset [Source:HGNC Symbol;Acc:HGNC
16	ENSG00000001	0.04	5e-04	0.6	37 x 25 hydroxysteroid (17-beta) dehydrogenase 7 [Source:HGNC S
17	ENSG00000001	0.01	5e-04	0.6	27 x 25 calcitonin-related polypeptide alpha [Source:HGNC Symbol;
18	ENSG00000001	0.06	6e-04	0.6	37 x 27 aldehyde dehydrogenase 4 family, member A1 [Source:HGNC
19	ENSG00000001	0.03	6e-04	0.6	31 x 31
20	ENSG00000001	0.01	6e-04	0.6	25 x 18 glycine dehydrogenase (decarboxylating) [Source:HGNC Syn

Global Geneset Analysis

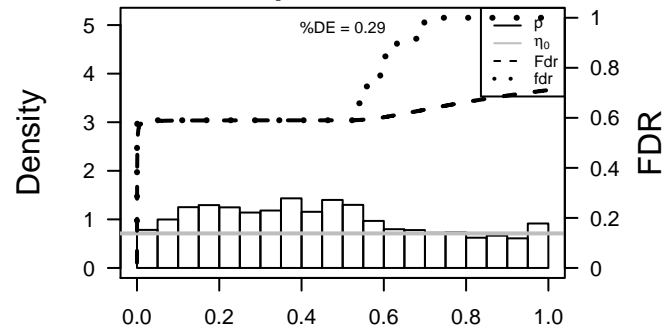
Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	24.33	0e+00	550	Cancer Lembecke_Normal vs Adenoma
2	23.63	0e+00	807	LymphomaLopp_June14_MMML937 tumors+controls_group.overexpression_
3	23.44	0e+00	811	LymphomaLIRTH_lymphoma937_spot D
4	19.36	3e-06	546	GSEA C2SOBERT_OLIGODENDROCYTE_DIFFERENTIATION_UP
5	18.51	1e-05	145	Glio WILLSCHER_GBM_Verhaak-CL_up (C
6	18.3	1e-05	668	GSEA C2MARSON_BOUND_BY_E2F4_UNSTIMULATED
7	18.25	1e-05	316	GSEA C2DUTERTRE ESTRADIOL_RESPONSE_24HR_UP
8	17.87	1e-05	400	GSEA C2VECCHI_GASTRIC_CANCER_EARLY_UP
9	17.31	2e-05	582	GSEA C2CAIRO_HEPATOBLASTOMA_CLASSES_UP
10	16.27	3e-03	16	Cancer SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
11	15.99	2e-05	282	GSEA C2MANALO_HYPOXIA_DN
12	15.74	2e-05	830	Colon CaReTrack_CRC_TCGA_corr_R_normal_DN
13	15.57	2e-05	138	GSEA C2ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUSTER
14	14.11	4e-05	446	GSEA C2SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6
15	14.09	4e-05	248	GSEA C2KOBAYASHI_EGFR_SIGNALING_24HR_DN
16	13.93	4e-05	8123	Colon CaReef_Colon
17	13.81	4e-05	975	GSEA C2NUYTEN_EZH2_TARGETS_DN
18	13.62	4e-05	747	GSEA C2PUJANA_CHEK2_PCC_NETWORK
19	13.31	4e-05	859	GSEA C2LEE_BMP2_TARGETS_DN
20	13.11	4e-05	10475	Colon CaReefA_Colon
<i>Underexpressed</i>				
1	-20.81	0e+00	844	Colon CaReefbke_TCGA-expr_kmeans_E_CIMP_H_UP_Cluster4_DN
2	-17.84	1e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
3	-17.1	2e-05	332	Colon CaReefTrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
4	-16.59	2e-05	368	GSEA C2LINDGREN_BLADEDER_CANCER_CLUSTER_2B
5	-15.89	2e-05	692	GSEA C2WONG_ADULT_TISSUE_STEM_MODULE
6	-15.89	2e-05	436	GSEA C2SMID_BREAST_CANCER_NORMAL_LIKE_UP
7	-15.55	2e-05	314	LymphomaLopp_June14_MMML937 tumors+controls_group.overexpression_
8	-15.46	3e-05	478	GSEA C2LIM_MAMMARY_STEM_CELL_UP
9	-15.37	3e-05	315	LymphomaLIRTH_lymphoma937_spot E
10	-15.29	3e-05	3109	Colon CaReefP_Colon
11	-15.18	3e-05	804	GSEA C2CUI_TCF21_TARGETS_2_DN
12	-14.37	3e-05	148	Colon CaReefTarsa_CRC-cluster-a
13	-14.3	3e-05	574	Cancer Lembecke_Colonc Inflammation
14	-13.89	4e-05	261	LymphomaLRENZ_Stromal signature 1
15	-13.66	4e-05	5039	LymphomaLopp_Repressed
16	-13.56	4e-05	263	GSEA C2WALLACE_PROSTATE_CANCER_RACE_UP
17	-13.5	4e-05	3507	CC plasma membrane
18	-13.39	4e-05	196	GSEA C2PICCALUGA_ANGIOIMMUNOBLASTIC_LYMPHOMA_UP
19	-13.3	4e-05	249	GSEA C2BOQUEST_STEM_CELL_UP
20	-13.17	4e-05	418	GSEA C2SWEET_LUNG_CANCER_KRAS_DN

Profile

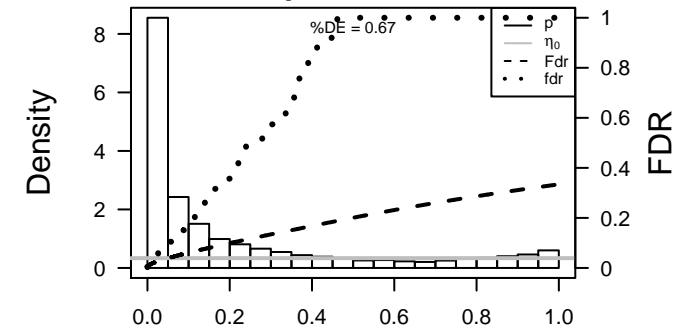
Regulated Spots



p-values



p-values



MLH1_adenomaHNPC

Local Summary

%DE = 0.83
 # metagenes = 19
 # genes = 457
 # genes in genesets = 449

 # genes with $fdr < 0.1$ = 187 (182 + / 5 -)
 # genes with $fdr < 0.05$ = 0 (0 + / 0 -)
 # genes with $fdr < 0.01$ = 0 (0 + / 0 -)

<r> metagenes = 0.99

<r> genes = 0.86

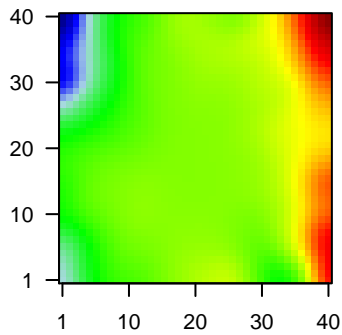
<FC> = 0.18

<t-score> = 1.74

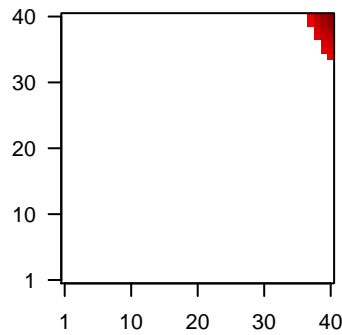
<p-value> = 0.2

<fdr> = 0.62

Profile



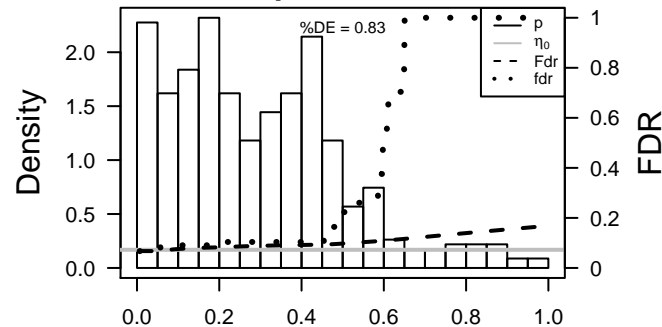
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	0.21	0.006	0.07	39 x 38 suppressor APC domain containing 2 [Source:HGNC Symbol]
2	ENSG0000001	0.19	0.008	0.07	37 x 40 solute carrier family 35 (adenosine 3'-phospho 5'-phospho)
3	ENSG0000001	0.23	0.009	0.07	39 x 37 hepatoma-derived growth factor [Source:HGNC Symbol;Acc:
4	ENSG0000000	0.28	0.010	0.07	38 x 39 TPX2, microtubule-associated [Source:HGNC Symbol;Acc:H
5	ENSG0000000	0.13	0.010	0.07	40 x 37 cytochrome b561 [Source:HGNC Symbol;Acc:HGNC:2571]
6	ENSG0000001	0.41	0.011	0.07	40 x 39 dual oxidase 2 [Source:HGNC Symbol;Acc:HGNC:13273]
7	ENSG0000001	0.24	0.012	0.07	38 x 40 ribonucleotide reductase M2 [Source:HGNC Symbol;Acc:HGI
8	ENSG0000002	0.41	0.012	0.07	40 x 40
9	ENSG0000001	0.24	0.012	0.07	40 x 38 ribophorin II [Source:HGNC Symbol;Acc:HGNC:10382]
10	ENSG0000001	0.13	0.012	0.07	40 x 35 cytochrome c oxidase assembly factor 4 homolog [Source:HC
11	ENSG0000001	0.15	0.012	0.07	38 x 40 mitochondrial ribosomal protein L17 [Source:HGNC Symbol;f
12	ENSG0000001	0.24	0.013	0.07	39 x 39 cyclin B2 [Source:HGNC Symbol;Acc:HGNC:1580]
13	ENSG0000001	0.29	0.014	0.07	40 x 39 cell division cycle 20 [Source:HGNC Symbol;Acc:HGNC:172:
14	ENSG0000001	0.17	0.015	0.07	39 x 37 MET proto-oncogene, receptor tyrosine kinase [Source:HGN
15	ENSG0000001	0.16	0.016	0.07	40 x 35 NOP10 ribonucleoprotein [Source:HGNC Symbol;Acc:HGNC
16	ENSG0000001	0.26	0.017	0.07	40 x 37 transaldolase 1 [Source:HGNC Symbol;Acc:HGNC:11559]
17	ENSG0000001	0.18	0.018	0.07	39 x 40 ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2 [S
18	ENSG0000001	0.15	0.019	0.07	38 x 38 transmembrane protein 97 [Source:HGNC Symbol;Acc:HGNC
19	ENSG0000001	0.23	0.020	0.07	39 x 38 anti-silencing function 1B histone chaperone [Source:HGNC
20	ENSG0000001	0.18	0.025	0.07	39 x 40 Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:F8\

p-values



MLH1_adenomaHNPC

Local Summary

%DE = 0.97
 # metagenes = 24
 # genes = 425
 # genes in genesets = 421

 # genes with $fdr < 0.1$ = 408 (0 + / 408 -)
 # genes with $fdr < 0.05$ = 407 (0 + / 407 -)
 # genes with $fdr < 0.01$ = 301 (0 + / 301 -)

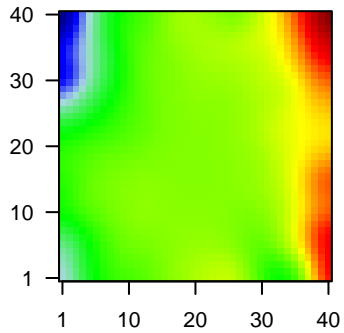
$\langle r \rangle$ metagenes = 0.94
 $\langle r \rangle$ genes = 0.78

 $\langle FC \rangle$ = -0.29
 $\langle t\text{-score} \rangle$ = -2.03
 $\langle p\text{-value} \rangle$ = 0.15
 $\langle fdr \rangle$ = 0.6

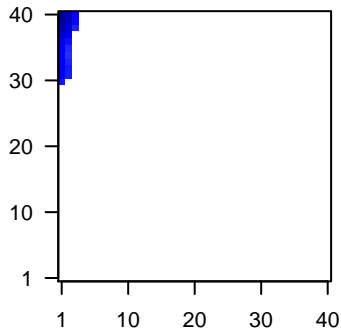
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.52	4e-04	0.002	1 x 31 jun B proto-oncogene [Source:HGNC Symbol;Acc:HGNC:62]
2	ENSG0000000	-0.3	4e-04	0.004	1 x 35 actin, beta [Source:HGNC Symbol;Acc:HGNC:132]
3	ENSG0000001	-1.02	8e-04	0.008	1 x 31 FBJ murine osteosarcoma viral oncogene homolog [Source:H
4	ENSG0000001	-0.59	8e-03	0.008	1 x 38 chromosome 8 open reading frame 4 [Source:HGNC Symbol
5	ENSG0000001	-0.57	9e-03	0.008	1 x 40 BTG family, member 2 [Source:HGNC Symbol;Acc:HGNC:11
6	ENSG0000001	-1.1	9e-03	0.008	1 x 32 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:H
7	ENSG0000001	-0.81	9e-03	0.008	1 x 31 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:HGNC:
8	ENSG0000001	-0.26	1e-02	0.008	1 x 36 yippee-like 5 [Source:HGNC Symbol;Acc:HGNC:18329]
9	ENSG0000001	-0.18	2e-02	0.008	2 x 37 fibrinogen-like 2 [Source:HGNC Symbol;Acc:HGNC:3696]
10	ENSG0000000	-0.41	2e-02	0.008	1 x 37 phosphatidic acid phosphatase type 2A [Source:HGNC Symb
11	ENSG0000001	-0.28	2e-02	0.008	1 x 35 proline-rich nuclear receptor coactivator 1 [Source:HGNC Sy
12	ENSG0000001	-0.85	3e-02	0.008	1 x 40 ras homolog family member B [Source:HGNC Symbol;Acc:H
13	ENSG0000001	-0.29	3e-02	0.008	2 x 39 gelsolin [Source:HGNC Symbol;Acc:HGNC:4620]
14	ENSG0000001	-0.69	3e-02	0.008	1 x 38 early growth response 1 [Source:HGNC Symbol;Acc:HGNC:3
15	ENSG0000001	-0.51	4e-02	0.008	1 x 31 metallothionein 2A [Source:HGNC Symbol;Acc:HGNC:7406]
16	ENSG0000001	-0.28	4e-02	0.008	3 x 40 related RAS viral (r-ras) oncogene homolog [Source:HGNC
17	ENSG0000001	-0.19	4e-02	0.008	2 x 32 lamin A/C [Source:HGNC Symbol;Acc:HGNC:6636]
18	ENSG0000001	-0.5	5e-02	0.008	1 x 40 tropomyosin 1 (alpha) [Source:HGNC Symbol;Acc:HGNC:12
19	ENSG0000000	-0.8	5e-02	0.008	1 x 36 vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
20	ENSG0000001	-0.43	5e-02	0.008	1 x 40 SH3 domain binding glutamate-rich protein like [Source:HGN

Profile



Spot



p-values

