

MLH1_adenomaHNPC

Global Summary

%DE = 0
 # 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> = -0.09
 <p-value> = 0.4
 <fdr> = 1

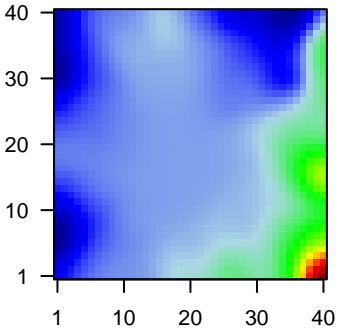
Global Genelist

Rank	ID	log(FC)	fdr p-value	Description Metagene
1	ENSG00000001	0.09	1e-06	1 36 x 3
2	ENSG00000000	0.04	5e-06	1 34 x 7 presenilin 1 [Source:HGNC Symbol;Acc:HGNC:9508]
3	ENSG00000001	0.06	2e-05	1 32 x 5 T-box 10 [Source:HGNC Symbol;Acc:HGNC:11593]
4	ENSG00000001	0	2e-05	1 23 x 18 chromosome 8 open reading frame 74 [Source:HGNC Symbc
5	ENSG00000001	0.11	2e-05	1 34 x 1 tetraspanin 7 [Source:HGNC Symbol;Acc:HGNC:11854]
6	ENSG00000001	0.05	4e-05	1 33 x 17 IQ motif containing E [Source:HGNC Symbol;Acc:HGNC:291
7	ENSG00000002	0	6e-05	1 21 x 5 UDP glucuronosyltransferase 2 family, polypeptide B11 [Sour
8	ENSG00000001	-0.02	6e-05	1 28 x 30 shisa family member 2 [Source:HGNC Symbol;Acc:HGNC:20
9	ENSG00000001	0.02	8e-05	1 18 x 35 PBX/knotted 1 homeobox 1 [Source:HGNC Symbol;Acc:HGN
10	ENSG00000000	0.06	2e-04	1 21 x 4 cell death-inducing p53 target 1 [Source:HGNC Symbol;Acc:
11	ENSG00000000	0.01	2e-04	1 8 x 2 mucosal vascular addressin cell adhesion molecule 1 [Source
12	ENSG00000001	0.06	2e-04	1 4 x 1 deoxyribonuclease I-like 3 [Source:HGNC Symbol;Acc:HGNC:
13	ENSG00000001	0.02	3e-04	1 23 x 6 gamma-glutamyltransferase 2 [Source:HGNC Symbol;Acc:Hi
14	ENSG00000000	0.2	3e-04	1 38 x 1 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:HGN
15	ENSG00000001	0.01	3e-04	1 28 x 16 hes family bHLH transcription factor 5 [Source:HGNC Symbol
16	ENSG00000000	0.43	5e-04	1 40 x 1 amine oxidase, copper containing 1 [Source:HGNC Symbol;A
17	ENSG00000001	0.01	5e-04	1 18 x 32 chromosome 9 open reading frame 24 [Source:HGNC Symbc
18	ENSG00000001	-0.3	5e-04	1 1 x 29 insulin-like growth factor binding protein 3 [Source:HGNC Sy
19	ENSG00000001	0.02	6e-04	1 27 x 5 carbonic anhydrase XIII [Source:HGNC Symbol;Acc:HGNC:1
20	ENSG00000001	0.05	6e-04	1 31 x 9 phospholipase C, epsilon 1 [Source:HGNC Symbol;Acc:HGN

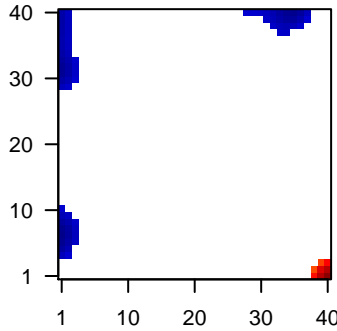
Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	13.44	4e-05	110	Colon CaMetsa_CRC-cluster-h
2	13.3	4e-05	616	Colon CaLembcke_TCGA-expr_kmeans_M_CIMP.H_DN
3	12.84	5e-05	10475	Colon CaMetsa_Colon
4	12.83	5e-05	14	MF glycine binding
5	12.61	6e-05	6761	Colon CaMetsa2_Colon
6	12.45	6e-05	507	Colon CaMetsa2_CRC_TCGA_corr_C_normal_UP
7	12.42	6e-05	8123	Colon CaMetsaF_Colon
8	11.47	8e-05	9930	Colon CaMetsa_Colon
9	11.38	8e-05	1169	Colon CaLembcke_TCGA-expr_kmeans_N_CIMP.H_DN
10	11.25	8e-05	9390	Colon CaMetsaF_Colon
11	11.24	8e-05	5889	Colon CaMetsaF_Colon
12	10.59	1e-04	9470	Colon CaMetsa3_Colon
13	9.81	2e-04	1624	GSEA C2DODD_NASOPHARYNGEAL_CARCINOMA_UP
14	9.29	2e-04	15	Glio neurons_glio
15	9.16	2e-04	21	GSEA C2REACTOME_LIGAND_GATED_ION_CHANNEL_TRANSPORT
16	9.13	2e-04	3112	Colon CaMetsa_Colon
17	8.67	3e-04	11791	Colon CaMetsa_Colon
18	8.26	4e-04	3122	Colon CaMetsaFhG1_Colon
19	8.24	4e-04	22	GSEA C2HASLINGER_B_CLL_WITH_11Q23_DELETION
20	8.19	4e-04	104	Colon CaMetsa2_CRC_TCGA_group.over_A_normal_UP
<i>Underexpressed</i>				
1	-15.42	3e-05	326	GSEA C2SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP
2	-14.73	3e-05	167	GSEA C2VECCHI_GASTRIC_CANCER_ADVANCED_VS_EARLY_UP
3	-14.35	3e-05	332	Colon CaMetsa2_CRC_TCGA_corr_J_msi-h_UP_mss_DN
4	-13.89	4e-05	148	Colon CaMetsa_CRC-cluster-a
5	-13.82	4e-05	198	HM HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
6	-13.72	4e-05	574	Cancer Lembcke_Colonc Inflammation
7	-11.99	6e-05	192	HM HALLMARK_TNFA_SIGNALING_VIA_NFKB
8	-11.84	6e-05	3109	Colon CaMetsaP_Colon
9	-11.22	9e-05	478	GSEA C2LIM_MAMMARY_STEM_CELL_UP
10	-11.17	9e-05	337	Colon CaMetsa2_CRC_TCGA_group.over_B_msi-h_UP
11	-10.49	1e-04	62	GSEA C2ANASTASSIOU_CANCER_MESENCHYMAL_TRANSITION_SIGN
12	-10.22	2e-04	314	LymphomaM10pp_June14_MMML937_tumors+controls_group.overexpression
13	-10.14	2e-04	945	GSEA C2NABA_MATRISOME
14	-10.06	2e-04	315	LymphomaM10WIRTH_lymphoma937_spot E
15	-10.04	2e-04	279	Glio WILLSCHEER_GBM_Verhaak-CL & MES_up
16	-9.98	2e-04	3406	Colon CaMetsaP_Colon
17	-9.64	2e-04	132	Colon CaMetsa_CRC-cluster-b
18	-9.61	2e-04	368	GSEA C2LINDGREN_BLADDER_CANCER_CLUSTER_2B
19	-9.38	2e-04	844	Colon CaLembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
20	-9.34	2e-04	445	GSEA C2CHARAFE_BREAST_CANCER_LUMINAL_VS_MESENCHYMAL

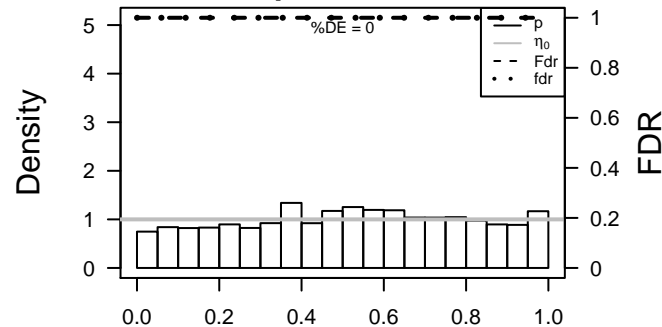
Profile



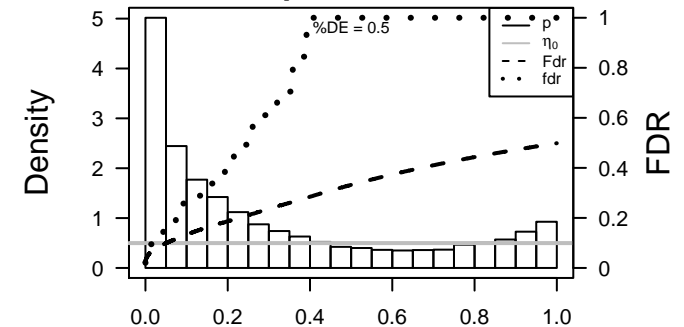
Regulated Spots



p-values



p-values



MLH1_adenomaHNPC

Local Summary

%DE = 0.14
 # metagenes = 8
 # genes = 172
 # genes in genesets = 169

 # genes with $fdr < 0.1 = 3$ (3 + / 0 -)
 # genes with $fdr < 0.05 = 3$ (3 + / 0 -)
 # genes with $fdr < 0.01 = 0$ (0 + / 0 -)

<r> metagenes = 0.96

<r> genes = 0.39

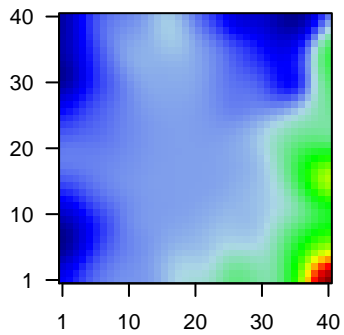
<FC> = 0.19

<t-score> = 1.64

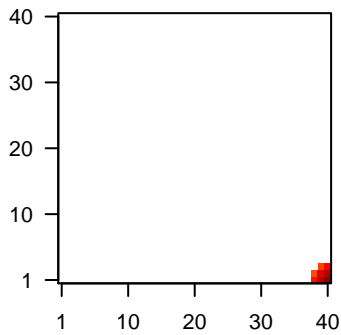
<p-value> = 0.24

<fdr> = 1

Profile



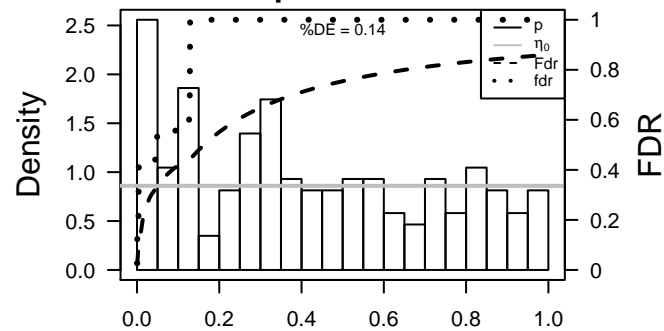
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000000	0.2	3e-04	0.03	38 x 1 collagen, type XVII, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2049]
2	ENSG00000000	0.43	5e-04	0.03	40 x 1 amine oxidase, copper containing 1 [Source:HGNC Symbol;Acc:HGNC:2049]
3	ENSG00000000	0.16	6e-04	0.03	40 x 1 hydroxysteroid (17-beta) dehydrogenase 2 [Source:HGNC Symbol;Acc:HGNC:2049]
4	ENSG00000001	0.58	7e-04	0.19	39 x 1 inhibitor of DNA binding 1, dominant negative helix-loop-helix [Source:HGNC Symbol;Acc:HGNC:2049]
5	ENSG00000001	0.15	3e-03	0.19	40 x 1 claudin 7 [Source:HGNC Symbol;Acc:HGNC:2049]
6	ENSG00000001	0.29	4e-03	0.19	40 x 1 syndecan binding protein (syntenin) 2 [Source:HGNC Symbol;Acc:HGNC:2049]
7	ENSG00000001	0.13	4e-03	0.44	38 x 1 protein kinase (cAMP-dependent, catalytic) inhibitor beta [Source:HGNC Symbol;Acc:HGNC:2049]
8	ENSG00000001	0.46	1e-02	0.44	40 x 1 chromosome 15 open reading frame 48 [Source:HGNC Symbol;Acc:HGNC:2049]
9	ENSG00000001	0.24	2e-02	0.44	40 x 1 transmembrane protein 45B [Source:HGNC Symbol;Acc:HGNC:2049]
10	ENSG00000001	0.28	3e-02	0.44	40 x 1 proline rich 15 [Source:HGNC Symbol;Acc:HGNC:22310]
11	ENSG00000002	1.01	3e-02	0.44	40 x 1 immunoglobulin lambda-like polypeptide 5 [Source:HGNC Symbol;Acc:HGNC:2049]
12	ENSG00000001	0.25	3e-02	0.44	40 x 1 keratin 19, type I [Source:HGNC Symbol;Acc:HGNC:6436]
13	ENSG00000001	0.26	3e-02	0.44	40 x 1 thiosulfate sulfurtransferase (rhodanese) [Source:HGNC Symbol;Acc:HGNC:2049]
14	ENSG00000001	0.43	3e-02	0.44	40 x 1 family with sequence similarity 3, member D [Source:HGNC Symbol;Acc:HGNC:2049]
15	ENSG00000001	0.23	3e-02	0.44	40 x 1 vesicle-associated membrane protein 8 [Source:HGNC Symbol;Acc:HGNC:2049]
16	ENSG00000001	0.91	4e-02	0.44	40 x 1 fatty acid binding protein 1, liver [Source:HGNC Symbol;Acc:HGNC:2049]
17	ENSG00000002	0.09	4e-02	0.44	38 x 2
18	ENSG00000002	0.46	5e-02	0.44	40 x 1 mucin 12, cell surface associated [Source:HGNC Symbol;Acc:HGNC:2049]
19	ENSG00000001	0.8	5e-02	0.44	40 x 1 polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:HGNC:2049]
20	ENSG00000002	0.38	5e-02	0.44	40 x 1 proline/histidine/glycine-rich 1 [Source:HGNC Symbol;Acc:HGNC:2049]

p-values



MLH1_adenomaHNPC

Local Summary

%DE = 0.05
 # metagenes = 19
 # genes = 302
 # genes in genesets = 285

 # 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 = 0.97
 <r> genes = 0.48

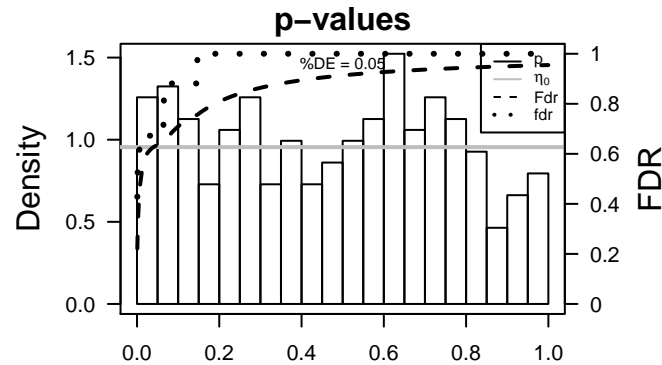
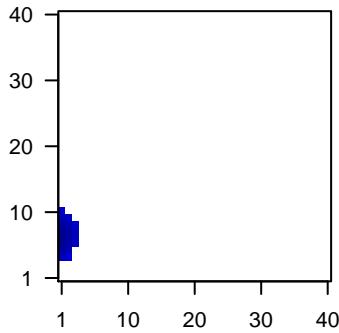
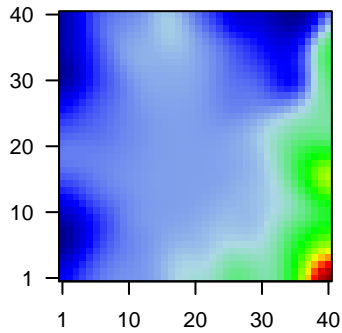
 <FC> = -0.07
 <t-score> = -1.07
 <p-value> = 0.34
 <fdr> = 1

Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG000002	-0.21	8e-04	0.4	3 x 7 chromosome 6 open reading frame 48 [Source:HGNC Symbc
2	ENSG000001	-0.16	2e-03	0.6	1 x 7 ribosomal protein S25 [Source:HGNC Symbol;Acc:HGNC:10-
3	ENSG000001	-0.2	6e-03	0.6	1 x 7 ribosomal protein S23 [Source:HGNC Symbol;Acc:HGNC:10-
4	ENSG000001	0.05	6e-03	0.7	2 x 5 septin 9 [Source:HGNC Symbol;Acc:HGNC:7323]
5	ENSG000001	-0.29	1e-02	0.7	1 x 4 DNA-damage-inducible transcript 4 [Source:HGNC Symbol;
6	ENSG000001	-0.14	2e-02	0.7	1 x 6 nucleosome assembly protein 1-like 1 [Source:HGNC Symbc
7	ENSG000000	-0.1	2e-02	0.7	2 x 9 transmembrane protein 230 [Source:HGNC Symbol;Acc:HGNC
8	ENSG000000	-0.1	2e-02	0.7	1 x 5 tribbles pseudokinase 2 [Source:HGNC Symbol;Acc:HGNC:3
9	ENSG000001	-0.16	2e-02	0.7	1 x 4 tumor necrosis factor, alpha-induced protein 3 [Source:HGNC
10	ENSG000001	-0.08	2e-02	0.7	3 x 7 GM2 ganglioside activator [Source:HGNC Symbol;Acc:HGNC
11	ENSG000001	-0.09	3e-02	0.7	1 x 4 ADP-ribosylation factor-like 4C [Source:HGNC Symbol;Acc:1
12	ENSG000002	-0.15	3e-02	0.7	1 x 9 nascent polypeptide-associated complex alpha subunit 2 [So
13	ENSG000001	-0.14	4e-02	0.7	3 x 6 cyclin L1 [Source:HGNC Symbol;Acc:HGNC:20569]
14	ENSG000001	-0.08	4e-02	0.7	3 x 7 formin binding protein 4 [Source:HGNC Symbol;Acc:HGNC:1
15	ENSG000001	-0.1	4e-02	0.7	1 x 9 NSA2 ribosome biogenesis homolog [Source:HGNC Symbol;
16	ENSG000001	-0.18	4e-02	0.7	1 x 4 ZFP36 ring finger protein-like 2 [Source:HGNC Symbol;Acc:t
17	ENSG000001	-0.09	4e-02	0.7	1 x 9 signal peptidase complex subunit 3 [Source:HGNC Symbol;A
18	ENSG000001	-0.04	4e-02	0.7	2 x 6 schlafen family member 5 [Source:HGNC Symbol;Acc:HGNC
19	ENSG000001	-0.1	5e-02	0.7	1 x 8 eukaryotic translation initiation factor 3, subunit L [Source:HG
20	ENSG000001	-0.12	5e-02	0.7	1 x 4 nuclear factor of kappa light polypeptide gene enhancer in B-

Profile

Spot



MLH1_adenomaHNPC

Local Summary

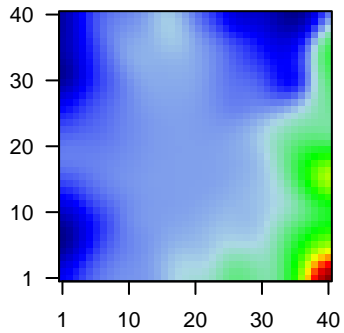
%DE = 0.35
 # metagenes = 28
 # genes = 443
 # genes in genesets = 438

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

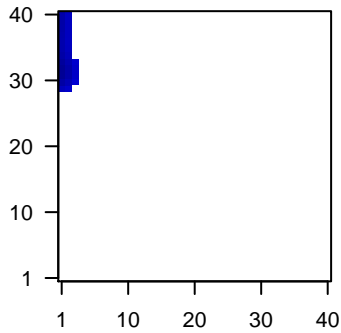
$\langle r \rangle$ metagenes = 0.93
 $\langle r \rangle$ genes = 0.74

 $\langle FC \rangle = -0.07$
 $\langle t\text{-score} \rangle = -1.31$
 $\langle p\text{-value} \rangle = 0.23$
 $\langle fdr \rangle = 1$

Profile



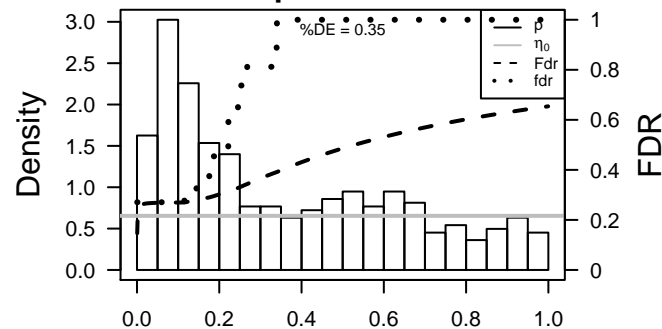
Spot



Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG00000001	-0.3	5e-04	0.3	1 x 29 insulin-like growth factor binding protein 3 [Source:HGNC Sy
2	ENSG00000001	-0.62	2e-03	0.3	1 x 31 FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC
3	ENSG00000001	-0.34	7e-03	0.3	1 x 40 tropomyosin 1 (alpha) [Source:HGNC Symbol;Acc:HGNC:126
4	ENSG00000001	-0.25	8e-03	0.3	1 x 38 chromosome 8 open reading frame 4 [Source:HGNC Symbol
5	ENSG00000001	-0.03	1e-02	0.3	1 x 30 mesenteric estrogen-dependent adipogenesis [Source:HGNC
6	ENSG00000001	-0.31	1e-02	0.3	1 x 32 dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC
7	ENSG00000000	-0.37	1e-02	0.3	1 x 36 vimentin [Source:HGNC Symbol;Acc:HGNC:12692]
8	ENSG00000001	-0.01	1e-02	0.3	1 x 29 inhibin, beta B [Source:HGNC Symbol;Acc:HGNC:6067]
9	ENSG00000001	-0.09	2e-02	0.3	1 x 35 proline-rich nuclear receptor coactivator 1 [Source:HGNC Sy
10	ENSG00000001	-0.56	2e-02	0.3	1 x 38 secreted protein, acidic, cysteine-rich (osteonectin) [Source:HGNC
11	ENSG00000001	-0.48	2e-02	0.3	1 x 30 biglycan [Source:HGNC Symbol;Acc:HGNC:1044]
12	ENSG00000001	-0.09	2e-02	0.3	1 x 40 dihydropyrimidinase-like 3 [Source:HGNC Symbol;Acc:HGNC
13	ENSG00000001	-0.11	2e-02	0.3	1 x 29 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 [S
14	ENSG00000001	-0.54	2e-02	0.3	1 x 31 ZFP36 ring finger protein [Source:HGNC Symbol;Acc:HGNC:
15	ENSG00000001	-0.57	2e-02	0.3	1 x 31 collagen, type I, alpha 1 [Source:HGNC Symbol;Acc:HGNC:2
16	ENSG00000001	-0.03	3e-02	0.3	1 x 30 ADAM metallopeptidase with thrombospondin type 1 motif, 4
17	ENSG00000001	-0.24	3e-02	0.3	1 x 29 plasminogen activator, urokinase [Source:HGNC Symbol;Acc
18	ENSG00000001	-0.21	3e-02	0.3	1 x 40 insulin-like growth factor binding protein 4 [Source:HGNC Sy
19	ENSG00000001	-0.31	3e-02	0.3	1 x 40 fibronectin 1 [Source:HGNC Symbol;Acc:HGNC:3778]
20	ENSG00000001	-0.19	3e-02	0.3	1 x 30 serpin peptidase inhibitor, clade E (nexin), plasminogen activa

p-values



MLH1_adenomaHNPC

Local Summary

%DE = 0.03
 # metagenes = 24
 # genes = 438
 # genes in genesets = 431

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

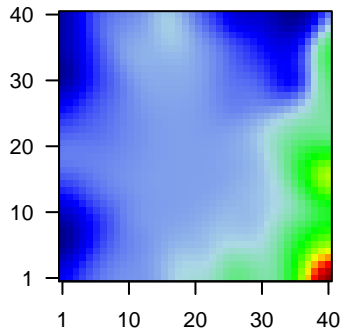
$\langle r \rangle$ metagenes = 0.99
 $\langle r \rangle$ genes = 0.71

 $\langle FC \rangle = -0.06$
 $\langle t\text{-score} \rangle = -0.92$
 $\langle p\text{-value} \rangle = 0.35$
 $\langle fdr \rangle = 1$

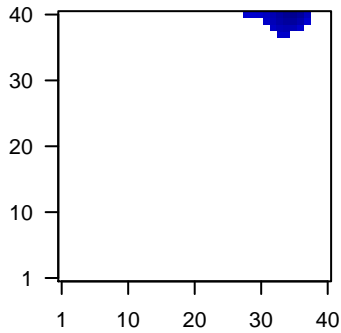
Local Genelist

Rank	ID	log(FC)	fdr	p-value	Description
1	ENSG0000001	-0.1	0.004	0.6	32 x 40 ribosomal L24 domain containing 1 [Source:HGNC Symbol;A
2	ENSG0000001	-0.31	0.006	0.6	36 x 40 solute carrier family 25 (mitochondrial carrier; adenine nucleo
3	ENSGR000001	-0.32	0.006	0.6	36 x 40
4	ENSG0000001	-0.16	0.006	0.6	37 x 40 oligosaccharyltransferase complex subunit (non-catalytic) [S
5	ENSG0000001	-0.12	0.007	0.8	33 x 40 heterogeneous nuclear ribonucleoprotein D (AU-rich element
6	ENSG0000001	-0.2	0.012	0.8	35 x 40 ribosomal protein L26 [Source:HGNC Symbol;Acc:HGNC:10
7	ENSG0000001	-0.15	0.013	0.8	35 x 40 ribosomal protein L19 [Source:HGNC Symbol;Acc:HGNC:10
8	ENSG0000001	-0.27	0.014	0.8	35 x 40 ribosomal protein L12 [Source:HGNC Symbol;Acc:HGNC:10
9	ENSG0000001	-0.05	0.017	0.8	32 x 38 WD repeat domain 75 [Source:HGNC Symbol;Acc:HGNC:25
10	ENSG0000001	-0.11	0.019	0.8	37 x 40 stathmin 1 [Source:HGNC Symbol;Acc:HGNC:6510]
11	ENSG0000002	0.1	0.019	0.8	35 x 40 translocase of outer mitochondrial membrane 6 homolog (yea
12	ENSG0000001	-0.21	0.021	0.8	32 x 40
13	ENSG0000001	-0.13	0.023	0.8	31 x 40 solute carrier family 43 (amino acid system L transporter), me
14	ENSG0000002	-0.35	0.036	0.8	37 x 40
15	ENSG0000002	-0.22	0.037	0.8	35 x 39
16	ENSG0000001	-0.21	0.037	0.8	35 x 40 ribosomal protein S4, X-linked [Source:HGNC Symbol;Acc:H
17	ENSG0000001	-0.12	0.038	0.8	34 x 40 ribosomal protein S7 [Source:HGNC Symbol;Acc:HGNC:104
18	ENSG0000000	-0.08	0.044	0.8	31 x 40 procollagen-llysine, 2-oxoglutarate 5-dioxygenase 1 [Source
19	ENSG0000001	-0.13	0.044	0.8	33 x 40 collagen beta(1-O)galactosyltransferase 1 [Source:HGNC Sy
20	ENSG0000001	-0.07	0.046	0.8	30 x 40 Fanconi anemia, complementation group L [Source:HGNC S

Profile



Spot



p-values

