



For further information on how to interpret these results please access <http://meme-suite.org/doc/ame-output-format.html>.
To get a copy of the MEME software please access <http://meme-suite.org>.

If you use AME in your research, please cite the following paper:

Robert McLeay and Timothy L. Bailey, "Motif Enrichment Analysis: A unified framework and method evaluation", *BMC Bioinformatics*, **11**:165, 2010, doi:10.1186/1471-2105-11-165. [\[full text\]](#)

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ENRICHED MOTIFS

Sequence motif score: avg_odds

Background model source: letter frequencies in (primary) sequences file (Galaxy195-bedtools_GetFastaBed_Merged_and_Narrowed_Hyper_regions.fasta)

Background model frequencies: 0.206554,0.293446,0.293446,0.206554

Total pseudocount added to a motif column: 0.1

Statistical test: Fisher's exact test (optimized over motif scores)

Labeling positives: all 107 primary sequences are labeled as 'positive'; all 1070 control sequences are labeled as 'negative'

Classifying positives: sequences with the motif scores $\geq$ 'TP Thresh' are classified as positive

E-value threshold for reporting results: 10

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Logo

Database 

ID 

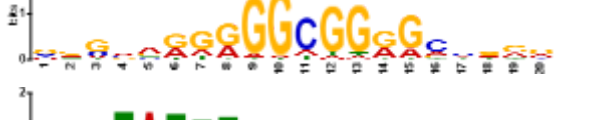
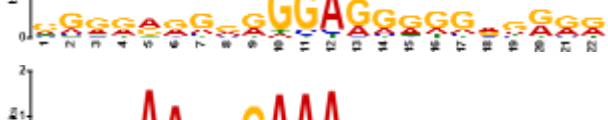
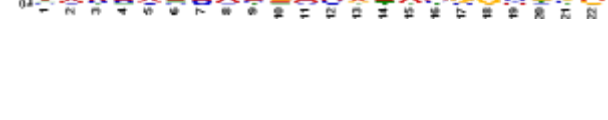
Alt
ID 

p-
value 

E-
value 

TP
Thresh 

TP
(%) 

Logo	Database ?	ID ?	Alt ID ?	p-value ?	E-value ?	TP Thresh ?	TP (%) ?
	HOCOMOCov11 full HUMAN mono meme format	ZBT17_HUMAN.H11MO.0.A		1.64e-13	1.26e-10	7.95	55 (51.4%)
	HOCOMOCov11 full HUMAN mono meme format	KLF15_HUMAN.H11MO.0.A		2.26e-11	1.74e-8	13.14	42 (39.3%)
	HOCOMOCov11 full HUMAN mono meme format	MAZ_HUMAN.H11MO.0.A		6.47e-11	4.97e-8	31.26	41 (38.3%)
	HOCOMOCov11 full HUMAN mono meme format	PATZ1_HUMAN.H11MO.0.C		1.12e-10	8.59e-8	5.67	55 (51.4%)
	HOCOMOCov11 full HUMAN mono meme format	SP4_HUMAN.H11MO.0.A		1.23e-10	9.48e-8	3.19	55 (51.4%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2C_HUMAN.H11MO.0.A		1.98e-10	1.53e-7	19.97	16 (15.0%)
	HOCOMOCov11 full HUMAN mono meme format	VEZF1_HUMAN.H11MO.0.C		2.02e-10	1.55e-7	7.08	59 (55.1%)
	HOCOMOCov11 full HUMAN mono meme format	STAT1_HUMAN.H11MO.1.A		6.28e-10	4.83e-7	2.27	51 (47.7%)
	HOCOMOCov11 full HUMAN mono meme format	EGR2_HUMAN.H11MO.0.A		1.10e-9	8.47e-7	7.36	46 (43.0%)
	HOCOMOCov11 full HUMAN mono meme format	ZN341_HUMAN.H11MO.0.C		2.54e-9	1.95e-6	6.71	50 (46.7%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	ZN467_HUMAN.H11MO.0.C		3.44e-9	2.64e-6	4.21	56 (52.3%)
	HOCOMOCov11 full HUMAN mono meme format	WT1_HUMAN.H11MO.0.C		3.83e-9	2.94e-6	4.81	50 (46.7%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2A_HUMAN.H11MO.0.A		4.74e-9	3.65e-6	16.25	17 (15.9%)
	HOCOMOCov11 full HUMAN mono meme format	NFAC1_HUMAN.H11MO.0.B		5.95e-9	4.57e-6	2.22	65 (60.7%)
	HOCOMOCov11 full HUMAN mono meme format	TAF1_HUMAN.H11MO.0.A		8.36e-9	6.43e-6	2.11	51 (47.7%)
	HOCOMOCov11 full HUMAN mono meme format	KLF6_HUMAN.H11MO.0.A		1.09e-8	8.38e-6	4.00	51 (47.7%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2B_HUMAN.H11MO.0.A		1.32e-8	1.02e-5	4.68	31 (29.0%)
	HOCOMOCov11 full HUMAN mono meme format	STAT2_HUMAN.H11MO.0.A		2.52e-8	1.94e-5	2.42	34 (31.8%)
	HOCOMOCov11 full HUMAN mono meme format	ETS2_HUMAN.H11MO.0.B		4.72e-8	3.63e-5	2.95	69 (64.5%)
	HOCOMOCov11 full HUMAN mono meme format	KLF3_HUMAN.H11MO.0.B		6.44e-8	4.96e-5	7.68	29 (27.1%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	EGR2_HUMAN.H11MO.1.A		9.68e-8	7.45e-5	10.60	28 (26.2%)
	HOCOMOCov11 full HUMAN mono meme format	IRF3_HUMAN.H11MO.0.B		1.06e-7	8.16e-5	1.35	63 (58.9%)
	HOCOMOCov11 full HUMAN mono meme format	VEZF1_HUMAN.H11MO.1.C		1.21e-7	9.27e-5	7.03	40 (37.4%)
	HOCOMOCov11 full HUMAN mono meme format	ZN263_HUMAN.H11MO.0.A		1.30e-7	9.96e-5	3.29	53 (49.5%)
	HOCOMOCov11 full HUMAN mono meme format	ZN281_HUMAN.H11MO.0.A		1.34e-7	1.03e-4	33.95	26 (24.3%)
	HOCOMOCov11 full HUMAN mono meme format	SP3_HUMAN.H11MO.0.B		1.97e-7	1.52e-4	8.94	33 (30.8%)
	HOCOMOCov11 full HUMAN mono meme format	SP4_HUMAN.H11MO.1.A		2.81e-7	2.16e-4	4.47	41 (38.3%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2D_HUMAN.H11MO.0.A		6.42e-7	4.94e-4	2.24	25 (23.4%)
	HOCOMOCov11 full HUMAN mono meme format	ANDR_HUMAN.H11MO.0.A		9.90e-7	7.61e-4	17.86	18 (16.8%)
	HOCOMOCov11 full HUMAN mono meme format	BC11A_HUMAN.H11MO.0.A		1.05e-6	8.04e-4	8.60	36 (33.6%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	FOXG1_HUMAN.H11MO.0.D		1.45e-6	1.11e-3	7.05	26 (24.3%)
	HOCOMOCov11 full HUMAN mono meme format	EGR1_HUMAN.H11MO.0.A		1.68e-6	1.29e-3	3.97	37 (34.6%)
	HOCOMOCov11 full HUMAN mono meme format	ZFP82_HUMAN.H11MO.0.C		1.89e-6	1.45e-3	2.69	35 (32.7%)
	HOCOMOCov11 full HUMAN mono meme format	KLF5_HUMAN.H11MO.0.A		2.37e-6	1.82e-3	6.48	34 (31.8%)
	HOCOMOCov11 full HUMAN mono meme format	FOXD3_HUMAN.H11MO.0.D		5.73e-6	4.40e-3	1.71	61 (57.0%)
	HOCOMOCov11 full HUMAN mono meme format	KLF16_HUMAN.H11MO.0.D		9.19e-6	7.07e-3	14.26	25 (23.4%)
	HOCOMOCov11 full HUMAN mono meme format	FLI1_HUMAN.H11MO.0.A		9.44e-6	7.26e-3	9.07	38 (35.5%)
	HOCOMOCov11 full HUMAN mono meme format	SP1_HUMAN.H11MO.0.A		1.03e-5	7.94e-3	29.04	15 (14.0%)
	HOCOMOCov11 full HUMAN mono meme format	PRDM6_HUMAN.H11MO.0.C		1.11e-5	8.55e-3	2.60	55 (51.4%)
	HOCOMOCov11 full HUMAN mono meme format	KLF1_HUMAN.H11MO.0.A		1.65e-5	1.27e-2	13.18	19 (17.8%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	E2F7_HUMAN.H11MO.0.B		1.71e-5	1.31e-2	2.28	47 (43.9%)
	HOCOMOCov11 full HUMAN mono meme format	NFAT5_HUMAN.H11MO.0.D		1.86e-5	1.43e-2	2.61	66 (61.7%)
	HOCOMOCov11 full HUMAN mono meme format	ZFP28_HUMAN.H11MO.0.C		2.07e-5	1.59e-2	2.05	21 (19.6%)
	HOCOMOCov11 full HUMAN mono meme format	FOXP1_HUMAN.H11MO.0.A		2.10e-5	1.61e-2	1.53	54 (50.5%)
	HOCOMOCov11 full HUMAN mono meme format	FUBP1_HUMAN.H11MO.0.D		2.34e-5	1.80e-2	4.37	28 (26.2%)
	HOCOMOCov11 full HUMAN mono meme format	ARI3A_HUMAN.H11MO.0.D		3.21e-5	2.47e-2	1.32	17 (15.9%)
	HOCOMOCov11 full HUMAN mono meme format	FOXJ3_HUMAN.H11MO.0.A		3.36e-5	2.58e-2	3.95	17 (15.9%)
	HOCOMOCov11 full HUMAN mono meme format	IRF1_HUMAN.H11MO.0.A		3.64e-5	2.80e-2	20.19	16 (15.0%)
	HOCOMOCov11 full HUMAN mono meme format	SP2_HUMAN.H11MO.0.A		3.80e-5	2.92e-2	3.56	38 (35.5%)
	HOCOMOCov11 full HUMAN mono meme format	TBX1_HUMAN.H11MO.0.D		4.09e-5	3.14e-2	3.07	35 (32.7%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	CPEB1_HUMAN.H11MO.0.D		4.30e-5	3.31e-2	1.26	22 (20.6%)
	HOCOMOCov11 full HUMAN mono meme format	PATZ1_HUMAN.H11MO.1.C		4.34e-5	3.33e-2	5.24	43 (40.2%)
	HOCOMOCov11 full HUMAN mono meme format	SOX10_HUMAN.H11MO.1.A		4.57e-5	3.52e-2	3.44	52 (48.6%)
	HOCOMOCov11 full HUMAN mono meme format	Z354A_HUMAN.H11MO.0.C		4.58e-5	3.52e-2	2.62	29 (27.1%)
	HOCOMOCov11 full HUMAN mono meme format	FOXJ2_HUMAN.H11MO.0.C		5.68e-5	4.37e-2	1.04	33 (30.8%)
	HOCOMOCov11 full HUMAN mono meme format	ERG_HUMAN.H11MO.0.A		5.89e-5	4.53e-2	1.79	57 (53.3%)
	HOCOMOCov11 full HUMAN mono meme format	ETV5_HUMAN.H11MO.0.C		5.96e-5	4.59e-2	2.91	62 (57.9%)
	HOCOMOCov11 full HUMAN mono meme format	FEV_HUMAN.H11MO.0.B		7.52e-5	5.78e-2	1.60	61 (57.0%)
	HOCOMOCov11 full HUMAN mono meme format	FLI1_HUMAN.H11MO.1.A		9.36e-5	7.19e-2	1.87	56 (52.3%)
	HOCOMOCov11 full HUMAN mono meme format	ZN148_HUMAN.H11MO.0.D		1.15e-4	8.87e-2	19.62	27 (25.2%)

file:///D:/Genetic HCM/TFBMs/AME using merged and narrowed regions/AME Hyper after narrowing with DNase.html

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	GATA3_HUMAN.H11MO.0.A		4.13e-4	3.18e-1	1.11	59 (55.1%)
	HOCOMOCov11 full HUMAN mono meme format	FOXP3_HUMAN.H11MO.0.D		4.13e-4	3.18e-1	1.02	49 (45.8%)
	HOCOMOCov11 full HUMAN mono meme format	ETV2_HUMAN.H11MO.0.B		5.24e-4	4.03e-1	1.23	40 (37.4%)
	HOCOMOCov11 full HUMAN mono meme format	TBP_HUMAN.H11MO.0.A		5.26e-4	4.04e-1	8.70	11 (10.3%)
	HOCOMOCov11 full HUMAN mono meme format	HXB13_HUMAN.H11MO.0.A		5.48e-4	4.21e-1	1.27	37 (34.6%)
	HOCOMOCov11 full HUMAN mono meme format	FOXK1_HUMAN.H11MO.0.A		5.71e-4	4.39e-1	1.11	64 (59.8%)
	HOCOMOCov11 full HUMAN mono meme format	HMGA1_HUMAN.H11MO.0.D		6.51e-4	5.00e-1	1.41	55 (51.4%)
	HOCOMOCov11 full HUMAN mono meme format	HXD11_HUMAN.H11MO.0.D		6.54e-4	5.03e-1	1.06	52 (48.6%)
	HOCOMOCov11 full HUMAN mono meme format	MAZ_HUMAN.H11MO.1.A		6.68e-4	5.13e-1	5.74	40 (37.4%)
	HOCOMOCov11 full HUMAN mono meme format	ZSC22_HUMAN.H11MO.0.C		6.75e-4	5.19e-1	1.63	47 (43.9%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	LYL1_HUMAN.H11MO.0.A		6.77e-4	5.20e-1	1.86	67 (62.6%)
	HOCOMOCov11 full HUMAN mono meme format	PURA_HUMAN.H11MO.0.D		9.21e-4	7.08e-1	5.09	30 (28.0%)
	HOCOMOCov11 full HUMAN mono meme format	ELF5_HUMAN.H11MO.0.A		9.96e-4	7.66e-1	1.16	53 (49.5%)
	HOCOMOCov11 full HUMAN mono meme format	TEF_HUMAN.H11MO.0.D		1.08e-3	8.32e-1	2.64	17 (15.9%)
	HOCOMOCov11 full HUMAN mono meme format	ETV4_HUMAN.H11MO.0.B		1.13e-3	8.73e-1	2.84	56 (52.3%)
	HOCOMOCov11 full HUMAN mono meme format	RXRA_HUMAN.H11MO.0.A		1.20e-3	9.21e-1	2.11	67 (62.6%)
	HOCOMOCov11 full HUMAN mono meme format	FOXM1_HUMAN.H11MO.0.A		1.21e-3	9.32e-1	2.95	32 (29.9%)
	HOCOMOCov11 full HUMAN mono meme format	ZN350_HUMAN.H11MO.0.C		1.23e-3	9.44e-1	1.25	61 (57.0%)
	HOCOMOCov11 full HUMAN mono meme format	ZN263_HUMAN.H11MO.1.A		1.26e-3	9.71e-1	5.52	37 (34.6%)
	HOCOMOCov11 full HUMAN mono meme format	BPTF_HUMAN.H11MO.0.D		1.45e-3	1.11e0	4.96	27 (25.2%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	HXC10_HUMAN.H11MO.0.D		1.50e-3	1.15e0	3.54	27 (25.2%)
	HOCOMOCov11 full HUMAN mono meme format	LMX1B_HUMAN.H11MO.0.D		1.63e-3	1.25e0	3.53	16 (15.0%)
	HOCOMOCov11 full HUMAN mono meme format	SP2_HUMAN.H11MO.1.B		1.71e-3	1.31e0	2.57	40 (37.4%)
	HOCOMOCov11 full HUMAN mono meme format	ZN394_HUMAN.H11MO.0.C		2.13e-3	1.64e0	1.58	63 (58.9%)
	HOCOMOCov11 full HUMAN mono meme format	BMAL1_HUMAN.H11MO.0.A		2.36e-3	1.81e0	1.39	25 (23.4%)
	HOCOMOCov11 full HUMAN mono meme format	EGR4_HUMAN.H11MO.0.D		2.49e-3	1.91e0	5.58	21 (19.6%)
	HOCOMOCov11 full HUMAN mono meme format	FOXO1_HUMAN.H11MO.0.A		2.68e-3	2.06e0	1.39	63 (58.9%)
	HOCOMOCov11 full HUMAN mono meme format	PO4F3_HUMAN.H11MO.0.D		2.81e-3	2.16e0	2.79	7 (6.5%)
	HOCOMOCov11 full HUMAN mono meme format	HXC13_HUMAN.H11MO.0.D		3.04e-3	2.34e0	1.49	30 (28.0%)
	HOCOMOCov11 full HUMAN mono meme format	SALL4_HUMAN.H11MO.0.B		3.14e-3	2.42e0	6.10	28 (26.2%)

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Logo	Database ?	ID ?	Alt ID ?	p-value ?	E-value ?	TP Thresh ?	TP (%) ?
	HOCOMOCov11 full HUMAN mono meme format	KLF4_HUMAN.H11MO.0.A		6.41e-3	4.93e0	2.81	32 (29.9%)
	HOCOMOCov11 full HUMAN mono meme format	HNF1B_HUMAN.H11MO.0.A		6.44e-3	4.95e0	1.46	19 (17.8%)
	HOCOMOCov11 full HUMAN mono meme format	PO4F1_HUMAN.H11MO.0.D		6.54e-3	5.03e0	10.25	6 (5.6%)
	HOCOMOCov11 full HUMAN mono meme format	FOXP2_HUMAN.H11MO.0.C		7.15e-3	5.50e0	1.58	36 (33.6%)
	HOCOMOCov11 full HUMAN mono meme format	NFAC1_HUMAN.H11MO.1.B		7.23e-3	5.56e0	2.96	36 (33.6%)
	HOCOMOCov11 full HUMAN mono meme format	SRY_HUMAN.H11MO.0.B		7.81e-3	6.00e0	1.18	53 (49.5%)
	HOCOMOCov11 full HUMAN mono meme format	FOXB1_HUMAN.H11MO.0.D		8.80e-3	6.76e0	4.49	8 (7.5%)
	HOCOMOCov11 full HUMAN mono meme format	USF2_HUMAN.H11MO.0.A		1.12e-2	8.60e0	6.31	7 (6.5%)
	HOCOMOCov11 full HUMAN mono meme format	SMAD3_HUMAN.H11MO.0.B		1.15e-2	8.82e0	2.76	57 (53.3%)
	HOCOMOCov11 full HUMAN mono meme format	HXA11_HUMAN.H11MO.0.D		1.18e-2	9.04e0	2.23	28 (26.2%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	FOXA1_HUMAN.H11MO.0.A		1.21e-2	9.30e0	1.04	32 (29.9%)
	HOCOMOCov11 full HUMAN mono meme format	ZNF713_HUMAN.H11MO.0.D		1.22e-2	9.38e0	2.57	37 (34.6%)
	HOCOMOCov11 full HUMAN mono meme format	ETV7_HUMAN.H11MO.0.D		1.25e-2	9.58e0	3.31	45 (42.1%)
	HOCOMOCov11 full HUMAN mono meme format	PRGR_HUMAN.H11MO.0.A		1.29e-2	9.94e0	1.14	41 (38.3%)
	HOCOMOCov11 full HUMAN mono meme format	TAL1_HUMAN.H11MO.1.A		1.30e-2	9.99e0	2.31	44 (41.1%)

INPUT FILES

Alphabet

Background source: built from the (primary) sequences

Background source: built from the (primary) sequences

Name	Bg.			Bg.	Name
Adenine	0.206554	A	~	T	Thymine
Cytosine	0.293446	C	~	G	Guanine

Name	Bg.			Bg.	Name
Adenine	0.206554	A	~	T	Thymine
Cytosine	0.293446	C	~	G	Guanine

Sequences

Primary Sequences	Number	Control Sequences	Number
Galaxy195-bedtools_GetFastaBed_Merged_and_Narrowed_Hyper_regions.fasta	107	primary sequences shuffled conserving 2-mer frequencies	1070
Primary Sequences	Number	Control Sequences	Number
Galaxy195-bedtools_GetFastaBed_Merged_and_Narrowed_Hyper_regions.fasta	107	primary sequences shuffled conserving 2-mer frequencies	1070

Motifs

Database	Source	Motif Count
HOCOMOCov11 full HUMAN mono meme format	db/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	769
HOCOMOCov11 full HUMAN mono meme format	db/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	769

AME version

5.1.15.1.1 (Release date: Wed Jan 29 15:00:42 2020 -0800Wed Jan 29 15:00:42 2020 -0800)

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Command line summary

```
ame --verbose 1 --oc . --scoring avg --method fisher --hit-lo-fraction 0.25 --evaluate-report-threshold 10.0 --control --shuffle-- --kmer 2
Galaxy195-bedtools_GetFastaBed_Merged_and_Narrowed_Hyper_regions.fasta db/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme
```




For further information on how to interpret these results please access <http://meme-suite.org/doc/ame-output-format.html>.
To get a copy of the MEME software please access <http://meme-suite.org>.

If you use AME in your research, please cite the following paper:
Robert McLeay and Timothy L. Bailey, "Motif Enrichment Analysis: A unified framework and method evaluation", *BMC Bioinformatics*, **11**:165, 2010, doi:10.1186/1471-2105-11-165. [\[full text\]](#)

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ENRICHED MOTIFS

Sequence motif score: avg_odds
Background model source: letter frequencies in (primary) sequences file (Galaxy196-bedtools_GetFastaBed_Merged_and_Narrowed_Hypo_regions.fasta)
Background model frequencies: 0.189588,0.310412,0.310412,0.189588
Total pseudocount added to a motif column: 0.1

Statistical test: Fisher's exact test (optimized over motif scores)
Labeling positives: all 42 primary sequences are labeled as 'positive'; all 1008 control sequences are labeled as 'negative'
Classifying positives: sequences with the motif scores $\geq$ 'TP Thresh' are classified as positive

E-value threshold for reporting results: 10
Sequence motif score: avg_odds
Background model source: letter frequencies in (primary) sequences file (Galaxy196-bedtools_GetFastaBed_Merged_and_Narrowed_Hypo_regions.fasta)
Background model frequencies: 0.189588,0.310412,0.310412,0.189588
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Statistical test: Fisher's exact test (optimized over motif scores)
Labeling positives: all 42 primary sequences are labeled as 'positive'; all 1008 control sequences are labeled as 'negative'
Classifying positives: sequences with the motif scores $\geq$ 'TP Thresh' are classified as positive

E-value threshold for reporting results: 10

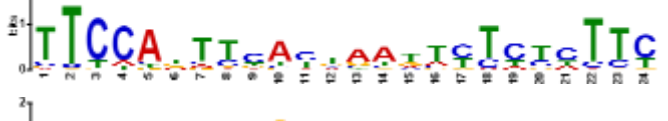
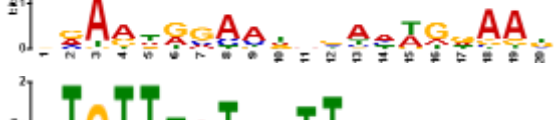
Logo	Database 	ID 	Alt ID 	p-value 	E-value 	TP Thresh 	TP (%) 
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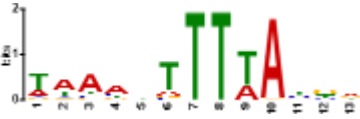
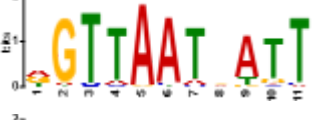
Logo	Database ?	ID ?	Alt ID ?	p-value ?	E-value ?	TP Thresh ?	TP (%) ?
	HOCOMOCov11 full HUMAN mono meme format	KLF15_HUMAN.H11MO.0.A		2.03e-9	1.56e-6	1.69	36 (85.7%)
	HOCOMOCov11 full HUMAN mono meme format	PO3F3_HUMAN.H11MO.0.D		2.12e-9	1.63e-6	2.14	24 (57.1%)
	HOCOMOCov11 full HUMAN mono meme format	SP3_HUMAN.H11MO.0.B		2.18e-9	1.68e-6	3.36	29 (69.0%)
	HOCOMOCov11 full HUMAN mono meme format	PATZ1_HUMAN.H11MO.0.C		1.43e-8	1.10e-5	3.90	31 (73.8%)
	HOCOMOCov11 full HUMAN mono meme format	GSX1_HUMAN.H11MO.0.D		1.52e-8	1.17e-5	5.47	15 (35.7%)
	HOCOMOCov11 full HUMAN mono meme format	SP2_HUMAN.H11MO.0.A		1.78e-8	1.37e-5	4.78	22 (52.4%)
	HOCOMOCov11 full HUMAN mono meme format	ZBT17_HUMAN.H11MO.0.A		4.02e-8	3.09e-5	5.41	28 (66.7%)
	HOCOMOCov11 full HUMAN mono meme format	SP4_HUMAN.H11MO.0.A		5.75e-8	4.42e-5	2.58	30 (71.4%)
	HOCOMOCov11 full HUMAN mono meme format	KLF6_HUMAN.H11MO.0.A		5.98e-8	4.60e-5	3.20	28 (66.7%)
	HOCOMOCov11 full HUMAN mono meme format	ZN467_HUMAN.H11MO.0.C		6.78e-8	5.22e-5	3.87	29 (69.0%)

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Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	WT1_HUMAN.H11MO.0.C		4.44e-6	3.42e-3	2.35	31 (73.8%)
	HOCOMOCov11 full HUMAN mono meme format	ZFX3_HUMAN.H11MO.0.D		4.56e-6	3.51e-3	2.46	9 (21.4%)
	HOCOMOCov11 full HUMAN mono meme format	SP4_HUMAN.H11MO.1.A		4.85e-6	3.73e-3	7.66	19 (45.2%)
	HOCOMOCov11 full HUMAN mono meme format	ZN263_HUMAN.H11MO.0.A		5.50e-6	4.23e-3	1.70	32 (76.2%)
	HOCOMOCov11 full HUMAN mono meme format	TBX15_HUMAN.H11MO.0.D		5.83e-6	4.48e-3	1.72	31 (73.8%)
	HOCOMOCov11 full HUMAN mono meme format	HXB2_HUMAN.H11MO.0.D		8.75e-6	6.73e-3	2.86	11 (26.2%)
	HOCOMOCov11 full HUMAN mono meme format	MAZ_HUMAN.H11MO.0.A		1.27e-5	9.78e-3	2.96	33 (78.6%)
	HOCOMOCov11 full HUMAN mono meme format	VEZF1_HUMAN.H11MO.0.C		1.35e-5	1.04e-2	2.87	35 (83.3%)
	HOCOMOCov11 full HUMAN mono meme format	SP2_HUMAN.H11MO.1.B		1.63e-5	1.25e-2	1.59	32 (76.2%)
	HOCOMOCov11 full HUMAN mono meme format	CPEB1_HUMAN.H11MO.0.D		1.78e-5	1.37e-2	1.27	14 (33.3%)

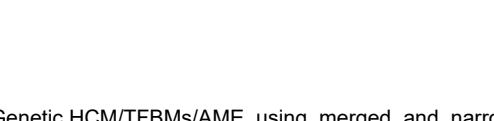
file:///D:/Genetic HCM/TFBMs/AME using merged and narrowed regions/AME Hypo after narrowing with DNase.html

Logo	Database ?	ID ?	Alt ID ?	p-value ?	E-value ?	TP Thresh ?	TP (%) ?
	HOCOMOCov11 full HUMAN mono meme format	PRDM6_HUMAN.H11MO.0.C		1.04e-4	8.02e-2	9.46	17 (40.5%)
	HOCOMOCov11 full HUMAN mono meme format	WT1_HUMAN.H11MO.1.B		1.10e-4	8.42e-2	2.26	31 (73.8%)
	HOCOMOCov11 full HUMAN mono meme format	EGR2_HUMAN.H11MO.0.A		1.18e-4	9.06e-2	1.12	35 (83.3%)
	HOCOMOCov11 full HUMAN mono meme format	ZFP82_HUMAN.H11MO.0.C		1.57e-4	1.20e-1	1.35	21 (50.0%)
	HOCOMOCov11 full HUMAN mono meme format	EGR1_HUMAN.H11MO.0.A		1.69e-4	1.30e-1	2.05	24 (57.1%)
	HOCOMOCov11 full HUMAN mono meme format	ZN394_HUMAN.H11MO.0.C		1.70e-4	1.30e-1	1.57	30 (71.4%)
	HOCOMOCov11 full HUMAN mono meme format	FOXJ3_HUMAN.H11MO.0.A		1.88e-4	1.45e-1	1.34	10 (23.8%)
	HOCOMOCov11 full HUMAN mono meme format	EGR2_HUMAN.H11MO.1.A		2.07e-4	1.59e-1	2.44	22 (52.4%)
	HOCOMOCov11 full HUMAN mono meme format	THA11_HUMAN.H11MO.0.B		2.68e-4	2.06e-1	1.47	10 (23.8%)
	HOCOMOCov11 full HUMAN mono meme format	E2F7_HUMAN.H11MO.0.B		2.69e-4	2.07e-1	3.00	19 (45.2%)

Logo	Database ?	ID ?	Alt ID ?	p-value ?	E-value ?	TP Thresh ?	TP (%) ?
	HOCOMOCov11 full HUMAN mono meme format	HXA11_HUMAN.H11MO.0.D		2.82e-4	2.17e-1	4.05	13 (31.0%)
	HOCOMOCov11 full HUMAN mono meme format	FOXG1_HUMAN.H11MO.0.D		3.70e-4	2.84e-1	1.06	18 (42.9%)
	HOCOMOCov11 full HUMAN mono meme format	ETV5_HUMAN.H11MO.0.C		3.90e-4	3.00e-1	4.21	22 (52.4%)
	HOCOMOCov11 full HUMAN mono meme format	KLF16_HUMAN.H11MO.0.D		4.30e-4	3.31e-1	2.38	23 (54.8%)
	HOCOMOCov11 full HUMAN mono meme format	SP1_HUMAN.H11MO.1.A		4.64e-4	3.57e-1	5.29	12 (28.6%)
	HOCOMOCov11 full HUMAN mono meme format	HNF1B_HUMAN.H11MO.1.A		4.78e-4	3.68e-1	4.58	8 (19.0%)
	HOCOMOCov11 full HUMAN mono meme format	DLX1_HUMAN.H11MO.0.D		5.92e-4	4.55e-1	5.38	10 (23.8%)
	HOCOMOCov11 full HUMAN mono meme format	MAZ_HUMAN.H11MO.1.A		6.94e-4	5.34e-1	5.07	20 (47.6%)
	HOCOMOCov11 full HUMAN mono meme format	PATZ1_HUMAN.H11MO.1.C		7.32e-4	5.63e-1	4.40	21 (50.0%)
	HOCOMOCov11 full HUMAN mono meme format	PO4F3_HUMAN.H11MO.0.D		7.40e-4	5.69e-1	1.29	6 (14.3%)

file:///D:/Genetic HCM/TFBMs/AME using merged and narrowed regions/AME Hypo after narrowing with DNase.html

file:///D:/Genetic HCM/TFBMs/AME using merged and narrowed regions/AME Hypo after narrowing with DNase.html

Logo	Database ?	ID ?	Alt ID ?	p-value ?	E-value ?	TP Thresh ?	TP (%) ?
	HOCOMOCov11 full HUMAN mono meme format	FLI1_HUMAN.H11MO.0.A		2.42e-3	1.86e0	1.89	27 (64.3%)
	HOCOMOCov11 full HUMAN mono meme format	GATA3_HUMAN.H11MO.0.A		2.52e-3	1.94e0	2.39	20 (47.6%)
	HOCOMOCov11 full HUMAN mono meme format	STAT2_HUMAN.H11MO.0.A		2.55e-3	1.96e0	1.12	16 (38.1%)
	HOCOMOCov11 full HUMAN mono meme format	JDP2_HUMAN.H11MO.0.D		2.66e-3	2.04e0	1.61	4 (9.5%)
	HOCOMOCov11 full HUMAN mono meme format	E2F6_HUMAN.H11MO.0.A		3.01e-3	2.31e0	4.09	17 (40.5%)
	HOCOMOCov11 full HUMAN mono meme format	ID4_HUMAN.H11MO.0.D		3.31e-3	2.54e0	1.76	21 (50.0%)
	HOCOMOCov11 full HUMAN mono meme format	CREB5_HUMAN.H11MO.0.D		3.38e-3	2.60e0	2.03	3 (7.1%)
	HOCOMOCov11 full HUMAN mono meme format	VSX1_HUMAN.H11MO.0.D		3.55e-3	2.73e0	1.16	13 (31.0%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2A_HUMAN.H11MO.0.A		3.86e-3	2.97e0	1.36	16 (38.1%)
	HOCOMOCov11 full HUMAN mono meme format	HXB3_HUMAN.H11MO.0.D		3.87e-3	2.98e0	11.21	7 (16.7%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2C_HUMAN.H11MO.0.A		4.18e-3	3.21e0	1.34	16 (38.1%)
	HOCOMOCov11 full HUMAN mono meme format	HSF2_HUMAN.H11MO.0.A		4.24e-3	3.26e0	4.29	10 (23.8%)
	HOCOMOCov11 full HUMAN mono meme format	HXD12_HUMAN.H11MO.0.D		4.29e-3	3.30e0	1.39	23 (54.8%)
	HOCOMOCov11 full HUMAN mono meme format	ZN350_HUMAN.H11MO.0.C		4.31e-3	3.32e0	26.21	8 (19.0%)
	HOCOMOCov11 full HUMAN mono meme format	HMGA1_HUMAN.H11MO.0.D		4.35e-3	3.34e0	1.36	26 (61.9%)
	HOCOMOCov11 full HUMAN mono meme format	LYL1_HUMAN.H11MO.0.A		4.40e-3	3.39e0	1.23	38 (90.5%)
	HOCOMOCov11 full HUMAN mono meme format	VENTX_HUMAN.H11MO.0.D		4.81e-3	3.70e0	1.37	14 (33.3%)
	HOCOMOCov11 full HUMAN mono meme format	BARH2_HUMAN.H11MO.0.D		4.91e-3	3.78e0	5.33	7 (16.7%)
	HOCOMOCov11 full HUMAN mono meme format	BC11A_HUMAN.H11MO.0.A		5.17e-3	3.98e0	5.40	18 (42.9%)
	HOCOMOCov11 full HUMAN mono meme format	HSF1_HUMAN.H11MO.0.A		5.28e-3	4.06e0	31.05	6 (14.3%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	FOXD2_HUMAN.H11MO.0.D		5.46e-3	4.20e0	1.51	4 (9.5%)
	HOCOMOCov11 full HUMAN mono meme format	RXRA_HUMAN.H11MO.0.A		6.18e-3	4.75e0	1.36	35 (83.3%)
	HOCOMOCov11 full HUMAN mono meme format	FOXP3_HUMAN.H11MO.0.D		6.19e-3	4.76e0	2.67	15 (35.7%)
	HOCOMOCov11 full HUMAN mono meme format	E2F4_HUMAN.H11MO.0.A		6.98e-3	5.37e0	1.75	18 (42.9%)
	HOCOMOCov11 full HUMAN mono meme format	ELK3_HUMAN.H11MO.0.D		7.41e-3	5.70e0	1.11	18 (42.9%)
	HOCOMOCov11 full HUMAN mono meme format	ATF7_HUMAN.H11MO.0.D		7.65e-3	5.88e0	1.54	3 (7.1%)
	HOCOMOCov11 full HUMAN mono meme format	ATF2_HUMAN.H11MO.1.B		7.65e-3	5.88e0	1.77	3 (7.1%)
	HOCOMOCov11 full HUMAN mono meme format	ZNF76_HUMAN.H11MO.0.C		7.71e-3	5.93e0	5.74	8 (19.0%)
	HOCOMOCov11 full HUMAN mono meme format	LHX9_HUMAN.H11MO.0.D		8.11e-3	6.24e0	1.04	10 (23.8%)
	HOCOMOCov11 full HUMAN mono meme format	MEIS1_HUMAN.H11MO.0.A		8.19e-3	6.30e0	1.64	14 (33.3%)

Logo	Database	ID	Alt ID	p-value	E-value	TP Thresh	TP (%)
	HOCOMOCov11 full HUMAN mono meme format	ETV7_HUMAN.H11MO.0.D		8.35e-3	6.42e0	2.95	21 (50.0%)
	HOCOMOCov11 full HUMAN mono meme format	CLOCK_HUMAN.H11MO.0.C		8.56e-3	6.58e0	3.91	6 (14.3%)
	HOCOMOCov11 full HUMAN mono meme format	MEF2D_HUMAN.H11MO.0.A		8.96e-3	6.89e0	2.15	11 (26.2%)
	HOCOMOCov11 full HUMAN mono meme format	ETS2_HUMAN.H11MO.0.B		9.88e-3	7.60e0	7.82	14 (33.3%)
	HOCOMOCov11 full HUMAN mono meme format	BRAC_HUMAN.H11MO.1.B		9.94e-3	7.64e0	1.11	28 (66.7%)
	HOCOMOCov11 full HUMAN mono meme format	BARH1_HUMAN.H11MO.0.D		1.04e-2	8.03e0	14.03	5 (11.9%)
	HOCOMOCov11 full HUMAN mono meme format	HXA10_HUMAN.H11MO.0.C		1.08e-2	8.32e0	1.16	14 (33.3%)
	HOCOMOCov11 full HUMAN mono meme format	GATA5_HUMAN.H11MO.0.D		1.15e-2	8.81e0	1.36	15 (35.7%)
	HOCOMOCov11 full HUMAN mono meme format	ZFP28_HUMAN.H11MO.0.C		1.16e-2	8.93e0	5.44	8 (19.0%)
	HOCOMOCov11 full HUMAN mono meme format	FOXD1_HUMAN.H11MO.0.D		1.20e-2	9.23e0	1.44	13 (31.0%)

INPUT FILES

Alphabet

Background source: built from the (primary) sequences

Background source: built from the (primary) sequences

Name ?	Bg. ?				Bg. ?	Name ?
Adenine	0.189588	A	~	T	0.189588	Thymine
Cytosine	0.310412	C	~	G	0.310412	Guanine

Name ?	Bg. ?				Bg. ?	Name ?
Adenine	0.189588	A	~	T	0.189588	Thymine
Cytosine	0.310412	C	~	G	0.310412	Guanine

Sequences

Primary Sequences	Number	Control Sequences	Number
Galaxy196-bedtools_GetFastaBed_Merged_and_Narrowed_Hypo_regions.fasta	42	primary sequences shuffled conserving 2-mer frequencies	1008

Primary Sequences	Number	Control Sequences	Number
Galaxy196-bedtools_GetFastaBed_Merged_and_Narrowed_Hypo_regions.fasta	42	primary sequences shuffled conserving 2-mer frequencies	1008

Motifs

Database	Source	Motif Count
HOCOMOCov11 full HUMAN mono meme format	db/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	769
HOCOMOCov11 full HUMAN mono meme format	db/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme	769

AME version

5.1.15.1.1 (Release date: Wed Jan 29 15:00:42 2020 -0800Wed Jan 29 15:00:42 2020 -0800)
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Command line summary

```
ame --verbose 1 --oc . --scoring avg --method fisher --hit-lo-fraction 0.25 --evaluate-report-threshold 10.0 --control --shuffle-- --kmer 2  
Galaxy196-bedtools_GetFastaBed_Merged_and_Narrowed_Hypo_regions.fasta db/HUMAN/HOCOMOCov11_full_HUMAN_mono_meme_format.meme
```

