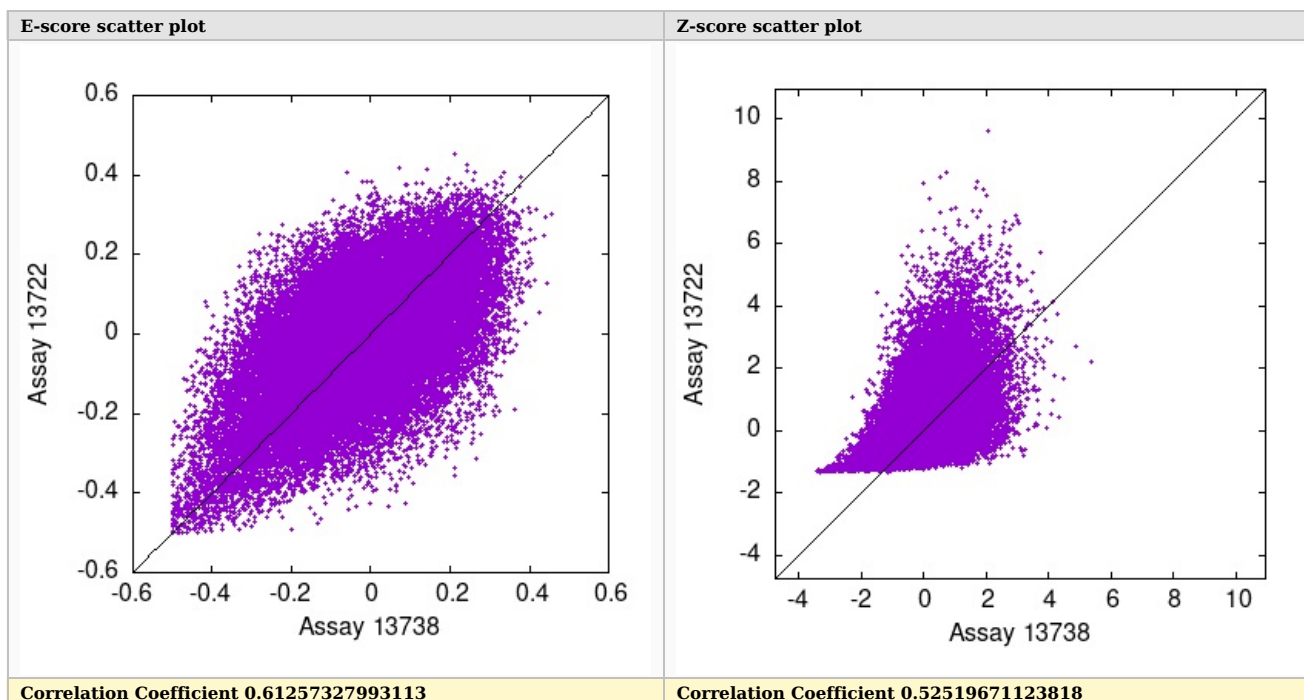


QC report



Top scoring motifs for Assay 13738

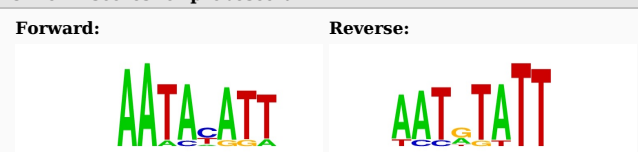
Protein ID: pTH14304.2 Gene: GPBP1.DBD Domain: Unknown Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
AAAATAAA	0.45617	AAAATAAA----
AATATATT	0.44587	--AATATATT--
ACAAAATA	0.44150	----TATTTTGT
AATAAATT	0.43711	--AATAAATT--
ACAAACCA	0.42438	ACAAACCA----
AATACATT	0.41735	--AATACATT--
ATATATTC	0.41445	---ATATATTC-
ATGTATCA	0.41398	-TGATACAT---
ATACATTA	0.40730	---ATACATTA-
CTGTATTA	0.40288	-TAATACAG--

8 mer Z-scores for probeset 'all'

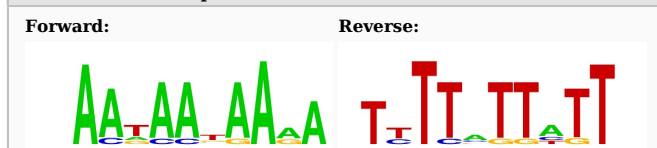


Top 10	Scores	Alignment
AATATATT	5.39326	----AATATATT--
ATATATTC	4.86783	-----ATATATTC-
GATATGTA	4.49334	-----TACATATC
ATACGTTA	4.33989	-----ATACGTTA-
AATAAATT	4.28384	-----AATAAATT--
TATTTGCA	4.21380	TGCAATA-----
AATACATT	4.13974	-----AATACATT--
CTGTATTA	4.12871	---TAATACAG---
ATATATTG	4.10663	-----ATATATTG-
ACAAACCA	4.07891	--ACAAACCA----

Top scoring motifs for Assay 13722

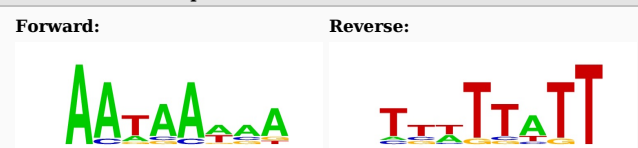
Protein ID: pTH14304.1 Gene: GPBP1.DBD Domain: Unknown Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
TACGAAA	0.45344	---TACGAAA
AAATAATA	0.42654	AAATAATA---
AAGCAGAA	0.41789	-AAGCAGAA--
TAATAAGA	0.41608	---TAATAAGA
AATAATAA	0.41179	-AATAATAA--
AAGACGAA	0.40690	-AAGACGAA--
ACAAATAA	0.40549	-ACAAATAA--
ATAATAAA	0.40491	--ATAATAAA--
AAAAATAA	0.39636	-AAAAATAA--
AATAAAAA	0.39442	-AATAAAAA--

8 mer Z-scores for probeset 'all'



Top 10	Scores	Alignment
AAATAATA	9.65174	AAATAATA--
AAGCAGAA	8.27751	-AAGCAGAA--
AAGCAAT	8.14113	-AAGCAAT--
ACAAATAA	7.98096	-ACAAATAA--
AATAAACA	7.94551	-AATAAACA--
ATAATAAA	7.82009	--ATAATAAA
AATAAAAA	7.73952	-AATAAAAA--
AATAATGG	7.53782	-AATAATGG--
ATAAACAC	7.44854	--ATAAACAC
ATAAAGAT	7.13254	--ATAAAGAT