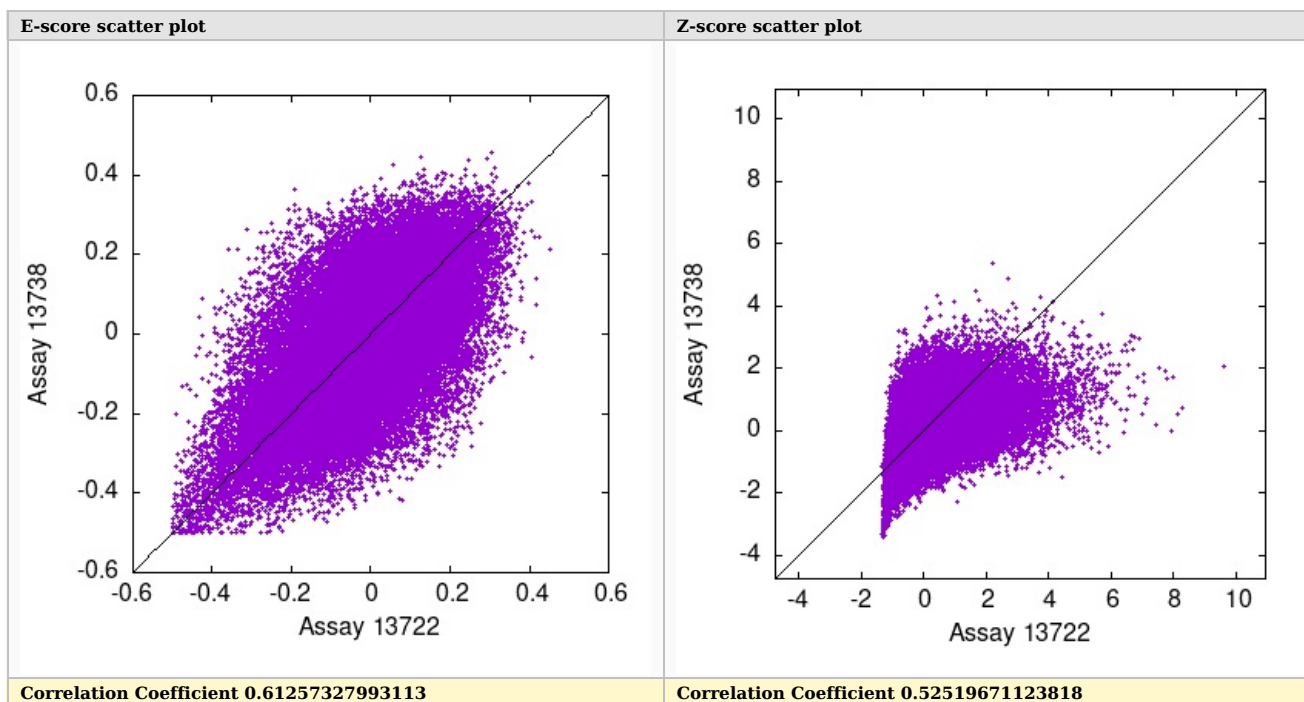




QC report





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'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
TAACGAAA	0.45344	- - - TAACGAAA
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'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AAATAATA	9.65174	AAATAATA--	
AAGCAGAA	8.27751	-AAGCAGAA-	
AAAGCAAT	8.14113	-AAAGCAAT-	
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	



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'

Forward:	Reverse:	
		
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'

Forward:		Reverse:	
			
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	TGCAAATA-----	
AATACATT	4.13974	-----AATACATT--	
CTGTATTA	4.12871	---TAATACAG---	
ATATATTG	4.10663	-----ATATATTG-	
ACAAACCA	4.07891	--ACAAACCA----	