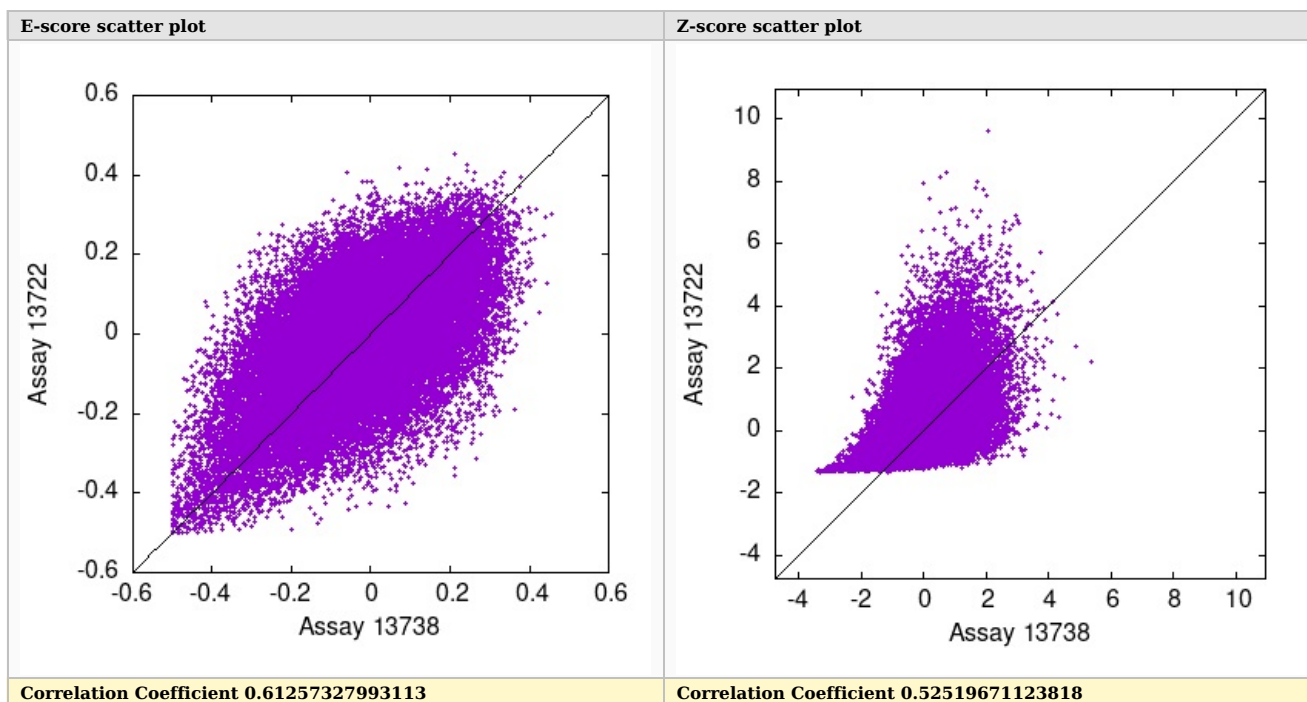


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AAAATAAA	0.45617	AAAATAAA----	AATATATT	5.39326	----AATATATT--
AATATATT	0.44587	--AATATATT--	ATATATTTC	4.86783	-----ATATATTTC-
ACAAAATA	0.44150	----TATTTTGT	GATATGTA	4.49334	-----TACATATC
AATAAATT	0.43711	--AATAAATT--	ATACGTTA	4.33989	-----ATACGTTA-
ACAAACCA	0.42438	ACAAACCA----	AATAAATT	4.28384	-----AATAAATT--
AATACATT	0.41735	--AATACATT--	TATTTGCA	4.21380	TGCAATA-----
ATATATTTC	0.41445	---ATATATTTC-	AATACATT	4.13974	-----AATACATT--
ATGTATCA	0.41398	-TGATACAT---	CTGTATTA	4.12871	---TAATACAG---
ATACATTA	0.40730	---ATACATTA--	ATATATTG	4.10663	-----ATATATTG-
CTGTATTA	0.40288	-TAATACAG---	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TAACGAAA	0.45344	---TAACGAAA	AAATAATA	9.65174	AAATAATA--
AAATAATA	0.42654	AAATAATA---	AAGCAGAA	8.27751	-AAGCAGAA-
AAGCAGAA	0.41789	-AAGCAGAA--	AAAGCAAT	8.14113	-AAAGCAAT-
TAATAAGA	0.41608	---TAATAAGA	ACAAATAA	7.98096	-ACAAATAA-
AATAATAA	0.41179	-AATAATAA--	AATAAACA	7.94551	-AATAAACA-
AAGACGAA	0.40690	-AAGACGAA--	ATAATAAA	7.82009	--ATAATAAA
ACAAATAA	0.40549	-ACAAATAA--	AATAAAAA	7.73952	-AATAAAAA-
ATAATAAA	0.40491	--ATAATAAA-	AATAATGG	7.53782	-AATAATGG-
AAAAATAA	0.39636	-AAAAATAA--	ATAAACAC	7.44854	--ATAAACAC
AATAAAAA	0.39442	-AATAAAAA--	ATAAAGAT	7.13254	--ATAAAGAT