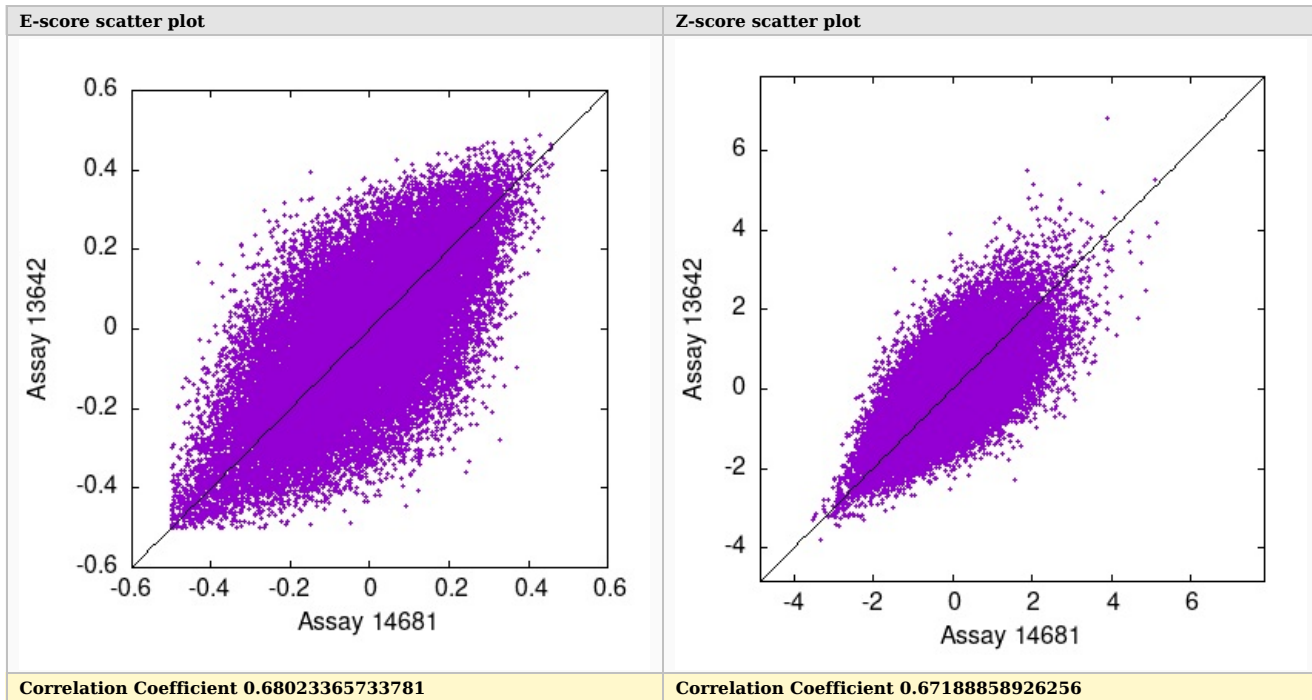


QC report



Top scoring motifs for Assay 14681

Protein ID: pTH13919.3 Gene: GLYR1.DBD Domain: AT_hook Flag: Backup_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
ATATATAT	0.46168	-ATATATAT-	ATTTAAAT	5.13180	--ATTTAAAT--
AAATATAT	0.45536	-AAATATAT-	AAATATAT	5.10548	--AAATATAT--
ATTTAAAT	0.45509	-ATTTAAAT-	ATAATATA	4.94166	--ATAATATA-
ATAATATA	0.45099	ATAATATA--	TTATATAA	4.87884	--TTATATAA-
TAAATTTA	0.44980	TAAATTTA--	ATATATTA	4.76412	--TAATATAT-
AATAATAA	0.44467	-AATAATAA-	ATTATATA	4.68903	--ATTATATA-
ATATATTA	0.44118	-TAATATAT-	ATATATAT	4.53674	--ATATATAT-
TTATATAA	0.43882	-TTATATAA-	AATAATAA	4.46489	TTATTATT---
ATAATTAT	0.43746	-ATAATTAT-	AAAATTTT	4.42557	--AAAATTTT-
ATTATATA	0.43596	--ATTATATA	TTTATAAA	4.23567	--TTTATAAA-

Top scoring motifs for Assay 13642

Protein ID: pTH13919.2 Gene: GLYR1.DBD Domain: AT_hook Flag: Backup_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
AATATATT	0.48709	--AATATATT	AATATATT	6.80307	--AATATATT--
AATAAATT	0.47669	--AATAAATT	AATTTAAA	5.49601	--TTTAAATT--
AATTTAAA	0.46807	--AATTTAAA	AAATATAT	5.25725	--AAATATAT--
AAATATTT	0.46748	-AAATATTT-	GAAATTTT	5.16522	-----GAAATTTT
ACAAAATA	0.46683	ACAAAATA--	AATAAATT	5.14720	--AATAAATT--
AAATATAT	0.46457	-AAATATAT-	TATTAATA	4.96037	--TATTAATA--
ATATATTG	0.45898	-CAATATAT-	AAAATAAA	4.88125	AAAATAAA----
TATTAATA	0.45591	--TATTAATA	ATAATTTT	4.79419	--ATAATTTT-
AAATTGAT	0.45416	-AAATTGAT-	GAATATTC	4.77199	--GAATATTC-
ATTTAAAT	0.45305	-ATTTAAAT-	AAATTAAT	4.58082	-AAATTAAT---