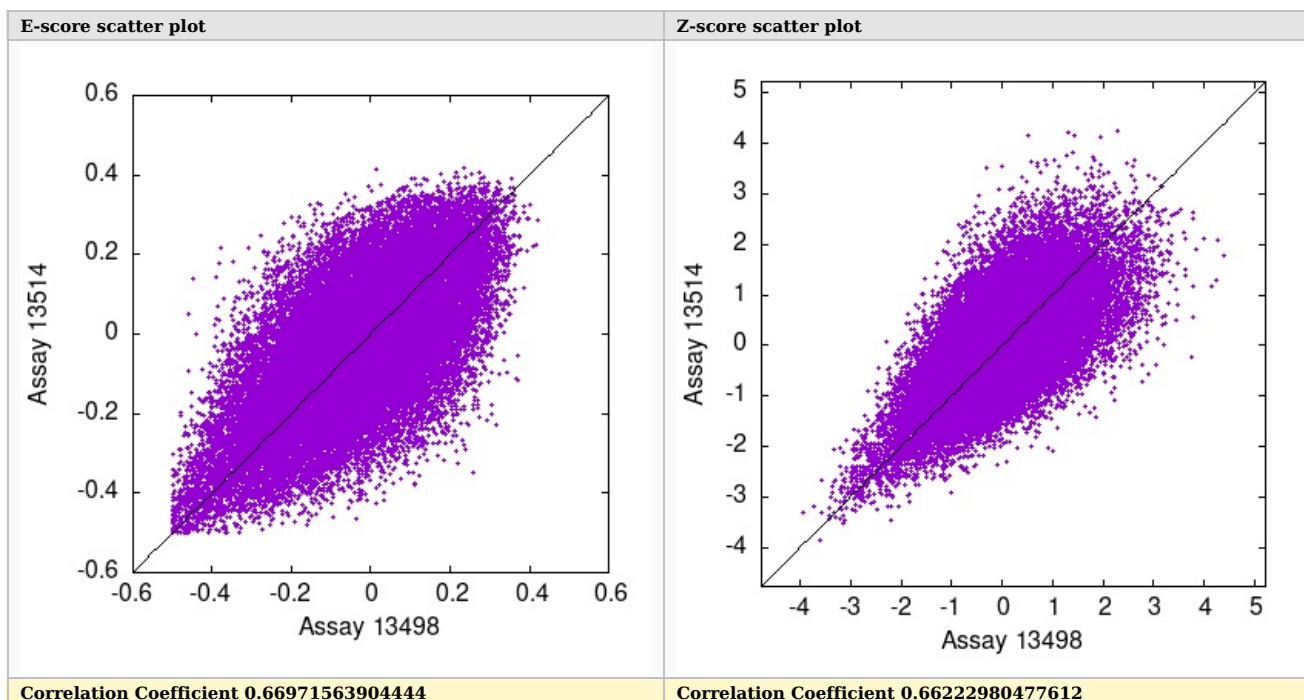




QC report





Top scoring motifs for Assay 13498

Protein ID: pTH13914.1 Gene: AKNA.DBD.1 Domain: AT_hook Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ATGTATAA	0.42295	-ATGTATAA--
TAACGAAA	0.41882	--TAACGAAA-
ATAATGCA	0.41023	--TGCAATAT-
ATATAAAT	0.40294	-ATATAAAT--
ATATATAA	0.39907	-ATATATAA--
ATTATATA	0.39308	--TATATAAT-
ATACAATA	0.39229	-ATACAATA--
ACAAATAA	0.38801	-ACAAATAA--
CATAATAC	0.38783	---GTATTATG
TAAATTTA	0.38537	TAAATTTA---



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ATGTATAA	4.39247	-ATGTATAA-	
ATATATAA	4.26458	-ATATATAA-	
ATTATATA	4.24762	--TATATAAT	
TAACGAAA	4.14867	--TAACGAAA	
ATGTTAAT	3.99572	-ATGTTAAT-	
AATATATG	3.84875	AATATATG--	
AGATATAT	3.80127	-AGATATAT-	
ATATAAAT	3.80046	-ATATAAAT-	
ATAATGCA	3.78109	--TGCATTAT	
ATCATTTA	3.77515	--TAAATGAT	



Top scoring motifs for Assay 13514

Protein ID: pTH13914.2 Gene: AKNA.DBD.1 Domain: AT_hook Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
GATATGTA	0.41972	---TACATATC
TACACACA	0.41441	---TACACACA
CTGTATTA	0.40618	TAATACAG--
ATAGTAAT	0.40606	--ATAGTAAT-
ATATTAAT	0.40397	--ATTAATAT-
CACATATA	0.40374	---CACATATA
ATACATAA	0.39632	--ATACATAA-
ATATCTTA	0.39371	--ATATCTTA-
AACACTTA	0.39292	-AACACTTA--
CACAAATA	0.39291	-CACAAATA--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ACAAAATA	4.25834	-ACAAAATA-
TATTTGCA	4.21344	-TGCAAATA-
AATTTAAA	4.16610	-AATTTAAA-
CACATATA	4.15070	-CACATATA-
ATATCTTA	4.12499	TAAGATAT--
GATATGTA	3.81935	-TACATATC-
GTAATGTA	3.75833	-GTAATGTA-
CACAAATA	3.73501	-CACAAATA-
AATATATT	3.68514	-AATATATT-
CTGTATTA	3.66898	--TAATACAG