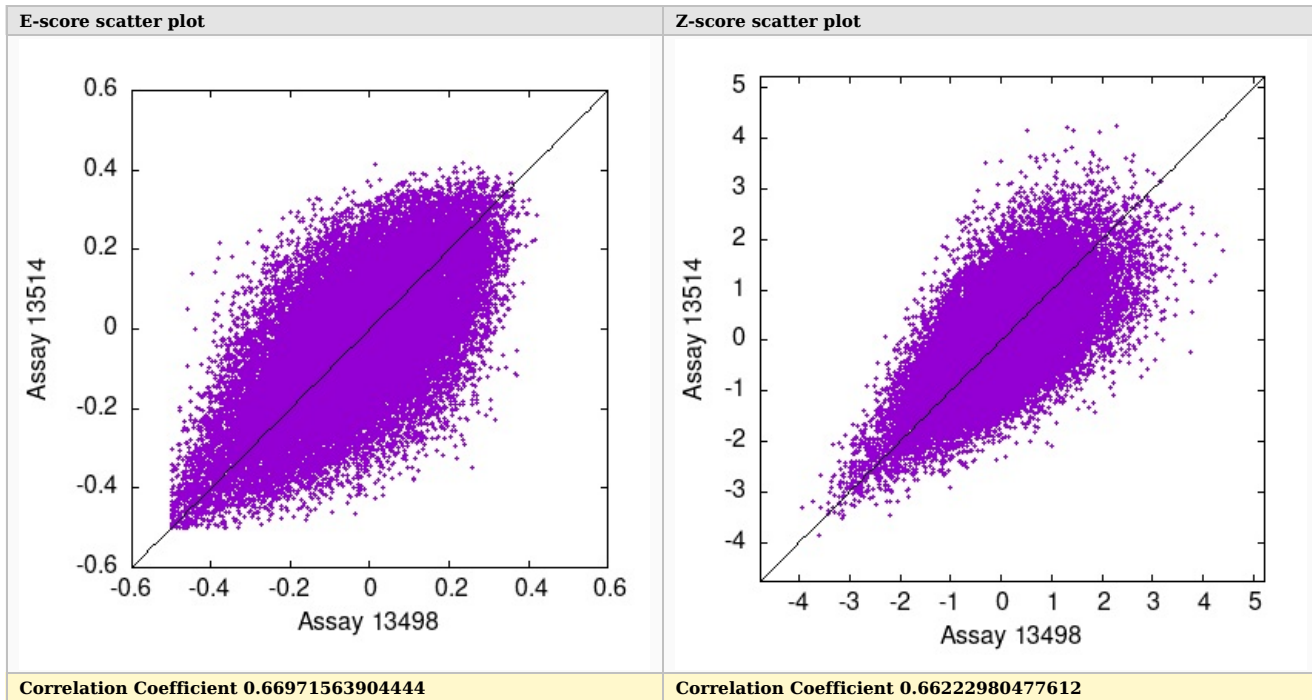


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATGTATAA	0.42295	-ATGTATAA--	ATGTATAA	4.39247	-ATGTATAA-
TAACGAAA	0.41882	--TAACGAAA-	ATATATAA	4.26458	-ATATATAA-
ATAATGCA	0.41023	--TGCAATAT-	ATTATATA	4.24762	--TATATAAT
ATATAAAT	0.40294	-ATATAAAT--	TAACGAAA	4.14867	--TAACGAAA
ATATATAA	0.39907	-ATATATAA--	ATGTTAAT	3.99572	-ATGTTAAT-
ATTATATA	0.39308	--TATATAAT-	AATATATG	3.84875	AATATATG--
ATACAATA	0.39229	-ATACAATA--	AGATATAT	3.80127	-AGATATAT-
ACAAATAA	0.38801	-ACAAATAA--	ATATAAAT	3.80046	-ATATAAAT-
CATAATAC	0.38783	---GTATTATG	ATAATGCA	3.78109	--TGCAATAT
TAAATTTA	0.38537	TAAATTTA--	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GATATGTA	0.41972	---TACATATC	ACAAAATA	4.25834	-ACAAAATA-
TACACACA	0.41441	---TACACACA	TATTTGCA	4.21344	-TGCAAAATA-
CTGTATTA	0.40618	TAATACAG---	AATTTAAA	4.16610	-AATTTAAA-
ATAGTAAT	0.40606	--ATAGTAAT-	CACATATA	4.15070	-CACATATA-
ATATTAAT	0.40397	--ATTAATAT-	ATATCTTA	4.12499	TAAGATAT--
CACATATA	0.40374	---CACATATA	GATATGTA	3.81935	-TACATATC-
ATACATAA	0.39632	--ATACATAA-	GTAATGTA	3.75833	-GTAATGTA-
ATATCTTA	0.39371	--ATATCTTA-	CACAAATA	3.73501	-CACAAATA-
AACACTTA	0.39292	---AACACTTA--	AATATATT	3.68514	-AATATATT-
CACAAATA	0.39291	-CACAAATA--	CTGTATTA	3.66898	--TAATACAG