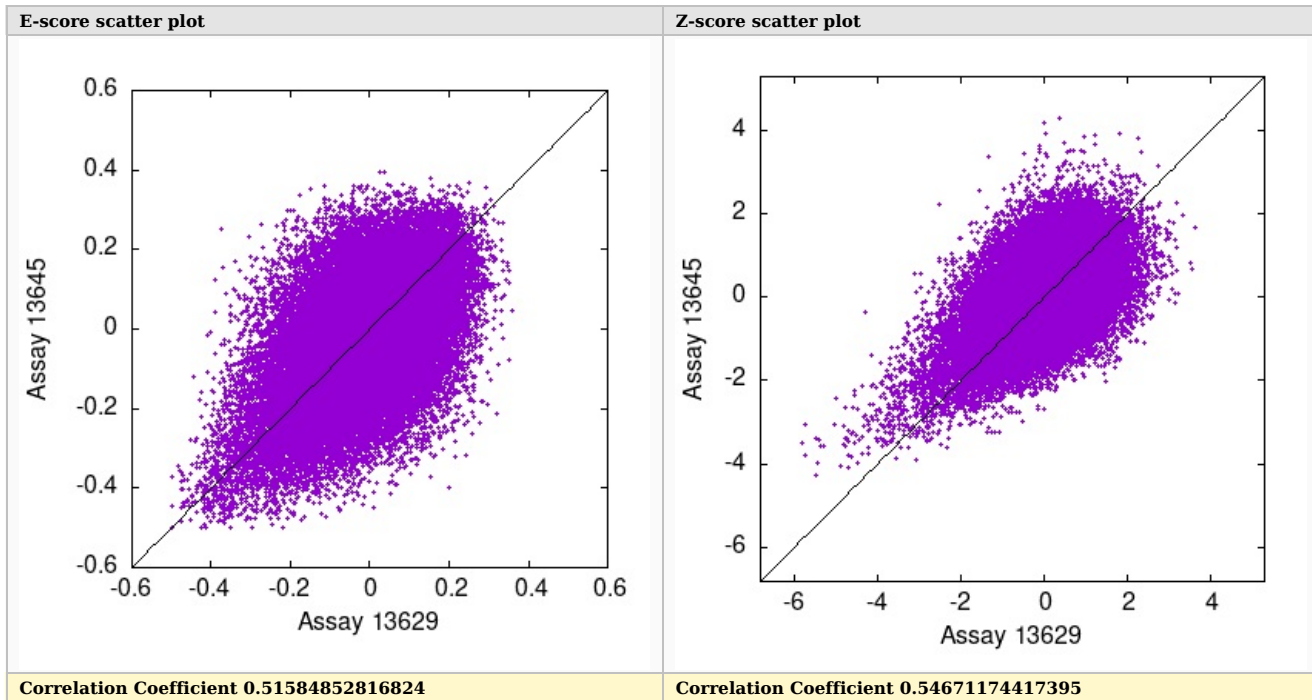


QC report



Top scoring motifs for Assay 13629

Protein ID: pTH14230.1 Gene: GATAD2B.DBD Domain: GATA 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
CGAACAGA	0.35976	----CGAACAGA	ACTGATTG	3.61947	CAATCAGT--
ACATACCG	0.35227	--ACATACCG--	GAACAACA	3.61863	--TGTTGTC
TACATACA	0.35076	--TACATACA--	AACTCAA	3.56207	--TTGAGTGT
AGTTGTCA	0.35035	--TGACAACT--	TAATAACA	3.54007	--TGTTATTA
ACTGATTG	0.34935	--CAATCAGT--	ACATTAGT	3.33254	ACATTAGT--
ACAAAACA	0.34841	--ACAAAACA--	TACCGACA	3.22968	--TGTCGGTA--
CGCAAAAC	0.34483	--CGCAAAAC--	GTGTGTAA	3.18945	--GTGTGTAA
TAATAACA	0.34014	--TAATAACA--	AATGTGAA	3.18338	--AATGTGAA--
TCGAGTAA	0.33786	TCGAGTAA----	ATTTGTAC	3.17723	--ATTTGTAC
ATACCAAT	0.33699	----ATACCAAT	CATTGTGA	3.17111	-CATTGTGA-

Top scoring motifs for Assay 13645

Protein ID: pTH14230.2 Gene: GATAD2B.DBD Domain: GATA 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
ATATCACA	0.39543	--ATATCACA-	AATTTAAA	4.29443	-TTTAAATT
GATATGTA	0.39351	-GATATGTA--	ATATCACA	4.21259	ATATCACA-
ATATTAAG	0.37865	--ATATTAAG-	TATTTGCA	3.93794	-TATTTGCA
CTGTATTA	0.36660	CTGTATTA---	GTCATGAC	3.92227	GTCATGAC-
ATCAGTAC	0.36363	--GTACTGAT-	ATATTAAG	3.91785	ATATTAAG-
GCACTATA	0.36204	---TATAGTGC	ATTATAAT	3.87726	ATTATAAT-
ACCACTAA	0.36161	-ACCACTAA--	CATATATG	3.82713	-CATATATG
AGTTTTTC	0.36144	---GAAAAACT	TATTAATA	3.72685	-TATTAATA
AATTCGGC	0.36129	---AATTCGGC	ATATTAAT	3.71627	ATATTAAT-
CATATATG	0.36114	-CATATATG--	ATCAGTAC	3.66757	GTACTGAT-