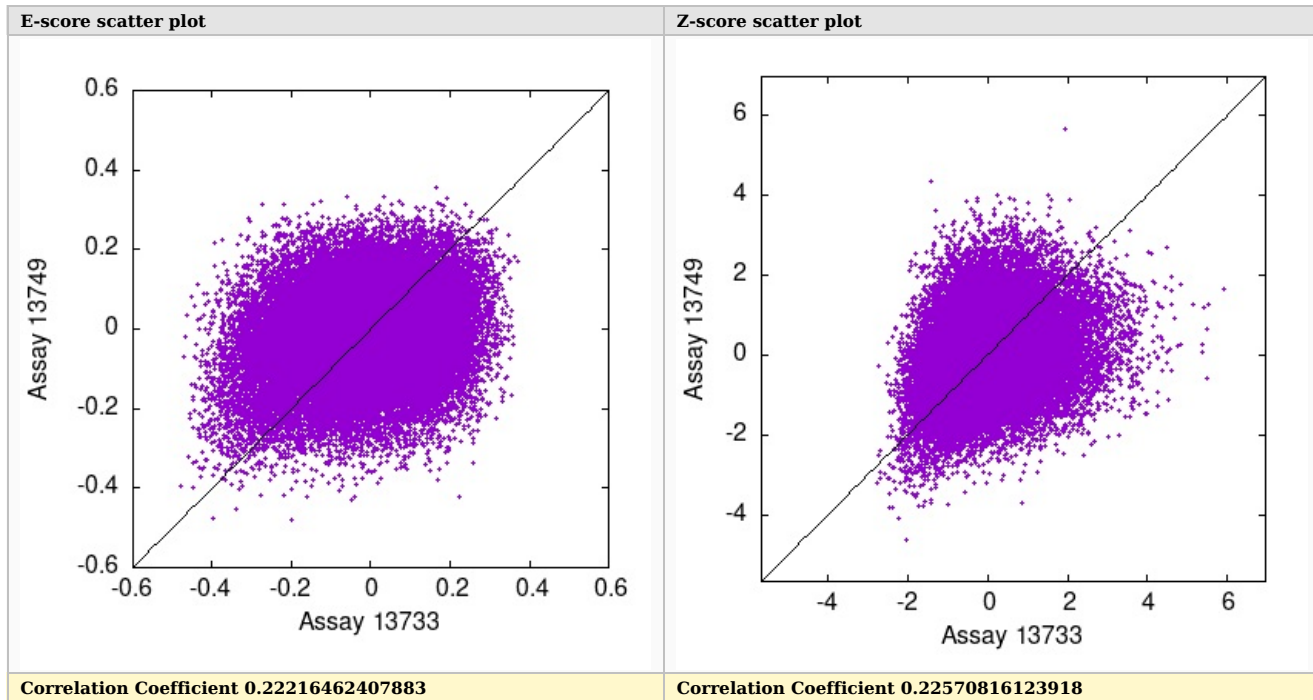


QC report



Top scoring motifs for Assay 13733

Protein ID: pTH14320.1 Gene: PURG.FL Domain: Unknown 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
TACGAAA	0.37126	-TTTCGTTA-	TACATACA	5.89974	--TGTATGTA--
GTACTTTA	0.36372	-GTACTTTA-	TATGTGAA	5.51919	--TATGTGAA--
AGACGAAA	0.35974	--TTTCGTCT	AGACGAAA	5.48783	---AGACGAAA-
ATATTTTA	0.35903	-ATATTTTA-	AATGAATC	5.47210	----AATGAATC
AAGAGATA	0.35712	TATCTCTT--	AATCAGTA	5.39950	---TACTGATT-
ATAATGCA	0.35451	-ATAATGCA-	ATATTTTA	5.36470	-ATATTTTA---
AAGATATA	0.35386	TATATCTT--	GAATAATA	5.36008	----TATTATTC
GTATAATA	0.35329	--TATTATAC	CATTGATA	5.12459	TATCAATG----
ATAAATAA	0.35181	-ATAAATAA-	ATATATGA	4.84249	-ATATATGA---
AATAATAA	0.35137	-TTATTATT-	AAGCAGAA	4.81645	---TTCTGCTT-

Top scoring motifs for Assay 13749

Protein ID: pTH14320.2 Gene: PURG.FL Domain: Unknown 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
GTAACATA	0.35733	---GTAACATA--	GTAACATA	5.63013	----TATGTTAC-
ATGCTTAC	0.33331	----ATGCTTAC-	CGCGTCCA	4.33044	---TGGACGCG---
GGTATACA	0.33262	-----TGTATACC	GCACGGTA	4.00229	---GCACGGTA--
TCAATTGA	0.33066	TCAATTGA-----	CACACAGC	3.99891	--CACACAGC---
CCTCGGCG	0.32218	--CCTCGGCG---	GTAACGTA	3.93256	----TACGTTAC-
ACCTACGT	0.32024	--ACCTACGT---	CATCGCAC	3.89799	----CATCGCAC-
ACTTGCAT	0.31571	--ACTTGCAT---	AATACAGC	3.89371	-----GCTGTATT
GTTCAAGC	0.31514	--GTTCAAGC---	TCAATTGA	3.87761	---TCAATTGA--
ATCTGGCG	0.31448	-ATCTGGCG----	ACGACGAT	3.85907	--ACGACGAT---
CATCGCAC	0.31360	--CATCGCAC---	ACAACCTCG	3.82845	ACAACCTCG-----