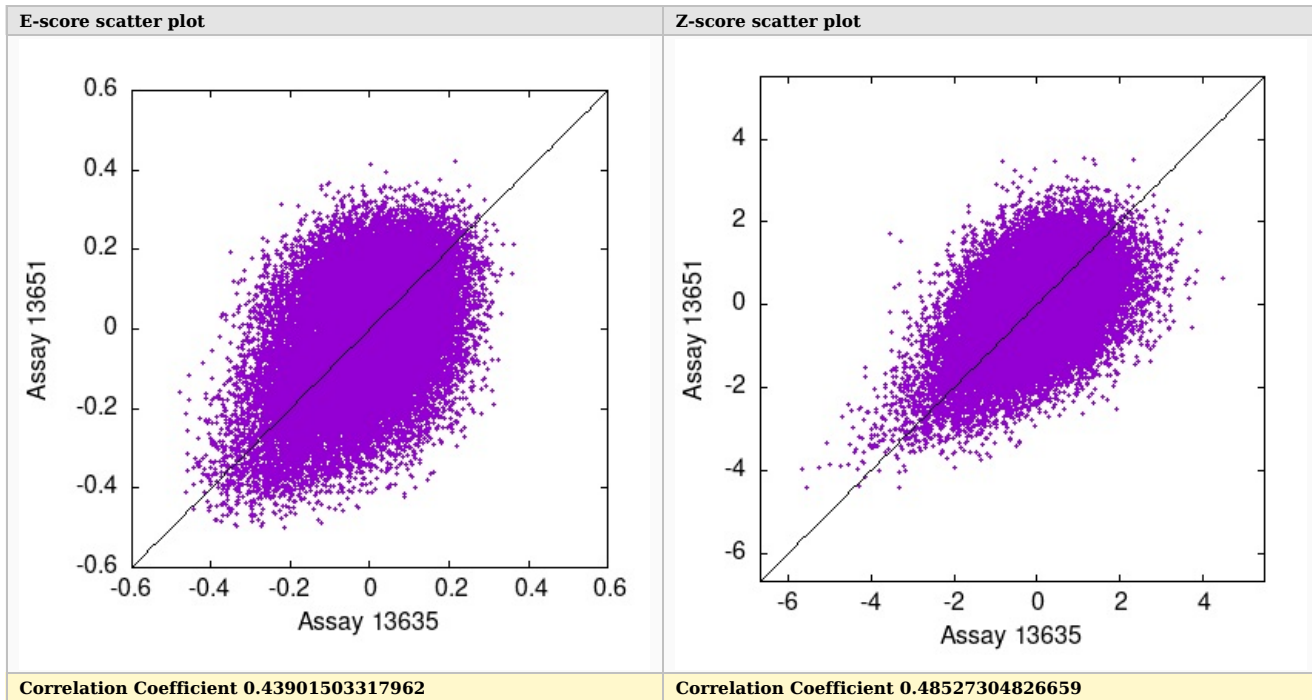


QC report



Top scoring motifs for Assay 13635

Protein ID: pTH14302.1 Gene: GLMP.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
CACAACAC	0.36119	--CACAACAC--	CACATTCA	4.49182	-----CACATTCA
CACATTCA	0.35986	--CACATTCA--	CGTTATAA	3.93562	CGTTATAA-----
GTTATAAC	0.33417	GTTATAAC----	ACAACGCA	3.86694	-ACAACGCA----
ATACACAT	0.33289	----ATACACAT	GTTTTGTA	3.81185	---TACAAAAC---
ATTATCTG	0.33178	--CAGATAAT--	ACCAGATA	3.76989	---ACCAGATA--
CAGACAAC	0.32769	--CAGACAAC--	ATATTGTA	3.69959	---TACAATAT--
CAACACCA	0.32447	----CAACACCA	AGACACAT	3.68969	--AGACACAT---
ATCTTTAC	0.32150	--ATCTTTAC--	ATACACAT	3.62571	--ATACACAT---
TCTTTACA	0.32142	-TCTTTACA---	GAATCCAA	3.59861	GAATCCAA-----
GTTTTGTA	0.31523	--TACAAAAC--	TCTTTACA	3.50631	-TCTTTACA----

Top scoring motifs for Assay 13651

Protein ID: pTH14302.2 Gene: GLMP.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
GTCATGAC	0.42261	----GTCATGAC-	AAACGTTT	3.52642	-----AAACGTTT-
AAACGTTT	0.41249	AAACGTTT-----	GTTTAAAC	3.51516	--GTTTAAAC-----
GCATATGC	0.39340	--GCATATGC---	GTCATGAC	3.49629	-GTCATGAC-----
ATTTGCAA	0.37551	----ATTTGCAA-	GCATATGC	3.46646	--GCATATGC-----
AATGTTTG	0.36670	-AATGTTTG----	CTTGCAAG	3.46116	---CTTGCAAG-----
ATCCGGAT	0.36589	----ATCCGGAT-	ACAAACAG	3.40362	----ACAAACAG---
ATCAGCTG	0.36274	----ATCAGCTG-	ACAATTCA	3.29458	ACAATTCA-----
TCGCGCGA	0.36088	----TCGCGCGA-	CTGTGATA	3.22475	--CTGTGATA-----
TTTGCAAA	0.36082	-----TTTGCAAA	ATCAGCTG	3.09325	----ATCAGCTG---
ATGCGCAT	0.36029	----ATGCGCAT-	AACGCGTT	3.09072	-----AACGCGTT-