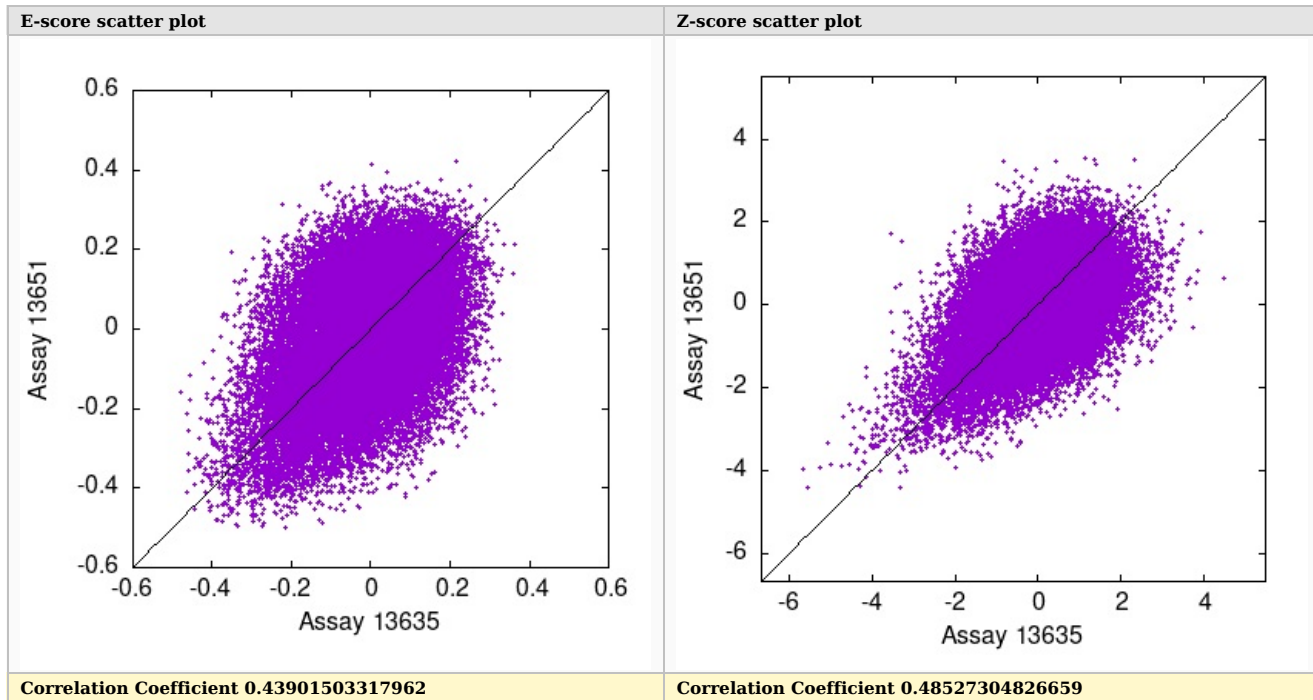


## QC report



## 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'

Forward:		Reverse:	
Top 10	Scores	Alignment	
CACAACAC	0.36119	--CACAACAC--	
CACATTCA	0.35986	--CACATTCA--	
GTTATAAC	0.33417	GTTATAAC---	
ATACACAT	0.33289	----ATACACAT	
ATTATCTG	0.33178	--CAGATAAT--	
CAGACAAC	0.32769	--CAGACAAC--	
CAACACCA	0.32447	----CAACACCA	
ATCTTTAC	0.32150	--ATCTTTAC--	
TCTTTACA	0.32142	-TCTTTACA--	
GTTTTGTA	0.31523	--TACAAAAC--	

## 8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
CACATTCA	4.49182	-----CACATTCA	
CGTTATAA	3.93562	CGTTATAA-----	
ACAACGCA	3.86694	-ACAACGCA----	
GTTTTGTA	3.81185	---TACAAAAC---	
ACCAGATA	3.76989	---ACCAGATA---	
ATATTGTA	3.69959	---TACAATAT---	
AGACACAT	3.68969	--AGACACAT---	
ATACACAT	3.62571	--ATACACAT---	
GAATCCAA	3.59861	GAATCCAA-----	
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'

Forward:		Reverse:	
Top 10	Scores	Alignment	
GTCATGAC	0.42261	----GTCATGAC-	
AAACGTTT	0.41249	AAACGTTT-----	
GCATATGC	0.39340	--GCATATGC---	
ATTTGCAA	0.37551	----ATTTGCAA-	
AATGTTTG	0.36670	-AATGTTTG----	
ATCCGGAT	0.36589	----ATCCGGAT-	
ATCAGCTG	0.36274	----ATCAGCTG-	
TCGCGCGA	0.36088	----TCGCGCGA-	
TTTGCAAA	0.36082	-----TTTGCAAA	
ATGCGCAT	0.36029	----ATGCGCAT-	

## 8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
AAACGTTT	3.52642	-----AAACGTTT-	
GTTTAAAC	3.51516	--GTTTAAAC-----	
GCATGAC	3.49629	-GTCATGAC-----	
GCATATGC	3.46646	--GCATATGC-----	
CTTGCAAG	3.46116	--CTTGCAAG-----	
ACAAACAG	3.40362	----ACAAACAG---	
ACAATTCA	3.29458	ACAATTCA-----	
CTGTGATA	3.22475	--CTGTGATA-----	
ATCAGCTG	3.09325	----ATCAGCTG---	
AACGCGTT	3.09072	-----AACGCGTT-	