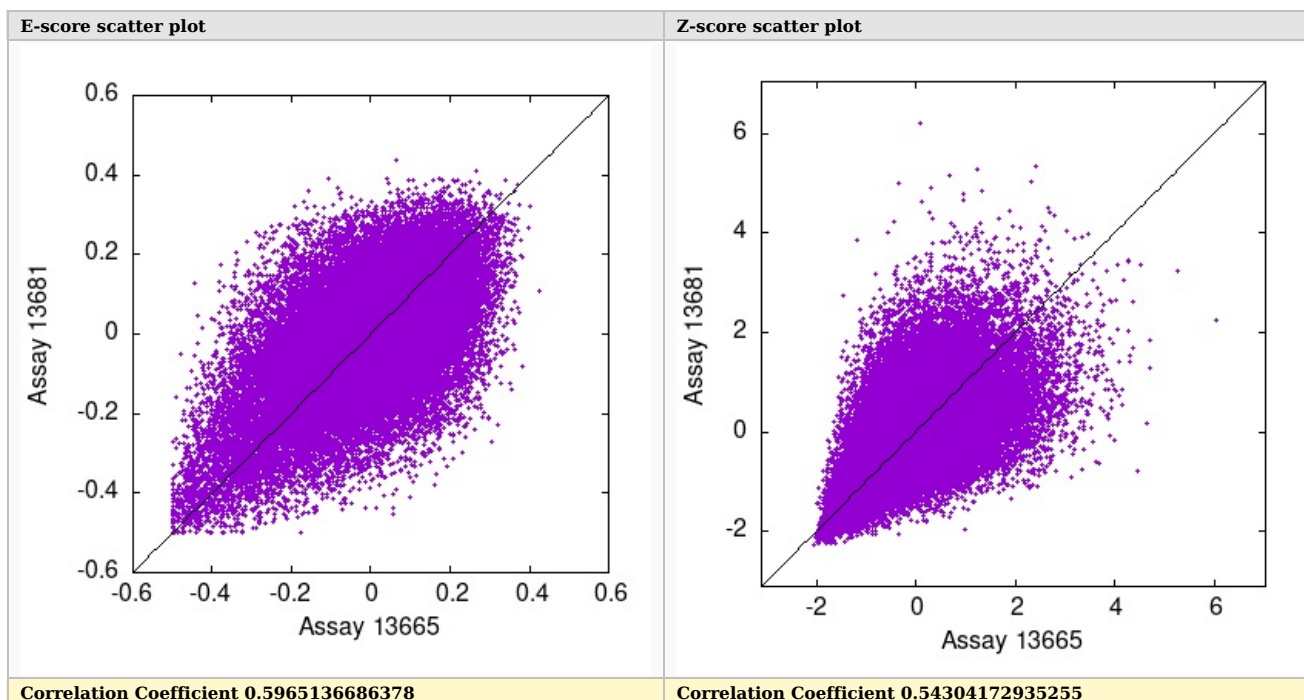


QC report



Top scoring motifs for Assay 13665

Protein ID: pTH14275.1 Gene: MYSM1.DBD Domain: Myb_DNA-binding Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TAACGAAA	0.42378	--TAACGAAA--	
GTACTTTA	0.40359	--TAAAGTAC--	
TGTATACA	0.39695	----TGTATACA	
ACATACAA	0.38190	----TTGTATGT	
AAGCAGAA	0.38063	--TTCTGCTT--	
ATAATGCA	0.38041	-ATAATGCA---	
ATGTACAT	0.37710	----ATGTACAT	
ATAATGTA	0.37429	-ATAATGTA---	
AACTGATA	0.37356	TATCAGTT----	
GTACTATA	0.37138	--TATAGTAC--	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TGTATACA	6.03105	-TGTATACA----	
GTACTTTA	5.27367	TAAAGTAC-----	
CACAACAC	4.71627	---CACAACAC--	
ATGTACAT	4.69855	--ATGTACAT---	
AATACTAA	4.65090	---AATACTAA--	
ATAATGTA	4.53628	-----TACATTAT	
AAGCAGAA	4.47215	--AAGCAGAA---	
AAGATATA	4.37320	-AAGATATA----	
ATTTGTAA	4.37320	----TTACAAAT-	
ACATACAA	4.32417	--ACATACAA---	

Top scoring motifs for Assay 13681

Protein ID: pTH14275.2 Gene: MYSM1.DBD Domain: Myb_DNA-binding Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
GTGTACAC	0.43736	---GTGTACAC---	
AAAATAAA	0.40993	----TTTATTTT--	
AAGCGCTT	0.39213	---AAGCGCTT---	
AAGTACTT	0.39149	---AAGTACTT---	
AACAATGA	0.39014	--TCATTGTT----	
TGTTAACA	0.38715	-----TGTTAACA	
GTATACTA	0.38598	---GTATACTA---	
TGACAAAA	0.38582	---TTTTGTCA---	
GATATGTA	0.38578	GATATGTA-----	
CTGTATTA	0.38573	---CTGTATTA---	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
GTGTACAC	6.19231	---GTGTACAC---	
ATGTTAAC	5.34920	---ATGTTAAC---	
AAAATAAA	5.26632	TTTATTTT-----	
AACAATGA	5.14901	TCATTGTT-----	
TGTTAACA	5.02825	----TGTTAACA	
CACAGAGA	4.98552	TCTCTGTG-----	
CTACATTA	4.89619	-CTACATTA---	
TATTTGCA	4.85786	----TATTTGCA	
GATGCATC	4.76689	--GATGCATC---	
TACACACA	4.65627	--TGTTGTGA---	