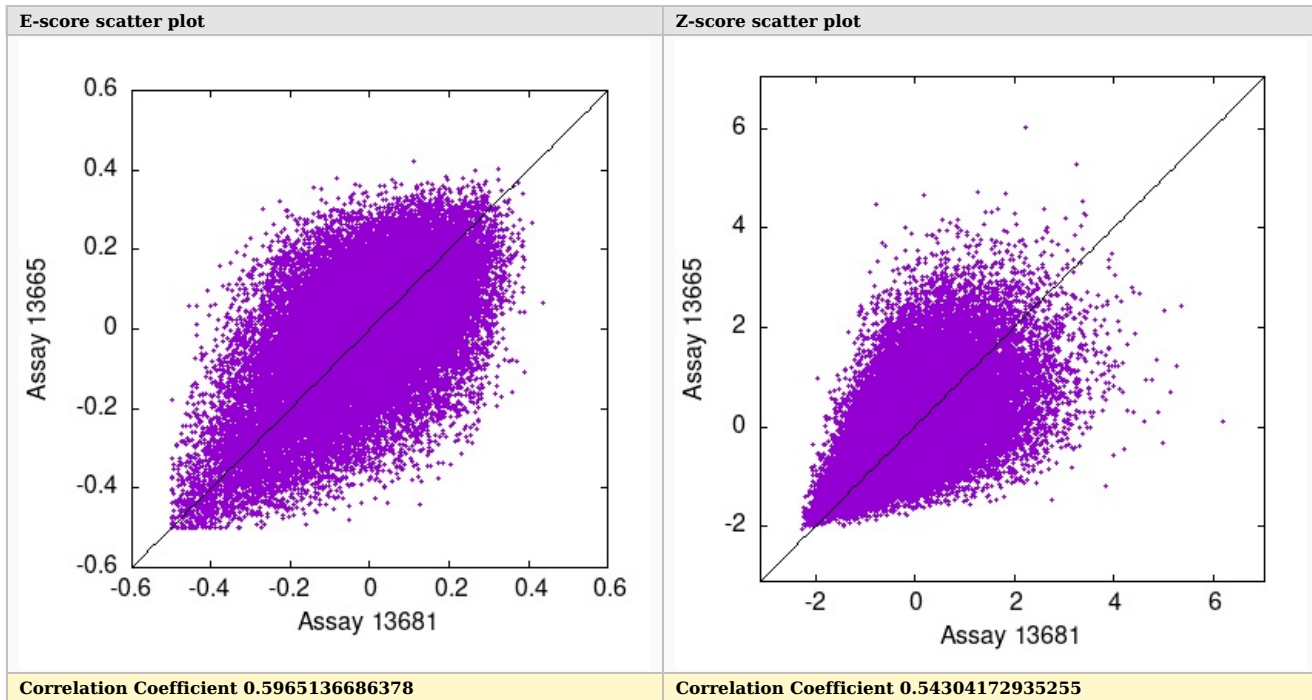


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GTGTACAC	0.43736	---GTGTACAC---	GTGTACAC	6.19231	---GTGTACAC---
AAAATAAA	0.40993	---TTTATTTT---	ATGTTAAC	5.34920	---ATGTTAAC---
AAGCGCTT	0.39213	---AAGCGCTT---	AAAATAAA	5.26632	TTTATTTT----
AAGTACTT	0.39149	---AAGTACTT---	AACAATGA	5.14901	TCATTGTT----
AACAATGA	0.39014	--TCATTGTT----	TGTTAACA	5.02825	----TGTTAACA
TGTTAACA	0.38715	-----TGTTAACA	CACAGAGA	4.98552	TCTCTGTG----
GTATACTA	0.38598	---GTATACTA---	CTACATTA	4.89619	--CTACATTA---
TGACAAAA	0.38582	---TTTTGTCA---	TATTTGCA	4.85786	----TATTTGCA
GATATGTA	0.38578	GATATGTA-----	GATGCATC	4.76689	--GATGCATC--
CTGTATTA	0.38573	---CTGTATTA---	TACACACA	4.65627	--TGTGTGTA--

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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TAACGAAA	0.42378	--TAACGAAA---	TGTATACA	6.03105	-TGTATACA----
GTACTTTA	0.40359	---TAAAGTAC---	GTACTTTA	5.27367	TAAAGTAC-----
TGTATACA	0.39695	-----TGTATACA	CACAACAC	4.71627	---CACAACAC--
ACATACAA	0.38190	----TTGTATGT-	ATGTACAT	4.69855	--ATGTACAT---
AAGCAGAA	0.38063	--TTCTGCTT---	AATACTAA	4.65090	---AATACTAA--
ATAATGCA	0.38041	---ATAATGCA---	ATAATGTA	4.53628	-----TACATTAT
ATGTACAT	0.37710	-----ATGTACAT-	AAGCAGAA	4.47215	--AAGCAGAA---
ATAATGTA	0.37429	---ATAATGTA---	AAGATATA	4.37320	-AAGATATA----
AACTGATA	0.37356	TATCAGTT-----	ATTTGTAA	4.37320	----TTACAAAT-
GTACTATA	0.37138	--TATAGTAC---	ACATACAA	4.32417	--ACATACAA---