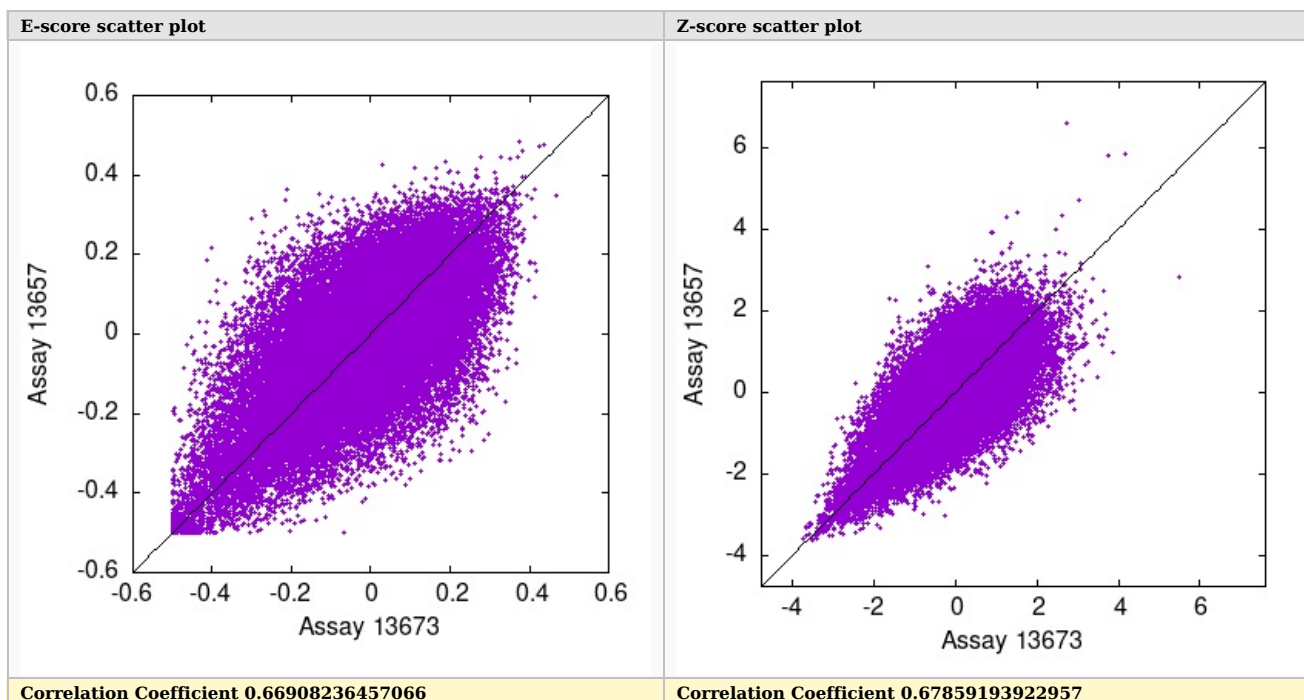




## QC report





### Top scoring motifs for Assay 13673

Protein ID: pTH14245.2 Gene: MKX.DBD Domain: Homeobox Flag: Pass\_matched\_pair Array: 1M-HK

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

Forward:		Reverse:
		
Top 10	Scores	Alignment
TGTTAACA	0.46859	---TGTTAACA
AACATGTT	0.43870	AACATGTT---
TACATGTA	0.42518	TACATGTA---
TATAACAA	0.41579	---TTGTTATA-
ATGTTACA	0.41522	---ATGTTACA-
TACACACA	0.41341	-TGTGTGTA--
AACAATGA	0.41238	TCATTGTT---
ATGTTAAC	0.41235	---ATGTTAAC-
GTGTACAC	0.40641	---GTGTACAC-
GTACAATA	0.40315	--TATTGTAC--



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

Forward:		Reverse:
		
Top 10	Scores	Alignment
TGTTAACA	5.48837	---TGTTAACA
TACATGTA	4.15788	--TACATGTA--
TACACACA	3.84909	--TGTGTGTA--
AACATGTT	3.73984	AACATGTT----
TATAACAA	3.70941	---TTGTTATA-
GTGTACAC	3.69476	--GTGTACAC-
TATGTTAA	3.64745	--TATGTTAA--
ACAAACAT	3.63814	---ATGTTTGT-
TACTAGTA	3.61915	--TACTAGTA--
GTAATGTA	3.52214	--TACATTAC--



### Top scoring motifs for Assay 13657

Protein ID: pTH14245.1 Gene: MKX.DBD Domain: Homeobox Flag: Pass\_matched\_pair Array: 1M-ME

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ATGTACAT	0.48388	---ATGTACAT
AACATGTT	0.47696	-AACATGTT---
TACATGTA	0.47362	-TACATGTA---
TGTATACA	0.45927	---TGTATACA-
CATGTACA	0.44673	---CATGTACA-
ACATGTAC	0.44579	--ACATGTAC--
ACATGTTA	0.44485	TAACATGT----
TTGTACAA	0.44090	----TTGTACAA
AAACATGT	0.43245	AAACATGT----
ACACGTGT	0.42474	--ACACGTGT--

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

Forward:		Reverse:
		
Top 10	Scores	Alignment
ATGTACAT	6.57901	---ATGTACAT
TACATGTA	5.84336	-TACATGTA---
AACATGTT	5.78880	-AACATGTT---
CATGTACA	4.69363	---CATGTACA-
ACATGTAC	4.38905	--ACATGTAC--
TGTATACA	4.34424	---TGTATACA-
TGTGCACA	4.28205	---TGTGCACA-
TTGTACAA	3.99069	----TTGTACAA
ACATGTTG	3.90922	CAACATGT----
ACATGTTA	3.90287	TAACATGT----