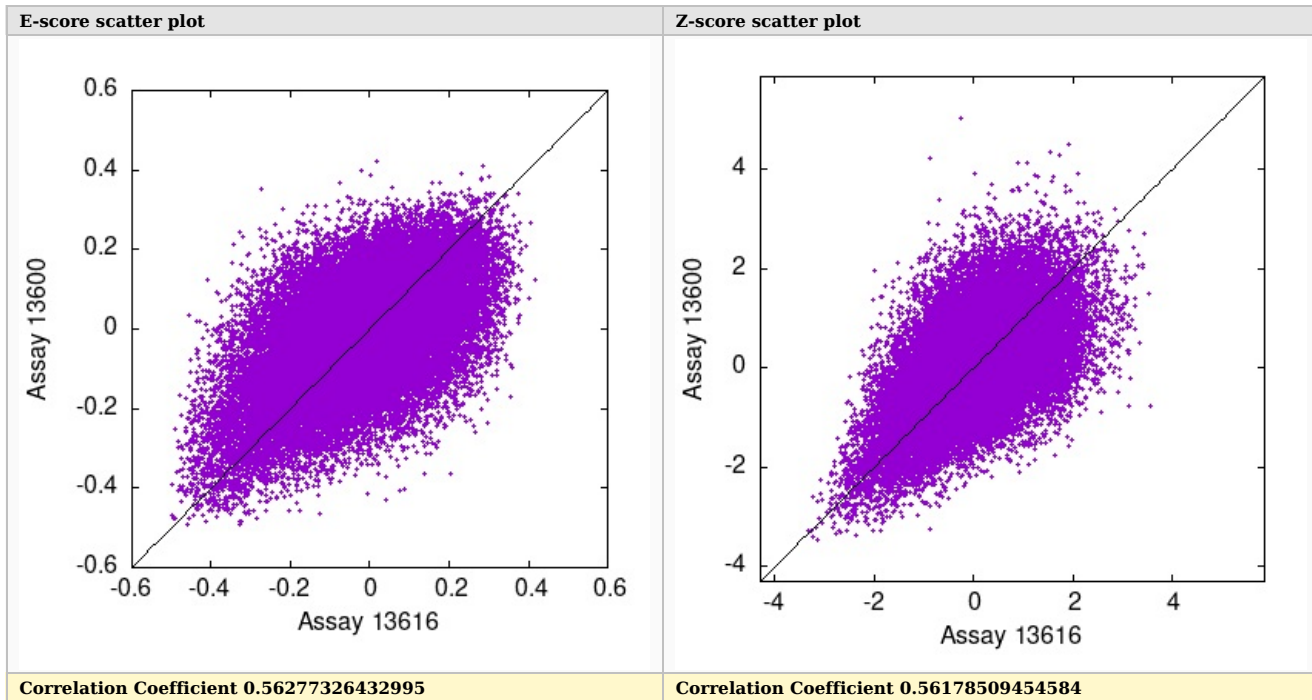


QC report



Top scoring motifs for Assay 13616

Protein ID: pTH14297.2 Gene: DACH1.DBD 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
GAATATTC	0.41638	----GAATATTC--	ATGTATAG	3.56079	ATGTATAG---
GTCATGAC	0.40486	---GTCATGAC---	CATATATG	3.52825	-CATATATG--
AAACGTTT	0.40232	----AAACGTTT--	ACATATAT	3.43676	ACATATAT---
ACTATTGA	0.39538	TCAATAGT-----	AAAATTTT	3.39963	AAAATTTT---
AAATCGAT	0.38402	----AAATCGAT--	AATGTACA	3.38852	-AATGTACA--
ATAAATTA	0.38305	----TAATTTAT--	AAACGTTT	3.33524	AAACGTTT---
ATAATGTA	0.38012	---ATAATGTA---	CGCGCGCG	3.32208	-CGCGCGCG--
AATGTACA	0.37894	----AATGTACA--	ATTATAAT	3.31819	-ATTATAAT--
ATTATTAG	0.37851	CTAATAAT-----	AAATCGAT	3.26072	AAATCGAT---
ACATATAT	0.37775	-----ATATATGT	ATAATGTA	3.25588	---TACATTAT

Top scoring motifs for Assay 13600

Protein ID: pTH14297.1 Gene: DACH1.DBD 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
TATATATA	0.42159	--TATATATA---	AGACGTCT	5.00740	---AGACGTCT--
ATTGTACA	0.41080	----ATTGTACA---	CAATTGCG	4.50598	CGCAATTG-----
ATATATAT	0.39781	---ATATATAT---	CAATTGTA	4.33494	--CAATTGTA---
CAATTGTA	0.39222	--CAATTGTA---	AATTAATT	4.26956	---AATTAATT--
GAATTCGA	0.38696	--GAATTCGA---	GACGCGTC	4.22760	---GACGCGTC---
AATTAATT	0.38270	---AATTAATT---	TTGTACAA	4.11827	-----TTGTACAA
ATTTGTAC	0.38000	---ATTTGTAC---	ATACACAT	4.11163	---ATGTGTAT---
CAATTGCG	0.37531	CGCAATTG-----	CAACGTTG	3.91662	--CAACGTTG---
TTGTACAA	0.36931	-----TTGTACAA	GAATTCGA	3.90439	--GAATTCGA---
AGACGTCT	0.36811	---AGACGTCT---	ATGACAAC	3.87007	----GTTGTCAT-