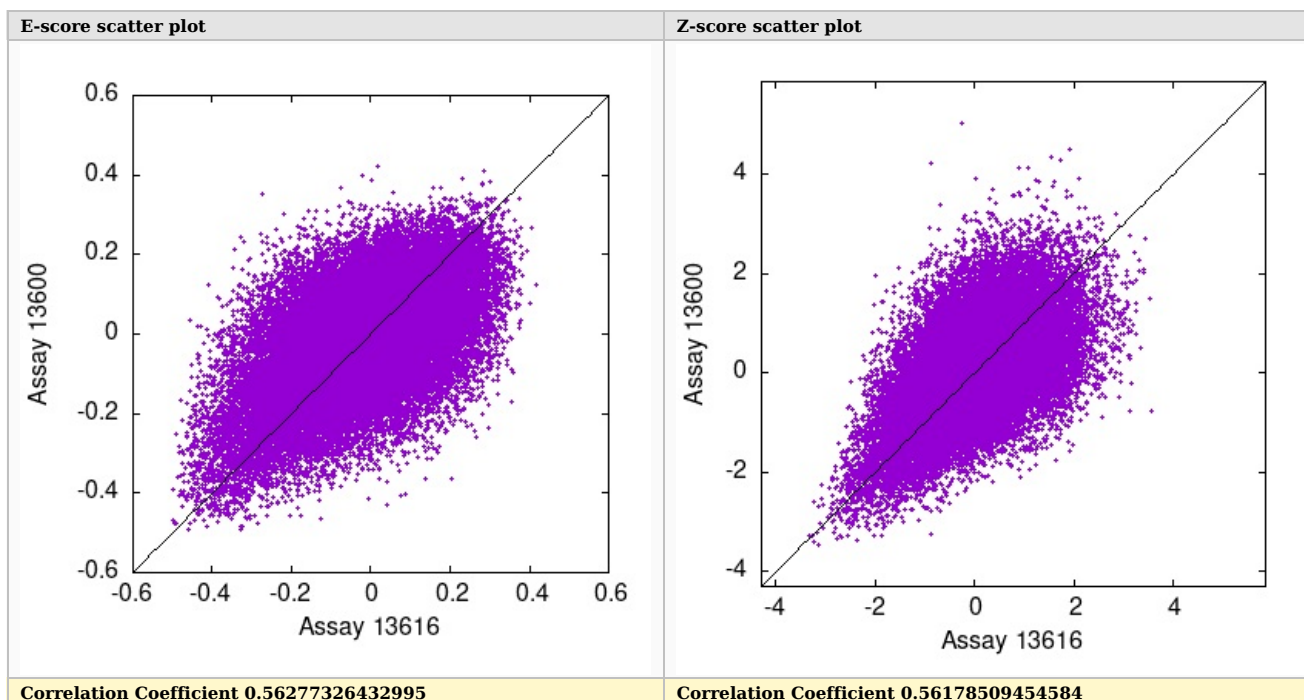


QC report



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'

Forward:		Reverse:	
Top 10	Scores	Alignment	
GAATATTC	0.41638	----GAATATTC--	
GTCATGAC	0.40486	---GTCATGAC---	
AAACGTTT	0.40232	----AAACGTTT--	
ACTATTGA	0.39538	TCAATAGT-----	
AAATCGAT	0.38402	----AAATCGAT--	
ATAAATTA	0.38305	----TAATTTAT--	
ATAATGTA	0.38012	---ATAATGTA---	
AATGTACA	0.37894	----AATGTACA--	
ATTATTAG	0.37851	CTAATAAT-----	
ACATATAT	0.37775	-----ATATATGT	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
ATGTATAG	3.56079	ATGTATAG---	
CATATATG	3.52825	-CATATATG--	
ACATATAT	3.43676	ACATATAT---	
AAAATTTT	3.39963	AAAATTTT---	
AATGTACA	3.38852	-AATGTACA--	
AAACGTTT	3.33524	AAACGTTT---	
CGCGCGCG	3.32208	-CGCGCGCG--	
ATTATAAT	3.31819	-ATTATAAT--	
AAATCGAT	3.26072	AAATCGAT---	
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'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TATATATA	0.42159	--TATATATA---	
ATTGTACA	0.41080	----ATTGTACA---	
ATATATAT	0.39781	---ATATATAT---	
CAATTGTA	0.39222	--CAATTGTA---	
GAATTCGA	0.38696	--GAATTCGA---	
AATTAATT	0.38270	---AATTAATT---	
ATTTGTAC	0.38000	---ATTTGTAC---	
CAATTGCG	0.37531	CGCAATTG-----	
TTGTACAA	0.36931	-----TTGTACAA	
AGACGTCT	0.36811	---AGACGTCT---	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
AGACGTCT	5.00740	---AGACGTCT---	
CAATTGCG	4.50598	CGCAATTG-----	
CAATTGTA	4.33494	--CAATTGTA---	
AATTAATT	4.26956	---AATTAATT---	
GACGCGTC	4.22760	---GACGCGTC---	
TTGTACAA	4.11827	-----TTGTACAA	
ATACACAT	4.11163	---ATGTGTAT---	
CAACGTTG	3.91662	--CAACGTTG---	
GAATTCGA	3.90439	--GAATTCGA---	
ATGACAAC	3.87007	----GTTGTCAT-	