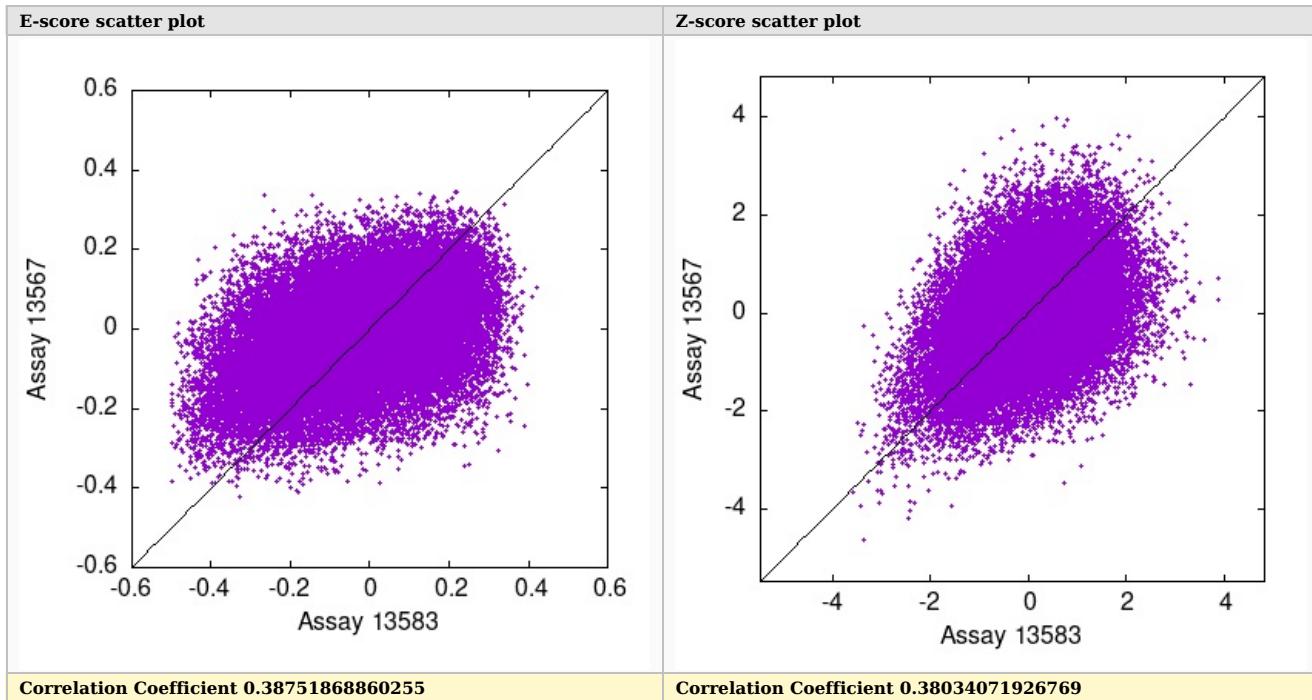


QC report



Top scoring motifs for Assay 13583

Protein ID: pTH13959.2 Gene: CPXCR1.DBD Domain: zf-C2H2 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
GATATGTA	0.42279	-GATATGTA--	AAACGTTT	3.87215	AAACGTTT---
AAACGTTT	0.40815	AAACGTTT---	GATATGTA	3.86657	-GATATGTA--
GATTAATA	0.39870	---TATTAATC	AATATATT	3.59491	-AATATATT--
GAATATTC	0.38963	GAATATTC---	AATATTAA	3.50563	-AATATTAA--
ATTAGGCA	0.38954	-ATTAGGCA--	AATTAGGC	3.37773	--AATTAGGC
AATATTAA	0.38849	-AATATTAA--	TATATGAA	3.37118	-TATATGAA--
TATATGAA	0.38643	-TATATGAA--	ACTAATTA	3.36477	-ACTAATTA--
ATACAAAT	0.38451	--ATACAAAT-	AAATTACG	3.34311	--AAATTACG-
AAATTACG	0.38355	--AAATTACG-	GAATATTC	3.32444	GAATATTC---
AATTAGGC	0.38347	---AATTAGGC	GCATATAA	3.30468	GCATATAA---

Top scoring motifs for Assay 13567

Protein ID: pTH13959.1 Gene: CPXCR1.DBD Domain: zf-C2H2 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
ATTATCTG	0.34453	---ATTATCTG--	TAAGTACA	3.96170	----TGTACTTA
ATACCAAT	0.34261	----ATACCAAT-	AATGAATC	3.94592	--AATGAATC--
GAGTGATA	0.34077	-----TATCACTC	ATCGAGAA	3.81762	-TTCTCGAT---
CTAAGCAC	0.33800	---CTAAGCAC--	ACCACTAT	3.81689	ATAGTGGT----
CAGACCAC	0.33692	---CAGACCAC--	CATCATCG	3.71597	-CGATGATG---
ACTATCAC	0.33315	---ACTATCAC--	ACACGAAT	3.62512	-ACACGAAT---
AGTGATAG	0.33227	----CTATCACT-	GTTAATCA	3.59316	--GTTAATCA-
TTGACAAA	0.33038	---TTTGTCAA--	ACTCAGCA	3.55684	-TGCTGAGT---
ATTCGTTA	0.32922	-----TAACGAAT	ATAGTGTC	3.45141	--ATAGTGTC--
ATAGTCTG	0.32874	CAGACTAT-----	CCAATCAG	3.44765	----CCAATCAG