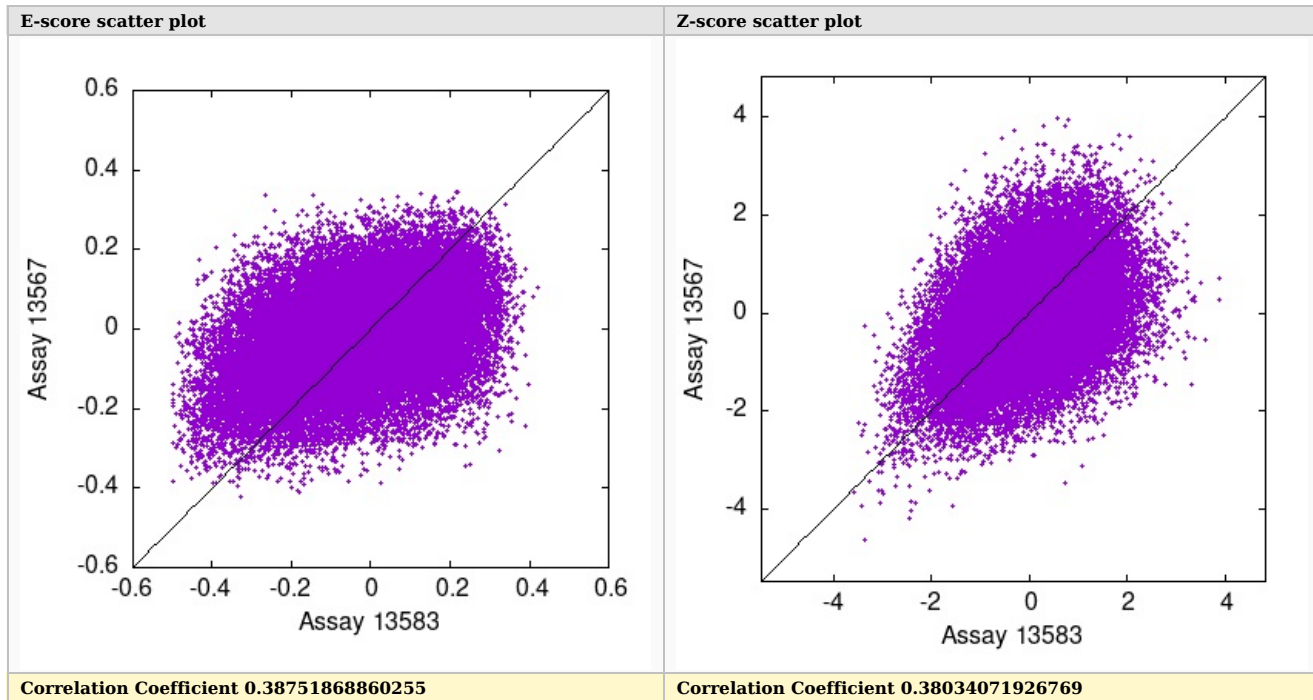


QC report



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'

Forward:

Reverse:



Top 10

Scores

Alignment

GATATGTA	0.42279	-GATATGTA--
AAACGTTT	0.40815	AAACGTTT---
GATTAATA	0.39870	---TATTAATC
GAATATTC	0.38963	GAATATTC---
ATTAGGCA	0.38954	-ATTAGGCA--
AATATTAA	0.38849	-AATATTAA--
TATATGAA	0.38643	-TATATGAA--
ATACAAAT	0.38451	--ATACAAAT-
AAATTACG	0.38355	--AAATTACG-
AATTAGGC	0.38347	---AATTAGGC

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AAACGTTT	3.87215	AAACGTTT---
GATATGTA	3.86657	-GATATGTA--
AATATATT	3.59491	-AATATATT--
AATATTAA	3.50563	-AATATTAA--
AATTAGGC	3.37773	--AATTAGGC
TATATGAA	3.37118	-TATATGAA--
ACTAATTA	3.36477	-ACTAATTA--
AAATTACG	3.34311	--AAATTACG-
GAATATTC	3.32444	GAATATTC---
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'

Forward:

Reverse:



Top 10

Scores

Alignment

ATTATCTG	0.34453	---ATTATCTG--
ATACCAAT	0.34261	----ATACCAAT-
GAGTGATA	0.34077	-----TATCACTC
CTAAGCAC	0.33800	---CTAAGCAC--
CAGACCAC	0.33692	---CAGACCAC--
ACTATCAC	0.33315	---ACTATCAC--
AGTGATAG	0.33227	----CTATCACT-
TTGACAAA	0.33038	----TTTGTCAA--
ATTCGTTA	0.32922	-----TAACGAAT
ATAGTCTG	0.32874	CAGACTAT-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAAGTACA	3.96170	----TGTACTTA
AATGAATC	3.94592	--AATGAATC--
ATCGAGAA	3.81762	-TTCTCGAT---
ACCACTAT	3.81689	ATAGTGGT----
CATCATCG	3.71597	-CGATGATG---
ACACGAAT	3.62512	-ACACGAAT---
GTTAATCA	3.59316	---GTTAATCA-
ACTCAGCA	3.55684	-TGCTGAGT---
ATAGTGTC	3.45141	--ATAGTGTC--
CCAATCAG	3.44765	----CCAATCAG