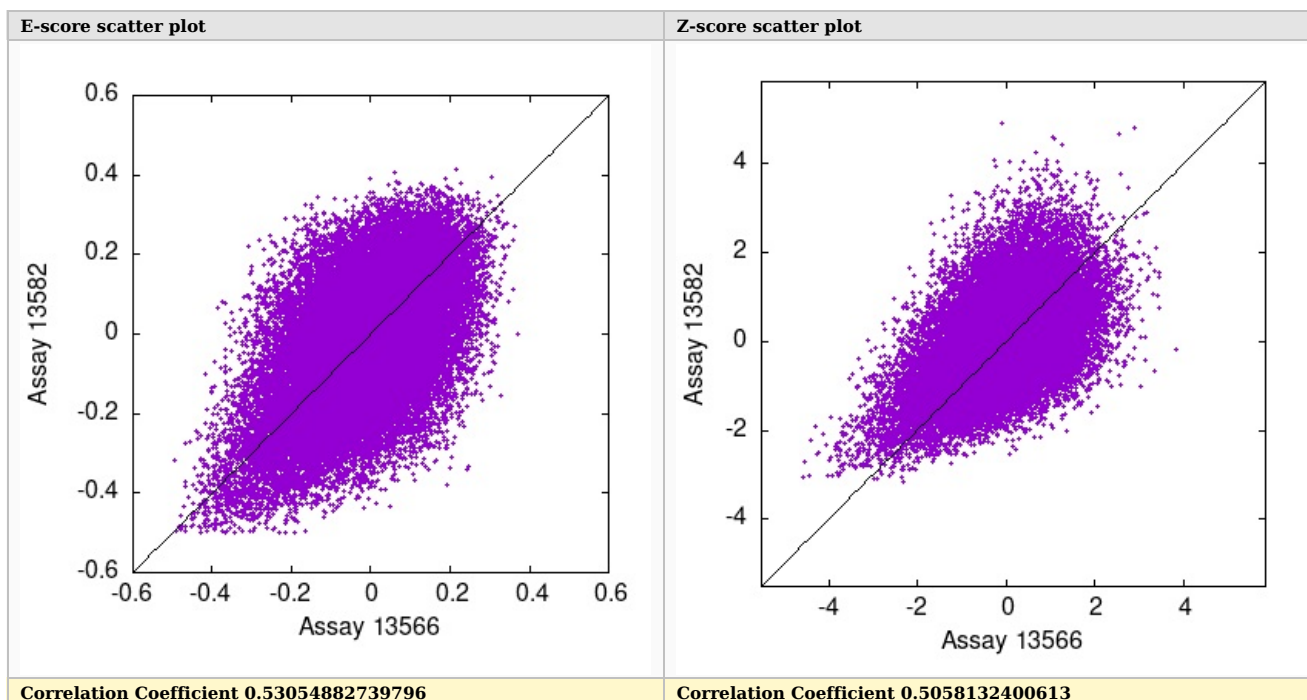


QC report



Top scoring motifs for Assay 13566

Protein ID: pTH13958.1 Gene: CPXCR1.FL Domain: zf-C2H2 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

AAAGTACA
AATTGTAG
TAAATTTA
ATGTATAA
ACATAACA
CACAAACAC
ATATGTAC
ACAACAAT
GAAATTA
AAATTGTT

CTTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT

Top 10

Scores

Alignment

AAAGTACA	0.37266	----TGTACTTT
AATTGTAG	0.36208	--AATTGTAG---
TAAATTTA	0.36029	TAAATTTA----
ATGTATAA	0.35846	---TTATACAT-
ACATAACA	0.34862	ACATAACA----
CACAAACAC	0.34736	---GTGTTGTG-
ATATGTAC	0.34197	-ATATGTAC---
ACAACAAT	0.34161	--ATTGTTGT--
GAAATTA	0.33539	TAATTTTC----
AAATTGTT	0.33519	AAATTGTT----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

?

?

Top 10

Scores

Alignment

AAAGTACA	3.84298	-AAAGTACA---
ACATATGT	3.46129	--ACATATGT--
TTGTACAA	3.44246	----TTGTACAA
ATATGTAC	3.42805	--ATATGTAC--
CACAAACAC	3.40954	---GTGTTGTG-
ACAATTGT	3.36387	CAAAATGT----
AATTATTG	3.32512	--AATTATTG--
AAAATTAT	3.32506	AAAATTAT----
AATTATAT	3.31347	--AATTATAT--
TAGTACAA	3.24295	----TTGTACTA

Top scoring motifs for Assay 13582

Protein ID: pTH13958.2 Gene: CPXCR1.FL Domain: zf-C2H2 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

AAAGTACA
AATTGTAG
TAAATTTA
ATGTATAA
ACATAACA
CACAAACAC
ATATGTAC
ACAACAAT
GAAATTA
AAATTGTT

CTTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT

Top 10

Scores

Alignment

TAACAAAA	0.41261	---TAACAAAA--
GTCATGAC	0.40688	--GTCATGAC---
AAATTGTA	0.39408	AAATTGTA-----
GATTAATA	0.38941	----TATTAATC-
ACTATAAT	0.38928	--ACTATAAT---
TTATAAAA	0.38470	---TTATAAAAA--
TTTCGAAA	0.38078	---TTTCGAAA--
CTCATATA	0.37920	--CTCATATA---
ATAAGATA	0.37822	-----ATAAGATA
AACAACCT	0.37757	AAGTTGTT-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

AAAGTACA
AATTGTAG
TAAATTTA
ATGTATAA
ACATAACA
CACAAACAC
ATATGTAC
ACAACAAT
GAAATTA
AAATTGTT

CTTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT
TCTCTAGT

Top 10

Scores

Alignment

GTCATGAC	4.89383	----GTCATGAC---
TTTCGAAA	4.80540	TTTCGAAA-----
AAATTGTA	4.65596	-----AAATTGTA--
ACATTTAG	4.59802	----ACATTTAG---
ACTATAAT	4.55199	-----ATTATAGT
ATAAGATA	4.42196	-----ATAAGATA---
AGTAATTA	4.25423	---AGTAATTA----
TGTAGCAA	4.08372	---TGTAGCAA----
AGTGATAT	4.06441	---AGTGATAT----
AATTTAAA	4.05075	-----AATTTAAA--