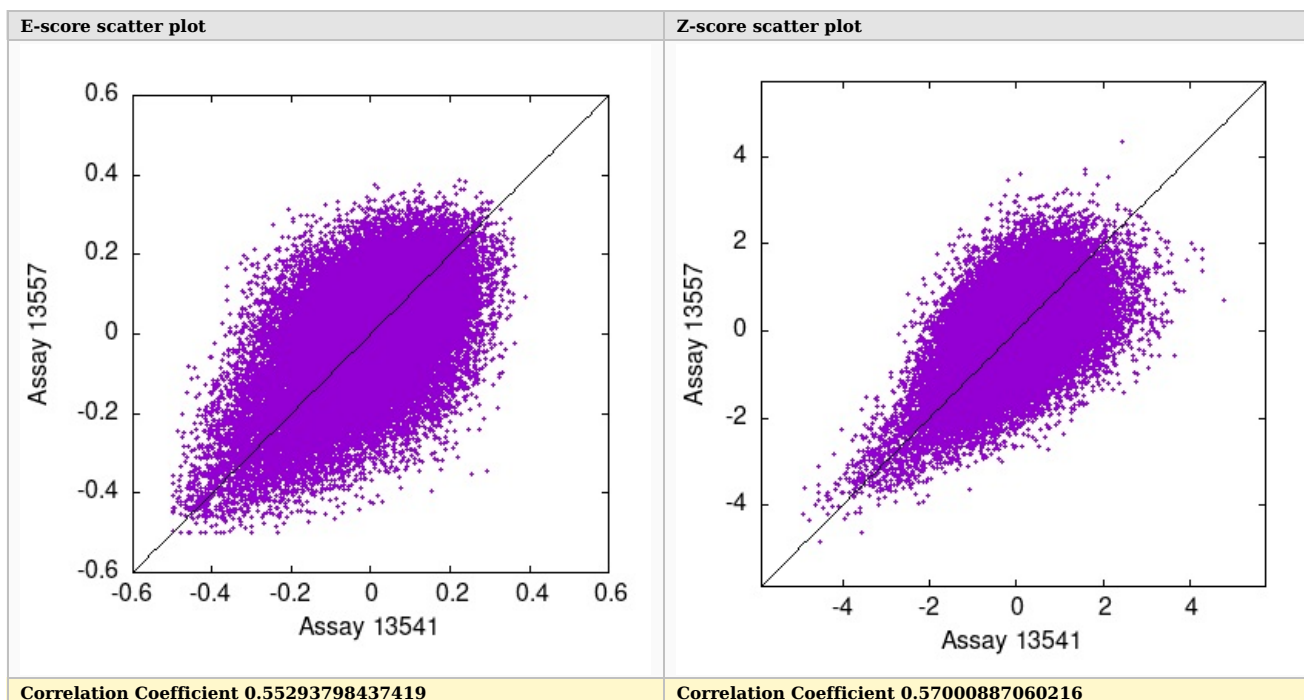


QC report



Top scoring motifs for Assay 13541

Protein ID: pTH14288.1 Gene: CENPT.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

AACATGAATT
TTGAACTT

TTTCTCAATGTT

Top 10

Scores

Alignment

TGTGCACA	0.39149	---TGTGCACA--
AAAGTACA	0.36464	----TGTACTTT
ACGTAACA	0.36305	--ACGTAACA---
ATATTGTA	0.36116	----ATATTGTA--
AACAAAGC	0.36001	-AACAAAGC----
ATGTACAT	0.35918	----ATGTACAT-
ATATATGA	0.35887	--TCATATAT---
ACAACAAT	0.35445	--ACAACAAT---
ATTCGTTA	0.35364	TAACGAAT----
ACATATAC	0.35255	--ACATATAC---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

ATTTGTGTA
TGTGCACA
ATGTACAT
ATTTATAA
ATTTGTAC
AACAAAGC
AACATGTT
ATGTTAAT

Top 10

Scores

Alignment

ATATTGTA	4.75439	ATATTGTA---
ATTCGTTA	4.27385	--ATTCGTTA--
ACAACAAT	4.27157	-ATTGTTGT--
TGTGCACA	4.26695	--TGTGCACA--
ATGTACAT	4.09826	---ATGTACAT
ATTTATAA	4.00548	-ATTTATAA--
ATTTGTAC	3.91244	-ATTTGTAC--
AACAAAGC	3.84111	GCTTTGTT---
AACATGTT	3.72651	AACATGTT---
ATGTTAAT	3.67272	-ATGTTAAT--

Top scoring motifs for Assay 13557

Protein ID: pTH14288.2 Gene: CENPT.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

?

?

Top 10

Scores

Alignment

AAGTACTT	0.38890	AAGTACTT-----
TACGCGTA	0.38234	---TACGCGTA---
GAAATTTT	0.37691	--GAAATTTT---
TCGCGCGA	0.37565	---TCGCGCGA---
TTGCGCAA	0.37157	-----TTGCGCAA
CGTCGGAA	0.36867	----CGTCGGAA--
TAGTTGCA	0.36505	---TAGTTGCA---
ATAATGTA	0.36428	---ATAATGTA---
GTACAGTA	0.35961	-----GTACAGTA
GTATACTA	0.35768	---TAGTATAC---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

?

?

Top 10

Scores

Alignment

TACGCGTA	4.35058	-----TACGCGTA
TTGCGCAA	3.69983	---TTGCGCAA---
ATAATGTA	3.60263	ATAATGTA-----
CACAGTAG	3.58399	CTACTGTG-----
ATATGTGC	3.53777	-----GCACATAT-
TCGCGCGA	3.45373	---TCGCGCGA---
ATTGTACA	3.35293	--ATTGTACA----
TATTTGCA	3.25446	-----TGCAAATA--
GTATTGTA	3.17908	GTATTGTA-----
GAATATTC	3.15232	-GAATATTC-----