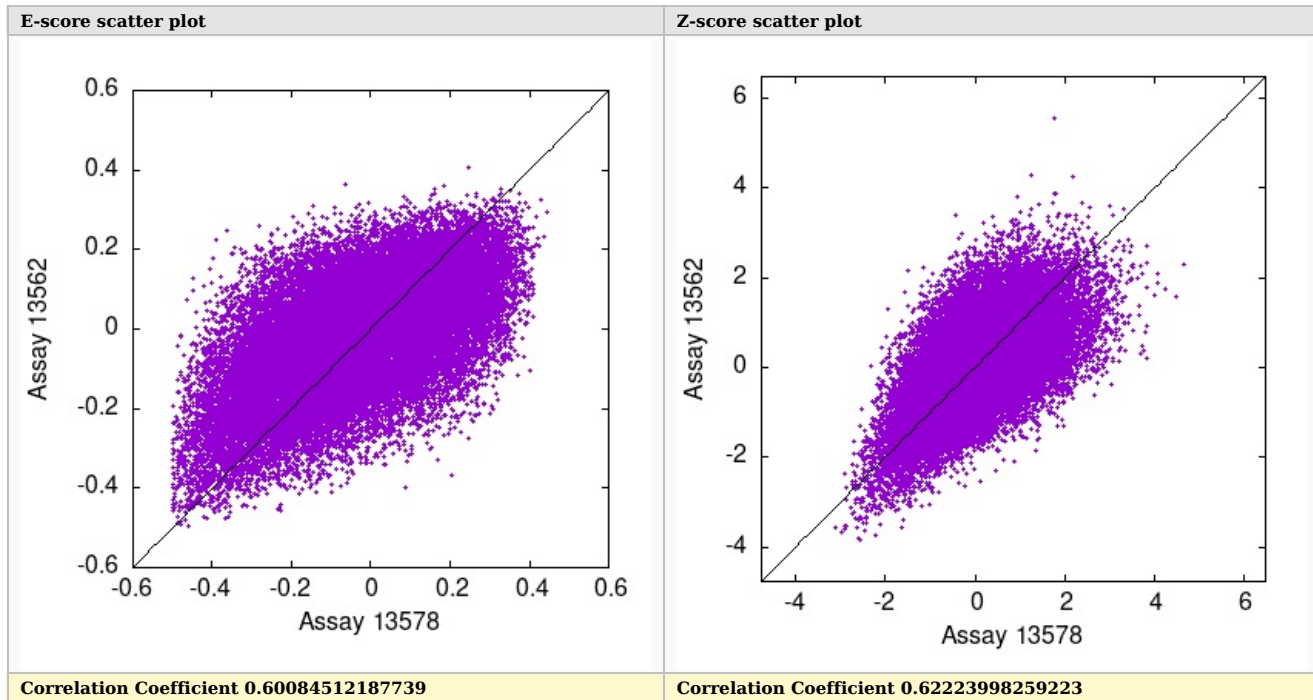


QC report



Top scoring motifs for Assay 13578

Protein ID: pTH13917.2 Gene: DNTTIP1.DBD Domain: AT_hook Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATATTAAT	0.44349	---ATATTAAT-
ATAGTAAT	0.43812	---ATAGTAAT-
AATATTAA	0.43018	--AATATTAA--
TATATGAA	0.42628	--TATATGAA--
CTGTATTA	0.42310	-CTGTATTA---
TATTAACA	0.41815	----TATTAACA
TATTAATA	0.41593	----TATTAATA
CATATAAC	0.41383	--CATATAAC--
AATAATAA	0.41112	--AATAATAA--
AATATAGA	0.41064	TCTATATT----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATATTAAT	4.66670	----ATATTAAT-
CATATAAC	4.48736	----CATATAAC--
GCATATAA	4.23368	---GCATATAA---
TATTAATA	4.08793	-----TATTAATA
TATTTGCA	4.06263	TGCAATA-----
CATATATG	4.00870	----CATATATG--
AATTTAAA	3.84191	----AATTTAAA--
AATATTAA	3.83866	----AATATTAA--
AATAATAA	3.83644	----AATAATAA--
ATATAAAC	3.82957	----ATATAAAC--

Top scoring motifs for Assay 13562

Protein ID: pTH13917.1 Gene: DNTTIP1.DBD Domain: AT_hook Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATGGTTTA	0.40562	----TAAACCAT
ATGAACTG	0.36517	---ATGAACTG-
ACATATAC	0.36044	---ACATATAC-
GATGAGTA	0.35390	--GATGAGTA--
GATATTAA	0.35129	GATATTAA----
AATAATAG	0.34954	---AATAATAG-
CGTAATAA	0.34836	----TTATTACG
AAATATAT	0.34221	---AAATATAT-
TATAAATA	0.34149	--TATAAATA--
ACGAAATG	0.34056	--ACGAAATG--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATGGTTTA	5.54310	-TAAACCAT----
ACATATAC	4.28014	ACATATAC-----
CGTAATAA	4.24388	--CGTAATAA--
ATACAATA	3.87864	--ATACAATA--
ATAATGCA	3.87218	---TGCATTAT--
ATACTCTA	3.80799	---ATACTCTA--
ACTGATTG	3.67477	-----CAATCAGT
ATTAATCG	3.65778	----CGATTAAAT-
AATCAGTA	3.63829	---AATCAGTA---
AATATATG	3.61372	-CATATATT-----