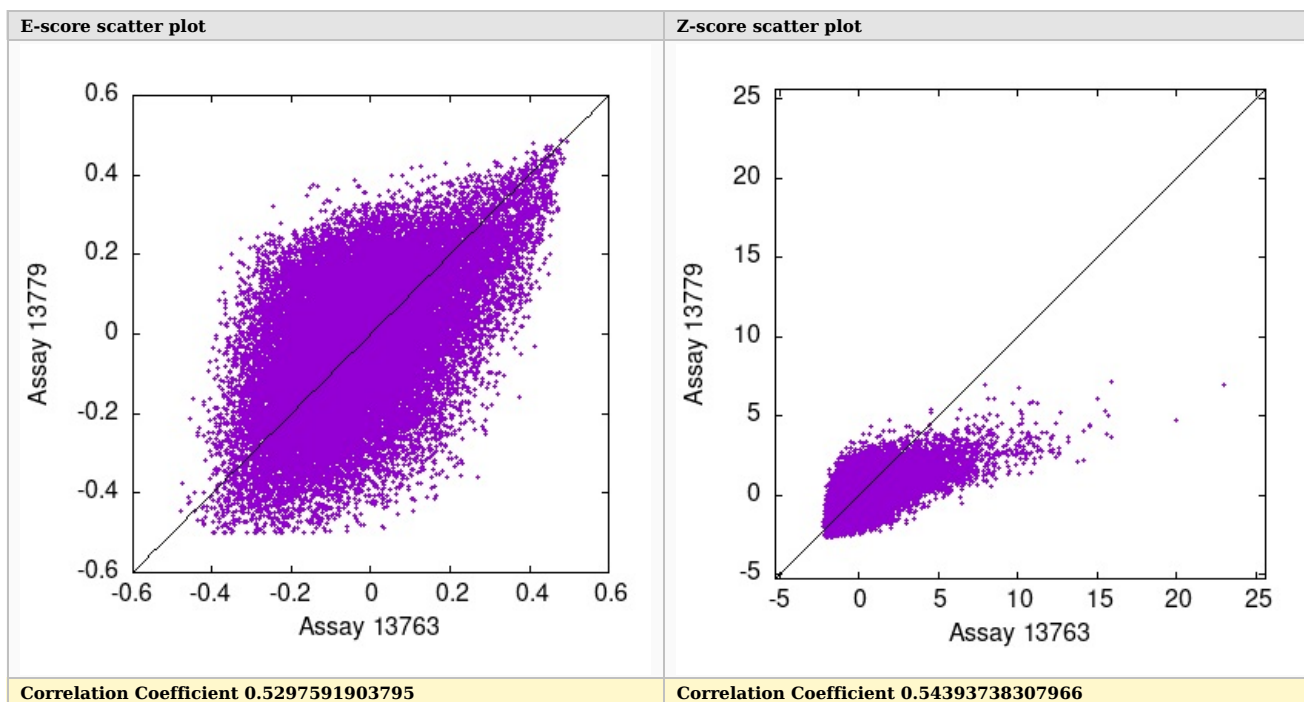


QC report



Top scoring motifs for Assay 13763

Protein ID: pTH14340.1 Gene: SP140L.DBD Domain: SAND Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TTACGTAA	0.49523	--TTACGTAA--
TGACGTAA	0.48807	--TGACGTAA--
ATTACGTA	0.48166	ATTACGTA--
GTTACGTA	0.48134	GTTACGTA--
TACGTCAA	0.48112	TTGACGTA--
TCACGTGA	0.47949	--TCACGTGA--
ACGTACGT	0.47421	---ACGTACGT
TGACGTCA	0.47337	--TGACGTCA--
TCACGTCA	0.47111	--TGACGTGA--
AATTACGT	0.47033	---ACGTAATT

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TTACGTAA	23.02625	--TTACGTAA--
TGACGTAA	19.92335	--TGACGTAA--
TCGTACGA	15.89911	---TCGTACGA
TCACGTGA	15.86988	-TCACGTGA--
TACGTCAA	15.65489	--TACGTCAA--
ATTACGTA	15.55499	ATTACGTA--
TGACGTCA	15.51546	-TGACGTCA--
ACGTACGT	15.02235	---ACGTACGT
ATACGTAA	14.51790	-ATACGTAA--
GATACGTA	14.51790	GATACGTA--

Top scoring motifs for Assay 13779

Protein ID: pTH14340.2 Gene: SP140L.DBD Domain: SAND Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TCACGTGA	0.48812	--TCACGTGA--
TTACGTAA	0.48426	--TTACGTAA--
TCGCGCGA	0.48167	TCGCGCGA--
ACGTACGA	0.47397	TCGTACGT--
CGTATACG	0.47213	--CGTATACG--
ATACGTAT	0.46564	---ATACGTAT--
TACGCGTA	0.46351	--TACGCGTA--
ACGTACGT	0.46340	ACGTACGT--
CGTACGTA	0.46263	--CGTACGTA--
TACGTAAA	0.46106	---TACGTAAA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TCACGTGA	7.18172	--TCACGTGA
TTACGTAA	6.98855	--TTACGTAA
TCGCGCGA	6.93633	TCGCGCGA--
CGTATACG	6.81344	-CGTATACG-
ACGTACGT	6.09151	ACGTACGT--
GTACGTAC	6.09151	--GTACGTAC
CGTACGTA	6.04972	-CGTACGTA-
TACGCGTA	5.92778	-TACGCGTA-
ACGTACGA	5.81248	TCGTACGT--
ATACGTAT	5.77620	--ATACGTAT