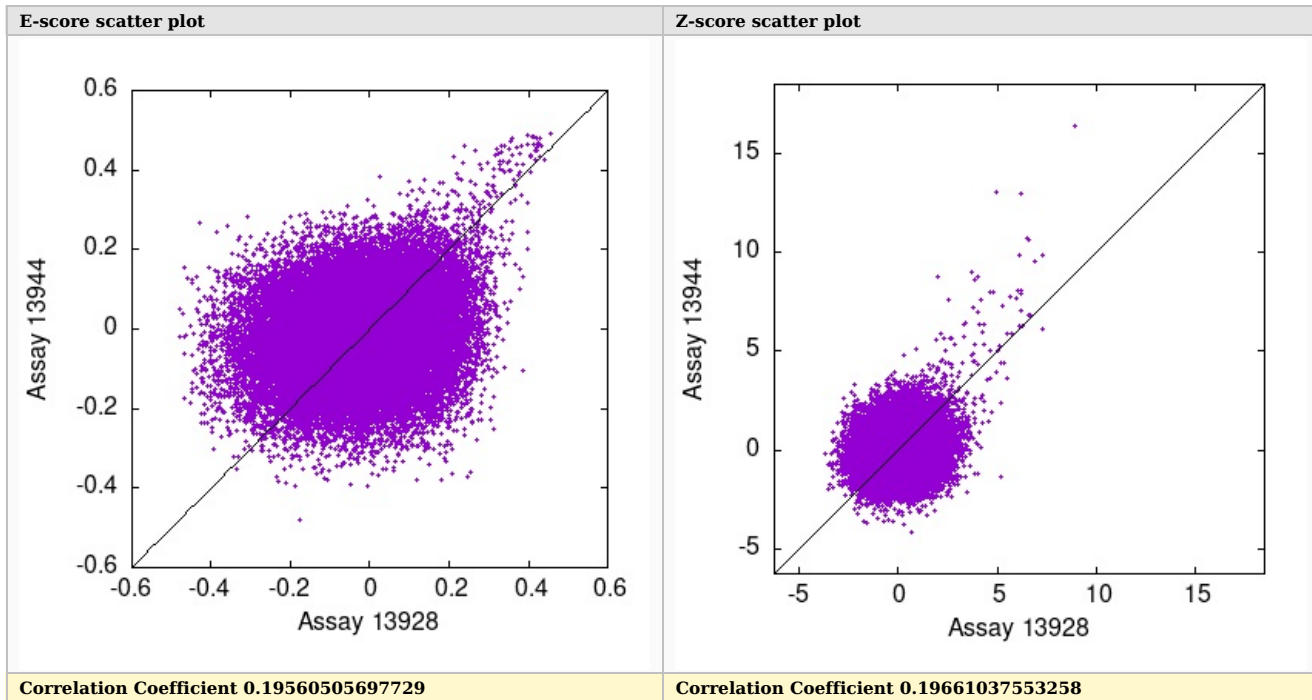


QC report



Top scoring motifs for Assay 13928

Protein ID: pTH14247.1 Gene: TPRX1.FL Domain: Homeobox Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

GGATTA

TAATCC

Top 10

Scores

Alignment

GATAATCC	0.45496	--GGATTATC
GGATTAAA	0.43951	--GGATTAAA
GCGATTAA	0.43397	-GGATTAA-
AAGGATTA	0.43095	AAGGATTA--
CGGATTAG	0.42938	-CGGATTAG-
ATAATCCA	0.42600	-TGGATTAT-
GCGGATTA	0.42450	GCGGATTA--
ACGGATTA	0.42291	ACGGATTA--
ATTAATCC	0.42155	--GGATTAAT
TAATCCGA	0.42043	TCGGATTA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

A GGATTA

TAATCC T

Top 10

Scores

Alignment

GATAATCC	8.96576	--GGATTATC
AAGGATTA	7.31758	AAGGATTA--
CGGATTAG	7.26945	-CGGATTAG-
ACGGATTA	6.91598	ACGGATTA--
ATAATCCA	6.65601	-TGGATTAT-
AGGGATTA	6.63253	AGGGATTA--
GGATTAAA	6.59555	--GGATTAAA
CATAATCC	6.50361	--GGATTATG
ACTAATCC	6.29683	--GGATTAGT
ATTAATCC	6.22036	--GGATTAAT

Top scoring motifs for Assay 13944

Protein ID: pTH14247.2 Gene: TPRX1.FL Domain: Homeobox Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

GATAATCC

GGATTA

Top 10

Scores

Alignment

GATAATCC	0.49086	-GATAATCC--
ATAATCCG	0.48718	--ATAATCCG-
AGGATTAT	0.48450	--ATAATCCT-
AGGGATTA	0.48331	---TAATCCCT
CATAATCC	0.48261	-CATAATCC--
AAGGATTA	0.48071	---TAATCCTT
GGATTAAC	0.47964	-GTTAATCC--
ACGGATTA	0.47889	---TAATCCGT
GATTATCC	0.47205	GGATAATC---
GCGGATTA	0.46749	---TAATCCGC

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

TAATCC

GGATTA

Top 10

Scores

Alignment

GATAATCC	16.46240	GATAATCC--
AGGATTAT	13.05041	-ATAATCCT-
ATAATCCG	12.98116	-ATAATCCG-
CATAATCC	10.75603	CATAATCC--
AGGGATTA	10.63371	--TAATCCCT
GCGGATTA	9.89660	--TAATCCGC
AAGGATTA	9.84274	--TAATCCTT
ACGGATTA	9.55166	--TAATCCGT
TGGATTAA	8.99445	-TTAATCCA-
GGATTAAC	8.80553	GTTAATCC--