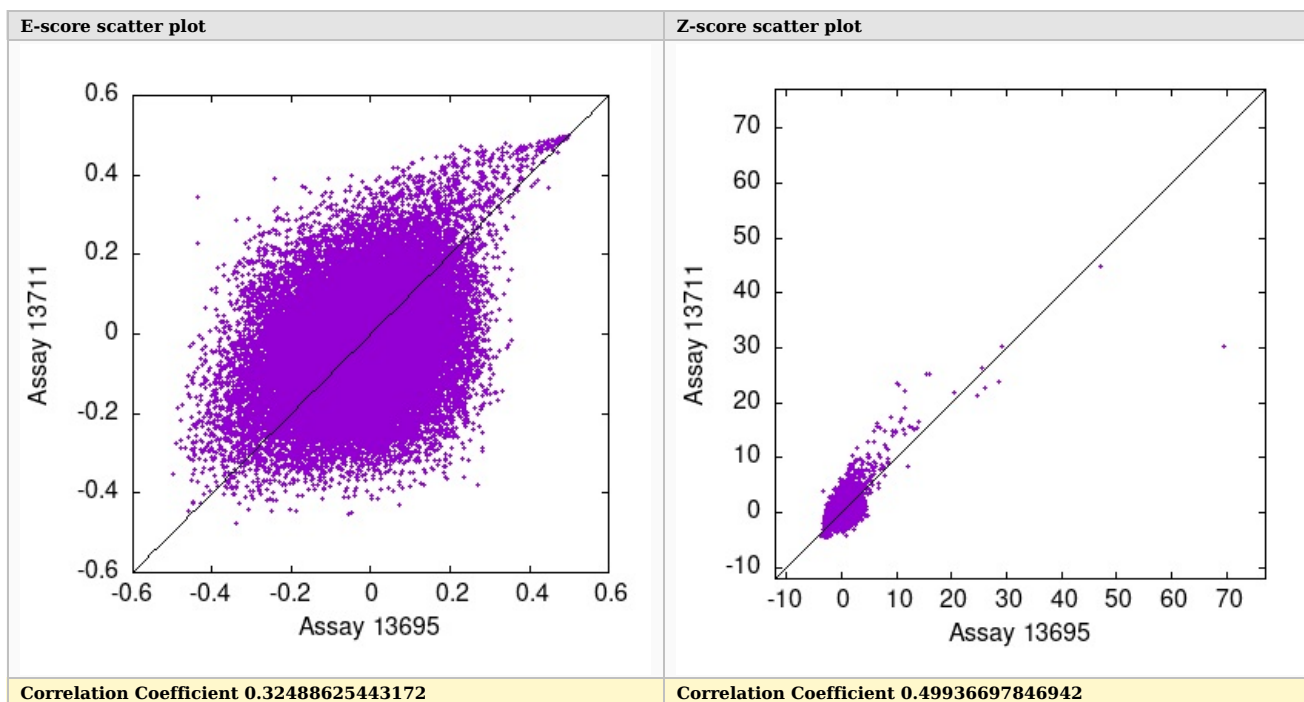


QC report



Top scoring motifs for Assay 13695

Protein ID: pTH13932.1 Gene: ZBED5.DBD Domain: zf-BED Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

CGG ACCcc

GgGGT CCG

Top 10

Scores

Alignment

GGAACCCC	0.49947	--GGAACCCC
CGGAACCC	0.49911	-CGGAACCC-
CGGCACCC	0.49699	-CGGCACCC-
CGGTACCC	0.49684	-CGGTACCC-
ACGGAACC	0.49599	ACGGAACC--
ACGGTACC	0.49561	ACGGTACC--
CGGTACCG	0.49449	-CGGTACCG-
GCGGTACC	0.49416	GCGGTACC--
GGGTACCC	0.49365	--GGTACCCC
GGCACCCC	0.49250	--GGCACCCC

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

CGG ACCcc

GgGGT CCG

Top 10

Scores

Alignment

GGAACCCC	69.62791	--GGAACCCC
CGGAACCC	47.06392	-CGGAACCC-
CGGTACCC	29.27901	-CGGTACCC-
ACGGTACC	28.52945	ACGGTACC--
ACGGAACC	26.15297	ACGGAACC--
CGGCACCC	25.58247	-CGGCACCC-
CGGTACCG	24.53248	-CGGTACCG-
GCGGTACC	20.46962	GCGGTACC--
GGCACCCC	15.89873	--GGCACCCC
GGGTACCC	15.35089	--GGGTACCC

Top scoring motifs for Assay 13711

Protein ID: pTH13932.2 Gene: ZBED5.DBD Domain: zf-BED Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

cGG ACCC C

G GGGT CC G

Top 10

Scores

Alignment

CGGAACCC	0.49935	-CGGAACCC-
GGAACCCC	0.49806	--GGAACCCC
GGGTACCC	0.49669	--GGGTACCC
CGGTACCC	0.49669	-CGGTACCC-
CGGCACCC	0.49626	-CGGCACCC-
AGGTTTCC	0.49618	--GGAACCCCT
ACGGAACC	0.49506	ACGGAACC--
GGGTACCC	0.49488	-GGGTACCC-
CGGGAACC	0.49464	GCGGAACC--
GGCACCCC	0.49452	--GGCACCCC

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

AcGG ACCC C

G GGGT CC GT

Top 10

Scores

Alignment

CGGAACCC	44.82538	-CGGAACCC-
GGAACCCC	30.35148	--GGAACCCC
CGGTACCC	30.26730	-CGGTACCC-
CGGCACCC	26.38172	-CGGCACCC-
GGCACCCC	25.14410	--GGCACCCC
GGGTACCC	25.14129	--GGGTACCC
ACGGTACC	23.75553	ACGGTACC--
GGGTACCC	23.63564	-GGGTACCC-
AGGTTTCC	23.22545	--GGAACCCCT
ACGGAACC	22.81193	ACGGAACC--