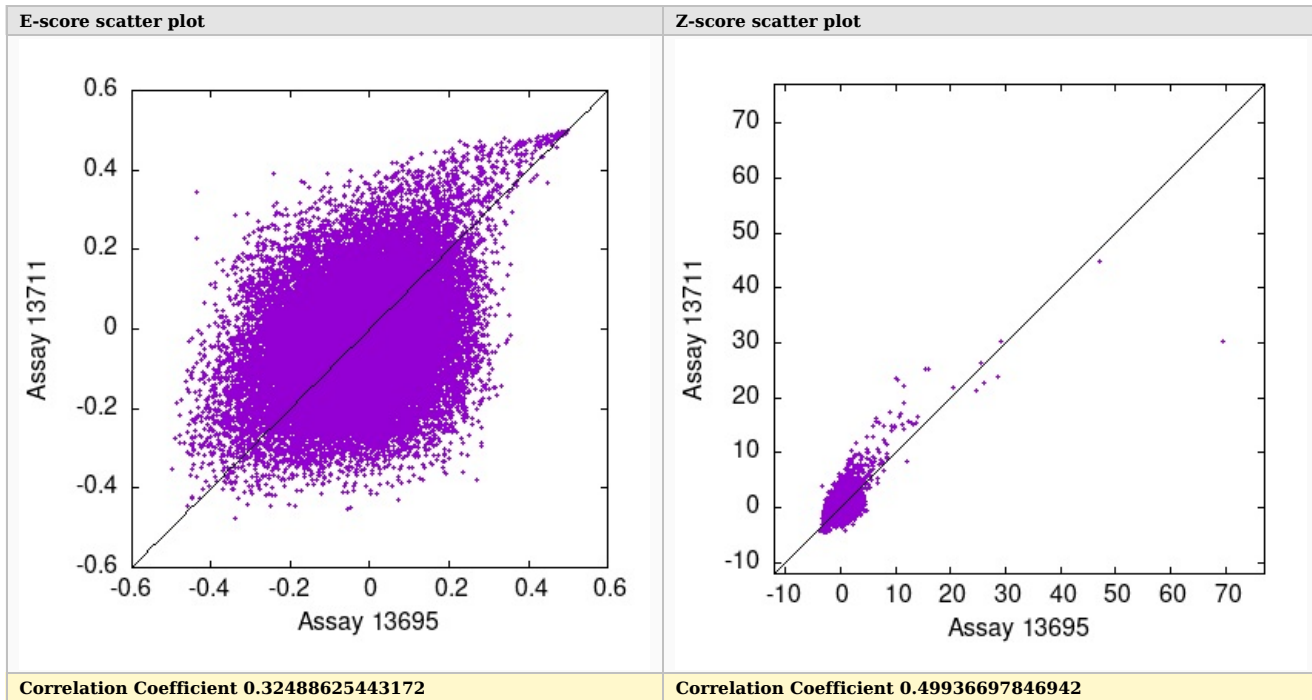


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:	Reverse:		Forward:	Reverse:	
Top 10	Scores	Alignment	Top 10	Scores	Alignment
GGAACCCC	0.49947	--GGAACCCC	GGAACCCC	69.62791	--GGAACCCC
CGGAACCC	0.49911	-CGGAACCC-	CGGAACCC	47.06392	-CGGAACCC-
CGGCACCC	0.49699	-CGGCACCC-	CGGTACCC	29.27901	-CGGTACCC-
CGGTACCC	0.49684	-CGGTACCC-	ACGGTACC	28.52945	ACGGTACC--
ACGGAACC	0.49599	ACGGAACC--	ACGGAACC	26.15297	ACGGAACC--
ACGGTACC	0.49561	ACGGTACC--	CGGCACCC	25.58247	-CGGCACCC-
CGGTACCG	0.49449	-CGGTACCG-	CGGTACCG	24.53248	-CGGTACCG-
GCGGTACC	0.49416	GCGGTACC--	GCGGTACC	20.46962	GCGGTACC--
GGGTACCC	0.49365	--GGTACCCC	GGCACCCC	15.89873	--GGCACCCC
GGCACCCC	0.49250	--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'			8 mer Z-scores for probeset 'all'		
Forward:	Reverse:		Forward:	Reverse:	
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CGGAACCC	0.49935	-CGGAACCC-	CGGAACCC	44.82538	-CGGAACCC-
GGAACCCC	0.49806	--GGAACCCC	GGAACCCC	30.35148	--GGAACCCC
GGGGTACC	0.49669	--GGGTACCC	CGGTACCC	30.26730	-CGGTACCC-
CGGTACCC	0.49669	-CGGTACCC-	CGGCACCC	26.38172	-CGGCACCC-
CGGCACCC	0.49626	-CGGCACCC-	GGCACCCC	25.14410	--GGCACCCC
AGGGTTCC	0.49618	--GGAACCCCT	GGGGTACC	25.14129	--GGGTACCCC
ACGGAACC	0.49506	ACGGAACC--	ACGGTACC	23.75553	ACGGTACC--
GGGTACCC	0.49488	-GGGTACCC-	GGGTACCC	23.63564	-GGGTACCC-
CGGGAACC	0.49464	GCGGAACC--	AGGGTTCC	23.22545	--GGAACCCCT
GGCACCCC	0.49452	--GGCACCCC	ACGGAACC	22.81193	ACGGAACC--