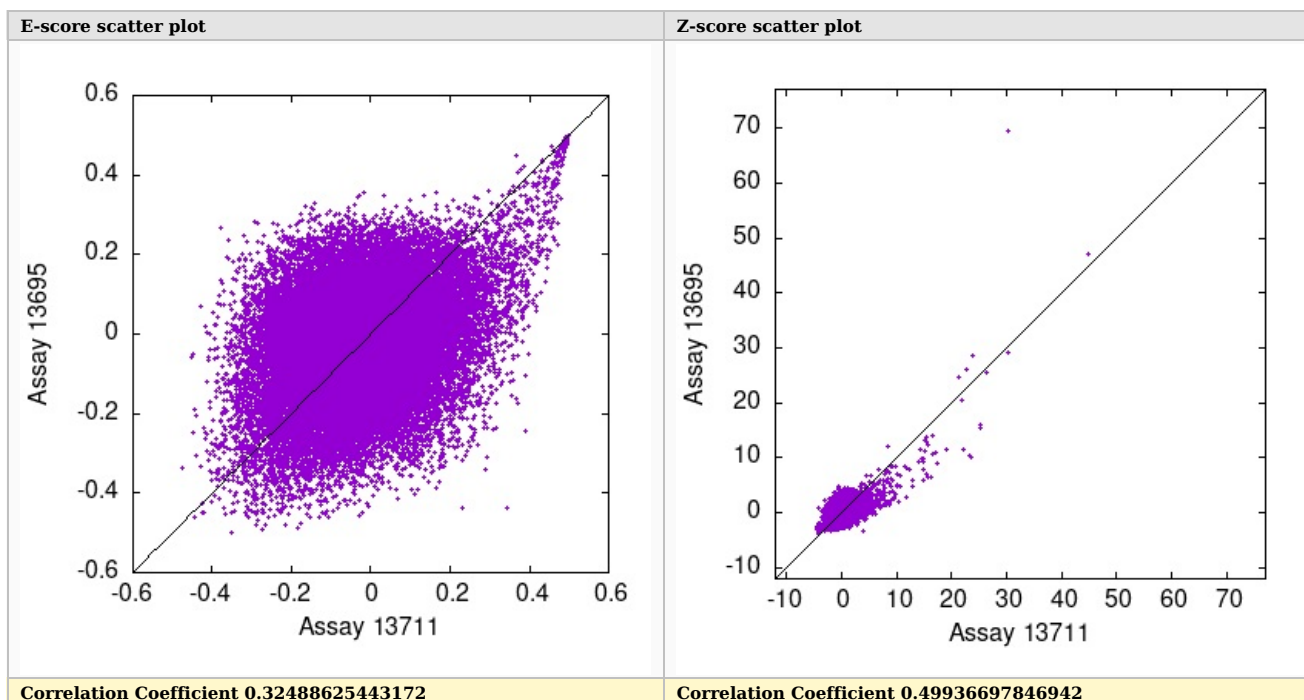




QC report





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:	
		
Top 10	Scores	Alignment
CGGAACCC	0.49935	-CGGAACCC-
GGAACCCC	0.49806	--GGAACCCC
GGGTACCC	0.49669	--GGTACCCC
CGGTACCC	0.49669	-CGGTACCC-
CGGCACCC	0.49626	-CGGCACCC-
AGGGTTCC	0.49618	--GGAACCCCT
ACGGAACC	0.49506	ACGGAACC--
GGGTACCC	0.49488	-GGGTACCC-
GCGGAACC	0.49464	GCGGAACC--
GGCACCCC	0.49452	--GGCACCCC

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
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	--GGTACCCC	
ACGGTACC	23.75553	ACGGTACC--	
GGGTACCC	23.63564	-GGGTACCC-	
AGGGTTCC	23.22545	--GGAACCCCT	
ACGGAACC	22.81193	ACGGAACC--	



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:	
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:	
			
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	--	GGTACCCC