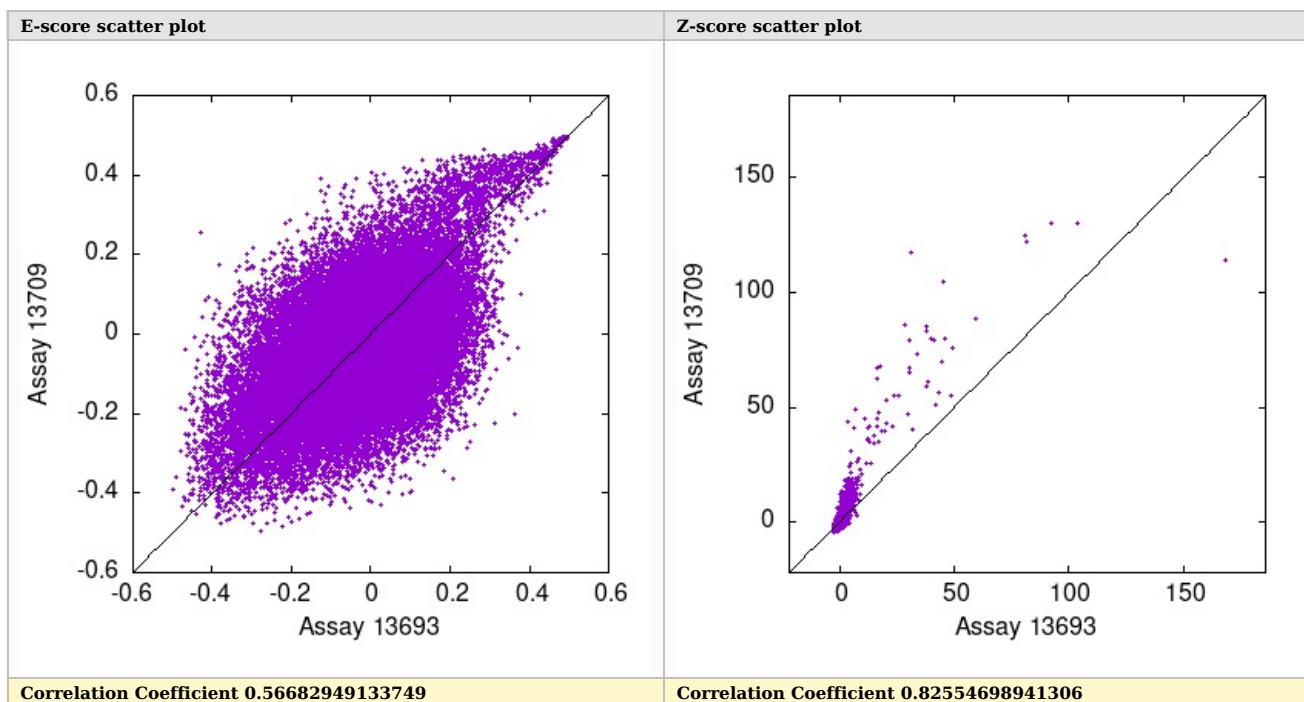


QC report



Top scoring motifs for Assay 13693

Protein ID: pTH13929.1 Gene: ZBED2.FL 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
CGAAACCC	0.49629	-CGAAACCC	CGAAACCC	168.48660	-CGAAACCC
ACGAAACC	0.49438	ACGAAACC-	ACGAAACC	103.96610	ACGAAACC-
ACGAAACT	0.49410	ACGAAACT-	ACGAAACT	92.15995	ACGAAACT-
CGAAACTC	0.49407	-CGAAACTC	CCGAAACC	81.47806	CCGAAACC-
CGAAACCC	0.49342	-CGAAACCC	CGAAACTC	80.82178	-CGAAACTC
GCGAAACC	0.49170	GCGAAACC-	CGAAACCC	59.36383	-CGAAACCC
CCGAAACC	0.49099	CCGAAACC-	AGTTTCGA	48.97310	TCGAAACT
GGTTTCGA	0.49040	TCGAAACC-	AGTTTCGC	48.88965	GCGAAACT-
CGAAACCG	0.48945	-CGAAACCG	GGTTTCGA	45.77455	TCGAAACC-
AGTTTCGA	0.48863	TCGAAACT-	CGAAACCG	45.50288	-CGAAACCG

Top scoring motifs for Assay 13709

Protein ID: pTH13929.2 Gene: ZBED2.FL 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
CGAAACTC	0.49675	-CGAAACTC	ACGAAACC	130.30217	ACGAAACC-
CGAAACCC	0.49612	-CGAAACCC	ACGAAACT	130.07036	ACGAAACT-
CCGAAACC	0.49607	CCGAAACC-	CGAAACTC	124.98604	-CGAAACTC
AGTTTCGG	0.49592	CCGAAACT-	CCGAAACC	121.83778	CCGAAACC-
ACGAAACC	0.49575	ACGAAACC-	CGAAACCA	117.45238	-CGAAACCA
ACGAAACT	0.49557	ACGAAACT-	CGAAACCC	114.36482	-CGAAACCC
CGAAACCA	0.49514	-CGAAACCA	CGAAACCG	104.99526	-CGAAACCG
CGAAACCG	0.49505	-CGAAACCG	CGAAACCC	88.76598	-CGAAACCC
GGTTTCGA	0.49353	TCGAAACC-	CGAAACTA	85.68332	-CGAAACTA
AGTTTCGA	0.49350	TCGAAACT-	AGTTTCGG	84.95335	CCGAAACT-