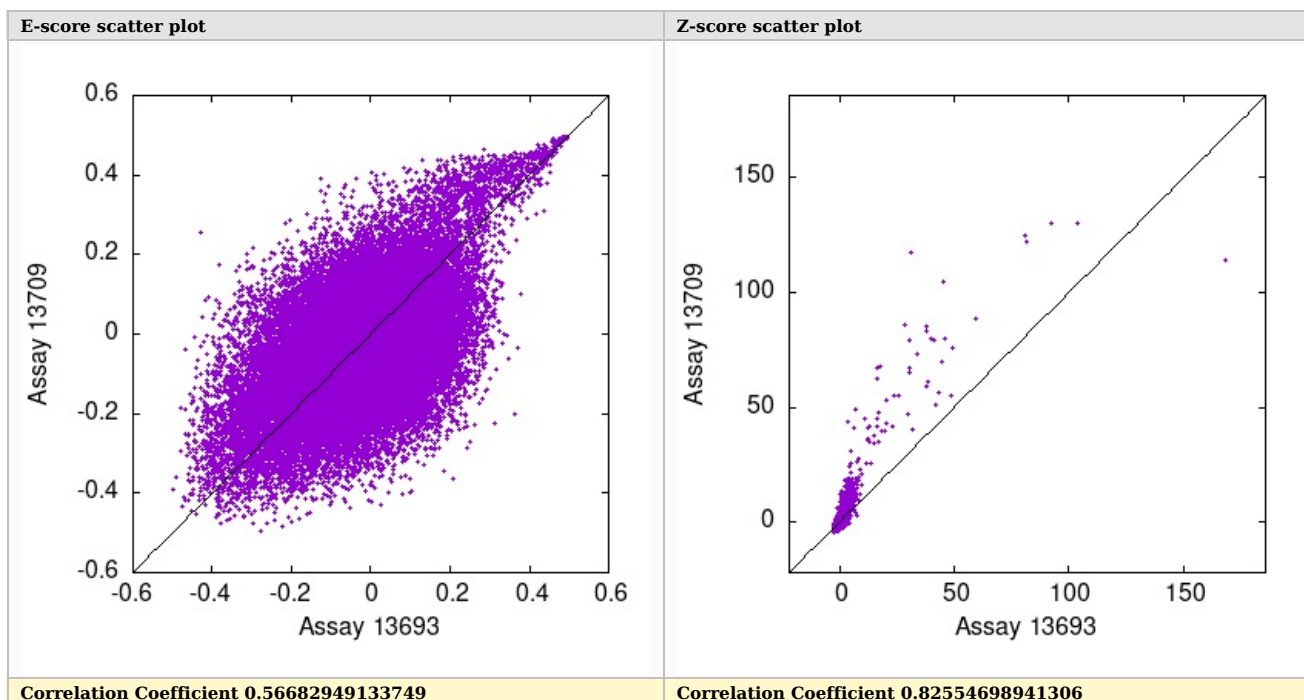


## QC report



### 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'

Forward:	Reverse:	
Top 10	Scores	Alignment
CGAAACCC	0.49629	-CGAAACCC
ACGAAACC	0.49438	ACGAAACC-
ACGAAACT	0.49410	ACGAAACT-
CGAAACTC	0.49407	-CGAAACTC
CGAACCCC	0.49342	-CGAACCCC
GCGAAACC	0.49170	GCGAAACC-
CCGAAACC	0.49099	CCGAAACC-
GGTTTCGA	0.49040	TCGAAACC-
CGAAACCG	0.48945	-CGAAACCG
AGTTTCGA	0.48863	TCGAAACT-

#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
CGAAACCC	168.48660	-CGAAACCC
ACGAAACC	103.96610	ACGAAACC-
ACGAAACT	92.15995	ACGAAACT-
CCGAAACC	81.47806	CCGAAACC-
CGAAACTC	80.82178	-CGAAACTC
CGAACCC	59.36383	-CGAACCC
AGTTTCGA	48.97310	TCGAAACT-
AGTTTCGC	48.88965	GCGAAACT-
GGTTTCGA	45.77455	TCGAAACC-
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'

Forward:	Reverse:	
Top 10	Scores	Alignment
CGAAACTC	0.49675	-CGAAACTC
CGAAACCC	0.49612	-CGAAACCC
CCGAAACC	0.49607	CCGAAACC-
AGTTTCGG	0.49592	CCGAAACT-
ACGAAACC	0.49575	ACGAAACC-
ACGAAACT	0.49557	ACGAAACT-
CGAAACCA	0.49514	-CGAAACCA
CGAAACCG	0.49505	-CGAAACCG
GGTTTCGA	0.49353	TCGAAACC-
AGTTTCGA	0.49350	TCGAAACT-

#### 8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ACGAAACC	130.30217	ACGAAACC -	
ACGAAACT	130.07036	ACGAAACT -	
CGAAACTC	124.98604	-CGAAACTC	
CCGAAACC	121.83778	CCGAAACC -	
CGAAACCA	117.45238	-CGAAACCA	
CGAAACCC	114.36482	-CGAAACCC	
CGAAACCG	104.99526	-CGAAACCG	
CGAACCCC	88.76598	-CGAACCCC	
CGAAACTA	85.68332	-CGAAACTA	
AGTTTCGG	84.95335	CCGAAACT -	