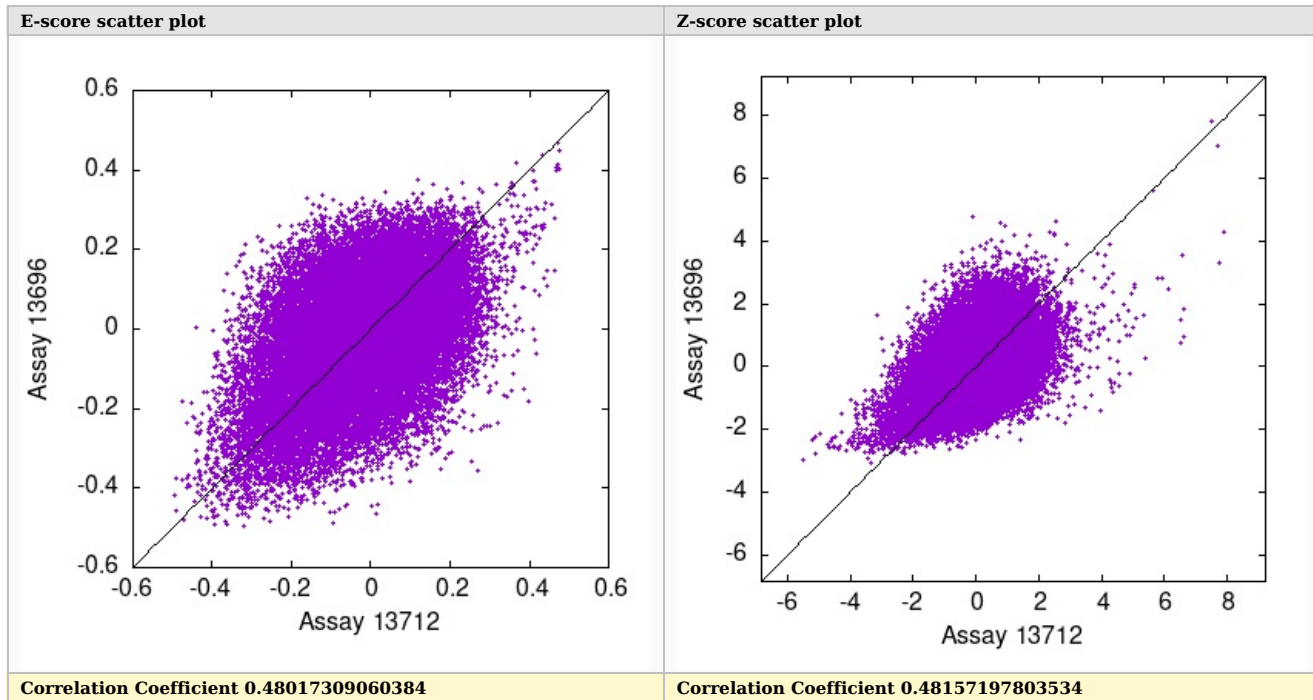


## QC report



### Top scoring motifs for Assay 13712

Protein ID: pTH13933.2 Gene: ZBED9.DBD Domain: zf-BED Flag: Pass\_matched\_pair Array: 1M-HK

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

Forward:

Reverse:



Top 10

Scores

Alignment

ACGGCCGG	0.47758	-ACGGCCGG-
AACGGCCG	0.47737	AACGGCCG--
ACGGCCGA	0.47294	-ACGGCCGA-
CGGGCCGAA	0.47136	--CGGGCCGAA
CGGGCCGA	0.46664	--CGGGCCGA
CGGCCGTA	0.46603	TACGGCCG--
GC GGCCCA	0.46562	-GC GGCCCA-
GGGGCCGA	0.46246	--GGGGCCGA
CGGCCCAA	0.45693	--CGGCCCAA
ACGGCCCA	0.44436	-ACGGCCCA-

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

Forward:

Reverse:



Top 10

Scores

Alignment

CGGGCCGAA	7.87713	--CGGGCCGAA
ACGGCCGG	7.76276	-ACGGCCGG-
AACGGCCG	7.69994	-AACGGCCG--
ACGGCCGA	7.49063	-ACGGCCGA-
GGGGCCGA	6.61453	--GGGGCCGA
GCGGCCCA	6.60512	-GCGGCCCA-
CGGCCGTA	6.56066	TACGGCCG--
ACGGCCCA	6.53691	-ACGGCCCA-
CGGCCCAA	6.53629	--CGGCCCAA
CGGCCGAG	6.11461	--CGGCCGAG

### Top scoring motifs for Assay 13696

Protein ID: pTH13933.1 Gene: ZBED9.DBD Domain: zf-BED Flag: Pass\_matched\_pair Array: 1M-ME

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

Forward:

Reverse:



Top 10

Scores

Alignment

ACGGCCGA	0.46969	--ACGGCCGA--
AACGGCCG	0.44846	-AACGGCCG--
ATCGGCCG	0.43932	---CGGCCGAT-
GGCCGAAA	0.41789	----GGCCGAAA
CGGGCCGAA	0.41364	---CGGGCCGAA-
CGGGCCGA	0.40457	---CGGGCCGA-
ACGGCCGG	0.40215	--ACGGCCGG--
CCGGCCGA	0.40061	--CCGGCCGA--
CGGCCGTA	0.39990	-TACGGCCG---
CTACAACA	0.37564	CTACAACA----

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

Forward:

Reverse:



Top 10

Scores

Alignment

ACGGCCGA	7.79632	--ACGGCCGA--
AACGGCCG	6.99725	-AACGGCCG--
ATCGGCCG	5.58540	---CGGCCGAT-
AACAACGC	4.77422	--AACAACGC--
CCGGCCGA	4.61157	--CCGGCCGA--
ACTGTATA	4.58360	--ACTGTATA--
ATAATGCA	4.47473	ATAATGCA----
CGGCCGAA	4.29148	---CGGCCGAA-
CATAATAC	4.27076	---GTATTATG
ATAACGAA	4.22849	--ATAACGAA--