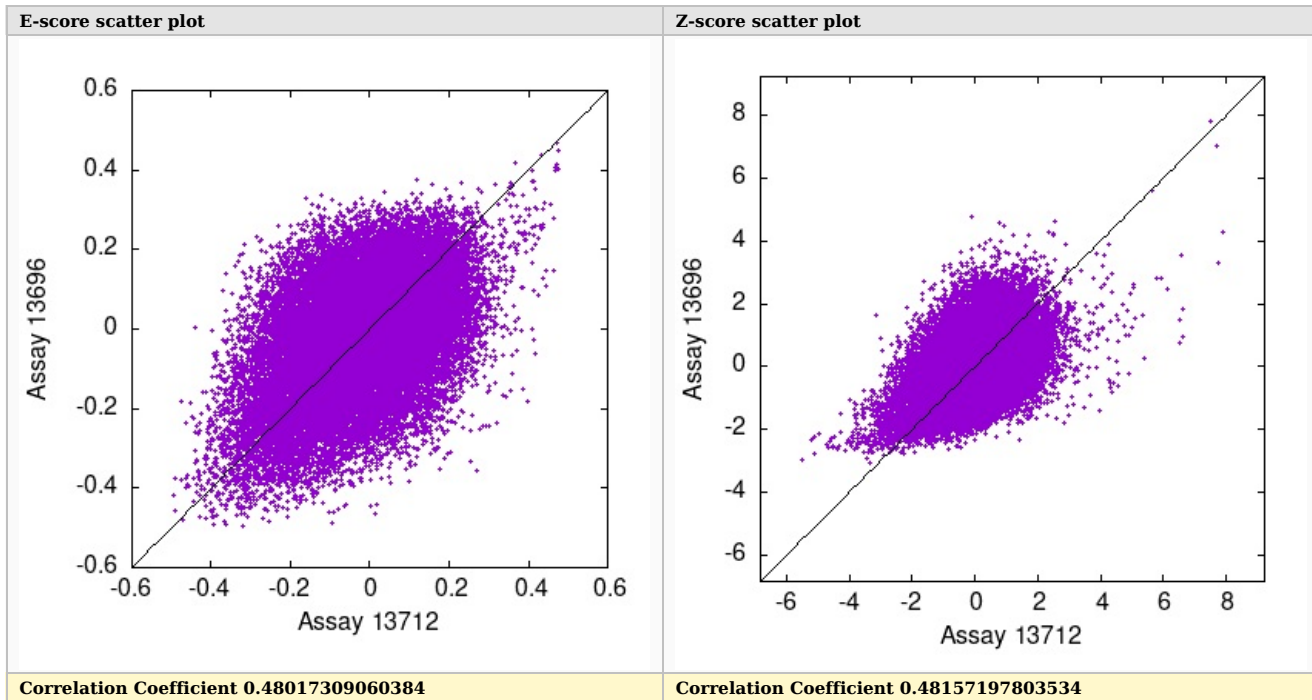


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACGGCCGG	0.47758	-ACGGCCG-	CGGCCGAA	7.87713	--CGGCCGAA
AACGGCCG	0.47737	AACGGCCG--	ACGGCCGG	7.76276	-ACGGCCGG-
ACGGCCGA	0.47294	-ACGGCCGA-	AACGGCCG	7.69994	AACGGCCG--
CGGCCGAA	0.47136	--CGGCCGAA	ACGGCCGA	7.49063	-ACGGCCGA-
CGGCCGGA	0.46664	--CGGCCGGA	GGGCCGCA	6.61453	--GGGCCGCA
CGGCCGTA	0.46603	TACGGCCG--	GCGGCCCA	6.60512	-GCGGCCCA-
GCGGCCCA	0.46562	-GCGGCCCA-	CGGCCGTA	6.56066	TACGGCCG--
GGGCCGCA	0.46246	--GGGCCGCA	ACGGCCCA	6.53691	-ACGGCCCA-
CGGCCCAA	0.45693	-CGGCCCAA	CGGCCCAA	6.53629	--CGGCCCAA
ACGGCCCA	0.44436	-ACGGCCCA-	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACGGCCGA	0.46969	--ACGGCCGA--	ACGGCCGA	7.79632	--ACGGCCGA--
AACGGCCG	0.44846	-AACGGCCG---	AACGGCCG	6.99725	-AACGGCCG---
ATCGGCCG	0.43932	---CGGCCGAT---	ATCGGCCG	5.58540	---CGGCCGAT---
GGCCGAAA	0.41789	----GGCCGAAA	AACAACGC	4.77422	--AACAACGC--
CGGCCGAA	0.41364	---CGGCCGAA-	CCGGCCGA	4.61157	--CCGGCCGA--
CGGCCGGA	0.40457	---CGGCCGGA-	ACTGTATA	4.58360	--ACTGTATA--
ACGGCCGG	0.40215	--ACGGCCGG--	ATAATGCA	4.47473	ATAATGCA----
CCGGCCGA	0.40061	-CCGGCCGA--	CGGCCGAA	4.29148	---CGGCCGAA-
CGGCCGTA	0.39990	-TACGGCCG---	CATAATAC	4.27076	---GTATTATG
CTACAACA	0.37564	CTACAACA----	ATAACGAA	4.22849	--ATAACGAA--