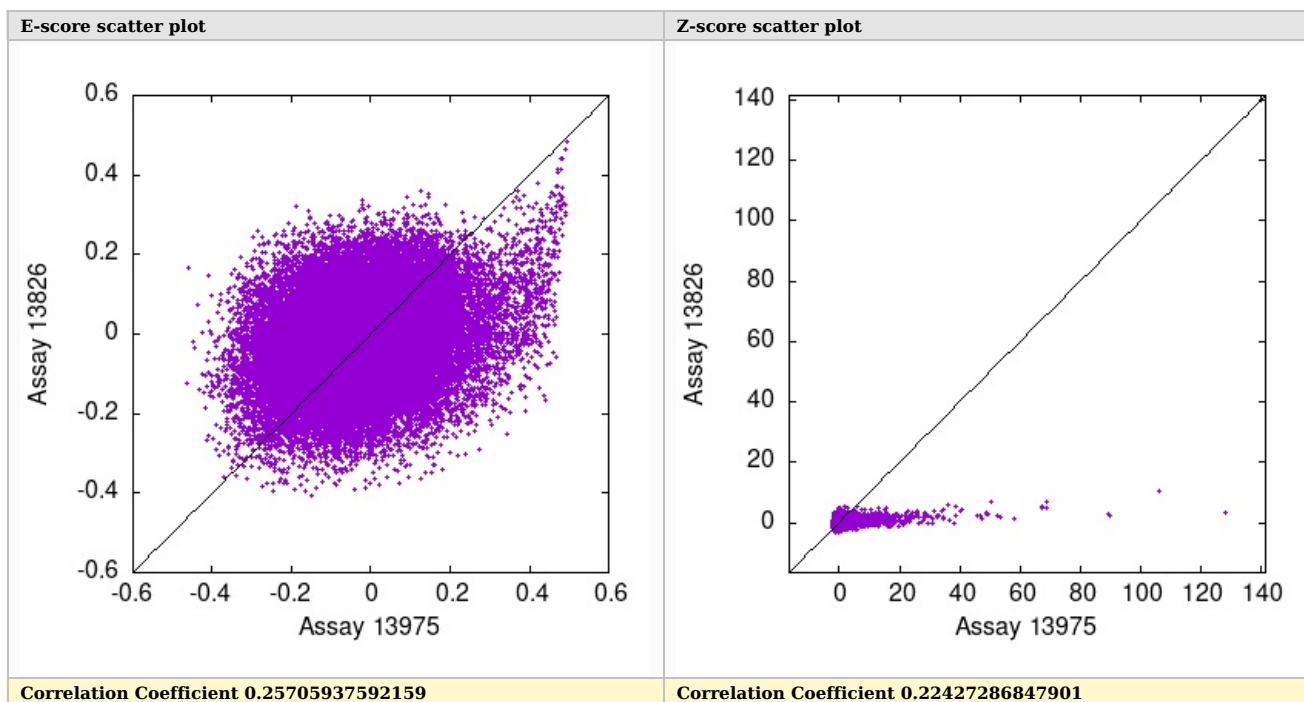




QC report





Top scoring motifs for Assay 13975

Protein ID: pTH13931.3 Gene: ZBED4 Domain: zf-BED Flag: Pass matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CGGTACCG	0.49340	-	CGGTACCG-
TGGTACCA	0.49241	-	TGGTACCA-
CGGTCCAA	0.49079	-	CGGTCCAA-
CGGTACCA	0.49026	-	CGGTACCA-
ATTGGACC	0.48954	- -	GGTCCAAT
CTGGTACC	0.48734	- -	GGTACCAG
AGGTTCCG	0.48486	-	CCGAACCT-
GCCGAACC	0.48390		GCCGAACC--
CCGGTACC	0.48389		CCGGTACC--
CCGAACCG	0.48200		-CCGAACCG-



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CGGTCCAA	128.23762	-CGGTCCAA--	
CGGTACCG	105.93106	-CGGTACCG--	
TGGTACCA	89.93481	-TGGTACCA--	
ATTGGACC	89.49647	--GGTCCAAT--	
CGGTACCA	69.00148	-CGGTACCA--	
CCGAACCA	68.77158	-CCGAACCA--	
CCGGTACC	67.43938	CCGGTACC---	
GCCGAACC	67.14504	GCCGAACC--	
ATTGGGTC	58.01877	---GACCCAAT	
CTGGTACC	53.46846	--GGTACCAG-	



Top scoring motifs for Assay 13826

Protein ID: pTH13931.1 Gene: ZBED4 Domain: zf-BED Flag: Pass matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
CGGTACCG	0.48308	CGGTACCG--
CGGTACCA	0.46619	TGGTACCG--
GGTTCCGA	0.44051	--GGTTCGGA--
CCGGTACC	0.44047	--GGTACCGG--
CCGAACCA	0.41598	TGGTTCCG--
CGGAACCG	0.41530	CGGAACCG--
GGTACCGA	0.40596	--GGTACCGA--
ACCGGTAC	0.38076	--GTACCGGT
GGTTCCGA	0.36996	--GGTTCGGA--
GGTACCAA	0.36985	--GGTACCAA--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
CGGTACCG	10.57487	---CGGTACCG--
GGTTCCGA	6.86183	---TCGGAACCG--
CGGTACCA	6.65803	---CGGTACCA--
GGTACCGA	5.74843	---TCGGTACC--
CCGGTACC	5.55751	---CCGGTACC--
CCGAACCA	5.51458	---CGGAACCA--
CATAATAC	5.44774	-----GTATTATG
ACCCAAC	5.14440	GTTTGGGT-----
GCCGAACC	5.07613	---GCCGAACC--
ATTATTAC	4.92334	-----GTAATAAT