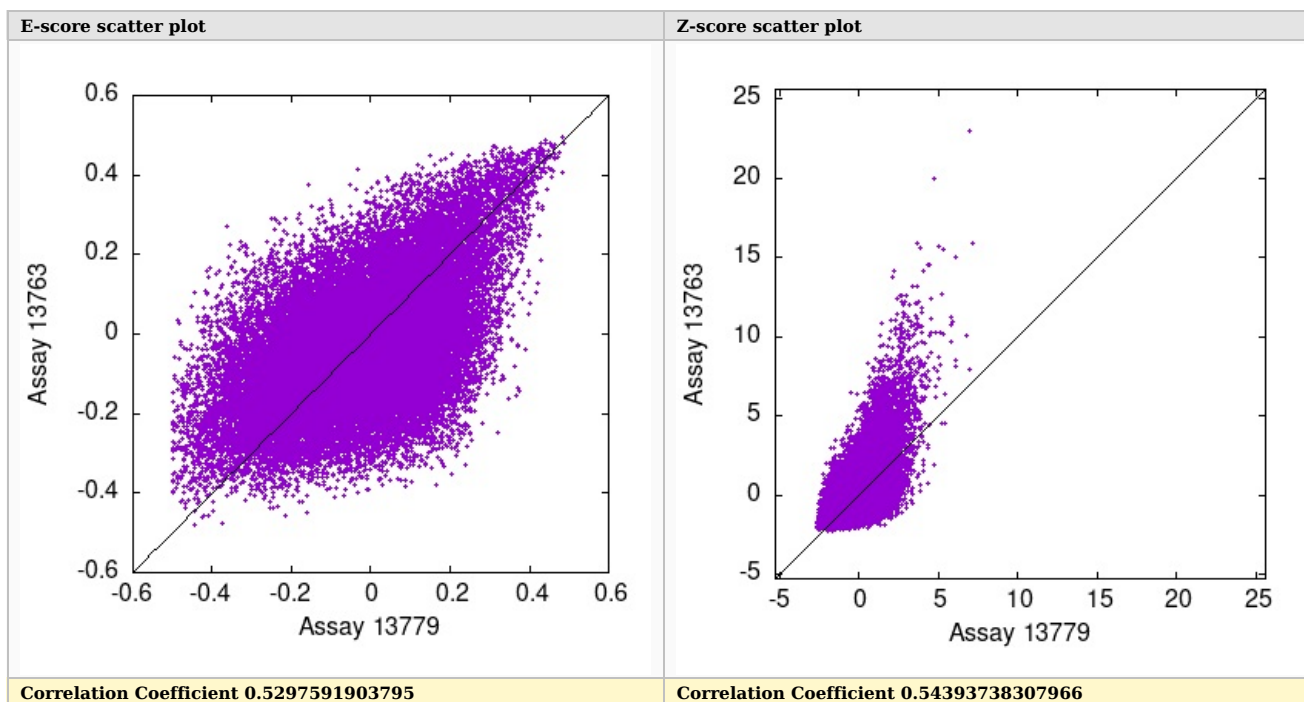




## QC report





### Top scoring motifs for Assay 13779

Protein ID: pTH14340.2 Gene: SP140L.DBD Domain: SAND Flag: Pass\_matched\_pair Array: 1M-HK

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
TCACGTGA	0.48812	--TCACGTGA--
TTACGTAA	0.48426	--TTACGTAA--
TCGCGCGA	0.48167	TCGCGCGA---
ACGTACGA	0.47397	TCGTACGT---
CGTATACG	0.47213	-CGTATACG--
ATACGTAT	0.46564	--ATACGTAT--
TACGCGTA	0.46351	-TACGCGTA--
ACGTACGT	0.46340	ACGTACGT---
CGTACGTA	0.46263	-CGTACGTA--
TACGTAAA	0.46106	---TACGTAAA



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

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
TCACGTGA	7.18172	- - TCACGTGA	
TTACGTAA	6.98855	- - TTACGTAA	
TCGCGCGA	6.93633	TCGCGCGA - -	
CGTATACG	6.81344	- CGTATACG -	
ACGTACGT	6.09151	ACGTACGT - -	
GTACGTAC	6.09151	- - GTACGTAC	
CGTACGTA	6.04972	- CGTACGTA -	
TACGCGTA	5.92778	- TACGCGTA -	
ACGTACGA	5.81248	TCGTACGT - -	
ATACGTAT	5.77620	- - ATACGTAT	

### Top scoring motifs for Assay 13763

Protein ID: pTH14340.1 Gene: SP140L.DBD Domain: SAND Flag: Pass\_matched\_pair Array: 1M-ME

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
TTACGTAA	0.49523	-TTACGTAA--
TGACGTAA	0.48807	-TGACGTAA--
ATTACGTA	0.48166	ATTACGTA---
GTTACGTA	0.48134	GTTACGTA---
TACGTCAA	0.48112	TTGACGTA---
TCACGTGA	0.47949	-TCACGTGA--
ACGTACGT	0.47421	---ACGTACGT
TGACGTCA	0.47337	-TGACGTCA--
TCACGTCA	0.47111	-TGACGTGA--
AATTACGT	0.47033	---ACGTAATT

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

Forward:		Reverse:
Top 10	Scores	Alignment
TTACGTAA	23.02625	- TTACGTAA - -
TGACGTAA	19.92335	- TGACGTAA - -
TCGTACGA	15.89911	- - - TCGTACGA
TCACGTGA	15.86988	- TCACGTGA - -
TACGTCAA	15.65489	- - TACGTCAA -
ATTACGTA	15.55499	ATTACGTA - - -
TGACGTCA	15.51546	- TGACGTCA - -
ACGTACGT	15.02235	- - - ACGTACGT
ATACGTAA	14.51790	- ATACGTAA - -
GATACGTA	14.51790	GATACGTA - - -