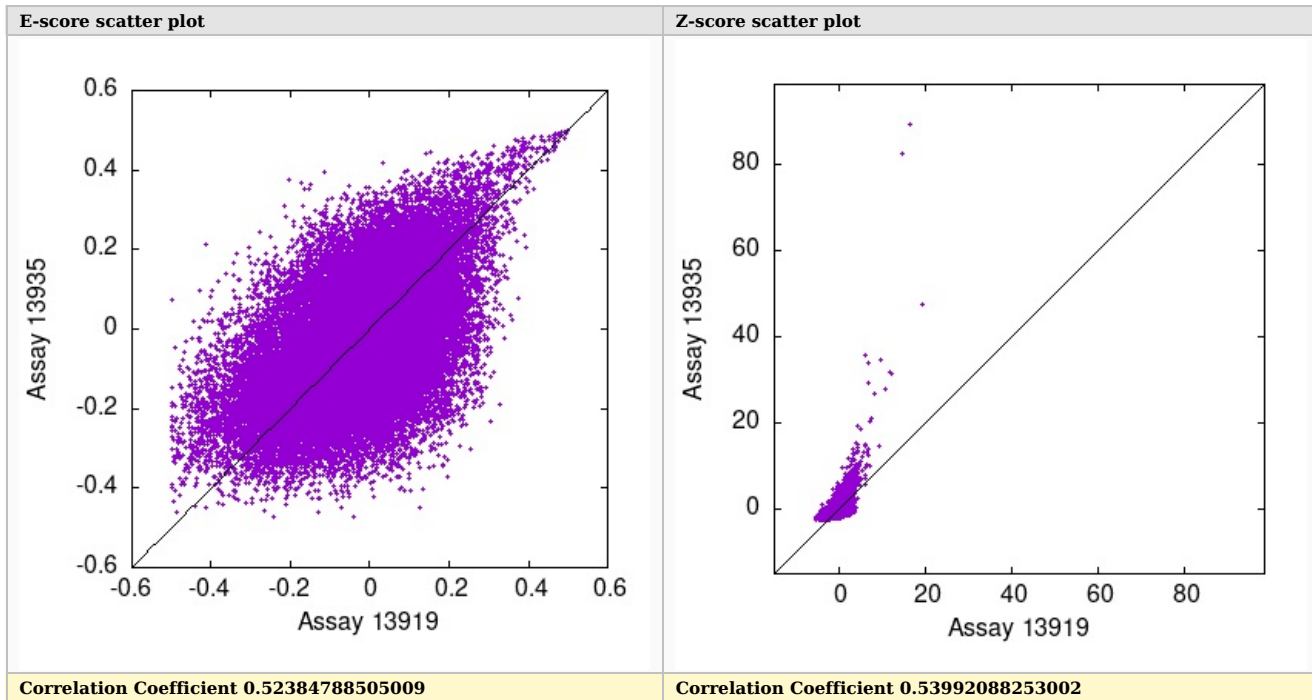




QC report





Top scoring motifs for Assay 13919

Protein ID: pTH14216.1 Gene: TIGD7.FL Domain: CENP-B_N Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AATTCGGA	0.49904	AATTCGGA--
ATTCGGAC	0.49872	-ATTCGGAC-
AGTCCGAA	0.49791	--TTCGGACT
GTCCGAAA	0.49616	-TTTCGGAC-
TGTCCGAA	0.49539	--TTCGGACA
ATTCGAA	0.49441	-ATTCGGAA-
TATTCGGA	0.49309	TATTCGGA--
GTCCGAAC	0.49109	-GTTCCGAC-
ATTTCGGA	0.48364	ATTTCGGA--
GGTCCGAA	0.48237	--TTCGGACC



8 mer Z-scores for probeset 'all'

Forward:	Reverse:
	
Top 10	Scores
AATTCGGA	19.31626
ATTCGGAC	16.65005
AGTCCGAA	14.74619
TGTCCGAA	12.26819
GTCCGAAA	11.87219
ATTCGGAA	10.98303
GTCCGAAC	9.76862
TATTCGGA	9.50040
ATTCCGAA	8.48378
AGTCCAAA	7.47218
Alignment	
AATTCGGA--	
-ATTCGGAC-	
--TTCGGACT	
--TTTCGGACA	
-TTTCGGAC-	
-ATTCGGAA-	
-GTTCCGAC-	
TATTCGGA--	
--TTCGGAAT	
--TTTGACT	



Top scoring motifs for Assay 13935

Protein ID: pTH14216.2 Gene: TIGD7.FL Domain: CENP-B_N Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ATTCGGAC	0.49868	-ATTCGGAC-
AGTCCGAA	0.49862	--TTCGGACT
AATTCGGA	0.49778	AATTCGGA--
GTCCGAAC	0.49462	-GTTCCGAC-
GTCCGAAA	0.49448	-TTTCGGAC-
GGTCCGAA	0.49380	--TTCGGACC
TGTCCGAA	0.49349	--TTCGGACA
ATTCGGAA	0.49194	-ATTCGGAA-
TTCCGAAA	0.49182	-TTTCGGAA-
ATTTGGAC	0.49004	-ATTTGGAC-

8 mer Z-scores for probeset 'all'

Forward:	Reverse:
	
Top 10	Scores
ATTCGGAC	89.08950
AGTCCGAA	82.61250
AATTCGGA	47.71935
TTCCGAAA	35.92735
GTCCGAAC	34.61777
GGTCCGAA	34.05659
GTCCGAAA	31.99658
TGTCCGAA	31.67130
ATTTGGAC	29.37974
ATTCGGAA	27.77642
Alignment	
- ATTCGGAC -	
- - TTCGGACT	
AATTCGGA - -	
- TTTCGGAA -	
- GTTCGGAC -	
- - TTCGGACC	
- TTTCGGAC -	
- - TTCGGACA	
- ATTTGGAC -	
- ATTCGGAA -	