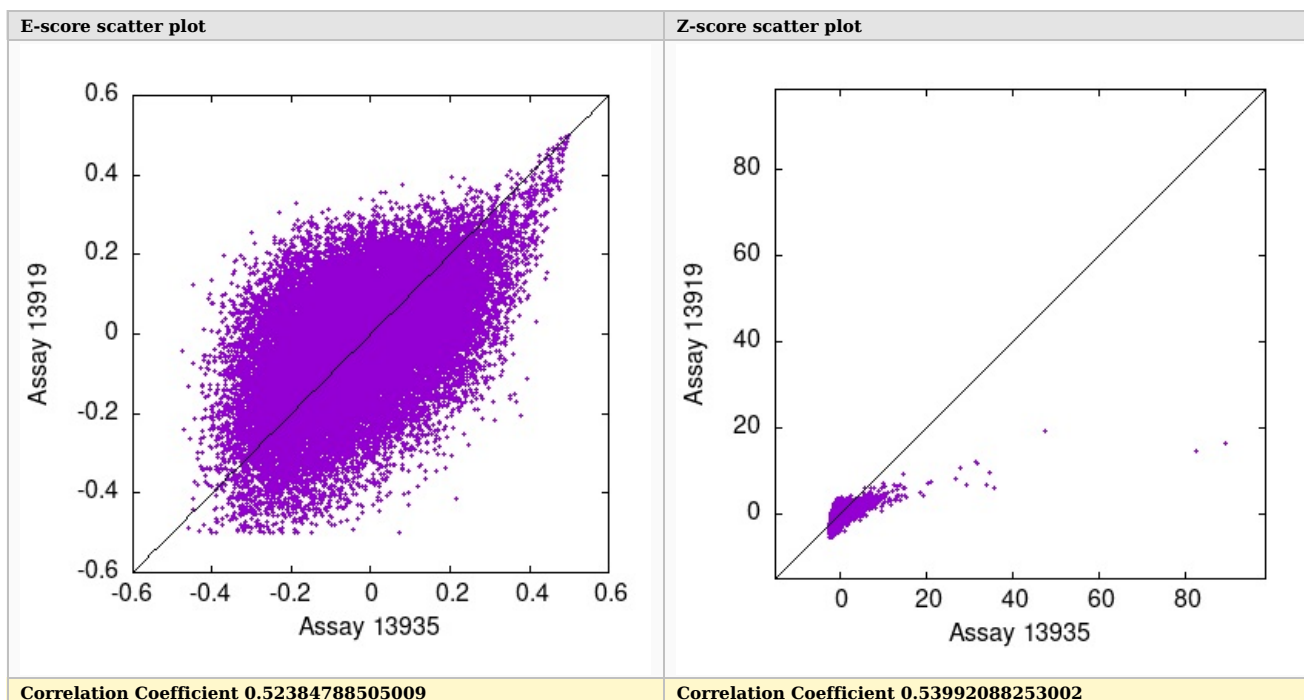




QC report





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	- GTTCGGAC-
GTCCGAAA	0.49448	- TTTCGGAC-
GGTCCGAA	0.49380	--TTCGGACC
TGTCCGAA	0.49349	--TTCGGACA
ATTCGGAA	0.49194	-ATTCGGAA-
TTCCGAAA	0.49182	-TTTCGGAA-
ATTGGGAC	0.49004	-ATTGGGAC-



8 mer Z-scores for probeset 'all'

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



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
ATTCGGAA	0.49441	-ATTCGGAA-
TATTCGGA	0.49309	TATTCGGA--
GTCCGAAC	0.49109	-GTTCCGAC-
ATTCGGA	0.48364	ATTCGGA--
GGTCCGAA	0.48237	--TTCGGACC

8 mer Z-scores for probeset 'all'

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