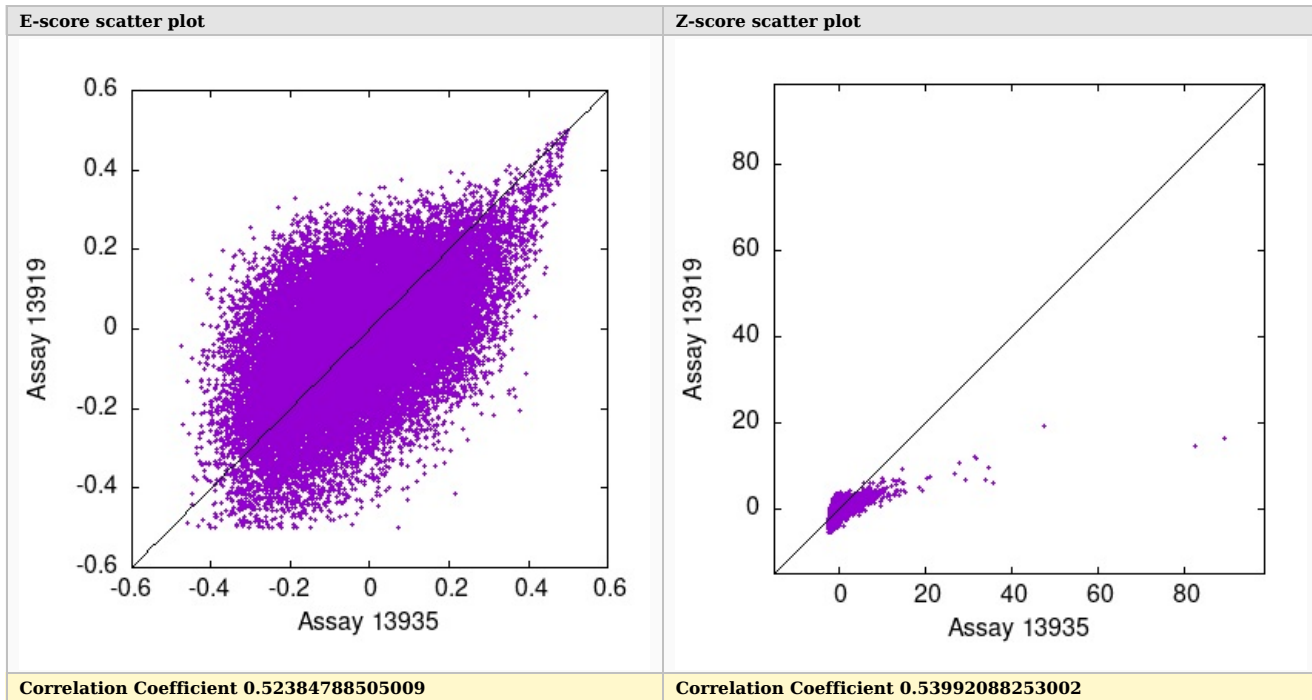


## QC report



## 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
ATTCGGAC	0.49868	-ATTCGGAC-	ATTCGGAC	89.08950	-ATTCGGAC-
AGTCCGAA	0.49862	--TTCGGACT	AGTCCGAA	82.61250	--TTCGGACT
AATTCGGA	0.49778	AATTCGGA--	AATTCGGA	47.71935	AATTCGGA--
GTCCGAAC	0.49462	-GTTCCGGAC-	TTCCGAAA	35.92735	-TTTCGGAA-
GTCCGAAA	0.49448	-TTTCGGAC-	GTCCGAAC	34.61777	-GTTCCGGAC-
GGTCCGAA	0.49380	--TTCGGACC	GGTCCGAA	34.05659	--TTCGGACC
TGTCCGAA	0.49349	--TTCGGACA	GTCCGAAA	31.99658	-TTTCGGAC-
ATTCGGAA	0.49194	-ATTCGGAA-	TGTCCGAA	31.67130	--TTCGGACA
TTCCGAAA	0.49182	-TTTCGGAA-	ATTTGGAC	29.37974	-ATTTGGAC-
ATTTCGAC	0.49004	-ATTTCGAC-	ATTCGAA	27.77642	-ATTCGAA-

## 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AATTCGGA	0.49904	AATTCGGA--	AATTCGGA	19.31626	AATTCGGA--
ATTCGGAC	0.49872	-ATTCGGAC-	ATTCGGAC	16.65005	-ATTCGGAC-
AGTCCGAA	0.49791	--TTCGGACT	AGTCCGAA	14.74619	--TTCGGACT
GTCCGAAA	0.49616	-TTTCGGAC-	TGTCCGAA	12.26819	--TTCGGACA
TGTCCGAA	0.49539	--TTCGGACA	GTCCGAAA	11.87219	-TTTCGGAC-
ATTCGGAA	0.49441	-ATTCGGAA-	ATTCGGAA	10.98303	-ATTCGGAA-
TATTCGGA	0.49309	TATTCGGA--	GTCCGAAC	9.76862	-GTTCCGGAC-
GTCCGAAC	0.49109	-GTTCCGGAC-	TATTCGGA	9.50040	TATTCGGA--
ATTCGGA	0.48364	ATTCGGA--	ATTCGAA	8.48378	--TTCGGAAT
GGTCCGAA	0.48237	--TTCGGACC	AGTCCAAA	7.47218	--TTTGGAAT