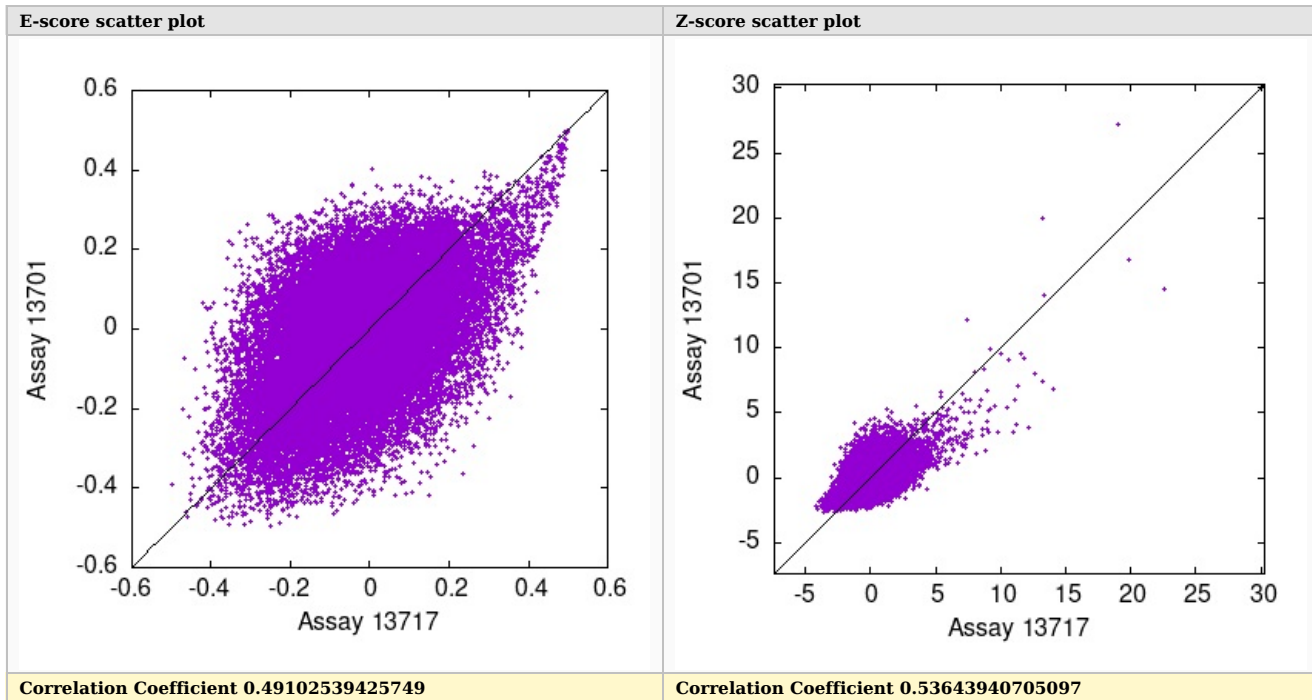


QC report



Top scoring motifs for Assay 13717

Protein ID: pTH14217.2 Gene: TIGD7.DBD 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
AGTCCGAA	0.49873	--TTCGGACT	AGTCCGAA	22.61628	AGTCCGAA--
ATTCGGAC	0.49799	-ATTCGGAC-	ATTCGGAC	19.89054	-GTCCGAAT-
AATTCGGA	0.49747	AATTCGGA--	AATTCGGA	19.06409	--TCCGAATT
GTCCGAAC	0.49578	-GTTCGGAC-	GTCCGAAC	14.04748	-GTCCGAAC-
GTCCGAAA	0.49448	-TTTCGGAC-	GTCCGAAA	13.39515	-GTCCGAAA-
GGTCCGAA	0.49342	--TTCGGACC	ATTCCGAA	13.20336	ATTCCGAA--
ATTCGGAA	0.49210	-ATTCGGAA-	ATTCGGAA	13.19241	-TTCCGAAT-
TGTCCGAA	0.49057	--TTCGGACA	GGTCCGAA	12.68992	GGTCCGAA--
AGTTCGGA	0.49029	AGTTCGGA--	AGTCCGGA	12.10545	AGTCCGGA--
ATTCCGAA	0.48980	--TTCGGAAT	TGTCCGAA	11.78252	TGTCCGAA--

Top scoring motifs for Assay 13701

Protein ID: pTH14217.1 Gene: TIGD7.DBD 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	0.49773	AATTCGGA--	AATTCGGA	27.14170	AATTCGGA--
ATTCGGAC	0.49662	-ATTCGGAC-	ATTCGGAA	19.99128	-ATTCGGAA-
ATTCGGAA	0.49481	-ATTCGGAA-	ATTCGGAC	16.75346	-ATTCGGAC-
AGTCCGAA	0.49465	--TTCGGACT	AGTCCGAA	14.54084	--TTCGGACT
GTCCGAAA	0.49058	-TTTCGGAC-	GTCCGAAA	14.07650	-TTTCGGAC-
TATTCGGA	0.48313	TATTCGGA--	TATTCGGA	12.14326	TATTCGGA--
TGTCCGAA	0.47830	--TTCGGACA	TGTCCAAA	9.91658	--TTTGGACA
GGTCCGAA	0.47791	--TTCGGACC	ATTTCCGGA	9.53518	ATTTCCGGA--
ATTCGGA	0.46629	ATTCGGA--	TTCCGAAA	9.53518	-TTTCGGAA-
TGTCCAAA	0.46510	--TTTGGACA	TGTCCGAA	9.20597	--TTCGGACA