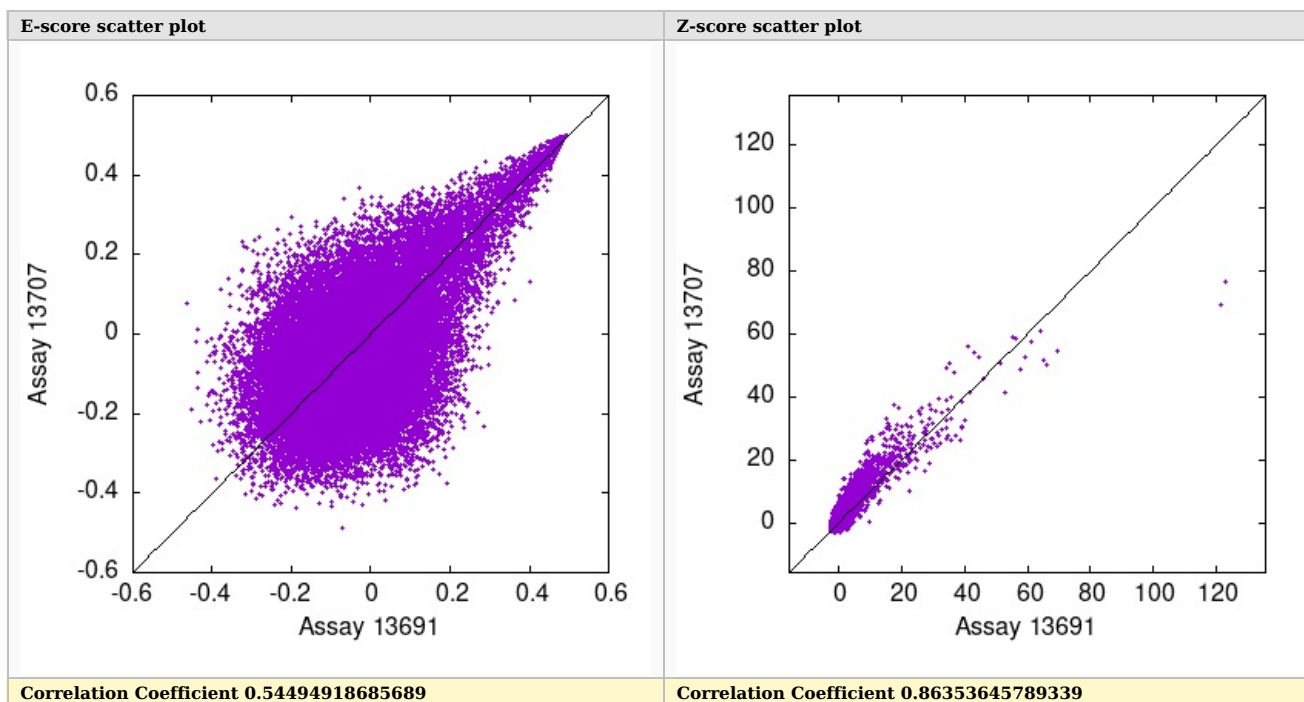


QC report



Top scoring motifs for Assay 13691

Protein ID: pTH13927.1 Gene: FAM200B.DBD Domain: zf-BED 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
GCGACCCA	0.49636	-GCGACCCA-	GCGACCCA	123.03463	-GCGACCCA-
CGCGACCC	0.49509	CGCGACCC--	CGCGACCC	121.24000	CGCGACCC--
ACGACCCC	0.49177	-ACGACCCC-	CACGACCC	69.65754	CACGACCC--
CGACCCAC	0.49163	--CGACCCAC	CGACCCAA	66.01732	--CGACCCAA
GGCGACCC	0.49102	GGCGACCC--	ACGACCCC	65.26430	-ACGACCCC-
ACGACCCA	0.49075	-ACGACCCA-	ACGACCCA	64.17999	-ACGACCCA-
GGGTCGCA	0.49006	TGCGACCC--	CGACCCAC	60.97356	--CGACCCAC
ATGGGTCG	0.48974	--CGACCCAT	GGCGACCC	59.06954	GGCGACCC--
CACGACCC	0.48913	CACGACCC--	AGGTCGCG	57.63452	-GCGACCC-
AGGGTCGC	0.48880	-GCGACCC-	GGGTCGCA	56.50584	TGCGACCC--

Top scoring motifs for Assay 13707

Protein ID: pTH13927.2 Gene: FAM200B.DBD Domain: zf-BED 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
GCGACCCA	0.49891	-GCGACCCA-	GCGACCCA	76.38583	-GCGACCCA-
CGCGACCC	0.49767	CGCGACCC--	CGCGACCC	69.39329	CGCGACCC--
ACGACCCA	0.49752	-ACGACCCA-	ACGACCCA	60.99655	-ACGACCCA-
ATGGGTCG	0.49718	--CGACCCAT	ATGGGTCG	58.94006	--CGACCCAT
GGGTCGCA	0.49688	TGCGACCC--	GGGTCGCA	58.62658	TGCGACCC--
CGACCCAC	0.49640	--CGACCCAC	CGACCCAC	57.72511	--CGACCCAC
GCGACCCC	0.49508	-GCGACCCC-	GCGACCCC	56.24566	-GCGACCCC-
CGACCCAA	0.49493	--CGACCCAA	CACGACCC	54.69189	CACGACCC--
GGGTCGTA	0.49461	TACGACCC--	GGGTCGTA	54.04737	TACGACCC--
GGCGACCC	0.49436	GGCGACCC--	CGGGTCGC	52.65244	-GCGACCCG-