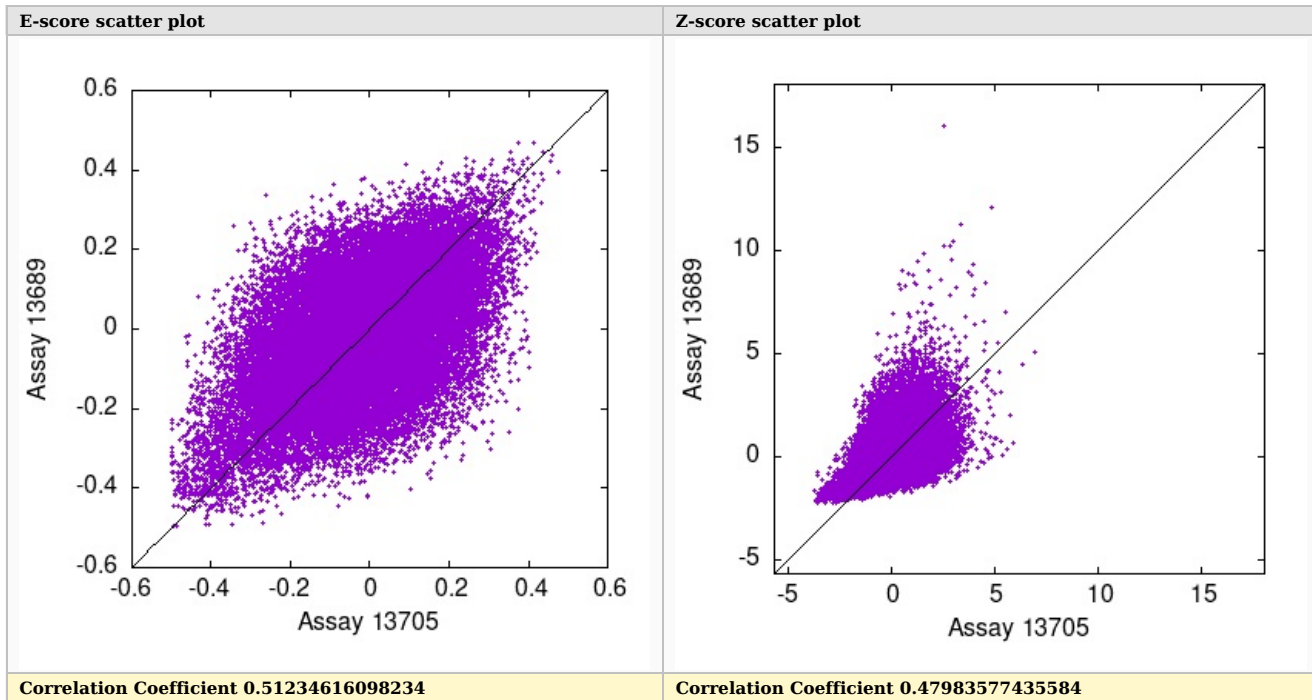


QC report



Top scoring motifs for Assay 13705

Protein ID: pTH12990.2 Gene: LIN28B.RBR Domain: CSD 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
GATATAAC	0.47755	GATATAAC -	AAAAAAC	6.94386	AAAAAAC -
GATAAGAC	0.45848	GATAAGAC -	GATATAAC	6.31862	GATATAAC -
AAAAAAC	0.45675	AAAAAAC -	AATATATT	5.90684	AATATATT -
ATATAACA	0.43821	-ATATAACA	ACACACCA	5.73294	-ACACACCA
AAAATAAC	0.43610	AAAATAAC -	GAAAAAAA	5.57524	GAAAAAAA -
AAAAAACC	0.43209	AAAAAACC -	GATAAGAC	5.51107	GATAAGAC -
GATAAAAC	0.43111	GATAAAAC -	GGTACACC	5.37806	GGTACACC -
AAAACAAC	0.42703	AAAACAAC -	GATATCAC	5.32862	GATATCAC -
AAAAAGAC	0.41966	AAAAAGAC -	AAAAAGAC	5.31106	AAAAAGAC -
ACAAACCA	0.41660	-ACAAACCA	ATGTTGTA	5.22736	--TACAACAT

Top scoring motifs for Assay 13689

Protein ID: pTH12990.1 Gene: LIN28B.RBR Domain: CSD 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
AAAAACAC	0.46790	--AAAAACAC	AAAAACAC	16.10903	--AAAAACAC
AAAAACA	0.46748	-AAAAACA-	AAAATAAC	12.10274	AAAATAAC -
AAAATAAC	0.44611	AAAATAAC -	ATACAACA	11.25010	-ATACAACA-
ATACAACA	0.44354	-ATACAACA-	GTTATTTA	10.43164	TAAATAAC -
GATAAGAC	0.43642	GATAAGAC -	AAAAAACA	10.25211	-AAAAAACA-
AAATAACC	0.42952	-AAATAACC-	ACACACAC	10.23174	--ACACACAC
AAACACT	0.42938	-AAACACT-	AAACAACG	9.89062	-AAACAACG-
AAAAGACA	0.42769	-AAAAGACA-	ATAAACA	9.59003	-ATAAACA-
GTGTTTTA	0.42684	--TAAACAC	TAAAAAAA	9.49169	-TAAAAAAA-
AAAAATA	0.42675	-AAAAATA-	AAATAACC	9.36848	-AAATAACC-