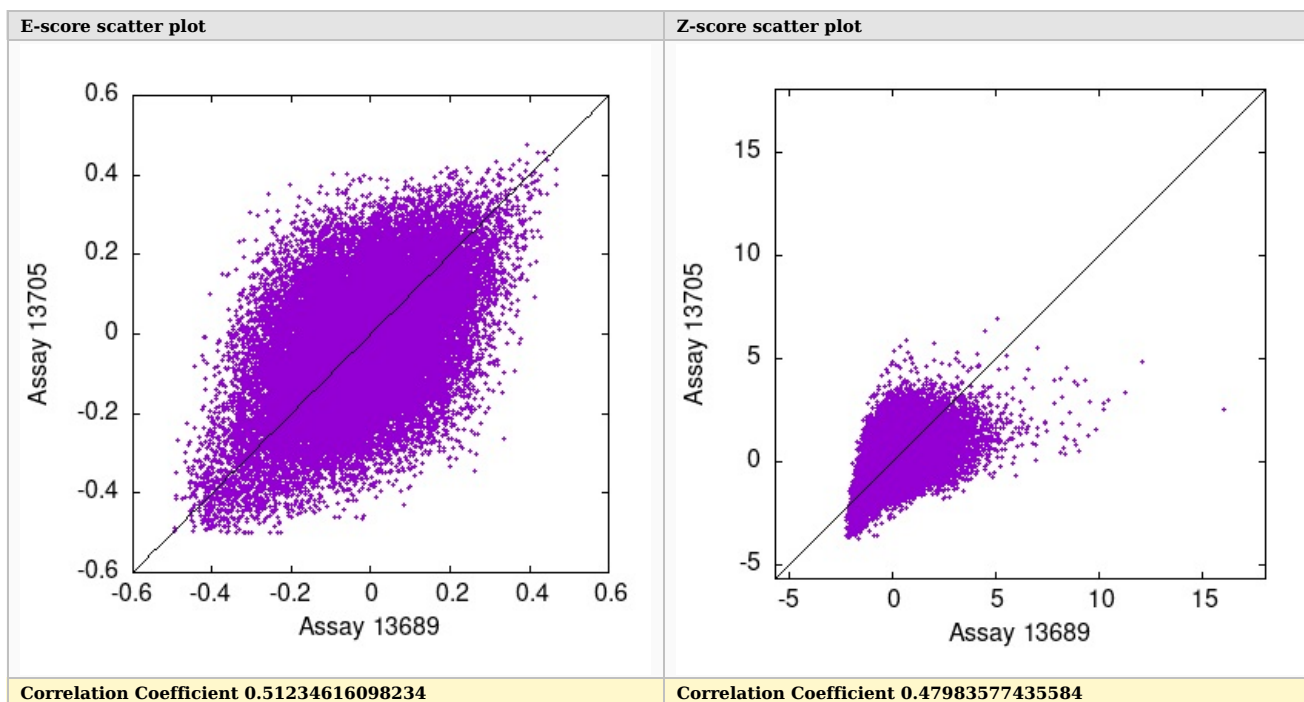




QC report





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'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AAAAACAC	0.46790	--AAAAACAC
AAAAAACA	0.46748	-AAAAAACA-
AAAATAAC	0.44611	AAAATAAC--
ATACAACA	0.44354	-ATACAACA-
GATAAGAC	0.43642	GATAAGAC--
AAATAACC	0.42952	-AAATAACC-
AAACACT	0.42938	-AAACACT-
AAAAGACA	0.42769	-AAAAGACA-
GTGTTT	0.42684	--TAAACAC
AAAAAATA	0.42675	-AAAAAATA-



8 mer Z-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AAAAACAC	16.10903	--AAAAACAC
AAAATAAC	12.10274	AAAATAAC--
ATACAACA	11.25010	-ATACAACA-
GTTATTTA	10.43164	TAAATAAC--
AAAAAACA	10.25211	-AAAAAACA-
ACACACAC	10.23174	--ACACACAC
AAACAACG	9.89062	-AAACAACG-
ATAAACA	9.59003	-ATAAACA-
TAAAAA	9.49169	-TAAAAA-
AAATAACC	9.36848	-AAATAACC-



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'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GATATAAC	0.47755	GATATAAC -
GATAAGAC	0.45848	GATAAGAC -
AAAAAAC	0.45675	AAAAAAC -
ATATAACA	0.43821	-ATATAACA
AAAATAAC	0.43610	AAAATAAC -
AAAAAACC	0.43209	AAAAAACC -
GATAAAC	0.43111	GATAAAC -
AAACAAC	0.42703	AAACAAC -
AAAAGAC	0.41966	AAAAGAC -
ACAAACCA	0.41660	-ACAAACCA

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AAAAAAC	6.94386	AAAAAAC--
GATATAAC	6.31862	GATATAAC--
AATATATT	5.90684	AATATATT--
ACACACCA	5.73294	-ACACACCA-
GAAAAA	5.57524	GAAAAA--
GATAAGAC	5.51107	GATAAGAC--
GGTACACC	5.37806	GGTACACC--
GATATCAC	5.32862	GATATCAC--
AAAAAGAC	5.31106	AAAAAGAC--
ATGTTGTA	5.22736	--TACAACAT