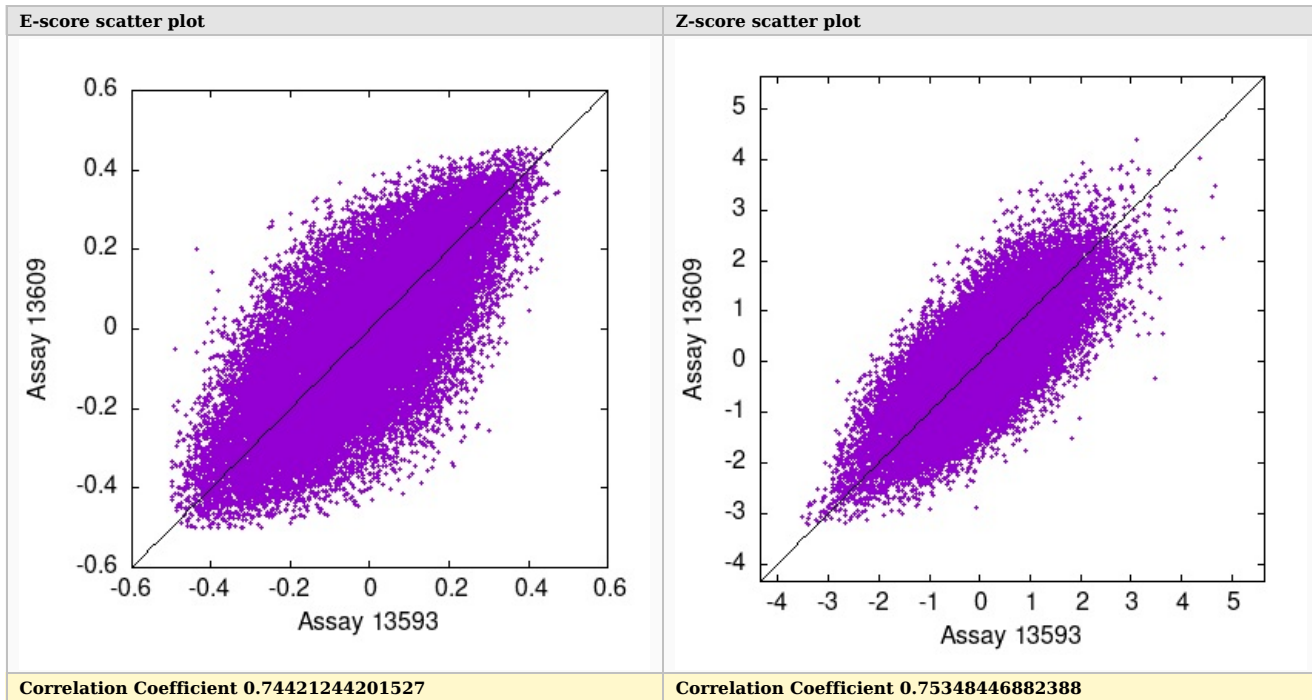


QC report



Top scoring motifs for Assay 13593

Protein ID: pTH14225.1 Gene: DMRTB1.FL Domain: DM 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
ATAATATA	0.47491	--TATATTAT--	ATAATATA	4.81308	--ATAATATA--
ATTATATA	0.46614	TATATAAT----	AAATATAT	4.66159	---AAATATAT-
AATATATT	0.45394	AATATATT----	TATTAATA	4.60997	TATTAATA----
ATATAATA	0.44894	-ATATAATA---	AACAATTA	4.43084	---TAATTGTT-
TATTAATA	0.44788	-TATTAATA---	AATATATT	4.37465	----AATATATT
AAATATAT	0.44585	-ATATATTT---	AATTGTTA	4.04187	--TAACAATT--
ATTTAAAT	0.44454	-ATTTAAAT---	ATATTAAA	3.99970	-TTTAATAT---
AACAATTA	0.43885	----TAATTGTT	ATTATATA	3.98952	--ATTATATA--
ATATTATA	0.43788	--TATAATAT--	AAATATTT	3.93271	--AAATATTT--
AAAAGAAT	0.43424	AAAAGAAT----	ATATAATA	3.92772	---TATTATAT-

Top scoring motifs for Assay 13609

Protein ID: pTH14225.2 Gene: DMRTB1.FL Domain: DM 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
AATAATAA	0.45852	--AATAATAA---	AATAATAA	4.39021	---TTATTATT
AATATTAA	0.45384	--AATATTAA---	AAATATTT	4.02987	---AATATATT-
ATAATAAT	0.45318	--ATAATAAT---	AATATTAA	3.97644	---AATATTAA-
ATTATTAA	0.44912	--TTAATAAT--	TTCATGAA	3.94286	--TTCATGAA--
ACATTATA	0.44909	ACATTATA----	TATTATAA	3.88661	-TATTATAA--
TATTATAA	0.44882	-TATTATAA---	AATAATGT	3.82457	ACATTATT---
AAAATAAT	0.44829	--AAAATAAT--	AAAATAAT	3.81141	---ATTATTTT-
AATATATT	0.44718	--AATATATT--	ATATTAAAT	3.80696	---ATATTAAAT
AATAATGT	0.44702	----AATAATGT	ATTATAAT	3.78847	---ATTATAAT-
TATTAACA	0.44608	---TATTAACA-	ATTATTAA	3.78772	---ATTATTAA-