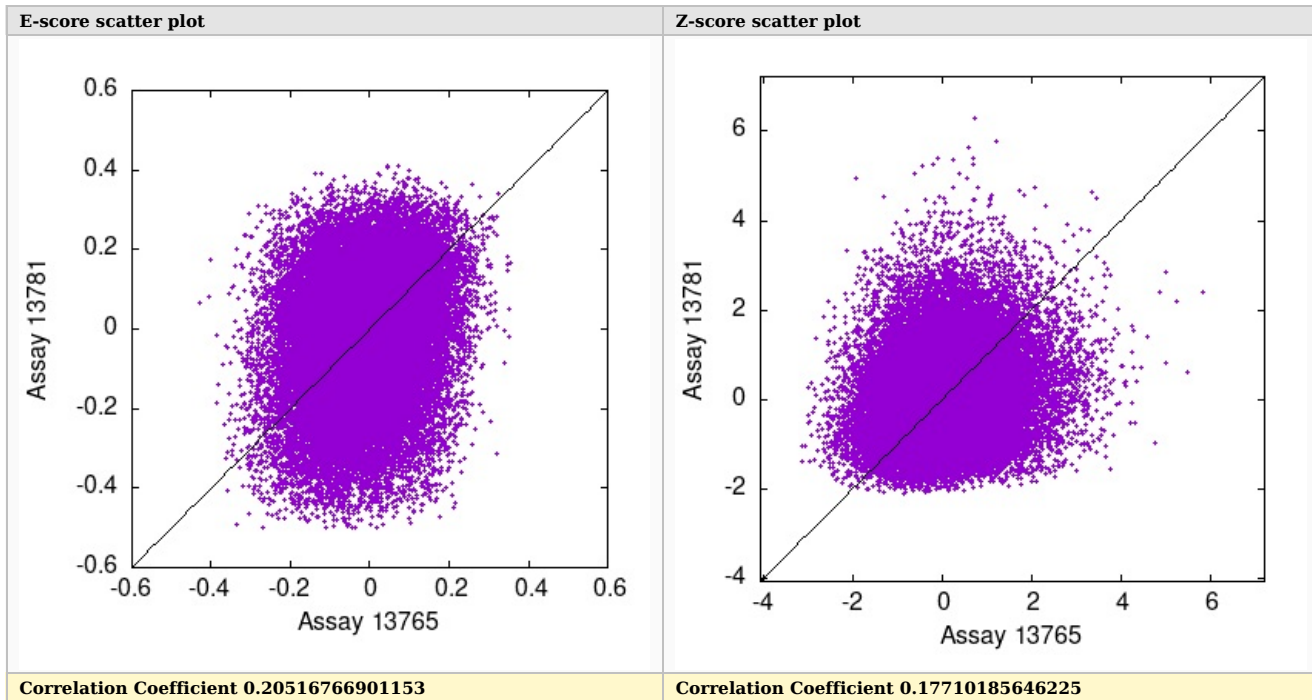


QC report



Top scoring motifs for Assay 13765

Protein ID: pTH14303.1 Gene: GPBP1.FL Domain: Unknown Flag: Reject 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
CGTAACAC	0.35417	-CGTAACAC---	CTAGTGTA	5.82198	----TACACTAG
TATATGGA	0.35212	TCCATATA---	TCCCAACA	5.49679	TCCCAACA----
ATAAATAA	0.34960	-ATAAATAA---	AATAATAG	5.24246	-AATAATAG--
ATAGTCTG	0.34850	---ATAGTCTG	TATGTGAA	5.00282	--TTCACATA--
CAAATACA	0.34719	--CAAATACA--	GGTAATAC	4.99865	-GGTAATAC---
ACAACATC	0.34630	----ACAACATC	ATCGATCA	4.86525	ATCGATCA----
TCCCAACA	0.34041	TCCCAACA----	GTGGGTGA	4.77531	---TAACCCAC-
GTGGGTGA	0.33860	---TAACCCAC-	CGTAACAC	4.59936	-CGTAACAC---
ATATAAAC	0.32326	---ATATAAAC-	AAATAATA	4.44144	AAATAATA----
AATAATAG	0.32129	---AATAATAG-	CAACTTGA	4.35566	---CAACTTGA-

Top scoring motifs for Assay 13781

Protein ID: pTH14303.2 Gene: GPBP1.FL Domain: Unknown Flag: Reject 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
GATGCATC	0.41159	GATGCATC----	TGTTAACA	6.27951	TGTTAACA-----
AGTATACT	0.40843	AGTATACT-----	TCTCGAGA	5.78811	---TCTCGAGA--
ATGCATCA	0.40548	-ATGCATCA----	TAACGTAA	5.64109	---TAACGTAA--
TCTCGAGA	0.40045	-TCTCGAGA----	ATAACGTA	5.38745	--ATAACGTA---
ATGCGCAT	0.39064	-ATGCGCAT----	ATGCATCA	5.38331	---TGATGCAT---
ATACATTA	0.38967	-ATACATTA----	GCATATGC	5.35124	-----GCATATGC
GTTTAAAC	0.38914	----GTTTAAAC-	GATGCATC	5.26041	----GATGCATC-
TAACGTAA	0.38907	-TTACGTTA----	AAGTTAGT	5.24209	-ACTAACTT----
ATTATAAT	0.38593	-----ATTATAAT	CTGTATTA	5.21009	---TAATACAG--
GTACAACA	0.38424	-GTACAACA----	AACAAATC	5.06531	----AACAAATC-