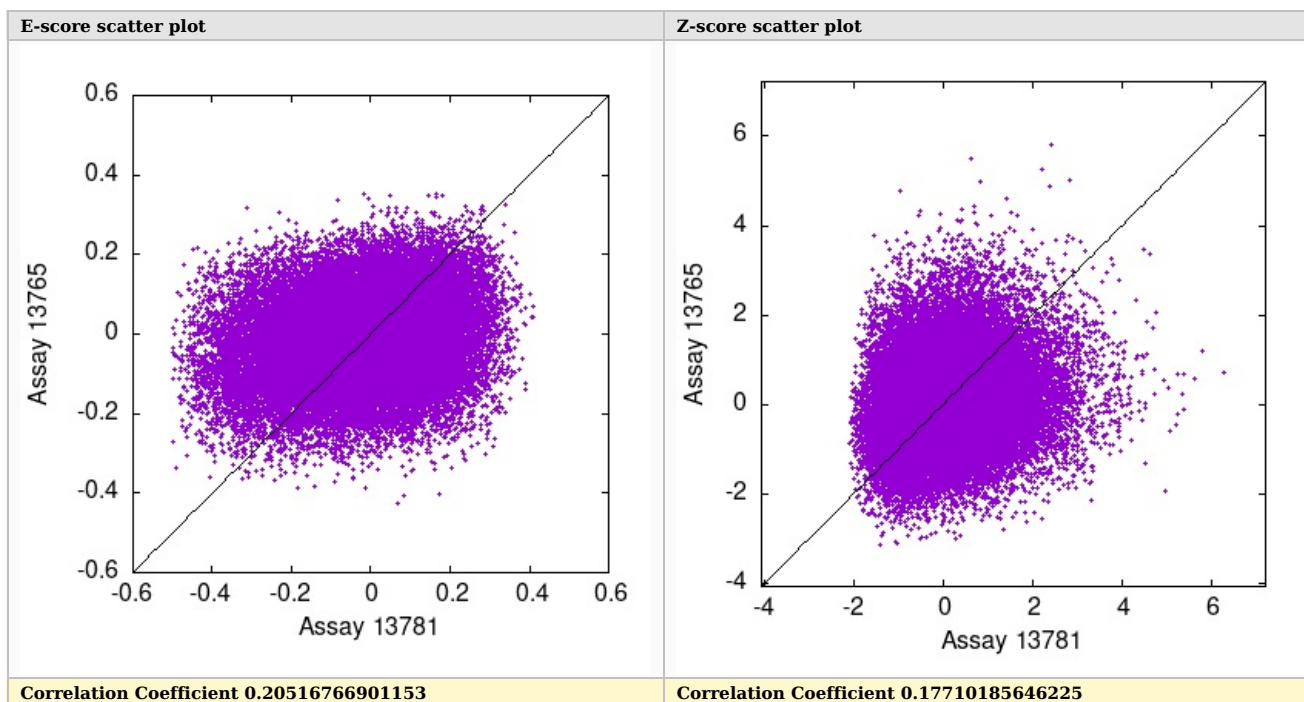


QC report



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'

Forward:

Reverse:



Top 10

Scores

Alignment

GATGCATC	0.41159	GATGCATC-----
AGTATACT	0.40843	AGTATACT-----
ATGCATCA	0.40548	-ATGCATCA-----
TCTCGAGA	0.40045	-TCTCGAGA-----
ATGCGCAT	0.39064	-ATGCGCAT-----
ATACATTA	0.38967	-ATACATTA-----
GTTTAAAC	0.38914	----GTTTAAAC--
TAACGTAA	0.38907	-TTACGTTA-----
ATTATAAT	0.38593	-----ATTATAAT
GTACAACA	0.38424	-GTACAACA-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TGTTAACA	6.27951	TGTTAACA-----
TCTCGAGA	5.78811	---TCTCGAGA--
TAACGTAA	5.64109	---TAACGTAA--
ATAACGTA	5.38745	--ATAACGTA---
ATGCATCA	5.38331	---TGATGCAT--
GCATATGC	5.35124	-----GCATATGC
GATGCATC	5.26041	-----GATGCATC-
AAGTTAGT	5.24209	-ACTAATCTT----
CTGTATTA	5.21009	---TAATACAG--
AACAAATC	5.06531	---AACAAATC--

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'

Forward:

Reverse:



Top 10

Scores

Alignment

CGTAACAC	0.35417	-CGTAACAC---
TATATGGA	0.35212	TCCATATA----
ATAAATAA	0.34960	---ATAAATAA---
ATAGTCTG	0.34850	---ATAGTCTG---
CAAATACA	0.34719	--CAAATACA---
ACAACATC	0.34630	----ACAACATC
TCCCAACA	0.34041	TCCCAACA-----
GTGGGTGA	0.33860	---TAACCCAC---
ATATAAAC	0.32326	---ATATAAAC---
AATAATAG	0.32129	---AATAATAG---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTAGTGTA	5.82198	----TACACTAG
TCCCAACA	5.49679	TCCCAACA----
AATAATAG	5.24246	-AATAATAG---
TATGTGAA	5.00282	--TTCACATA--
GGTAATAC	4.99865	-GGTAATAC---
ATCGATCA	4.86525	ATCGATCA----
GTGGGTGA	4.77531	---TAACCCAC---
CGTAACAC	4.59936	-CGTAACAC---
AAATAATA	4.44144	AAATAATA----
CAACTTGA	4.35566	---CAACTTGA-