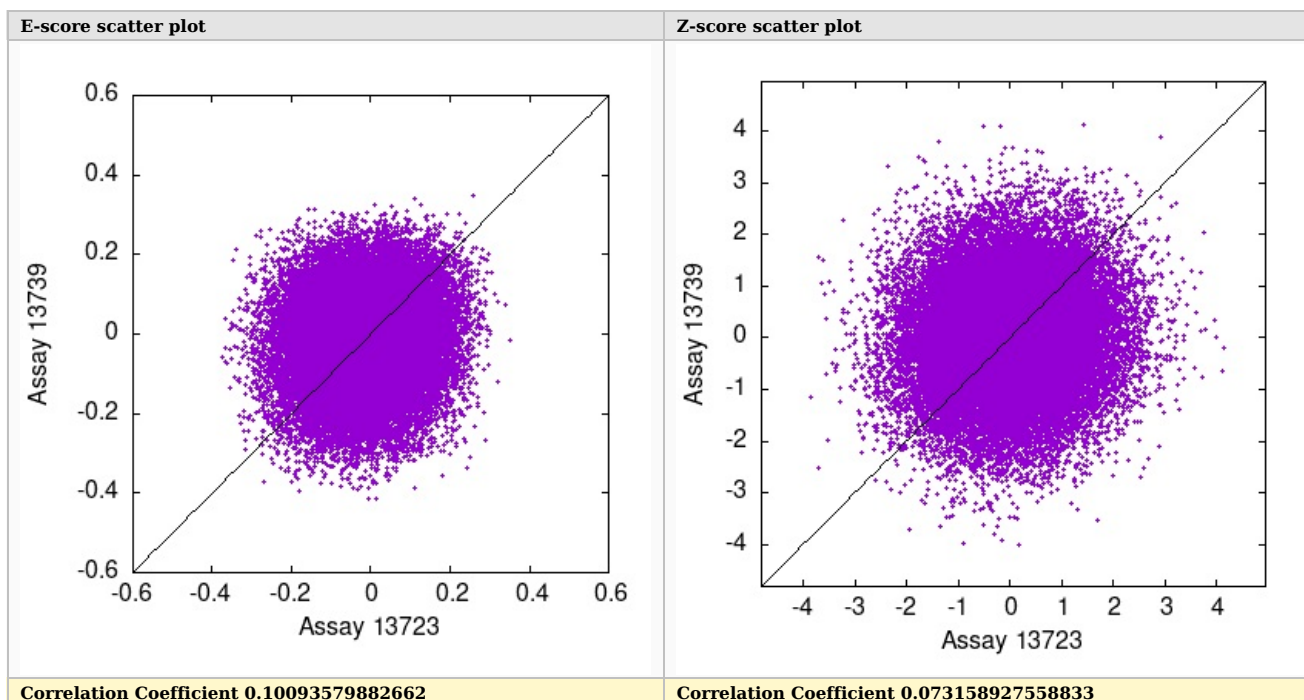


## QC report



### Top scoring motifs for Assay 13723

Protein ID: pTH14305.1 Gene: GPBP1L1.FL Domain: Unknown Flag: Reject Array: 1M-ME

#### 8 mer E-scores for probeset 'all'

Forward:

Reverse:

#### Top 10

#### Scores

#### Alignment

Sequence	Score	Alignment
ATGTCACG	0.34998	CGTGACAT----
GTAACACG	0.34144	-GTAACACG---
GCATCGAA	0.32143	----GCATCGAA
ATAGAGAT	0.31899	-ATCTCTAT---
AATCAATG	0.31312	CATTGATT----
AACACGAG	0.30679	-AACACGAG---
TAACAGCA	0.30011	--TAACAGCA--
ATGTATAA	0.30000	ATGTATAA----
TCCAGCCA	0.29782	---TCCAGCCA-
ATTACAAC	0.29705	-ATTACAAC---

#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:

#### Top 10

#### Scores

#### Alignment

Sequence	Score	Alignment
ATGTCACG	4.13534	-CGTGACAT----
ATAGAGAT	4.11204	--ATAGAGAT---
GTAACACG	3.98725	---GTAACACG---
AGATATAT	3.95398	ATATATCT-----
ATAACAGC	3.79799	--ATAACAGC---
ATTACAAC	3.76845	---ATTACAAC---
ACGGTCAA	3.72603	---TTGACCGT---
GCATCGAA	3.69649	-----GCATCGAA
CAATGTTC	3.69192	---GAACATTG---
TAACAGCA	3.62037	---TAACAGCA--

### Top scoring motifs for Assay 13739

Protein ID: pTH14305.2 Gene: GPBP1L1.FL Domain: Unknown Flag: Reject Array: 1M-HK

#### 8 mer E-scores for probeset 'all'

Forward:

Reverse:

#### Top 10

#### Scores

#### Alignment

Sequence	Score	Alignment
CGGATCCG	0.34938	-----CGGATCCG-
AAAGTTGT	0.33947	----AAAGTTGT---
GCAAAAAA	0.32680	--GCAAAAAA-----
CAGTACAA	0.32327	-----CAGTACAA--
GATGCTTA	0.31941	----TAAGCATC---
ATGCAAAA	0.31539	ATGCAAAA-----
GCAATGA	0.31422	---GCAATGA----
ACTGATAT	0.30938	-----ATATCAGT
AAAATATC	0.30629	----AAAATATC---
GTAATTAC	0.30506	----GTAATTAC---

#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:

#### Top 10

#### Scores

#### Alignment

Sequence	Score	Alignment
AGTTAACT	4.12263	AGTTAACT---
AACAACCTA	4.09666	-AACAACCTA--
CAACTGCA	4.07481	---CAACTGCA
CGGATCCG	3.89115	-CGGATCCG--
AAATAACG	3.77905	AAATAACG---
AACATACT	3.67281	-AACATACT---
GCAAAAAA	3.65919	--GCAAAAAA--
AAAACCTA	3.60710	-AAAACCTA---
CTGTTTTT	3.60045	-GAAAACAG---
CATCACTA	3.58557	-CATCACTA--