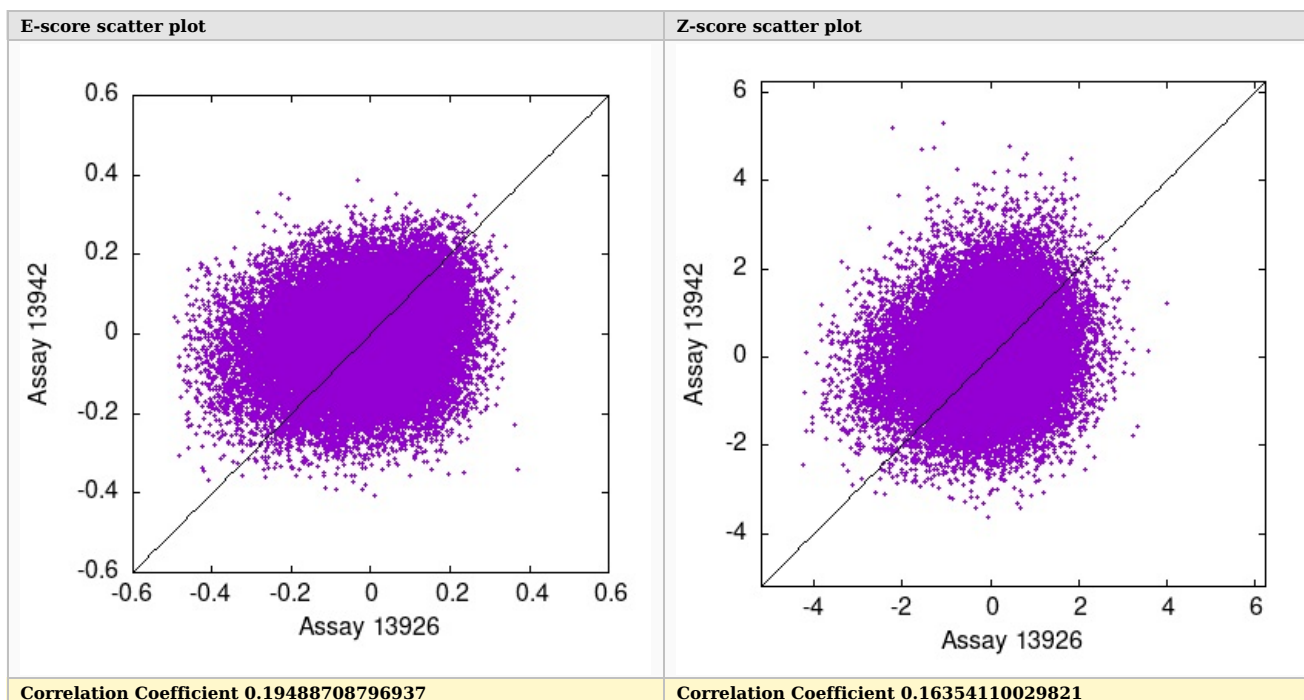


## QC report



### Top scoring motifs for Assay 13926

Protein ID: pTH14235.1 Gene: GTF2IRD2B Domain: GTF2I Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



Top 10	Scores	Alignment
CAAATTTG	0.36901	-CAAATTTG----
ACATATGT	0.36411	ACATATGT-----
AATTGTTA	0.36152	--AATTGTTA--
GTTGGAAC	0.35908	---GTTGGAAC--
GTACGTAC	0.35840	---GTACGTAC--
AACGCGTT	0.35463	-AACGCGTT----
ATTGAAA	0.34889	--ATTGAAA---
ATTGTACA	0.34314	---ATTGTACA--
ATAATATA	0.33852	---TATATTAT--
TGTTAACA	0.33467	-----TGTTAACA

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

Forward:

Reverse:



Top 10	Scores	Alignment
AACGCGTT	3.99124	-AACGCGTT---
AGTAATGA	3.59397	--AGTAATGA--
ACATATGT	3.32919	--ACATATGT--
CGACATGA	3.23306	---CGACATGA--
CAATTATA	3.22789	----CAATTATA
CAAATTTG	3.22350	---CAAATTTG--
AACGAATT	3.22334	-AACGAATT---
ATTGTACA	3.14230	TGTACAAT----
AACATTAA	3.10740	---TTAATGTT-
GATTAATC	3.09752	-GATTAATC---

### Top scoring motifs for Assay 13942

Protein ID: pTH14235.2 Gene: GTF2IRD2B Domain: GTF2I Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



Top 10	Scores	Alignment
TAAATTTA	0.38720	TAAATTTA---
TATATTGA	0.35311	TCAATATA---
ACCCACCC	0.35152	---ACCCACCC
ATACAAAA	0.34984	---ATACAAAA
ATGGGAGG	0.33909	--ATGGGAGG--
AGAATGCA	0.33538	---AGAATGCA
AAATTTAA	0.32815	-AAATTTAA--
CGTCACAA	0.32415	TTGTGACG---
AAGACAGC	0.32285	--AAGACAGC-
CTGCTTTA	0.31998	-TAAGACAG--

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

Forward:

Reverse:



Top 10	Scores	Alignment
AAGACAGC	5.29232	---AAGACAGC--
ATGGGAGG	5.19781	---ATGGGAGG--
GGTAATAC	4.77979	GGTAATAC-----
AAATGCCT	4.76203	---AGGCATT--
ACCCACCC	4.72609	----ACCCACCC-
AGAATGCA	4.58907	----AGAATGCA-
TAAATTTA	4.50746	-TAAATTTA----
ATACAAAA	4.49266	----ATACAAAA-
ACTCCTCT	4.26050	----ACTCCTCT-
GACAAACA	4.22075	-----GACAAACA