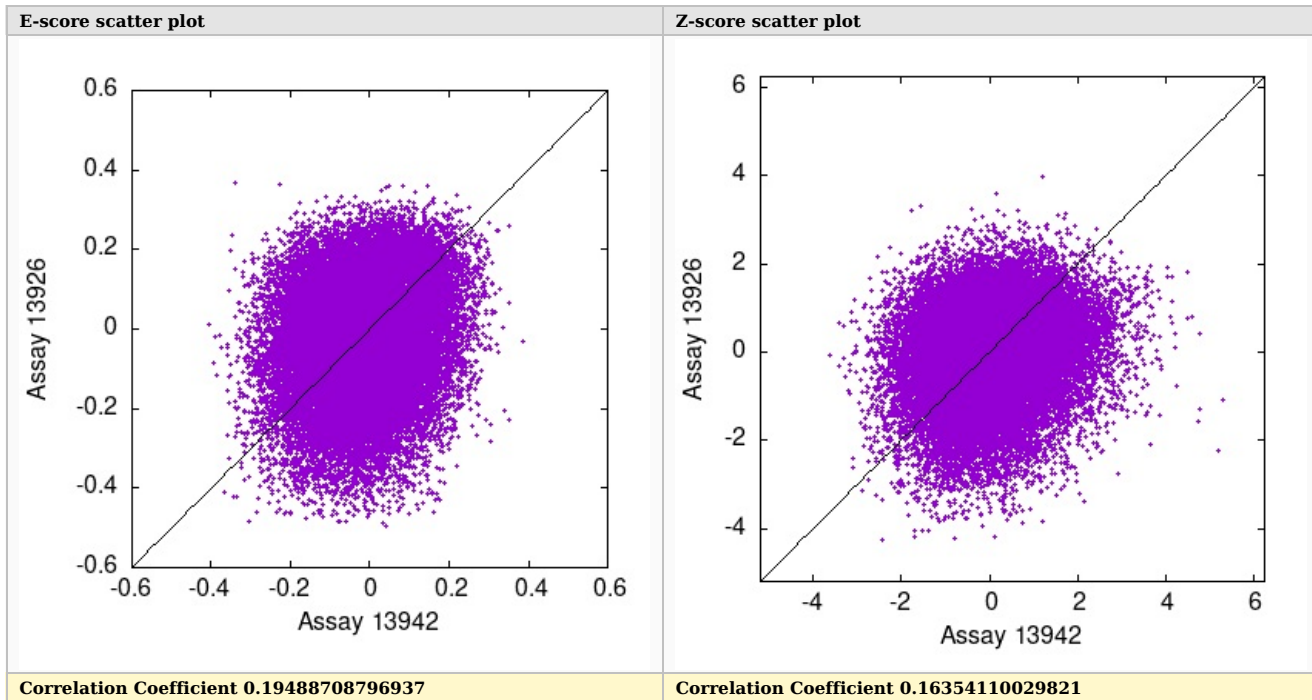


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TAAATTTA	0.38720	TAAATTTA---	AAGACAGC	5.29232	---AAGACAGC--
TATATTGA	0.35311	TCAATATA---	ATGGGAGG	5.19781	---ATGGGAGG--
ACCCACCC	0.35152	---ACCCACCC	GGTAATAC	4.77979	GGTAATAC----
ATACAAAA	0.34984	---ATACAAAA	AAATGCCT	4.76203	---AGGCATT--
ATGGGAGG	0.33909	--ATGGGAGG-	ACCCACCC	4.72609	----ACCCACCC-
AGAATGCA	0.33538	---AGAATGCA	AGAATGCA	4.58907	----AGAATGCA-
AAATTTAA	0.32815	-AAATTTAA--	TAAATTTA	4.50746	-TAAATTTA----
CGTCACAA	0.32415	TTGTGACG---	ATACAAAA	4.49266	----ATACAAAA
AAGACAGC	0.32285	--AAGACAGC-	ACTCCTCT	4.26050	----ACTCCTCT-
CTGTCTTA	0.31998	-TAAGACAG--	GACAAACA	4.22075	-----GACAAACA

### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CAAATTTG	0.36901	-CAAATTTG----	AACGCGTT	3.99124	-AACGCGTT---
ACATATGT	0.36411	ACATATGT-----	AGTAATGA	3.59397	--AGTAATGA--
AATTGTTA	0.36152	---AATTGTTA---	ACATATGT	3.32919	--ACATATGT--
GTTTGAAC	0.35908	---GTTTGAAC--	CGACATGA	3.23306	---CGACATGA-
GTACGTAC	0.35840	---GTACGTAC--	CAATTATA	3.22789	----CAATTATA
AACGCGTT	0.35463	-AACGCGTT----	CAAATTTG	3.22350	---CAAATTTG-
ATTTGAAA	0.34889	--ATTTGAAA---	AACGAATT	3.22334	-AACGAATT---
ATTGTACA	0.34314	---ATTGTACA--	ATTGTACA	3.14230	TGTACAAT----
ATAATATA	0.33852	---TATATTAT--	AACATTAA	3.10740	---TTAATGTT-
TGTTAACA	0.33467	-----TGTTAACA	GATTAATC	3.09752	-GATTAATC---