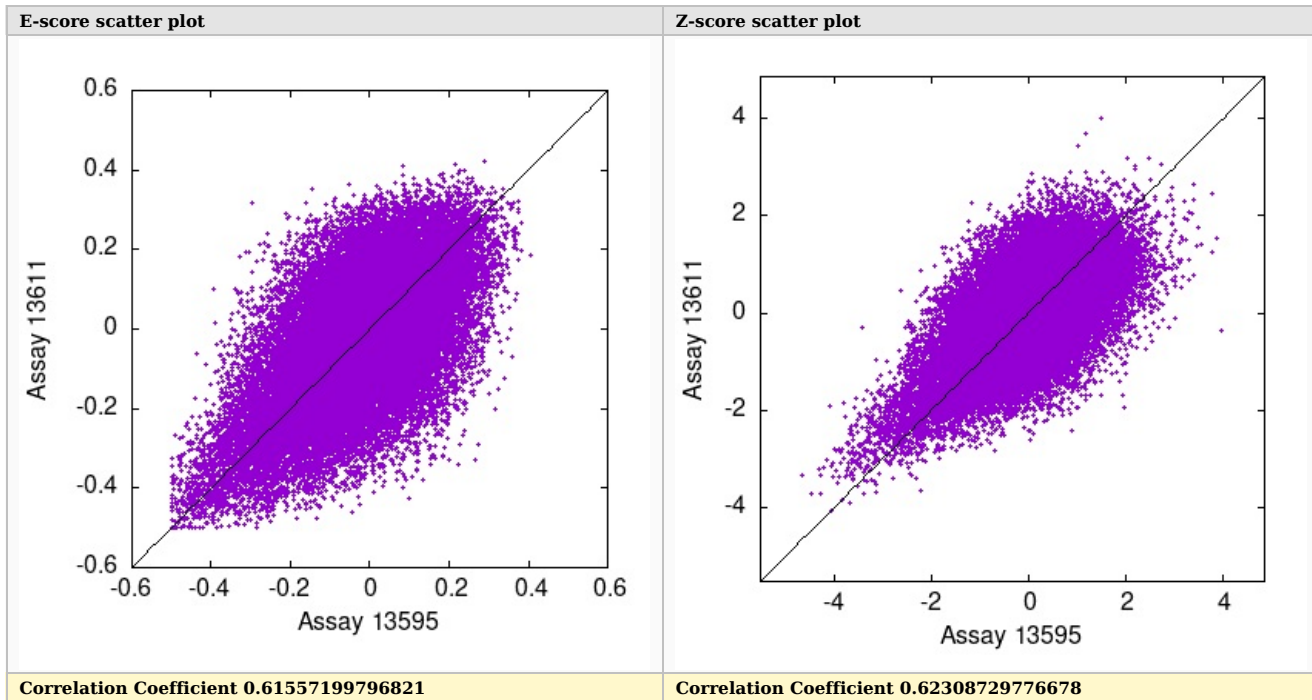


QC report



Top scoring motifs for Assay 13595

Protein ID: pTH14292.1 Gene: CSRNPI.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
CAAATTTG	0.40650	CAAATTTG----	GACGCGTC	3.95376	--GACGCGTC--
ATTGTGAC	0.38123	---ATTGTGAC-	TGTATACA	3.87855	TGTATACA----
CGAATTCG	0.38065	CGAATTCG----	AACATGTT	3.77897	--AACATGTT--
AACATGTT	0.37656	--AACATGTT--	ATGTTAAC	3.77897	-GTTAACAT---
ACAACAAT	0.37628	---ATTGTTGT-	ATACACAT	3.55038	-ATACACAT---
AATGCATT	0.37398	---AATGCATT	CAAATTTG	3.47557	----CAAATTTG
ATACAACA	0.37384	---TGTGTAT-	CGAATTCG	3.44361	----CGAATTCG
ACATATAT	0.37282	-ATATATGT---	TGTTAACA	3.40674	TGTTAACA----
TGTATACA	0.37166	---TGTATACA	AAGTACTT	3.38591	-AAGTACTT---
CGTTTCGA	0.36948	--CGTTTCGA--	ACATATGT	3.38113	---ACATATGT-

Top scoring motifs for Assay 13611

Protein ID: pTH14292.2 Gene: CSRNPI.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
TCACGTGA	0.42290	---TCACGTGA-	ATTATAAT	3.98652	----ATTATAAT
ATTATAAT	0.41325	----ATTATAAT	TATTATAA	3.67165	---TATTATAA-
TATTATAA	0.41031	---TATTATAA-	AATTAAA	3.42753	---AATTAAA-
ACTAACAT	0.39836	----ACTAACAT	TCACGTGA	3.18579	---TCACGTGA-
TATTAATA	0.39762	---TATTAATA-	ACTAACAT	3.16076	----ACTAACAT
ATTGCTAC	0.39240	---ATTGCTAC	TATTAATA	3.04527	---TATTAATA-
CTGTATTA	0.39085	CTGTATTA----	AAAACAAT	3.01903	----AAAACAAT
TATTTGCA	0.38839	---TATTTGCA-	AAAATTTT	2.96644	-AAAATTTT---
AATTGCAA	0.38593	---AATTGCAA-	ACACATTA	2.88884	ACACATTA----
ACACATTA	0.38401	ACACATTA----	TATTTGCA	2.88483	---TATTTGCA-