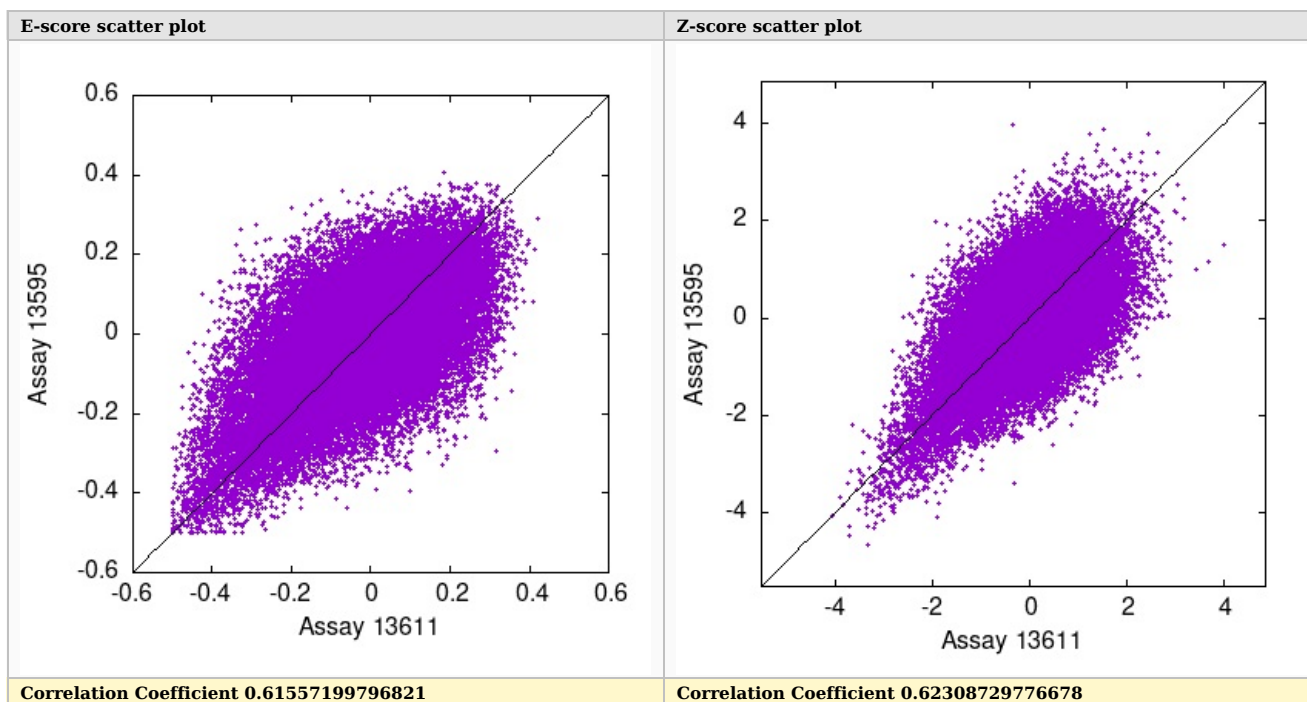


QC report



Top scoring motifs for Assay 13611

Protein ID: pTH14292.2 Gene: CSRN1.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TCACGTGA	0.42290	---TCACGTGA-
ATTATAAT	0.41325	---ATTATAAT
TATTATAA	0.41031	---TATTATAA-
ACTAACAT	0.39836	---ACTAACAT
TATTAATA	0.39762	---TATTAATA-
ATTGCTAC	0.39240	---ATTGCTAC
CTGTATTA	0.39085	CTGTATTA----
TATTGCA	0.38839	---TATTGCA-
AATTGCAA	0.38593	---AATTGCAA-
ACACATTA	0.38401	ACACATTA----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ATTATAAT	3.98652	----ATTATAAT
TATTATAA	3.67165	---TATTATAA-
AATTTAAA	3.42753	---AATTTAAA-
TCACGTGA	3.18579	---TCACGTGA-
ACTAACAT	3.16076	---ACTAACAT
TATTAATA	3.04527	---TATTAATA-
AAAACAAT	3.01903	----AAAACAAT
AAAATTTT	2.96644	---AAAATTTT---
ACACATTA	2.88884	ACACATTA----
TATTGCA	2.88483	---TATTGCA-

Top scoring motifs for Assay 13595

Protein ID: pTH14292.1 Gene: CSRN1.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CAAATTG	0.40650	CAAATTG----
ATTTGTAC	0.38123	---ATTTGTAC-
CGAATTCG	0.38065	CGAATTCG----
AACATGTT	0.37656	---AACATGTT--
ACAACAAT	0.37628	---ATTGTTGT-
AATGCATT	0.37398	---AATGCATT
ATACAACA	0.37384	---TGTTGTAT-
ACATATAT	0.37282	---ATATATGT---
TGTATACA	0.37166	---TGTATACA-
CGTTTCGA	0.36948	--CGTTTCGA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GACGCGTC	3.95376	--GACGCGTC--
TGTATACA	3.87855	TGTATACA----
AACATGTT	3.77897	--AACATGTT--
ATGTTAAC	3.77897	-GTTAACAT---
ATACACAT	3.55038	-ATACACAT---
CAAATTG	3.47557	----CAAATTG
CGAATTCG	3.44361	----CGAATTCG
TGTTAACA	3.40674	TGTTAACA----
AAGTACTT	3.38591	--AAGTACTT---
ACATATGT	3.38113	---ACATATGT-