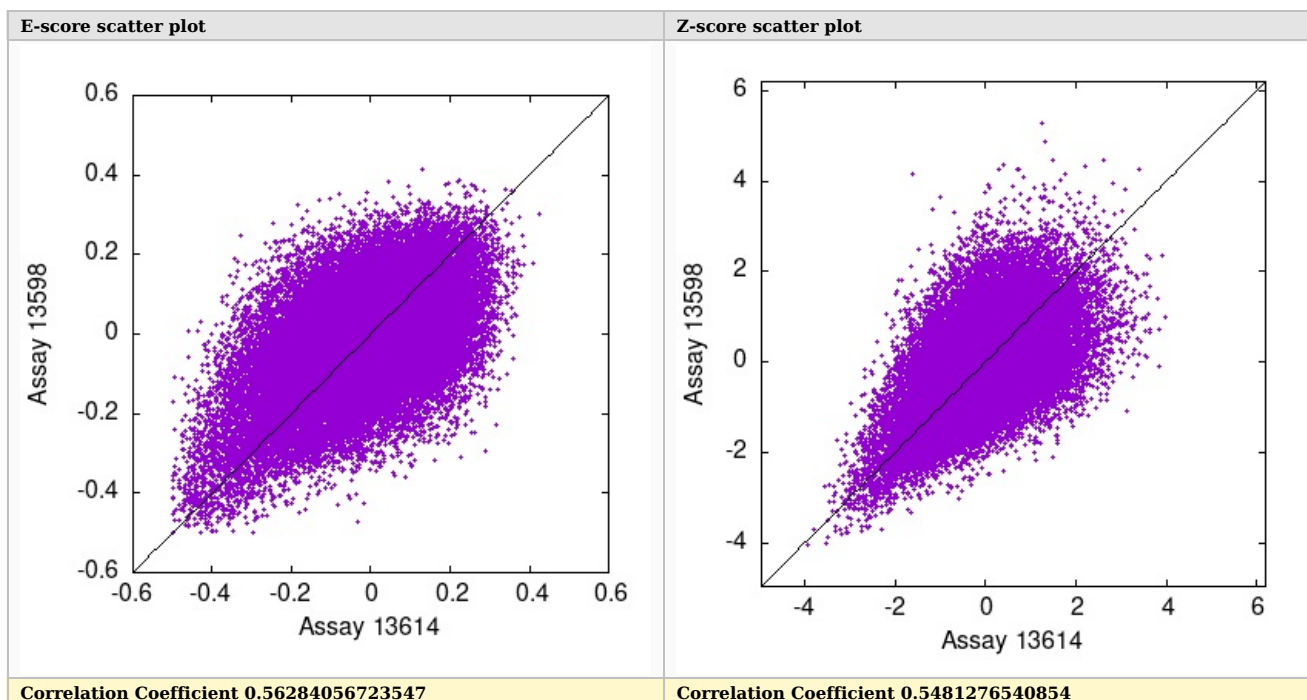


## QC report



### Top scoring motifs for Assay 13614

Protein ID: pTH14295.2 Gene: CSRN2.DBD Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



Top 10	Scores	Alignment
AAACGTTT	0.42558	----AAACGTTT
AGTTGCAT	0.41073	---AGTTGCAT-
GATATCAA	0.38797	--GATATCAA--
ATTATAAT	0.38767	---ATTATAAT-
AAATCGAT	0.38152	---AAATCGAT-
ACGTATTG	0.37910	---CAATACGT-
AATATTAA	0.37522	---AATATTAA--
GTTATAAC	0.37381	GTTATAAC----
TACAATCA	0.37047	-TACAATCA---
AATGCATT	0.37001	----AATGCATT

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

Forward:

Reverse:



Top 10	Scores	Alignment
ACGTATTG	3.98351	---ACGTATTG
AAACGTTT	3.92061	-AAACGTTT--
AATATTAA	3.84932	--TTAATATT-
GATTAATA	3.83525	--GATTAATA-
AATGCATT	3.79116	--AATGCATT-
AGTCGACT	3.65107	-AGTCGACT--
AGTTGCAT	3.64432	-AGTTGCAT--
ATTATATC	3.63770	--ATTATATC-
CGATAACA	3.62017	CGATAACA---
TAGTTGCA	3.59927	TAGTTGCA---

### Top scoring motifs for Assay 13598

Protein ID: pTH14295.1 Gene: CSRN2.DBD Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



Top 10	Scores	Alignment
CAAATTTG	0.41504	-----CAAATTTG
AAGTACTT	0.38614	---AAGTACTT----
TGTGCACA	0.38304	---TGTGCACA----
TAACAGTA	0.38184	---TACTGTTA----
TGTATACA	0.37954	---TGTATACA----
ATGCATCA	0.37615	---TGATGCAT----
AACAACGC	0.37536	--GCGTTGTT-----
TTTCGAAA	0.37192	---TTTCGAAA----
TGTTGCAA	0.37132	---TGTTGCAA----
ACCGGTTA	0.37105	ACCGGTTA-----

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

Forward:

Reverse:



Top 10	Scores	Alignment
TTTCGAAA	5.26563	--TTTCGAAA--
TAACAGTA	4.88139	-TAACAGTA---
AAGTACTT	4.46267	---AAGTACTT
GCGCAACA	4.45934	---GCGCAACA
AGACGCTC	4.36111	AGACGCTC----
CATATATG	4.32629	---CATATATG-
TGTATACA	4.26722	--TGTATACA--
TCGAGTAA	4.24981	--TCGAGTAA--
AACGCGTT	4.24404	-AACGCGTT---
GTGCGCAC	4.24313	--GTGCGCAC--