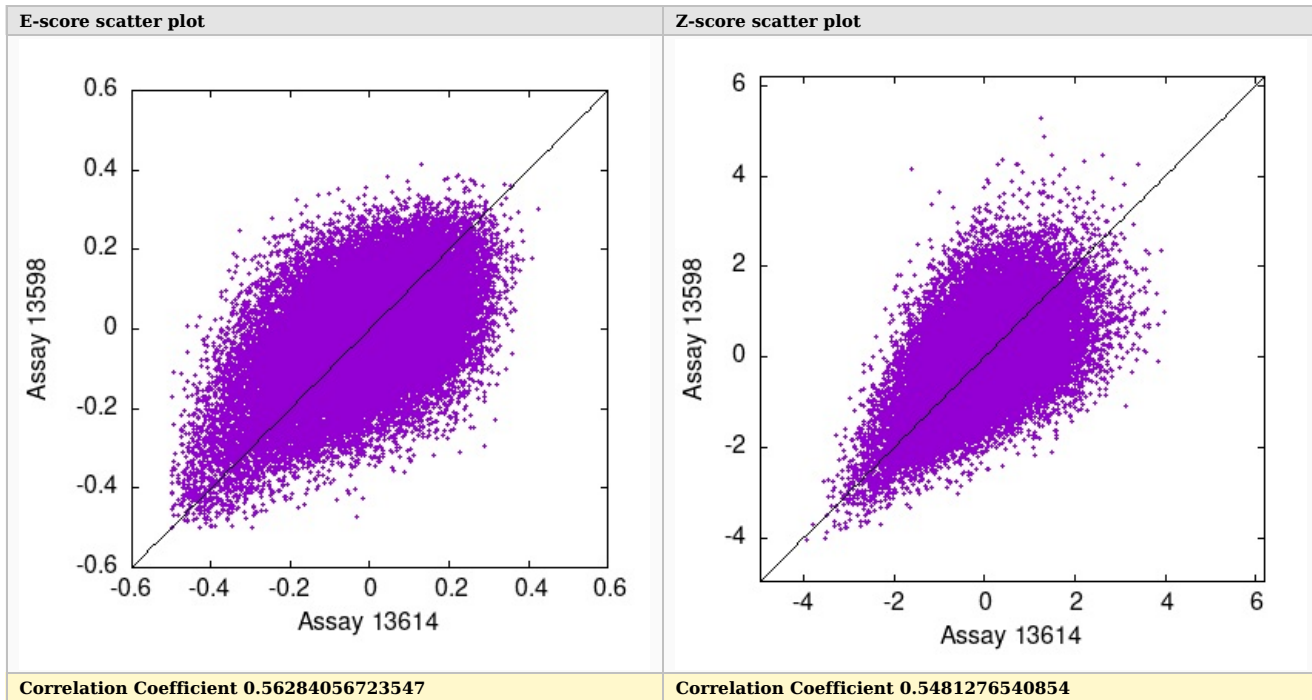


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AAACGTTT	0.42558	----AAACGTTT	ACGTATTG	3.98351	---ACGTATTG
AGTTGCAT	0.41073	---AGTTGCAT-	AAACGTTT	3.92061	-AAACGTTT--
GATATCAA	0.38797	--GATATCAA--	AATATTAA	3.84932	--TTAATATT-
ATTATAAT	0.38767	---ATTATAAT-	GATTAATA	3.83525	--GATTAATA-
AAATCGAT	0.38152	---AAATCGAT-	AATGCATT	3.79116	--AATGCATT-
ACGTATTG	0.37910	---CAATACGT-	AGTCGACT	3.65107	-AGTCGACT--
AATATTAA	0.37522	---AATATTAA--	AGTTGCAT	3.64432	-AGTTGCAT--
GTTATAAC	0.37381	GTTATAAC----	ATTATATC	3.63770	--ATTATATC-
TACAATCA	0.37047	-TACAATCA---	CGATAACA	3.62017	CGATAACA---
AATGCATT	0.37001	----AATGCATT	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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CAAATTTG	0.41504	-----CAAATTTG	TTTCGAAA	5.26563	--TTTCGAAA--
AAGTACTT	0.38614	---AAGTACTT----	TAACAGTA	4.88139	-TAACAGTA---
TGTGCACA	0.38304	---TGTGCACA----	AAGTACTT	4.46267	----AAGTACTT
TAACAGTA	0.38184	---TACTGTTA----	GCGCAACA	4.45934	----GCGCAACA
TGTATACA	0.37954	---TGTATACA----	AGACGCTC	4.36111	AGACGCTC----
ATGCATCA	0.37615	---TGATGCAT----	CATATATG	4.32629	---CATATATG-
AACAACGC	0.37536	--GCGTTGTT-----	TGTATACA	4.26722	--TGTATACA--
TTTCGAAA	0.37192	---TTTCGAAA----	TCGAGTAA	4.24981	--TCGAGTAA--
TGTTGCAA	0.37132	---TGTTGCAA----	AACGCGTT	4.24404	-AACGCGTT---
ACCGGTTA	0.37105	ACCGGTTA-----	GTGCGCAC	4.24313	--GTGCGCAC--