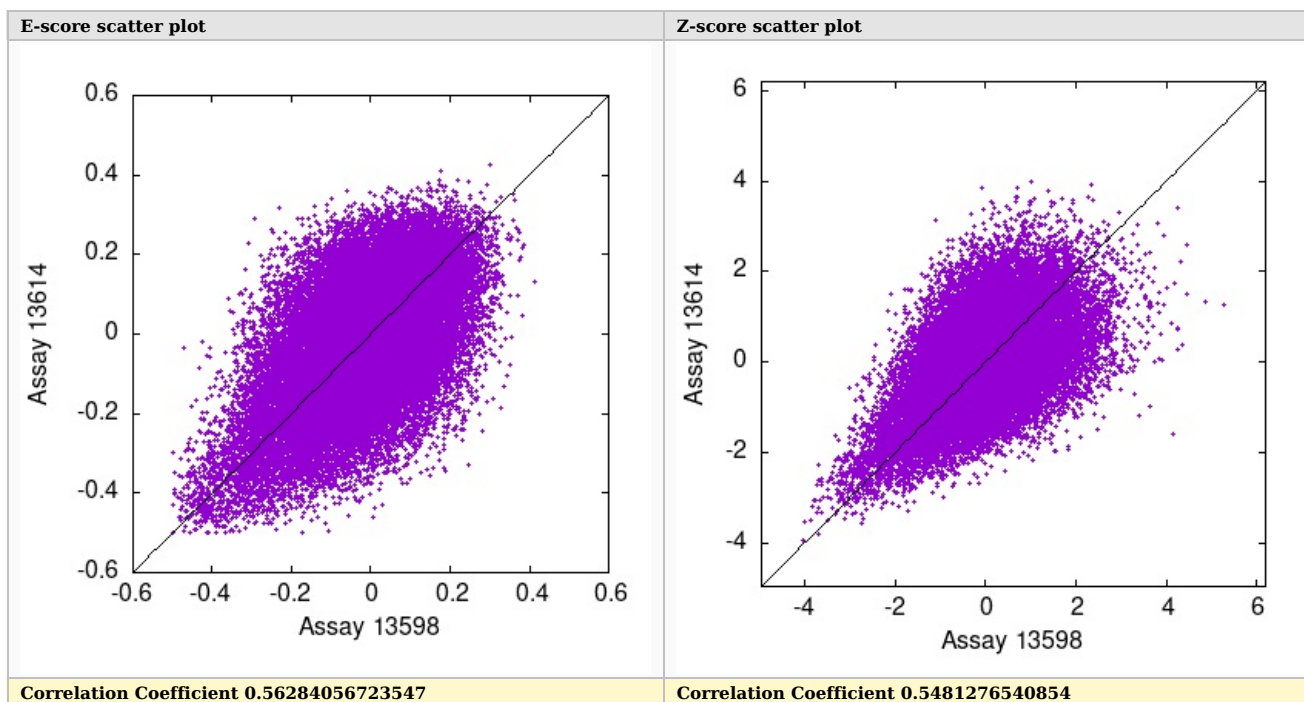


QC report



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---	AGACGTCT	4.36111	AGACGTCT----
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--

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---