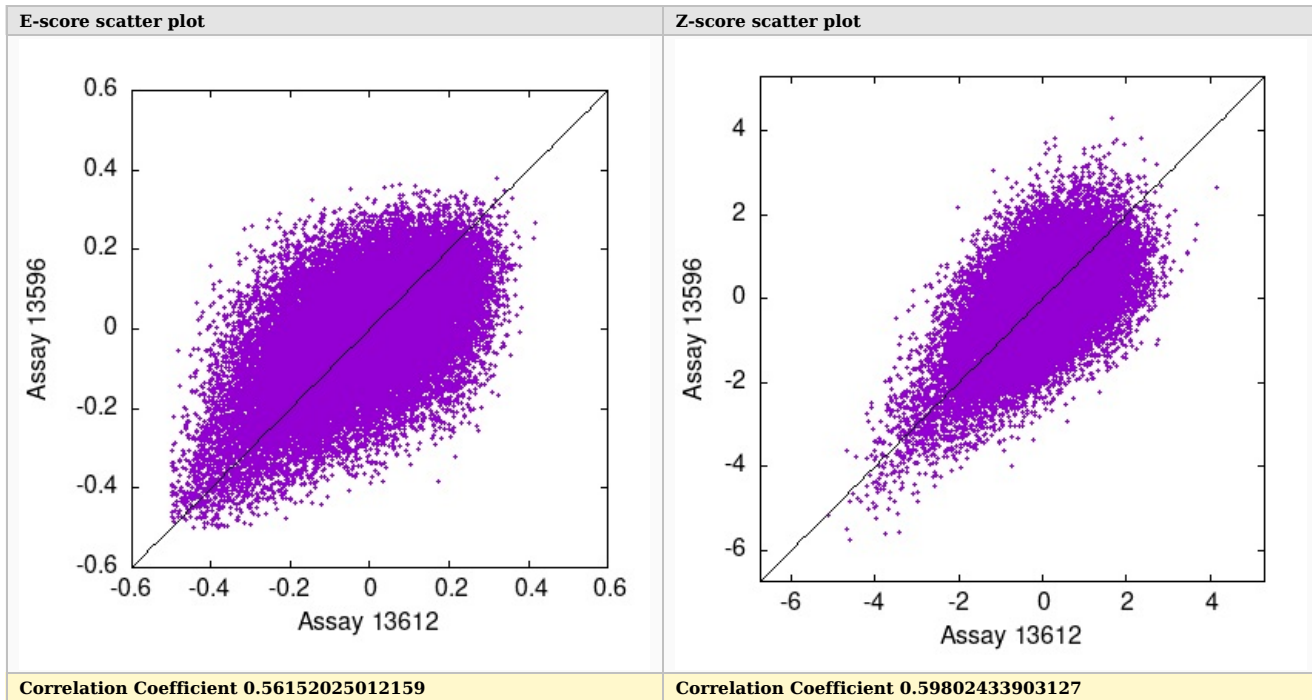


## QC report



### Top scoring motifs for Assay 13612

Protein ID: pTH14293.2 Gene: CSRN1.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	0.41560	--AAACGTTT--	AAACGTTT	4.17595	AAACGTTT--
GTCATGAC	0.41356	-GTCATGAC--	ATAATGTA	3.66373	--TACATTAT
GAATATTC	0.38411	GAATATTC--	GTCATGAC	3.66113	-GTCATGAC
CATAGACA	0.37948	---TGCTATG	CACACAGA	3.47266	-CACACAGA
GATATGTA	0.37790	-GATATGTA--	ATTATAAT	3.46298	-ATTATAAT
ATAATGTA	0.37732	-ATAATGTA--	TACGTCAA	3.32590	-TACGTCAA
GTATGTTA	0.37400	--GTATGTTA--	GAAATTC	3.17118	-GAAATTC
GACAAACA	0.37079	-GACAAACA--	TAATAATA	3.14059	TAATAATA
GAAATTC	0.36833	-GAAATTC--	AATATTAA	3.06690	-AATATTAA
ACTATTGA	0.36798	-ACTATTGA--	GAATATTC	3.04781	GAATATTC-

### Top scoring motifs for Assay 13596

Protein ID: pTH14293.1 Gene: CSRN1.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
TTTCGAAA	0.37894	--TTTCGAAA--	AACATGTT	4.29626	--AACATGTT--
AACAACGC	0.36205	---AACAACGC--	ACATGTTA	3.84373	---ACATGTTA--
CAAATTTG	0.36038	-----CAAATTTG	ATGTACAT	3.82259	-ATGTACAT---
ATGTATAA	0.35915	ATGTATAA-----	TTTGCAAA	3.78273	TTTGCAAA----
ACATGTTA	0.35588	----ACATGTTA--	ATACACAT	3.73928	-ATACACAT---
CGACATGA	0.35216	---CGACATGA---	CTGTATAC	3.70940	-GTATACAG---
ATGACACA	0.34886	-ATGACACA----	CATATATG	3.69968	--CATATATG--
TCGCGCGA	0.34717	TCGCGCGA-----	ATGACACA	3.65368	ATGACACA----
CGTTAATA	0.34687	---TATTAACG--	GTTTCAAC	3.64318	-GTTTCAAC---
GTACAAAC	0.34567	--GTACAAAC---	CAAATTTG	3.60835	----CAAATTTG