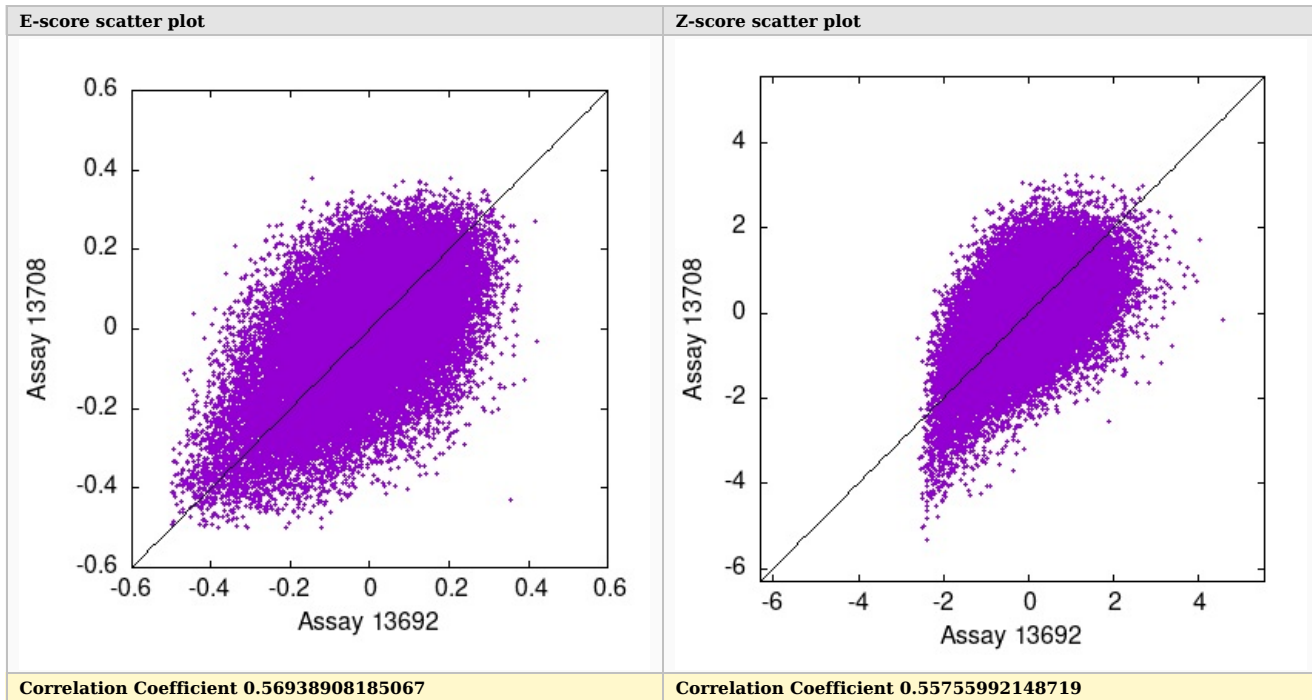


QC report



Top scoring motifs for Assay 13692

Protein ID: pTH13928.1 Gene: SGSM2.DBD Domain: zf-BED 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
AACATGTT	0.42263	AACATGTT-----	AACATGTT	4.56457	AACATGTT---
TAAATTTA	0.41608	----TAAATTTA----	GTTGCAAC	4.03121	--GTTGCAAC--
AATTCGAA	0.39118	-----TTCGAATT--	TGTGCACA	3.94177	TGTGCACA---
GCAATTGC	0.37699	-----GCAATTGC--	TAAATTTA	3.87385	TAAATTTA---
ATGTACAT	0.37311	----ATGTACAT----	ACTATAGT	3.73834	--ACTATAGT--
TTGTACAA	0.37152	----TTGTACAA----	GCAATTGC	3.66229	GCAATTGC---
ATTCGAAT	0.37151	----ATTCGAAT----	TTGTACAA	3.64974	---TTGTACAA--
GTTGCAAC	0.37037	----GTTGCAAC----	ATTTATTG	3.55070	---ATTTATTG--
TGTTGCAA	0.36932	----TGTTGCAA----	TAACAGTA	3.44958	TAACAGTA---
GTATAATA	0.36670	----TATTATAC----	ATTCGAAT	3.41695	--ATTCGAAT--

Top scoring motifs for Assay 13708

Protein ID: pTH13928.2 Gene: SGSM2.DBD Domain: zf-BED 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
AGTTTTTC	0.38012	---AGTTTTTC--	TATTTGCA	3.23367	----TGCAAATA--
TATTTGCA	0.37927	-----TGCAAATA	TATAAGCA	3.23262	----TGCTTATA--
TTCATGAA	0.37212	---TTCATGAA----	ACAATTTG	3.19088	-----CAAATTGT
CGTAACAA	0.37207	-----CGTAACAA	ATATGTGC	3.16268	---GCACATAT---
ACTTTCTA	0.36948	TAGAAAGT-----	ATACATAT	3.08935	---ATACATAT---
AAAGCTTA	0.36273	---AAAGCTTA---	ATCATACA	3.08371	ATCATACA-----
AATGTAAC	0.36079	---AATGTAAC---	TTCATGAA	3.06014	-----TTCATGAA--
ATATGTGC	0.35052	---ATATGTGC---	ACCATACT	3.05205	-----ACCATACT--
ACGTAACA	0.35002	----ACGTAACA----	ACAGTGAT	3.03816	---ACAGTGAT---
ATATCACA	0.34874	----ATATCACA----	ACAATACG	3.02855	ACAATACG-----