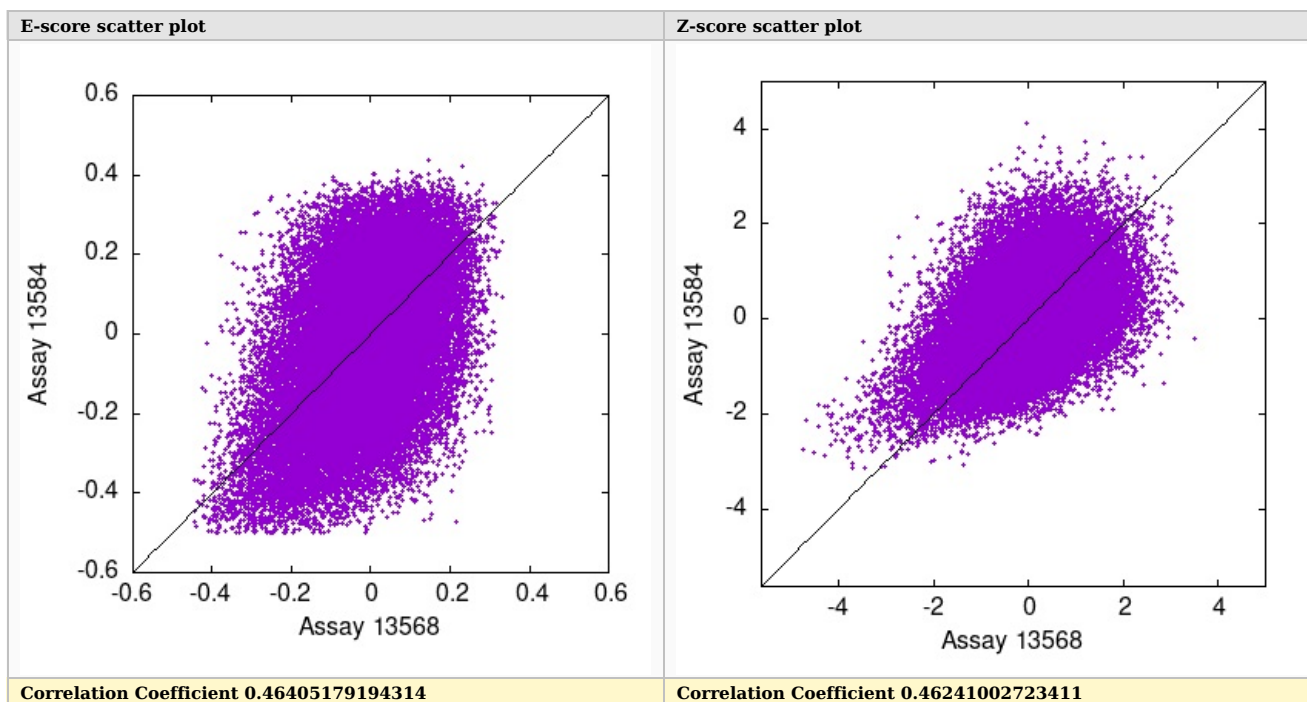


QC report



Top scoring motifs for Assay 13568

Protein ID: pTH13960.1 Gene: DZIP1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

ACAATGTA	0.33318	----ACAATGTA--
CTGGTAGA	0.33170	TCTACCAG-----
TACCAATA	0.32532	--TACCAATA----
ACAAATAT	0.31669	---ACAAATAT---
ACTTTAAT	0.31649	---ACTTTAAT---
ACAAAACA	0.31631	---ACAAAACA---
AATCATTA	0.31544	--AATCATTA----
ACCGGTTA	0.31326	---ACCGGTTA---
AATGTAGT	0.31139	-----AATGTAGT
AGTAGTAT	0.31119	-ATACTACT-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AAGCGCGA	3.48286	----AAGCGCGA---
CAACATTG	3.22502	----CAACATTG---
AATAGTGT	3.19100	-----ACACTATT-
GTTACTAA	3.12008	TTAGTAAC-----
ATGACAAC	3.11093	-----ATGACAAC-
ATGTAGAC	3.09874	-----GTCTACAT
ACCCAAAA	3.09682	-----ACCCAAAA-
ACTGCGAA	3.08951	---TTCGCAGT----
TAACACTA	3.08930	---TAACACTA----
AATTTTAC	3.03811	---GTAAATT-----

Top scoring motifs for Assay 13584

Protein ID: pTH13960.2 Gene: DZIP1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTGTATTA	0.43754	CTGTATTA--
ATAGTAAT	0.42068	--ATAGTAAT
ATATTAAT	0.41142	--ATATTAAT
TATTTGCA	0.40929	-TATTTGCA-
TATATGAA	0.40583	-TATATGAA-
AAAACCTA	0.40281	-AAAACCTA-
TACACACA	0.40278	-TGTGTGTA-
GATATGTA	0.40184	-GATATGTA-
GAAATTC	0.39711	-GAAATTC-
ACAAAATA	0.39597	-TATTTTGT-

Forward:

Reverse:



Top 10

Scores

Alignment

CTGTATTA	4.10800	--TAATACAG-
GCATATAA	3.81530	--GCATATAA-
TAATATAA	3.72981	--TAATATAA-
ATAGTAAT	3.69828	ATTACTAT---
TAATAATA	3.63271	--TAATAATA-
ATATCTTA	3.61135	--TAAGATAT-
GATATGTA	3.59688	---GATATGTA
ATATTAAT	3.49932	ATTAATAT---
TACACACA	3.48835	-TGTGTGTA--
CATATAAC	3.48615	---CATATAAC