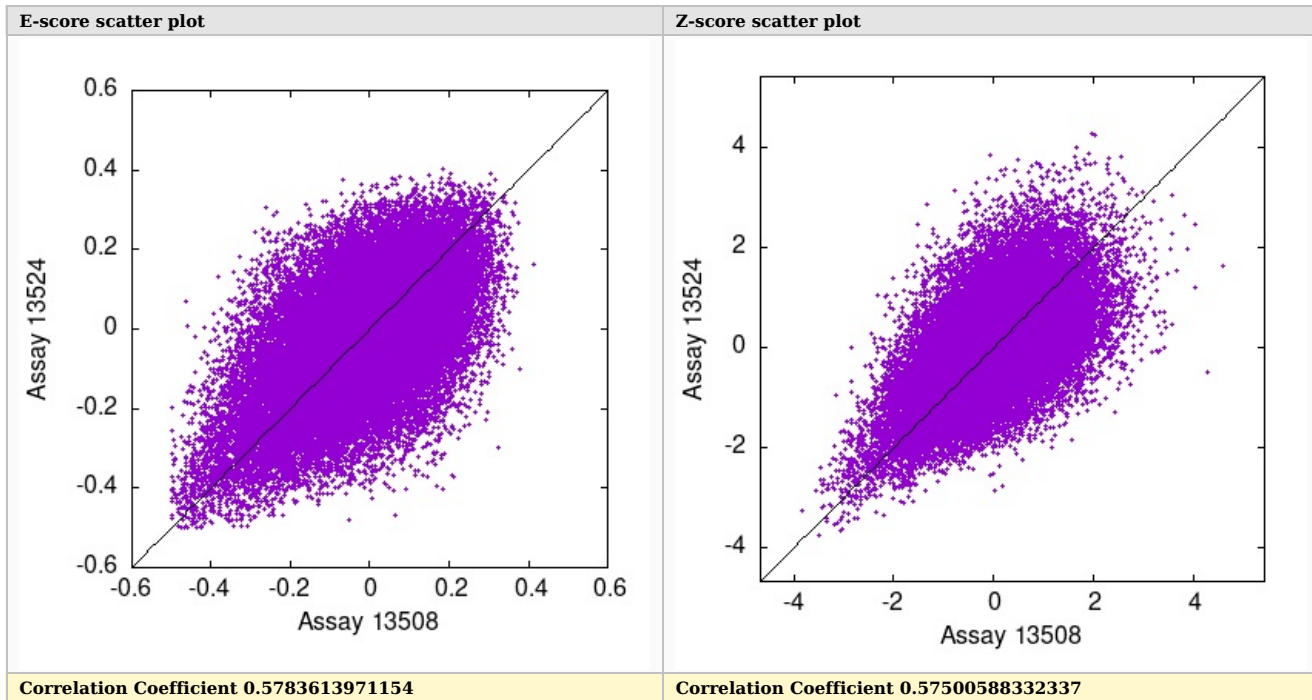


QC report



Top scoring motifs for Assay 13508

Protein ID: pTH13953.1 Gene: ATMIN.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

TATAAATA	0.41382	---TATAAATA
ATTTACTA	0.38050	--TAGTAAAT-
ATGTATAA	0.37306	--TTATACAT-
ACTACTAT	0.37265	--ATAGTAGT-
AACGAAAT	0.37253	--AACGAAAT-
ATATAAAT	0.36695	--ATATAAAT-
TAACGAAA	0.36681	--TAACGAAA--
AAACATAA	0.36577	AAACATAA---
ACATACAA	0.36483	--ACATACAA--
ATATATCA	0.36392	--ATATATCA-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

TATAAATA	4.58360	TATTTATA---
ATTTACTA	4.27085	-ATTTACTA--
ATAATGCA	4.04240	--TGCATTAT-
AATAATAA	4.03150	---TTATTATT
ACATACAA	3.89224	-ACATACAA--
AACATACA	3.82662	AACATACA---
AGAAAAGA	3.66445	TCCTTTCT---
ATATAGTA	3.57793	-ATATAGTA--
ACGTAATA	3.57752	-ACGTAATA--
ATATATCA	3.56020	-ATATATCA--

Top scoring motifs for Assay 13524

Protein ID: pTH13953.2 Gene: ATMIN.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

GATATGTA	0.40239	----TACATATC
ACAAAATA	0.39254	--ACAAAATA--
ATGTAGTA	0.39249	-TACTACAT---
AATAAATT	0.38777	--AATAAATT--
TATCAACA	0.38364	TATCAACA----
ATAATAGA	0.38117	--ATAATAGA--
TGACAAAA	0.38075	TGACAAAA----
AGAGATAT	0.38013	---AGAGATAT--
TATTTGCA	0.37787	---TGCAAAATA--
ATATTAGC	0.37590	----ATATTAGC

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10

Scores

Alignment

TATTTGCA	4.28604	TGCAAAATA-----
ACAAAATA	4.26013	-----TATTTTGT-
GTACAATA	4.01885	-----GTACAATA--
AATACATT	3.88079	-----AATACATT---
ACCACTAA	3.84938	-----ACCACTAA---
ATGTAGTA	3.83061	---TACTACAT----
GTAATACA	3.82250	--GTAATACA-----
ACATTACT	3.78291	-----ACATTACT
AACACTTA	3.75513	-----AACACTTA---
AAAATAAA	3.74851	--AAAATAAA-----