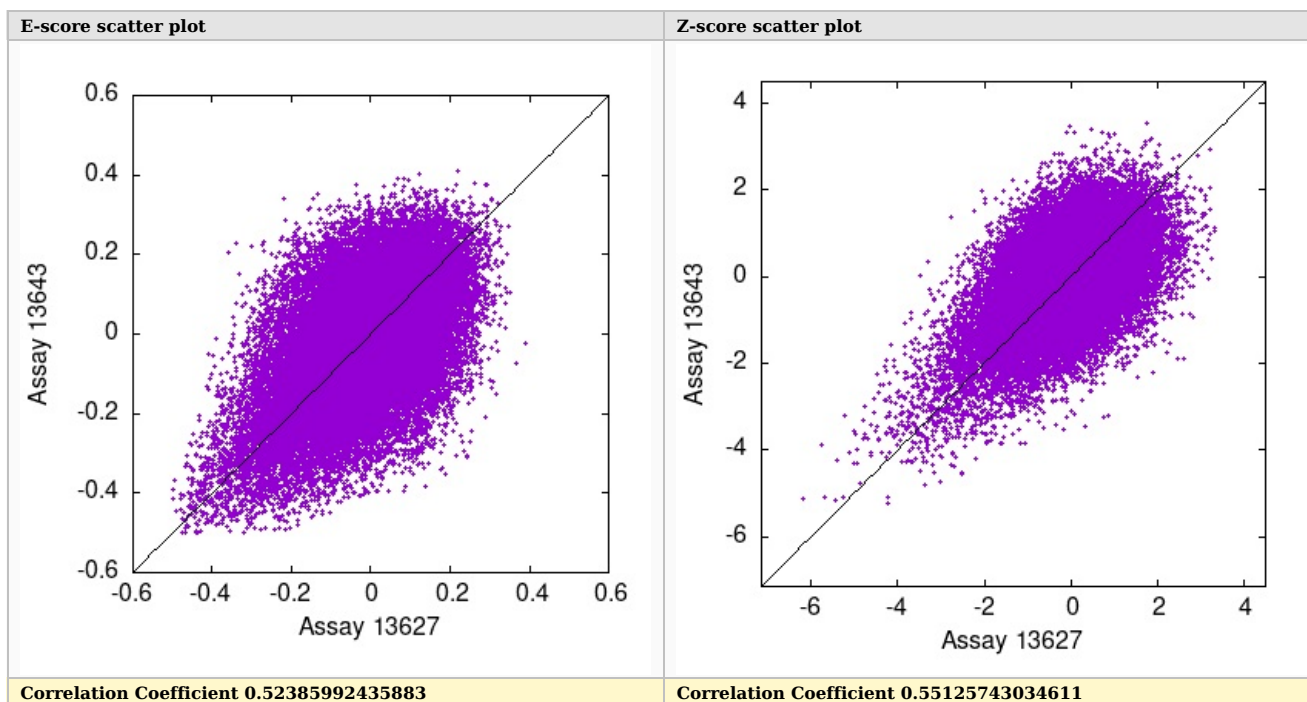


QC report



Top scoring motifs for Assay 13627

Protein ID: pTH14228.1 Gene: GATAD2A.DBD Domain: GATA Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

CAAA

TTGT

Top 10

Scores

Alignment

CCACAACA	0.39037	-CCACAACA---
TACAACTA	0.36552	--TACAACTA--
CACAACAC	0.35298	--CACAACAC--
TATACAAA	0.34910	TATACAAA----
ATTAGTTG	0.34514	----CAACTAAT
GATCCGAA	0.34465	GATCCGAA----
CGTTTTGC	0.34162	-GCAAAACG---
GTTTTGTA	0.33994	--TACAAAAC--
AAATGCAT	0.33980	-ATGCATTT---
GACAACTA	0.33273	--GACAACTA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

AACA

TGT

Top 10

Scores

Alignment

AATCGAAC	3.30045	AATCGAAC----
TATACAAA	3.29949	TATACAAA----
CAACAATC	3.22444	----CAACAATC
ACACATAC	3.22136	---ACACATAC--
AACGCGTT	3.21166	--AACGCGTT--
AACAGACA	3.19092	--AACAGACA--
GACAACTA	3.18982	--GACAACTA--
TACAACTA	3.18541	--TACAACTA--
ACTGATTG	3.16697	----CAATCAGT
AAACAACG	3.14770	-AAACAACG---

Top scoring motifs for Assay 13643

Protein ID: pTH14228.2 Gene: GATAD2A.DBD Domain: GATA Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

CA

TG

Top 10

Scores

Alignment

TACGCGTA	0.41137	----TACGCGTA
GATGCATC	0.40236	--GATGCATC--
GCGCGCGC	0.39127	-GCGCGCGC---
AAACGCGC	0.39122	-AAACGCGC---
CAATTGTC	0.38803	----GACAATTG
AACGGTTG	0.38113	--CAACCGTT--
TTCATGAA	0.37461	TTCATGAA----
ACATACAA	0.37452	-ACATACAA---
ATTTAAAA	0.37448	-ATTTAAAA---
AAACAAC	0.37425	---AAACAAC-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

CA

TG

Top 10

Scores

Alignment

AACGTTTC	3.51649	----GAAACGTT----
AATTTAAA	3.44841	AATTTAAA-----
AAACGCGC	3.39672	-----AAACGCGC---
GTACAACA	3.33225	--GTACAACA-----
TTCATGAA	3.30641	-----TTCATGAA--
GCGCGCGC	3.29938	-----GCGCGCGC---
AGTATACT	3.28963	--AGTATACT-----
CGCAACAA	3.26796	-----CGCAACAA--
ATCAGTAC	3.21310	-----ATCAGTAC---
GCGCGCGC	3.18081	-----GCGCGCGC---