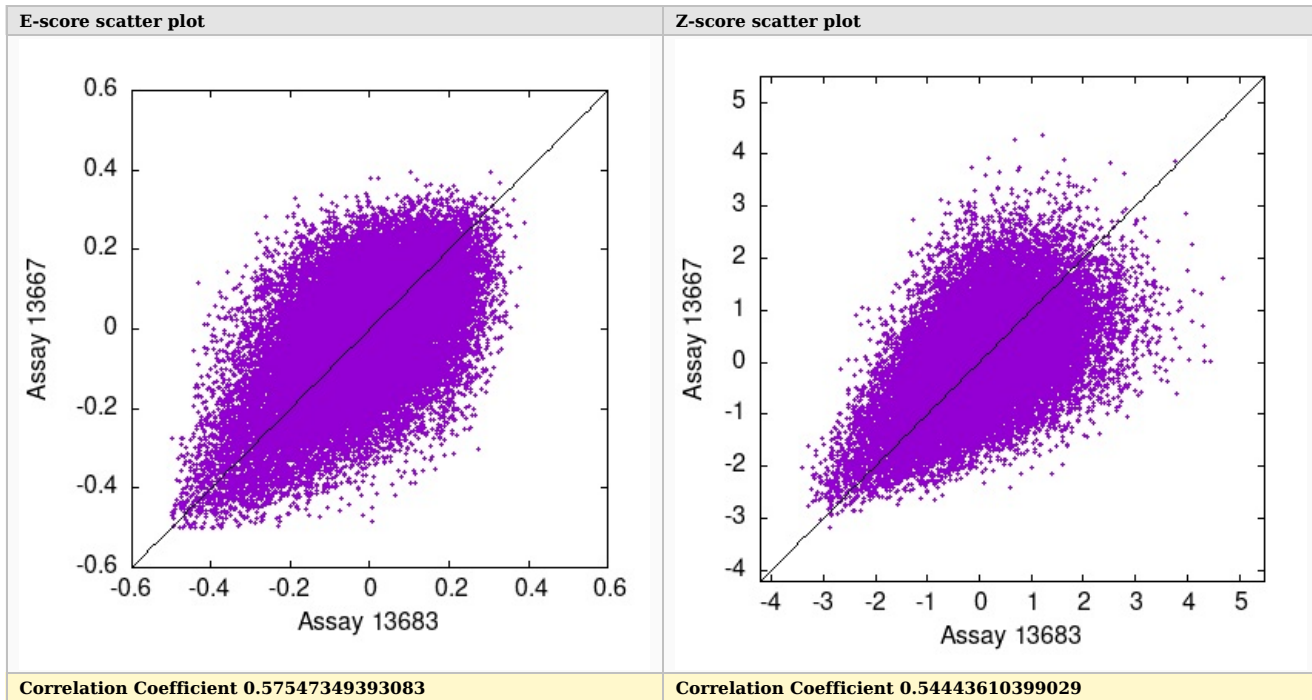


QC report



Top scoring motifs for Assay 13683

Protein ID: pTH14279.2 Gene: TTF1.DBD Domain: Myb_DNA-binding Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TGTTAACA	0.39165	---TGTTAACA
GAAATTGA	0.37870	-GAAATTGA--
AATTTTAC	0.37224	--AATTTTAC-
TACACACA	0.36593	-TGTGTGTA--
ATGTTAAC	0.36233	--ATGTTAAC-
GATCACAC	0.35691	-GTGTGATC-
ATGTCACA	0.35568	--ATGTCACA-
ATAAGATA	0.35406	-TATCTTAT--
TAATATAA	0.34801	TTATATTA---
AGTGTGAA	0.34584	-AGTGTGAA--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TGTTAACA	4.67983	-TGTTAACA----
AATTTTAC	4.45543	--AATTTTAC----
CATTGTTA	4.33931	----TAACAATG--
TATAACAA	4.33512	--TATAACAA----
CACATAGA	4.31645	--CACATAGA----
TACACACA	4.26036	--TACACACA----
GTAATACA	4.12399	TGTATTAC-----
GAAATTGA	4.10495	-----TCAATTTT
TATGCATA	4.10356	--TATGCATA----
GATCACAC	4.03116	--GATCACAC----

Top scoring motifs for Assay 13667

Protein ID: pTH14279.1 Gene: TTF1.DBD Domain: Myb_DNA-binding Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GAAATTAA	0.39506	----GAAATTAA
CAATTTCA	0.39485	--CAATTTCA---
ATGTACAT	0.38086	--ATGTACAT---
TGTGCACA	0.37869	---TGTGCACA-
AAACGTAT	0.37649	AAACGTAT----
TATGTGAA	0.36617	-TATGTGAA---
CTGTAATA	0.36264	--CTGTAATA--
ATGTATAA	0.36123	--ATGTATAA--
CAATTGCG	0.35961	--CAATTGCG---
GTACTATA	0.35921	----GTACTATA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

GAAATTAA	4.37505	--GAAATTAA--
ATGTACAT	4.26338	ATGTACAT----
AAACGTAT	3.91196	--ATACGTTT--
TACTTTAA	3.90213	---TACTTTAA--
TATGTGAA	3.86608	---TATGTGAA--
GTACTTTA	3.81949	--GTACTTTA--
AACAATTG	3.75668	---AACAATTG--
TGTGCACA	3.75222	-TGTGCACA---
AATTGGCG	3.69140	-----AATTGGCG
AGACGTCT	3.65874	--AGACGTCT--