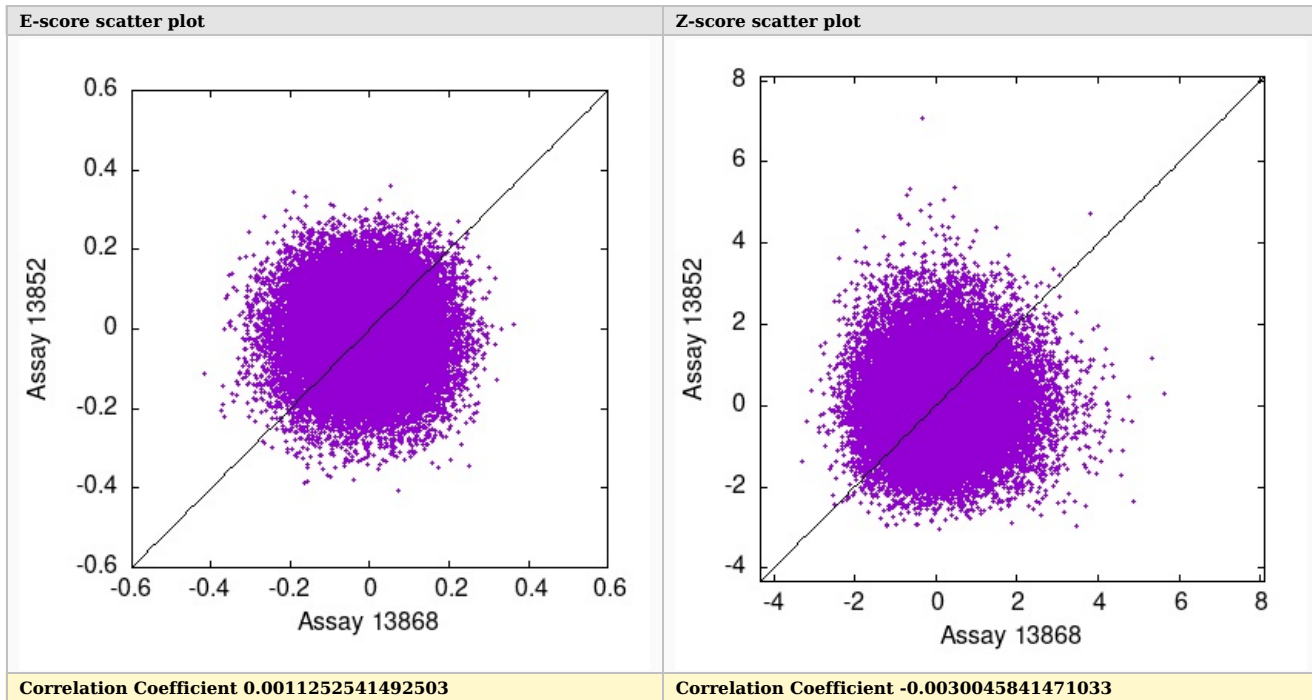


QC report



Top scoring motifs for Assay 13868

Protein ID: pTH14252.2 Gene: ZHX3.DBD.2 Domain: Homeobox Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

AGCCTCGA	0.36359	----AGCCTCGA--
AGACGTCT	0.33232	----AGACGTCT--
AACTGATC	0.32019	-----AACTGATC
ATTACGAA	0.31820	-----TTCGTAAT
CAGGCCTG	0.31522	---CAGGCCTG---
CAGTCGGG	0.30860	---CAGTCGGG---
ACATAAGT	0.30140	--ACATAAGT---
CCAAGAAC	0.30043	--CCAAGAAC---
GAGGCTCC	0.29770	---GAGGCTCC---
GAGCAAGC	0.29703	GAGCAAGC-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CAATAAAC	5.61757	-----CAATAAAC----
CGCTTAAG	5.30861	-----CGCTTAAG----
CAGGCCTG	4.85479	----CAGGCCTG-----
TCGGTAAA	4.81963	----TCGGTAAA-----
AAGAAAAC	4.73800	----AAGAAAAC-----
CGGTCCAG	4.61952	----CGGTCCAG-----
AGCCTCGA	4.60731	AGCCTCGA-----
TTACCGAA	4.55215	---TTACCGAA-----
AAACAGCC	4.36047	-----AAACAGCC----
ATTTTGG	4.32495	-----CCAAAAAT----

Top scoring motifs for Assay 13852

Protein ID: pTH14252.1 Gene: ZHX3.DBD.2 Domain: Homeobox Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

CTGCAGTC	0.35938	CTGCAGTC-----
TAACGTTA	0.34371	-TAACGTTA----
ATGGAGAC	0.33463	-----GTCTCCAT
CTTGTTCA	0.32341	-----TGAACAAG
ACTCGGCT	0.31169	-ACTCGGCT-----
ATACATAC	0.30856	----ATACATAC---
CCGTCCGA	0.30814	---CCGTCCGA---
GTTATAAC	0.30347	-----GTTATAAC
CCGTCACA	0.29767	---CCGTCACA---
AAACCCAG	0.29497	-----AAACCCAG-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10

Scores

Alignment

TAACGTTA	7.06436	-TAACGTTA--
CTGCAGTC	5.36879	--CTGCAGTC--
ACTCCCC	5.34590	---GGGGGAGT
CTTGTTCA	5.17152	---TGAACAAG
CAAGAGGC	5.07864	--CAAGAGGC--
ATGGAGAC	4.95604	--ATGGAGAC--
ACTCGGCT	4.79663	---AGCCGAGT
AGGCATTG	4.72024	CAATGCCT---
GTTGCAAC	4.69102	--GTTGCAAC--
GTTATAAC	4.67075	--GTTATAAC--