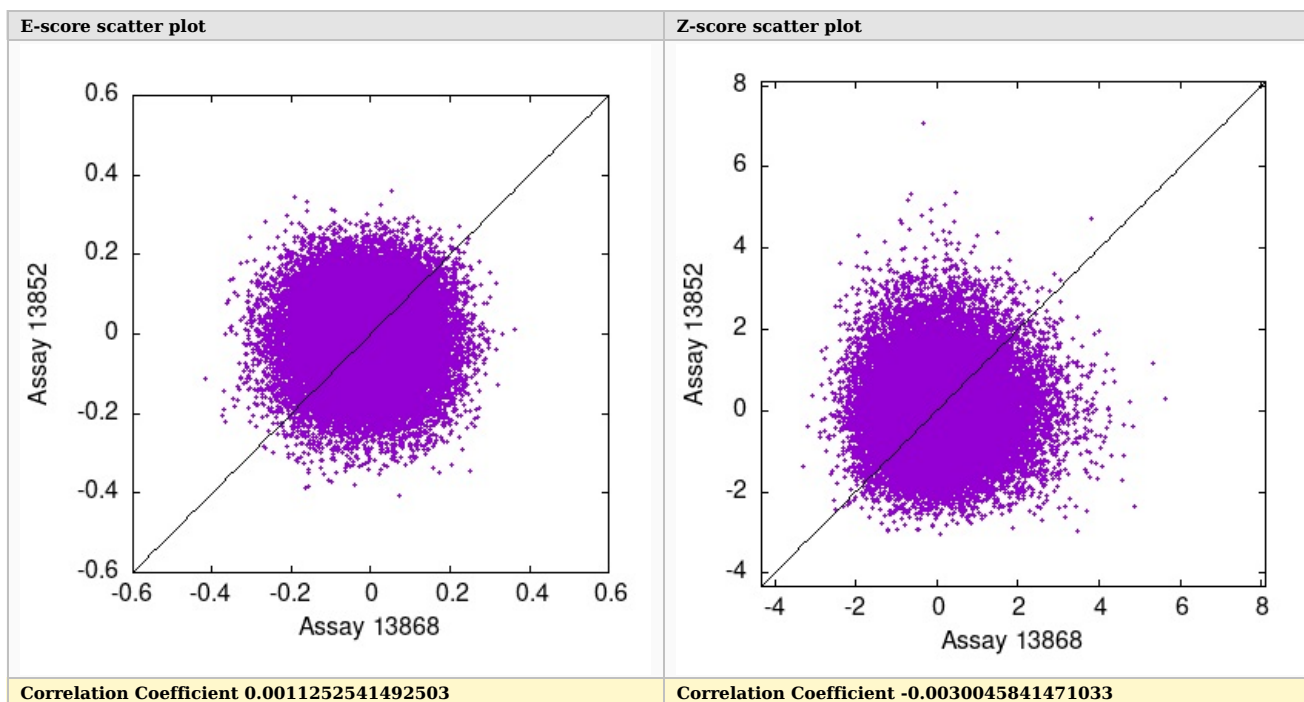


## QC report



### 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:



#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
AGCCTCGA	0.36359	----AGCCTCGA--	CAATAAAC	5.61757	-----CAATAAAC----
AGACGTCT	0.33232	----AGACGTCT--	CGCTTAAG	5.30861	-----CGCTTAAG----
AACTGATC	0.32019	-----AACTGATC	CAGGCCTG	4.85479	----CAGGCCTG----
ATTACGAA	0.31820	-----TTCGTAAT	TCGGTAAA	4.81963	----TCGGTAAA----
CAGGCCTG	0.31522	---CAGGCCTG---	AAGAAAAC	4.73800	----AAGAAAAC----
CAGTCGGG	0.30860	---CAGTCGGG---	CGGTCCAG	4.61952	----CGGTCCAG----
ACATAAGT	0.30140	--ACATAAGT---	AGCCTCGA	4.60731	AGCCTCGA-----
CCAAGAAC	0.30043	--CCAAGAAC----	TTACCGAA	4.55215	---TTACCGAA-----
GAGGCTCC	0.29770	---GAGGCTCC---	AAACAGCC	4.36047	-----AAACAGCC
GAGCAAGC	0.29703	GAGCAAGC-----	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:



#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
CTGCAGTC	0.35938	CTGCAGTC-----	TAACGTTA	7.06436	-TAACGTTA--
TAACGTTA	0.34371	-TAACGTTA----	CTGCAGTC	5.36879	--CTGCAGTC--
ATGGAGAC	0.33463	-----GTCTCCAT	ACTCCCC	5.34590	---GGGGGAGT
CTTGTTCA	0.32341	----TGAACAAG	CTTGTTCA	5.17152	---TGAACAAG
ACTCGGCT	0.31169	-ACTCGGCT----	CAAGAGGC	5.07864	--CAAGAGGC--
ATACATAC	0.30856	----ATACATAC-	ATGGAGAC	4.95604	--ATGGAGAC--
CCGTCCGA	0.30814	---CCGTCCGA--	ACTCGGCT	4.79663	---AGCCGAGT
GTTATAAC	0.30347	----GTTATAAC	AGGCATTG	4.72024	CAATGCCT---
CCGTCACA	0.29767	---CCGTCACA--	GTTGCAAC	4.69102	--GTTGCAAC-
AAACCCAG	0.29497	----AAACCCAG-	GTTATAAC	4.67075	--GTTATAAC-