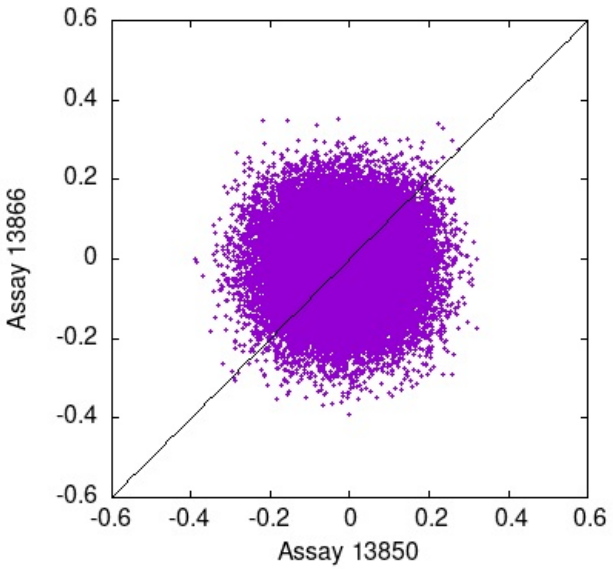
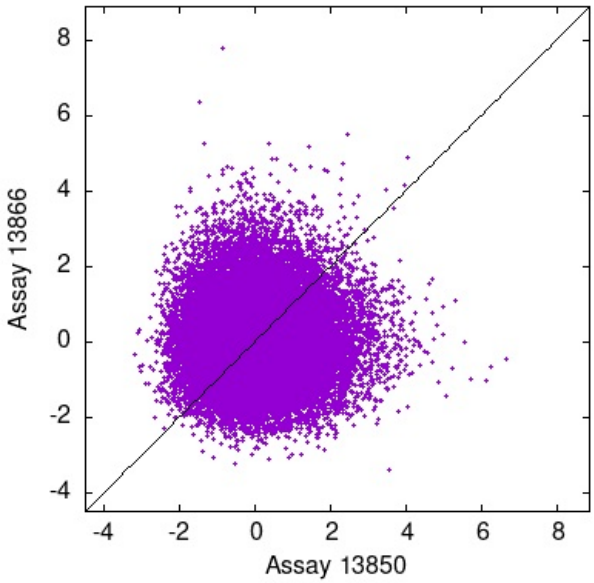
QC report

E-score scatter plot	Z-score scatter plot
	
Correlation Coefficient 0.0068335134865469	**Correlation Coefficient 0.01245051654323**

Top scoring motifs for Assay 13850
Protein ID: pTH14250.1 **Gene:** ZHX2.DBD.2 **Domain:** Homeobox **Flag:** Reject **Array:** 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GGCGCGCA	0.32024	GGCGCGCA----
GTTCAAGA	0.31960	----GTTCAAGA
CAGGTTTC	0.31352	--CAGGTTTC--
ATACATAC	0.30940	-GTATGTAT---
CAGTCTGA	0.30811	--CAGTCTGA--
GTAAGTGA	0.30376	-TCACTTAC---
CAGGTATA	0.29936	--CAGGTATA--
ATGGAGAC	0.29921	---ATGGAGAC-
CCGGGAGA	0.29868	--CCGGGAGA--
ACTCACTC	0.29846	--GAGTGAGT--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GTTCAAGA	6.66517	---GTTCAAGA--
GTAAGTGA	6.27342	-----GTAAGTGA
GGCGCGCA	6.14099	-----TGCGCGCC
CTCATTCC	5.71459	----CTCATTCC-
CAGTCTGA	5.57350	CAGTCTGA-----
CAGGTTTC	5.31678	----CAGGTTTC-
ACAGCAGT	5.25207	---ACTGCTGT--
CTGATGTC	5.08286	----CTGATGTC-
AAACGTAA	5.00995	-----TTACGTTT
ACTCACTC	4.98949	--GAGTGAGT---

Top scoring motifs for Assay 13866
Protein ID: pTH14250.2 **Gene:** ZHX2.DBD.2 **Domain:** Homeobox **Flag:** Reject **Array:** 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ATTACGAA	0.35283	-ATTACGAA-----
AACTGATC	0.34920	---AACTGATC---
GACGCTCC	0.34778	------GGAGCGTC
CAGTGATC	0.34145	---CAGTGATC---
CCGTTGAC	0.33744	GTCAACGG------
CTGGACTC	0.32882	-----CTGGACTC-
GAGGCTCC	0.30456	------GGAGCCTC
ATGATCCG	0.30345	-----ATGATCCG-
CTCAGTTC	0.30235	--GAACTGAG----
CCTACCGA	0.30228	-CCTACCGA-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ATTACGAA	7.76292	ATTACGAA-----
AACTGATC	6.36475	--AACTGATC---
CTCAGTTC	5.47718	-GAACTGAG----
CCTACCGA	5.24245	CCTACCGA-----
AGGTTCCG	5.23561	----CGGAACCT-
GGTAATCA	5.15544	-----TGATTACC
AAGGGCGC	4.87657	--AAGGGCGC---
CTAGCTAG	4.83759	CTAGCTAG-----
GAGGCTCC	4.83096	-----GGAGCCTC
CAGTGATC	4.73585	--CAGTGATC---