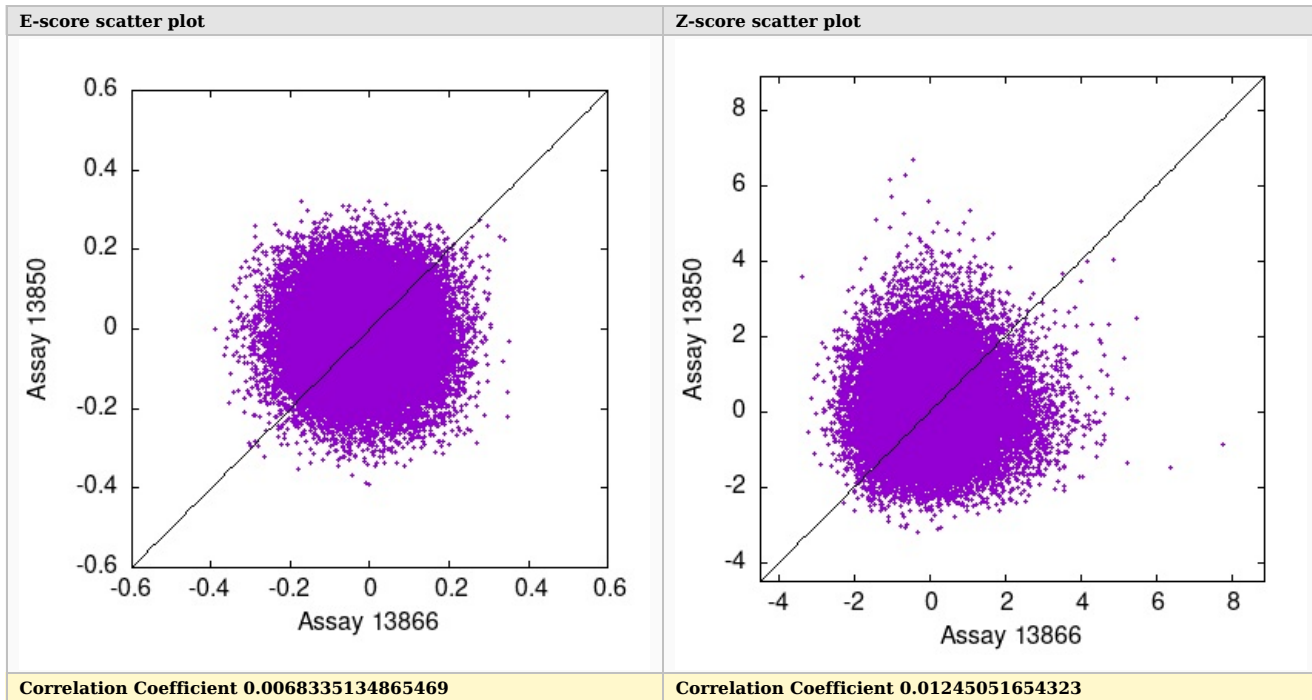


## QC report



### 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	--GAAGTGA-----
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----

### 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---