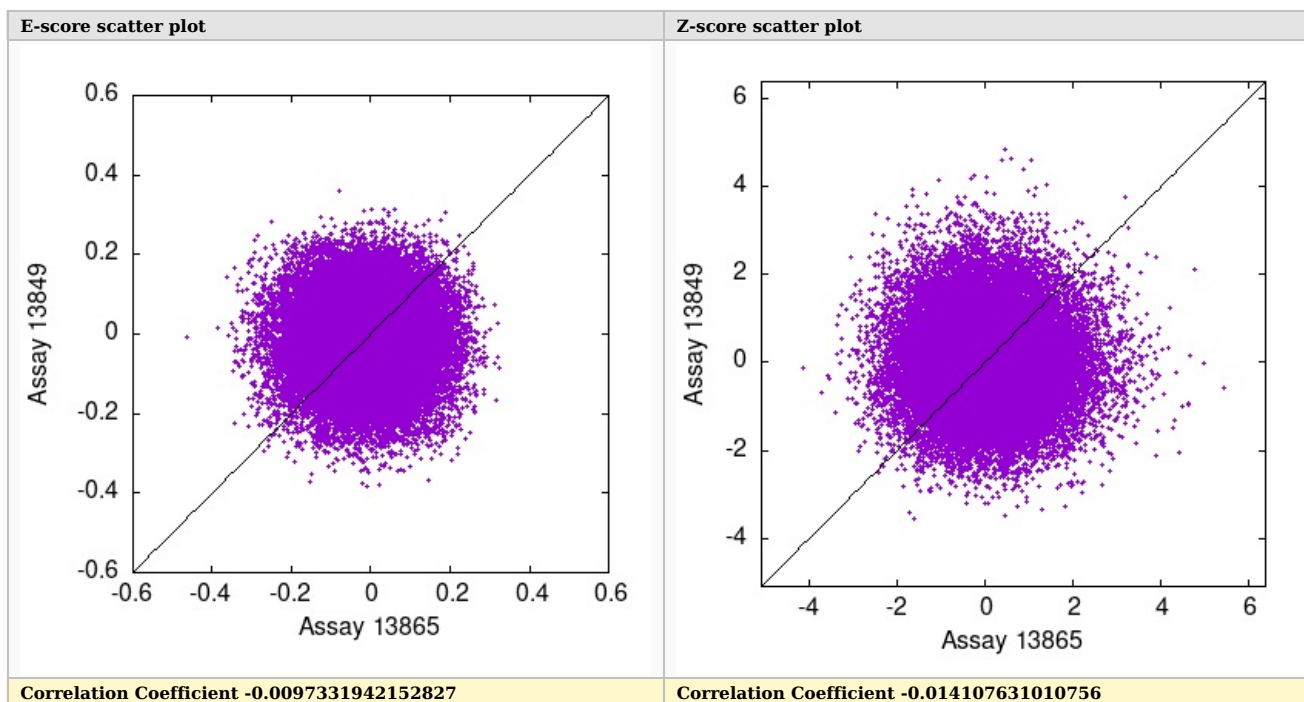


QC report



Correlation Coefficient -0.0097331942152827

Correlation Coefficient -0.014107631010756

Top scoring motifs for Assay 13865

Protein ID: pTH14249.2 Gene: ZHX2.DBD.1 Domain: Homeobox Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

GG A A A

T C T C C

Top 10

Scores

Alignment

AGAGGTAA	0.32355	--AGAGGTAA--
TTCCGGAA	0.32184	TTCCGGAA----
CGCCAGGA	0.31955	--TCTGGCG--
GCAATATGC	0.31840	--GCATATGC--
CGCCAGGA	0.31331	---CGCCAGGA--
ATTTGTAG	0.31257	--ATTTGTAG--
TCTCCCAA	0.30183	--TTGGGAGA--
ACCGGTAG	0.29217	--ACCGGTAG--
CAATATAA	0.29073	---CAATATAA--
GAAAGACA	0.28964	----GAAAGACA

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

T C T C C

G C T C C

Top 10

Scores

Alignment

TTCCGGAA	5.41426	TTCCGGAA-----
ATCTCAAG	4.97964	--ATCTCAAG----
CCCCAGCG	4.74142	---CCCCAGCG--
AGGGCCGC	4.63692	--AGGGCCGC--
ATTTGTAG	4.62630	--ATTTGTAG--
CCGGTAGC	4.60606	--CCGGTAGC--
ATAGTTTC	4.46473	-----GAAACTAT
CGTGTATA	4.39506	--CGTGTATA--
CTTCGATA	4.32140	CTTCGATA-----
TACATTGA	4.28856	TCAATGTA-----

Top scoring motifs for Assay 13849

Protein ID: pTH14249.1 Gene: ZHX2.DBD.1 Domain: Homeobox Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

C A G G C C

G C C C T G

Top 10

Scores

Alignment

CAGTGGCG	0.35938	--CAGTGGCG--
CAGGCTCC	0.31482	--CAGGCTCC--
AGCCTCAG	0.31249	CTGAGGCT-----
AGGGCGTG	0.31161	---CACGCCCT--
CAGGTACC	0.30804	--CAGGTACC--
CAAAGTCG	0.30505	---CAAAGTCG--
AGTCGCAC	0.30465	---AGTCGCAC--
ACATAGCT	0.29782	ACATAGCT-----
ATTGCCTG	0.29484	---CAGGCAAT--
CATTGAAC	0.29185	-----GTTCAATG

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

C A G C C

G C C C T G

Top 10

Scores

Alignment

AGCCTCAG	4.83811	--CTGAGGCT--
CAGTGGCG	4.61818	--CAGTGGCG--
TCCAGTAA	4.57713	TCCAGTAA-----
ATGATCAT	4.57665	---ATGATCAT--
TGGCGCCA	4.37256	-----TGGCGCCA
AGCATTCC	4.22405	AGCATTCC-----
ATCTGTAC	4.21371	ATCTGTAC-----
AGGGCGTG	4.17525	---AGGGCGTG--
CGGATCCG	4.15133	--CGGATCCG--
CGCATCTA	4.02254	--TAGATGCG--