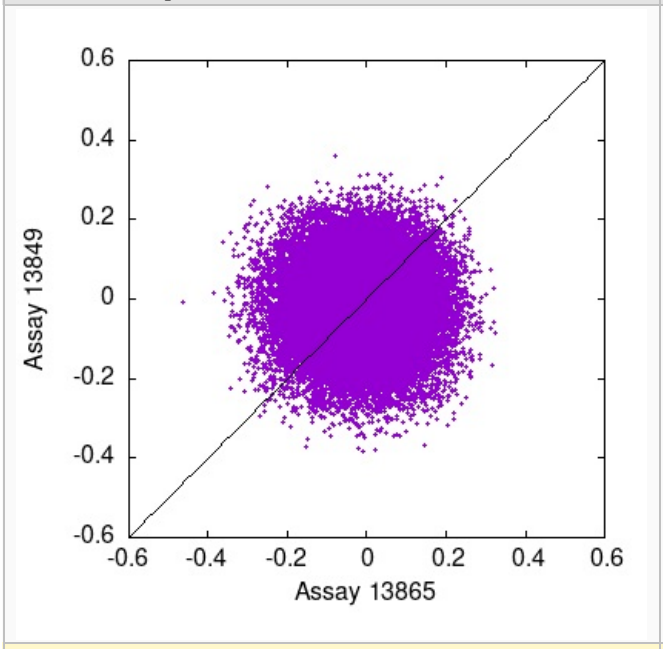
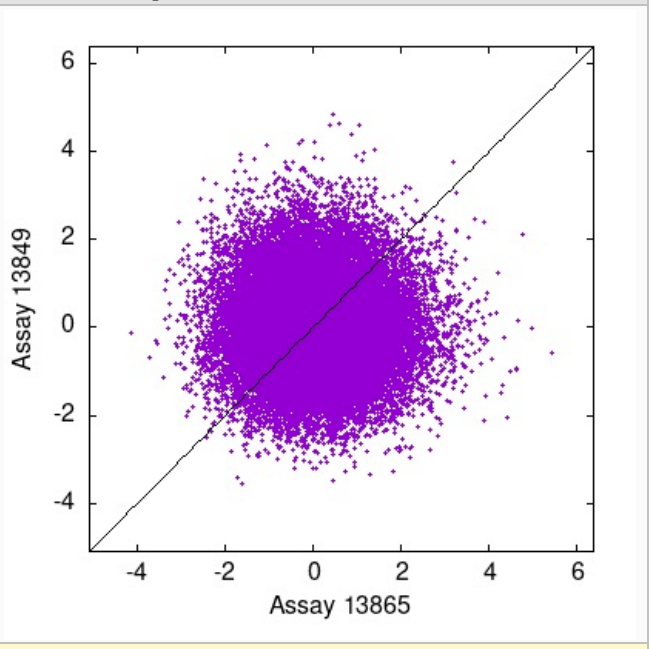
PBM database

QC report

E-score scatter plot	Z-score scatter plot
	
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'			8 mer Z-scores for probeset 'all'		
Forward:	**Reverse:**		**Forward:**	**Reverse:**	
Top 10	**Scores**	**Alignment**	**Top 10**	**Scores**	**Alignment**
AGAGGTAA	0.32355	-AGAGGTAA---	TTCCGGAA	5.41426	TTCCGGAA-----
TTCCGGAA	0.32184	TTCCGGAA----	ATCTCAAG	4.97964	-ATCTCAAG----
CGCCCAGA	0.31955	-TCTGGGCG---	CCCCAGCG	4.74142	---CCCCAGCG--
GCATATGC	0.31840	-GCATATGC---	AGGGCCGC	4.63692	--AGGGCCGC---
CGCCAGGA	0.31331	---CGCCAGGA-	ATTTGTAG	4.62630	-ATTTGTAG----
ATTTGTAG	0.31257	-ATTTGTAG---	CCGGTAGC	4.60606	--CCGGTAGC---
TCTCCCAA	0.30183	--TTGGGAGA--	ATAGTTTC	4.46473	-----GAAACTAT
ACCGGTAG	0.29217	-ACCGGTAG---	CGTGTATA	4.39506	--CGTGTATA---
CAATATAA	0.29073	---CAATATAA-	CTTCGATA	4.32140	CTTCGATA-----
GAAAGACA	0.28964	----GAAAGACA	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'			8 mer Z-scores for probeset 'all'		
Forward:	**Reverse:**		**Forward:**	**Reverse:**	
Top 10	**Scores**	**Alignment**	**Top 10**	**Scores**	**Alignment**
CAGTGGCG	0.35938	--CAGTGGCG---	AGCCTCAG	4.83811	--CTGAGGCT---
CAGGCTCC	0.31482	--CAGGCTCC---	CAGTGGCG	4.61818	--CAGTGGCG---
AGCCTCAG	0.31249	CTGAGGCT-----	TCCAGTAA	4.57713	TCCAGTAA-----
AGGGCGTG	0.31161	--CACGCCCT---	ATGATCAT	4.57665	---ATGATCAT--
CAGGTACC	0.30804	--CAGGTACC---	TGGCGCCA	4.37256	-----TGGCGCCA
CAAAGTCG	0.30505	--CAAAGTCG---	AGCATTCC	4.22405	AGCATTCC-----
AGTCGCAC	0.30465	---AGTCGCAC--	ATCTGTAC	4.21371	ATCTGTAC-----
ACATAGCT	0.29782	ACATAGCT-----	AGGGCGTG	4.17525	----AGGGCGTG-
ATTGCCTG	0.29484	--CAGGCAAT---	CGGATCCG	4.15133	--CGGATCCG---
CATTGAAC	0.29185	-----GTTCAATG	CGCATCTA	4.02254	--TAGATGCG---