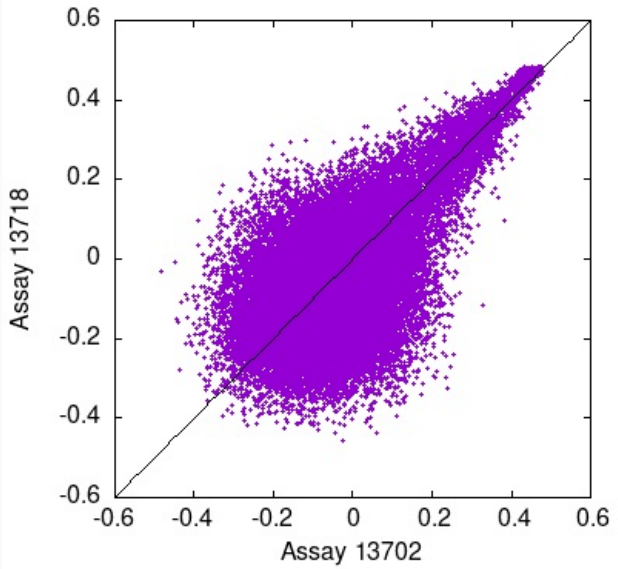
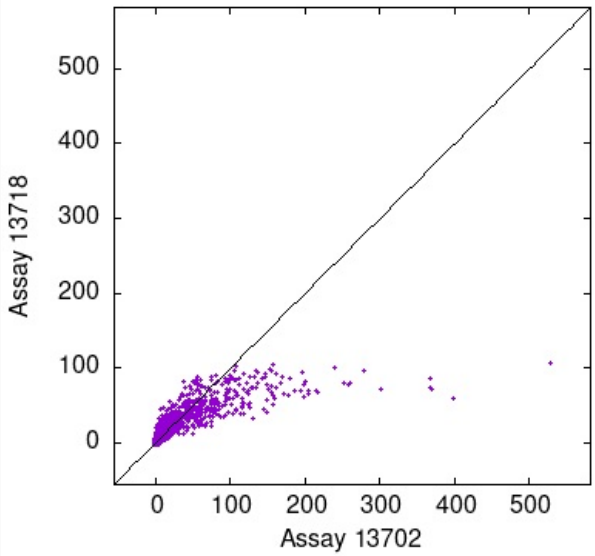
PBM database

QC report

E-score scatter plot	Z-score scatter plot
	
Correlation Coefficient 0.61711682053217	**Correlation Coefficient 0.80029895226132**

Top scoring motifs for Assay 13702
Protein ID: pTH14232.1 **Gene:** ZGLP1.DBD **Domain:** GATA **Flag:** Pass_matched_pair **Array:** 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ACGATCGT	0.47792	--ACGATCGT--
ATCGATCG	0.47661	-ATCGATCG---
CGATCGGA	0.47639	---CGATCGGA-
GATCGATC	0.47568	GATCGATC----
ATGATCAT	0.47527	--ATGATCAT--
GATGATCA	0.47189	---TGATCATC-
GCGATCGA	0.46965	--TCGATCGC--
GATCATCA	0.46917	----GATCATCA
CGATCGCA	0.46907	---CGATCGCA-
ATCGATCA	0.46883	-ATCGATCA---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GATCGATC	528.82813	---GATCGATC
ATCGATCG	397.56767	--CGATCGAT-
ACGATCGT	369.66832	-ACGATCGT--
ATCGATCA	368.03588	--TGATCGAT-
ATGATCAT	367.16833	-ATGATCAT--
GATGATCA	367.16833	GATGATCA---
GCGATCGA	300.66634	-GCGATCGA--
GCGATCGC	278.29637	-GCGATCGC--
CGATCGCG	259.18618	CGCGATCG---
CGATCGCA	258.52797	TGCGATCG---

Top scoring motifs for Assay 13718
Protein ID: pTH14232.2 **Gene:** ZGLP1.DBD **Domain:** GATA **Flag:** Pass_matched_pair **Array:** 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GATCGATC	0.48419	---GATCGATC
GATGATCA	0.48404	GATGATCA---
CGATCACG	0.48360	CGTGATCG---
CGATCGCC	0.48360	GGCGATCG---
GCGATCGC	0.48221	-GCGATCGC--
TTGATCAA	0.48195	-TTGATCAA--
CGTGATCA	0.48155	CGTGATCA---
GTGATCAA	0.48102	-GTGATCAA--
TGATCAAA	0.48014	--TGATCAAA-
AGCGATCG	0.48001	AGCGATCG---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GATCGATC	106.37461	GATCGATC---
TTGATCAA	104.45268	--TTGATCAA-
CGTGATCA	102.28186	-CGTGATCA--
AGCGATCG	100.08916	-AGCGATCG--
CGATCGCC	98.86468	-GGCGATCG--
GTGATCAC	97.39004	--GTGATCAC-
CACGATCG	96.82296	---CGATCGTG
GCGATCGC	96.70618	--GCGATCGC-
AGCGATCA	96.50692	-AGCGATCA--
CGATCATC	95.43301	---CGATCATC