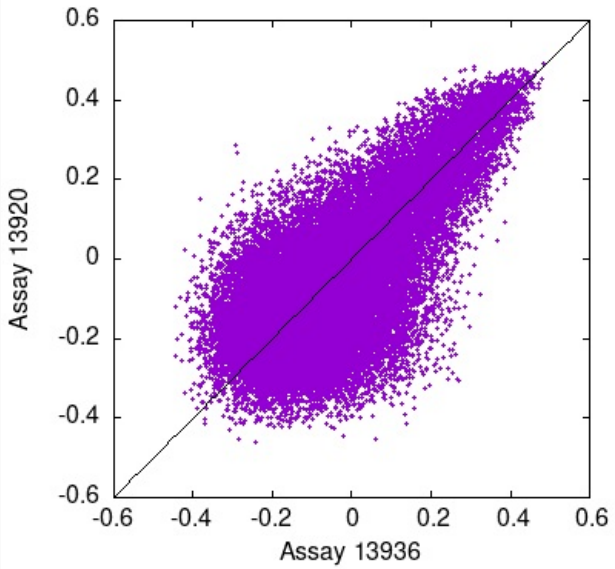
PBM database

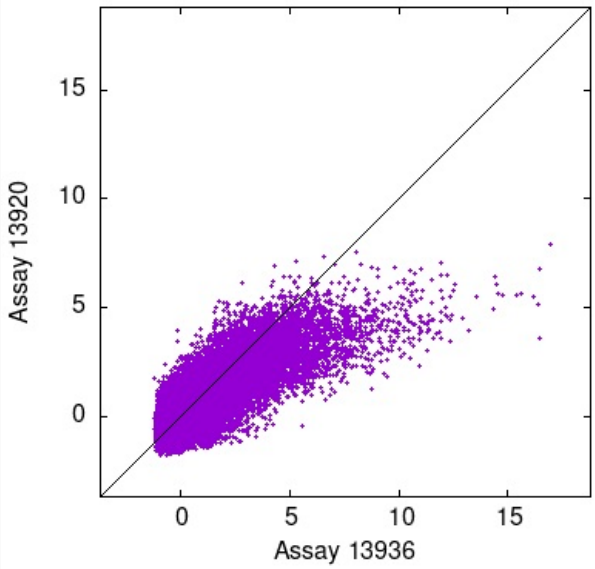
QC report

E-score scatter plot



Correlation Coefficient 0.72226286001598

Z-score scatter plot



Correlation Coefficient 0.81582802220326

Top scoring motifs for Assay 13936
Protein ID: pTH14220.2 **Gene:** CXXC4 **Domain:** zf-CXXC **Flag:** Pass_matched_pair **Array:** 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ACGTACGT	0.48399	--ACGTACGT---
CACGTACG	0.48061	-CACGTACG----
ACGTTGCG	0.47242	--ACGTTGCG---
ACGCAACG	0.47230	--ACGCAACG---
ACGACGTC	0.46311	-----GACGTCGT
CTACGTAC	0.46180	CTACGTAC-----
GCGTACGC	0.46094	--GCGTACGC---
CGCGTACG	0.45588	-CGCGTACG----
ACGTAAAT	0.45489	--ACGTAAAT---
GTACGCAA	0.45481	----GTACGCAA-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ACGTACGT	16.91192	-----ACGTACGT
ACGACGTC	16.48418	--ACGACGTC---
CGACGTCC	16.46381	---CGACGTCC--
CTACGTAC	16.37540	---CTACGTAC--
ACGCAACG	16.20114	ACGCAACG-----
CACGTACG	15.63391	----CACGTACG-
ACGTTGCG	15.37336	-CGCAACGT----
ACGTCGTA	14.74815	-TACGACGT----
ACGCGACG	14.52302	ACGCGACG-----
CGTGACGC	14.46683	-CGTGACGC----

Top scoring motifs for Assay 13920
Protein ID: pTH14220.1 **Gene:** CXXC4 **Domain:** zf-CXXC **Flag:** Pass_matched_pair **Array:** 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ACGTACGT	0.49282	----ACGTACGT--
CGCGCGCG	0.48515	---CGCGCGCG---
CACGTGCG	0.47790	---CACGTGCG---
CGACGTCG	0.47636	--CGACGTCG----
ACGTCGCG	0.47485	CGCGACGT------
CGTCGCGC	0.47440	------GCGCGACG
ACGTGCGC	0.47427	----ACGTGCGC--
ACGCGTTA	0.47383	----ACGCGTTA--
CGTAACGC	0.47382	-----CGTAACGC-
ACGCACGC	0.47308	----GCGTGCGT--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
ACGTACGT	7.94023	----ACGTACGT--
CACGTGCG	7.55875	---CACGTGCG---
ACGCACGC	7.32779	----GCGTGCGT--
CGCGCGCG	7.11353	---CGCGCGCG---
ACGTGACG	7.04952	CGTCACGT------
GCACGTGC	7.01928	--GCACGTGC----
CGACGTCG	7.01769	--CGACGTCG----
CGTCGCGC	6.92845	------GCGCGACG
CGTACGTC	6.86325	---GACGTACG---
CGTAACGC	6.85282	-----CGTAACGC-