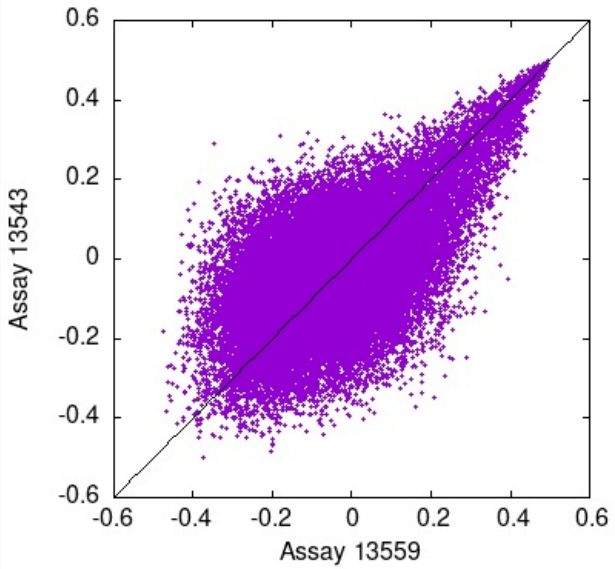
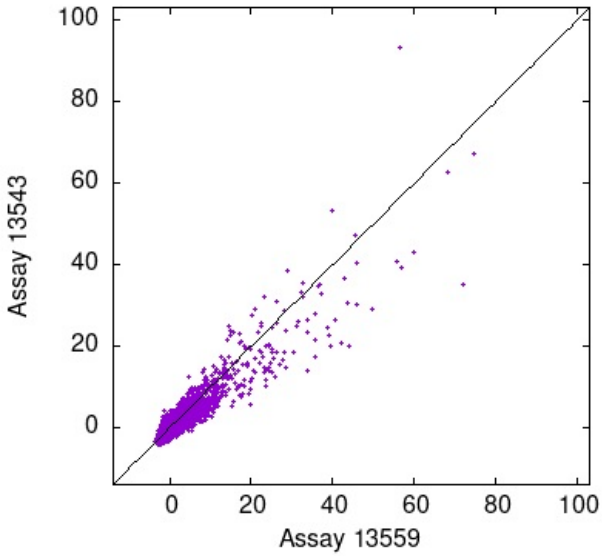
PBM database

QC report

E-score scatter plot	Z-score scatter plot
	
Correlation Coefficient 0.60942295959127	**Correlation Coefficient 0.85116730912065**

Top scoring motifs for Assay 13559
Protein ID: pTH14290.2 **Gene:** CGGBP1.FL **Domain:** Unknown **Flag:** Pass_matched_pair **Array:** 1M-HK

8 mer E-scores for probeset 'all'

Forward: **Reverse:**

Top 10	Scores	Alignment
CGCCGCCG	0.49670	CGCCGCCG--
GCCGCCGA	0.49533	-GCCGCCGA-
CGCCGCAG	0.49479	CGCCGCAG--
ACGGCGGC	0.49466	-GCCGCCGT-
ACCGCCGA	0.49418	-ACCGCCGA-
CGGCGGCA	0.49334	TGCCGCCG--
CCGCCGAA	0.49265	--CCGCCGAA
GCCGCGGC	0.49139	-GCCGCGGC-
CACCGCCG	0.49131	CACCGCCG--
GCCGCAGA	0.49074	-GCCGCAGA-

8 mer Z-scores for probeset 'all'

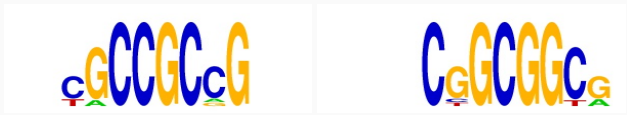
Forward: **Reverse:**

Top 10	Scores	Alignment
CGCCGCCG	74.59760	CGCCGCCG-
ACGGCGGC	72.24044	-GCCGCCGT
GCCGCCGA	68.19641	-GCCGCCGA
GCCGCGGC	60.08075	-GCCGCGGC
CGCCGCAG	56.86047	CGCCGCAG-
CGGCGGCA	56.56005	TGCCGCCG-
ACCGCCGA	55.68139	-ACCGCCGA
GCCGCGGA	49.64600	-GCCGCGGA
CCGCGGCG	46.06611	CGCCGCGG-
CTGCGGCA	46.00378	TGCCGCAG-

Top scoring motifs for Assay 13543
Protein ID: pTH14290.1 **Gene:** CGGBP1.FL **Domain:** Unknown **Flag:** Pass_matched_pair **Array:** 1M-ME

8 mer E-scores for probeset 'all'

Forward: **Reverse:**



Top 10	Scores	Alignment
CGGCGGCA	0.49916	TGCCGCCG--
GCCGCCGA	0.49833	-GCCGCCGA-
CGCCGCCG	0.49770	CGCCGCCG--
GCCGCCGC	0.49630	-GCCGCCGC-
CCGCCGAA	0.49504	--CCGCCGAA
ACGGCGGC	0.49318	-GCCGCCGT-
CCGGCGGC	0.49303	-GCCGCCGG-
ACCGCCGA	0.49302	-ACCGCCGA-
CCGCGGCG	0.49246	CGCCGCGG--
CGCCGCAG	0.49240	CGCCGCAG--

8 mer Z-scores for probeset 'all'

Forward: **Reverse:**

Top 10	Scores	Alignment
CGGCGGCA	93.36270	TGCCGCCG--
CGCCGCCG	67.19254	CGCCGCCG--
GCCGCCGA	62.90803	-GCCGCCGA-
GCCGCCGC	53.13536	-GCCGCCGC-
CCGCCGAA	47.25810	--CCGCCGAA
GCCGCGGC	43.04293	-GCCGCGGC-
ACCGCCGA	41.02491	-ACCGCCGA-
CCGCGGCG	40.47387	CGCCGCGG--
CGCCGCAG	39.52276	CGCCGCAG--
CCGCCGCG	38.59859	--CCGCCGCG