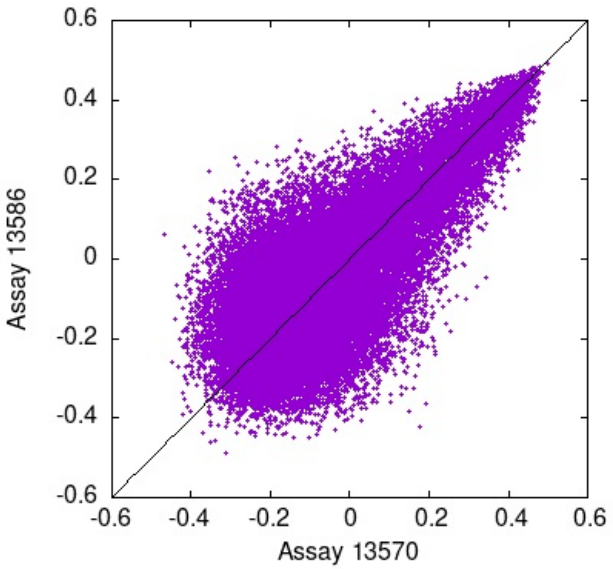
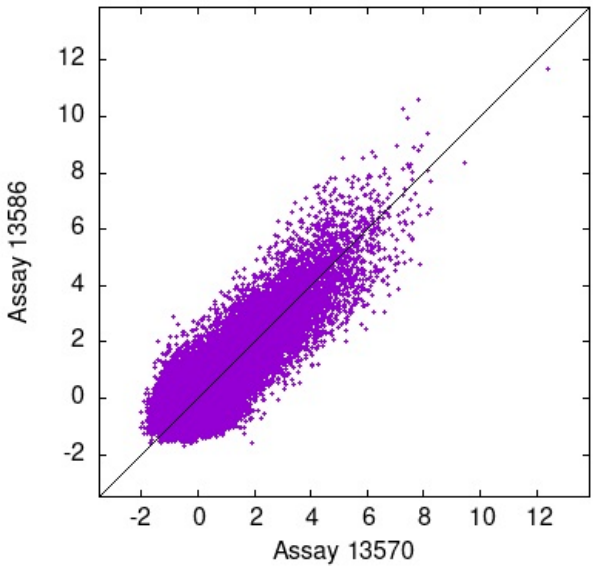
QC report

E-score scatter plot	Z-score scatter plot
	
Correlation Coefficient 0.75012532552496	**Correlation Coefficient 0.85153343147091**

Top scoring motifs for Assay 13570
Protein ID: pTH14221.1 **Gene:** zf-CXXC4.DBD **Domain:** zf-CXXC **Flag:** Pass_matched_pair **Array:** 1M-ME

8 mer E-scores for probeset 'all'

Forward: **Reverse:**

Top 10	Scores	Alignment
ACGTACGT	0.49725	----ACGTACGT
ACGTCACG	0.48667	CGTGACGT----
ACGACGTC	0.47953	-ACGACGTC---
CACGTACG	0.47843	---CACGTACG-
ACGTGACG	0.47790	CGTCACGT----
CACGTGCG	0.47761	---CACGTGCG-
ACGCACGC	0.47633	----ACGCACGC
CGACGTCG	0.47628	--CGACGTCG--
AACGCGTT	0.47626	-AACGCGTT---
AACGTACG	0.47614	---AACGTACG-

8 mer Z-scores for probeset 'all'

Forward: **Reverse:**

Top 10	Scores	Alignment
ACGTACGT	12.43537	---ACGTACGT-
ACGTCACG	9.46349	---ACGTCACG-
CACGTGCG	8.27013	CGCACGTG----
ACGTAACG	8.25909	---ACGTAACG-
ACGTAGCG	8.14898	---ACGTAGCG-
TGACGTCA	8.14374	-TGACGTCA---
ACGTGACG	8.12515	---ACGTGACG-
GCGTACGC	7.90629	---GCGTACGC-
ACGCACGA	7.88820	---ACGCACGA-
CGTGCGCA	7.86670	----CGTGCGCA

Top scoring motifs for Assay 13586
Protein ID: pTH14221.2 **Gene:** zf-CXXC4.DBD **Domain:** zf-CXXC **Flag:** Pass_matched_pair **Array:** 1M-HK

8 mer E-scores for probeset 'all'

Forward: **Reverse:**

Top 10	Scores	Alignment
ACGTACGT	0.48971	-ACGTACGT--
CACGTACG	0.48196	CACGTACG---
GCGTACGC	0.48126	-GCGTACGC--
ACGTACGC	0.48016	-ACGTACGC--
ACGCACGT	0.47903	-ACGCACGT--
CGTACGTA	0.47701	--CGTACGTA-
GCACGTGC	0.47671	---GCACGTGC
ACGTAACG	0.47568	-ACGTAACG--
ACGCAACG	0.47478	-ACGCAACG--
GTACGTAC	0.47388	---GTACGTAC

8 mer Z-scores for probeset 'all'

Forward: **Reverse:**

Top 10	Scores	Alignment
ACGTACGT	11.69088	----ACGTACGT
CACGTACG	10.59068	---CACGTACG-
ACGCACGT	10.29530	----ACGCACGT
GCACGTGC	9.97501	--GCACGTGC--
ACGTGACG	9.40951	CGTCACGT----
GCGTACGC	8.97791	----GCGTACGC
ACGCAACG	8.96734	----ACGCAACG
ACGTACGC	8.90466	----ACGTACGC
ACGACGTC	8.78493	-ACGACGTC---
CTACGTAG	8.74858	--CTACGTAG--