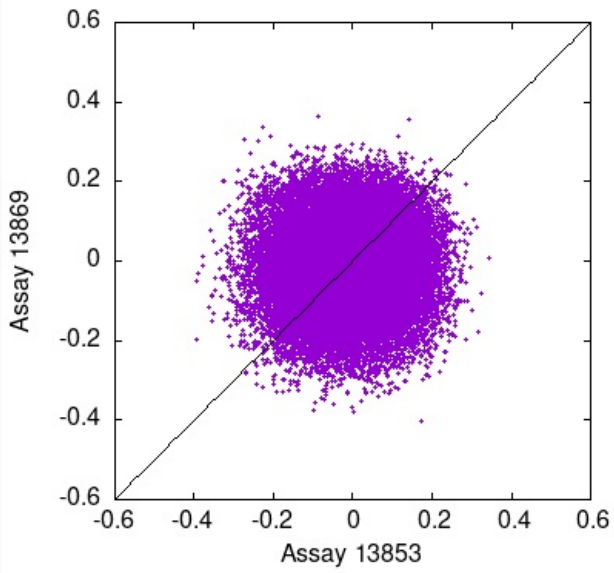
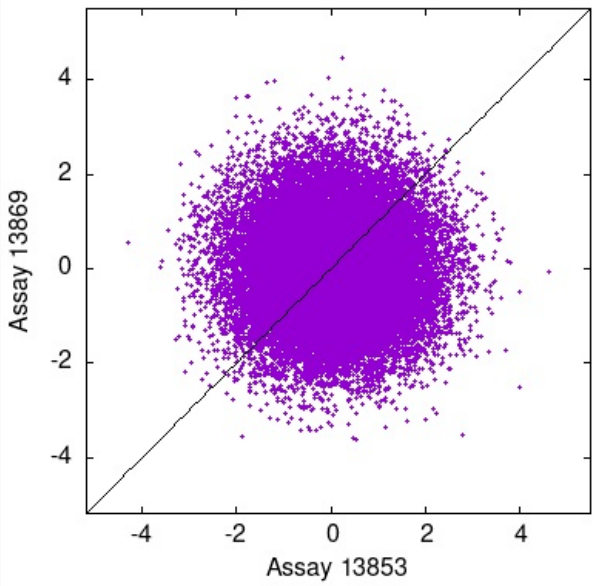
QC report

E-score scatter plot	Z-score scatter plot
	
Correlation Coefficient 0.0046883428418297	**Correlation Coefficient -0.0027925773471673**

Top scoring motifs for Assay 13853
Protein ID: pTH14253.1 **Gene:** POU5F2.FL **Domain:** Homeobox **Flag:** Reject **Array:** 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GACATAAC	0.34502	-----GACATAAC
CGGTTGAG	0.32307	----CGGTTGAG-
ATGATCAT	0.31648	----ATGATCAT-
AGGTGTTC	0.31245	----AGGTGTTC-
GAGTGCTA	0.30581	----GAGTGCTA-
AGAAATTA	0.30125	---AGAAATTA--
GGGTTTAA	0.29745	----GGGTTTAA-
ACTAGCCG	0.29613	----CGGCTAGT-
AACCGGTT	0.29000	-AACCGGTT----
CCGCGGCA	0.28914	TGCCGCGG-----

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GACATAAC	4.61721	--GACATAAC----
ATAATTAT	4.01796	ATAATTAT------
CGGTTGAG	4.00815	---CTCAACCG---
ACCCTGCT	3.80261	------AGCAGGGT
GCAGGCGA	3.74643	-----TCGCCTGC-
ACTAGCCG	3.70585	---ACTAGCCG---
GCCAATAA	3.65413	-TTATTGGC-----
ATGATCAT	3.60509	---ATGATCAT---
CGATCTTC	3.57298	----CGATCTTC--
AATTTGTA	3.53352	--AATTTGTA----

Top scoring motifs for Assay 13869
Protein ID: pTH14253.2 **Gene:** POU5F2.FL **Domain:** Homeobox **Flag:** Reject **Array:** 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
AAATTGGT	0.36326	-AAATTGGT----
ATTTGTAG	0.35513	---ATTTGTAG--
GGTCGACC	0.33694	---GGTCGACC--
AAGTGCAA	0.31458	-----TTGCACTT
AATTCCTC	0.31217	--AATTCCTC---
GCTCGGTA	0.30548	--GCTCGGTA---
TCAAGAGA	0.30181	TCTCTTGA-----
ATTGGTAC	0.29418	---ATTGGTAC--
TATGAGGA	0.29408	--TATGAGGA---
GAGGCCAA	0.28987	----TTGGCCTC-

8 mer Z-scores for probeset 'all'

Forward:

Reverse:

Top 10	Scores	Alignment
GGTCGACC	4.46164	-----GGTCGACC--
AAATTGGT	4.04449	----AAATTGGT---
AAGTGCAA	3.96606	-------TTGCACTT
CCATGTCC	3.95013	----CCATGTCC---
CGATTGGC	3.78764	----CGATTGGC---
CCATATGG	3.77931	----CCATATGG---
CCTAGGAC	3.69842	---GTCCTAGG----
CTATCGGC	3.67441	----CTATCGGC---
ATCTGAAA	3.65235	TTTCAGAT-------
ACCTTACT	3.64745	----AGTAAGGT---