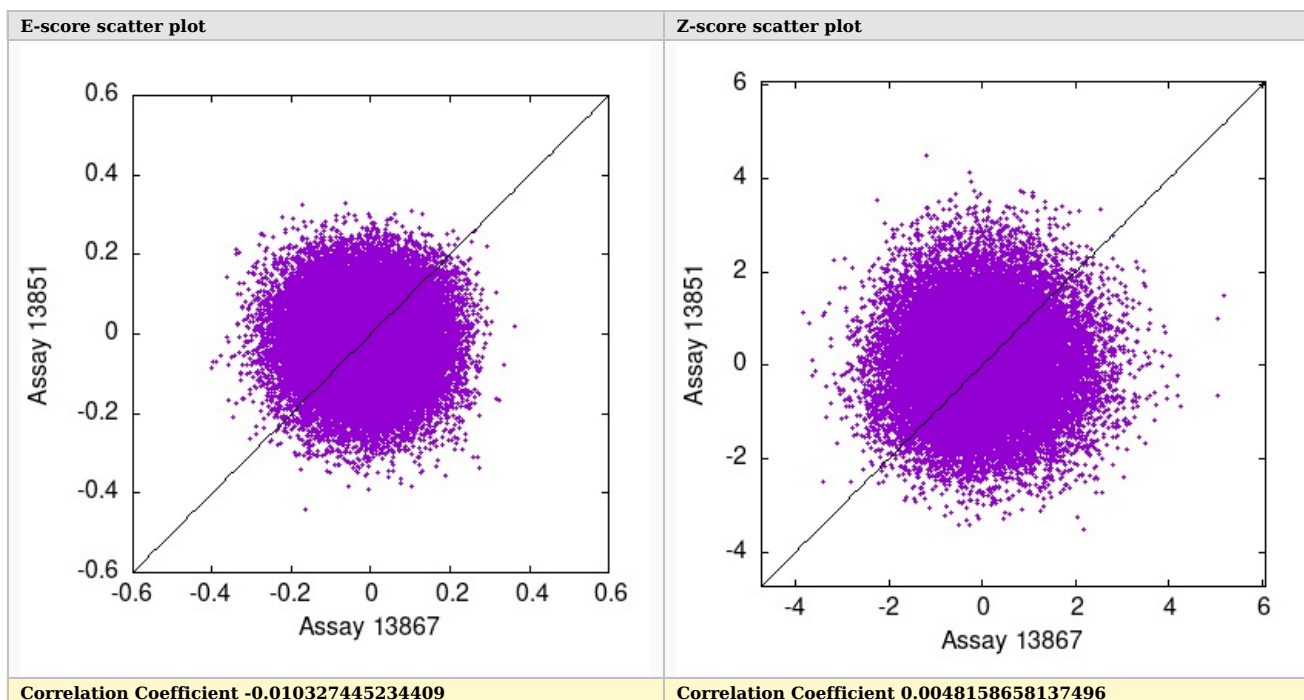


## QC report



### Top scoring motifs for Assay 13867

Protein ID: pTH14251.2 Gene: ZHX3.DBD.1 Domain: Homeobox Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CAATATTG	0.36246	CAATATTG----	CGCCTTAA	5.17006	--CGCCTTAA--
ATTGTAG	0.33740	---ATTGTAG-	CATCATGG	5.05897	---CCATGATG
CCACCTGC	0.32253	-GCAGGTGG--	CAATATTG	5.05158	--CAATATTG--
AACAAATG	0.31844	AACAAATG----	CTTCGCAC	4.24590	-GTGCGAAG---
TAATTGGA	0.31584	--TAATTGGA--	CGCTATGA	4.18749	--CGCTATGA--
CGCCTTAA	0.30314	-TTAAGGCG--	CGCCCAAC	4.18503	--GTTGGGCG-
CATCATGG	0.29982	CATCATGG----	AATTGCT	4.02602	---AATTGCT-
GGAATTGA	0.29262	-GGAATTGA--	GTCTATCA	3.97171	--GTCTATCA--
CCTGTACC	0.29228	----CCTGTACC	GAGGCTCC	3.94365	GAGGCTCC----
CGCACAAAC	0.29181	----GTTGTGCG	CGTCTATC	3.92396	--CGTCTATC--

### Top scoring motifs for Assay 13851

Protein ID: pTH14251.1 Gene: ZHX3.DBD.1 Domain: Homeobox Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AGAATTAG	0.33096	---CTAATTCT-	AAGTATTA	4.50572	AAGTATTA--
TACCTCGA	0.32643	---TACCTCGA	CGTGAGCA	4.14142	CGTGAGCA--
GGCTTTAC	0.30988	GGCTTTAC----	CCGATCGG	3.91656	-CCGATCGG-
ACTCACTC	0.30247	--ACTCACTC--	AGACCACT	3.71771	--AGACCACT
CGTGAGCA	0.30186	-TGCTCAGC--	ATTATCGG	3.71771	-ATTATCGG-
TTCAAGAA	0.30161	---TTCAAGAA--	GGCTTGTA	3.69153	--GGCTTGTA
GACTGTCA	0.30136	-GACTGTCA--	CAGGACGA	3.68650	CAGGACGA--
GAATAGCA	0.29865	-GAATAGCA--	ATGATCAT	3.66670	-ATGATCAT-
TAATGTAA	0.29768	--TTACATTA--	TGTTATAA	3.65395	TGTTATAA--
AGGGCGTG	0.29530	-CACGCCCT--	ACATCGGG	3.64589	--ACATCGGG