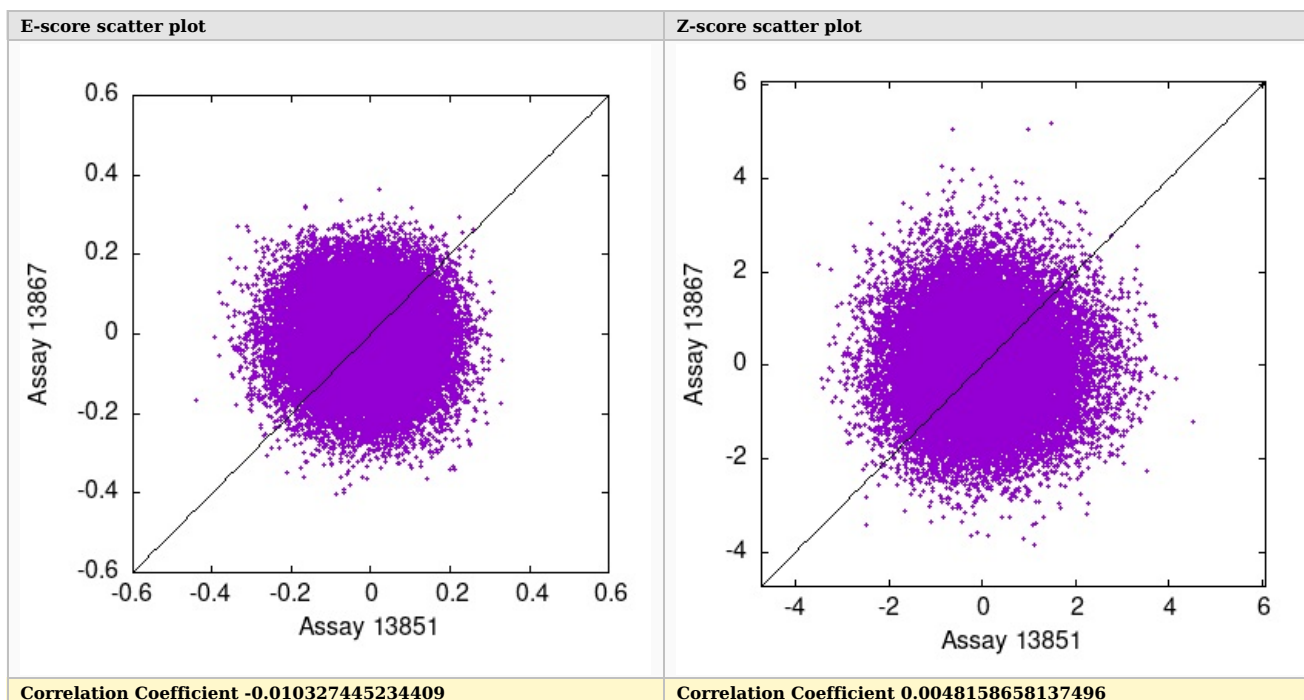


QC report



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'

Forward:

Reverse:



Top 10	Scores	Alignment
AGAATTAG	0.33096	---CTAATTCT-
TACCTCGA	0.32643	---TACCTCGA
GGCTTTAC	0.30988	GGCTTTAC----
ACTCACTC	0.30247	--ACTCACTC--
CGTGAGCA	0.30186	-TGCTCACG---
TTCAAGAA	0.30161	---TTCAAGAA--
GACTGTCA	0.30136	-GACTGTCA---
GAATAGCA	0.29865	-GAATAGCA---
TAATGTAA	0.29768	--TTACATTA--
AGGGCGTG	0.29530	-CACGCCCT---

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
AAGTATTA	4.50572	AAGTATTA--
CGTGAGCA	4.14142	CGTGAGCA--
CCGATCGG	3.91656	--CCGATCGG--
AGACCACT	3.71771	--AGACCACT--
ATTATCGG	3.71771	-ATTATCGG--
GGCTTGTA	3.69153	--GGCTTGTA--
CAGGACGA	3.68650	CAGGACGA--
ATGATCAT	3.66670	-ATGATCAT--
TGTTATAA	3.65395	TGTTATAA--
ACATCGGG	3.64589	--ACATCGGG--

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'

Forward:

Reverse:



Top 10	Scores	Alignment
CAATATTG	0.36246	CAATATTG----
ATTTGTAG	0.33740	---ATTTGTAG--
CCACCTGC	0.32253	-GCAGGTGG---
AACAAATG	0.31844	AACAAATG----
TAATTGGA	0.31584	--TAATTGGA--
CGCCTTAA	0.30314	---TTAAGGCG---
CATCATGG	0.29982	CATCATGG----
GGAATTGA	0.29262	---GGAATTGA---
CCTGTACC	0.29228	----CCTGTACC--
CGCACAAAC	0.29181	----GTTGTGCG--

8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment
CGCCTTAA	5.17006	--CGCCTTAA--
CATCATGG	5.05897	---CATCATGG--
CAATATTG	5.05158	--CAATATTG--
CTTCGCAC	4.24590	--GTGCGAAG---
CGCTATGA	4.18749	--CGCTATGA--
CGCCCAAC	4.18503	---GTTGGGCG---
AATTTGCT	4.02602	---AATTTGCT--
GTCTATCA	3.97171	--GTCTATCA--
GAGGCTCC	3.94365	GAGGCTCC----
CGTCTATC	3.92396	-CGTCTATC---