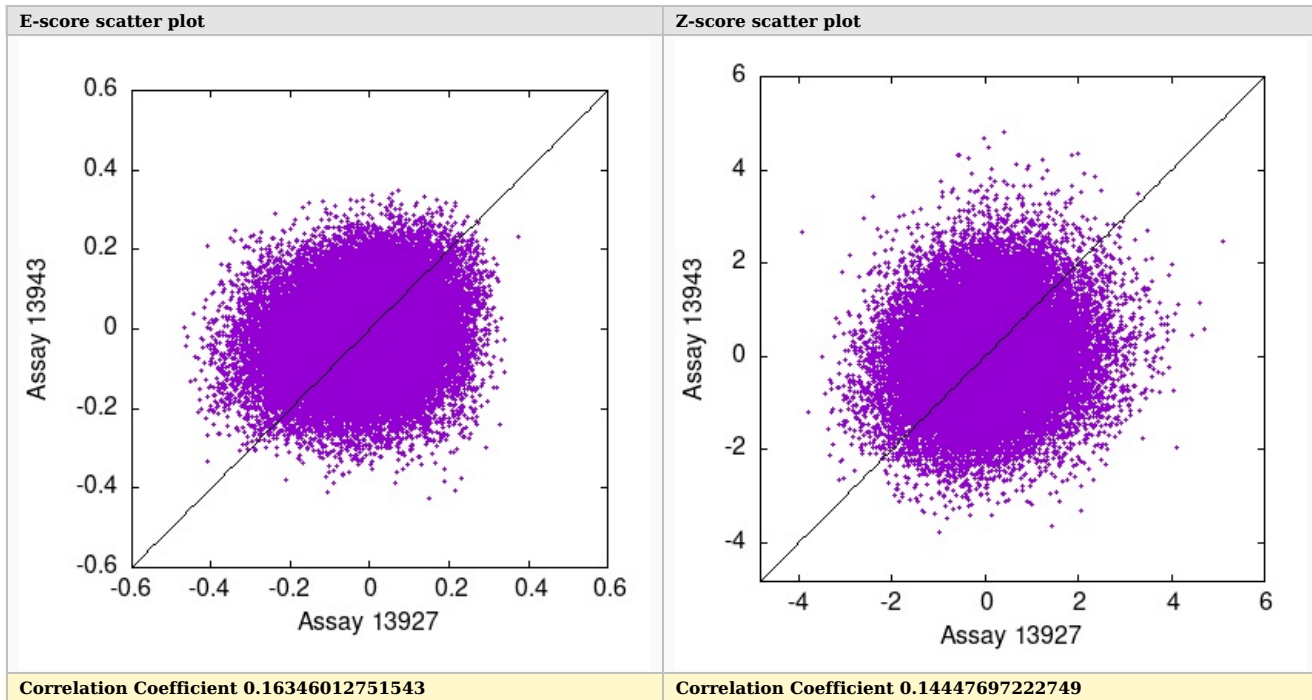


QC report



Top scoring motifs for Assay 13927

Protein ID: pTH14244.1 Gene: MKX.FL 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
AACAAAGC	0.37407	--AACAAAGC--	AACAAAGC	5.09609	--GCTTTGTT---
AACTAGTG	0.33884	--CACTAGTT--	GCAACAA	4.69167	-----TTGTTTGC
AACGTTGT	0.33866	-ACAACGTT---	CAGCAACG	4.59416	---CGTTGCTG--
ACACTAAT	0.33356	-ACACTAAT---	AACGTTGT	4.44998	-AACGTTGT----
TGGTTAAA	0.33201	---TTTAACCA-	AACGTTGT	4.13141	--TTGCAGTT---
GCAATTGC	0.32665	-GCAATTGC---	GCAATTGC	4.10810	-GCAATTGC----
TTGACAAA	0.32483	TTGACAAA----	ATGTACAA	4.09185	-----TTGTACAT
ATTATTAC	0.32162	-GTAATAAT---	GGATAAAA	4.05932	---TTTTATCC--
CAACTTCG	0.32081	----CGAAGTTG	CACAACAC	4.05330	--GTGTTGTG--
AACACTAA	0.32057	AACACTAA----	CAACGTTG	4.00079	CAACGTTG----

Top scoring motifs for Assay 13943

Protein ID: pTH14244.2 Gene: MKX.FL 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
ATATACAA	0.34991	-TTGTATAT--	CATAATAC	4.80063	---GTATTATG--
CTTATAAG	0.34012	--CTTATAAG-	ATTACTAC	4.68572	GTAGTAAT-----
AAAGAAAG	0.33565	-CTTCTTTT--	AGCATGGG	4.48470	---AGCATGGG--
GTAATGTA	0.33166	--TACATTAC-	GACGTTAA	4.34646	---TTAACGTC--
TATACCGA	0.32905	TCGGTATA---	CATGATCC	4.32918	-GGATCATG----
CATGATCC	0.32679	---GGATCATG	GTAATGTA	4.32918	---GTAATGTA--
CTGTATTA	0.32665	-CTGTATTA--	AATCGATT	4.30729	-----AATCGATT
GAGATATA	0.32335	--TATATCTC-	AGTGTGTG	4.26438	-----AGTGTGTG
CGTTCGAC	0.32230	---GTCGAACG	TACATGTA	4.22464	---TACATGTA--
ATTACTAC	0.32160	---GTAGTAAT	ACACACAC	4.12125	----GTGTGTGT-