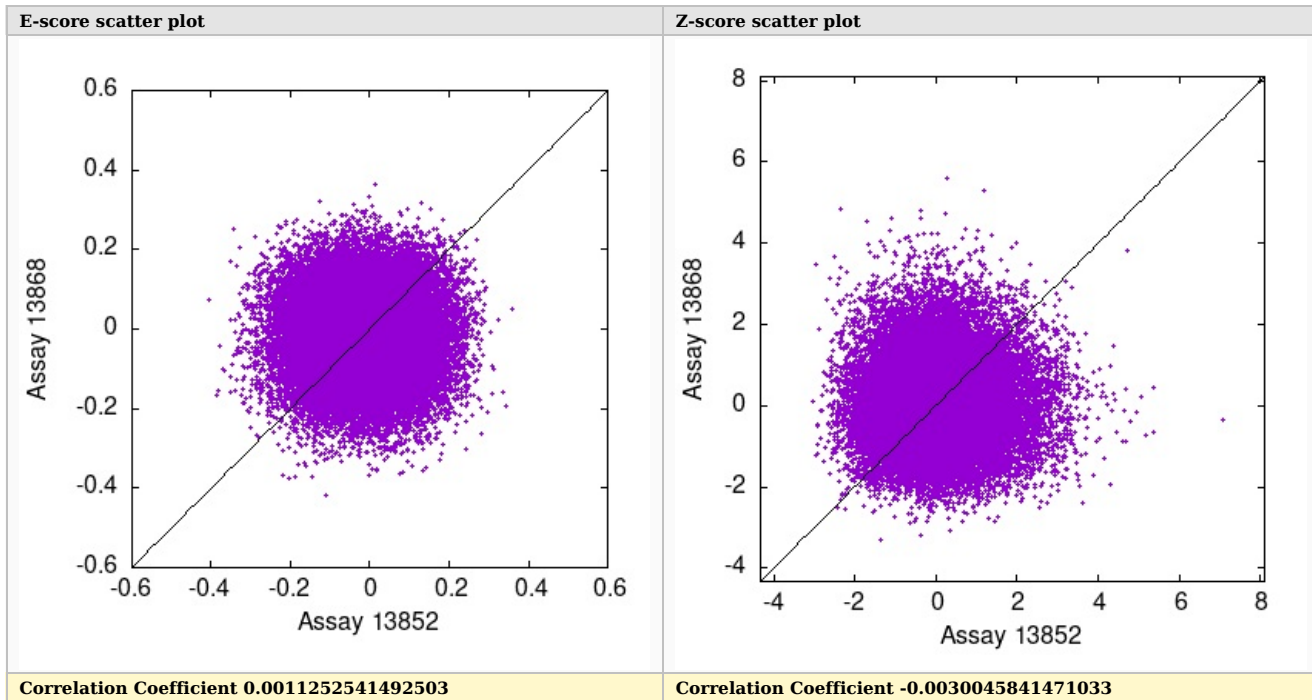


QC report



Top scoring motifs for Assay 13852

Protein ID: pTH14252.1 Gene: ZHX3.DBD.2 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
CTGCAGTC	0.35938	CTGCAGTC----	TAACGTTA	7.06436	-TAACGTTA--
TAACGTTA	0.34371	-TAACGTTA----	CTGCAGTC	5.36879	--CTGCAGTC-
ATGGAGAC	0.33463	----GTCTCCAT	ACTCCCCC	5.34590	---GGGGAGT
CTTGTTCA	0.32341	----TGAACAAG	CTTGTTCA	5.17152	---TGAACAAG
ACTCGGCT	0.31169	-ACTCGGCT----	CAAGAGGC	5.07864	--CAAGAGGC-
ATACATAC	0.30856	----ATACATAC-	ATGGAGAC	4.95604	--ATGGAGAC-
CCGTCCGA	0.30814	---CCGTCCGA--	ACTCGGCT	4.79663	---AGCCGAGT
GTTATAAC	0.30347	----GTTATAAC	AGGCATTG	4.72024	CAATGCCT---
CCGTACAC	0.29767	---CCGTACAC--	GTTGCAAC	4.69102	--GTTGCAAC-
AAACCCAG	0.29497	----AAACCCAG-	GTTATAAC	4.67075	--GTTATAAC-

Top scoring motifs for Assay 13868

Protein ID: pTH14252.2 Gene: ZHX3.DBD.2 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
AGCCTCGA	0.36359	----AGCCTCGA--	CAATAAAC	5.61757	-----CAATAAAC----
AGACGTCT	0.33232	----AGACGTCT--	CGCTTAAG	5.30861	-----CGCTTAAG----
AACTGATC	0.32019	-----AACTGATC	CAGGCTG	4.85479	-----CAGGCTG-----
ATTACGAA	0.31820	-----TTCGTAAT	TCGGTAAA	4.81963	-----TCGGTAAA-----
CAGGCCTG	0.31522	---CAGGCCTG---	AAGAAAAC	4.73800	-----AAGAAAAC-----
CAGTCGGG	0.30860	---CAGTCGGG---	CGGTCCAG	4.61952	-----CGGTCCAG-----
ACATAAGT	0.30140	--ACATAAGT----	AGCCTCGA	4.60731	AGCCTCGA-----
CCAAGAAC	0.30043	---CCAAGAAC---	TTACCGAA	4.55215	---TTACCGTAA-----
GAGGCTCC	0.29770	---GAGGCTCC---	AAACAGCC	4.36047	-----AAACAGCC-----
GAGCAAGC	0.29703	GAGCAAGC-----	ATTTTGG	4.32495	-----CCAAAAAT-----