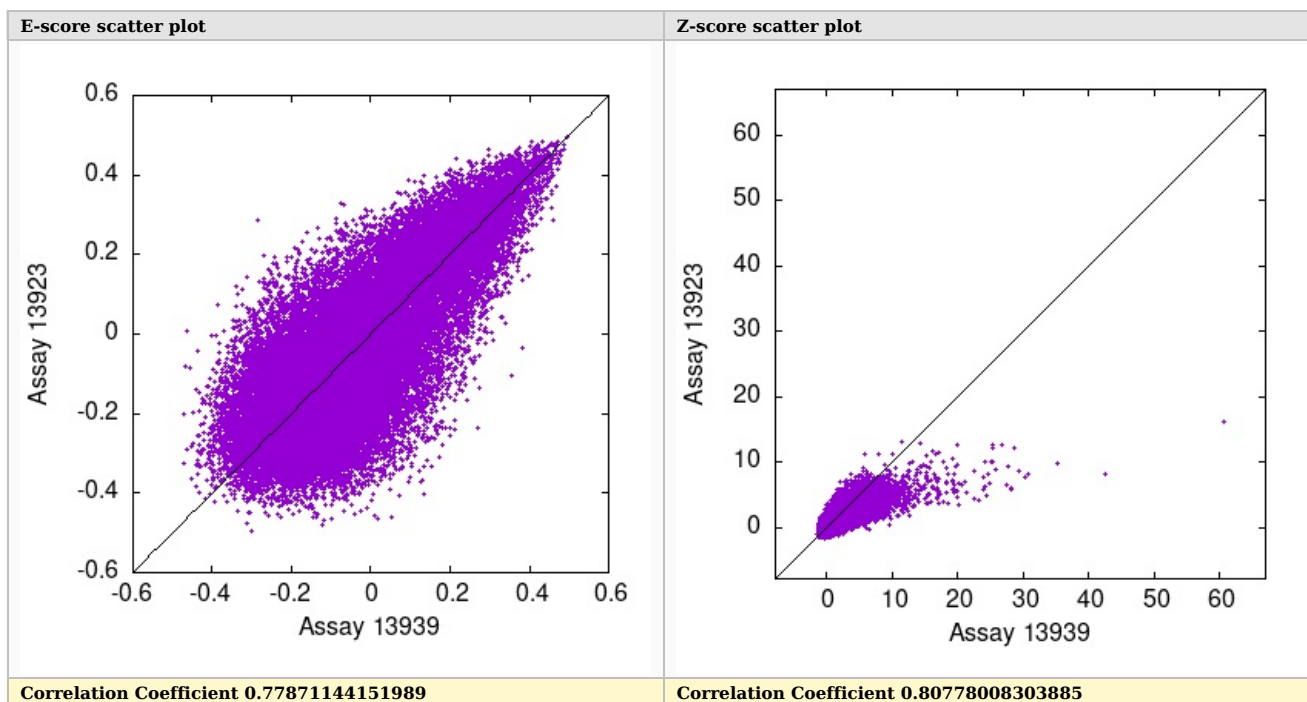


QC report



Top scoring motifs for Assay 13939

Protein ID: pTH14224.2 Gene: TET3 Domain: zf-CXXC Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:

Reverse:



8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACGTACGT	0.49348	ACGTACGT----	ACGTACGT	60.77964	ACGTACGT----
CACGTACG	0.48775	-CGTACGTG---	CACGTACG	42.50194	-CGTACGTG---
CTACGTAC	0.48552	--GTACGTAG--	CTACGTAC	35.25481	--GTACGTAG--
ACGTAACG	0.47964	----ACGTAACG	TTACGTAA	30.80576	---TTACGTAA---
CCTACGTA	0.47897	-CCTACGTA---	GTACGTAA	30.39577	--GTACGTAA---
TACGTAAA	0.47806	---TACGTAAA--	TACGTAAA	29.38805	---TACGTAAA--
GTACGTAA	0.47642	--GTACGTAA--	GTTACGTA	28.61336	---TACGTAAAC--
CTACGTAG	0.47586	--CTACGTAG--	AGGGGGGA	28.27380	-AGGGGGGA----
ATACGTAA	0.47507	--ATACGTAA--	ACGTTGCG	28.12513	----CGCAACGT
CGTACGTC	0.47244	-CGTACGTC---	ACGTAACG	27.83867	----ACGTAACG-

Top scoring motifs for Assay 13923

Protein ID: pTH14224.1 Gene: TET3 Domain: zf-CXXC Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:

Reverse:



8 mer Z-scores for probeset 'all'

Forward:

Reverse:



Top 10	Scores	Alignment	Top 10	Scores	Alignment
ACGTACGT	0.49355	---ACGTACGT-	ACGTACGT	16.27967	---ACGTACGT-
GGGGGGGA	0.48511	---TCCCCCCC-	GGGGGGGA	13.12314	---TCCCCCCC-
CCCCCCCC	0.48468	---CCCCCCCC-	CGCGTACG	12.82485	---CGTACGCG
ACGTACGC	0.48323	---ACGTACGC-	CGTACGTC	12.73670	--GACGTACG--
CGTACGTC	0.48256	--GACGTACG--	ACGTACGC	12.64737	---ACGTACGC-
CGTACGTA	0.48172	--TACGTACG--	CGTACGTA	12.62628	--TACGTACG--
GTTACGTA	0.47916	GTTACGTA----	GTACGTAC	12.20438	-GTACGTAC---
CGCGTACG	0.47870	----CGTACGCG	GTTACGTA	12.16962	GTTACGTA----
CGACGTAC	0.47785	-CGACGTAC---	ACGTAGCG	11.70842	---ACGTAGCG-
ACGTAGCG	0.47701	---ACGTAGCG-	CGGTACGC	11.60819	---CGGTACGC-