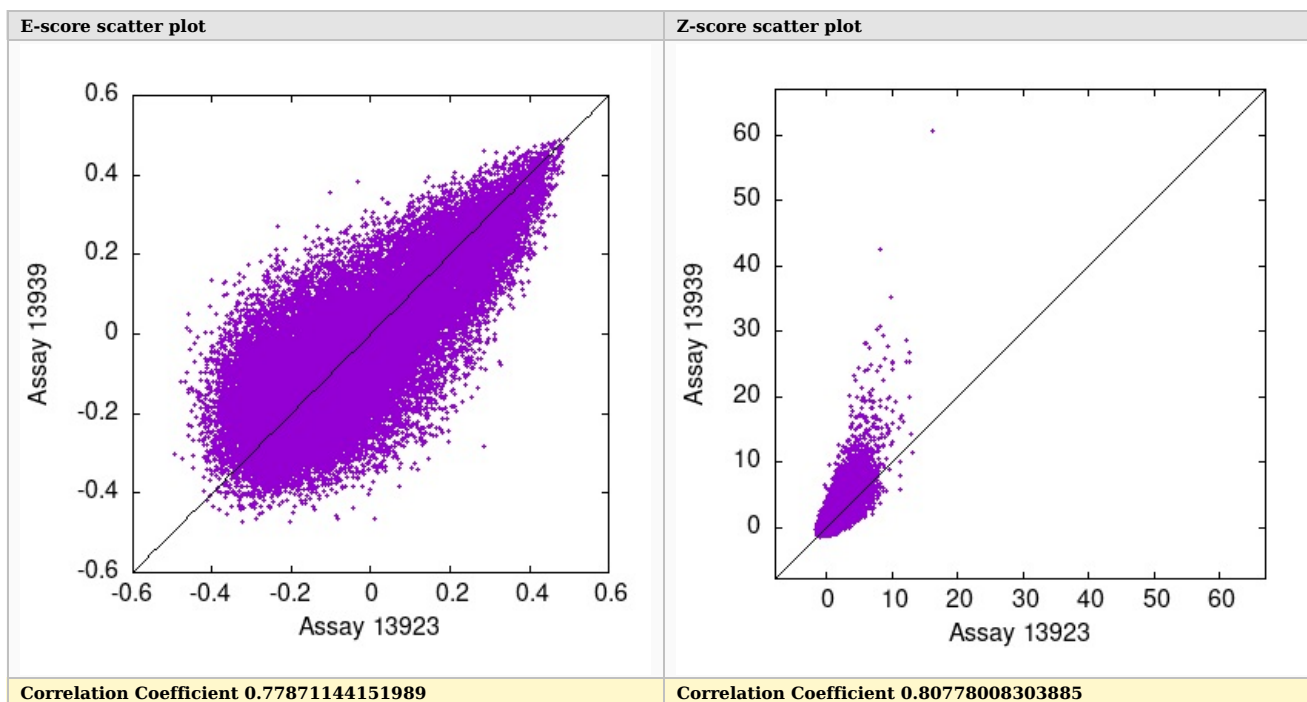


QC report





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:	
Top 10	Scores	Alignment	
ACGTACGT	0.49355	---ACGTACGT-	
GGGGGGGA	0.48511	---TCCCCCCC-	
CCCCCCCC	0.48468	---CCCCCCCC-	
ACGTACGC	0.48323	---ACGTACGC-	
CGTACGTC	0.48256	--GACGTACG--	
CGTACGTA	0.48172	--TACGTACG--	
GTTACGTA	0.47916	GTTACGTA----	
CGCGTACG	0.47870	---CGTACGCG	
CGACGTAC	0.47785	-CGACGTAC---	
ACGTAGCG	0.47701	---ACGTAGCG-	



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ACGTACGT	16.27967	---ACGTACGT-	
GGGGGGGA	13.12314	---TCCCCCCC-	
CGCGTACG	12.82485	---CGTACGCG	
CGTACGTC	12.73670	--GACGTACG--	
ACGTACGC	12.64737	---ACGTACGC-	
CGTACGTA	12.62628	--TACGTACG--	
GTACGTAC	12.20438	-GTACGTAC---	
GTTACGTA	12.16962	GTTACGTA---	
ACGTAGCG	11.70842	---ACGTAGCG-	
GCGTACGC	11.60819	---GCGTACGC-	



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:	
		
Top 10	Scores	Alignment
ACGTACGT	0.49348	ACGTACGT----
CACGTACG	0.48775	-CGTACGTG---
CTACGTAC	0.48552	--GTACGTAG--
ACGTAACG	0.47964	----ACGTAACG
CCTACGTA	0.47897	---CCTACGTA---
TACGTAAA	0.47806	---TACGTAAA---
GTACGTAA	0.47642	--GTACGTAA--
CTACGTAG	0.47586	--CTACGTAG--
ATACGTAA	0.47507	--ATACGTAA---
CGTACGTC	0.47244	-CGTACGTC---

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
ACGTACGT	60.77964	ACGTACGT-----
CACGTACG	42.50194	-CGTACGTG-----
CTACGTAC	35.25481	--GTACGTAG-----
TTACGTAA	30.80576	--TTACGTAA-----
GTACGTAA	30.39577	--GTACGTAA-----
TACGTAAA	29.38805	---TACGTAAA-----
GTTACGTA	28.61336	---TACGTAA-----
AGGGGGGA	28.27380	-AGGGGGGA-----
ACGTTGCG	28.12513	----CGCAACGT-----
ACGTAACG	27.83867	----ACGTAACG-----