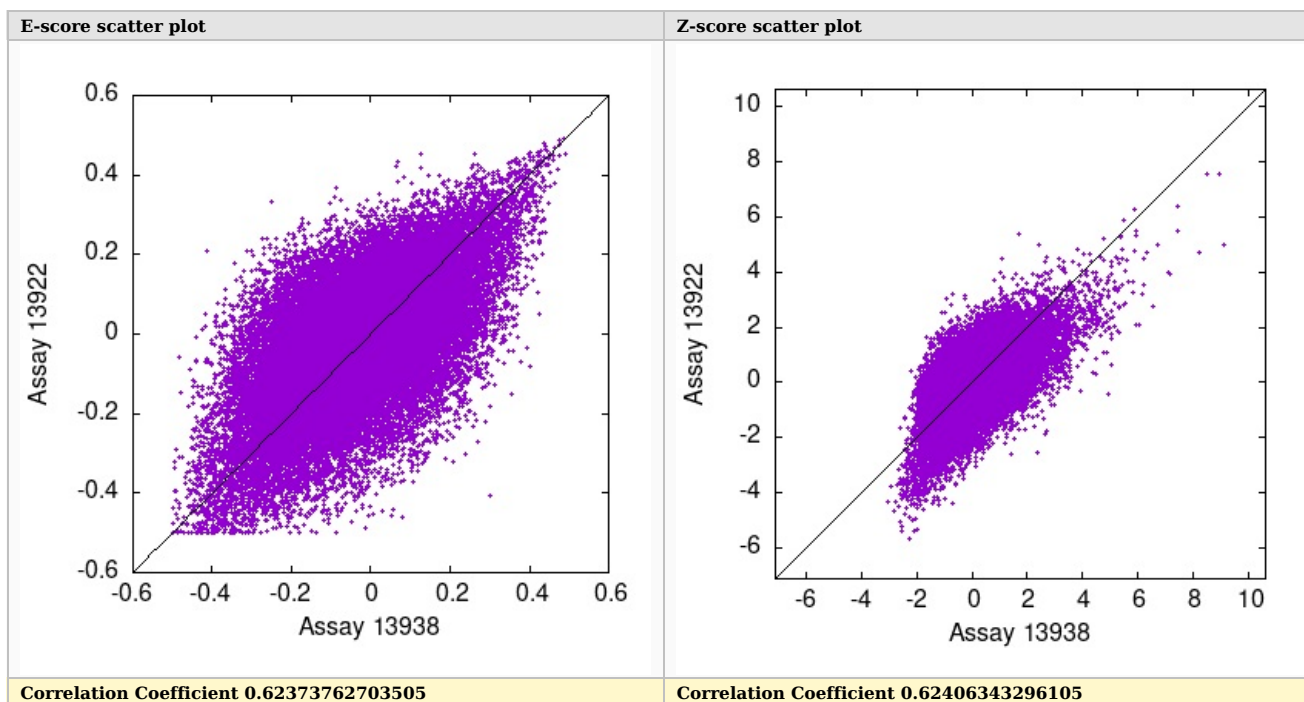




QC report





Top scoring motifs for Assay 13938

Protein ID: pTH14223.2 Gene: KDM2A.DBD Domain: zf-CXXC Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
TCGCGCGA	0.49053	TCGCGCGA----
CGCGCGCG	0.48578	-CGCGCGCG---
GCGCGCGC	0.47717	GCGCGCGC----
TACGCGTA	0.47512	-TACGCGTA---
TTACGTAA	0.47389	--TTACGTAA--
CGCGCGAA	0.47256	-CGCGCGAA---
GCGATCGC	0.46556	GCGATCGC----
TACGTAAA	0.46267	---TACGTAAA--
CGGTACGC	0.46143	----GCGTACGC--
CGCGCGTA	0.46034	-CGCGCGTA---

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
TCGCGCGA	9.15609	TCGCGCGA - - -
CGCGCGCG	8.97293	- CGCGCGCG - - -
TACGCGTA	8.51206	- TACGCGTA - - -
TTACGTAA	8.21350	- - TTACGTAA - -
GCGCGCGC	7.47813	GCGCGCGC - - -
GCGATCGC	7.43904	- - - GCGATCGC -
TACGTAAA	7.17926	- TACGTAAA - - -
CGCGCGAA	7.10477	- CGCGCGAA - - -
CGTACGTA	6.72384	- CGTACGTA - - -
ACGTACGA	6.54474	ACGTACGA - - -



Top scoring motifs for Assay 13922

Protein ID: pTH14223.1 Gene: KDM2A.DBD Domain: zf-CXXC Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
CGCGCGCG	0.49329	---CGCGCGCG---	
TACGCGTA	0.48626	---TACGCGTA---	
ACGTACGT	0.48059	---ACGTACGT---	
GCGCGCGC	0.47718	---GCGCGCGC---	
CGCGTAAC	0.47211	---GTTACGCG---	
GCGATCGC	0.46795	GCGATCGC----	
ATCGCGCG	0.46528	---ATCGCGCG---	
ACGCGTAA	0.46023	---TTACGCGT---	
ATACGTAT	0.46004	---ATACGTAT---	
CGATCGCG	0.45733	-CGATCGCG---	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
TACGCGTA	7.56474	TACGCGTA---
CGCGCGCG	7.56077	--CGCGCGCG--
GCGCGCGC	6.36709	-GCGCGCGC---
CGCGTAAC	6.27990	--CGCGTAAC-
ACGTACGT	5.88930	---ACGTACGT---
ACGCGTAA	5.52059	-ACGCGTAA---
GCGATCGC	5.48057	---GCGATCGC---
CGAATTCG	5.38351	--CGAATTCG---
AATACGTA	5.32068	AATACGTA---
ATACGTAT	5.32068	-ATACGTAT--