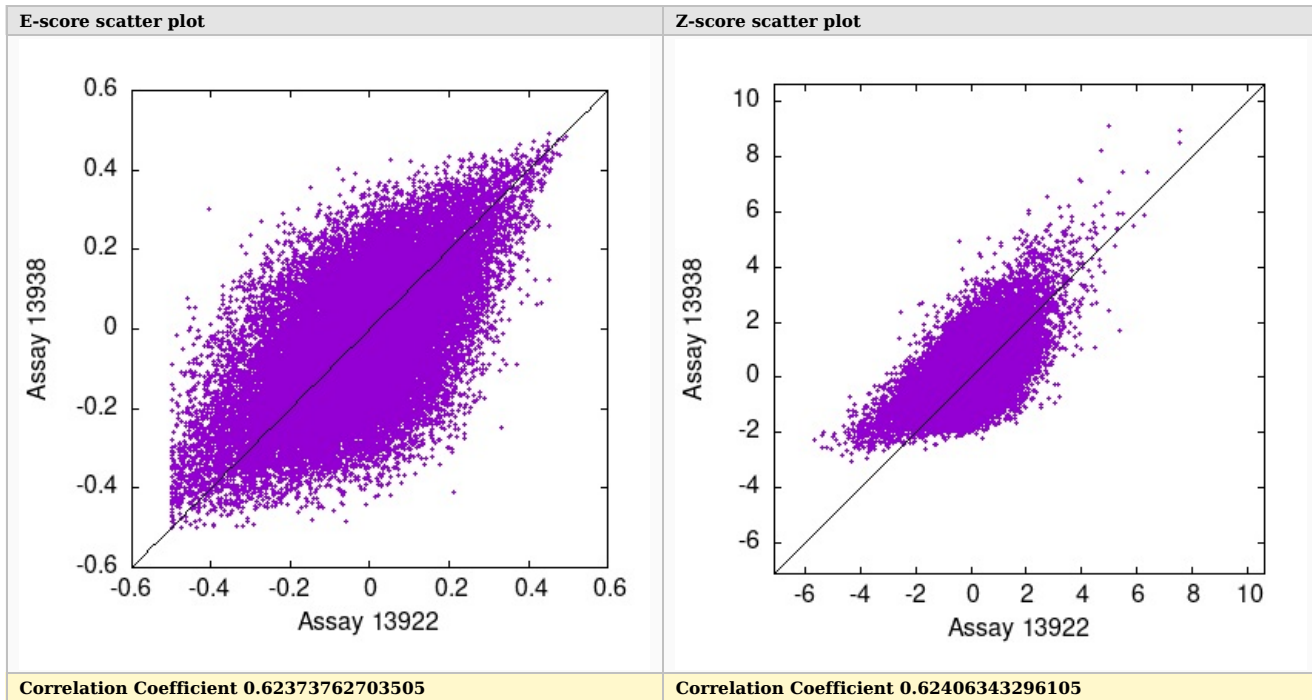


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
CGCGCGCG	0.49329	---CGCGCGCG--	TACGCGTA	7.56474	TACGCGTA---
TACGCGTA	0.48626	---TACGCGTA--	CGCGCGCG	7.56077	--CGCGCGCG--
ACGTACGT	0.48059	---ACGTACGT--	GCGCGCGC	6.36709	-GCGCGCGC--
GCGCGCGC	0.47718	---GCGCGCGC--	CGCGTAAC	6.27990	--CGCGTAAC--
CGCGTAAC	0.47211	---GTTACGCG--	ACGTACGT	5.88930	---ACGTACGT--
GCGATCGC	0.46795	GCGATCGC----	ACGCGTAA	5.52059	-ACGCGTAA--
ATCGCGCG	0.46528	---ATCGCGCG--	GCGATCGC	5.48057	---GCGATCGC--
ACGCGTAA	0.46023	---TTACGCGT--	CGAATTCG	5.38351	--CGAATTCG--
ATACGTAT	0.46004	---ATACGTAT--	AATACGTA	5.32068	AATACGTA---
CGATCGCG	0.45733	-CGATCGCG---	ATACGTAT	5.32068	-ATACGTAT--

### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TCGCGCGA	0.49053	TCGCGCGA----	TCGCGCGA	9.15609	TCGCGCGA----
CGCGCGCG	0.48578	-CGCGCGCG---	CGCGCGCG	8.97293	--CGCGCGCG---
GCGCGCGC	0.47717	GCGCGCGC----	TACGCGTA	8.51206	-TACGCGTA---
TACGCGTA	0.47512	-TACGCGTA---	TTACGTAA	8.21350	--TTACGTAA--
TTACGTAA	0.47389	--TTACGTAA--	GCGCGCGC	7.47813	GCGCGCGC----
CGCGCGAA	0.47256	-CGCGCGAA---	GCGATCGC	7.43904	---GCGATCGC--
GCGATCGC	0.46556	GCGATCGC----	TACGTAAA	7.17926	-TACGTAAA---
TACGTAAA	0.46267	---TACGTAAA--	CGCGCGAA	7.10477	-CGCGCGAA---
GCGTACGC	0.46143	----GCGTACGC--	CGTACGTA	6.72384	-CGTACGTA---
CGCGCGTA	0.46034	-CGCGCGTA---	ACGTACGA	6.54474	ACGTACGA----