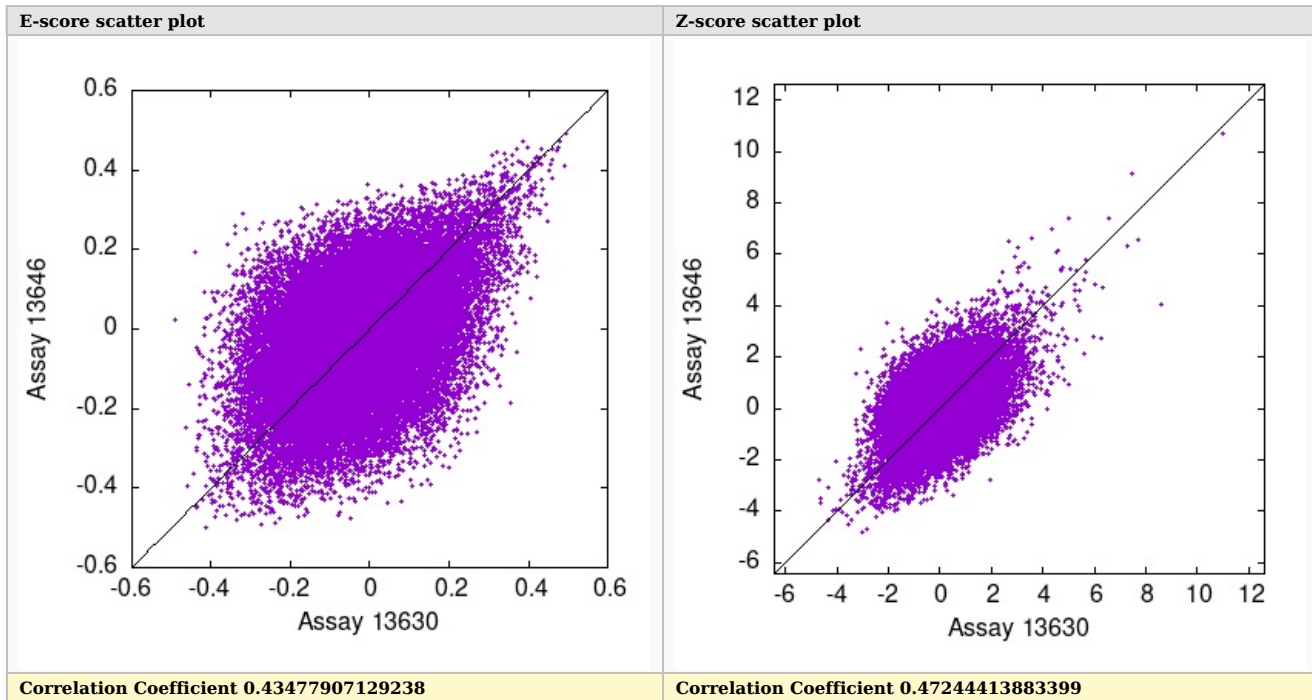


QC report



Top scoring motifs for Assay 13630

Protein ID: pTH14233.1 Gene: GRHL3.DBD Domain: CP2 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
AACCGGTT	0.49681	-AACCGGTT-	AACCGGTT	11.01874	-AACCGGTT-
ACCGGTTC	0.48984	--ACCGGTTC	ACCGGTTC	8.61804	--ACCGGTTC
AAACCGGT	0.47982	AAACCGGT--	AACCGATT	7.67055	-AACCGATT-
AACCGATT	0.47685	-AACCGATT-	AAACCGGT	7.48107	AAACCGGT--
AACCGGTC	0.47221	-AACCGGTC-	AACCGGTC	7.28075	-AACCGGTC-
AACTTGTC	0.46067	AACTTGTC--	ACCGTTTA	6.53757	--ACCGTTTA
ACCGGTTA	0.45931	--ACCGGTTA	AACCGGAT	6.30572	-AACCGGAT-
AAACAGT	0.45907	AAACAGT--	AACAGGTC	6.24569	-AACAGGTC-
AACCGGAT	0.45440	-AACCGGAT-	AAACCTGC	6.04000	AAACCTGC--
AACTTGCC	0.45357	-AACTTGCC-	AAGTTGCC	5.96651	-AAGTTGCC-

Top scoring motifs for Assay 13646

Protein ID: pTH14233.2 Gene: GRHL3.DBD Domain: CP2 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
AACCGGTT	0.49017	--AACCGGTT----	AACCGGTT	10.67278	-AACCGGTT-
AAACCGGT	0.47297	-AAACCGGT-----	AAACCGGT	9.14692	AAACCGGT--
GTTGCAAC	0.47060	-----GTTGCAAC	ACCGTTTA	7.40347	--ACCGTTTA
AACCGATT	0.45511	--AACCGATT-----	AACCGGTA	7.37637	-AACCGGTA-
ACCGTTTG	0.45501	---ACCGTTTG----	ACCGTTTG	6.96859	--ACCGTTTG
ACCGTTTA	0.45483	---ACCGTTTA----	AACTAGTT	6.62897	-AACTAGTT-
AAAACCGG	0.45454	AAAACCGG-----	AACCGATT	6.52992	-AACCGATT-
AACTAGTT	0.45113	--AACTAGTT-----	AAACTTGT	6.49956	AAACTTGT--
AACCGGTA	0.45101	-AACCGGTA-----	AACCGGTC	6.34843	-AACCGGTC-
AACCGGTC	0.44963	--AACCGGTC-----	AAACAAC	6.25752	-AAACAAC-