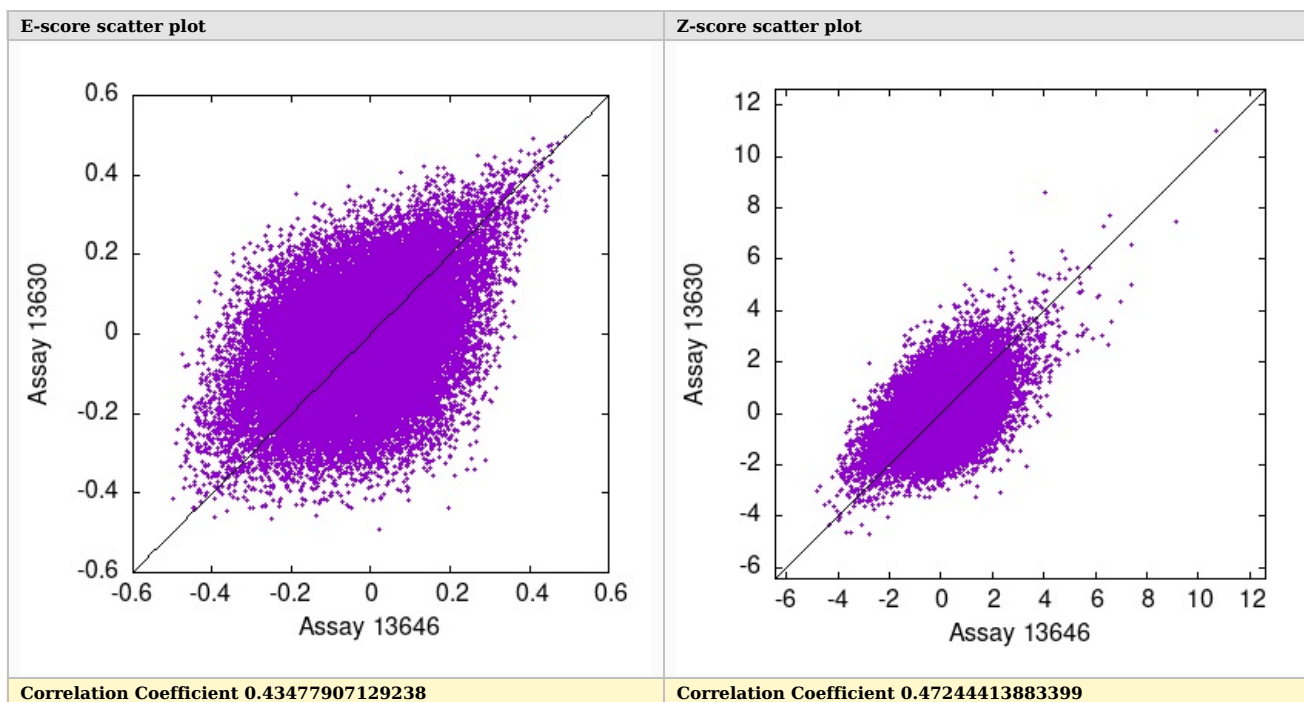




QC report





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'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AACCGGTT	0.49017	--	AACCGGTT----
AAACCGGT	0.47297	--	AAACCGGT-----
GTTGCAAC	0.47060	-----	GTTGCAAC
AACCAAGT	0.45511	--	AACCAAGT-----
ACCGGTTG	0.45501	---	ACCGGTTG----
ACCGGTTA	0.45483	---	ACCGGTTA----
AAAACCGG	0.45454	AAAACCGG	-----
AACTAGTT	0.45113	--	AACTAGTT-----
AACCGGTA	0.45101	--	AACCGGTA-----
AACCGGTC	0.44963	--	AACCGGTC-----



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AACCGGTT	10.67278	-	AACCGGTT-
AAACCGGT	9.14692		AAACCGGT--
ACCGGTTA	7.40347	--	-ACCGGTTA
AACCGGTA	7.37637	-	-AACCGGTA-
ACCGGTTG	6.96859	--	-ACCGGTTG
AACTAGTT	6.62897	-	-AACTAGTT-
AACCAAGT	6.52992	-	-AACCAAGT-
AACTTGT	6.49956		AACTTGT--
AACCGGTC	6.34843	-	-AACCGGTC-
AAACAAC	6.25752	-	-AAACAAC-



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'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AACCGGTT	0.49681	-AACCGGTT-
ACCGGTTT	0.48984	--ACCGGTTT
AAACCGGT	0.47982	AAACCGGT--
AACCAAGT	0.47685	-AACCAAGT-
AACCGGTC	0.47221	-AACCGGTC-
AAACTTGC	0.46067	AAACTTGC--
ACCGGTTA	0.45931	--ACCGGTTA
AAACCAAGT	0.45907	AAACCAAGT--
AACCGGAT	0.45440	-AACCGGAT-
AACTTGCC	0.45357	-AACTTGCC-

8 mer Z-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AACCGGTT	11.01874	-AACCGGTT-
ACCGGTTC	8.61804	--ACCGGTTC
AACCAAGT	7.67055	-AACCAAGT-
AAACCGGT	7.48107	AAACCGGT--
AACCGGTC	7.28075	-AACCGGTC-
ACCGGTTA	6.53757	--ACCGGTTA
AACCGGAT	6.30572	-AACCGGAT-
AACAGGTC	6.24569	-AACAGGTC-
AAACCTGC	6.04000	AAACCTGC--
AAGTTGCC	5.96651	-AAGTTGCC-