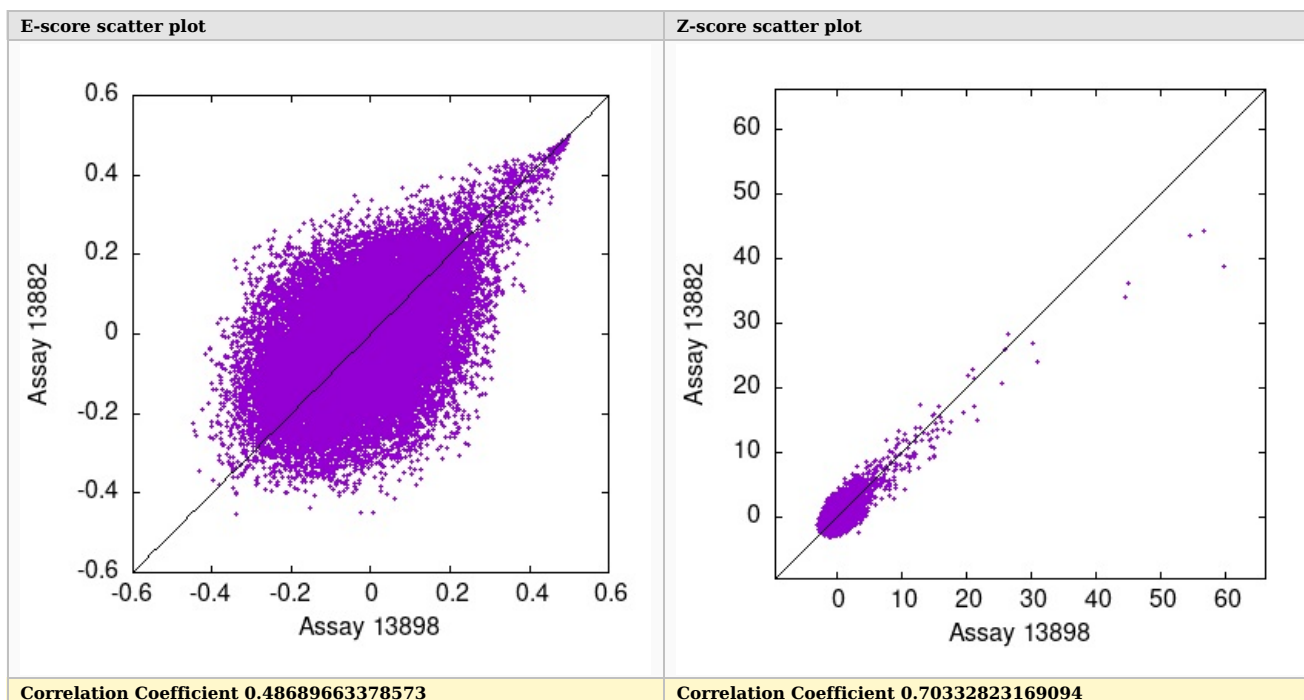


QC report



Top scoring motifs for Assay 13898

Protein ID: pTH14278.2 Gene: TERF1 Domain: Myb_DNA-binding Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AACCCTAG	0.49945	--AACCCTAG
TAACCCTA	0.49927	-TAACCCTA-
AACCCTAA	0.49918	--AACCCTAA
CAACCCTA	0.49841	-CAACCCTA-
GAACCCTA	0.49836	-GAACCCTA-
TAGGGTAA	0.49669	-TTACCCTA-
AACCCTAC	0.49625	--AACCCTAC
AGGGTTAC	0.49455	GTAACCCT--
AGGGTTCA	0.49395	TGAACCCT--
AACCCTAT	0.49373	--AACCCTAT

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AACCCTAA	59.99796	--AACCCTAA
AACCCTAG	56.84303	--AACCCTAG
TAACCCTA	54.69533	-TAACCCTA-
CAACCCTA	45.10027	-CAACCCTA-
GAACCCTA	44.51927	-GAACCCTA-
TAGGGTAA	31.05236	-TTACCCTA-
AACCCTAC	30.25508	--AACCCTAC
AAACCCTA	26.53109	-AAACCCTA-
AACCCTAT	26.12791	--AACCCTAT
AGGGTTAC	25.58657	GTAACCCT--

Top scoring motifs for Assay 13882

Protein ID: pTH14278.1 Gene: TERF1 Domain: Myb_DNA-binding Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AACCCTAG	0.49743	--AACCCTAG
TAACCCTA	0.49704	-TAACCCTA-
AACCCTAA	0.49599	--AACCCTAA
CAACCCTA	0.49579	-CAACCCTA-
GAACCCTA	0.49496	-GAACCCTA-
AACCCTAC	0.49342	--AACCCTAC
TAGGGTAA	0.49232	-TTACCCTA-
AAACCCTA	0.49194	-AAACCCTA-
AGGGTTAG	0.49129	CTAACCCT--
AACCCTAT	0.49090	--AACCCTAT

Forward:	Reverse:

Top 10	Scores	Alignment
AACCCTAG	44.29370	-AACCCTAG
TAACCCTA	43.75437	TAACCCTA-
AACCCTAA	38.99789	-AACCCTAA
CAACCCTA	36.27410	CAACCCTA-
GAACCCTA	34.22661	GAACCCTA-
AAACCCTA	28.41413	AAACCCTA-
AACCCTAC	26.96859	-AACCCTAC
AACCCTAT	26.09133	-AACCCTAT
TAGGGTAA	24.22745	TTACCCTA-
CTAGGGTA	23.06647	-TACCCTAG