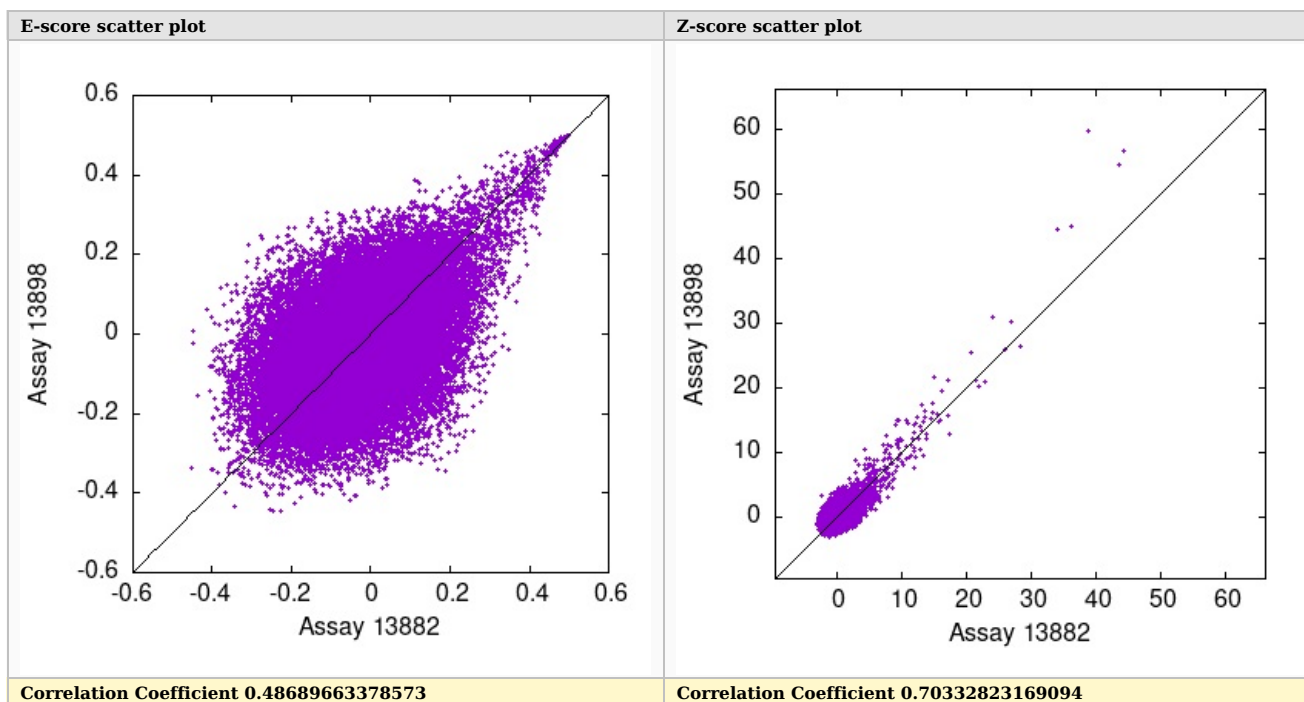


QC report



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
AACCCCTAG	0.49743	--AACCCCTAG
TAACCCCTA	0.49704	-TAACCCCTA-
AACCCCTAA	0.49599	--AACCCCTAA
CAACCCCTA	0.49579	-CAACCCCTA-
GAACCCCTA	0.49496	-GAACCCCTA-
AACCCCTAC	0.49342	--AACCCCTAC
TAGGGTAA	0.49232	-TTACCCCTA-
AAACCCCTA	0.49194	-AAACCCCTA-
AGGGTTAG	0.49129	CTAACCCCT--
AACCCCTAT	0.49090	--AACCCCTAT

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AACCCCTAG	44.29370	-AACCCCTAG
TAACCCCTA	43.75437	TAACCCCTA-
AACCCCTAA	38.99789	-AACCCCTAA
CAACCCCTA	36.27410	CAACCCCTA-
GAACCCCTA	34.22661	GAACCCCTA-
AAACCCCTA	28.41413	AAACCCCTA-
AACCCCTAC	26.96859	-AACCCCTAC
AACCCCTAT	26.09133	-AACCCCTAT
TAGGGTAA	24.22745	TTACCCCTA-
CTAGGGTAA	23.06647	-TACCCCTAG

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
AACCCCTAG	0.49945	--AACCCCTAG
TAACCCCTA	0.49927	-TAACCCCTA-
AACCCCTAA	0.49918	--AACCCCTAA
CAACCCCTA	0.49841	-CAACCCCTA-
GAACCCCTA	0.49836	-GAACCCCTA-
TAGGGTAA	0.49669	-TTACCCCTA-
AACCCCTAC	0.49625	--AACCCCTAC
AGGGTTAC	0.49455	GTAACCCCT--
AGGGTTCA	0.49395	TGAACCCCT--
AACCCCTAT	0.49373	--AACCCCTAT

8 mer Z-scores for probeset 'all'

Forward:	Reverse:

Top 10	Scores	Alignment
AACCCCTAA	59.99796	--AACCCCTAA
AACCCCTAG	56.84303	--AACCCCTAG
TAACCCCTA	54.69533	-TAACCCCTA-
CAACCCCTA	45.10027	-CAACCCCTA-
GAACCCCTA	44.51927	-GAACCCCTA-
TAGGGTAA	31.05236	-TTACCCCTA-
AACCCCTAC	30.25508	--AACCCCTAC
AAACCCCTA	26.53109	-AAACCCCTA-
AACCCCTAT	26.12791	--AACCCCTAT
AGGGTTAC	25.58657	GTAACCCCT--