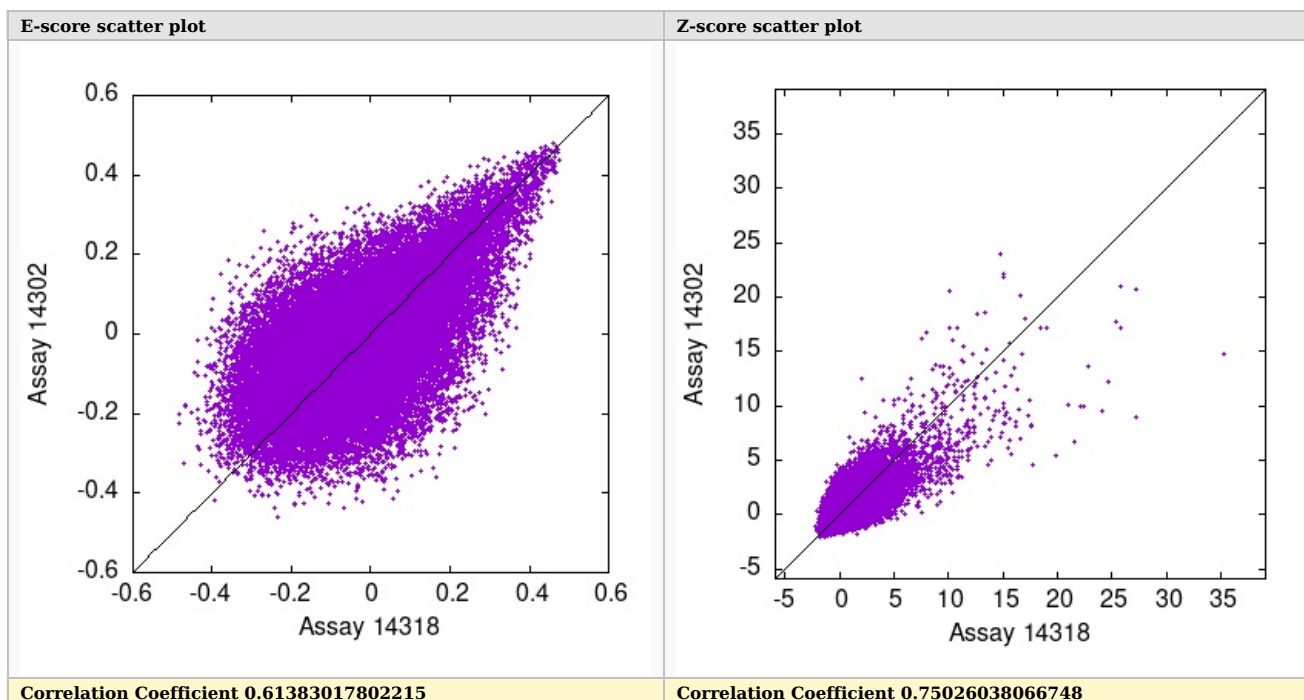


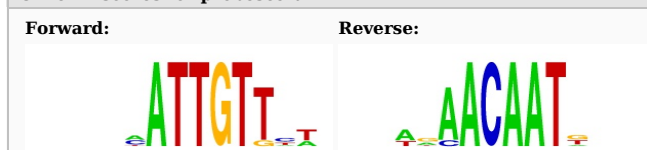
QC report



Top scoring motifs for Assay 14318

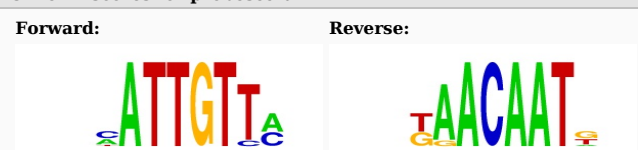
Protein ID: pTH15519.2 Gene: SRY Domain: HMG_box Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
AACAATGG	0.47653	-CCATTGTT--
AGAACAAT	0.47272	---ATTGTTCT
AACAATTA	0.47154	-TAATTGTT--
AATTGTTA	0.46905	--AATTGTTA--
GAACAATA	0.46893	--TATTGTTCT-
AACAATGT	0.46744	-ACATTGTT--
AACAACAAT	0.46578	---ATTGTGTT
ACAATTAT	0.46559	ATAATTGT---
ATTGTTTA	0.46508	---ATTGTTTA
CATTGTTT	0.46504	--CATTGTTC-

8 mer Z-scores for probeset 'all'

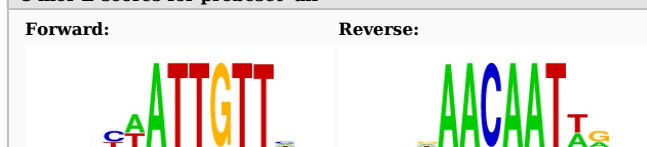


Top 10	Scores	Alignment
AACAATGG	35.34472	CCATTGTT--
AACAATGT	27.22762	ACATTGTT--
AGAACAAT	27.17836	--ATTGTTCT
GAACAATA	25.78984	-TATTGTTCT-
AATTGTTA	25.75857	-AATTGTTA-
AACAATTA	25.41173	TAATTGTT--
ATTGTTAC	24.66473	--ATTGTTAC
CATTGTTA	24.13667	-CATTGTTA-
CATTGTTT	22.89531	-CATTGTTCT-
AATTGTCA	22.37364	-AATTGTCA-

Top scoring motifs for Assay 14302

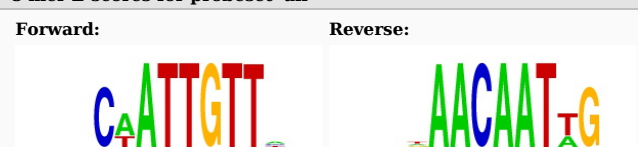
Protein ID: pTH15519.1 Gene: SRY Domain: HMG_box Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
ATTGTTAA	0.47864	---ATTGTTAA
ATTGTTTC	0.47353	---ATTGTTTC
AATTGTTA	0.47206	--AATTGTTA--
GAACAATA	0.47152	--TATTGTTCT-
ACAATTGT	0.46876	ACAATTGT---
AACAATA	0.46576	--TATTGTTT-
AACAATTA	0.46429	-TAATTGTT--
AATTGTTT	0.46243	--AATTGTTCT-
AACAATAG	0.46050	-CTATTGTT--
ATTGTTTCG	0.46016	---ATTGTTTCG

8 mer Z-scores for probeset 'all'



Top 10	Scores	Alignment
ATTGTTAA	23.91460	---ATTGTTAA
ATTGTTTC	22.10543	---ATTGTTTC
AAACAATA	21.82503	--TATTGTTT-
AATTGTTA	21.01741	-AATTGTTA-
AGAACAAT	20.64843	---ATTGTTCT
ACAATTGT	20.53113	ACAATTGT---
AATTGTTT	20.09391	--AATTGTTCT-
AACAATAG	18.52336	-CTATTGTT--
AACAATTG	18.49283	-CAATTGTT--
ATAACAAT	18.00106	---ATTGTTAT