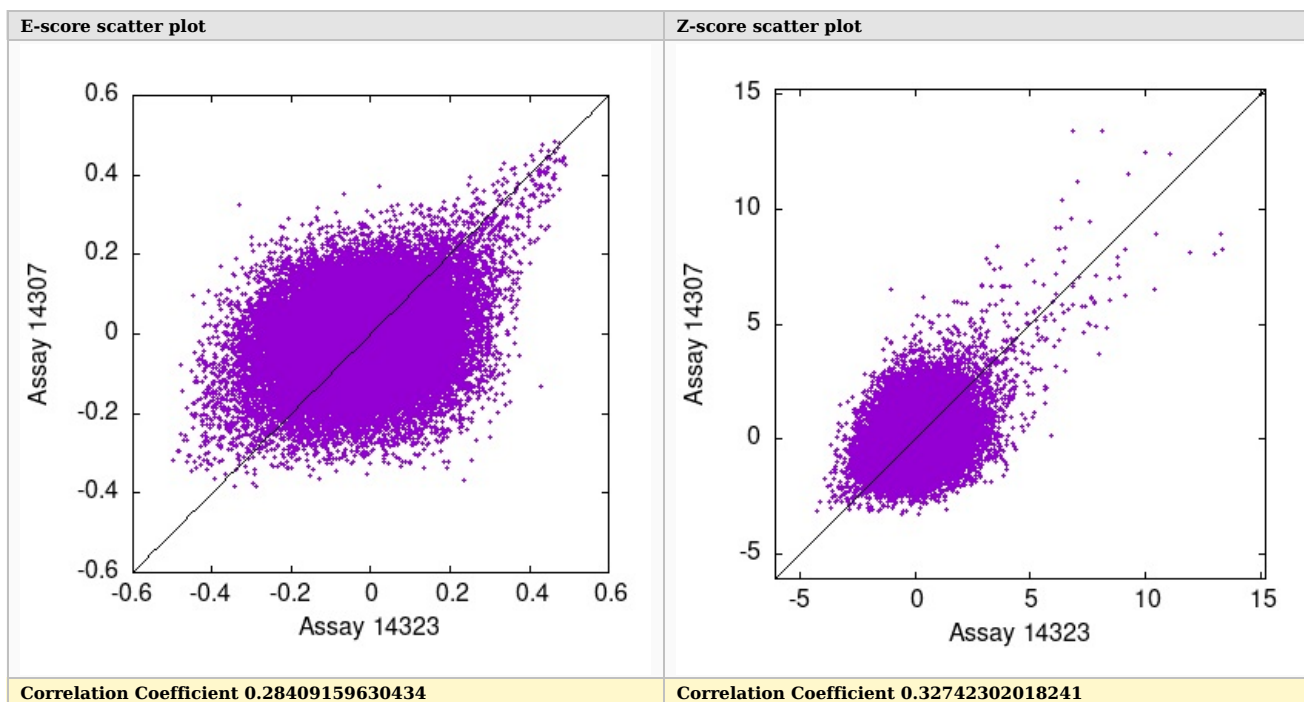


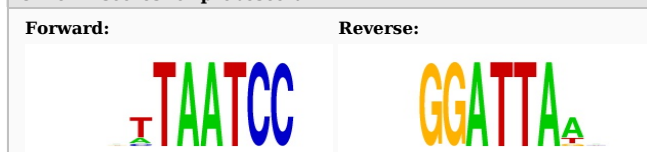
QC report



Top scoring motifs for Assay 14323

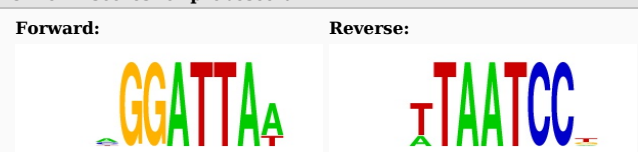
Protein ID: pTH14243.4 Gene: LEUTX.FL Domain: Homeobox Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
TGGATTAA	0.49042	--TTAATCCA
ATTAATCC	0.48696	-ATTAATCC-
GGATTAAA	0.48602	-TTAATCC-
CGGATTAA	0.48175	--TTAATCCG
GATAATCC	0.47733	-GATAATCC-
AGGATTAT	0.47642	--ATAATCCT
AGGATTAA	0.47564	--TTAATCCT
GGATTAAAC	0.47341	-GTTAATCC-
ACTAATCC	0.46605	-ACTAATCC-
ATTTAATC	0.46598	ATTTAATC--

8 mer Z-scores for probeset 'all'

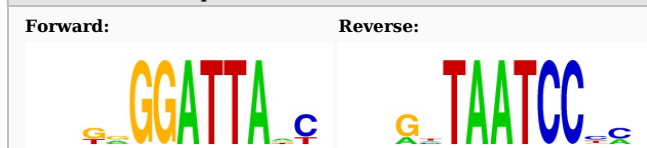


Top 10	Scores	Alignment
TGGATTAA	13.32906	-TGGATTAA-
ATTAATCC	13.24625	--GGATTAAAT
GGATTAAA	13.02418	--GGATTAAA
CGGATTAA	11.92880	-CGGATTAA-
GATAATCC	11.04751	--GGATTATC
AGGATTAA	10.45232	-AGGATTAA-
AGGATTAT	10.37830	-AGGATTAT-
GGATTAAAC	9.96320	--GGATTAAAC
GCGGATTA	9.27739	GCGGATTA--
AAGGATTA	9.11641	AAGGATTA--

Top scoring motifs for Assay 14307

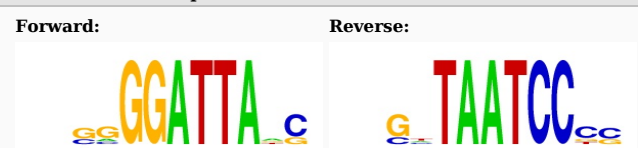
Protein ID: pTH14243.3 Gene: LEUTX.FL Domain: Homeobox Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
GGGATTAA	0.48284	-GGGATTAA-
GATAATCC	0.47970	--GGATTATC
GGGGATTA	0.47468	GGGGATTA--
GGATTAAAC	0.46847	--GGATTAAAC
AGGATTAG	0.46126	-AGGATTAG-
ATAATCCC	0.46071	-GGGATTAT-
GCGGATTA	0.45568	GCGGATTA--
GCTAATCC	0.44994	--GGATTAGC
TAATCCTA	0.44613	TAGGATTA--
ATTAATCC	0.44537	--GGATTAAAT

8 mer Z-scores for probeset 'all'



Top 10	Scores	Alignment
GGGGATTA	13.42688	GGGGATTA--
GGGATTAA	13.38667	-GGGATTAA-
GGATTAAAC	12.43916	--GGATTAAAC
GATAATCC	12.35876	--GGATTATC
GCGGATTA	11.51239	GCGGATTA--
ATAATCCC	11.20117	-GGGATTAT-
AGGATTAG	10.38565	-AGGATTAG-
CGGGATTA	9.57061	CGGGATTA--
CTTAATCC	9.43718	--GGATTAAAG
GCTAATCC	9.16636	--GGATTAGC