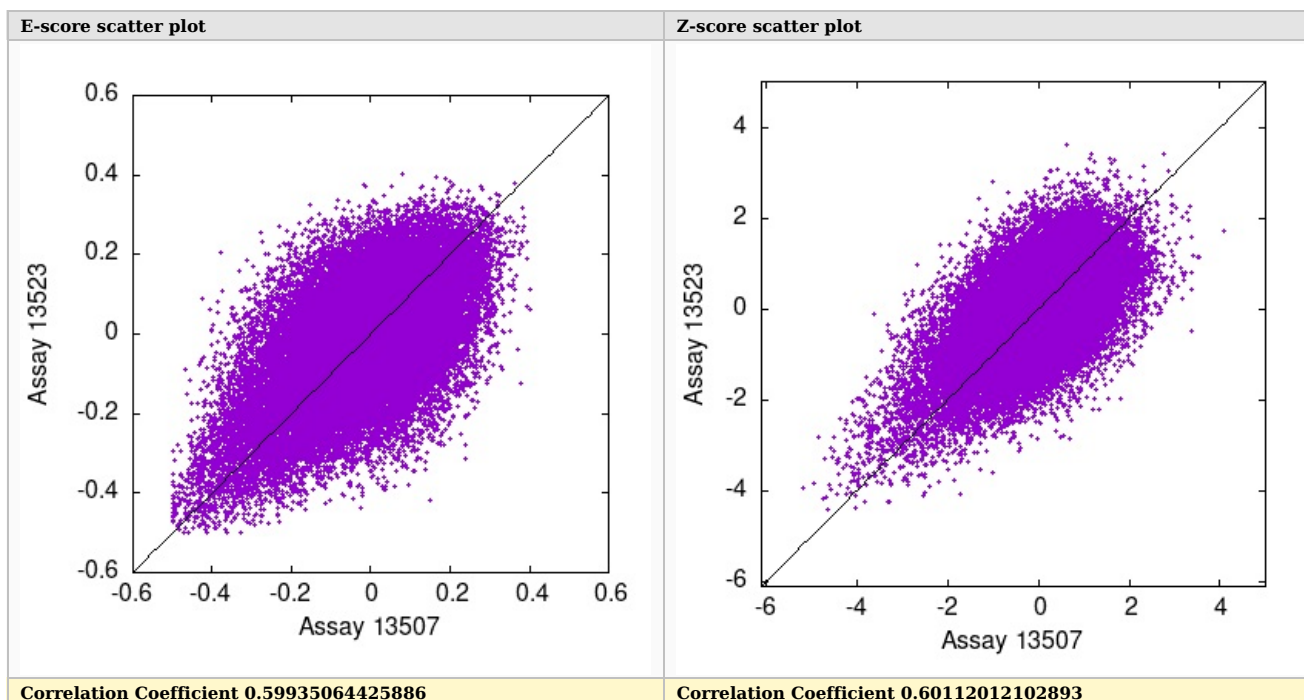


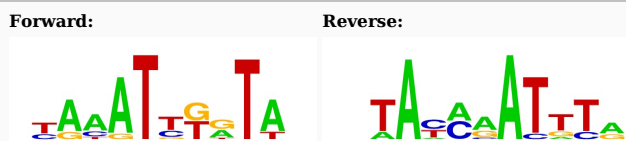
## QC report



### Top scoring motifs for Assay 13507

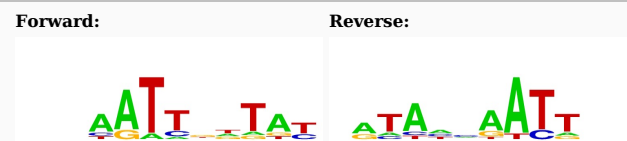
Protein ID: pTH13952.1 Gene: ANKZF1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-ME

#### 8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
CACATTCA	0.40307	TGAATGTG---
ATCGATAC	0.40288	---ATCGATAC
CAAAATTG	0.39610	CAAAATTG---
AACCAACA	0.39386	--TGTTGGTT--
AAATTTGT	0.39377	-AAATTTGT--
ACATCGAT	0.38650	-ACATCGAT--
AATTGTTA	0.38621	--AATTGTTA--
CATCGATA	0.38287	--CATCGATA--
AATTTGTA	0.38108	--AATTTGTA--
TAAATTTA	0.38081	TAAATTTA---

#### 8 mer Z-scores for probeset 'all'



Top 10	Scores	Alignment
ATTAAAT	4.07799	---ATTAAAT
AACCAACA	3.53531	--TGTTGGTT--
ATCGATAC	3.50481	---ATCGATAC
CGAATTCG	3.40612	CGAATTCG---
CAAAATTG	3.38452	-CAAAATTG--
CATCGATA	3.38356	--CATCGATA--
ATAATTAT	3.38351	---ATAATTAT
AAATTTGT	3.36737	-AAATTTGT--
AATTGTTA	3.35179	--AATTGTTA--
AGTTGTTG	3.31475	--AGTTGTTG--

### Top scoring motifs for Assay 13523

Protein ID: pTH13952.2 Gene: ANKZF1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-HK

#### 8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
CGCGAAAA	0.40117	----TTTTCGCG--
AACATTATT	0.39439	-AACATTATT----
AACAATGT	0.39238	--ACATTGTT---
GTAACAAA	0.38143	-TTTGTTAC----
AAACGTTT	0.38048	AAACGTTT-----
AACACTGT	0.37674	-AACACTGT-----
ATATGTGC	0.37368	GCACATAT-----
TGTTAACA	0.37333	---TGTTAACA---
AACGTTTC	0.37310	-AACGTTTC-----
TTTCGAAA	0.37201	-----TTTCGAAA

#### 8 mer Z-scores for probeset 'all'



Top 10	Scores	Alignment
AACTAACG	3.61429	-AACTAACG-----
ATAACGTA	3.42914	---ATAACGTA----
AAACGTTT	3.41948	---AAACGTTT---
CAAAATAC	3.30742	-----CAAAATAC---
TGTTAACA	3.30185	-TGTTAACA-----
AACAATGT	3.26686	--AACAATGT-----
CCTATCAA	3.23829	-----CCTATCAA
GTCATGAC	3.21805	GTCATGAC-----
TTTCGAAA	3.14637	-----TTTCGAAA---
GAATATTC	3.07929	----GAATATTC---