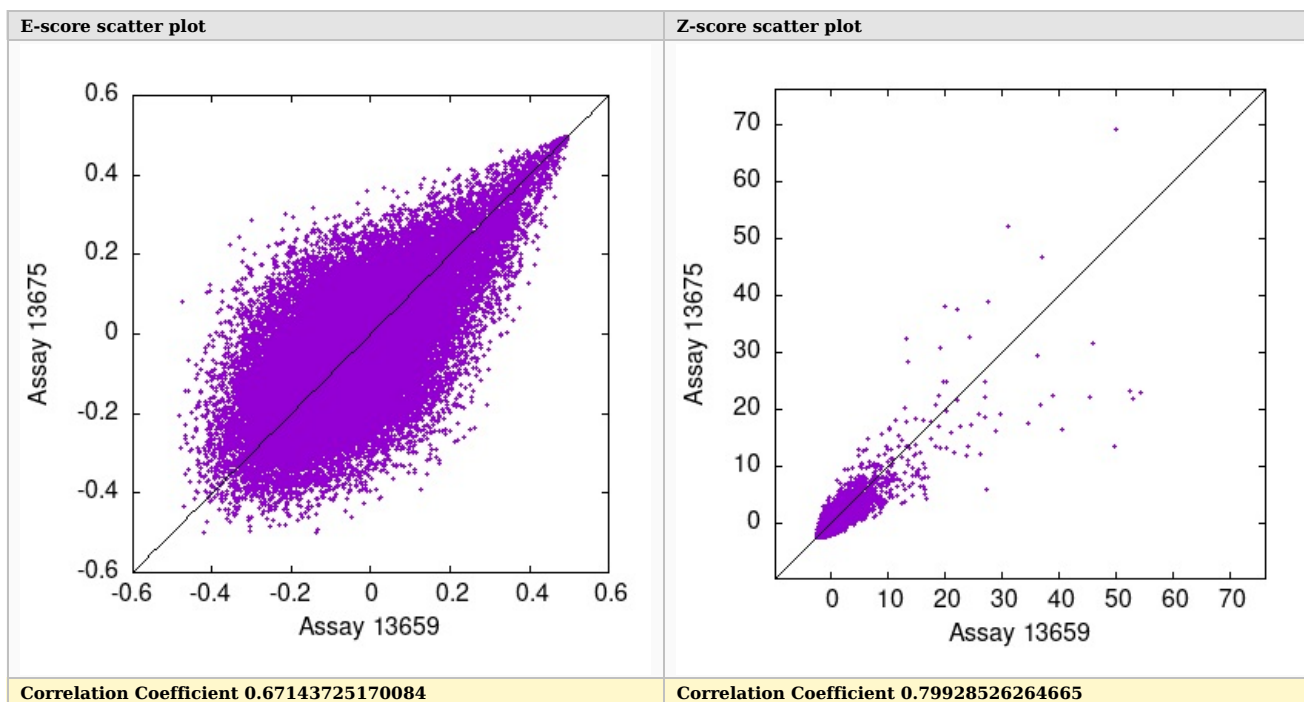


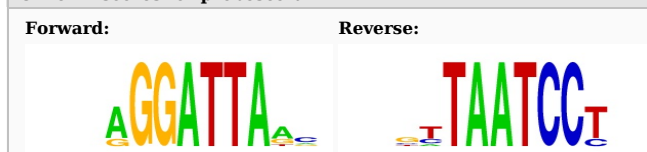
QC report



Top scoring motifs for Assay 13659

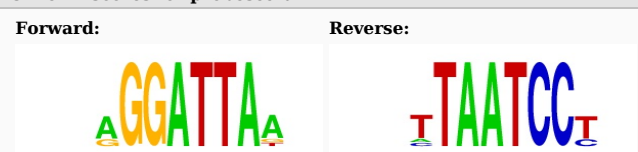
Protein ID: pTH14248.1 Gene: TPRX1.DBD Domain: Homeobox Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
GGGATTAA	0.49470	-GGGATTAA-
GATAATCC	0.49422	--GGATTATC
TAATCCTA	0.49328	TAGGATTA--
CTTAATCC	0.49187	--GGATTAAG
AAGGATTA	0.49182	AAGGATTA--
AGGATTAA	0.49167	--AGGATTAA-
GGATTAAAC	0.49081	--GGATTAAC
GGATTAAA	0.49062	--GGATTAAA
AGGATTAG	0.49048	-AGGATTAG-
GCTAATCC	0.49046	--GGATTAGC

8 mer Z-scores for probeset 'all'

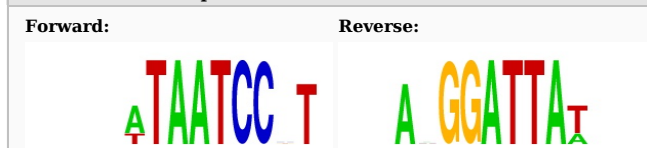


Top 10	Scores	Alignment
TAATCCTA	54.28061	TAGGATTA--
GGGATTAA	52.94116	-GGGATTAA-
AGGATTAA	52.49688	-AGGATTAA-
GATAATCC	50.18861	--GGATTATC
CTTAATCC	49.87366	--GGATTAAG
AAGGATTA	46.14275	AAGGATTA--
GGATTAAAC	45.54511	--GGATTAAC
GGATTAAA	40.52280	--GGATTAAA
GCTAATCC	38.90113	--GGATTAGC
ATTAATCC	37.22747	--GGATTAAT

Top scoring motifs for Assay 13675

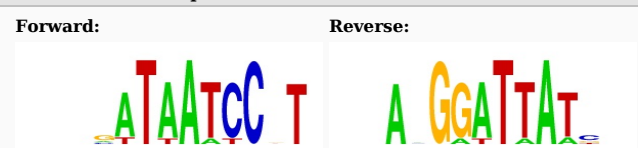
Protein ID: pTH14248.2 Gene: TPRX1.DBD Domain: Homeobox Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'



Top 10	Scores	Alignment
GATAATCC	0.49725	-GATAATCC--
AGGATTAT	0.49502	--ATAATCCT-
ATAATCCG	0.49389	--ATAATCCG-
AAGGATTA	0.49385	---TAATCCTT
GATTATCC	0.49326	GGATAATC---
AGGGATTA	0.49199	---TAATCCCT
CATAATCC	0.49194	-CATAATCC--
ATTAATCC	0.49187	-ATTAATCC--
ACGGATTA	0.49124	---TAATCCGT
GGGATTAA	0.48984	--TTAATCCC-

8 mer Z-scores for probeset 'all'



Top 10	Scores	Alignment
GATAATCC	69.09617	-GATAATCC--
AGGATTAT	52.09617	--ATAATCCT-
ATTAATCC	46.93881	-ATTAATCC--
ATAATCCG	39.09929	---ATAATCCG-
GATTATCC	38.26687	GGATAATC---
ACGGATTA	37.56249	---TAATCCGT
AGGGATTA	32.84479	---TAATCCCT
GATTAATC	32.61177	-GATTAATC--
AAGGATTA	31.67124	---TAATCCTT
CATAATCC	31.02225	-CATAATCC--