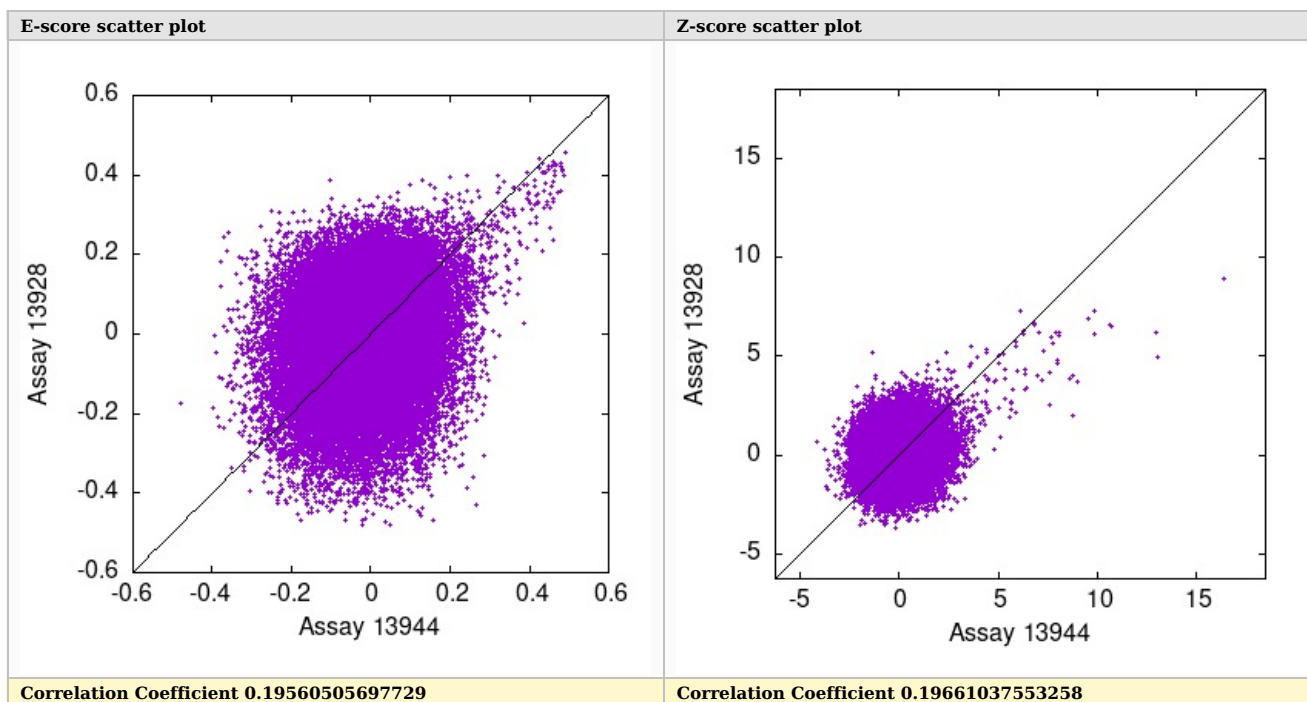




QC report





Top scoring motifs for Assay 13944

Protein ID: pTH14247.2 Gene: TPRX1.FL Domain: Homeobox Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GATAATCC	0.49086	-GATAATCC--
ATAATCCG	0.48718	--ATAATCCG--
AGGATTAT	0.48450	--ATAATCCT--
AGGGATTA	0.48331	---TAATCCCT
CATAATCC	0.48261	-CATAATCC--
AAGGATTA	0.48071	---TAATCCTT
GGATTAAC	0.47964	-GTTAATCC--
ACGGATTA	0.47889	---TAATCCGT
GATTATCC	0.47205	GGATAATC---
GCGGATTA	0.46749	---TAATCCGC



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
GATAATCC	16.46240	GATAATCC--	
AGGATTAT	13.05041	-ATAATCCT-	
ATAATCCG	12.98116	-ATAATCCG-	
CATAATCC	10.75603	CATAATCC--	
AGGGATTA	10.63371	--TAATCCCT	
GCGGATTA	9.89660	--TAATCCGC	
AAGGATTA	9.84274	--TAATCCTT	
ACGGATTA	9.55166	--TAATCCGT	
TGGATTAA	8.99445	-TTAATCCA-	
GGATTAAC	8.80553	GTTAATCC--	



Top scoring motifs for Assay 13928

Protein ID: pTH14247.1 Gene: TPRX1.FL Domain: Homeobox Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GATAATCC	0.45496	--GGATTATC
GGATTAAA	0.43951	--GGATTAAA
GGGATTAA	0.43397	-GGGATTAA-
AAGGATTA	0.43095	AAGGATTA--
CGGATTAG	0.42938	-CGGATTAG-
ATAATCCA	0.42600	-TGGATTAT-
GCGGATTA	0.42450	GCGGATTA--
ACGGATTA	0.42291	ACGGATTA--
ATTAATCC	0.42155	--GGATTAAT
TAATCCGA	0.42043	TCGGATTA--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
GATAATCC	8.96576	--	GGATTATC
AAGGATTA	7.31758		AAGGATTA--
CGGATTAG	7.26945	-	CGGATTAG-
ACGGATTA	6.91598		ACGGATTA--
ATAATCCA	6.65601	-	TGGATTAT-
AGGGATTA	6.63253		AGGGATTA--
GGATTAAA	6.59555	--	GGATTAAA
CATAATCC	6.50361	--	GGATTATG
ACTAATCC	6.29683	--	GGATTAGT
ATTAATCC	6.22036	--	GGATTAAT