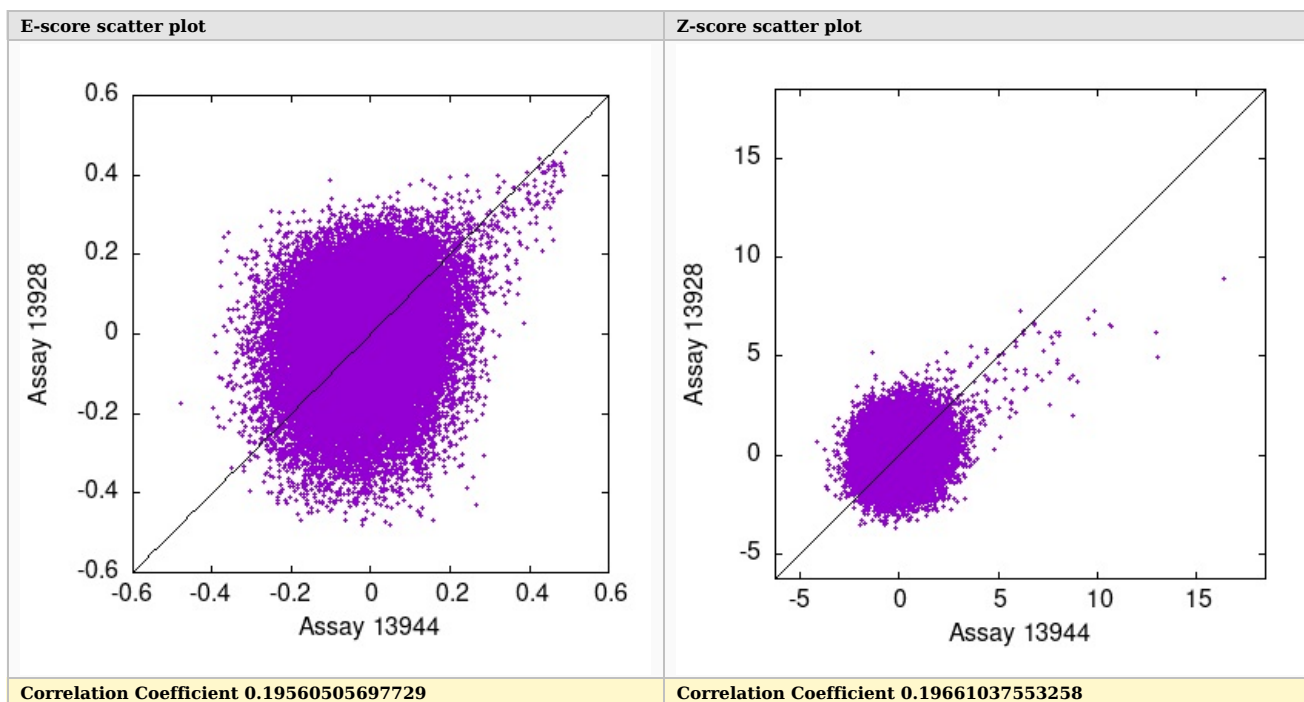


## QC report



## 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