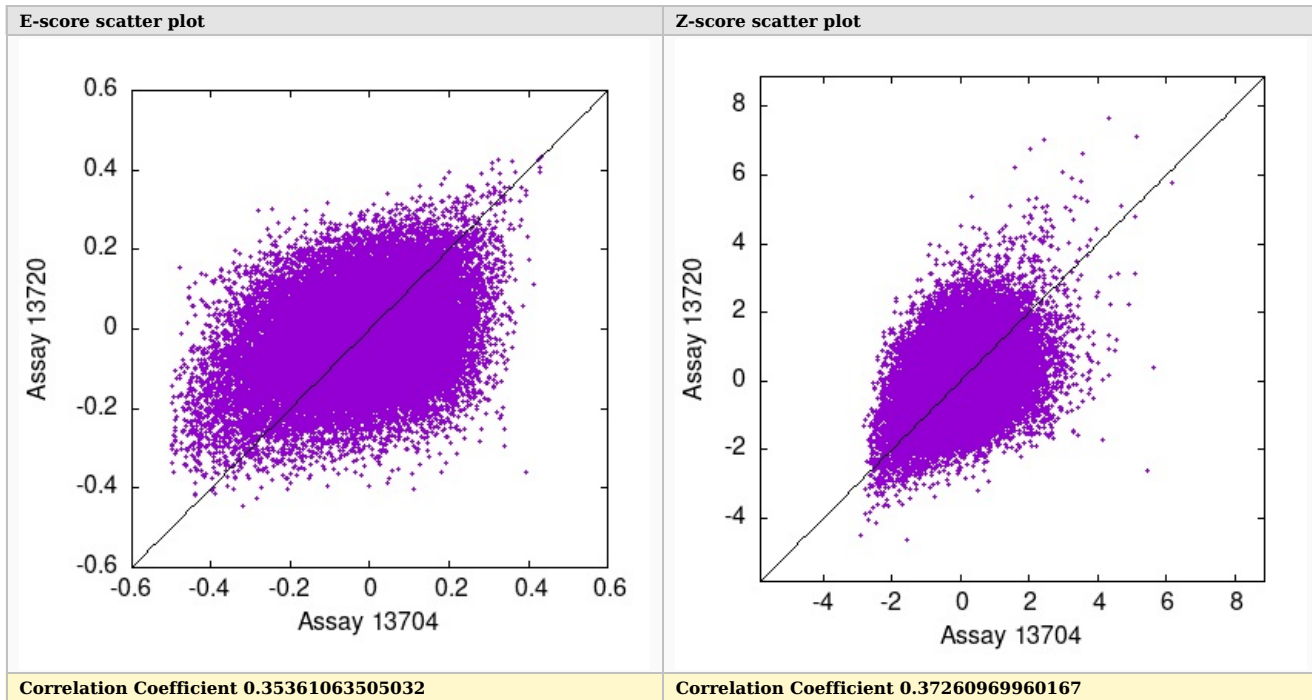




QC report





Top scoring motifs for Assay 13704

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

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
GATTAATC	0.43309	--GATTAATC
TAATCCGA	0.43005	TCGGATTA--
GGGATTAA	0.42727	-GGGATTAA--
ATTAATCC	0.42490	--GGATTAAT-
CAATTTCA	0.41413	TGAAATTG--
TGTGCACA	0.40283	TGTGCACA--
CGAGATTA	0.39904	CGAGATTA--
GGATTAAAC	0.39563	--GGATTAAAC-
AGACGTCT	0.39475	-AGACGTCT--
ATAATCCA	0.39330	-TGATTAT--

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
TAATCCGA	6.15762	TCGGATTA--
CAATTTCA	5.61245	TGAAATTG--
AGACGTCT	5.45101	-AGACGTCT-
ATTAATCC	5.12337	--GGATTAAT
GGGATTAA	5.10558	-GGGATTAA-
AGGATTAG	5.07770	-AGGATTAG-
AGATTAAA	4.92667	--AGATTAAA
GGATTAAAC	4.66748	--GGATTAAAC
CGAGATTA	4.61610	CGAGATTA--
GTTATCAA	4.54658	-GTTATCAA-

Top scoring motifs for Assay 13720

Protein ID: pTH14243.2 Gene: LEUTX.FL Domain: Homeobox Flag: Unsure Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
Top 10	Scores	Alignment
GATTAATC	0.43313	GATTAATC---
GATAATCC	0.42598	-GATAATCC--
ATTAATCC	0.42464	-ATTAATCC--
AGATTAA	0.42332	-ATTAATCT--
ATAATCCG	0.41845	--ATAATCCG-
TAATCCGA	0.40787	---TAATCCGA
GGATTATA	0.40186	-TATAATCC--
ACATAATC	0.39508	ACATAATC---
CGGATTAA	0.39506	--TTAATCCG-
GGGATTAA	0.39415	--TTAATCCC-

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
Top 10	Scores	Alignment
GATTAATC	7.64218	- - - GATTAATC
ATTAATCC	7.12662	- - GGATTAAT -
ATAATCCG	7.03122	- CGGATTAT - -
GGATTATA	6.74488	- - GGATTATA -
GATAATCC	6.60320	- - GGATTATC -
ACGGATTA	6.20739	ACGGATTA - - -
TGGATTAA	6.08343	- TGGATTAA - -
GCGGATTA	5.91461	GCGGATTA - - -
CGGATTAA	5.80027	- CGGATTAA - -
TAATCCGA	5.78347	TCGGATTA - - -