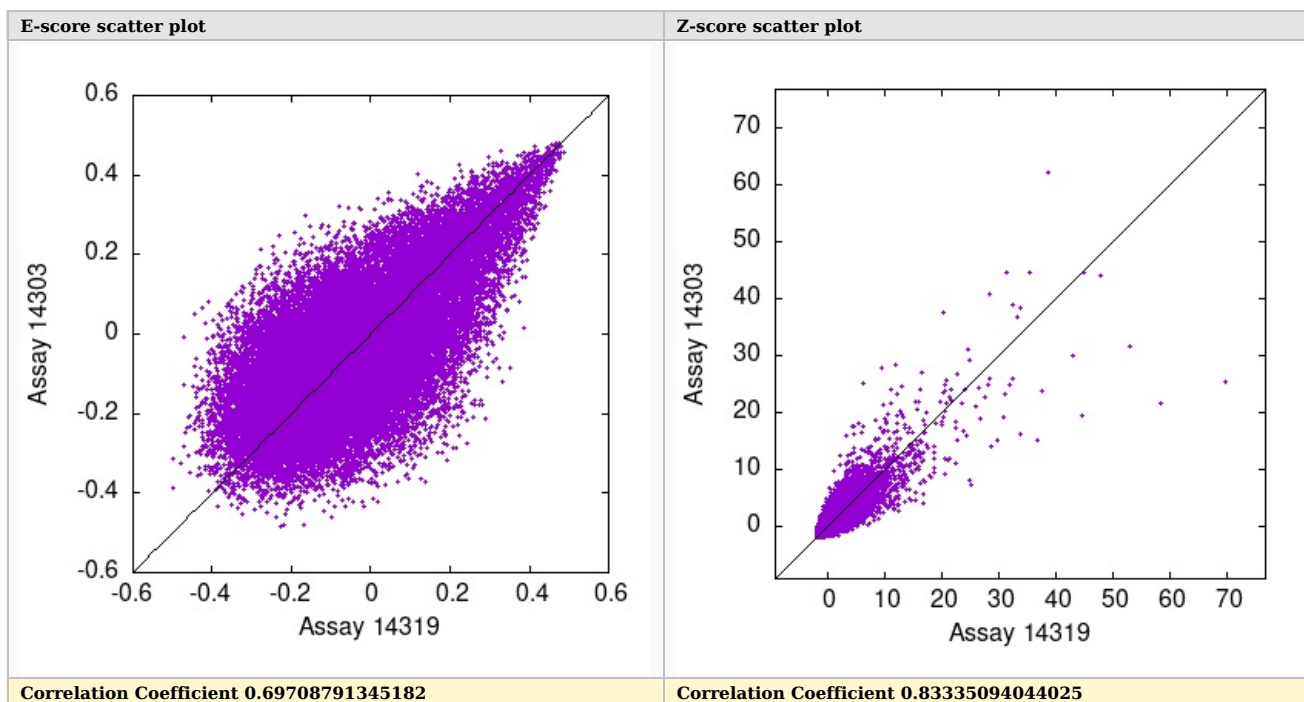




QC report





Top scoring motifs for Assay 14319

Protein ID: pTH15520.2 Gene: SOX15 Domain: HMG_box Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AACAATGG	0.48613	- - AACAATGG
AGAACAAAT	0.47932	AGAACAAAT - -
AACAATAA	0.47862	- - AACAATAA
CATTGTTA	0.47767	-TAACAATG-
AACAATAG	0.47635	- - AACAATAG
ATTGTTAA	0.47635	TTAACAAT - -
GAACAATA	0.47628	-GAACAATA-
ATAACAAT	0.47584	ATAACAAT - -
AATACAAT	0.47566	AATACAAT - -
CATTGTTC	0.47392	-GAACAATG-



8 mer Z-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AACAATGG	69.68676	CCATTGTT--
CATTGTTA	58.37989	--CATTGTTA--
ATAACAAT	53.04627	--ATTGTTAT
AGAACAAAT	47.87200	--ATTGTTCT
ATTGTTAA	44.83975	--ATTGTTAA
CATTGTTC	44.58092	--CATTGTTC--
AACAATAA	43.05705	TTATTGTT--
AACAATAG	38.70843	CTATTGTT--
AATACAAT	37.70771	--ATTGTATT
AACAATGT	36.79082	ACATTGTT--



Top scoring motifs for Assay 14303

Protein ID: pTH15520.1 Gene: SOX15 Domain: HMG_box Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AACAATAG	0.48044	--AACAATAG-
ATAACAAT	0.47932	ATAACAAT---
AAACAATA	0.47817	--AAACAATA--
GAACAATA	0.47691	-GAACAATA--
ATTGTTAA	0.47636	TTAACAAT---
TACAATA	0.47622	--TAACAATA--
AACAATTG	0.47420	--AACAATTG--
AATTGTTA	0.47326	--TAACAATT--
ACAATTGT	0.47275	---ACAATTGT
AGAACAAAT	0.47067	AGAACAAAT---

8 mer Z-scores for probeset 'all'

Forward:	Reverse:	
		
Top 10	Scores	Alignment
AACAATAG	62.39182	--AACAATAG
AAACAATA	44.79887	--AAACAATA-
ATTGTTAA	44.77750	TTAACAAT--
TAACAATA	44.68571	--TAACAATA-
AGAACAAAT	44.05493	AGAACAAAT--
AACAATTG	40.93879	--AACAATTG
AACAATTA	39.05317	--AACAATTA
GAACAATA	38.60100	--GAACAATA-
ATTGTTTC	37.80146	GAAACAAT--
AAACAATG	36.78954	--AAACAATG-