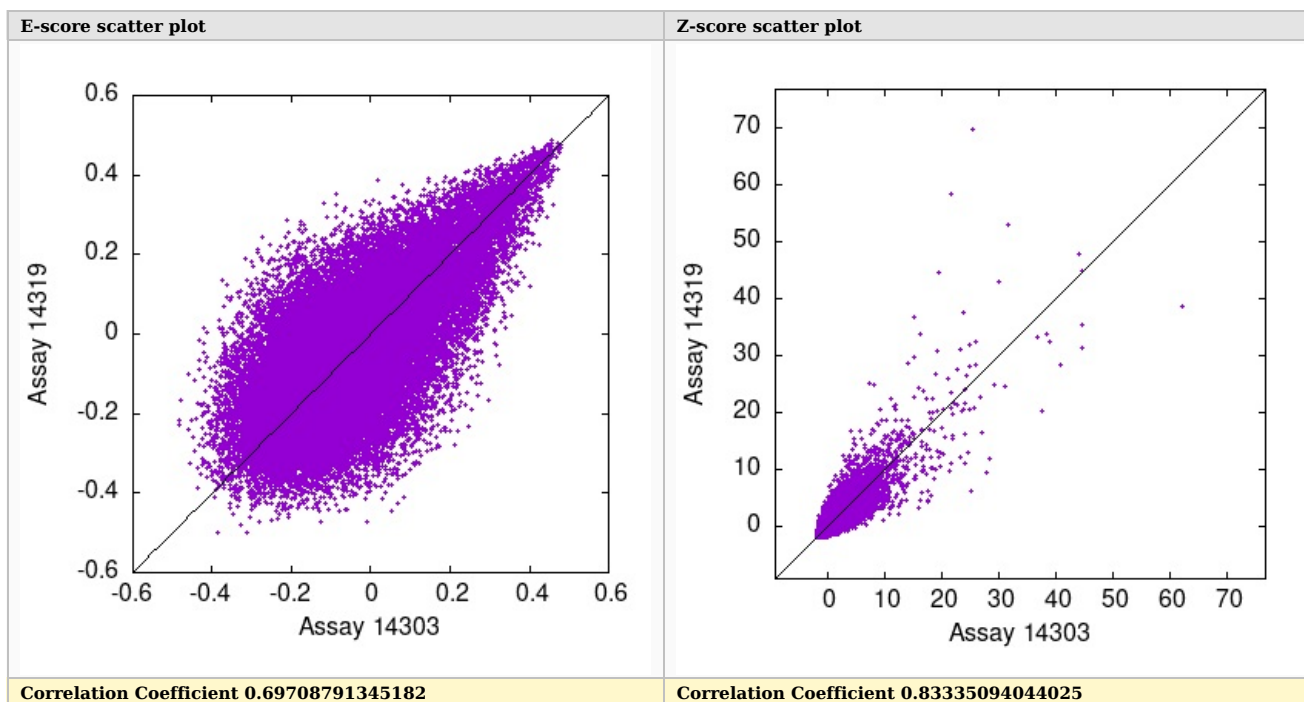


QC report



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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AACAATAG	0.48044	--AACAATAG-	AACAATAG	62.39182	--AACAATAG
ATAACAAT	0.47932	ATAACAAT--	AAACAATA	44.79887	-AAACAATA-
AAACAATA	0.47817	-AAACAATA--	ATTGTTAA	44.77750	TTAACAAT--
GAACAATA	0.47691	-GAACAATA--	TAACAATA	44.68571	-TAACAATA-
ATTGTTAA	0.47636	TTAACAAT--	AGAACAAT	44.05493	AGAACAAT--
TAACAATA	0.47622	-TAACAATA--	AACAATTG	40.93879	--AACAATTG
AACAATTG	0.47420	--AACAATTG-	AACAATTA	39.05317	--AACAATTA
AATTGTTA	0.47326	-TAACAATT--	GAACAATA	38.60100	-GAACAATA-
ACAATTGT	0.47275	---ACAATTGT	ATTGTTTC	37.80146	GAAACAAT--
AGAACAAT	0.47067	AGAACAAT--	AAACAATG	36.78954	-AAACAATG-

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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AACAATGG	0.48613	--AACAATGG	AACAATGG	69.68676	CCATTGTT--
AGAACAAT	0.47932	AGAACAAT--	CATTGTTA	58.37989	-CATTGTTA-
AACAATAA	0.47862	--AACAATAA	ATAACAAT	53.04627	--ATTGTTAT
CATTGTTA	0.47767	-TAACAATG-	AGAACAAT	47.87200	--ATTGTTCT
AACAATAG	0.47635	--AACAATAG	ATTGTTAA	44.83975	--ATTGTTAA
ATTGTTAA	0.47635	TTAACAAT--	CATTGTTT	44.58092	-CATTGTTT-
GAACAATA	0.47628	-GAACAATA-	AACAATAA	43.05705	TTATTGTT--
ATAACAAT	0.47584	ATAACAAT--	AACAATAG	38.70843	CTATTGTT--
AATACAAT	0.47566	AATACAAT--	AATACAAT	37.70771	--ATTGTTAT
CATTGTTC	0.47392	-GAACAATG-	AACAATGT	36.79082	ACATTGTT--