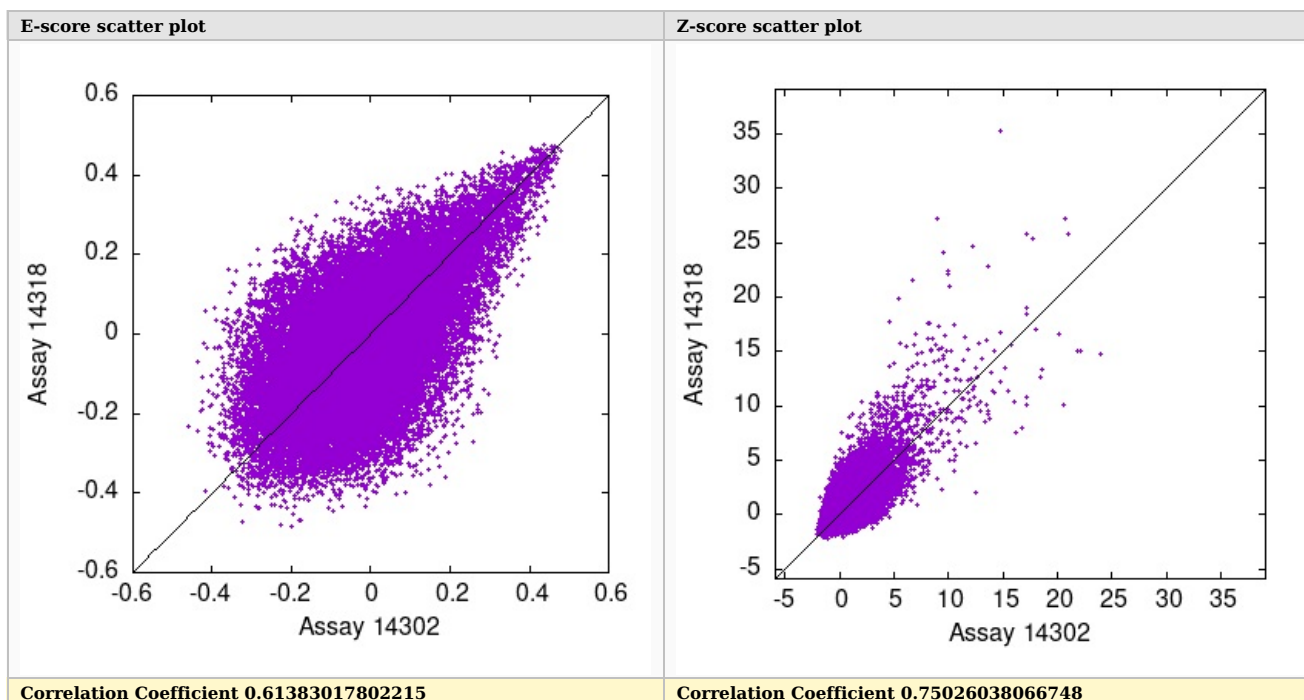


QC report



Top scoring motifs for Assay 14302

Protein ID: pTH15519.1 Gene: SRY Domain: HMG_box Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
ATTGTTAA	0.47864	---ATTGTTAA	
ATTGTTTC	0.47353	---ATTGTTTC	
AATTGTTA	0.47206	--AATTGTTA-	
GAACAATA	0.47152	--TATTGTTT-	
ACAATTGT	0.46876	ACAATTGT---	
AAACAATA	0.46576	--TATTGTTT-	
AACAATTA	0.46429	-TAATTGTT--	
AATTGTTC	0.46243	--AATTGTTC-	
AACAATAG	0.46050	-CTATTGTT--	
ATTGTTTG	0.46016	---ATTGTTTG	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
ATTGTTAA	23.91460	---ATTGTTAA	
ATTGTTTC	22.10543	---ATTGTTTC	
AAACAATA	21.82503	--TATTGTTT-	
AATTGTTA	21.01741	--AATTGTTA-	
AGACAAT	20.64843	---ATTGTTCT	
ACAATTGT	20.53113	ACAATTGT---	
AATTGTTC	20.09391	--AATTGTTC-	
AACAATAG	18.52336	-CTATTGTT--	
AACAATTG	18.49283	-CAATTGTT--	
ATAACAAT	18.00106	---ATTGTTAT	

Top scoring motifs for Assay 14318

Protein ID: pTH15519.2 Gene: SRY Domain: HMG_box Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
AACAATGG	0.47653	-CCATTGTT--	
AGACAAT	0.47272	---ATTGTTCT	
AACAATTA	0.47154	--TAATTGTT--	
AATTGTTA	0.46905	--AATTGTTA-	
GAACAATA	0.46893	--TATTGTTT-	
AACAATGT	0.46744	-ACATTGTT--	
AACAATTA	0.46578	---ATTGTTGT	
ACAATTAT	0.46559	ATAATTGTT--	
ATTGTTTA	0.46508	---ATTGTTTA	
CATTGTTC	0.46504	--CATTGTTC-	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
AACAATGG	35.34472	CCATTGTT--	
AACAATGT	27.22762	ACATTGTT--	
AGACAAT	27.17836	--ATTGTTCT	
GAACAATA	25.78984	-TATTGTTT-	
AATTGTTA	25.75857	-AATTGTTA-	
AACAATTA	25.41173	TAATTGTT--	
ATTGTTAC	24.66473	--ATTGTTAC	
CATTGTTA	24.13667	-CATTGTTA-	
CATTGTTC	22.89531	-CATTGTTC-	
AATTGTCA	22.37364	-AATTGTCA-	