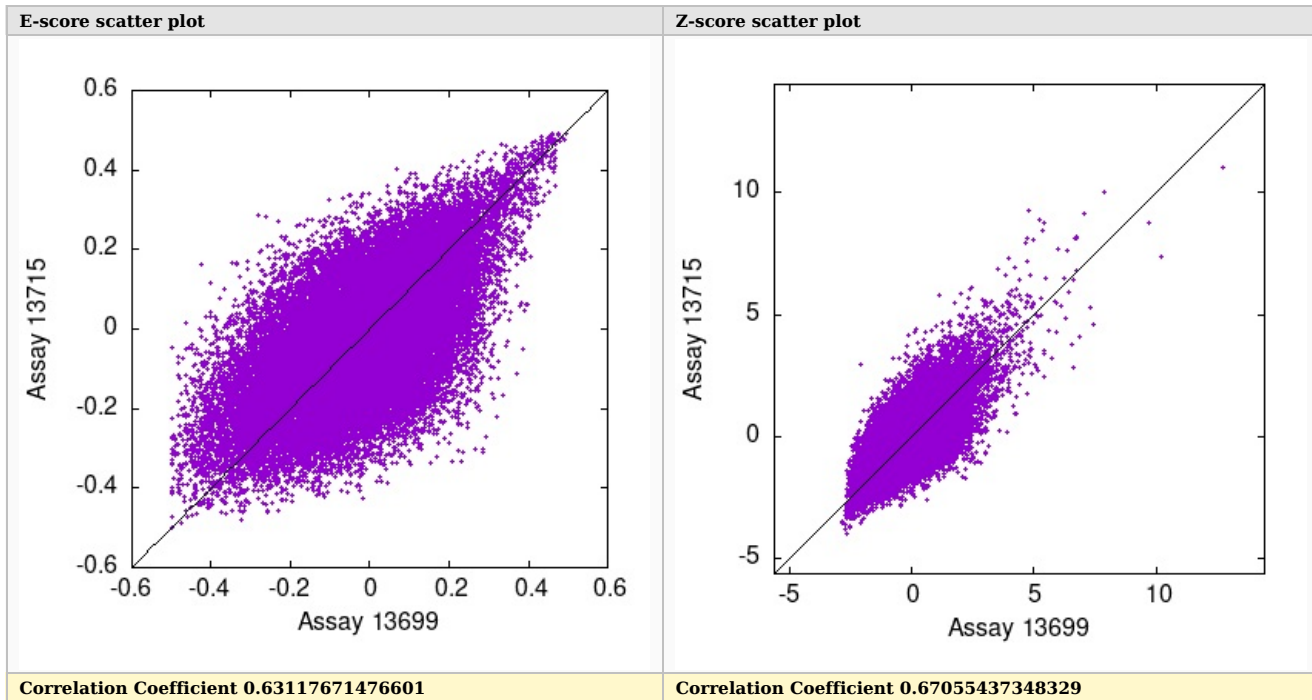


QC report



Top scoring motifs for Assay 13699

Protein ID: pTH14212.1 Gene: TIGD3.DBD Domain: CENP-B_N Flag: Pass_matched_pair Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TATGCATA	0.49540	TATGCATA---	
GAATATTC	0.49119	---GAATATTC	
ATGCATAA	0.48664	-ATGCATAA--	
AGTGAATA	0.48134	AGTGAATA---	
ATTATGCA	0.47668	--TGCATAAT-	
GTTATGCA	0.47546	--TGCATAAC-	
GCATATGC	0.46845	---GCATATGC	
TATATTCA	0.46806	--TGAATATA-	
TATTCACA	0.46801	TATTCACA---	
ATGCGCAT	0.46731	-ATGCGCAT--	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TATGCATA	12.74771	---TATGCATA	
GAATATTC	10.17627	GAATATTC---	
ATGCATAA	9.69973	--TTATGCAT-	
ATTATGCA	7.84913	-ATTATGCA--	
TATATTCA	7.46007	-TATATTCA--	
TATATGCA	7.32461	-TATATGCA--	
GTTATGCA	7.02562	-GTTATGCA--	
ATATGCAC	6.85615	--ATATGCAC-	
GCATATGC	6.76697	GCATATGC---	
ATTATTCA	6.72857	-ATTATTCA--	

Top scoring motifs for Assay 13715

Protein ID: pTH14212.2 Gene: TIGD3.DBD Domain: CENP-B_N Flag: Pass_matched_pair Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TATGCATA	0.49246	TATGCATA--	
ATTATGCA	0.49228	--TGCATAAT	
GTTATTCA	0.49115	--TGAATAAC	
GTTATGCA	0.48814	--TGCATAAC	
GTGAATAA	0.48596	-GTGAATAA-	
CATGAATA	0.48471	CATGAATA--	
CTGAATAA	0.48398	-CTGAATAA-	
ATGCATAA	0.48186	-ATGCATAA-	
ACTGAATA	0.48099	ACTGAATA--	
TTATGCAA	0.47977	-TTGCATAA-	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
TATGCATA	11.02486	TATGCATA--	
ATTATGCA	10.03849	--TGCATAAT	
GTTATTCA	9.24222	--TGAATAAC	
GTTATGCA	9.10610	--TGCATAAC	
CATGAATA	8.87183	CATGAATA--	
TTATGCAA	8.75568	-TTGCATAA-	
ATGCATAA	8.74709	-ATGCATAA-	
GTGAATAA	8.43279	-GTGAATAA-	
ATTATTCA	8.16283	--TGAATAAT	
TATTCACA	8.14408	TATTCACA--	