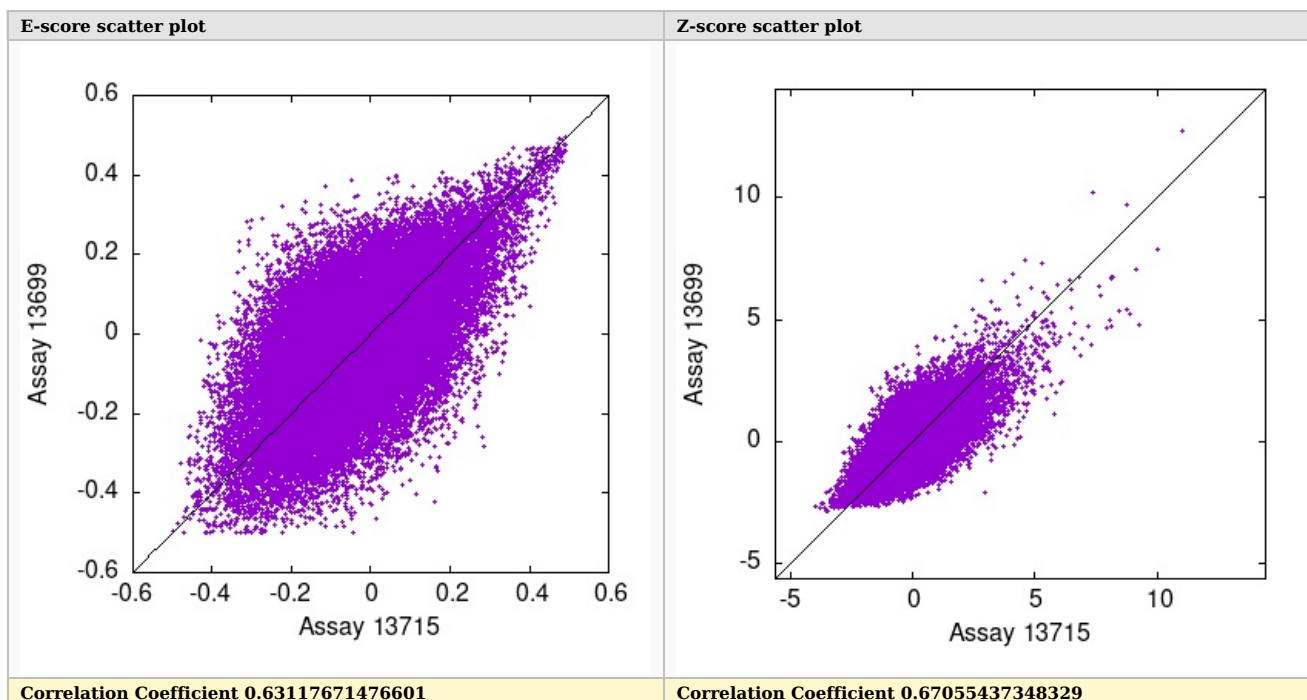




QC report





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	
TATTCA	8.14408	TATTCA--	



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 - -