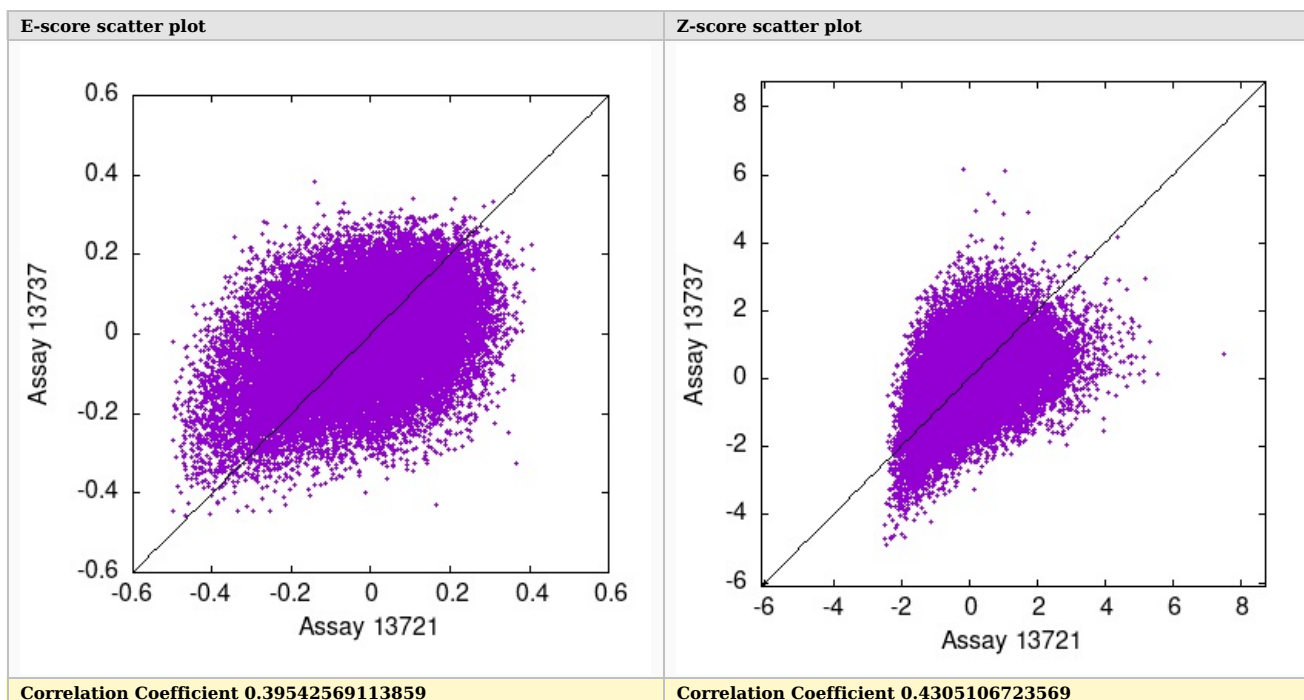


QC report





Correlation Coefficient 0.39542569113859

Correlation Coefficient 0.4305106723569



Top scoring motifs for Assay 13721

Protein ID: pTH14300.1 Gene: DR1.FL Domain: Unknown Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AGAATTCT	0.41021	--AGAATTCT--	
TAAATTTA	0.40568	-TAAATTTA---	
TATATACA	0.38791	---TATATACA-	
TGATATCA	0.38403	TGATATCA---	
GTTGCAAC	0.38391	--GTTGCAAC--	
AATTACGT	0.38304	---AATTACGT	
AACTGATA	0.37854	---AACTGATA-	
ATATTTTA	0.37666	--ATATTTTA--	
ATATTTAC	0.37148	--ATATTTAC--	
AATTGTTA	0.36845	-AATTGTTA---	



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AGAATTCT	7.50831	-AGAATTCT-	
ACATTATC	5.56728	GATAATGT--	
ATATTTTA	5.35578	--TAAATAT-	
TAAATTTA	5.18569	-TAAATTTA-	
ATAATATA	5.17795	-ATAATATA-	
ATATATTA	5.17795	--TAATATAT	
ATTATATA	5.17795	-ATTATATA-	
ACAAACAT	5.01084	ACAAACAT--	
TCTATAGA	5.00425	-TCTATAGA-	
ATAACAAT	4.92264	-ATAACAAT-	



Top scoring motifs for Assay 13737

Protein ID: pTH14300.2 Gene: DR1.FL Domain: Unknown Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AGTTTTTC	0.38469	-AGTTTTTC-
CATTTGCA	0.33963	--CATTTGCA-
AGTCTACA	0.33899	-AGTCTACA-
AACGTAAC	0.33135	--GTTACGTT
ACAATGTC	0.33092	GACATTGT--
AAAGTCAC	0.32857	GTGACTTT--
CGCAACAA	0.32287	--TTGTTGCG
TAATAATA	0.31546	-TATTATTA-
CGAGAGCC	0.31448	--GGCTCTCG
ACAAATAG	0.31252	--CTATTGTG

8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
AGTTTTTC	6.15337	-AGTTTTTC--	
AGTCTACA	6.09858	--AGTCTACA-	
CAGCTAAC	5.43669	---GTTAGCTG	
CATTTGCA	5.20628	--CATTTGCA-	
CGTATACG	4.94688	--CGTATACG-	
CGCAACAA	4.88908	--TTGTTGCG-	
ACAAATAG	4.82954	-CTATTTGT--	
ACAATGTC	4.19659	GACATTGT---	
TTTCGAAA	4.14968	---TTTCGAAA	
GTAAGTTA	4.10358	-TAACTTAC--	