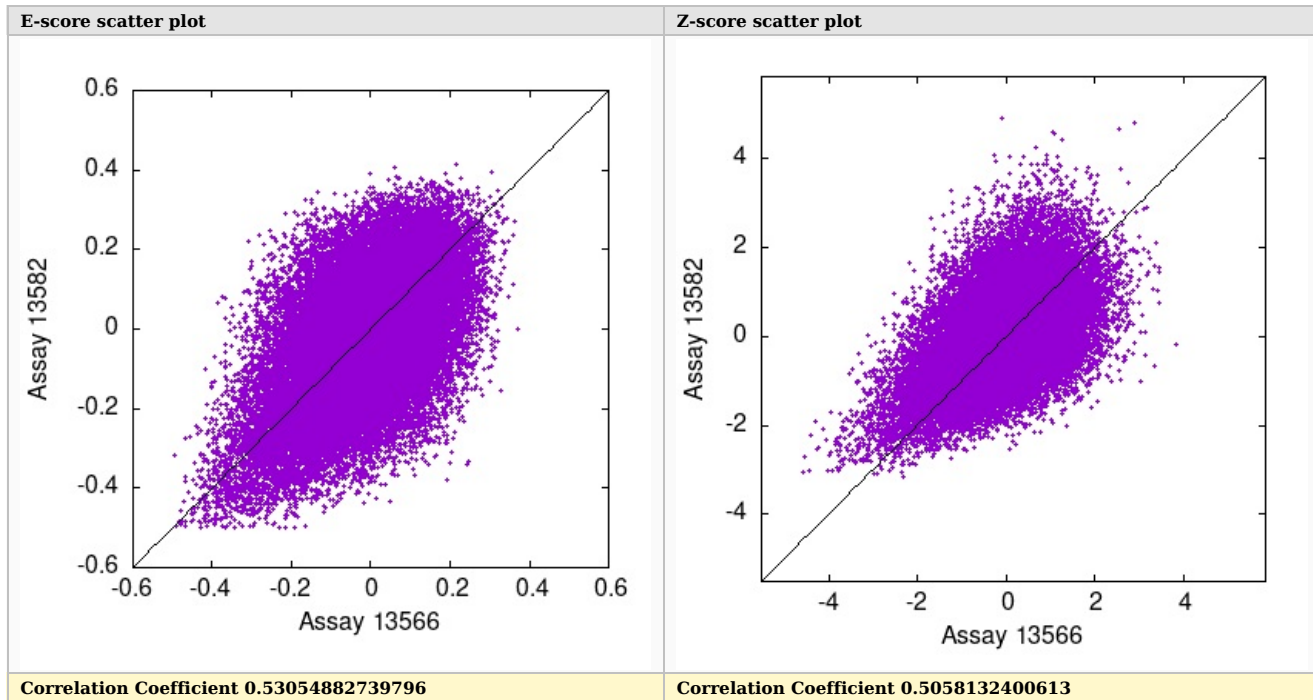




QC report



Top scoring motifs for Assay 13566

Protein ID: pTH13958.1 Gene: CPXCR1.FL Domain: zf-C2H2 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AAAGTACA	0.37266	---TGTACTTT
AATTGTAG	0.36208	-AATTGTAG---
TAAATTTA	0.36029	TAAATTTA----
ATGTATAA	0.35846	---TTATACAT-
ACATAACA	0.34862	ACATAACA----
CACAACAC	0.34736	---GTGTTGTG-
ATATGTAC	0.34197	-ATATGTAC---
ACAACAAT	0.34161	--ATTGTTGT--
GAAATTA	0.33539	TAATTTTC----
AAATTGTT	0.33519	AAATTGTT----



8 mer Z-scores for probeset 'all'

Forward:		Reverse:	
Top 10	Scores	Alignment	
AAAGTACA	3.84298	-AAAGTACA---	
ACATATGT	3.46129	--ACATATGT--	
TTGTACAA	3.44246	----TTGTACAA	
ATATGTAC	3.42805	--ATATGTAC--	
CACAACAC	3.40954	---GTGTTGTG-	
ACAATTGT	3.36387	CAAATTGT----	
AATTATTG	3.32512	--AATTATTG--	
AAAATTAT	3.32506	AAAATTAT----	
AATTATAT	3.31347	--AATTATAT--	
TAGTACAA	3.24295	----TTGTACTA	



Top scoring motifs for Assay 13582

Protein ID: pTH13958.2 Gene: CPXCR1.FL Domain: zf-C2H2 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
TAACAAAA	0.41261	---TAACAAAA--	
GTCATGAC	0.40688	--GTCATGAC---	
AAATTGTA	0.39408	AAATTGTA-----	
GATTAATA	0.38941	----TATTAATC-	
ACTATAAT	0.38928	--ACTATAAT---	
TTATAAAA	0.38470	---TTATAAAA--	
TTTCGAAA	0.38078	---TTTCGAAA--	
CTCATATA	0.37920	--CTCATATA---	
ATAAGATA	0.37822	-----ATAAGATA	
AACAACCT	0.37757	AAGTTGTT-----	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
GTCATGAC	4.89383	---GTCATGAC---
TTTCGAAA	4.80540	TTTCGAAA-----
AAATTGTA	4.65596	-----AAATTGTA--
ACATTTAG	4.59802	----ACATTTAG---
ACTATAAT	4.55199	-----ATTATAGT
ATAAGATA	4.42196	-----ATAAGATA---
AGTAATTA	4.25423	---AGTAATTA----
TGTAGCAA	4.08372	---TGTAGCAA----
AGTGATAT	4.06441	---AGTGATAT----
AATTTAAA	4.05075	-----AATTTAAA--