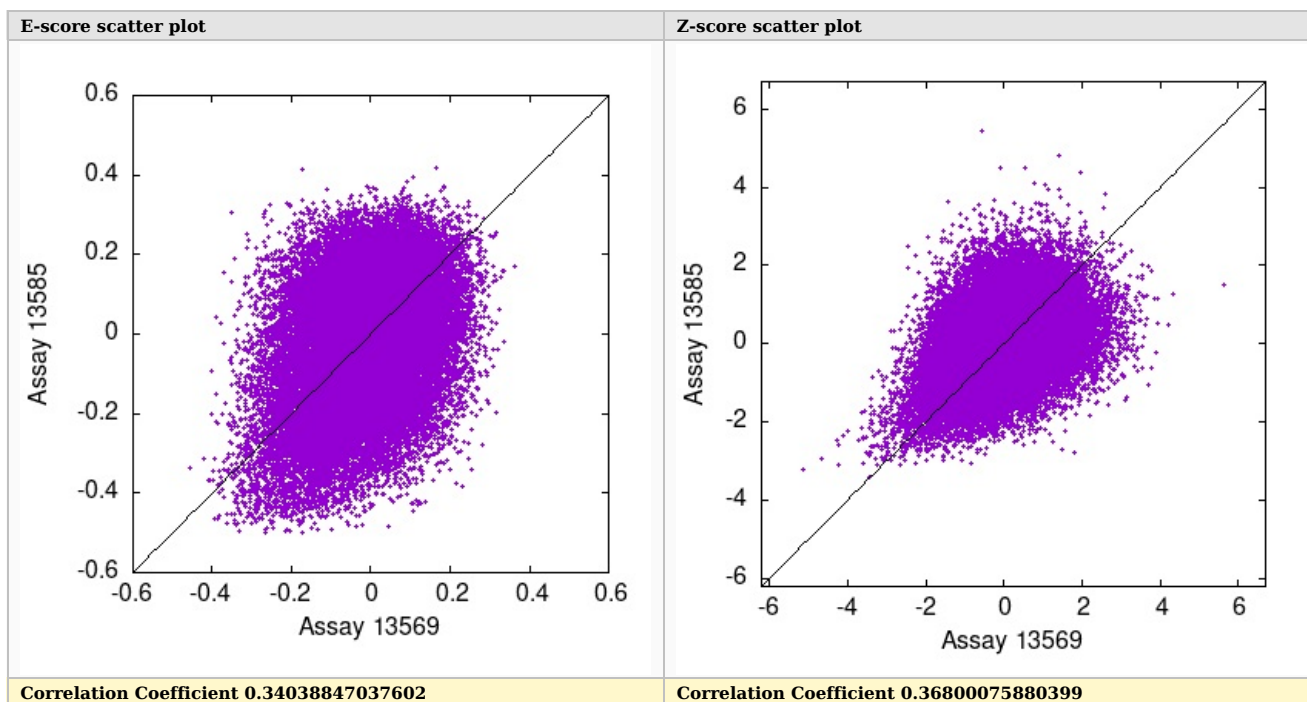




QC report





Top scoring motifs for Assay 13569

Protein ID: pTH13961.1 Gene: EEA1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-ME

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
CCAACAAC	0.36306	--CCAACAAC-	
CAACTTCG	0.33629	---CAACTTCG	
AATGAATC	0.33467	--AATGAATC-	
ACACAAC	0.33387	ACACAAC---	
ACAACATC	0.32917	---ACAACATC-	
GAATGTAC	0.32594	---GTACATTC	
ACACTACA	0.32189	ACACTACA---	
TGTGCACA	0.31712	TGTGCACA---	
TAAGTACA	0.31591	TAAGTACA---	
TGCCGACA	0.31591	TGCCGACA---	



8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
CCAACAAC	5.62895	---CCAACAAC--
CGCGTTAA	4.33447	---TTAACGCG--
AATGAATC	4.21126	---AATGAATC--
ATTACACG	3.95237	---ATTACACG--
CAACTTCG	3.92081	CAACTTCG----
CCATCAAC	3.90731	---CCATCAAC--
ATGTACTC	3.87718	--ATGTACTC---
TCGGTGAA	3.79031	-----TTCACCGA
ACTTACAC	3.76951	--ACTTACAC---
CAACGTAG	3.70591	CAACGTAG----



Top scoring motifs for Assay 13585

Protein ID: pTH13961.2 Gene: EEA1.DBD Domain: zf-C2H2 Flag: Reject Array: 1M-HK

8 mer E-scores for probeset 'all'

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
ACACGTAT	0.41701	---ACACGTAT--	
AAAATTTT	0.41456	---AAAATTTT--	
AAACGTTT	0.39314	----AAACGTTT	
TACAATCA	0.38382	--TACAATCA---	
TTTTAAAA	0.37221	TTTTAAAA-----	
ACAAACAT	0.37172	----ACAAACAT--	
AACAATGA	0.36807	---AACAATGA---	
AATTTTCA	0.36740	--TGAAAAATT---	
ATATCACA	0.36730	----ATATCACA---	
ATATACAA	0.36636	ATATACAA-----	

8 mer Z-scores for probeset 'all'

Forward:		Reverse:
		
Top 10	Scores	Alignment
AAAATTTT	5.42744	--AAAATTTT----
ACACGTAT	4.81019	---ATACGTGT---
AACAATGA	4.49148	---TCATTGTT---
TTTTAAAA	4.48754	---TTTTAAAA---
AAACGTTT	4.38089	---AAACGTTT---
GTAACGTA	4.11841	-----TACGTTAC--
CGTTACAA	4.08193	-----TTGTAACG
ATATCACA	3.93376	-----TGTGATAT---
ATATGGTA	3.93087	---ATATGGTA---
CATATATG	3.81445	CATATATG-----