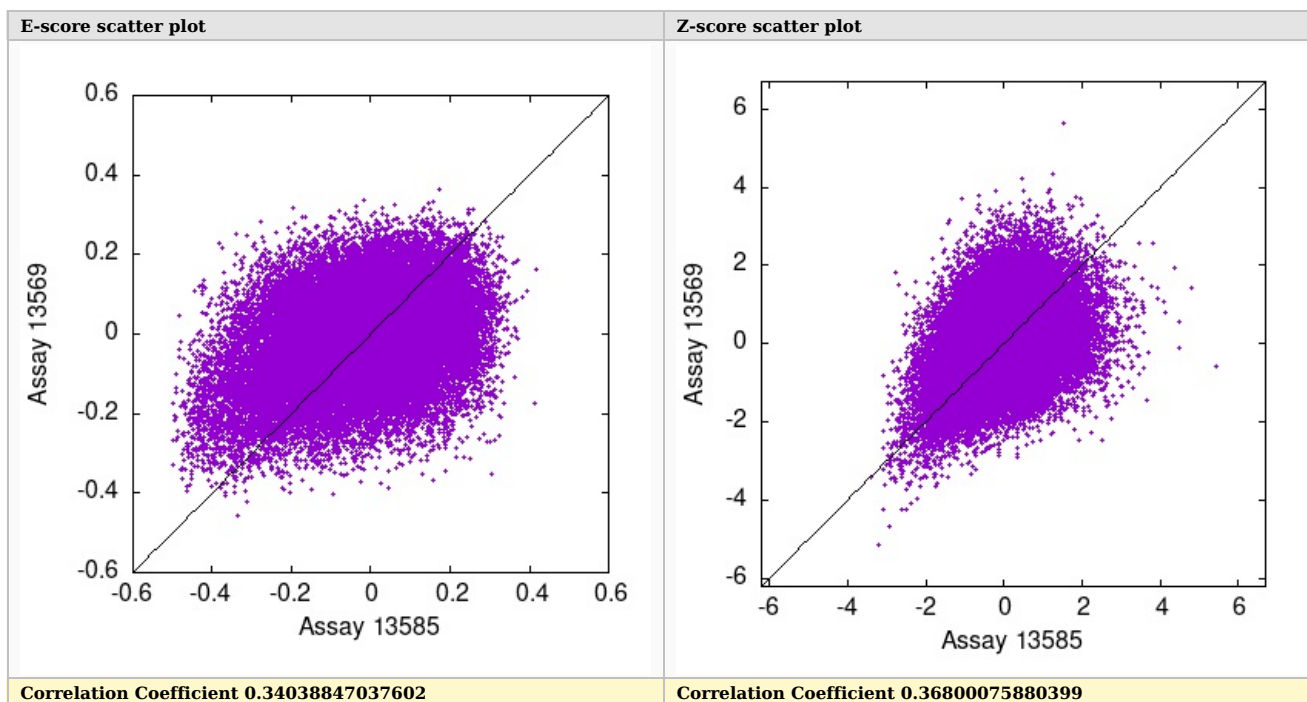


## QC report



### 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	--TGAATTTT---
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-----

### 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---
GATGTAC	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-----