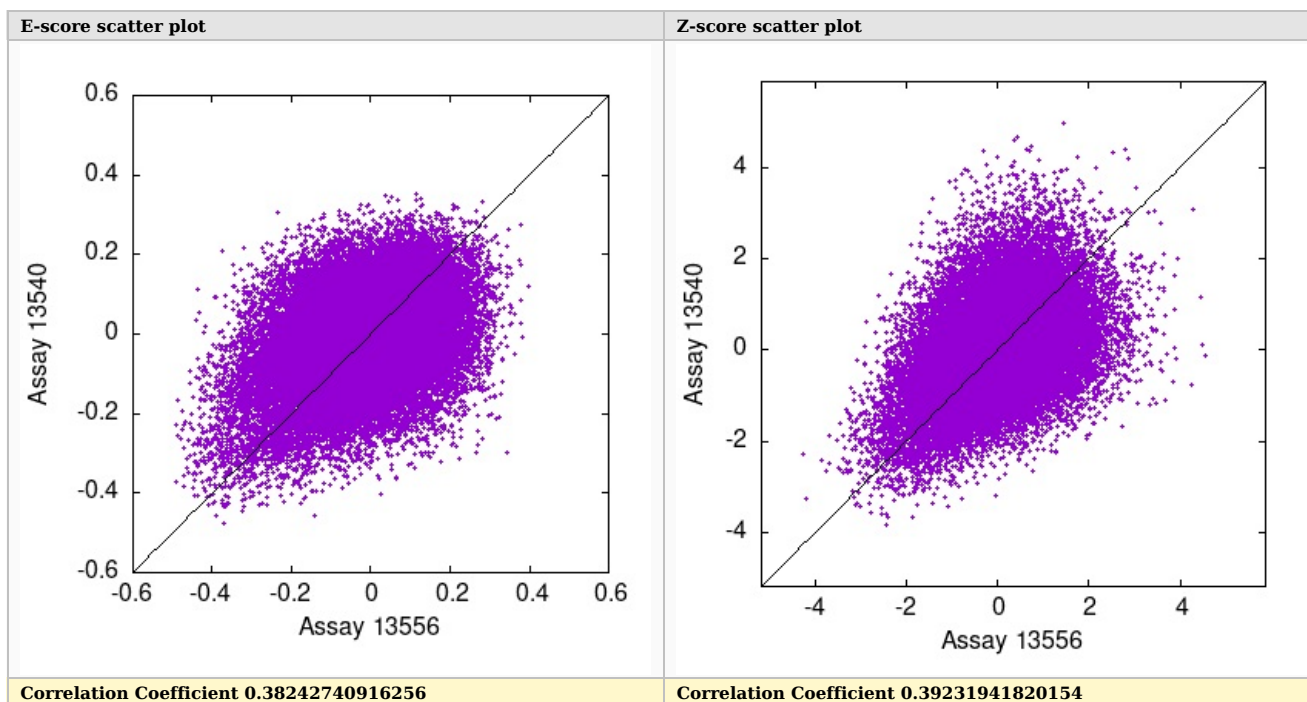


## QC report



### Top scoring motifs for Assay 13556

Protein ID: pTH14286.2 Gene: CENPA.FL Domain: Unknown Flag: Reject Array: 1M-HK

#### 8 mer E-scores for probeset 'all'

Forward:

Reverse:

AACA A

T TTT

#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:

AAC

GT

#### Top 10

#### Scores

#### Alignment

TCAACACA	0.39649	--TCAACACA--
TTCATGAA	0.38411	--TTCATGAA--
TTTGCAAA	0.37837	--TTTGCAAA--
CTAACATA	0.37800	--CTAACATA--
ATACGTAT	0.37679	---ATACGTAT-
AACGTTTG	0.37672	----AACGTTTG
GTTTAAAC	0.37507	-GTTTAAAC---
GCGCAAAA	0.36487	GCGCAAAA----
AACACTGT	0.36319	---AACACTGT
ACAACATA	0.35650	--ACAACATA--

#### Top 10

#### Scores

#### Alignment

AACACTGT	4.55844	----AACACTGT
TCAACACA	4.48236	--TCAACACA--
TGTTAACA	4.46985	TGTTAACA----
TTTGCAAA	4.29039	--TTTGCAAA--
TCCAACGA	4.24200	-TCCAACGA---
GTCAACAC	3.96105	-GTCAACAC---
AGAATTCT	3.91655	--AGAATTCT--
GAAATTTT	3.89302	-GAAATTTT---
AACAACAT	3.87999	-AACAACAT---
AACGTTTG	3.86480	----AACGTTTG

### Top scoring motifs for Assay 13540

Protein ID: pTH14286.1 Gene: CENPA.FL Domain: Unknown Flag: Reject Array: 1M-ME

#### 8 mer E-scores for probeset 'all'

Forward:

Reverse:

TACAAAT

AT TGT

#### 8 mer Z-scores for probeset 'all'

Forward:

Reverse:

CAAA

T TGT

#### Top 10

#### Scores

#### Alignment

AACGAATT	0.35069	-----AACGAATT
TACTATAA	0.34694	--TTATAGTA---
CCAGTTAC	0.34330	CCAGTTAC-----
AACATGCA	0.34166	-AACATGCA----
GACGCAAC	0.33771	---GACGCAAC--
CGTACAAA	0.33698	---CGTACAAA--
TATACAAA	0.33434	---TATACAAA--
ATACACAT	0.33323	----ATACACAT-
TCAAAACA	0.32662	---TCAAAACA--
ATGTATAA	0.32662	--TTATACAT---

#### Top 10

#### Scores

#### Alignment

GAAACGTA	4.95382	-GAAACGTA-
ACAACCAA	4.67493	-ACAACCAA-
TACTATAA	4.60512	TACTATAA--
ATCGACGA	4.45291	ATCGACGA--
AACGTTGT	4.40086	-ACAACGTT-
AACATGCA	4.39700	AACATGCA--
ATGAACGT	4.36126	--CAGTTCAT
CTAGACGA	4.35250	-CTAGACGA-
AACAGACA	4.32350	AACAGACA--
CGACCTTA	4.21723	--CGACCTTA