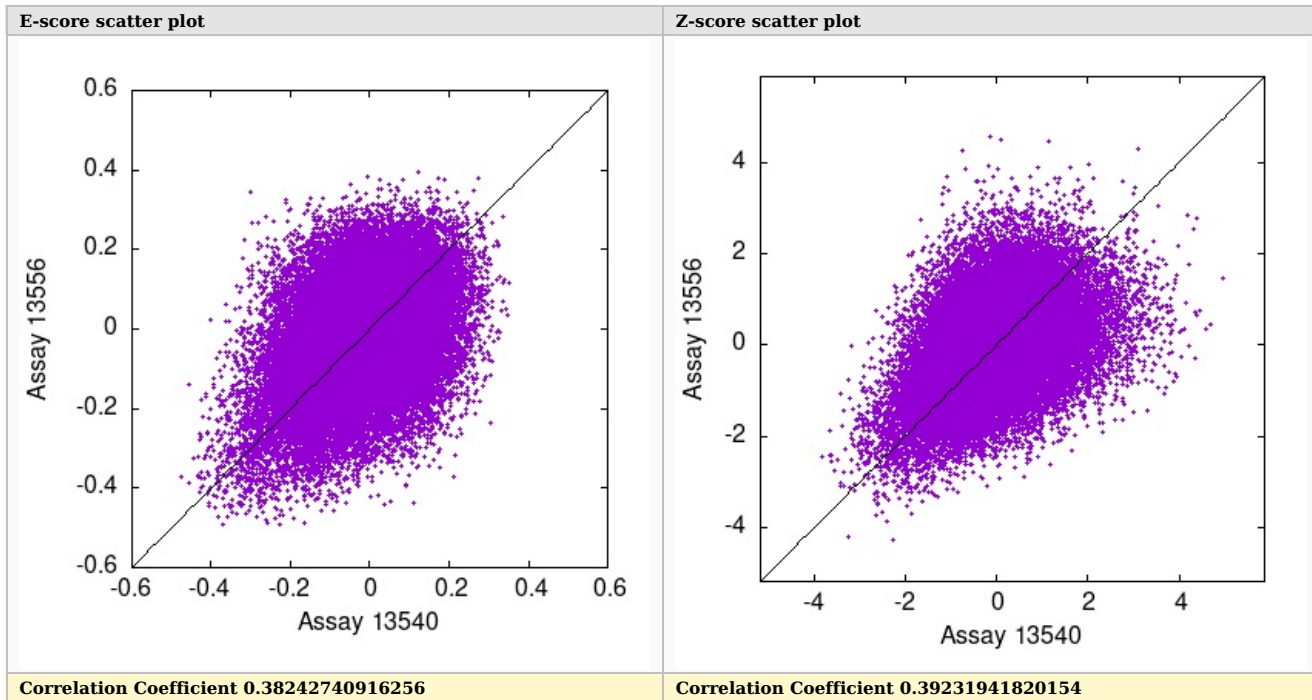


## QC report



### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
AACGAATT	0.35069	-----AACGAATT	GAAACGTA	4.95382	-GAAACGTA-
TACTATAA	0.34694	--TTATAGTA---	ACAACCAA	4.67493	--ACAACCAA-
CCAGTTAC	0.34330	CCAGTTAC----	TACTATAA	4.60512	TACTATAA--
AACATGCA	0.34166	-AACATGCA----	ATCGACGA	4.45291	ATCGACGA--
GACGCAAC	0.33771	---GACGCAAC--	AACGTTGT	4.40086	-ACAACGTT-
CGTACAAA	0.33698	---CGTACAAA--	AACATGCA	4.39700	AACATGCA--
TATACAAA	0.33434	---TATACAAA--	ATGAACTG	4.36126	--CAGTTCAT
ATACACAT	0.33323	---ATACACAT--	CTAGACGA	4.35250	-CTAGACGA-
TCAAAACA	0.32662	---TCAAAACA--	AACAGACA	4.32350	AACAGACA--
ATGTATAA	0.32662	--TTATACAT--	CGACCTTA	4.21723	--CGACCTTA

### 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'			8 mer Z-scores for probeset 'all'		
Forward:		Reverse:	Forward:		Reverse:
Top 10	Scores	Alignment	Top 10	Scores	Alignment
TCAACACA	0.39649	--TCAACACA--	AACACTGT	4.55844	---AACACTGT
TTCATGAA	0.38411	-TTCATGAA---	TCAACACA	4.48236	--TCAACACA--
TTTGCAAA	0.37837	---TTTGCAAA--	TGTTAACA	4.46985	TGTTAACA---
CTAACATA	0.37800	--CTAACATA--	TTTGCAAA	4.29039	--TTTGCAAA--
ATACGTAT	0.37679	---ATACGTAT--	TCCAACGA	4.24200	-TCCAACGA---
AACGTTTG	0.37672	---AACGTTTG--	GTCAACAC	3.96105	-GTCAACAC---
GTTTAAAC	0.37507	-GTTTAAAC---	AGAATTCT	3.91655	--AGAATTCT--
GCGCAAAA	0.36487	GCGCAAAA----	GAAATTTT	3.89302	-GAAATTTT---
AACACTGT	0.36319	---AACACTGT--	AACAACAT	3.87999	-AACAACAT---
ACAACATA	0.35650	--ACAACATA--	AACGTTTG	3.86480	---AACGTTTG