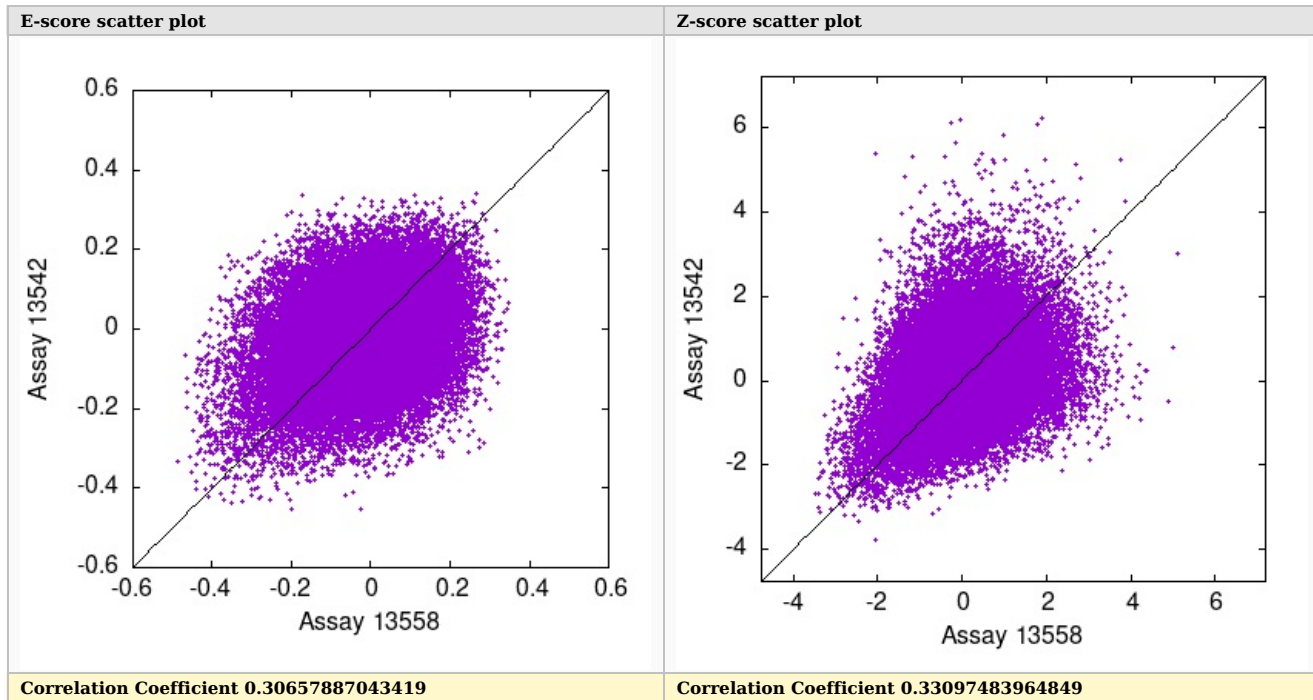


## QC report



### Top scoring motifs for Assay 13558

Protein ID: pTH14289.2 Gene: CENPX.FL Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

CAGTGAC	0.34617	GTGCACTG----
GCTTATAA	0.34244	----GCTTATAA
TACACACA	0.34080	---TACACACA-
CGACTCAA	0.34012	--CGACTCAA--
AAACGTTT	0.33649	----AAACGTTT
ACTCATGA	0.33277	----ACTCATGA
ATATAGCA	0.32883	----ATATAGCA
AATCTTGA	0.32662	----AATCTTGA
GAAATTGC	0.32468	---GAAATTGC
ATTTGTGC	0.32220	--GCACAAAT--

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

ACAGTTAC	5.10239	GTAAGTGT----
AAACGTTT	5.00556	--AAACGTTT--
ACTACCAT	4.88543	--ATGGTAGT--
ATTTGTGC	4.38658	--ATTTGTGC--
CACAGTTA	4.34110	-TAACTGTG---
CTCAAAAC	4.23592	-TGTTTGAG---
GCTTATAA	4.22779	--TTATAAGC--
ACTCATGA	4.21373	TCATGAGT----
TTGCGCAA	4.18961	----TTGCGCAA
CGACTCAA	4.11180	----TTGAGTCG

### Top scoring motifs for Assay 13542

Protein ID: pTH14289.1 Gene: CENPX.FL Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

CCAACAAA	0.34087	---CCAACAAA--
TGGCGAAA	0.33796	----TGGCGAAA--
TATACAAA	0.33656	----TATACAAA--
CCAGTTAC	0.32978	---GTAAGTGG--
CTGCTAAC	0.32876	CTGCTAAC-----
GTGCGCAC	0.32741	---GTGCGCAC--
ACCGGTAA	0.32381	----TAACCGGT--
ATAACCAA	0.32300	---ATAACCAA--
ACGTGACC	0.32267	-ACGTGACC-----
AACCTTAT	0.32057	-----AACCTTAT

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

CTGCTAAC	6.19841	-CTGCTAAC---
GTGGTAGA	6.17779	GTGGTAGA----
GTGCGCAC	6.08312	-GTGCGCAC---
TATACAAA	6.07695	-TATACAAA---
AAACGTAC	5.80845	-AAACGTAC---
TGGAGTAA	5.61789	-TGGAGTAA---
CTGACCTA	5.38968	CTGACCTA----
CGACATGA	5.37617	----CGACATGA
TGGGTCAA	5.31198	-TGGGTCAA---
TGGCGAAA	5.29720	-TGGCGAAA---