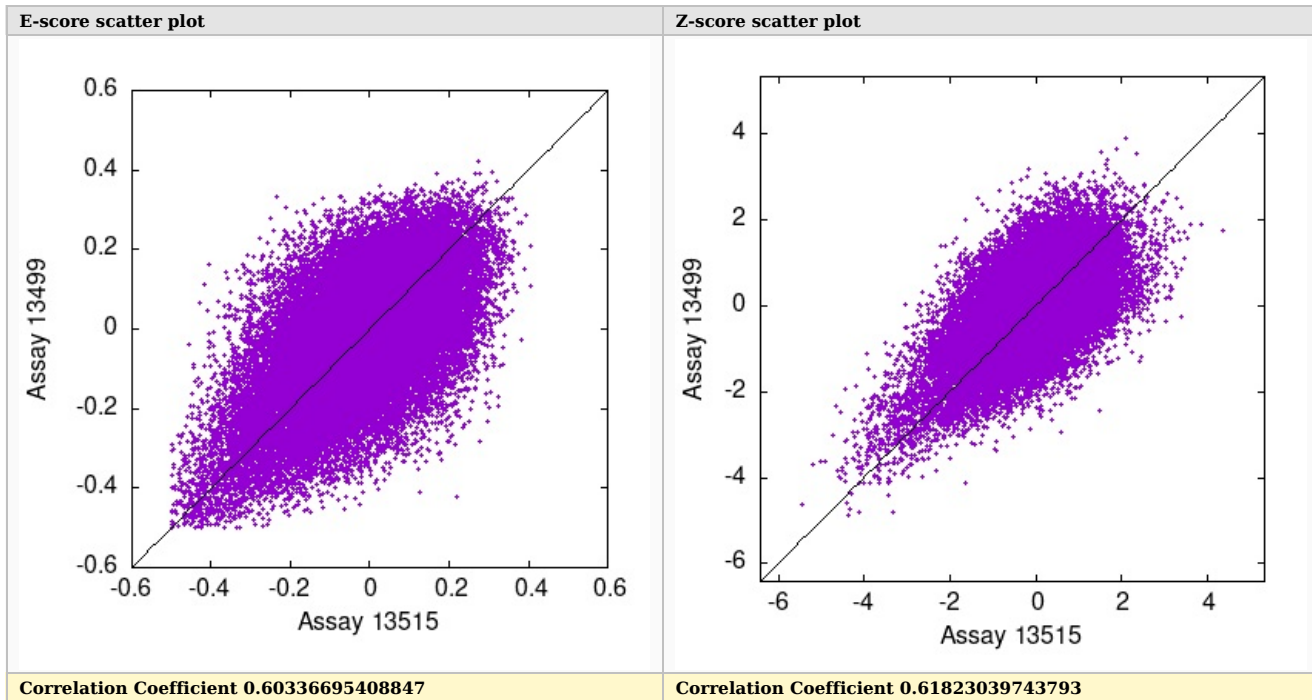


## QC report



### Top scoring motifs for Assay 13515

Protein ID: pTH13934.2 Gene: HLHA9.FL Domain: HLH Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



Top 10	Scores	Alignment
ATGCGCAT	0.40751	----ATGCGCAT
CGATAACA	0.40549	---CGATAACA-
TGTTAACA	0.39493	---TGTTAACA-
TATTAATA	0.38933	---TATTAATA-
ATTGTTGC	0.38217	-ATTGTTGC---
CGCGCGCG	0.38125	---CGCGCGCG-
GTTTAAAC	0.37560	---GTTTAAAC-
GCGCAAAA	0.37418	---GCGCAAAA-
CAATGTCA	0.37105	CAATGTCA----
GTTATAAC	0.36778	----GTTATAAC

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

Forward:

Reverse:



Top 10	Scores	Alignment
TGTTAACA	4.35698	--TGTTAACA----
ATTGTTGC	3.87656	ATTGTTGC-----
CAACGTTG	3.61733	-----CAACGTTG-
AGTTAACT	3.55370	--AGTTAACT----
CGATAACA	3.46063	--CGATAACA----
TGTTTAA	3.45116	TGTTTAA-----
AAACGTTT	3.40775	-----AAACGTTT-
ACAAACAG	3.39530	---ACAAACAG----
CAGTACTG	3.38004	--CAGTACTG----
AACGTTTG	3.37657	-----AACGTTTG

### Top scoring motifs for Assay 13499

Protein ID: pTH13934.1 Gene: HLHA9.FL Domain: HLH Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



Top 10	Scores	Alignment
ACAACAAT	0.42379	-----ATTGTTGT--
TTTCGAAA	0.39567	TTTCGAAA-----
ATTGTGAC	0.39199	-----ATTGTGAC---
CAACAATA	0.39149	-----TATTGTTG---
ATAATATA	0.39128	----TATATTAT----
AATTGTTA	0.39113	-----AATTGTTA---
AAATTTGT	0.37428	-----AAATTTGT----
AAATTGTT	0.37070	-----AAATTGTT----
CGTTAACG	0.36907	-----CGTTAACG---
AATTTGTA	0.36836	-----AATTTGTA----

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

Forward:

Reverse:



Top 10	Scores	Alignment
TTTCGAAA	3.91971	--TTTCGAAA----
AACGCGTT	3.65111	-AACGCGTT-----
AATTGTTA	3.59535	--AATTGTTA----
ACAACAAT	3.54209	---ATTGTTGT----
TAAATTTA	3.41221	--TAAATTTA----
CGTTAACG	3.30314	-----CGTTAACG---
ATTTACTA	3.20429	--ATTTACTA----
ATGATCAT	3.19706	---ATGATCAT----
ACATATGT	3.11320	ACATATGT-----
AGCAATTG	3.09215	-CAATTGCT-----