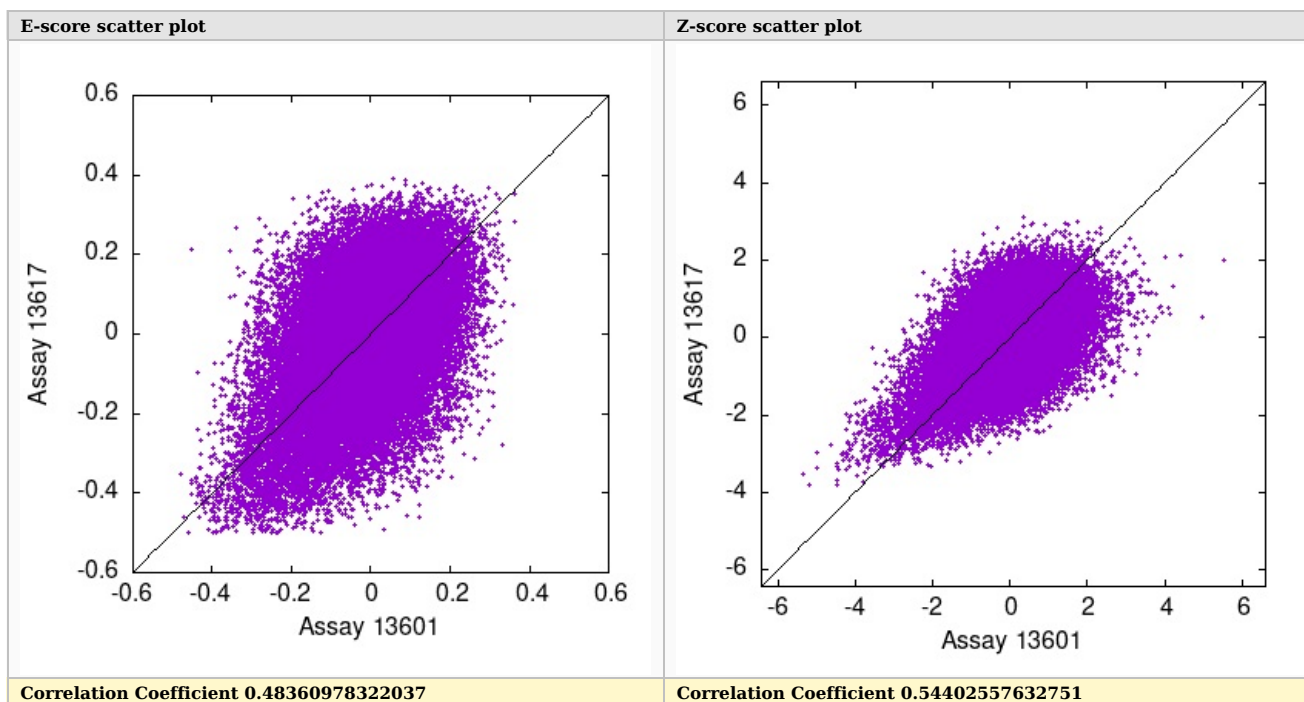


## QC report



### Top scoring motifs for Assay 13601

Protein ID: pTH14298.1 Gene: DACH2.FL Domain: Unknown Flag: Reject Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GTTATAAC	0.36254	--GTTATAAC--
CTTGTAAC	0.36251	GTTACAAG---
TGTGCACA	0.35863	TGTGCACA--
AACAAAGC	0.34658	--AACAAAGC--
AACTTTGG	0.33983	---CCAAAGTT
ACAGTTCT	0.33627	--ACAGTTCT
CAGACAAC	0.33510	--CAGACAAC--
ATTCGTTA	0.33255	-TAACGAAT--
CCAACAAC	0.33236	CCAACAAC--
AAACCAAA	0.33150	-AAACCAAA--

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GTTATAAC	5.52356	---GTTATAAC----
TGTGCACA	4.96173	---TGTGCACA----
CTTGTAAC	4.43213	---CTTGTAAC----
TGCATGCA	4.23014	-TGCATGCA-----
AACAAAGC	4.13010	-GCTTTGTT-----
GATCGTTA	4.11350	-----TAACGATC-
GTTGCAAC	4.01313	---GTTGCAAC-----
ACAGTTCT	3.92501	ACAGTTCT-----
AACTTTGG	3.89666	-----AACTTTGG
CCAACAAC	3.85665	---CCAACAAC----

### Top scoring motifs for Assay 13617

Protein ID: pTH14298.2 Gene: DACH2.FL Domain: Unknown Flag: Reject Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

GATATGTA	0.39117	GATATGTA--
ATTAATAA	0.38532	-ATTAATAA--
ACAAACAG	0.38018	-ACAAACAG--
ATCATACA	0.37680	--TGTATGAT-
ACAAATCA	0.37457	-ACAAATCA--
AACGTTTT	0.37281	-AACGTTTT--
GTCATGAC	0.37280	--GTCATGAC-
TATTAATA	0.37216	TATTAATA--
ATTATTAA	0.37126	--TTAATAAT-
CGTTATAA	0.36921	---TTATAACG

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

ATCATACA	3.12503	ATCATACA--
GAAATTC	3.00935	GAAATTC--
ATAAACGA	2.97313	-TCGTTTAT-
ACAAACAG	2.95469	ACAAACAG--
GATATGTA	2.91639	GATATGTA--
ATTATAAT	2.90411	ATTATAAT--
ATTATTAA	2.89790	ATTATTAA--
AATATTAA	2.86220	AATATTAA--
ATTGTTGC	2.85373	ATTGTTGC--
GATTAATA	2.84843	--TATTAATC