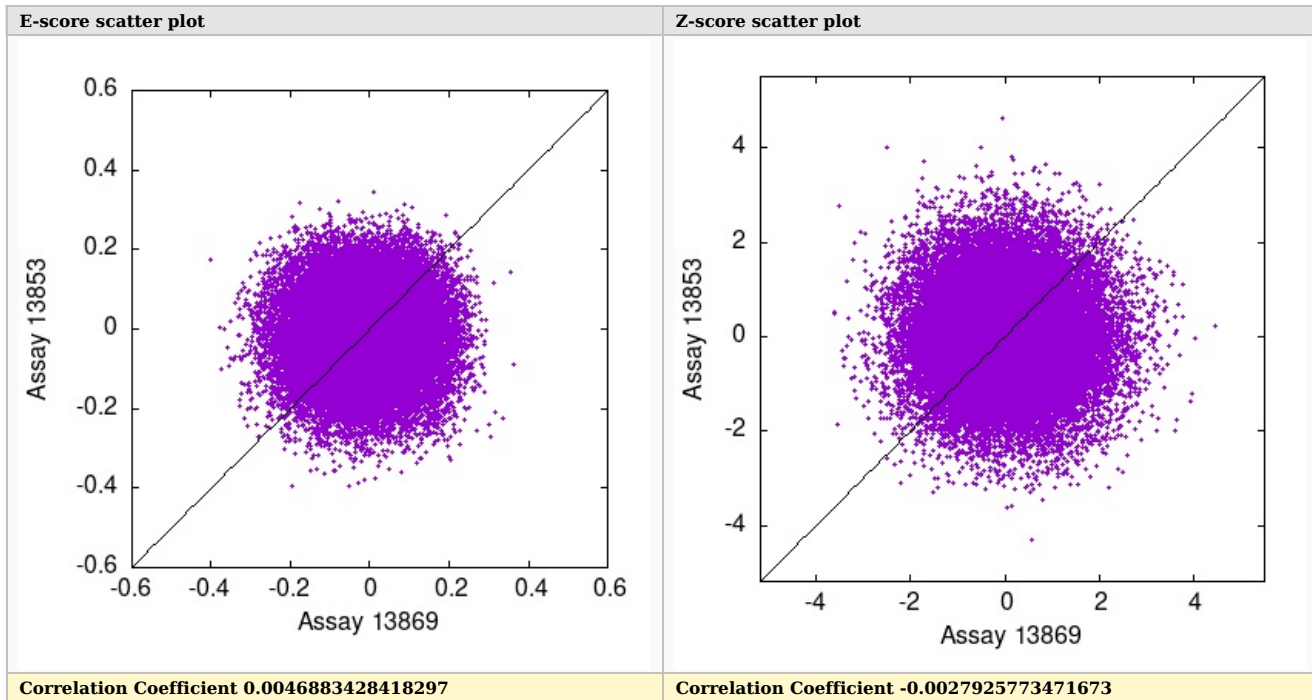


## QC report



### Top scoring motifs for Assay 13869

Protein ID: pTH14253.2 Gene: POU5F2.FL Domain: Homeobox Flag: Reject Array: 1M-HK

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

Forward:

Reverse:

AAATTGGT  
ATTTGTAG  
GGTCGACC  
AAGTGCAA  
AATTCTCT  
GCTCGGTA  
TCAAGAGA  
ATTGGTAC  
TATGAGGA  
GAGGCCAA

TTTCAAGG  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA

#### Top 10

#### Scores

#### Alignment

AAATTGGT	0.36326	AAATTGGT----
ATTTGTAG	0.35513	---ATTTGTAG--
GGTCGACC	0.33694	---GGTCGACC--
AAGTGCAA	0.31458	-----TTGCACTT
AATTCTCT	0.31217	--AATTCTCT---
GCTCGGTA	0.30548	--GCTCGGTA---
TCAAGAGA	0.30181	TCTCTTGA-----
ATTGGTAC	0.29418	---ATTGGTAC--
TATGAGGA	0.29408	--TATGAGGA---
GAGGCCAA	0.28987	----TTGGCCTC-

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

Forward:

Reverse:

GGTCGACC  
AAATTGGT  
AAGTGCAA  
CCATGTCC  
CGATTGGC  
CCATATGG  
CTAGGAC  
CTATCGGC  
ATCTGAAA  
ACCTTACT

TTTCAAGG  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA

#### Top 10

#### Scores

#### Alignment

GGTCGACC	4.46164	-----GGTCGACC--
AAATTGGT	4.04449	-----AAATTGGT---
AAGTGCAA	3.96606	-----TTGCACTT
CCATGTCC	3.95013	-----CCATGTCC---
CGATTGGC	3.78764	-----CGATTGGC---
CCATATGG	3.77931	-----CCATATGG---
CCTAGGAC	3.69842	---GTCCTAGG----
CTATCGGC	3.67441	-----CTATCGGC---
ATCTGAAA	3.65235	TTTCAGAT-----
ACCTTACT	3.64745	----AGTAAGGT---

### Top scoring motifs for Assay 13853

Protein ID: pTH14253.1 Gene: POU5F2.FL Domain: Homeobox Flag: Reject Array: 1M-ME

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

Forward:

Reverse:

GACATAAC  
CGGTTGAG  
ATGATCAT  
AGGTGTTC  
GAGTGCTA  
AGAAATTA  
GGGTTTAA  
ACTAGCCG  
AACCGGTT  
CCGCGGCA

TTTCAAGG  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA

#### Top 10

#### Scores

#### Alignment

GACATAAC	0.34502	-----GACATAAC
CGGTTGAG	0.32307	-----CGGTTGAG--
ATGATCAT	0.31648	-----ATGATCAT--
AGGTGTTC	0.31245	-----AGGTGTTC--
GAGTGCTA	0.30581	-----GAGTGCTA--
AGAAATTA	0.30125	-----AGAAATTA--
GGGTTTAA	0.29745	-----GGGTTTAA--
ACTAGCCG	0.29613	-----CGGCTAGT--
AACCGGTT	0.29000	-----AACCGGTT---
CCGCGGCA	0.28914	TGCCGCGG-----

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

Forward:

Reverse:

GACATAAC  
ATAATTAT  
CGGTTGAG  
ACCTTGCT  
GCAGGCGA  
ACTAGCCG  
GCCAATAA  
ATGATCAT  
CGATCTTC  
AATTGTGA

TTTCAAGG  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA  
TCTCTTGA

#### Top 10

#### Scores

#### Alignment

GACATAAC	4.61721	--GACATAAC-----
ATAATTAT	4.01796	ATAATTAT-----
CGGTTGAG	4.00815	---CTCAACCG-----
ACCTTGCT	3.80261	-----AGCAGGGT
GCAGGCGA	3.74643	-----TCGCCTGC---
ACTAGCCG	3.70585	---ACTAGCCG-----
GCCAATAA	3.65413	-TTATTGGC-----
ATGATCAT	3.60509	---ATGATCAT-----
CGATCTTC	3.57298	----CGATCTTC----
AATTGTGA	3.53352	--AATTGTGA-----