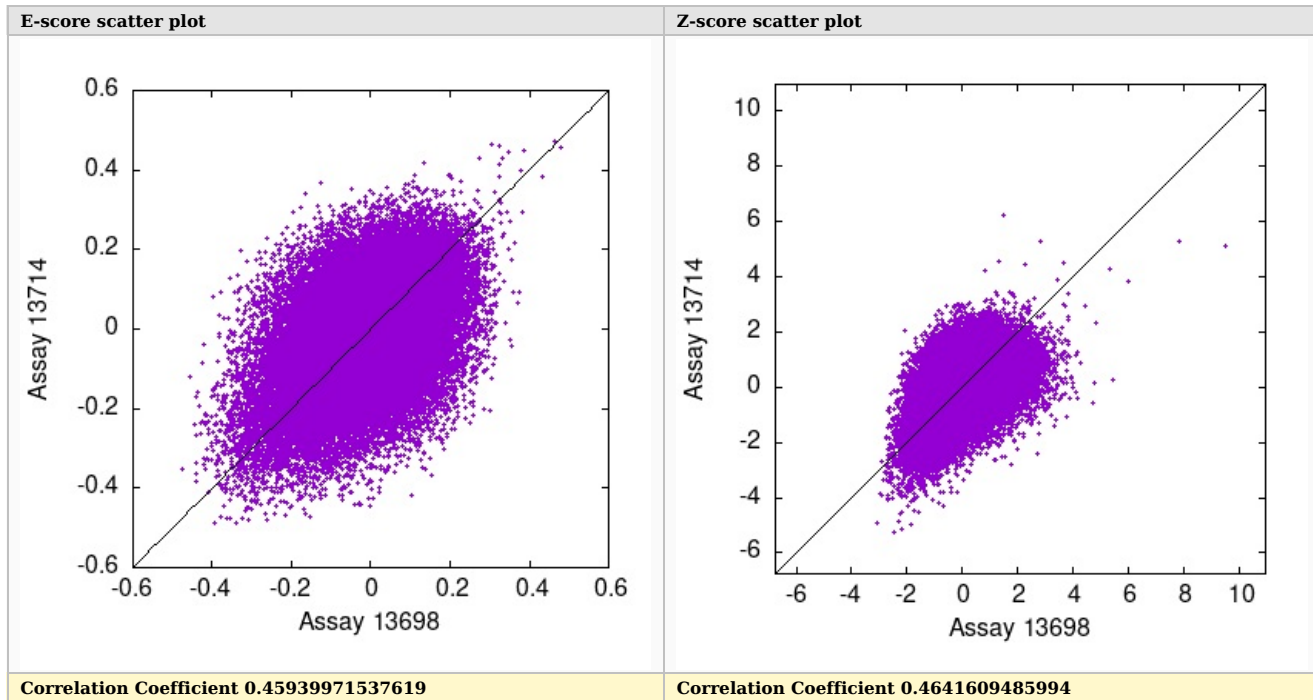


## QC report



### Top scoring motifs for Assay 13698

Protein ID: pTH14210.1 Gene: JRK.DBD Domain: CENP-B\_N Flag: Pass\_matched\_pair Array: 1M-ME

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

Forward:

Reverse:



#### Top 10

#### Scores

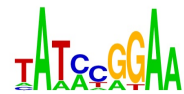
#### Alignment

ATCCGGAA	0.47778	---ATCCGGAA--
TATCCGGA	0.46404	--TATCCGGA--
ATTCCGGA	0.43337	---TCCGGAAT
TAACCGGA	0.38804	--TAACCGGA--
AATCCGGA	0.38396	--AATCCGGA--
CCGATAA	0.38008	--TTATCCGG--
TATACAGA	0.37557	--TATACAGA--
TATAAATA	0.37071	--TATAAATA--
GTACTTTA	0.36481	--GTACTTTA--
CGGATACA	0.36007	TGTATCCG----

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

ATCCGGAA	9.49685	-----ATCCGGAA--
TATCCGGA	7.84255	-----TATCCGGA--
ATTCCGGA	6.03276	-----TCCGGAAT
TATAAATA	5.45596	-----TATAAATA--
TAACCGGA	5.31828	-----TAACCGGA--
AATCCGGA	4.85837	-----AATCCGGA--
TATACAGA	4.77276	-----TATACAGA--
ACAAATGG	4.71254	-----ACAAATGG--
ATAATGTA	4.46040	TACATTAT-----
TATATGGA	4.29098	-----TATATGGA--

### Top scoring motifs for Assay 13714

Protein ID: pTH14210.2 Gene: JRK.DBD Domain: CENP-B\_N Flag: Pass\_matched\_pair Array: 1M-HK

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

TATCCGGA	0.47249	TATCCGGA--
AACCGGAA	0.46408	-AACCGGAA--
TTCCGGAA	0.45914	-TTCCGGAA--
ATCCGGAA	0.45839	-ATCCGGAA--
TAACCGGA	0.44737	TAACCGGA--
CATCCGGA	0.44384	CATCCGGA--
ATCCGGAT	0.42865	-ATCCGGAT--
ATCCGGAC	0.42777	-ATCCGGAC--
CTTCCGGA	0.41662	--TCCGGAAG
TCCGGAAG	0.41412	--TCCGGAAG

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

Forward:

Reverse:



#### Top 10

#### Scores

#### Alignment

TTCCGGAA	6.24708	-TTCCGGAA--
AACCGGAA	5.27728	-AACCGGAA--
TATCCGGA	5.26893	TATCCGGA--
ATCCGGAA	5.10310	-ATCCGGAA--
ATCCGGAT	4.56572	-ATCCGGAT--
CATCCGGA	4.51451	CATCCGGA--
TCCGGAAG	4.43473	--TCCGGAAG
TAACCGGA	4.29781	TAACCGGA--
CTTCCGGA	4.25531	--TCCGGAAG
ATCCGGAC	3.90314	-ATCCGGAC--