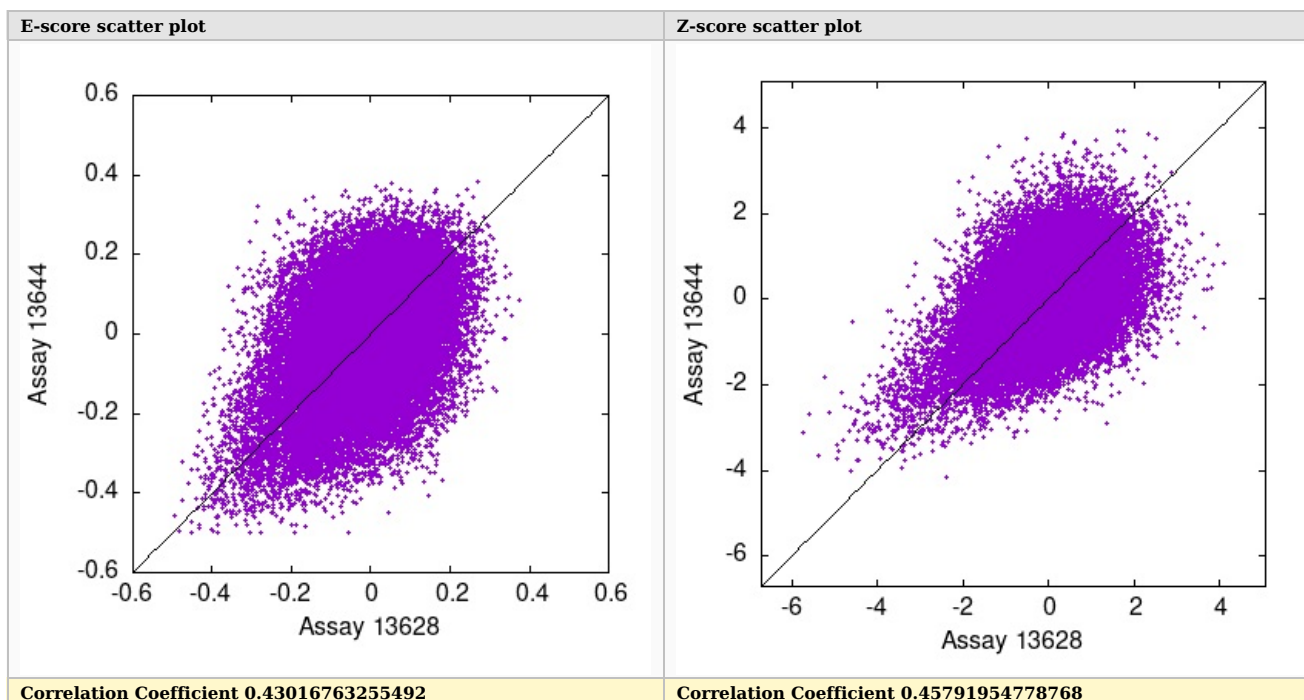


## QC report



### Top scoring motifs for Assay 13628

Protein ID: pTH14229.1 Gene: GATAD2B.FL Domain: GATA Flag: Reject Array: 1M-ME

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

Forward:	Reverse:

Top 10	Scores	Alignment
ACAACACG	0.37458	CGTGTGTG---
ACAACAAT	0.35726	ATTGTTGT---
ATGTTGTC	0.35208	-ATGTTGTC--
ATGTTGAG	0.34812	-ATGTTGAG--
ACAACCTGA	0.34046	TCAGTTGT---
CACAACAC	0.33989	-GTGTTGTG--
CCAACAAC	0.33870	---GTTGTTGG
GTGTAGTA	0.33837	-GTGTAGTA--
GAATCCAA	0.33479	-TTGGATTC--
AGTCAGGA	0.32015	--TCCTGACT-

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

Forward:	Reverse:

Top 10	Scores	Alignment
GTGTAGTA	4.09035	TACTACAC---
ATGTTGTC	3.97185	GACAACAT---
AAACCAAC	3.86439	-AAACCAAC--
ACAACACG	3.79441	-ACAACACG--
ACAACAAT	3.73220	-ACAACAAT--
ATTACGAC	3.70325	--ATTACGAC
CCAACAAC	3.63409	-CCAACAAC--
AACATGTT	3.63201	---AACATGTT
AGTATTGA	3.62044	-TCAATACT--
CGAACAGA	3.57866	-CGAACAGA--

### Top scoring motifs for Assay 13644

Protein ID: pTH14229.2 Gene: GATAD2B.FL Domain: GATA Flag: Reject Array: 1M-HK

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

Forward:	Reverse:

Top 10	Scores	Alignment
GTCATGAC	0.38185	-GTCATGAC----
TATGCATA	0.37821	-TATGCATA----
ACAATTCA	0.36977	-----TGAAGTGT
TACGCGTA	0.36536	-TACGCGTA----
CGCGCGCG	0.36499	-CGCGCGCG----
CGCGCGAA	0.36466	-CGCGCGAA----
TCGCGCGA	0.36282	TCGCGCGA-----
ATCACACA	0.36058	-TGTGTGAT----
GGTCTAGA	0.35857	--GGTCTAGA----
ACTGTAAA	0.35813	-ACTGTAAA----

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

Forward:	Reverse:

Top 10	Scores	Alignment
ACAAACAG	3.93093	----ACAAACAG--
TCGCGCGA	3.92404	----TCGCGCGA--
TATGCATA	3.85353	---TATGCATA---
CGCGCGCG	3.84057	--CGCGCGCG---
TATAACGA	3.77131	--TATAACGA----
ACGAAACG	3.75244	---ACGAAACG---
GAAATTTT	3.73879	GAAATTTT-----
ATTTCAAC	3.70199	---ATTTCAAC---
ACACTTCA	3.67082	-----ACACTTCA
ATCACACA	3.62801	--ATCACACA---