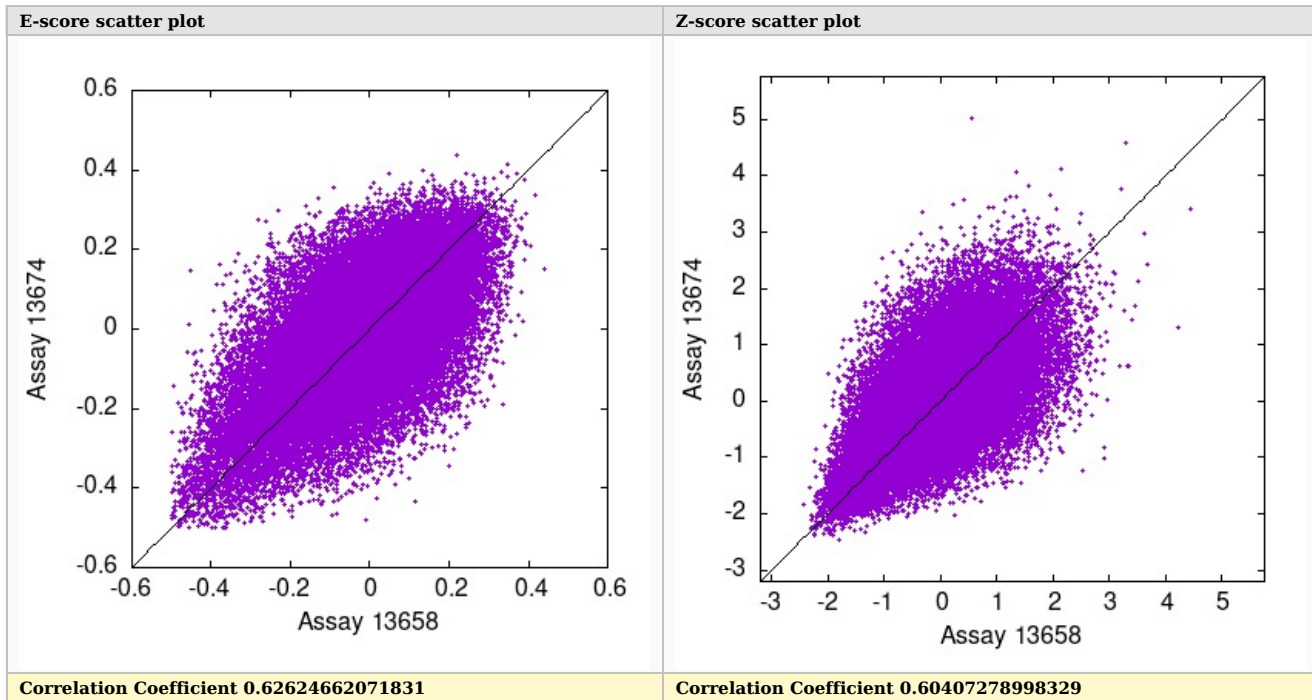




## QC report





### Top scoring motifs for Assay 13658

Protein ID: pTH14246.1 Gene: NANOGNB.FL Domain: Homeobox Flag: Reject Array: 1M-ME

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

Forward:	Reverse:	
		
Top 10	Scores	Alignment
ATGTACAT	0.43971	---ATGTACAT--
AATGCATT	0.41810	AATGCATT-----
AACATGTT	0.40690	AACATGTT-----
TAAATTTA	0.39528	TAAATTTA-----
TGTGCACA	0.39489	----TGTGCACA-
CGTTATCA	0.39038	-----TGATAACG-
AACGTTGT	0.38977	AACGTTGT-----
GTTTAAAC	0.38974	-----GTTTAAAC
ATATTTAA	0.38475	-ATATTTAA-----
ACATGTTA	0.38327	-ACATGTTA----



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

Forward:		Reverse:
		
Top 10	Scores	Alignment
AATGCATT	4.45242	--AATGCATT--
ATGTACAT	4.22338	-ATGTACAT---
TAAATTTA	3.68024	----TAAATTTA
GTTTAAAC	3.61846	-GTTTAAAC---
AACATGTT	3.49998	----AACATGTT
TTGCGCAA	3.44384	-TTGCGCAA---
TGTGCACA	3.39401	--TGTGCACA--
ATATTTAA	3.33756	-ATATTTAA---
GTTGCGCA	3.32308	GTTGCGCA----
TTTGCAAA	3.27860	--TTTGCAAA--



### Top scoring motifs for Assay 13674

Protein ID: pTH14246.2 Gene: NANOGNB.FL Domain: Homeobox Flag: Reject Array: 1M-HK

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

Forward:		Reverse:	
			
Top 10	Scores	Alignment	
GTGTACAC	0.43616	-GTGTACAC-	
TTTGCAAA	0.41605	TTTGCAAA--	
ATTATAAT	0.39983	-ATTATAAT-	
GTCATGAC	0.39663	-GTCATGAC-	
ATGTTAAC	0.39213	-ATGTTAAC-	
ATGCATAC	0.39055	-ATGCATAC-	
ATGGTCCA	0.38917	-ATGGTCCA-	
GATGCATC	0.38865	GATGCATC--	
GTGTAACA	0.38681	--TGTTACAC	
TGTTAACA	0.38249	--TGTTAACA	

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

Forward:		Reverse:
		
Top 10	Scores	Alignment
GTGTACAC	5.01188	--GTGTACAC-
TTTGCAAA	4.59370	-TTTGCAAA--
GTCATGAC	4.11942	--GTCATGAC-
ACGTACTA	4.06079	---TAGTACGT
TAACGTAA	3.81336	TTACGTTA--
ATGTTAAC	3.76490	--ATGTTAAC-
GTGTAACA	3.65843	---TGTTACAC
TACACACA	3.62363	-TGTGTGTA--
CTGTATTA	3.62275	CTGTATTA--
ATTATAAT	3.58240	--ATTATAAT-