N6-Methyladenine DNA modification in *Xanthomonas oryzae* pv. *oryzicola* genome

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Table S1. The datasets of seven Xoc strains in this study

Strain	Sample ID	SMRT cell	Total length of subreads (Gb)	Coverage	Reference link
BLS256	SAMN03612250	5	1.94	421x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233712
BLS279	SAMN03612248	4	1.66	362x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233507
CFBP2286	SAMN03612252	6	2.03	425x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233505
CFBP7331	SAMN03612260	7	2.11	442x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233509
CFBP7341	SAMN03612287	4	1.85	387x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233510
L8	SAMN03612258	4	1.33	291x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233511
RS105	SAMN03612254	4	1.80	395x	https://www.ncbi.nlm.nih.gov/genome/529?genome_assembly_id=233512

Table S2. The stop codon usage in seven strains

Strain	Normal stop codon			6mA stop codon		
	TGA	TAA	TAG	TGA	TAA	TAG
BLS256	2681 (67.63%)	817 (20.61%)	466 (11.76%)	56 (49.56%)	47 (41.59%)	10 (8.85%)
BLS279	2697 (68.19%)	805 (20.35%)	453 (11.46%)	66 (51.56%)	49 (38.28%)	13 (10.16%)
CFBP2286	2807 (67.51%)	860 (20.68%)	491 (11.81%)	80 (60.15%)	42 (31.58%)	11 (8.27%)
CFBP7331	2762 (67.28%)	866 (21.10%)	477 (11.62%)	73 (50.69%)	59 (40.97%)	12 (8.34%)
CFBP7341	2803 (67.32%)	874 (20.98%)	487 (11.70%)	45 (47.37%)	47 (49.47%)	3 (3.16%)
L8	2714 (67.85%)	831 (20.78%)	455 (11.37%)	42 (55.26%)	26 (34.21%)	8 (10.53%)
RS105	2696 (68.20%)	807 (20.42%)	450 (11.38%)	59 (48.76%)	49 (40.50%)	13 (10.74%)

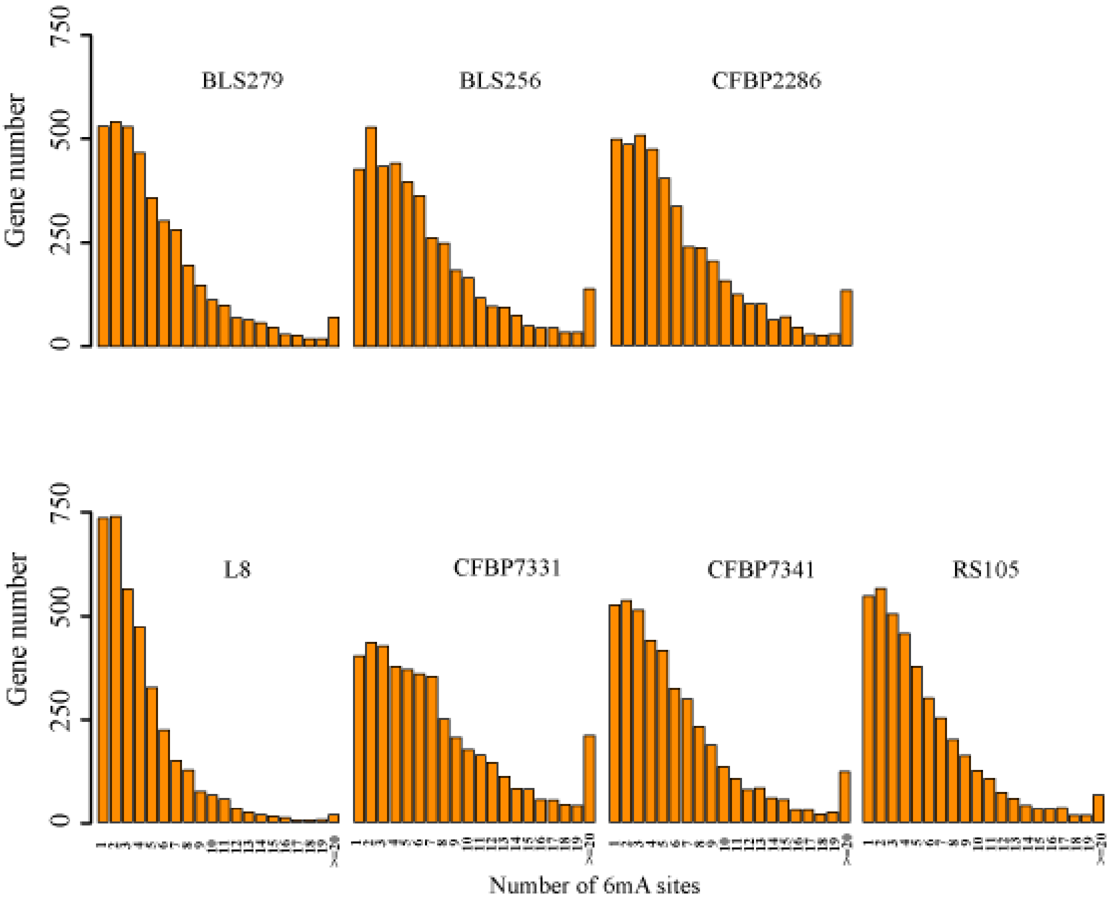


Figure S1. The located 6mA sites number of all genes in seven strains.

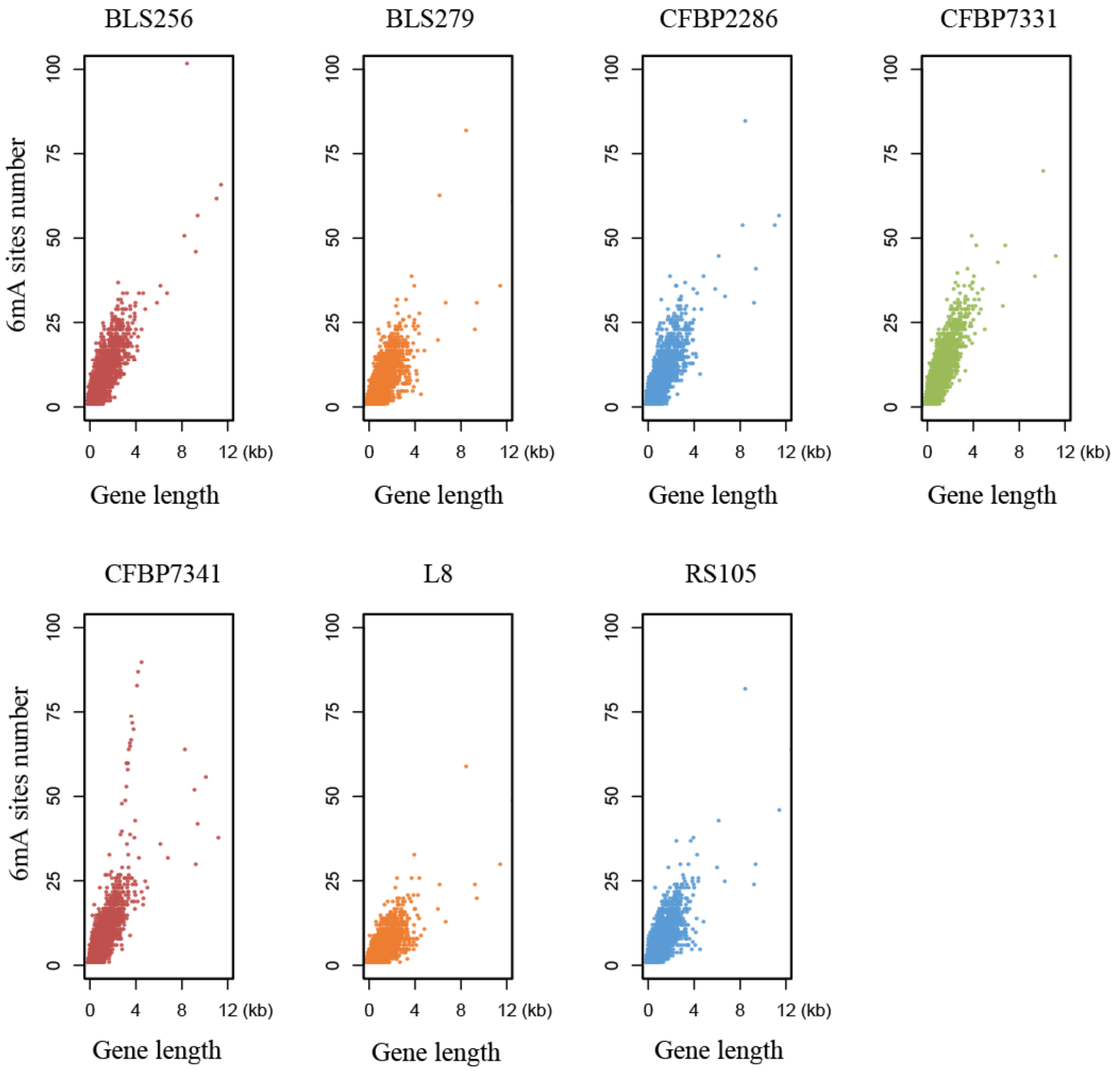
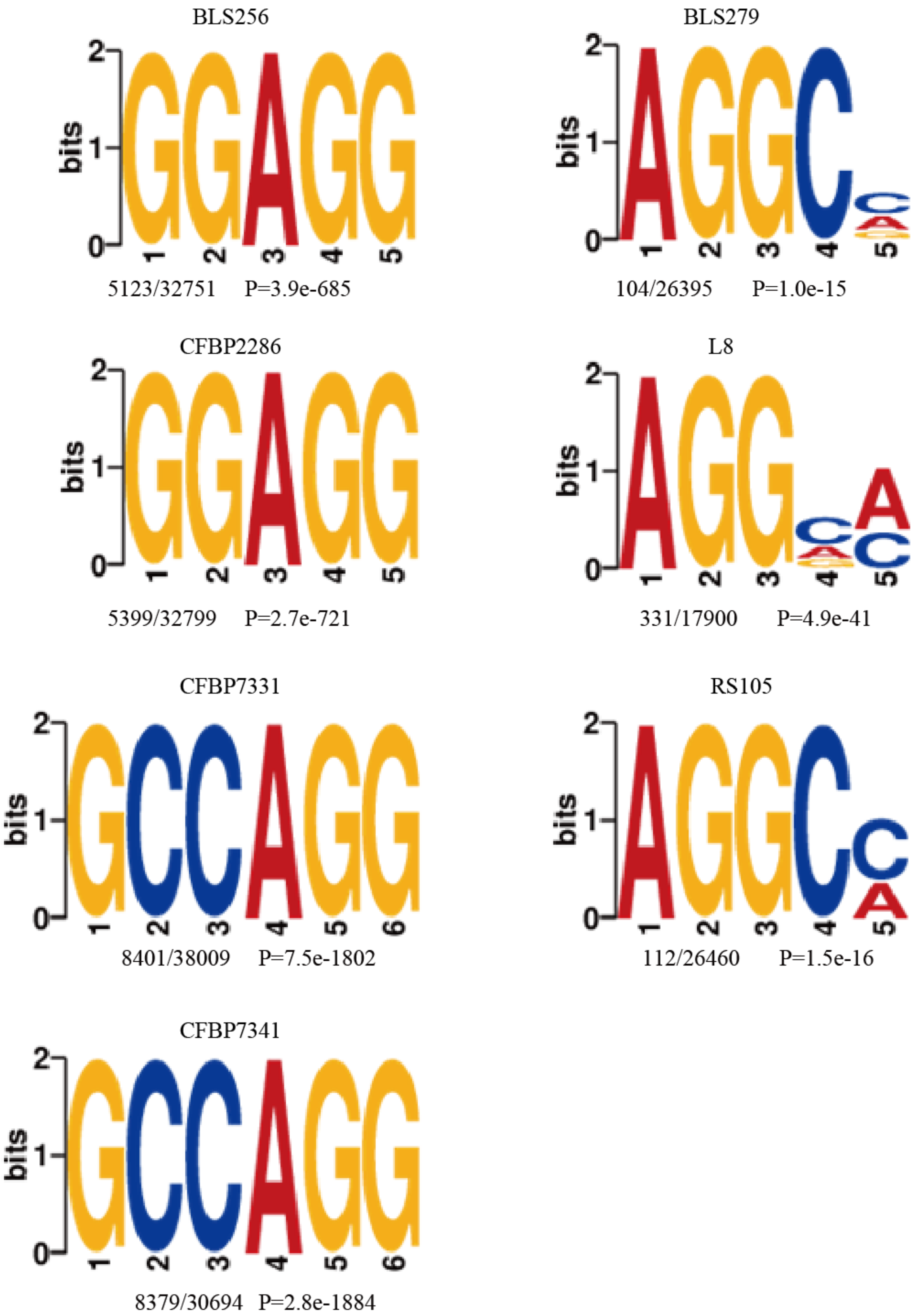


Figure S2. The scatter plot of 6mA sites numbers and gene length in seven strains.



BLS256
5123/32751 P=3.9e-685

BLS279
104/26395 P=1.0e-15

CFBP2286
5399/32799 P=2.7e-721

L8
331/17900 P=4.9e-41

CFBP7331
8401/38009 P=7.5e-1802

RS105
112/26460 P=1.5e-16

CFBP7341
8379/30694 P=2.8e-1884

Figure S3. The identified consensus motifs containing 6mA sites in seven strains.

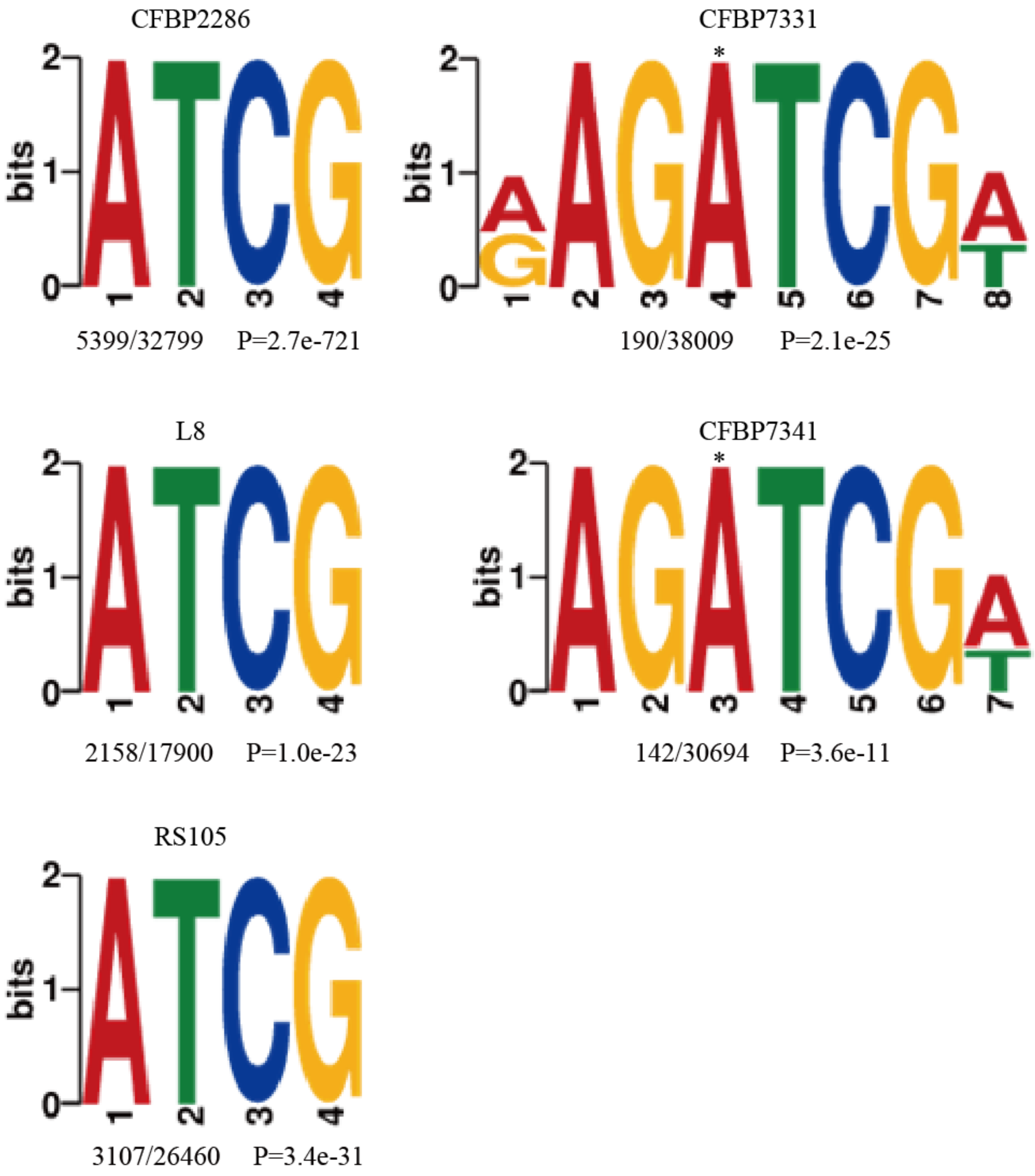


Figure S4. The identified ATCG motif containing 6mA sites in partial strains.