Supplementary tables

	Contigs assembly only with PE reads	Assembly with PE and MP reads	Assembly with PE, MP and SLR reads	Assembly with PE, MP, SLR and ONT reads
Sf21 genome				
# sequences (>= 1 Kb)	47,866	17,588	11,871	4,020
Largest scaffold (bp)	264,592	1,209,752	2,608,367	2,900,257
Total length (bp)	430,604,418	477,599,629	488,468,751	463,041,686
N50 (bp)	18,101	140,626	307,038	364,523
L50	6,168	843	383	315
GC (%)	36.20	36.33	38.59	38.42
# N's per 100 Kb	27.82	3559.42	776.82	681.43
Tni genome				
# sequences (>= 1 Kb)	53,137	22,485	14,683	2,954
Largest scaffold (bp)	101,314	595,205	1,711,767	1,722,548
Total length (bp)	355,056,269	393,087,391	407,374,447	332,103,479
N50 (bp)	8,666	82,532	252,810	326,309
L50	9,637	1,114	395	293
GC (%)	36.08	35.82	36.51	36.30
Number of N's per 100 Kb	57.75	1183.12	575.45	499.33

Table S1: Short summary of Sf21 and Tni *de novo* genome assemblies using progressively different types of reads. The N50 value is defined as the sequence length of the shortest contig

at 50% of the total genome length. L50 value represent the smallest number of contigs to which their cumulative length represents half of genome size.

	Sf21	**Tni**
RNA-Seq data		
Total number of PE/SE reads	91,741,494	240,178,919
Number of PE/SE reads after adaptor and quality trimming	86,754,674	164,941,193
Number of PE/SE reads after duplicate removal	77,650,737 (#PE: 75,773,152 #SE:1,877,585)	129,473,322 (#PE: 124,582,705 #SE: 4,890,617)
Transcriptome assembly		
Number of assembled transcripts	28,339	57,600
Number of assembled transcripts (>= 1000 bp)	9,948	21,534
GC (%)	41.31	42.93
Total assembled bases	31,697,415	67,831,071
N50 (bp)	1,956	2,076
Median transcript length (bp)	611	648
Mean transcript length (bp)	1,118.51	1,177.65
Largest transcript (bp)	24,940	20,156
# Full length transcripts (>= 80%)	3,211	3,669
Percentage of mapped RNAseq PE/SE reads	~ 97% (proper pairs)	~ 69% (proper pairs)
Number of transcripts after CD-HIT run (90% similarity)	24,992	41,041

Table S2: Sf21 and Tni *de novo* transcriptome sequencing data and assembly features. This table presents the total number of sequencing paired-end (PE) reads and the number of processed reads after trimming and duplicate removal. The filtered reads were then used for transcriptome assembly. The shown metrics cover the number of assembled transcripts, the GC percent, the cumulative length of the assembly, the N50, the median, the mean and the

maximum length of the transcripts, the full-length transcript coverage and the number of RNAseq PE reads mapping back to the assembled sequences. Finally, the assembled transcripts were clustered, before the gene prediction step, using CD-HIT to remove duplications and clean up the dataset.

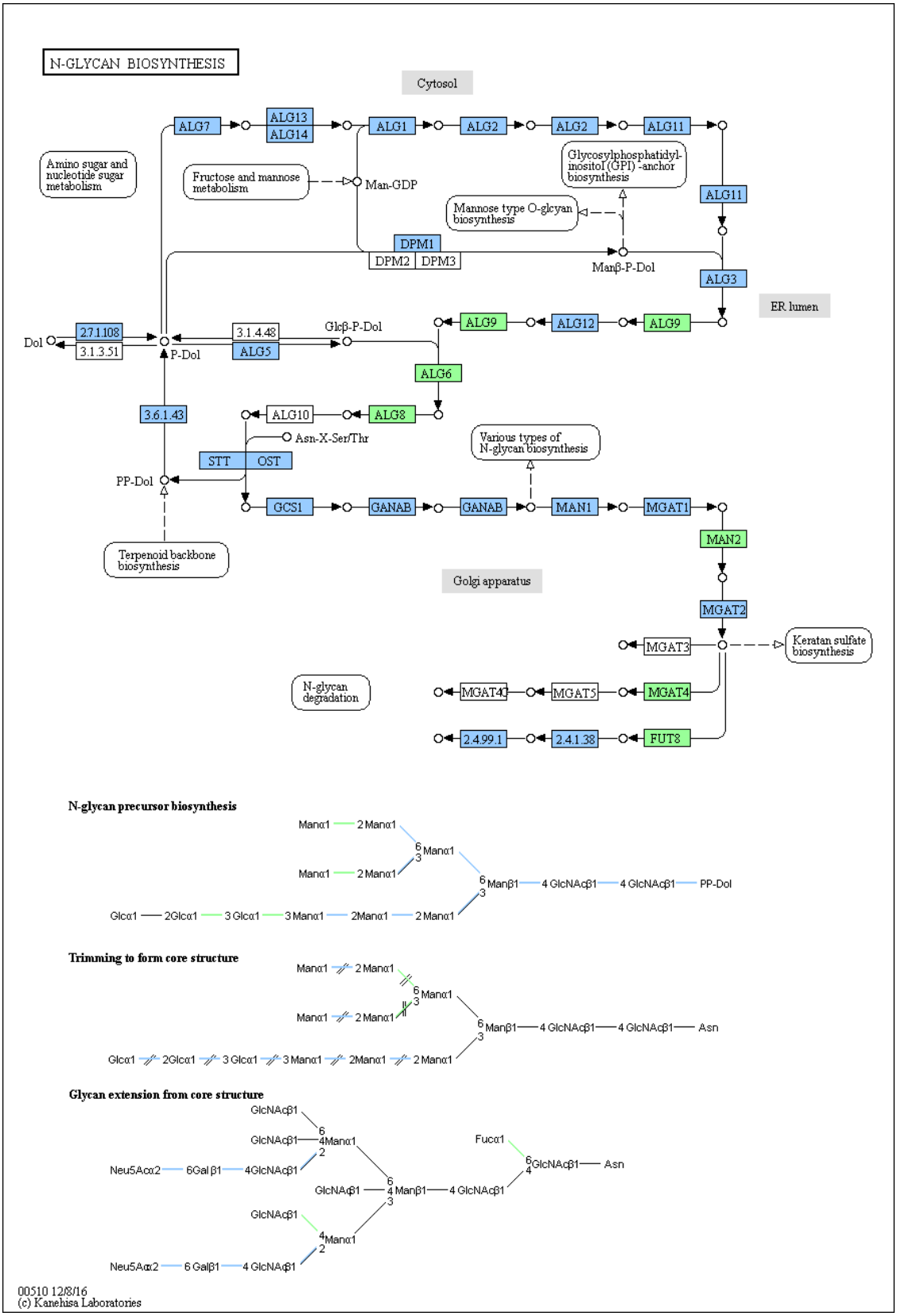
	Sf21	**Tni**
Main features		
Number of tRNAs	1,233 (311 pseudos)	1,965 (1,166 pseudos)
Number of ncRNAs	396	249
Number of repeats (excluding low complexity regions and satellites)	431,477	390,271
Number of protein-coding genes	21,506	14,159
Exon statistics		
Exon count	110,027	89,378
Average number of exons/gene	~5.12	~6.31
Exon space count (bp)	30,421,075	20,631,338
Average exon size (bp)	276	231
Median exon size (bp)	160	156
Minimum exon size (bp)	14,440	14,890
Maximum exon size (bp)	3	3
Intron statistics		
Intron count	88,521	75,220
Number of introns/gene	~4.12	~5.31
Intron space count (bp)	94,576,984	77,902,387
Average intron size (bp)	1086	1036

Median intron size (bp)	649	597
Minimum intron size (bp)	86,400	79,230
Maximum intron size (bp)	21	22
Intergenic space statistics		
Intergenic space count	13,035	8,735
Intergenic space size (bp)	353,235,779	248,980,732
Average intergenic space distance (bp)	31,190	33,600
Median intergenic space distance (bp)	12,840	15,390
Minimum intergenic space distance (bp)	1	1
Maximum intergenic space distance (bp)	977,500	584,000

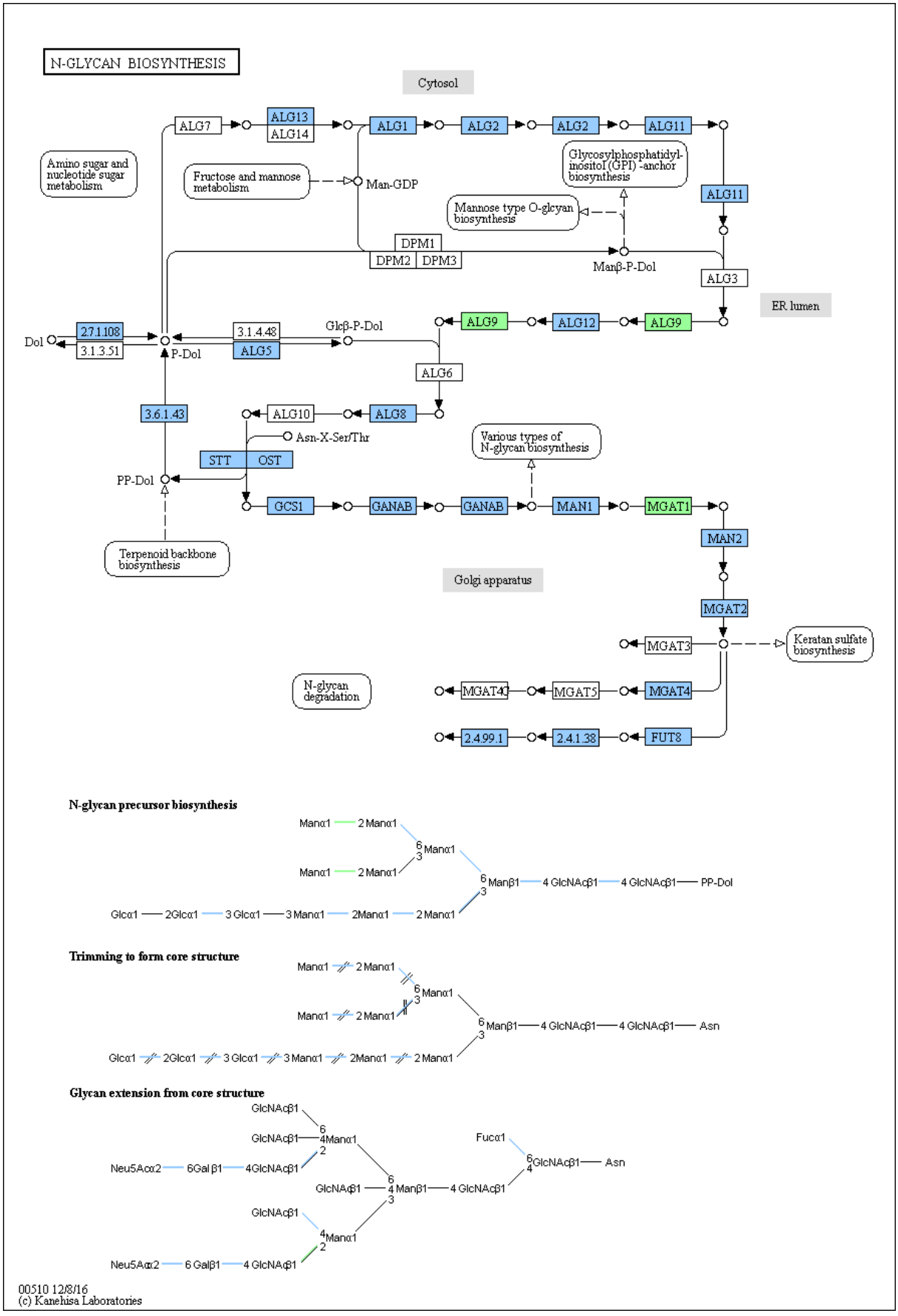
Table S3. Genomics feature count. This table represents the genomics feature characteristics and statistics for the Sf21 and Tni genomes.

Supplementary figures

Sf21



Tni


N-GLYCAN BIOSYNTHESIS
Cytosol
ALG7
ALG13
ALG14
ALG1
ALG2
ALG2
ALG11
Amino sugar and nucleotide sugar metabolism
Fructose and mannose metabolism
Man-GDP
Glycosylphosphatidyl-inositol (GPI) -anchor biosynthesis
ALG11
Mannose type O-glcyan biosynthesis
DPM1
DPM2
DPM3
Manβ-P-Dol
ALG3
ER lumen
Dol
2.7.1.108
3.1.3.51
P-Dol
3.1.4.48
ALG5
Glcβ-P-Dol
ALG9
ALG12
ALG9
ALG6
3.6.1.43
ALG10
ALG8
Asn-X-Ser/Thr
Various types of N-glycan biosynthesis
STT
OST
PP-Dol
GCS1
GANAB
GANAB
MAN1
MGAT1
MAN2
Terpenoid backbone biosynthesis
Golgi apparatus
MGAT2
MGAT3
Keratan sulfate biosynthesis
N-glycan degradation
MGAT4
MGAT5
MGAT4
2.4.99.1
2.4.1.38
FUT8
N-glycan precursor biosynthesis
Manα1 2 Manα1
6 3 Manα1
Manα1 2 Manα1
6 3 Manβ1 4 GlcNAcβ1 4 GlcNAcβ1 PP-Dol
Glcα1 2Glcα1 3 Glcα1 3 Manα1 2Manα1 2 Manα1
Trimming to form core structure
Manα1 2 Manα1
6 3 Manα1
Manα1 2 Manα1
6 3 Manβ1 4 GlcNAcβ1 4 GlcNAcβ1 Asn
Glcα1 2Glcα1 3 Glcα1 3 Manα1 2Manα1 2 Manα1
Glycan extension from core structure
GlcNAcβ1
6 4Manα1
GlcNAcβ1
2
Neu5Acα2 6Galβ1 4GlcNAcβ1
6
GlcNAcβ1 4 Manβ1 4 GlcNAcβ1
3
Fucα1
6 4 GlcNAcβ1 Asn
GlcNAcβ1
4 Manα1
2
Neu5Acα2 6 Galβ1 4 GlcNAcβ1
00510 12/8/16
(c) Kanehisa Laboratories

B. mori

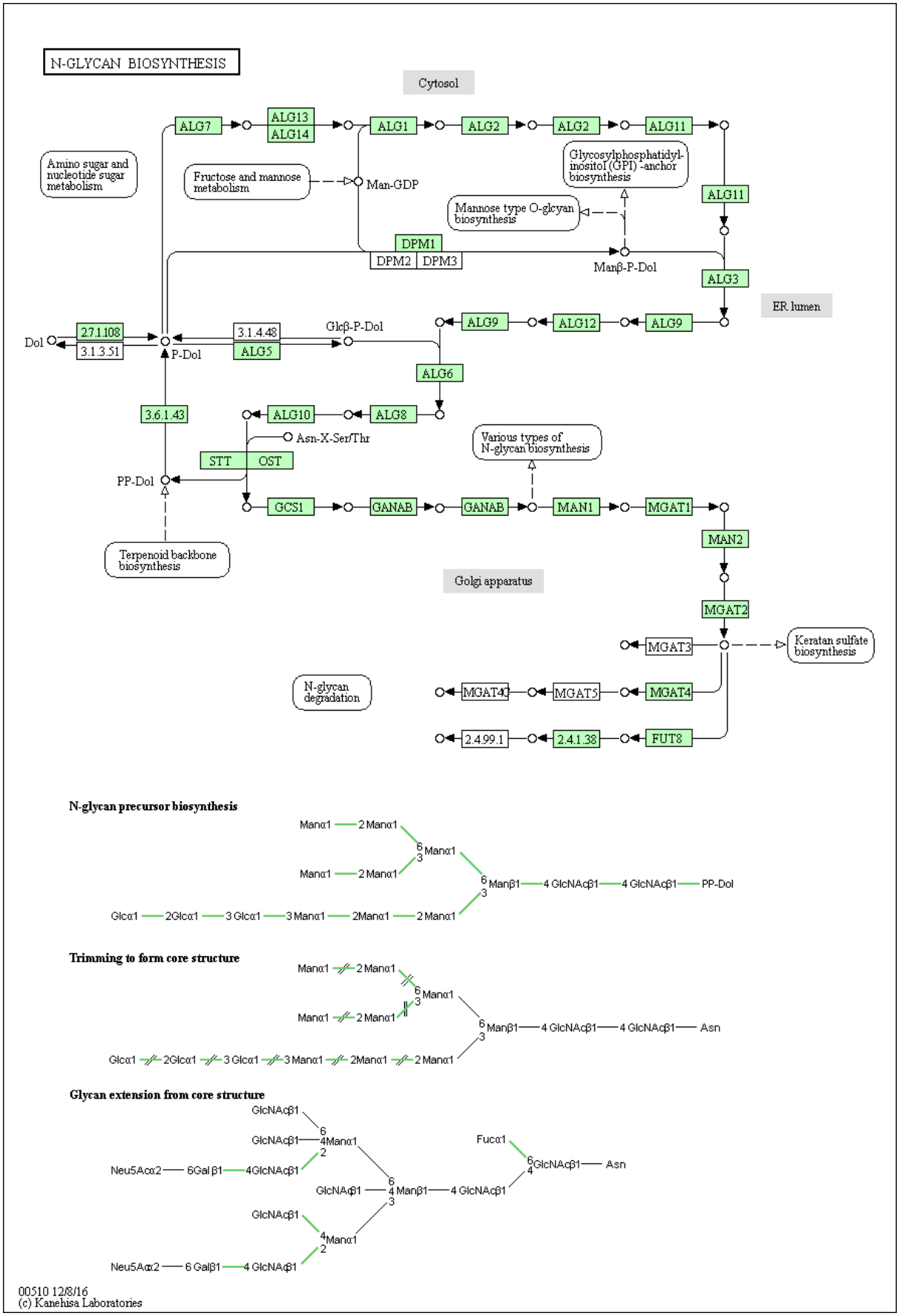

N-GLYCAN BIOSYNTHESIS
Cytosol
ALG7
ALG13
ALG14
ALG1
ALG2
ALG2
ALG11
Amino sugar and nucleotide sugar metabolism
Fructose and mannose metabolism
Man-GDP
Glycosylphosphatidyl-inositol (GPI) -anchor biosynthesis
Mannose type O-glcyan biosynthesis
ALG11
DPM1
DPM2
DPM3
Manβ-P-Dol
ALG3
ER lumen
Dol
2.7.1.108
3.1.3.51
P-Dol
3.1.4.48
ALG5
Glcβ-P-Dol
ALG9
ALG12
ALG9
ALG6
3.6.1.43
ALG10
ALG8
Asn-X-Ser/Thr
STT
OST
Various types of N-glycan biosynthesis
PP-Dol
GCS1
GANAB
GANAB
MAN1
MGAT1
MAN2
Terpenoid backbone biosynthesis
Golgi apparatus
MGAT2
MGAT3
Keratan sulfate biosynthesis
N-glycan degradation
MGAT4
MGAT5
MGAT4
2.4.99.1
2.4.1.38
FUT8
N-glycan precursor biosynthesis
Manα1 2 Manα1
Manα1 2 Manα1
Manα1
Manβ1 4 GlcNAcβ1 4 GlcNAcβ1 PP-Dol
Glcα1 2Glcα1 3 Glcα1 3 Manα1 2Manα1 2 Manα1
Trimming to form core structure
Manβ1 4 GlcNAcβ1 4 GlcNAcβ1 Asn
Glycan extension from core structure
GlcNAcβ1
GlcNAcβ1 4Manα1
Neu5Acα2 6Galβ1 4GlcNAcβ1
GlcNAcβ1 4 Manβ1 4 GlcNAcβ1
Fucα1
GlcNAcβ1 Asn
Neu5Acα2 6 Galβ1 4 GlcNAcβ1
00510 12/8/16
(c) Kanehisa Laboratories

Figure S1. N-glycan pathway. N-glycan pathway representations for SF21 and Tni, as well as Bombyx Mori. Predicted genes, based on the genomic analysis, are marked with green and predicted and expressed, based on the genomic and transcriptomic analysis, are represented in blue.