

## Complete Genome Structure of the Nitrogen-fixing Symbiotic Bacterium *Mesorhizobium loti* (Supplement)

Takakazu KANEKO, Yasukazu NAKAMURA, Shusei SATO, Erika ASAMIZU, Tomohiko KATO, Shigemi SASAMOTO, Akiko WATANABE, Kumi IDESAWA, Atsuko ISHIKAWA, Kumiko KAWASHIMA, Takaharu KIMURA, Yoshie KISHIDA, Chiaki KIYOKAWA, Mitsuyo KOHARA, Midori MATSUMOTO, Ai MATSUNO, Yoko MOCHIZUKI, Shinobu NAKAYAMA, Naomi NAKAZAKI, Sayaka SHIMPO, Masako SUGIMOTO, Chie TAKEUCHI, Manabu YAMADA, and Satoshi TABATA\*

*Kazusa DNA Research Institute, 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan*

(Received 22 November 2000)

---

Communicated by Mituru Takanami

\* To whom correspondence should be addressed. Tel. +81-438-52-3933, Fax. +81-438-52-3934

Table 1. Codon-anticodon recognition pattern for the *M. loti* genome.

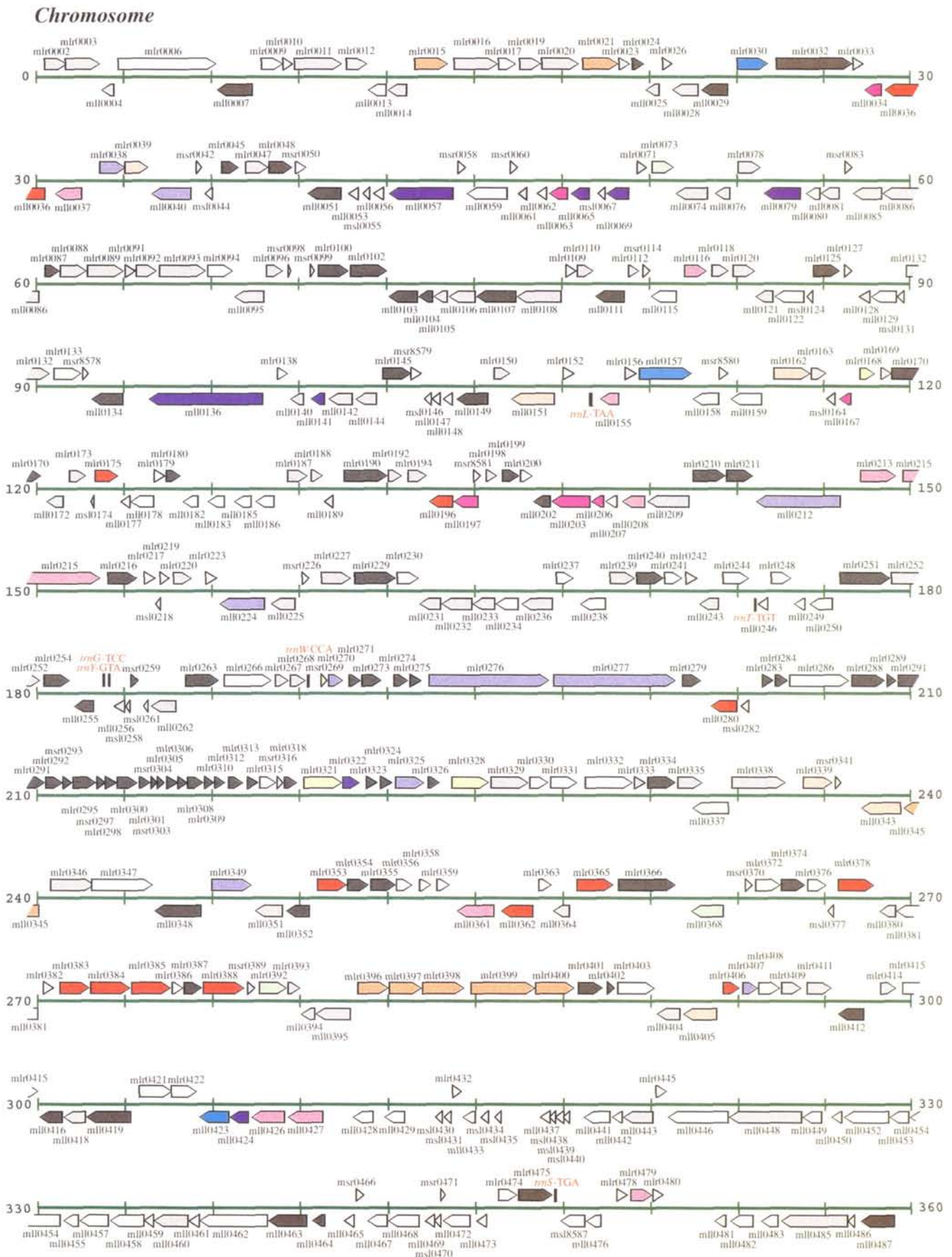
UUU	F	<i>trnF-GAA</i>	UCU	S	<i>trnS-GGA</i>	UAU	Y	<i>trnY-GUA</i>	UGU	C	<i>trnC-GCA</i>
UUC	F		UCC	S		UAC	Y		UGC	C	
UUA	L	<i>trnL-UAA</i>	UCA	S	<i>trnS-UGA</i>	UAA	-		UGA	-	
UUG	L	<i>trnL-CAA</i>	UCG	S	<i>trnS-CGA</i>	UAG	-		UGG	W	<i>trnW-CCA</i>
CUU	L	<i>trnL-GAG</i>	CCU	P	<i>trnP-GGG</i>	CAU	H	<i>trnH-GUG</i>	CGU	R	
CUC	L		CCC	P		CAC	H		CGC	R	<i>trnR-ACG</i>
CUA	L	<i>trnL-UAG</i>	CCA	P	<i>trnP-UGG</i>	CAA	Q	<i>trnQ-UUG</i> <sup>(2)</sup>	CGA	R	
CUG	L	<i>trnL-CAG</i>	CCG	P	<i>trnP-CGG</i>	CAG	Q	<i>trnQ-CUG</i>	CGG	R	<i>trnR-CCG</i>
AUU	I	<i>trnI-GAU</i> <sup>(2)</sup>	ACU	T	<i>trnT-GGU</i>	AAU	N	<i>trnN-GUU</i>	AGU	S	<i>trnS-GCU</i>
AUC	I		ACC	T		AAC	N		AGC	S	
AUA	I	<i>trnI-UAU</i>	ACA	T	<i>trnT-UGU</i>	AAA	K	<i>trnK-UUU</i>	AGA	R	<i>trnR-UCU</i>
AUG	M	<i>trnM-CAU</i> <sup>(2)</sup> <i>trnM-CAU</i> <sup>(2)</sup>	ACG	T	<i>trnT-CGU</i>	AAG	K	<i>trnK-CUU</i>	AGG	R	<i>trnR-CCU</i>
GUU	V	<i>trnV-GAC</i>	GCU	A	<i>trnA-GGC</i>	GAU	D	<i>trnD-GUC</i>	GGU	G	<i>trnG-GCC</i>
GUC	V		GCC	A		GAC	D		GGC	G	
GUA	V	<i>trnV-UAC</i>	GCA	A	<i>trnA-UGC</i> <sup>(2)</sup>	GAA	E	<i>trnE-UUC</i>	GGA	G	<i>trnG-UCC</i>
GUG	V	<i>trnV-CAC</i>	GCG	A	<i>trnA-CGC</i>	GAG	E	<i>trnE-CUC</i>	GGG	G	<i>trnG-CCC</i>

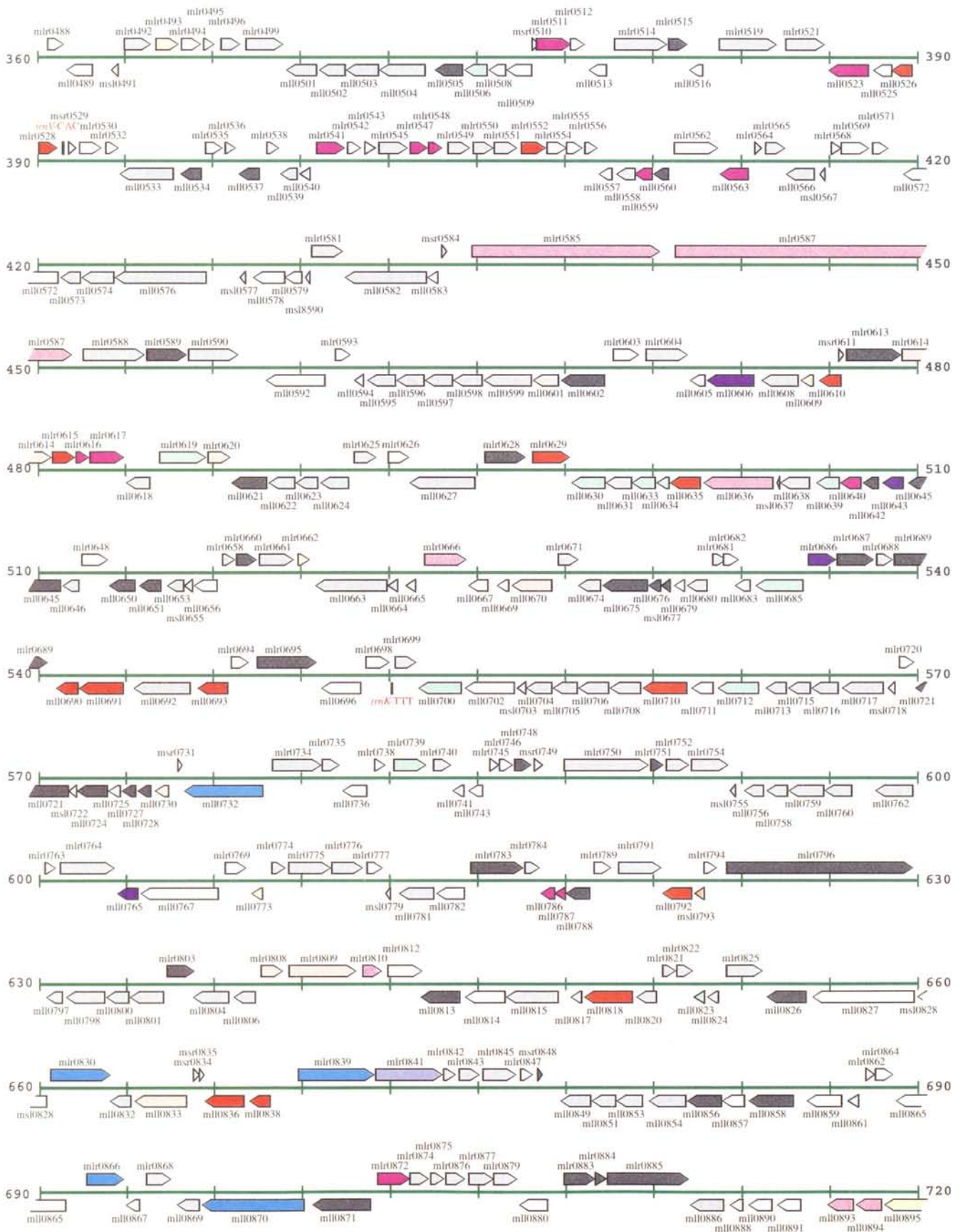
Corresponding amino acids and tRNA species are given by one-letter abbreviation and italic letters. Numerals in the parentheses indicate the number of genes on the chromosome.

Table 2. Codon usage frequency for the *M. loti* genome.

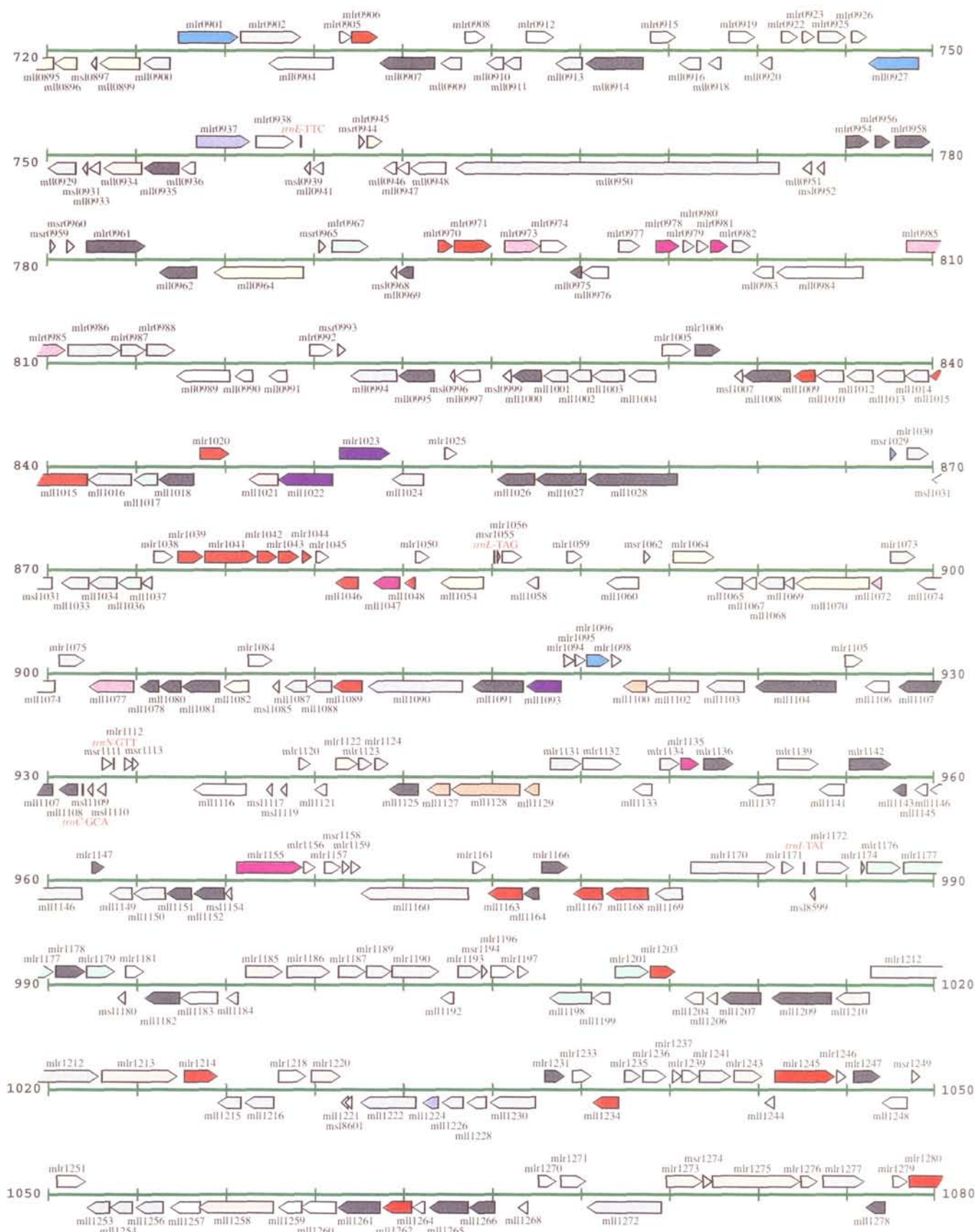
	Chromosome			pMLa	pMLb
	total	non-sym	sym		
UUU	7.3 ( 14818)	7.0 ( 13129)	10.4 ( 1689)	11.3 ( 1080)	10.9 ( 542)
UUC	31.2 ( 63663)	31.7 ( 59589)	25.1 ( 4074)	24.4 ( 2334)	24.5 ( 1216)
UUA	0.6 ( 1192)	0.5 ( 874)	2.0 ( 318)	1.8 ( 175)	1.2 ( 60)
UUG	9.8 ( 20054)	9.4 ( 17663)	14.8 ( 2391)	14.3 ( 1367)	14.9 ( 739)
CUU	10.8 ( 21950)	10.3 ( 19301)	16.3 ( 2649)	17.2 ( 1642)	16.6 ( 825)
CUC	26.8 ( 54610)	26.7 ( 50117)	27.7 ( 4493)	27.6 ( 2639)	26.9 ( 1336)
CUA	1.7 ( 3422)	1.4 ( 2667)	4.7 ( 755)	4.5 ( 429)	3.3 ( 165)
CUG	48.5 ( 98933)	49.6 ( 93143)	35.7 ( 5790)	34.4 ( 3292)	36.1 ( 1793)
AUU	7.3 ( 14842)	6.9 ( 12987)	11.4 ( 1855)	13.2 ( 1261)	10.8 ( 535)
AUC	43.8 ( 89396)	44.6 ( 83694)	35.2 ( 5702)	36.1 ( 3456)	34.5 ( 1715)
AUA	2.7 ( 5446)	2.5 ( 4691)	4.7 ( 755)	4.8 ( 463)	4.4 ( 217)
AUG	24.3 ( 49498)	24.4 ( 45899)	22.2 ( 3599)	22.6 ( 2158)	22.3 ( 1105)
GUU	7.2 ( 14748)	6.8 ( 12761)	12.3 ( 1987)	12.2 ( 1166)	12.5 ( 620)
GUC	37.7 ( 76891)	38.3 ( 71976)	30.3 ( 4915)	30.6 ( 2928)	32.6 ( 1617)
GUA	2.3 ( 4659)	2.0 ( 3828)	5.1 ( 831)	5.5 ( 528)	4.0 ( 199)
GUG	26.8 ( 54774)	27.2 ( 51144)	22.4 ( 3630)	22.4 ( 2139)	21.4 ( 1062)
UCU	2.1 ( 4188)	1.8 ( 3358)	5.1 ( 830)	4.4 ( 420)	4.8 ( 237)
UCC	12.0 ( 24493)	12.0 ( 22574)	11.8 ( 1919)	12.8 ( 1221)	13.3 ( 662)
UCA	3.1 ( 6313)	2.8 ( 5345)	6.0 ( 968)	6.1 ( 584)	5.8 ( 289)
UCG	22.3 ( 45410)	22.6 ( 42535)	17.7 ( 2875)	18.4 ( 1756)	19.0 ( 942)
CCU	4.2 ( 8515)	3.9 ( 7360)	7.1 ( 1155)	7.7 ( 733)	7.7 ( 380)
CCC	12.5 ( 25566)	12.5 ( 23524)	12.6 ( 2042)	12.7 ( 1216)	12.8 ( 634)
CCA	4.3 ( 8783)	4.0 ( 7425)	8.4 ( 1358)	7.8 ( 746)	8.1 ( 400)
CCG	29.4 ( 59895)	29.8 ( 55964)	24.3 ( 3931)	23.9 ( 2281)	22.6 ( 1121)
ACU	2.8 ( 5648)	2.5 ( 4772)	5.4 ( 876)	5.2 ( 493)	4.7 ( 233)
ACC	26.8 ( 54757)	27.4 ( 51522)	20.0 ( 3235)	19.8 ( 1889)	20.9 ( 1040)
ACA	4.4 ( 8981)	4.2 ( 7838)	7.1 ( 1143)	7.4 ( 712)	7.5 ( 372)
ACG	18.9 ( 38656)	19.0 ( 35751)	17.9 ( 2905)	18.3 ( 1748)	18.7 ( 927)
CCU	8.9 ( 18160)	8.3 ( 15662)	15.4 ( 2498)	15.6 ( 1489)	14.2 ( 706)
CCC	60.4 (123144)	61.7 (115908)	44.6 ( 7236)	44.1 ( 4220)	48.0 ( 2385)
CCA	11.0 ( 22405)	10.5 ( 19635)	17.1 ( 2770)	17.5 ( 1670)	16.1 ( 801)
CCG	43.2 ( 88033)	43.5 ( 81718)	39.0 ( 6315)	37.6 ( 3596)	39.1 ( 1943)
UAU	11.6 ( 23665)	11.6 ( 21857)	11.2 ( 1808)	11.5 ( 1102)	11.3 ( 561)
UAC	10.5 ( 21469)	10.5 ( 19702)	10.9 ( 1767)	10.8 ( 1031)	9.8 ( 489)
UAA	0.5 ( 1000)	0.5 ( 914)	0.5 ( 86)	0.6 ( 58)	0.7 ( 36)
UAG	0.8 ( 1616)	0.8 ( 1498)	0.7 ( 118)	0.7 ( 70)	1.1 ( 55)
CAU	10.7 ( 21926)	10.6 ( 19931)	12.3 ( 1995)	11.2 ( 1066)	11.5 ( 571)
CAC	9.8 ( 19934)	9.5 ( 17922)	12.4 ( 2012)	10.7 ( 1020)	10.1 ( 502)
CAA	6.0 ( 12316)	5.6 ( 10610)	10.5 ( 1706)	10.1 ( 965)	9.6 ( 477)
CAG	24.9 ( 50700)	25.0 ( 47007)	22.8 ( 3693)	24.0 ( 2293)	24.0 ( 1191)
AAU	9.8 ( 20044)	9.8 ( 18349)	10.5 ( 1695)	11.0 ( 1047)	9.7 ( 481)
AAC	17.3 ( 35235)	17.4 ( 32627)	16.1 ( 2608)	16.7 ( 1595)	16.6 ( 824)
AAA	8.0 ( 16260)	7.8 ( 14573)	10.4 ( 1687)	10.8 ( 1034)	11.5 ( 569)
AAG	28.9 ( 59044)	29.4 ( 55244)	23.4 ( 3800)	24.0 ( 2290)	25.1 ( 1247)
GAU	19.5 ( 39689)	19.2 ( 36003)	22.7 ( 3686)	23.6 ( 2259)	23.5 ( 1167)
GAC	37.2 ( 75890)	37.7 ( 70803)	31.4 ( 5087)	31.5 ( 3009)	33.8 ( 1677)
GAA	22.9 ( 46629)	22.7 ( 42710)	24.2 ( 3919)	26.1 ( 2492)	24.4 ( 1212)
GAG	30.6 ( 62333)	30.4 ( 57088)	32.4 ( 5245)	30.5 ( 2918)	30.5 ( 1513)
UGU	1.2 ( 2540)	1.1 ( 2066)	2.9 ( 474)	2.5 ( 241)	1.8 ( 91)
UGC	7.3 ( 14835)	7.1 ( 13242)	9.8 ( 1593)	9.0 ( 864)	6.6 ( 326)
UGA	2.0 ( 4136)	2.0 ( 3760)	2.3 ( 376)	2.0 ( 192)	2.4 ( 118)
UGG	13.6 ( 27650)	13.6 ( 25454)	13.5 ( 2196)	13.5 ( 1292)	15.4 ( 766)
CGU	6.7 ( 13657)	6.4 ( 11966)	10.4 ( 1691)	10.5 ( 1000)	9.3 ( 464)
CGC	36.9 ( 75373)	37.3 ( 70120)	32.4 ( 5253)	30.5 ( 2913)	34.2 ( 1699)
CGA	3.6 ( 7419)	3.1 ( 5868)	9.6 ( 1551)	8.9 ( 847)	8.6 ( 425)
CGG	14.2 ( 28953)	13.9 ( 26038)	18.0 ( 2915)	17.8 ( 1697)	17.4 ( 862)
AGU	2.3 ( 4754)	2.2 ( 4076)	4.2 ( 678)	4.4 ( 425)	5.2 ( 256)
AGC	14.6 ( 29809)	14.5 ( 27211)	16.0 ( 2598)	15.4 ( 1477)	15.8 ( 786)
AGA	1.9 ( 3889)	1.7 ( 3251)	3.9 ( 638)	3.4 ( 328)	3.9 ( 192)
AGG	5.5 ( 11244)	5.4 ( 10092)	7.1 ( 1152)	7.4 ( 703)	7.8 ( 386)
GGU	9.7 ( 19726)	9.4 ( 17657)	12.8 ( 2069)	13.4 ( 1285)	11.8 ( 588)
GGC	61.2 (124830)	62.9 (118130)	41.3 ( 6700)	40.8 ( 3902)	43.7 ( 2171)
GGA	6.3 ( 12847)	5.9 ( 11072)	10.9 ( 1775)	12.1 ( 1156)	10.7 ( 529)
GGG	9.3 ( 18873)	9.0 ( 16832)	12.6 ( 2041)	12.6 ( 1200)	12.3 ( 612)

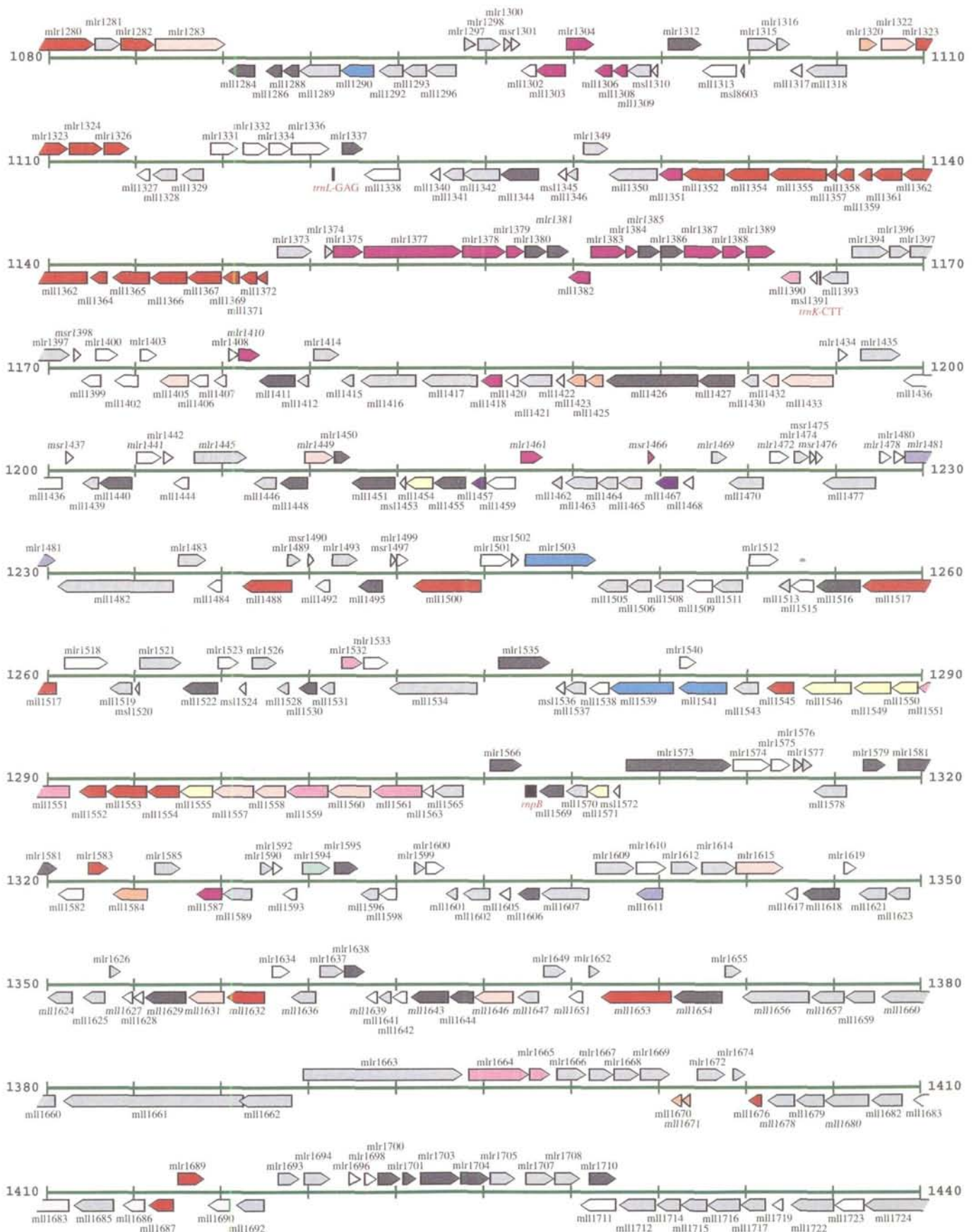
The frequency of the usage of each codon in the chromosome and the two plasmids was shown in permillage of overall counts. Genes in the chromosome were further divided into those inside (sym) and outside (non-sym) the symbiotic island. The numerals in parentheses indicate the actual number of codons.



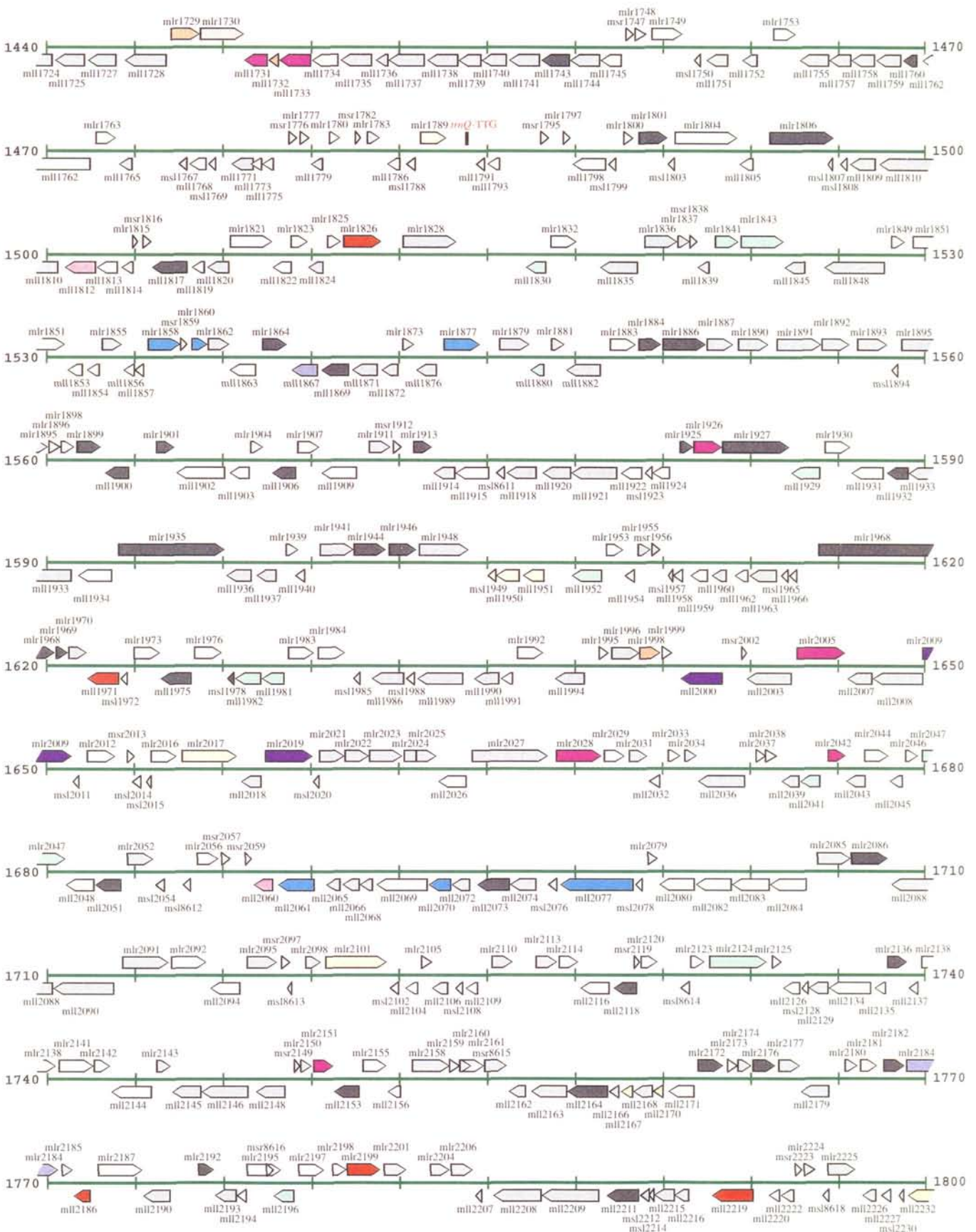






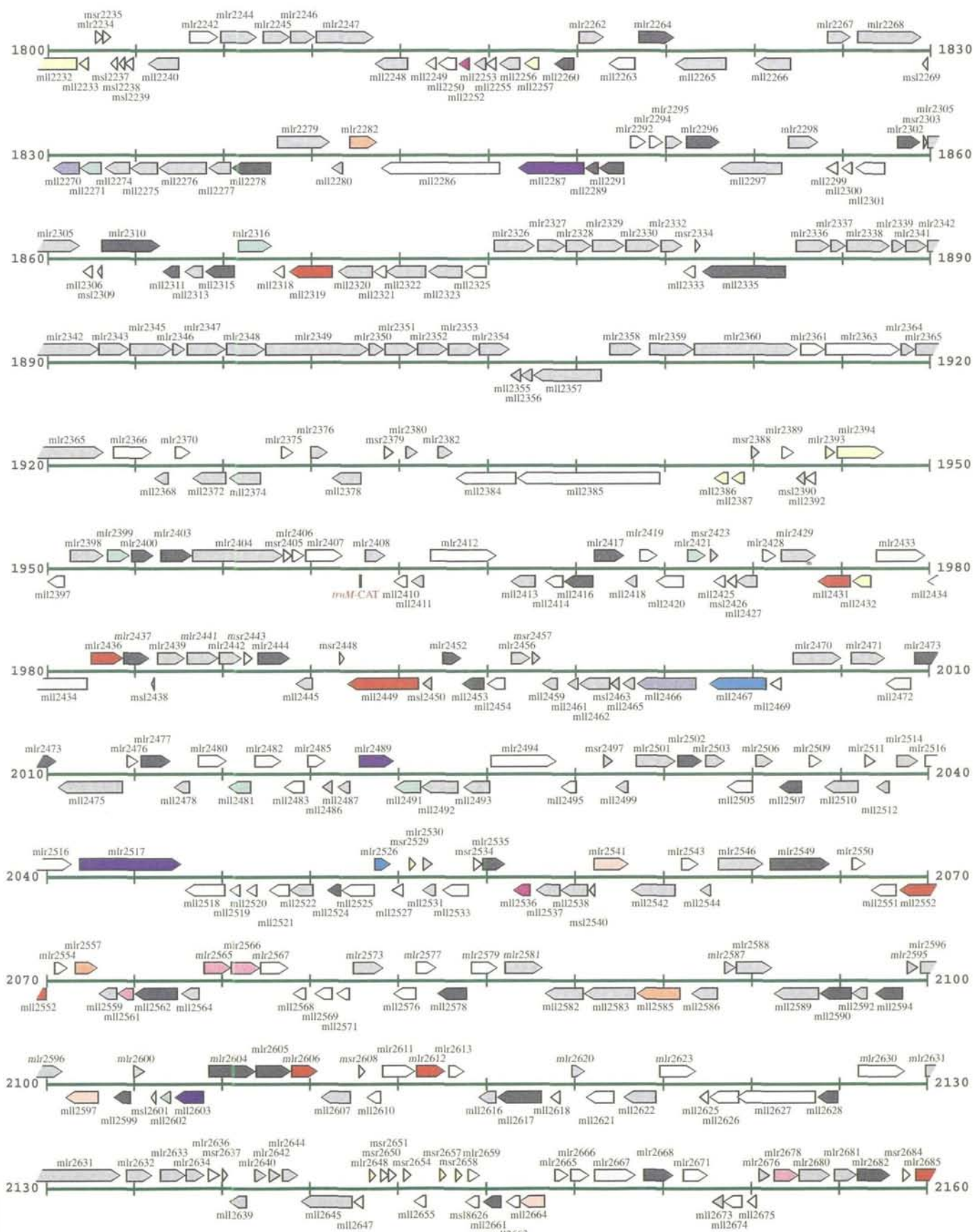


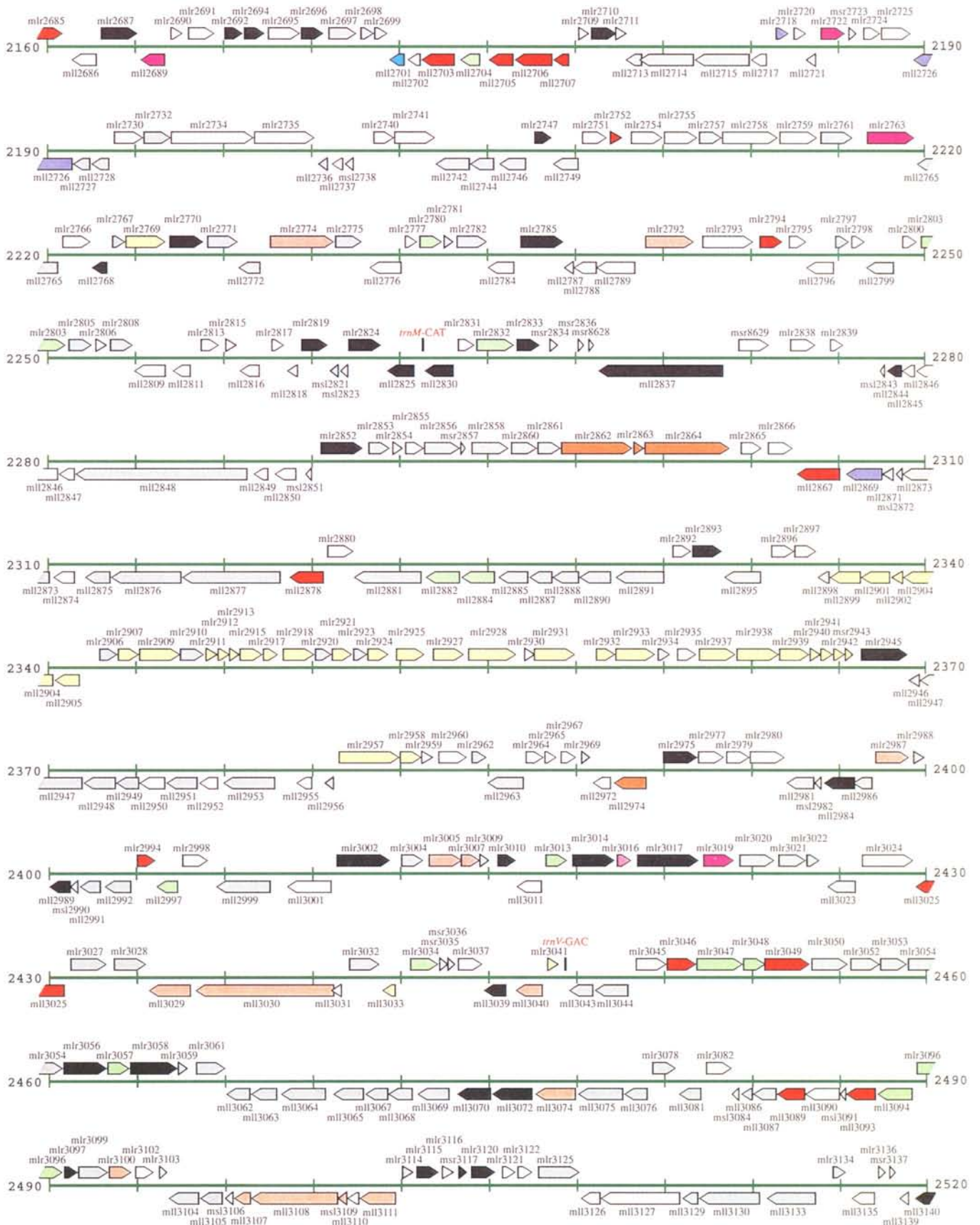




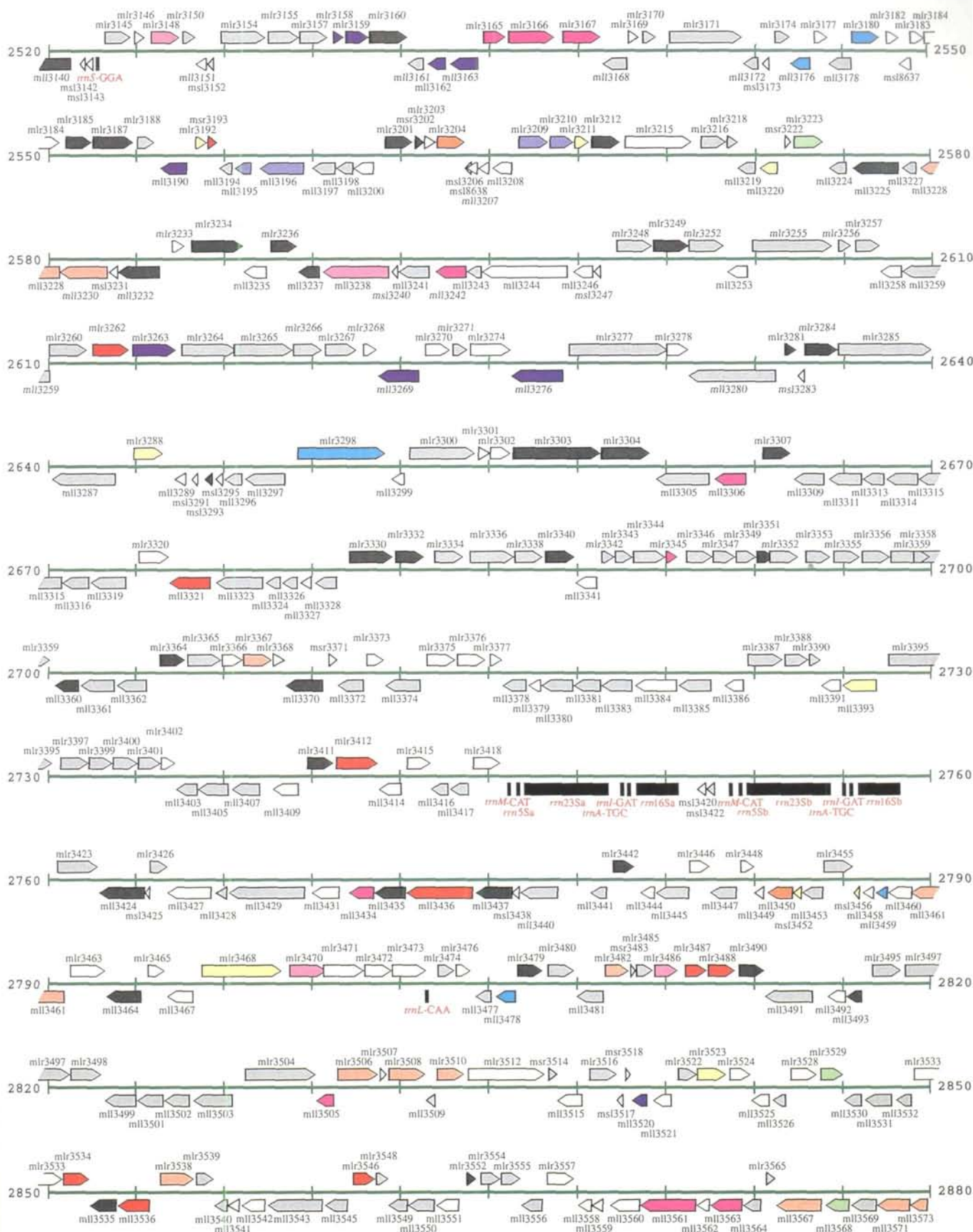
Downloaded from https://academic.oup.com/dna/research/article/7/6/381/471132 by guest on 20 August 2022







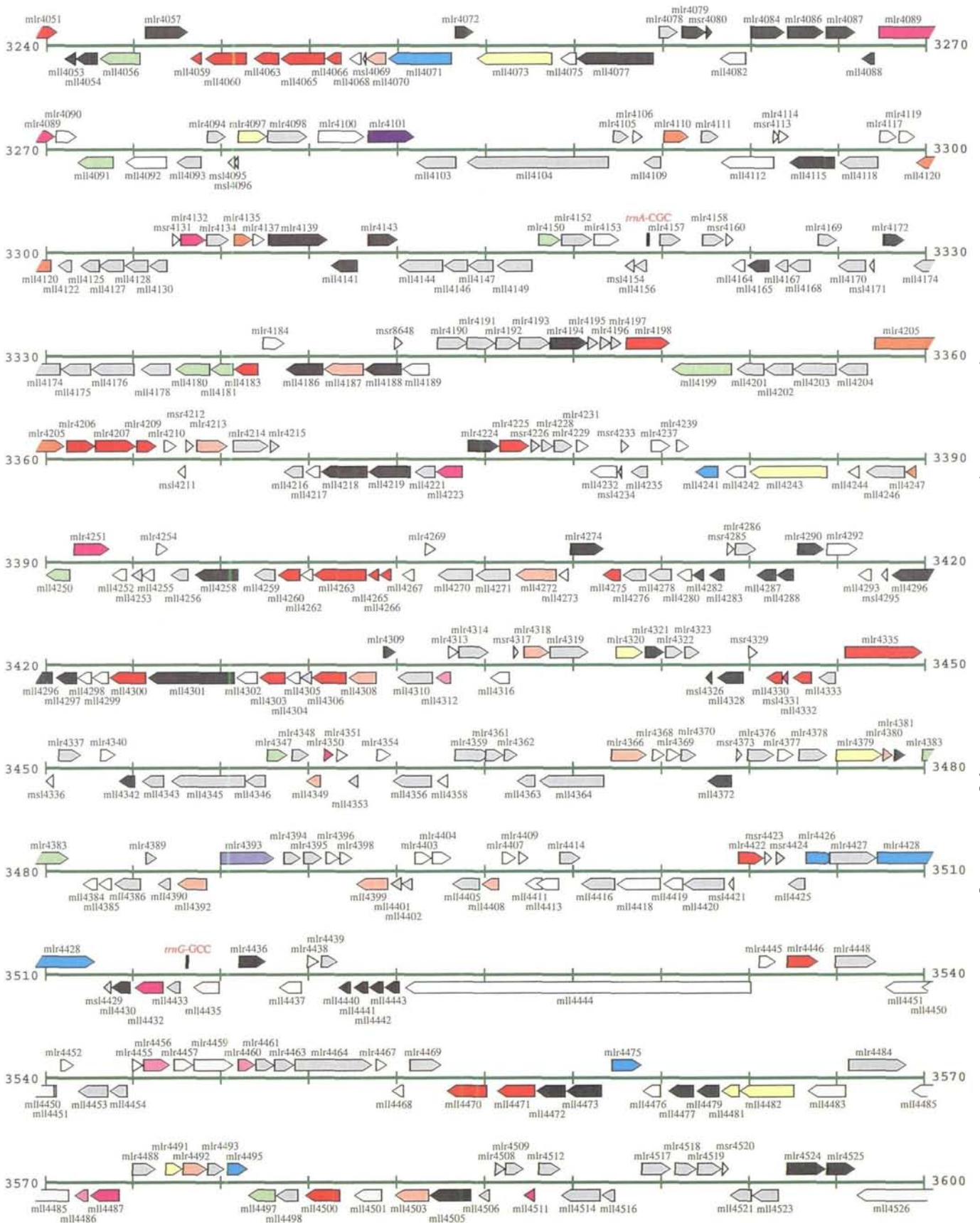




Downloaded from https://academic.oup.com/dna/research/article/7/6/391/471132 by guest on 20 August 2022

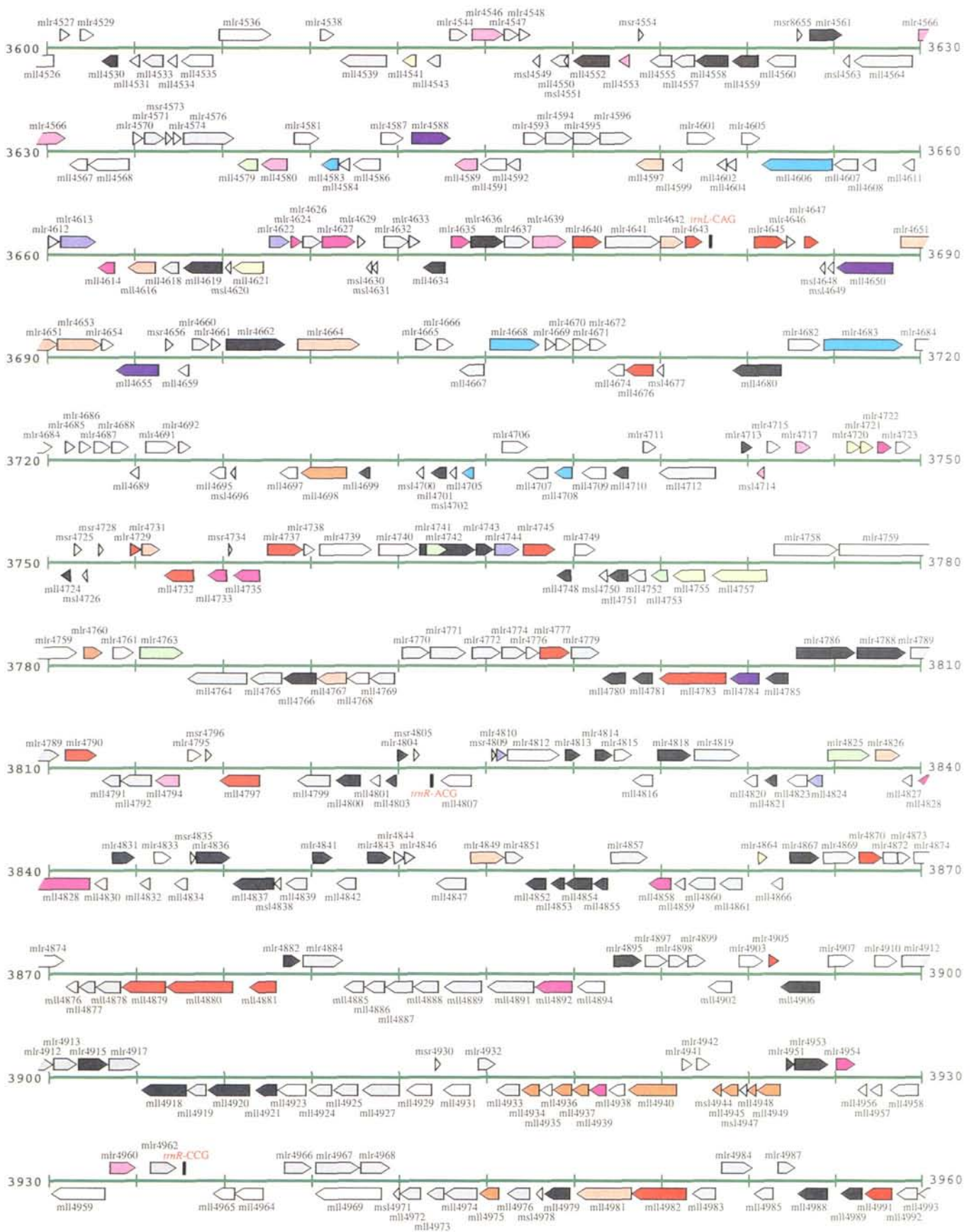




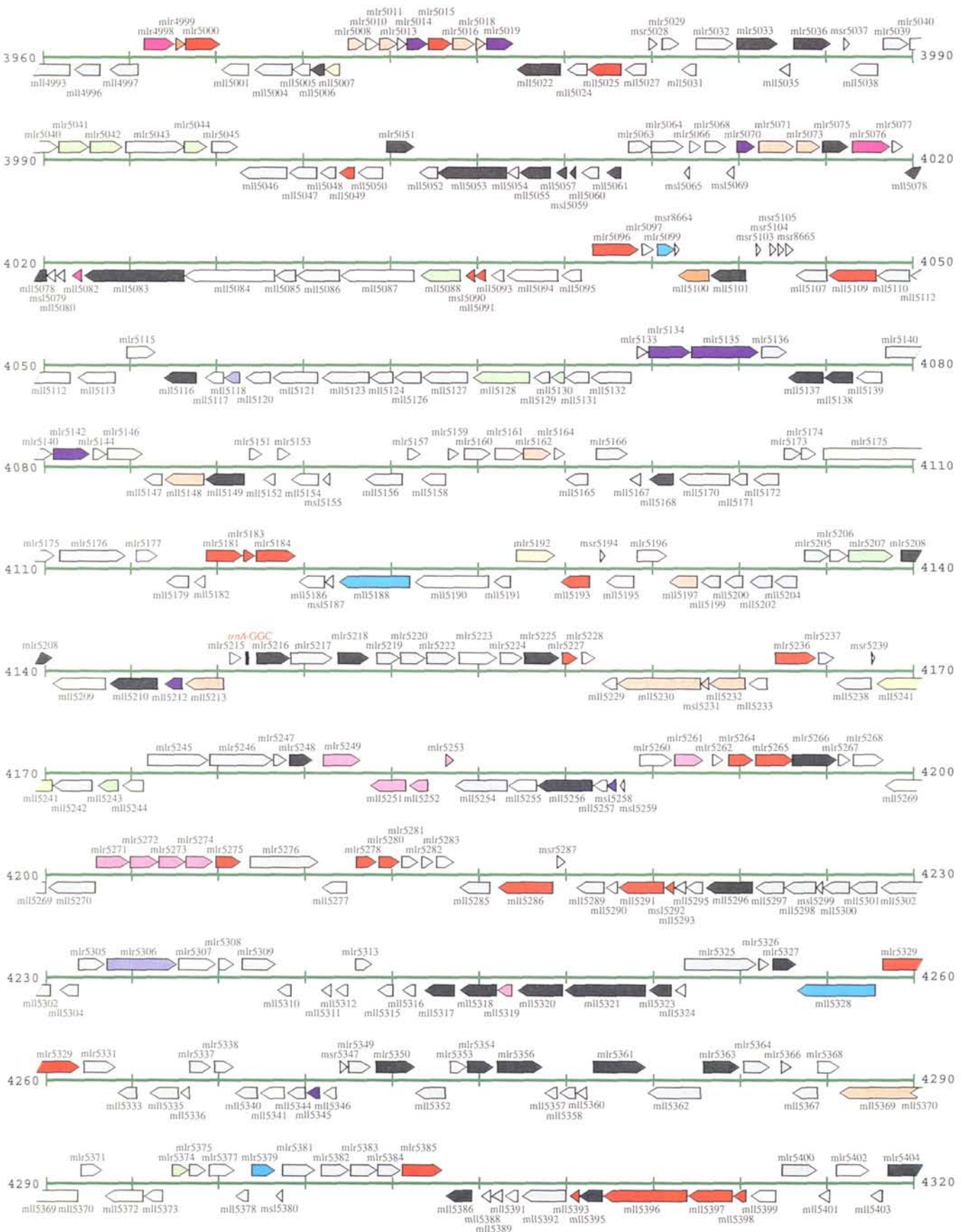


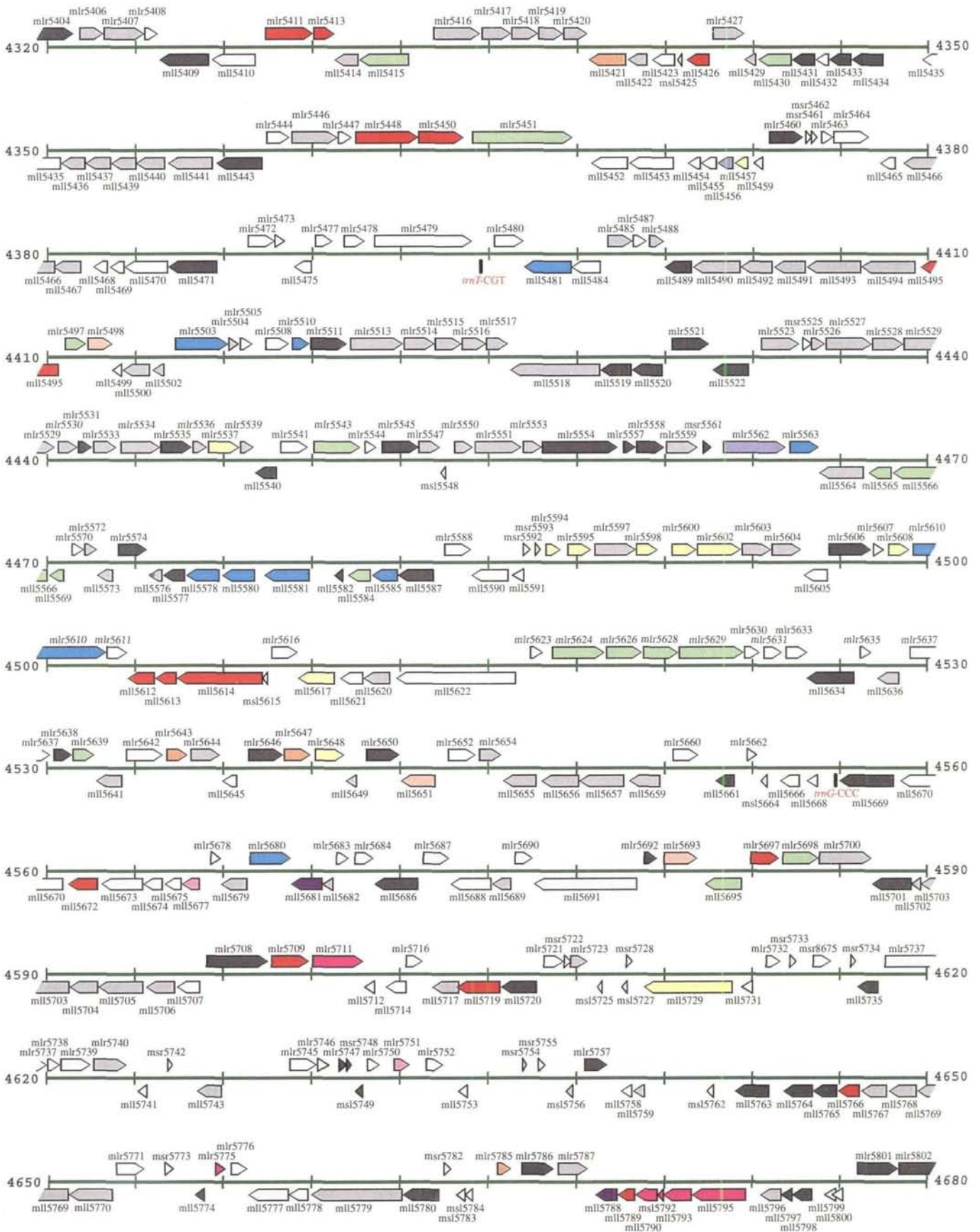
Downloaded from https://academic.oup.com/dnaresearch/article/7/6/381/471132 by guest on 20 August 2022







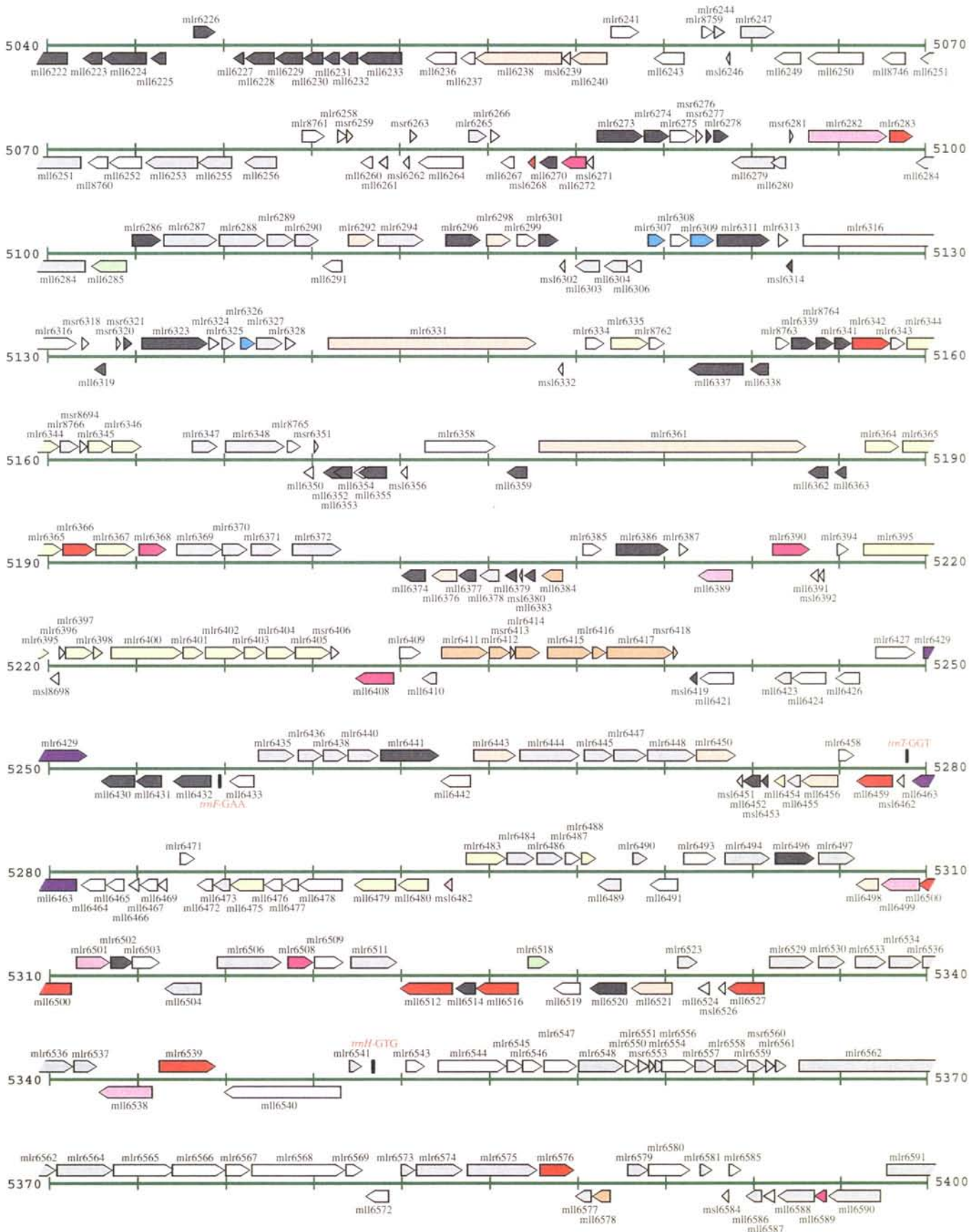




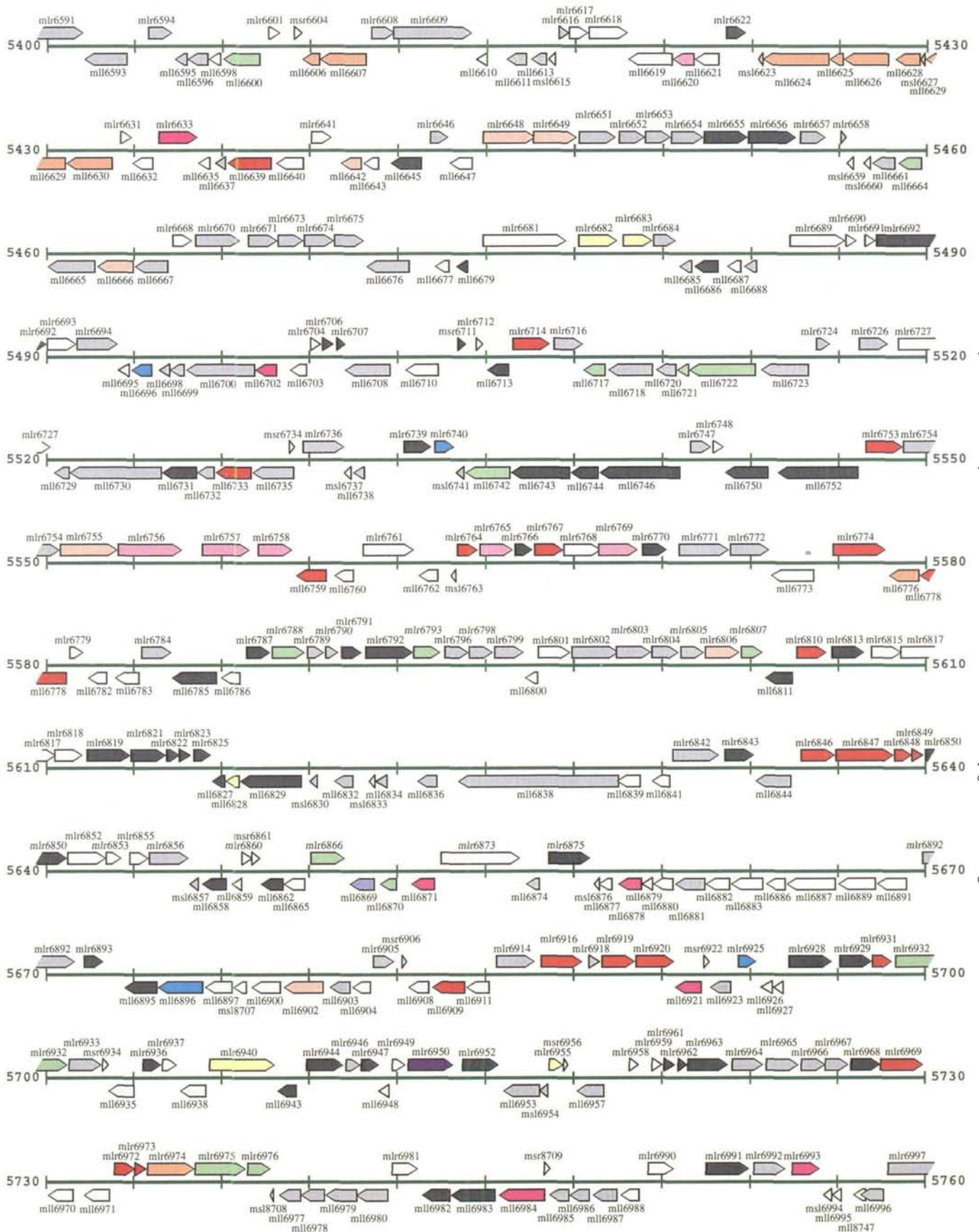




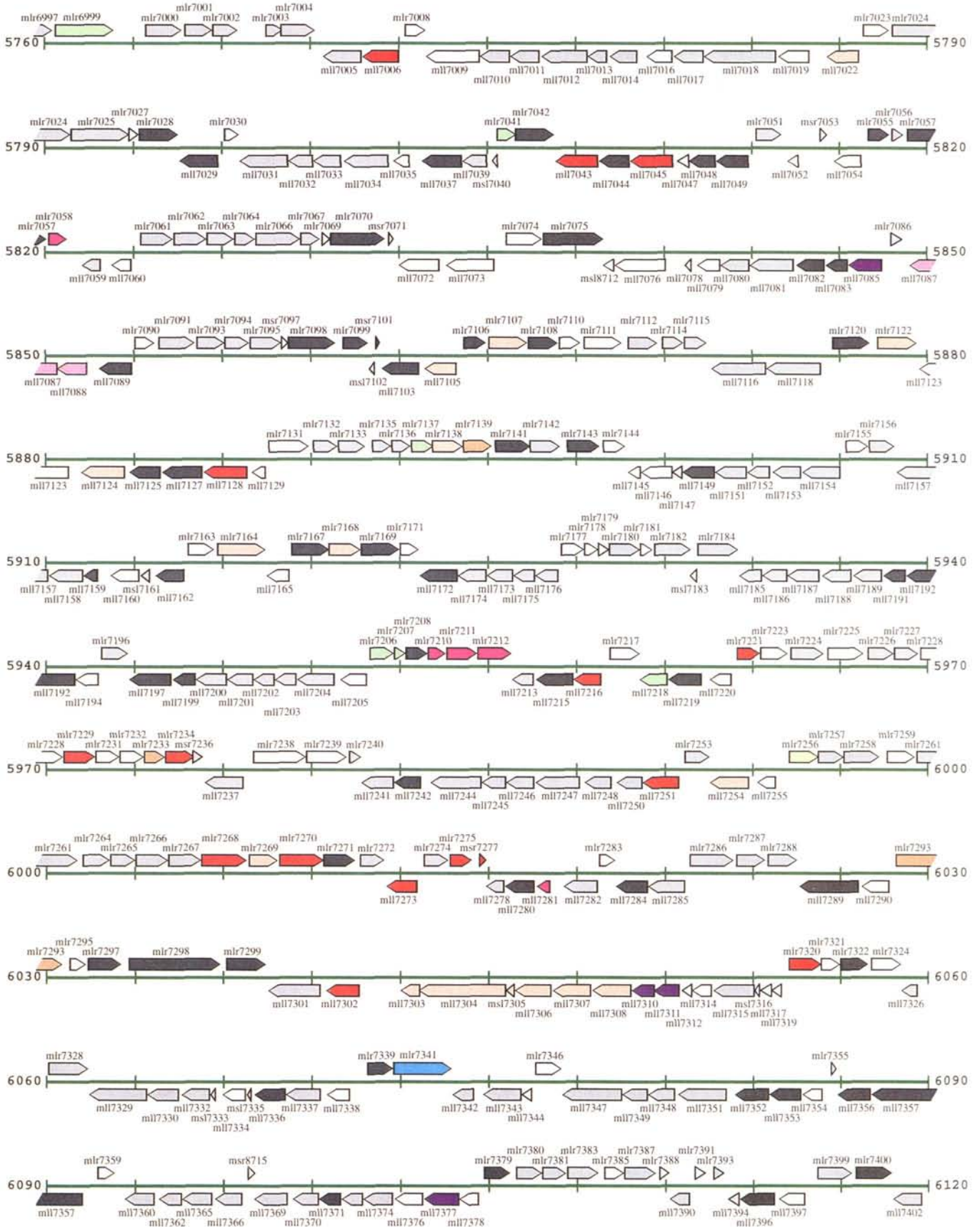




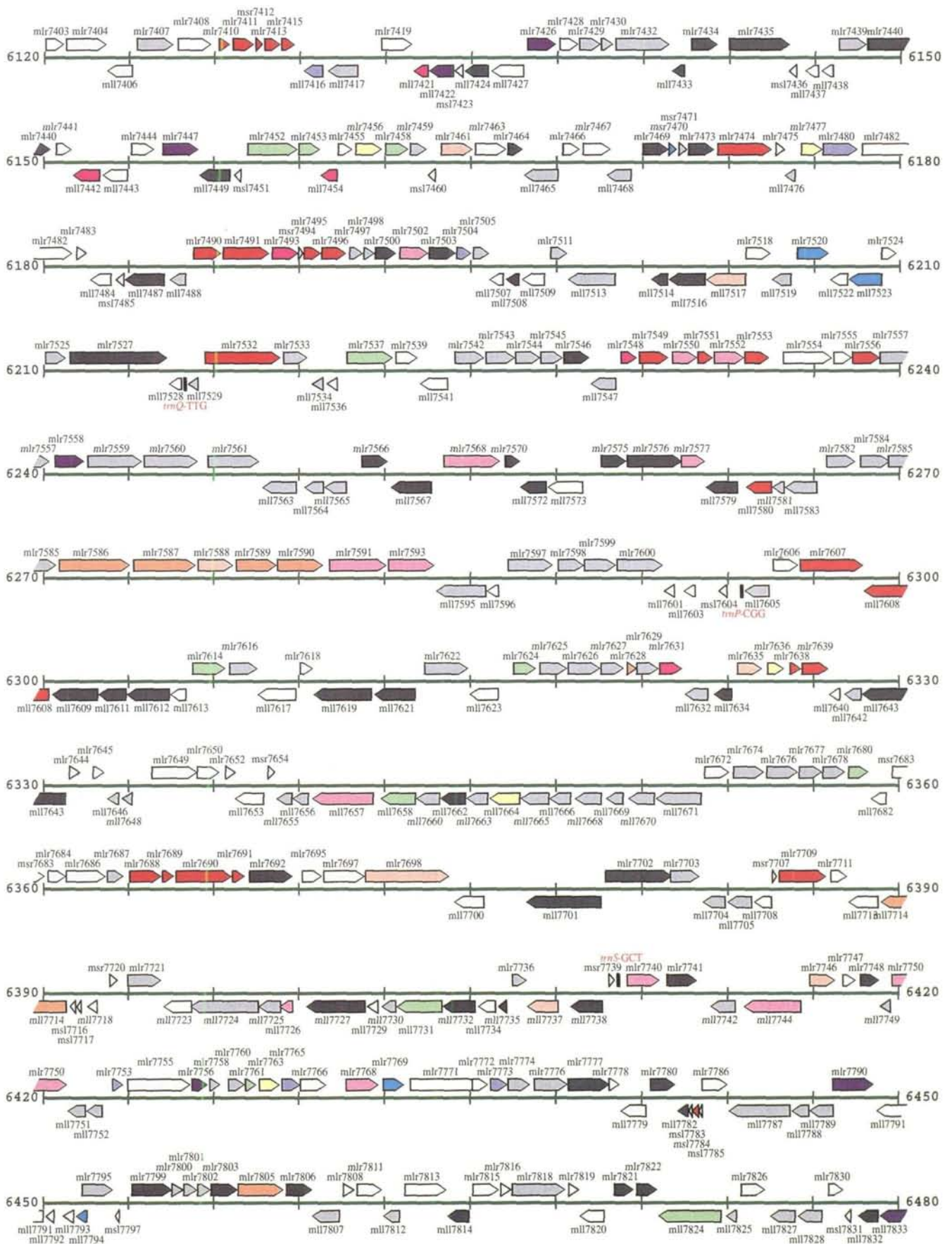
Downloaded from <https://academic.oup.com/dnaresearch/article/7/6/381/471132> by guest on 20 August 2022

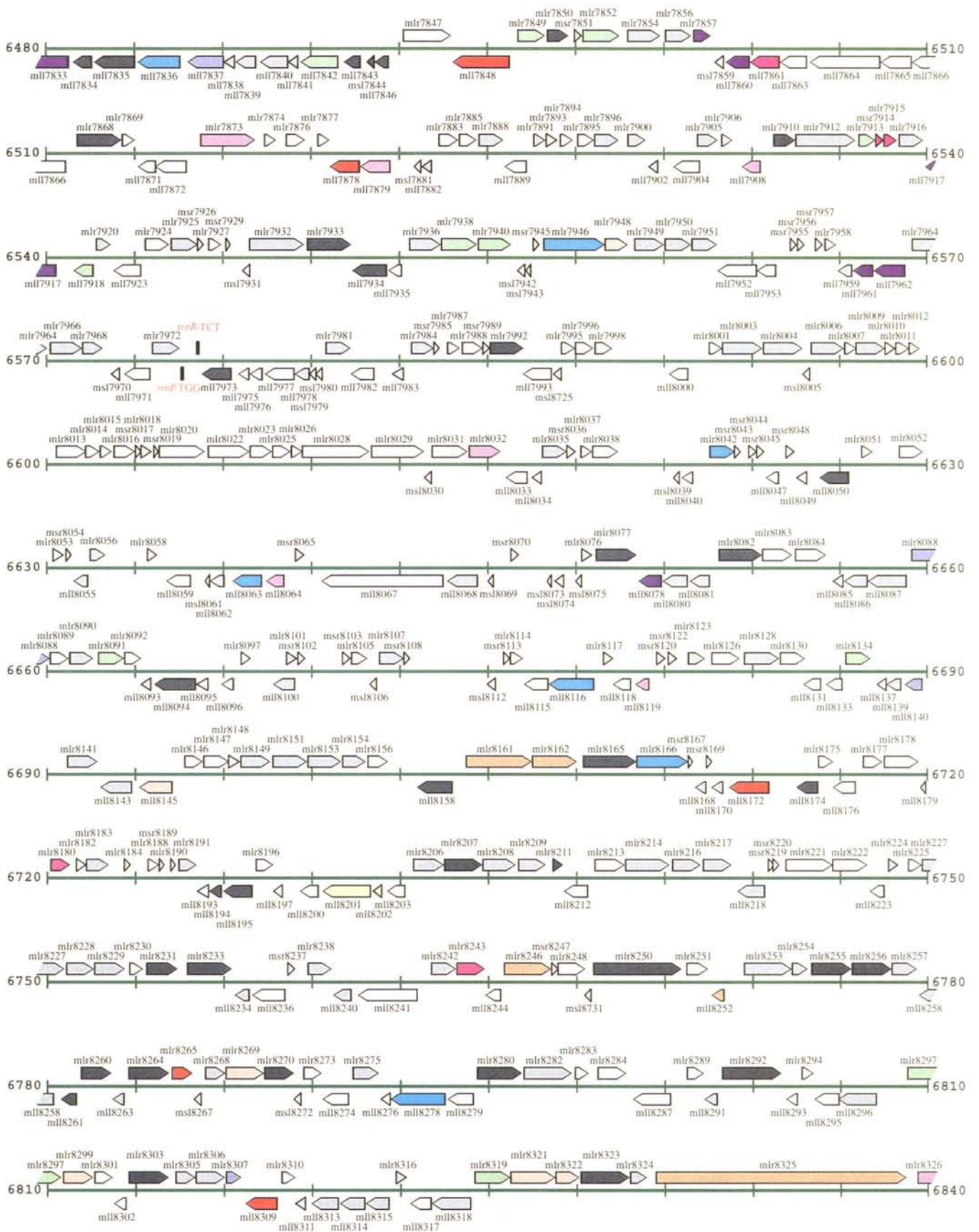




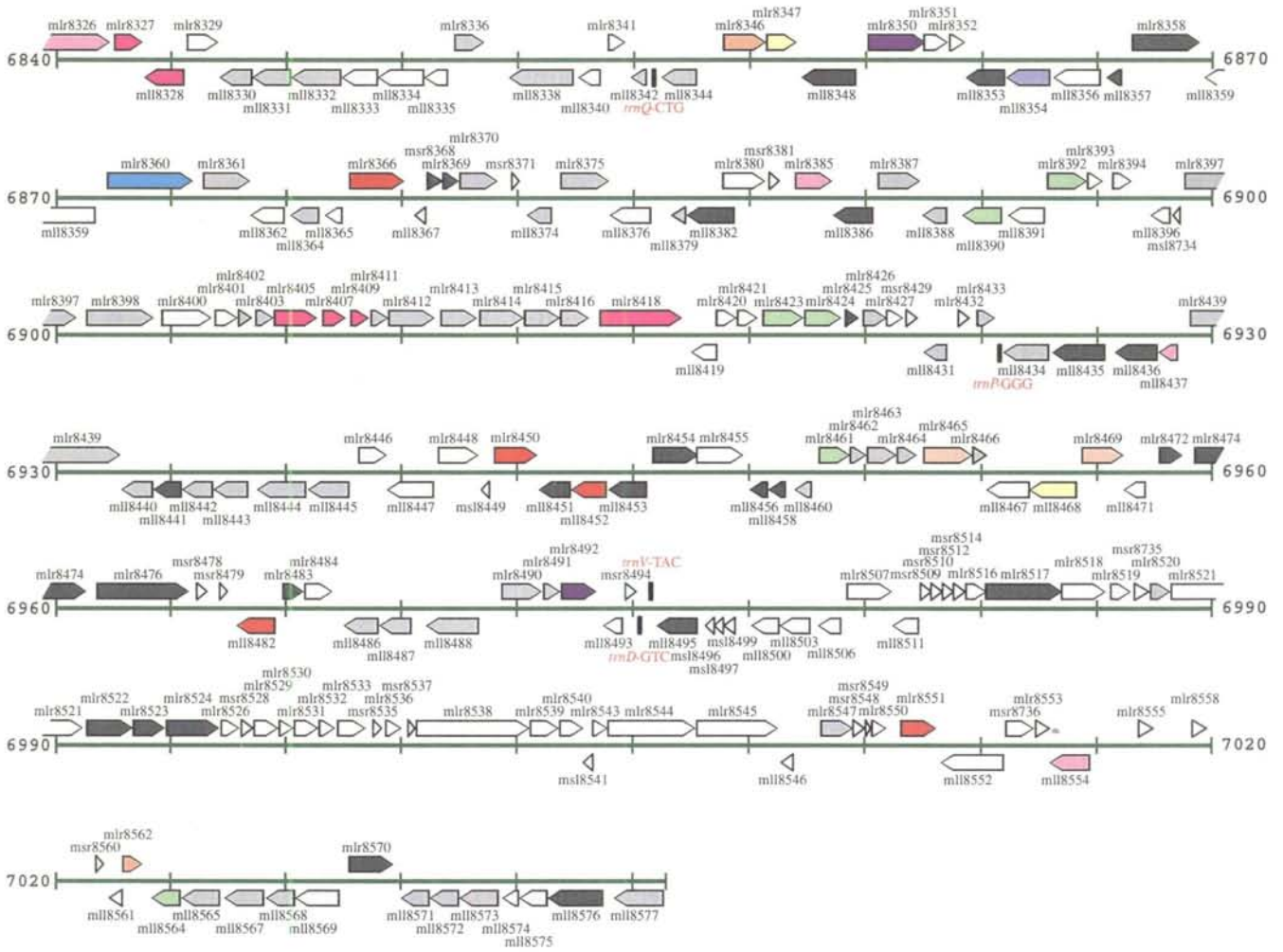






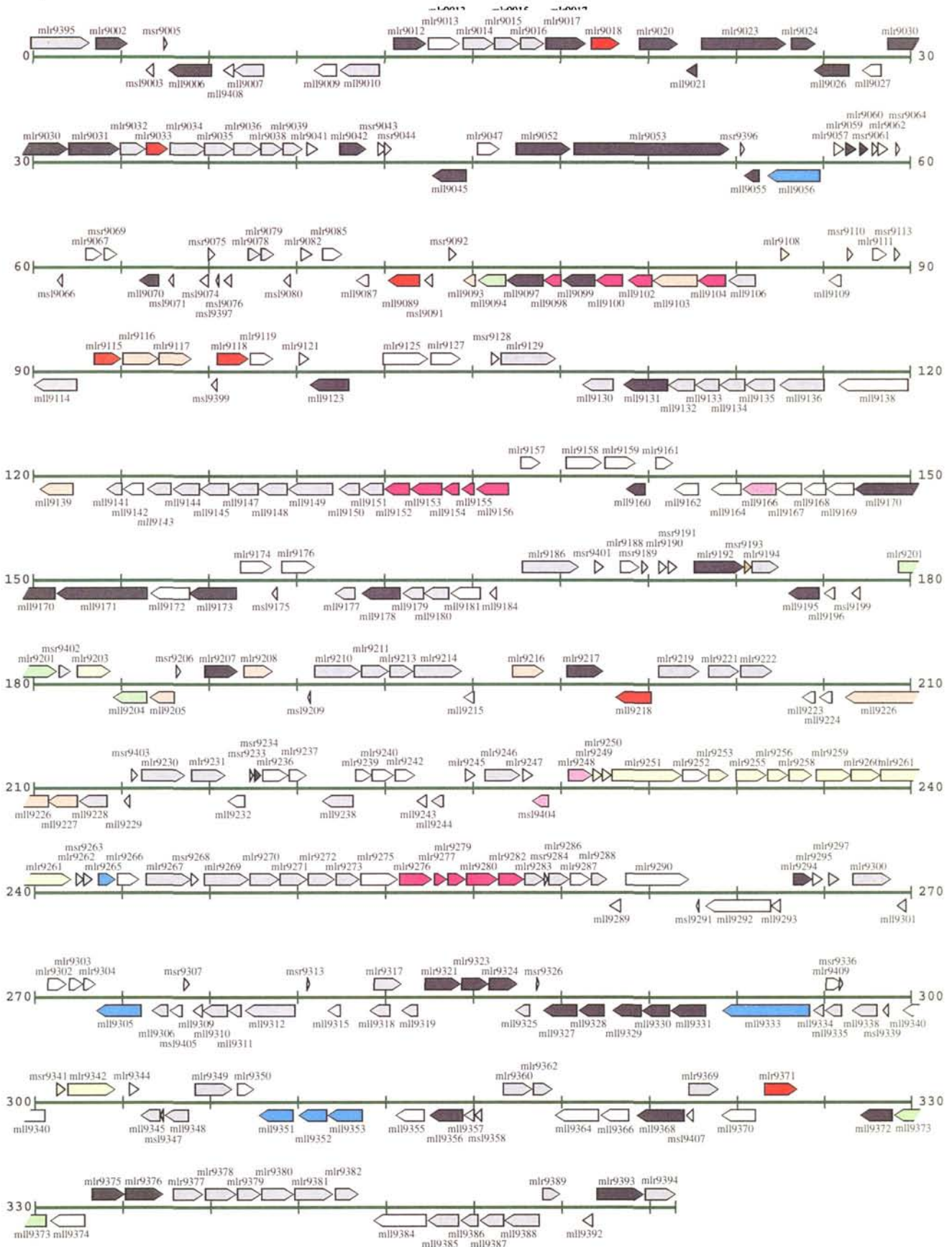








**pMLa**



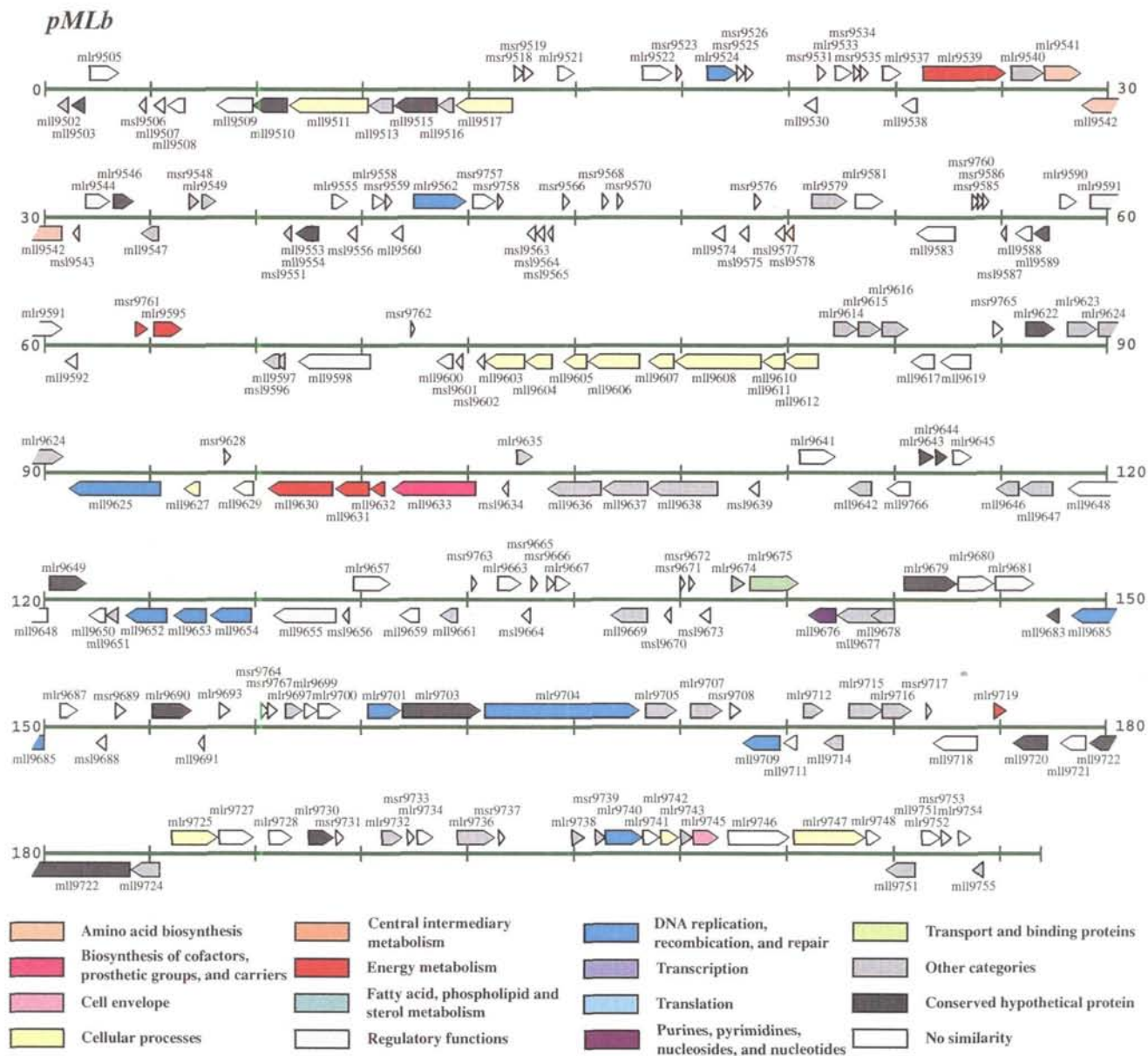


Fig. 1. The gene map of the chromosome and the plasmids of *M. loti*. The circular chromosome (7,036,076 bp) and the two plasmids, pMLa (351,911 bp) and pMLb (208,315 bp), of *M. loti* MAFF303099 were opened at the recognition sites of *Pac* I for the chromosome and pMLa, and *Spe* I for pMLb, and are represented by a linear map starting from this junction (map position 0/100). Green bars show the scale in 3 kb with numerals in kb. On both sides of the scale, the potential protein-coding genes assigned on the basis of computer prediction and similarity search are shown by boxes with arrowheads indicating the reading direction. The detailed assignment procedures are described in the main article in this issue (pp331–338). The potential genes of which the function could be evaluated by similarity search were classified into 14 functional categories, and are indicated by different color codes. The RNA coding genes were shown by black bars and boxes. The sequences as well as the gene information shown in this paper are available in the Web database, RhizoBase, at <http://www.kazusa.or.jp/rhizobase/>. The sequence data analyzed have been registered in the DDBJ/GenBank/EMBL databases by dividing into 24 entries. The accession numbers are as follows: AP002994 (nucleotide positions 1–347,660), AP002995 (347,655–694,550), AP002996 (694,545–1,044,163), AP002997 (1,044,158–1,373,866), AP002998 (1,373,861–1,721,610), AP002999 (1,721,605–2,067,898), AP003000 (2,067,893–2,415,969), AP003001 (2,415,964–2,761,746), AP003002 (2,761,741–3,111,238), AP003003 (3,111,233–3,460,348), AP003004 (3,460,343–3,798,921), AP003005 (3,798,916–4,131,550), AP003006 (4,131,545–4,473,431), AP003007 (4,473,426–4,821,836), AP003008 (4,821,831–5,168,650), AP003009 (5,168,645–5,508,325), AP003010 (5,508,320–5,849,176), AP003011 (5,849,171–6,195,680), AP003012 (6,195,675–6,542,221), AP003013 (6,542,216–6,890,165), and AP003014 (6,890,160–7,036,071) for the chromosome; AP003015 (1–307,548) and AP003016 (307,543–351,911) for pMLa; AP003017 (1–208,315) for pMLb.

Aminoacyl stem	D domain stem loop	stem	Anticodon domain stem	loop	stem	Variable region	T <sub>ψ</sub> C stem	domain loop	stem	Aminoacyl stem
<i>tmL-UAA</i> (109035-108953)	CGC A AGGGA CTTAAAA TCCCT CGATCTCTGATCGT						ACGGG	TTCGATT	CCCGT	CGTCCGC A
<i>tmT-UGU</i> (174674-174602)	GAGC A GCGGT TTTGTAA ACCGA AGGTC						GGCGG	TTCGATT	CCGTC	CGGGGGC A
<i>tmY-GUA</i> (182332-182413)	GGG G ACGGA CTGTAAA TCCGT TGGCTTAGCCTAC						GTTCG	TTCGAAT	CCAACT	CGTCTCC A
<i>tmG-UCC</i> (182507-182577)	GAGC A GCAGC CTTCCAA GCTGA ATAT						GGGGG	TTCGATT	CCGCG	TACCCGC T
<i>tmW-CCA</i> (189335-189407)	GAGC G GCGGT CTCCAA ACCGC AGGTC						GTAGG	TTCGAGC	CCTGC	TGCGCGT G
<i>tmS-UGA</i> (347728-347814)	GGC A CCGGT CTTGAAA ACCGG CGTGGCGCAAGTTCCAC						GTGGG	TTCGAAT	CCGAC	TCCCTCC G
<i>tmV-CAC</i> (390847-390918)	GAGC A CACCC TTCACAC GGSTG GGGTC						GCAGS	TTCAAATC	CCTGC	ATCGCCC A
<i>tmK-UUU</i> (552148-552076)	GAGC A ACTGA CTTTAA TCAGT AGGTC						ATGGG	TTCGAAT	CCCAT	CGCGCTC A
<i>tmE-UUC</i> (758542-758613)	GGC A CCGCC CTTTAC GCGCG TAAC						AGGGG	TTCGATT	CCCTT	TGGCGGT A
<i>tmL-UAG</i> (885121-885202)	CGC C CTGGA TTTAGT TCCAG TGCCGAAAGGCGT						GGGGG	TTCGAGT	CCCTT	CATCCGC A
<i>tmC-GCA</i> (931216-931146)	CGC A GAGGA CTGCAA TCCTT GCAC						CCCGG	TTCGATT	CCGGG	CGAGGCC T
<i>tmN-GUU</i> (932217-932288)	GAGC A ACCGG CTGTAA CCGGT TGSTC						GCTGG	TTCGAAT	CCGGG	CGGGGGA G
<i>tmI-UAU</i> (985562-985636)	GAGC A TCAGA CTTATA TCTGA CTGTC						GAAGG	TTCGATT	CCCTC	TCCCAAG C
<i>tmL-GAG</i> (1119857-1119776)	CGC G CAGCG TTGAGT CGTGS TGGGGCAACCCCGT						GGAAG	TTCGAGT	CTTCT	CGACCCG A
<i>tmK-UUU</i> (1166425-1166353)	GAGC A GCTGA CTCTTA TCAGC GGGTC						CACAG	TTCAAATC	CTGTG	CGCAACC A
<i>tmQ-UUG</i> (1484315-1484385)	GGC A GCGCC CTTTGA GCGGT GAAT						CGTGG	TTCGAGC	CCATG	AGCGGGA A
<i>tmM-CAU</i> (1960723-1960651)	GAGC C GGGGG CTCATA CCGCT TGGTT						GGGGG	TTCGAGT	CCCTC	CGGGCCC A
<i>tmM-CAU</i> (2262783-2262856)	GAGC A CCGGA ATCATA TCCTG GGGTC						GGGGG	TTCGAAT	CCCTC	TCCCGCT A
<i>tmV-GAC</i> (2447616-2447687)	GAGC A CTGCA TTGACAT TSCAG GGGTC						ACAGG	TTCAAATC	CCTGT	CGCGCCC A
<i>tmS-GGA</i> (2521735-2521849)	GGC G CAGCG CTGAAA GTGTG TTTACGGGAGACCGTAAAC						CGGGG	TTCGAAT	CCCGC	TCTCTCC G
<i>tmM-CAU</i> (2745746-2745673)	GCTC G TCAGG CTCATA CCTGA AGGTC						ACAGG	TTCAAAT	CCTGT	CCCCGCA A
<i>tmA-UGC</i> (2749583-2749511)	GAGC G CCGCC TTTGCAA GCAGG ATGTC						GTCCG	TTCGATC	CCGTC	CGCTCC A
<i>tmI-GAU</i> (2749710-2749637)	GAGC G CCGCC TTGATA GCGTG AGGTC						GGAGG	TTCAAAT	CCTCC	CAGGCCC A
<i>tmM-CAU</i> (2753235-2753162)	GCTC G TCAGG CTCATA CCTGA AGGTC						ACAGG	TTCAAAT	CCTGT	CCCCGCA A
<i>tmA-UGC</i> (2757096-2757024)	GAGC G CCGCC TTTGCAA GCAGG ATGTC						GTCCG	TTCGATC	CCGTC	CGCTCC A
<i>tmS-GGA</i> (2757223-2757150)	GAGC G CCGCC TTGATA GCGTG AGGTC						GGAGG	TTCAAAT	CCTCC	CAGGCCC A
<i>tmL-CAA</i> (2803017-2802936)	CGC G CTGGA CTCAAA TCGAG TTCGCAAGGAGT						GCTGG	TTCGATC	CCCGC	TAGGGGC A
<i>tmR-CCU</i> (2888030-2888103)	GAGC G GCAGA TTCCTAA TCTGT AGGTC						ACAGG	TTCGATT	CCTGT	CGGGATC A
<i>tmE-CUC</i> (3010459-3010388)	GGC A CCGCC CTCTCAC GCGCG GAAC						AGGGG	TTCGATT	CCCTC	TGGCGGT A
<i>tmS-CGA</i> (3212915-3213001)	TGC A CCGCA CTCGAAA TCGCG CATGGGTGCAAGCCCATC						GGGGG	TTCGAAT	CCCTC	TCTCTCC G
<i>tmA-CGC</i> (3320516-3320588)	GAGC G CATCG TTCGAAA TGATG AGGTC						AGGGG	TTCGATC	CCCTC	CAGCTCC A
<i>tmG-GCC</i> (3514870-3514941)	GAGC A CAACC TTGCAA GCTTG GGGTC						GAGCG	TTCGAAT	CCGTT	CACCCGC T
<i>tmL-CAG</i> (3682635-3682716)	CGC G CAGCG TTCAGGT CCGTG TTCGCAAGGAGT						GGAGG	TTCGAGT	CCTCT	TCTGGGC A
<i>tmR-ACG</i> (3823185-3823112)	GAGC A CCAGA CTCAGAA TCTGG GGGTC						AGGAG	TTCGAAT	CTCTT	CGGGCGC G
<i>tmR-CCG</i> (3934619-3934692)	GAGC G CTGCC CTCGAAA GGCAG AGGTC						ACAGG	TTCGAAT	CCTGT	CGGGTGC G
<i>tmA-GGC</i> (4147037-4147109)	GAGC G CTTGA ATGGCAT TCAAG AGGTC						GTCCG	TTCGATT	CCGAT	TGGCTCC A
<i>tmT-CGU</i> (4394764-4394692)	GAGC A CATCA TTCGTAA TGATG GGGTC						AGGTG	TTCGAGT	CACCT	AAGCGGC A
<i>tmG-CCC</i> (4556900-4556830)	GCTC G TCAGC TTCCTAA GCTGA ACGC						GCGGG	TTCGATT	CCCGC	TACCCGC T
<i>tmF-GAA</i> (5255843-5255771)	GAGC A GCGGA CTGAAA TCAGC GTGTC						GGTGG	TTCGAAT	CCCGC	TCTGGGC A
<i>tmT-GGU</i> (5279355-5279426)	GAGC A CTCCC TTGTAAA GGGAG AGGTC						GAGAG	TTCAAATC	CTCTC	TGCGAGC A
<i>tmH-GUG</i> (5351043-5351116)	GAGC G CCGGA TTGTGGA TCGCG AGGTC						GCTGG	TTCGATC	CCAGC	TAACGGT A
<i>tmQ-UUG</i> (6215006-6214935)	GGC A TCGGT TTTTGGT ACCGA CATT						CCAGG	TTCGAAT	CCTGG	CGCCCCA G
<i>tmP-CGG</i> (6294516-6294443)	GCGC A CCTCG TTCGAAA CGAGG GGGTC						GCAGG	TTCAAAT	CCTGC	TACTCCG A
<i>tmS-GCU</i> (6410150-6410244)	GGC G CTCCC CTGCTAA GGGAG TAGAGGTCAAAGCTCTCT						GTGGG	TTCGAAT	CCCAT	TCTCTCC G
<i>tmP-UGG</i> (6574654-6574581)	GCGC A TCTGG TTTGGGA CCAGA GGGTC						GGGAG	TTCGAAT	CTCTC	TACTCCG A
<i>tmR-UCU</i> (6575132-6575205)	GAGC A CCGCC CTTCTAA GCGCA TGSTC						ACAAG	TTCGAAT	CCTGT	CGGGATC G
<i>tmQ-CUG</i> (6855558-6855488)	GACC C ACGGA CTCTGAC TCGGT TAGT						CCTGG	TTCGAAT	CCAGG	TTCCTCA G
<i>tmP-GGG</i> (6924523-6924450)	GCGC A CTGGA CTGGGGG TCAAG GGGTC						GTCCG	TTCGAAT	CCCGC	TACTCCG A
<i>tmD-GUC</i> (6975241-6975168)	GAGT G CCGCC CTGCTAC GCGCG AGGTC						GCGGG	TTCGAGC	CCGCT	TACTCCG G
<i>tmV-UAC</i> (6975459-6975531)	GAGC G CTTCG TTTACAC CSAAG ATGTC						GGCGG	TTCGAGC	CCGTC	ATCGCCC A

Fig. 2. Structure of the tRNA genes in the genome of *M. loti*. The nucleotide sequences, nucleotide positions in the genome and the structural domains for the to 50 tRNA genes are tabulated.