Compilation of small ribosomal subunit RNA sequences

Jean-Marc Neefs, Yves Van de Peer, Lydia Hendriks and Rupert De Wachter*
Departement Biochemie, Universiteit Antwerpen, UIA, Universiteitsplein 1, B-2610 Antwerp, Belgium

INTRODUCTION

Table 1 lists 275 small ribosomal subunit RNA (further abbreviated as srRNA) sequences (references 1–270) that have been published, or submitted to the EMBL or GenBank nucleotide sequence libraries, to our knowledge. The previous compilation (271) listed 106 srRNA sequences. There is a tendency towards publication of partial, rather than complete sequences. This is a consequence of the availability of new techniques for sequencing or DNA amplification, that allow to collect results faster, but do not allow to determine the complete sequence up to the termini. One such method uses reverse transcription of the RNA with primers complementary to universally conserved sequence areas (272), in which case the sequence adjacent to the 3'-terminus cannot be determined. In another approach (27), the rDNA is amplified by the polymerase chain reaction (273) rather than by cloning. Since the primers for the PCR bind to conserved sequences close to the termini but within the boundaries of the srRNA gene, neither of the terminal sequences is comprised in the analysis. Both these methods, however, can yield a continuous sequence spanning more than 90% of the molecule, provided a sufficient number of primers is used. Some authors (e.g. reference 274) use a limited set of primers, in which case a discontinuous set of partial sequences is obtained, which can nevertheless be aligned with complete sequences from other species and used for phylogenetic studies.

The set of 270 different srRNA sequences listed in Table 1 comprises complete sequences and continuous partial sequences, but no discontinuous partial sequences. In order to limit the space needed for the alignment, we have restricted it to 60 sequences. This comprises all the complete sequences that were published, or have become accessible in sequence libraries, since the last compilation (271), plus 8 previously listed sequences added as references in order to allow a comparison of the present alignment and secondary structure scheme with the previous one.

SEQUENCE ALIGNMENT

The 60 sequences are listed in 5 groups, consisting of eukaryotic (cytoplasmic) -, archaebacterial -, eubacterial -, plastidial – and mitochondrial srRNAs. Each group comprises a sequence already aligned in the previous compilation, viz. *Homo sapiens* for the eukaryotic cytoplasmic srRNAs, *Halobacterium cutirubrum* for the archaebacterial srRNAs, *Escherichia coli* for the eubacterial srRNAs, *Zea mays* for the plastid srRNAs. Because of the extreme variability in length and secondary structure of mitochondrial srRNA sequences, an animal -, a plant -, a fungal – and a flagellate sequence were added as references in this group. The species chosen are *H. sapiens*, *Glycine max*, *Saccharomyces cerevisiae* and *Leishmania tarentolae*. The sequences are identified on each alignment page by a number corresponding with that in Table 1 and with the literature reference, and by the initials of the species name.

Alignment positions are numbered at the top and bottom of each page. In addition, *E. coli* srRNA nucleotide positions counting from its 5'-terminus are indicated above the eubacterial sequences. Regardless of the analytical method used, all sequences are listed using the ribonucleotide symbols U, C, A, and G. Posttranscriptional modifications are known for few sequences and not indicated in the alignment, but if data are available this is mentioned by a footnote in the last column of Table 1. The symbol X is used for unidentified -, and the symbols Y (pyrimidine nucleotide) and R (purine nucleotide) for incompletely identified nucleotides. These symbols point to uncertainty in the identification of a nucleotide in the case of analyses performed on cloned or amplified DNA, which examine the structure of a single gene. In the case of sequencing by reverse transcription of srRNA, however, they can point either to analytical uncertainty or to sequence heterogeneity, since the srRNA used as template may be a mixture of different sequences. Gaps introduced in order to optimize the alignment are filled with hyphens. On the contrary, dots are used for an interruption of the sequence due to partial sequencing. Hence, a sequence interrupted by 10 dots means that partial sequences are known to the left and to the right of the interruption, but that the length of the separating stretch is unknown. An interruption by 10 X's means that exactly 10 nucleotides are present, but their identity is unknown. A sequence starting or ending with dots means that sequencing has not reached the terminus. Lower case characters at termini are used to indicate length heterogeneity of the RNA molecules.

It should be noted that the alignment of the sequences for optimal similarity is straightforward in areas of relatively conserved primary and secondary structure, but is much more arbitrary in the structurally more variable areas. Alignment rests mostly on the periodic occurrence of conserved sequence motifs and on the observation of compensating substitutions in complementary areas of the secondary structure (see below). In the variable areas, conserved sequence motifs are rarer and at the same time the sequences differ in length. Whether compensating substitutions are seen or not then depends on how the gaps are placed, which makes their observation less meaningful.

Sequence segments presumedly involved in base pairing according to the secondary structure model described below are indicated by shading superimposed on the alignment. Shaded

* To whom correspondence should be addressed

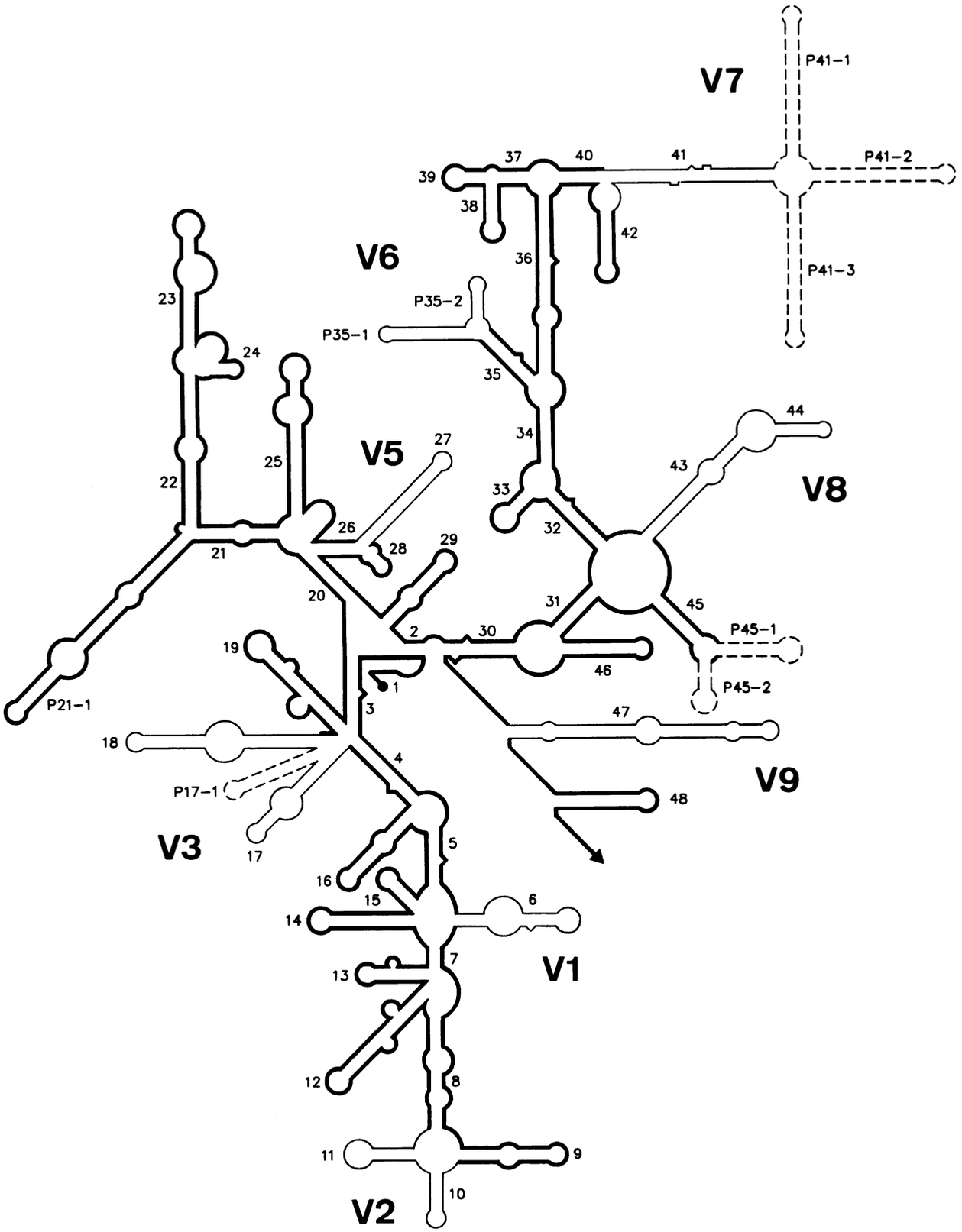

Fig. 1. Secondary structure model for prokaryotic srRNAs.
The 5′-terminus is symbolized by a filled circle and the 3′-terminus by an arrowhead. Helices are numbered in the order of occurrence from 5′- to 3′-terminus. Helices bearing a single number are common to the prokaryotic and eukaryotic (Fig. 2) models. A composite number preceded by P points to a prokaryote-specific helix. Relatively conserved areas are drawn in bold lines, areas of sequence–and length variability in thin lines. Eight variable areas, numbered V1 to V9, are distinguished, V4 being absent in prokaryotic srRNAs. Helices drawn in broken lines are present in a small number of known structures only. Archaebacterial sequences follow the prokaryotic pattern except for helix 35, which is unbranched as in eukaryotes.

areas corresponding to complementary strands of helices 1 to 48 of the secondary structure model are numbered 1 and 1′ to 48 and 48′. Helix numbers are listed twice, the uppermost row applying to the eukaryotic sequences, and the lowermost row to the bacterial -, plastidial -, and mitochondrial sequences. Internal loops and bulges in a helix are indicated by interruption of the shading. Bases suspected to belong to pairs other than the Watson-Crick pairs G·C, A·U, or the wobble pair G·U, because they are intercalated between Watson-Crick and/or wobble pairs, are put in parentheses.

SECONDARY STRUCTURE MODEL

The secondary structure models adopted for indication of the double stranded areas in the alignment are shown in Fig. 1 and 2. The prokaryotic model of Fig. 1 applies to archaebacterial, eubacterial, plastidial, and mitochondrial srRNAs. The model of Fig. 2 applies to eukaryotic srRNAs. Helices common to both models, further called universal helices, are numbered 1 to 48, in the order of occurrence of the 5′-proximal strand when the sequence is scanned from 5′ to 3′-end. Helix numbers change

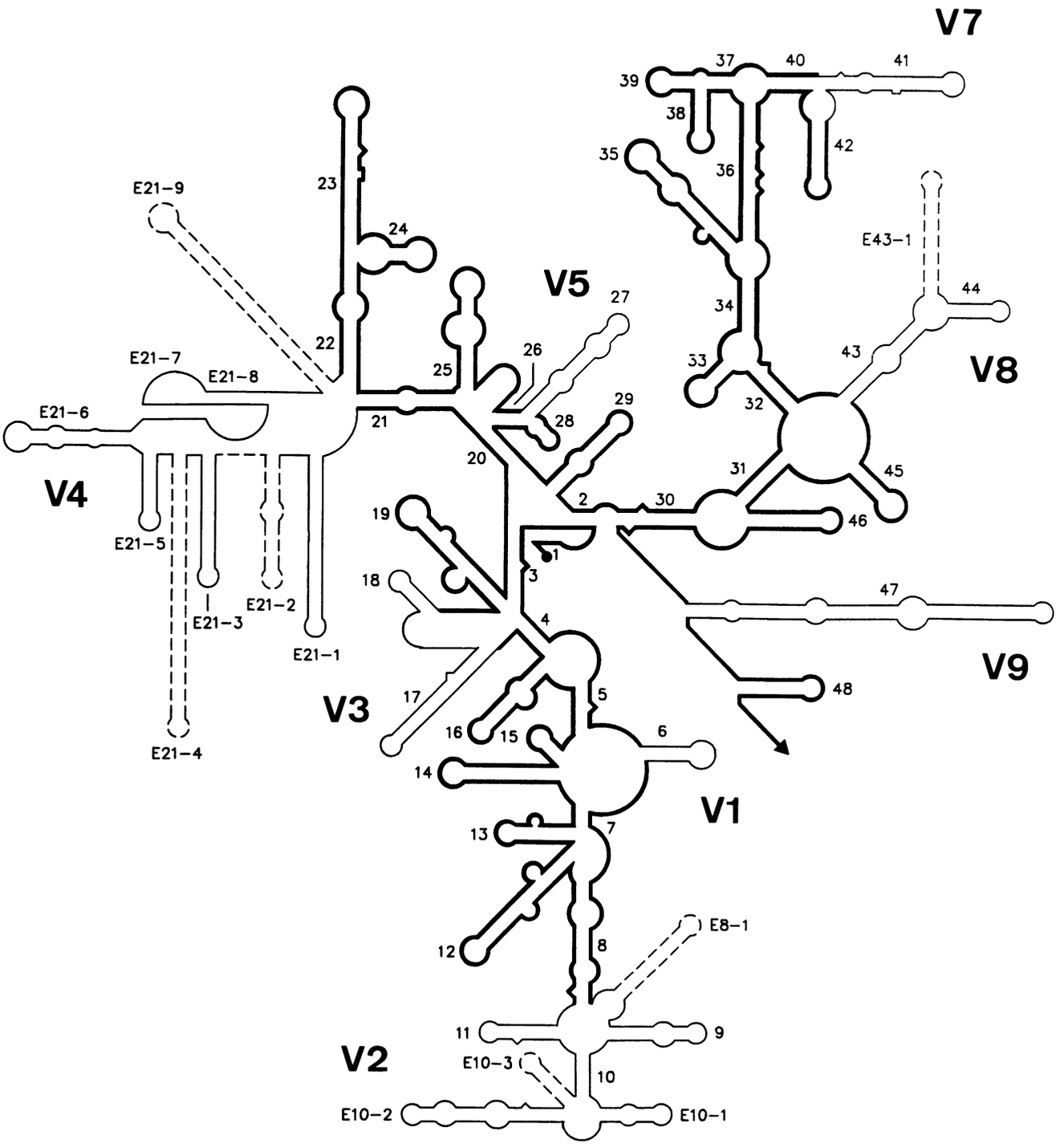

Fig. 2. Secondary structure model for eukaryotic srRNAs.
Symbols are as in Fig. 1. Helices bearing a composite number preceded by E are eukaryote-specific. Variable area V6 is missing in eukaryotic srRNAs.

at branching points and at pseudoknot loops, not at internal- and bulge loops. Helices specific to the prokaryotic model are numbered Pa-b, where a is the number of the preceding universal helix and b is a serial number. Helices specific to the eukaryotic model are similarly numbered Ea-b.

Structurally conserved areas are drawn in bold lines, whereas structurally variable areas, labeled V1 to V9, are drawn in thin lines. Helices that are present in a limited number of species are drawn in broken lines. Such is the case for e.g. helices P41-1 to P41-3, specific for plant mitochondrial srRNAs, or helix E10-3, hitherto found only in *Euglena gracilis* cytoplasmic srRNA. Conversely, helices can be absent in certain srRNAs. As an example, the diplomonad *Giardia lamblia* misses helices E21-1 to E21-4. Even the 'universal' helices do not occur in all srRNAs, the exceptions being found among the mitochondrial srRNAs. Those from animal mitochondria retain only 36 of the universal helices, with most of the missing ones belonging to variable areas. In flagellate mitochondrial srRNAs the structure retains only 25 universal helices, with the entire area consisting of helices 31 to 45 missing. The Fig. 1 model should therefore be regarded, not so much as a general prokaryotic model, but rather as a model for eubacterial and plastidial srRNA secondary structure, from which mitochondrial srRNA structures can be derived by addition (in the case of plant mitochondria) or subtraction of sets of helices. As for the archaebacterial srRNAs, these differ from the eubacterial ones only by lacking the branching point leading to helices P35-1 and P35-2.

The models of Fig. 1 and 2 concur with those proposed by Gutell et al. (275) as far as the conserved areas are concerned, and for a fraction of the variable areas. However, we propose a structure for a long insertion in area V7 found in plant mitochondrial srRNAs, and for area V4 in eukaryotic srRNAs, both left undefined in (275). The latter structure is different from that adopted in the previous compilation (271) and comprises a pseudoknot. In addition, for areas V2 and V3 of the eukaryotic model, we propose a base pairing scheme slightly different from that of Gutell et al. (275). Although most of the structures that we propose in the variable areas are supported by observation of compensating substitutions, (unpublished) they should nevertheless be regarded as tentative in view of the difficulties connected with alignment in these areas explained above.

AVAILABILITY OF THE DATA

Of the 270 different srRNA sequences listed in Table 1, 197 were in our computer file at the time of writing, in aligned form and with delimitation of secondary structure elements. The remaining ones, which are not listed in the papers reporting them but have been submitted to GenBank, have only recently become available in the file server of this library. They will be aligned as soon as possible. The sequences will be available on floppy disks, readable on microcomputers operating under MS-DOS, in the following three formats:

1) In the form of an alignment with indication of secondary structure elements. Aligned sequences will be listed on 42 pages each containing 100 alignment positions of all the sequences. This format is most useful for those wishing to produce a hardcopy of the complete alignment, rather than the sample of 60 sequences listed here. From this file, the complete alignment can be printed using a wide carriage printer, condensed print and reduced line spacing. Note, however, that this takes about 252 pages of 15 inch wide printer paper.

2) The sequences, listed one by one, without indication of secondary structure elements, but interspersed with the gaps required for alignment, i.e. with homologous nucleotides in the same position in each sequence.

3) The sequences, listed one by one, written continuously without gaps or secondary structure-describing symbols. The number of formatted floppy disks of different types that should be sent in order to obtain each of these files is listed in Table 2.

In addition, all these files can be obtained on a TK50 tape, suitable for a MicroVax computer operating under VMS 5.0 or higher.

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Table 1. List of *sr*RNA sequences.

Nr (a)	Species	Specification (b)	Taxonomic position (c)		Length (d)	Access. (e)	Method (f)	Remark
	EUKARYOTES							
* 1	Homo sapiens		Chordata (Ph.)	Mammalia (Cl.)	1869	X03205		g
2	Homo sapiens		Chordata (Ph.)	Mammalia (Cl.)	1868	M10098		
3	Homo sapiens	pB pA4	Chordata (Ph.)	Mammalia (Cl.)	1870	K03432		
4	Mus musculus		Chordata (Ph.)	Mammalia (Cl.)	1869	X00686		
5	Rattus norvegicus	Male Sprague-Dawley, liver	Chordata (Ph.)	Mammalia (Cl.)	1869	M11188		
6	Rattus norvegicus	Male Sprague-Dawley, liver	Chordata (Ph.)	Mammalia (Cl.)	1874	X01117		
* 7	Oryctolagus cuniculus	Reticulocytes	Chordata (Ph.)	Mammalia (Cl.)	1863	X06778		h
8	Xenopus laevis		Chordata (Ph.)	Amphibia (Cl.)	1826	X04025		g
9	Xenopus borealis		Chordata (Ph.)	Amphibia (Cl.)	1825			g
10	Artemia salina	Cysts	Arthropoda (Ph.)	Crustacea (Cl.)	1810	X01723		
* 11	Eurypelma californica	Whole organism	Arthropoda (Ph.)	Arachnida (Cl.)	1814	X13457		
* 12	Tenebrio molitor	Larvae	Arthropoda (Ph.)	Insecta (Cl.)	1921	X07801		
* 13	Drosophila melanogaster		Arthropoda (Ph.)	Insecta (Cl.)	1995			
14	Caenorhabditis elegans		Nemathelminthes (Ph.)	Nematoda (Cl.)	1759	X03680		
15	Oryza sativa		Angiospermae (Ph.)	Monocotyledoneae (Cl.)	1812	X00755		
* 16	Lycopersicon esculentum		Angiospermae (Ph.)	Monocotyledoneae (Cl.)	1800	X51576		
17	Zea mays	Cultivar Black Mexican, leaves	Angiospermae (Ph.)	Monocotyledoneae (Cl.)	1809	K02202		
18	Glycine max	Variety Wayne lambda-SR1	Angiospermae (Ph.)	Dicotyledoneae (Cl.)	1807	X02623		
* 19	Arabidopsis thaliana	Variety Co 10	Angiospermae (Ph.)	Dicotyledoneae (Cl.)	1804	X16077		
* 20	Zamia pumila	Leaves	Gymnospermae (Ph.)	Cycadopsida (Cl.)	1813			
21	Chlamydomonas reinhardtii		Chlorophyceae (Cl.)	Volvocales (O.)	1791			
* 22	Volvox carteri	f. nagariensis, HK 10 (UTEX 1885)	Chlorophyceae (Cl.)	Volvocales (O.)	1788			
* 23	Chlorella vulgaris	Type strain 211-11b	Chlorophyceae (Cl.)	Chlorococcales (O.)	1798	X13688	PCR	
* 24	Nanochlorum eucaryotum		Chlorophyceae (Cl.)		1796	X06425		
25	Ochromonas danica		Chrysophyceae (Cl.)	Chrysomonadales (O.)	1789			
26	Costaria costata	Sporophytes	Phaeophyceae (Cl.)	Laminariales (O.)	(1595)			
* 27	Skeletonema costatum	Culture 18/C, British Columbia	Bacilariophyceae (Cl.)		1798		PCR	
28	Neurospora crassa		Ascomycotina (Ph.)	Pyrenomycetes (Cl.)	1795	X04971		
29	Saccharomyces cerevisiae	Strain A364A	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1798	V01335		
* 30	Pneumocystis carinii	Isolate from rat lung			1774	X12708		
31	Achlya bisexualis		Mastigomycotina (Ph.)	Oomycetes (Cl.)	1809			
32	Dictyostelium discoideum	Strain Ax3	Myxomycota (Ph.)	Acrasiomycetes (Cl.)	1872	K02641		h
* 33	Physarum polycephalum	Strain CL	Myxomycota (Ph.)	Myxomycetes (Cl.)	1964	X13160		
34	Euplotes aediculatus		Ciliata (Ph.)	Spirotricha (O.)	1882	X03949		
35	Oxytricha nova		Ciliata (Ph.)	Spirotricha (O.)	1771	X03948		
36	Stylonychia pustulata		Ciliata (Ph.)	Spirotricha (O.)	1771	X03947		
37	Tetrahymena thermophila	Strain A-17682a (intron+), ATTC 30377	Ciliata (Ph.)	Holotricha (O.)	1753	M10932		
38a	Tetrahymena pigmentosa	Strain UM 1286 (intron-)	Ciliata (Ph.)	Holotricha (O.)	1752			
38b	Tetrahymena hyperangularis	Strain EN 101, ATCC 30273	Ciliata (Ph.)	Holotricha (O.)	1752			
38c	Tetrahymena nanneyi	Strain XQ5, ATCC 30840	Ciliata (Ph.)	Holotricha (O.)	1752			
39	Tetrahymena hegewischi	Strain KP7 (intron-), ATCC 30832	Ciliata (Ph.)	Holotricha (O.)	1752			
40	Tetrahymena australis	Strain MGO (intron-), ATCC 30831	Ciliata (Ph.)	Holotricha (O.)	1752			
41	Tetrahymena capricornis	Strain AU-F1-1 (intron-), ATCC 30291	Ciliata (Ph.)	Holotricha (O.)	1752			
42	Tetrahymena patula	Strain LFF (intron-), ATCC 50064	Ciliata (Ph.)	Holotricha (O.)	1752			
43a	Tetrahymena borealis	Strain UM 731 (intron-)	Ciliata (Ph.)	Holotricha (O.)	1752			
43b	Tetrahymena canadensis	Strain UM 1215, ATCC 30368	Ciliata (Ph.)	Holotricha (O.)	1752			
44	Tetrahymena tropicalis	Strain TC3 (intron-), ATCC 30352	Ciliata (Ph.)	Holotricha (O.)	1752			
45	Tetrahymena pyriformis	Strain GL-C (intron-, a-micronuclear)	Ciliata (Ph.)	Holotricha (O.)	1752			
46	Tetrahymena malaccensis	Strain MP75 (intron+), ATCC 50066	Ciliata (Ph.)	Holotricha (O.)	1753			
47	Paramecium tetraurelia		Ciliata (Ph.)	Holotricha (O.)	1753	X03772		
48	Prorocentrum micans	Strain LB113614	Dinoflagellates (Assemblage)		1798	M14649		
49	Plasmodium berghei	Strain NUY2	Sporozoa (Ph.)	Haemosporidia (O.)	2059	M14599		
50	Plasmodium berghei		Sporozoa (Ph.)	Haemosporidia (O.)	2058			
* 51	Plasmodium falciparum		Sporozoa (Ph.)	Haemosporidia (O.)	2091			
* 52	Plasmodium falciparum		Sporozoa (Ph.)	Haemosporidia (O.)	2148			
* 53	Plasmodium lophurae		Sporozoa (Ph.)	Haemosporidia (O.)	2118	X13706		
54	Plasmodium vivax		Sporozoa (Ph.)	Haemosporidia (O.)	(1602)	X13926		
55	Acanthamoeba castellanii		Rhizopoda (Ph.)	Amoebina (O.)	2303	M13435		
* 56	Naegleria gruberi		Rhizopoda (Ph.)	Amoebina (O.)	2019	M18732		
57	Trypanosoma brucei		Euglenozoa (Assemblage)	Kinetoplastidea	2255	M12676		
58	Crithidia fasciculata		Euglenozoa (Assemblage)	Kinetoplastidea	2206	X03450		
* 59	Leishmania donovani	Strain Sudan 1	Euglenozoa (Assemblage)	Kinetoplastidea	2204	X07773		
60	Euglena gracilis		Euglenozoa (Assemblage)	Euglenophyta	2305	M12677		
61	Vairimorpha necatrix		Microsporidia (Assemblage)	Microsporidia (Ph.)	1244	Y00266		
* 62	Giardia lamblia	Strain Portland 1	Polymastigotes (Assemblage)		1453	M19500		

Table 1. continued

Nr (a)	Species	Specification (b)	Taxonomic position (c)		Length (d)	Access. (e)	Method (f)	Remark
	ARCHAEBACTERIA							
* 63	Halobacterium cutirubrum		Halobacteria		1472	K02971		
64	Halobacterium halobium	Strain RI	Halobacteria		1473	M11583		
65	Halobacterium volcanii		Halobacteria		1472	K00421		
66	Halococcus morrhuae	ATCC 17082	Halobacteria		1475	X00662		
67	Methanospirillum hungatei	Strain JF1	Methanomicrobium group		1464			
* 68	Methanothrix soehngenii		Methanomicrobium group		1471	X16932		
69	Methanococcus vannielii	DSM 1224	Methanococcus group		1466			
70	Methanobacterium formicicum	DSM 1312	Methanobacter group		1476			
71	Methanobacterium thermoautotrophicum	Strain Marburg	Methanobacter group		1496	X15364		
* 72	Thermococcus celer	DSM 2476	Thermococcus group		1486			
* 73	Thermoplasma acidophilum	122-1B2	Thermoplasma group		1471			
74	Desulfurococcus mobilis		Extreme thermophiles		1495			
* 75	Pyrodictium occultum	Strain PL-19 DSM 2709	Extreme thermophiles		1497	M21087		
76	Sulfolobus solfataricus	Strain P1	Extreme thermophiles		1493	X03235		h
77	Thermoproteus tenax		Extreme thermophiles		1504			
78	Archaeoglobus fulgidus	Strain VC-16			1492	X05567		
	EUBACTERIA							
79	Agrobacterium tumefaciens	DSM 30105	Proteobacteria (Cl.)	alpha group (SCl.)	1489	M11223		
80	Brucella abortus	Strain 11/19	Proteobacteria (Cl.)	alpha group (SCl.)	(1429)	X13695	RT	
81	Ehrlichia risticii	ATCC VR986	Proteobacteria (Cl.)	alpha group (SCl.)	(1489)	M21290		
82	Hyphomicrobium vulgare	Strain MC-750	Proteobacteria (Cl.)	alpha group (SCl.)	(1373)		RT	
83	Rickettsia prowazekii		Proteobacteria (Cl.)	alpha group (SCl.)	1508	M21789		
84	Rickettsia rickettsii	ATCC VR891	Proteobacteria (Cl.)	alpha group (SCl.)	(1443)	M21293	RT	
85	Rickettsia typhi		Proteobacteria (Cl.)	alpha group (SCl.)	(1444)	M20499	RT	
86	Rochalimaea quintana	Strain Fuller	Proteobacteria (Cl.)	alpha group (SCl.)	1492	M11927		
87	Alcaligenes faecalis	ATCC 8750	Proteobacteria (Cl.)	beta group (SCl.)	(1473)	M22508		
88	Alcaligenes xylosoxidans	ATCC 15173, subsp. denitrificans	Proteobacteria (Cl.)	beta group (SCl.)	(1463)	M22509		
89	Chromobacterium fluviatale	ATCC 33051	Proteobacteria (Cl.)	beta group (SCl.)	(1470)	M22511	RT	
90	Chromobacterium violaceum	ATCC 12472	Proteobacteria (Cl.)	beta group (SCl.)	(1472)	M22510	RT	
91	Eikenella corrodens	ATCC 23834	Proteobacteria (Cl.)	beta group (SCl.)	(1487)	M22512	RT	
92a	Eikenella corrodens	FDC 373	Proteobacteria (Cl.)	beta group (SCl.)	(1486)	M22513	RT	
92b	Eikenella corrodens	FDC 558	Proteobacteria (Cl.)	beta group (SCl.)	(1486)	M22514	RT	
92c	Eikenella corrodens	FDC 1073	Proteobacteria (Cl.)	beta group (SCl.)	(1486)	M22515	RT	
93	Kingella denitrificans	ATCC 33394	Proteobacteria (Cl.)	beta group (SCl.)	(1472)	M22516	RT	
94	Kingella kingae	ATCC 23330	Proteobacteria (Cl.)	beta group (SCl.)	(1473)	M22517	RT	
* 95	Neisseria gonorrhoeae	NCTC 8375	Proteobacteria (Cl.)	beta group (SCl.)	1544	X07714		
* 96	Pseudomonas aeruginosa	ATCC 11996	Proteobacteria (Cl.)	beta group (SCl.)	1537	X06684		
97	Pseudomonas cepacia	ATCC 25416	Proteobacteria (Cl.)	beta group (SCl.)	(1471)	M22518	RT	
98	Pseudomonas testosteroni	ATCC 11996	Proteobacteria (Cl.)	beta group (SCl.)	1536	M11224		
99	Vitreoscilla stercoraria	VT1	Proteobacteria (Cl.)	beta group (SCl.)	(1487)	M22519	RT	
*100	Acyrthosyphon pisum symbiont P		Proteobacteria (Cl.)	gamma group (SCl.)	1547	M27039		
*101	Acyrthosyphon pisum symbiont S		Proteobacteria (Cl.)	gamma group (SCl.)	1542	M27040		
*102	Chromatium vinosum		Proteobacteria (Cl.)	gamma group (SCl.)	1526	M26629		
103	Coxiella burnetii	Strain Q177	Proteobacteria (Cl.)	gamma group (SCl.)	(1484)	M21291	RT	
104	Ectothiorhodospira halophila		Proteobacteria (Cl.)	gamma group (SCl.)	(1494)	M26630		
*105	Escherichia coli	Operon rrnB	Proteobacteria (Cl.)	gamma group (SCl.)	1542	V00348		i
106	Proteus vulgaris		Proteobacteria (Cl.)	gamma group (SCl.)	1544	J01874		h
107	Ruminobacter amylophilus	DSM 1361	Proteobacteria (Cl.)	gamma group (SCl.)	1539			
108	Wolbachia persica	ATCC VR331	Proteobacteria (Cl.)	gamma group (SCl.)	(1475)	M21292	RT	
109	Desulfosarcina variabilis		Proteobacteria (Cl.)	delta group (SCl.)	(1527)	M26632		
110	Desulfotobacter postgatei		Proteobacteria (Cl.)	delta group (SCl.)	(1519)	M26633		
111	Desulfovibrio desulfuricans	ATCC 27774	Proteobacteria (Cl.)	delta group (SCl.)	1551			
112	Desulfuromonas acetoxidans		Proteobacteria (Cl.)	delta group (SCl.)	(1522)	M26634		
113	Myxococcus xanthus	Strain MD207	Proteobacteria (Cl.)	delta group (SCl.)	1537			
114	Wolinella succinogenes		Proteobacteria (Cl.)	uncertain affiliation	(1503)		RT	
115	Acholeplasma entomophilum	Strain TAC, ATCC 43706	Firmicuta (Ph.)	low G+C	(1476)	M23931		
116	Acholeplasma florum	Strain L1, ATCC 33453	Firmicuta (Ph.)	low G+C				
117	Acholeplasma laidlawii	Strain JA1	Firmicuta (Ph.)	low G+C	1508	M23932		
118	Acholeplasma modicum	Strain PG49, ATCC 29102	Firmicuta (Ph.)	low G+C	(1473)	M23933		
119	Anaeroleplasma abactoclasticum	Strain 6-1, ATCC 27879	Firmicuta (Ph.)	low G+C	(1453)	M25050		
120	Anaeroleplasma bactoclasticum	Strain JR, ATCC 27112	Firmicuta (Ph.)	low G+C	(1436)	M25049		
121	Anaeroleplasma intermedium	Strain 5LA	Firmicuta (Ph.)	low G+C				
122	Anaeroleplasma varium	Strain A-2, ATCC 43167	Firmicuta (Ph.)	low G+C		M23934		
123	Asteroleplasma anaerobium	Strain 161, ATCC 27880	Firmicuta (Ph.)	low G+C	(1471)	M22351		
124	Bacillus subtilis	Operon rrnB	Firmicuta (Ph.)	low G+C	1550			
125	Clostridium innocuum	Strain B-3, ATCC 14501	Firmicuta (Ph.)	low G+C	1544	M23732		
126	Clostridium ramosum	Strain 113-I, ATCC 25582	Firmicuta (Ph.)	low G+C	1530	M23731		
127	Clostridium sticklandii		Firmicuta (Ph.)	low G+C	(1476)	M26494		
128	Erysipelothrix rhusiopathiae	Strain alpha-P15, ATCC 19414	Firmicuta (Ph.)	low G+C	(1487)	M23728		
129	Lactobacillus catenaforme	Strain 1871, ATCC 25536	Firmicuta (Ph.)	low G+C	1549	M23729		
130	Lactobacillus confusus	DSM 20196	Firmicuta (Ph.)	low G+C		M23036	RT	

Table 1. continued.

Nr (a)	Species	Specification (b)	Taxonomic position (c)		Length (d)	Access. (e)	Method (f)	Re-mark
131	Lactobacillus haloterans	DSM 20190	Firmicuta (Ph.)	low G+C		M23037	RT	
132	Lactobacillus kandleri	DSM 20593	Firmicuta (Ph.)	low G+C		M23038	RT	
133	Lactobacillus minor	DSM 20014	Firmicuta (Ph.)	low G+C		M23039	RT	
134	Lactobacillus viridescens	ATCC 12706	Firmicuta (Ph.)	low G+C		M23040	RT	
135	Lactobacillus vitulinus	Strain 185, ATCC 27783	Firmicuta (Ph.)	low G+C	(1477)	M23727		
136	Lactococcus garvieae	NCDO 2156	Firmicuta (Ph.)	low G+C	(1475)		RT	
137	Lactococcus lactis	NCDO 2118, subsp. lactis	Firmicuta (Ph.)	low G+C	(1472)		RT	
138	Lactococcus plantarum	NCDO 1869	Firmicuta (Ph.)	low G+C	(1473)		RT	
139	Lactococcus raffinolactis	NCDO 617	Firmicuta (Ph.)	low G+C	(1479)		RT	
140	Leuconostoc cremoris	DSM 20346	Firmicuta (Ph.)	low G+C		M23034	RT	
141	Leuconostoc lactis	DSM 20202	Firmicuta (Ph.)	low G+C		M23031	RT	
142	Leuconostoc mesenteroides	DSM 20343	Firmicuta (Ph.)	low G+C		M23035	RT	
143	Leuconostoc oenos	DSM 20252	Firmicuta (Ph.)	low G+C		M23032	RT	
144	Leuconostoc paramesenteroides	DSM 20288	Firmicuta (Ph.)	low G+C		M23033	RT	
145	Mycoplasma agalactiae	Strain PG2, NCTC 10123	Firmicuta (Ph.)	low G+C	(1463)	M24290		
146	Mycoplasma arginini	Strain G230, ATCC 23838	Firmicuta (Ph.)	low G+C	(1474)	M24579		
147	Mycoplasma arthritidis	Strain PG6, ATCC 19611	Firmicuta (Ph.)	low G+C	(1480)	M24580		
148	Mycoplasma bovigenitalium	Strain PG11, ATCC 19852	Firmicuta (Ph.)	low G+C	(1464)	M24291		
149	Mycoplasma californicum	Strain ST-6, ATCC 33461	Firmicuta (Ph.)	low G+C	(1480)	M24582		
150	Mycoplasma capricolum	Operon rrnB	Firmicuta (Ph.)	low G+C	1521	X00921		
151	Mycoplasma ellychniae	Strain ELCN-1, ATCC 43707	Firmicuta (Ph.)	low G+C	(1475)	M24292		
152	Mycoplasma fermentans	Strain PG18, ATCC 19989	Firmicuta (Ph.)	low G+C	(1461)	M24289		
*153	Mycoplasma gallisepticum		Firmicuta (Ph.)	low G+C	1519	M22441		
154	Mycoplasma hominis	Strain PG21, ATCC 23114	Firmicuta (Ph.)	low G+C	(1468)	M24473		
155	Mycoplasma hyopneumoniae	ATCC 27719	Firmicuta (Ph.)	low G+C	1537	Y00149		
156	Mycoplasma hyorhinis	ATCC 17981	Firmicuta (Ph.)	low G+C	(1470)	M24658		
157	Mycoplasma iowae	Strain 695, ATCC 33552	Firmicuta (Ph.)	low G+C	(1463)	M24293		
158	Mycoplasma lipophilum	Strain MaBy, ATCC 27104	Firmicuta (Ph.)	low G+C	(1480)	M24581		
159	Mycoplasma mobile	Strain 1634, ATCC 43663	Firmicuta (Ph.)	low G+C	(1466)	M24480		
160	Mycoplasma muris	Strain RIII4, ATCC 33757	Firmicuta (Ph.)	low G+C	(1464)	M23939		
161	Mycoplasma mycoides	Strain UM30847, subsp. mucoides	Firmicuta (Ph.)	low G+C	(1474)	M23943		
162	Mycoplasma neurolyticum	Strain type A, ATCC 19988	Firmicuta (Ph.)	low G+C	(1480)	M23944		
163	Mycoplasma orale	Strain CH19299, ATCC 23714	Firmicuta (Ph.)	low G+C	(1463)	M24659		
164	Mycoplasma pirum	Strain 70-159, ATCC 25960	Firmicuta (Ph.)	low G+C	(1465)	M23940		
165	Mycoplasma pneumoniae	Strain FH, ATCC 15531	Firmicuta (Ph.)	low G+C	(1465)	M29061		
166	Mycoplasma pulmonis	Strain PG34, ATCC 19612	Firmicuta (Ph.)	low G+C	(1476)	M23941		
167	Mycoplasma putrefaciens	Strain KS-1, ATCC 15718	Firmicuta (Ph.)	low G+C		M23938		
168	Mycoplasma salivarum	Strain PG20, ATCC 23064	Firmicuta (Ph.)	low G+C	(1476)	M24661		
169	Mycoplasma sualvi	Strain Mayfield B, ATCC 33004	Firmicuta (Ph.)	low G+C	(1497)	M23936		
170	Mycoplasma sp.	Strain 831-C4, ATCC 49193	Firmicuta (Ph.)	low G+C	(1475)	M24479		
171	Mycoplasma sp.	Strain PG 50, Operon rrnA	Firmicuta (Ph.)	low G+C	1523	M10588		
172	Mycoplasma sp.	Strain M1, ATCC 49191	Firmicuta (Ph.)	low G+C	(1474)	M24478		
*173	Oenothera hookeri MLO		Firmicuta (Ph.)	low G+C	1535			
174	Spiroplasma apis	Strain B-31, ATCC 33834	Firmicuta (Ph.)	low G+C	(1469)	M23937		
175	Spiroplasma citri	Strain Maroc, ATCC 27556	Firmicuta (Ph.)	low G+C	1523	M23942		
176	Spiroplasma group II	Strain DW1, ATCC 43153	Firmicuta (Ph.)	low G+C	(1468)	M24483		
177	Spiroplasma group IX (beetle)	Strain CN-5, ATCC 33827	Firmicuta (Ph.)	low G+C	(1464)	M24474		
178	Spiroplasma group VI	Strain Y32, ATCC 33835	Firmicuta (Ph.)	low G+C	(1473)	M24477		
179	Spiroplasma group VII (wasp)	Strain MQ-1, ATCC 33825	Firmicuta (Ph.)	low G+C	(1458)	M24481		
180	Spiroplasma group XII (beetle)	Strain DM-1, ATCC 43210	Firmicuta (Ph.)	low G+C	(1460)	M24482		
181	Spiroplasma group XXIII (horsefly)	Strain TG-1, ATCC 43525	Firmicuta (Ph.)	low G+C	(1469)	M24475		
182	Spiroplasma mirum	Strain SMCA, ATCC 29335	Firmicuta (Ph.)	low G+C	(1468)	M24662		
183	Spiroplasma taiwanense group XXII	Strain CT-1, ATCC 43302	Firmicuta (Ph.)	low G+C	(1467)	M24476		
184	Streptococcus pleomorphus	Strain 60B, ATCC 29734	Firmicuta (Ph.)	low G+C	1577	M23730		
185	Ureaplasma urealyticum	Strain 960, NCTC 10177	Firmicuta (Ph.)	low G+C	(1464)	M23935		
186	Vagococcus fluvialis	NCDO 2497	Firmicuta (Ph.)	low G+C	(1484)		RT	
187	Corynebacterium polymorphus	NCDO 2097	Firmicuta (Ph.)	high G+C	(1458)		RT	
*188	Megasphaera elsdenii		Firmicuta (Ph.)	high G+C	1567	M26493		
*189	Mycobacterium bovis	Strain BCG	Firmicuta (Ph.)	high G+C	1536			
190	Mycobacterium kansasii	DSM 43224	Firmicuta (Ph.)	high G+C	(1463)	X15916	PCR	
191	Nocardioides albus	DSM 43109	Firmicuta (Ph.)	high G+C	(1444)		RT	
192	Nocardioides jensenii	DSM 29641	Firmicuta (Ph.)	high G+C	(1443)		RT	
193	Nocardioides luteus	NCIB 11455	Firmicuta (Ph.)	high G+C	(1441)		RT	
194	Pimelobacter simplex	NCIB 8929	Firmicuta (Ph.)	high G+C	(1444)		RT	
195	Propionibacterium acidipropionici	DSM 20272	Firmicuta (Ph.)	high G+C	(1351)		RT	
196	Propionibacterium acnes	DSM 1897	Firmicuta (Ph.)	high G+C	(1359)		RT	
197	Propionibacterium freudenreichii	DSM 20271	Firmicuta (Ph.)	high G+C	(1468)		RT	
198	Propionibacterium jensenii	DSM 20535	Firmicuta (Ph.)	high G+C	(1365)		RT	
199	Propionibacterium propionicus	DSM 43307	Firmicuta (Ph.)	high G+C	(1214)		RT	
200	Propionibacterium thoenii	DSM 20276	Firmicuta (Ph.)	high G+C	(1365)		RT	
*201	Streptomyces ambofaciens	Operon rrnD	Firmicuta (Ph.)	high G+C	1528	M27245		
202	Streptomyces coelicolor	Strain A3 (2) M145, Operon rrnD	Firmicuta (Ph.)	high G+C	1526	Y00411		
*203	Streptomyces lividans	Strain TK21 Operon rrnB	Firmicuta (Ph.)	high G+C	1531			

Table 1. continued.

Nr (a)	Species	Specification (b)	Taxonomic position (c)		Length (d)	Access. (e)	Method (f)	Remark
204	Terrabacter tumescens	NCIB 8914	Firmicuta (Ph.)	high G+C	(1444)		RT	
205	Tsukamurella paurometabolum	DSM 20162, NCTC 10741	Firmicuta (Ph.)	high G+C	(1341)			
206	Heliobacterium chlorum		Firmicuta (Ph.)	photosynthetic org.	1522	M11212		
*207	Thermus thermophilus	Strain HB8	Radioresistant micrococci & rel.(Ph.)	Thermophiles group	1515	X07998		
*208	Deinococcus radiodurans	Strain UWO 298	Radioresistant micrococci & rel.(Ph.)	Deinococcus group	1502	M21413		
209	Bacteroides fragilis	ATCC 25285	Bacteroides,Flavobact.,Cytophaga(Ph.)	Bacteroides	1533	M11656		
210	Cytophaga heparina	IFO 12017 (ATCC 13125)	Bacteroides,Flavobact.,Cytophaga(Ph.)	Flavobacterium group	1528	M11657		
211	Chlamydia psittaci	Strain 6BC	Chlamydiae (Ph.)		1556	M13769		
212	Chloroflexus aurantiacus	J10FL (lyophilized cells)	Green non sulfur bacteria & rel.(Ph.)	Chloroflexus group	1484			
213	Herpetosiphon aurantiacus	ATCC 23779 (frozen cell pellet)	Green non sulfur bacteria & rel.(Ph.)	Chloroflexus group	1483			
214	Thermomicrobium roseum	ATCC 27502 (frozen cell pellet)	Green non sulfur bacteria & rel.(Ph.)	Thermomicrobium group	1525			
215	'Clathrochloris sulfurica'	Strain 1	Green sulfur dependent (Ph.)		(1335)		RT	
216	Anacystis nidulans	Strain 6301 (Berkeley)	Cyanobacteria		1487	X01296		
217	Thermotoga maritima	Strain MSB 8, DSM 3109	Thermophilic eubacteria		1563			
218	Arhodomonas oleiferhydrans				(1487)	M26631		
219	Desulfomonile tiedjei				(1505)	M26635		
220	Syntrophomonas wolfei				(1532)	M26492		
221	Syntrophospora bryantii				(1532)	M26491		
	PLASTIDS							
*222	Zea mays chl.		Angiospermae (Ph.)	Monocotyledoneae (Cl.)	1490	Z00028		
*223	Oryza sativa chl.		Angiospermae (Ph.)	Monocotyledoneae (Cl.)	1491	X15901		
224	Nicotiana tabacum chl.	Variety Bright Yellow 4	Angiospermae (Ph.)	Dicotyledoneae (Cl.)	1486	V00165		
*225	Glycine max chl.		Angiospermae (Ph.)	Dicotyledoneae (Cl.)	1470	X06428		
226	Marchantia polymorpha chl.		Bryophyta (Ph.)	Hepaticae (Cl.)	1496	X04465		
227	Chlamydomonas reinhardtii chl.		Chlorophyceae (Cl.)	Volvocales (O.)	1475	X03269		
*228	Chlamydomonas moewusii chl.		Chlorophyceae (Cl.)	Volvocales (O.)	1481			
*229	Chlamydomonas eugametos chl.		Chlorophyceae (Cl.)	Volvocales (O.)	1481			
*230	Chlorella ellipsoidea chl.	Strain IAM-C87	Chlorophyceae (Cl.)	Chlorococcales (O.)	1583	X12742		
*231	Chlorella vulgaris chl.	Strain 211-11b	Chlorophyceae (Cl.)	Chlorococcales (O.)	1494	X16579	PCR	
232	Ochromonas danica chr.	Strain 933-7	Mastigomycotina (Ph.)	Oomycetes (Cl.)	(1355)		RT	
233	Euglena gracilis chl.	Strain Z	Euglenozoa (Assemblage)	Euglenophyta	1491			
	MITOCHONDRIA							
*234	Homo sapiens mit.	Placenta	Chordata (Ph.)	Mammalia (Cl.)	954	V00710		
235	Pan troglodytes mit.	Cultured cells	Chordata (Ph.)	Mammalia (Cl.)	948			
236	Pan paniscus mit.	Frozen tissue	Chordata (Ph.)	Mammalia (Cl.)	949			
237	Gorilla gorilla mit.	Frozen tissue	Chordata (Ph.)	Mammalia (Cl.)	948			
238	Pongo pigmaeus mit.	Frozen tissue	Chordata (Ph.)	Mammalia (Cl.)	950			
239	Mus musculus mit.	L-cell, C2-1 line	Chordata (Ph.)	Mammalia (Cl.)	956			
240	Rattus norvegicus mit.	Liver	Chordata (Ph.)	Mammalia (Cl.)	953	V00680		
*241	Rattus norvegicus mit.	Variant A	Chordata (Ph.)	Mammalia (Cl.)	954	X14848		
242	Bos taurus mit.	Heart	Chordata (Ph.)	Mammalia (Cl.)	955	V00654		
*243	Rana catesbeiana mit.		Chordata (Ph.)	Amphibia (Cl.)	937	X12841		
244	Xenopus laevis mit.		Chordata (Ph.)	Amphibia (Cl.)	819	X02890		
245	Drosophila yakuba mit.	Stock 2371.6, Ivory coast	Arthropoda (Ph.)	Insecta (Cl.)	789	X03240		
246	Drosophila virilis mit.	Stock 2375.8, Chile	Arthropoda (Ph.)	Insecta (Cl.)	789			
*247	Strongylocentrotus purpuratus mit.		Echinodermata (Ph.)	Echinoidea (Cl.)	865	X12631		
*248	Paracentrotus lividus mit.	Fresh eggs	Echinodermata (Ph.)	Echinoidea (Cl.)	878	J04815		
249	Zea mays mit.		Spermatophyta (Ph.)	Monocotyledoneae (Cl.)	1964	X00794		
250	Zea mays mit.		Spermatophyta (Ph.)	Monocotyledoneae (Cl.)	1967	M10248		
251	Zea diploperennis mit.	Seedlings	Spermatophyta (Ph.)	Monocotyledoneae (Cl.)	1964			
252	Triticum aestivum mit.		Spermatophyta (Ph.)	Monocotyledoneae (Cl.)	1955	K01229		
*253	Glycine max mit.	Cultivar Williams	Spermatophyta (Ph.)	Dicotyledoneae (Cl.)	1990	M16859		
254	Oenothera sp. mit.		Spermatophyta (Ph.)	Dicotyledoneae (Cl.)	1897			
*255	Chlamydomonas reinhardtii mit.		Chlorophyceae (Cl.)	Volvocales (O.)	1199	M22648		j
*256	Saccharomyces cerevisiae mit.	Strain MH41-7B	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)		V00702		
257	Saccharomyces cerevisiae mit.	Strain D273-10B, wild-type	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1686	V00704		
*258	Saccharomyces cerevisiae mit.	Strain 777-3A	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1651	X07799		
259	Saccharomyces cerevisiae mit.	Strain KL14-4A	Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1649	X07800		
*260	Aspergillus nidulans mit.	Strain paba A1, bi A1	Ascomycotina (Ph.)	Plectomycetes (Cl.)	1554			
*261	Schizosaccharomyces pombe mit.		Ascomycotina (Ph.)	Hemiascomycetes (Cl.)	1422	X15738		
*262	Podospora anserina mit.	Race A	Ascomycotina (Ph.)	Plectomycetes (Cl.)	1978	X14734		
263	Tetrahymena pyriformis mit.	Strain ST	Ciliata (Ph.)	Holotricha (O.)	1659	X05203		
264	Tetrahymena pyriformis mit.	Strain ST	Ciliata (Ph.)	Holotricha (O.)	1668	M12714		k
265	Paramecium primaurelia mit.	Stock 513 (Edinburgh)	Ciliata (Ph.)	Holotricha (O.)	1691?	K01750		
266	Paramecium tetraurelia mit.	Stock 51 (Edinburgh)	Ciliata (Ph.)	Holotricha (O.)	1690?	K01751		
267	Trypanosoma brucei mit.	Strain 427	Euglenozoa (Assemblage)	Kinetoplastidea	611	V01390		
268	Crithidia fasciculata mit.		Euglenozoa (Assemblage)	Kinetoplastidea	612	X02548		
*269	Leishmania tarentolae mit.		Euglenozoa (Assemblage)	Kinetoplastidea	610			
*270	Leptomonas sp. mit.		Euglenozoa (Assemblage)	Kinetoplastidea	611			

Table 2. Number of formatted disks to be sent in order to obtain a copy of the database.

Disk type		Database format (see text)		
Size	Capacity	Format 1	Format 2	Format 3
5.25″	DSDD (360 Kbytes)	15	4	2
5.25″	DSHD (1.2 Mbytes)	5	2	1
3.5″	DSDD (720 Kbytes)	8	2	1
3.5″	DSHD (1.44 Mbytes)	4	1	1

Footnotes to Table 1

a) This number corresponds with the literature reference and is preceded by an asterisk if the sequence is printed in the alignment. The same number, and the initials of the species name, precede or follow the sequence on each alignment page. Identical numbers, followed by a different lower case character, are attributed to srRNAs from related species, or from different strains of the same species, that have the same sequence (e.g. *Tetrahymena canadensis* and *Tetrahymena borealis*). In such cases only one sequence is listed in our computer file.

b) This column contains the following data, if specified by the authors:
- Strain name for laboratory animals, (cultivated) variety for plants, culture collection and strain number in the case of microorganisms.
- Tissue from which the DNA used for cloning or amplification was extracted in the case of differentiated organisms.
- Ribosomal RNA operon to which belongs the cloned srRNA gene in the case of bacteria.

c) The taxonomic position is described according to the following references: 277 for the metazoa (No. 1 to 14), 278 for the higher plants (No. 15 to 20), 279 for the algae (No. 21 to 27), 280 for the fungi (No. 28 to 33). The taxonomic position of the protista (No. 34–62) is described according to Wetzel (281) for the species numbered 34–47 and 49–56, but according to Corliss (282) for Prorocentrum micans (No. 48) and for Euglenozoa, Microsporida and Polymastigotes (57–62). The archaebacteria are classified according to Woese (283). The classification of the eubacteria is according to Stackebrandt et al. (284) for the Proteobacteria, according to Wayne et al. (285) for the Firmicuta, and according to Woese (283) for the remaining taxa. We have no information yet on the taxonomic position of species 218–221. Taxon designations corresponding to an established taxonomic level are followed by the abbreviation Ph. (phylum), Sph. (subphylum), Cl. (class), O. (order).

d) The srRNA termini are located experimentally (e.g. by S1 nuclease mapping) by some authors, but more often deduced by comparison with structures from related species. In case of length heterogeneity the length of the longest variant is listed. A question mark following the length denotes uncertainty on the location of the termini. A number enclosed in brackets means that the sequence has been determined partially and gives the length of the sequenced area. No length is mentioned for sequences not yet accessible in sequence libraries at the time of writing.

e) Accession number in the EMBL and Genbank nucleotide sequence libraries. The accession number for a sequence is the same in both libraries but there can be a delay before a sequence submitted to one library arrives in the other one.

f) PCR: the DNA was amplified by the polymerase chain reaction.
RT: the srRNA was sequenced by the dideoxynucleotide method using reverse transcriptase.
In the remaining cases DNA was amplified by cloning and sequencing was performed in most cases by the dideoxynucleotide method.

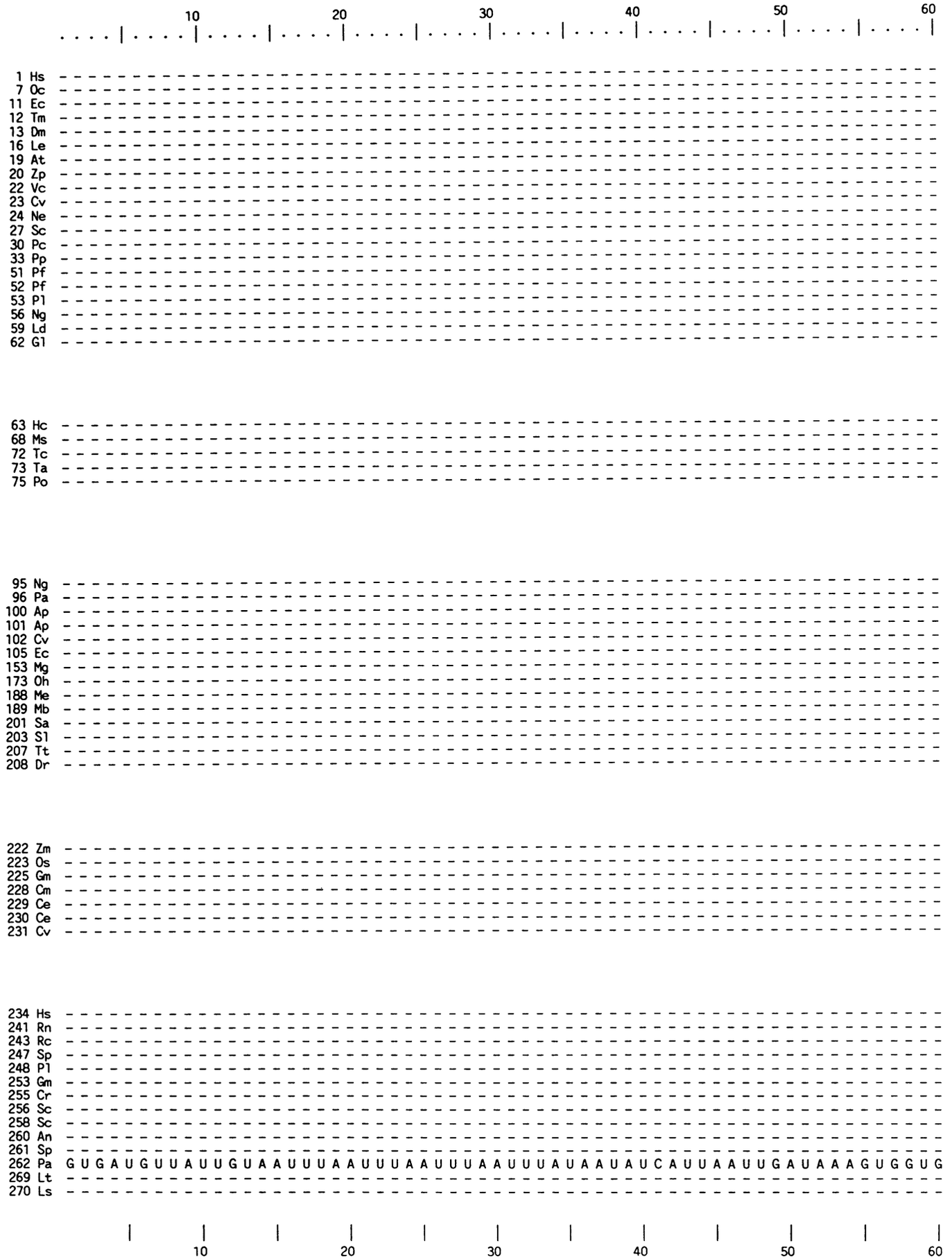
g) Complete data on nucleoside modification can be found in the paper reporting this sequence.

h) Partial data on modified nucleosides are mentioned in this paper or other papers cited therein.

i) Complete data on nucleoside modification can be found in (276), but the sequence listed there misses 1 nucleotide and has been corrected in (105).

j) *Chlamydomonas reinhardtii* mitochondrial srRNA consists of a set of 4 discontinuous fragments, which in the rDNA are interspersed with genes coding for tRNAs, large ribosomal subunit RNA fragments, and proteins. The interruptions between the fragments correspond with alignment positions 239 to 312, 911 to 930, and 2643 to 2811.

k) In the mature RNA, the nucleotides in alignment positions 431 to 618 are deleted by processing.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63 Hc
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Ec 11
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Dm 13
Le 16
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Zp 20
Vc 22
Cv 23
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Sc 27
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Pp 33
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Pf 52
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Ld 59
Gl 62
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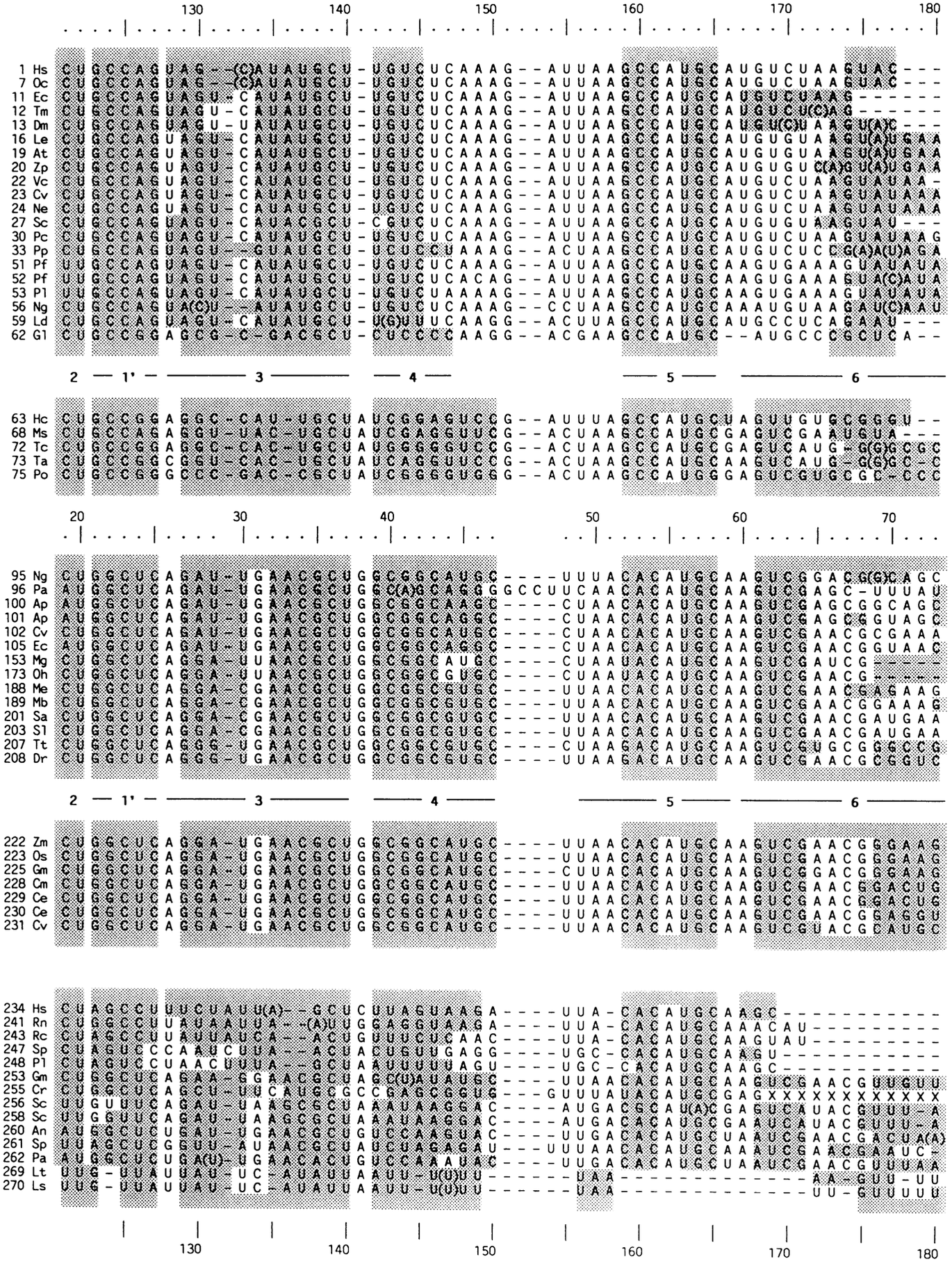

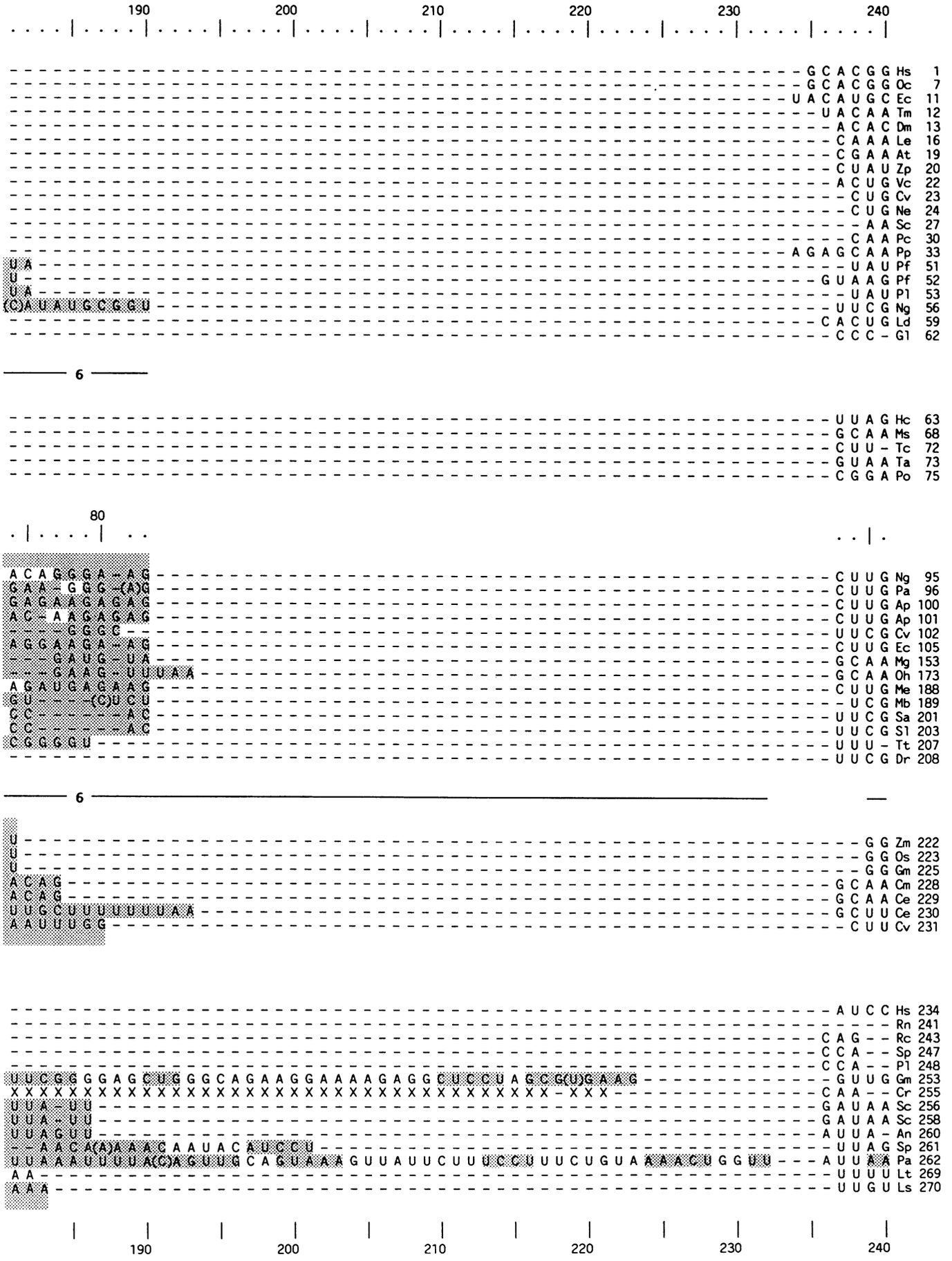
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Ld 59
Gl 62
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Hc 63
Ms 68
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Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
6
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
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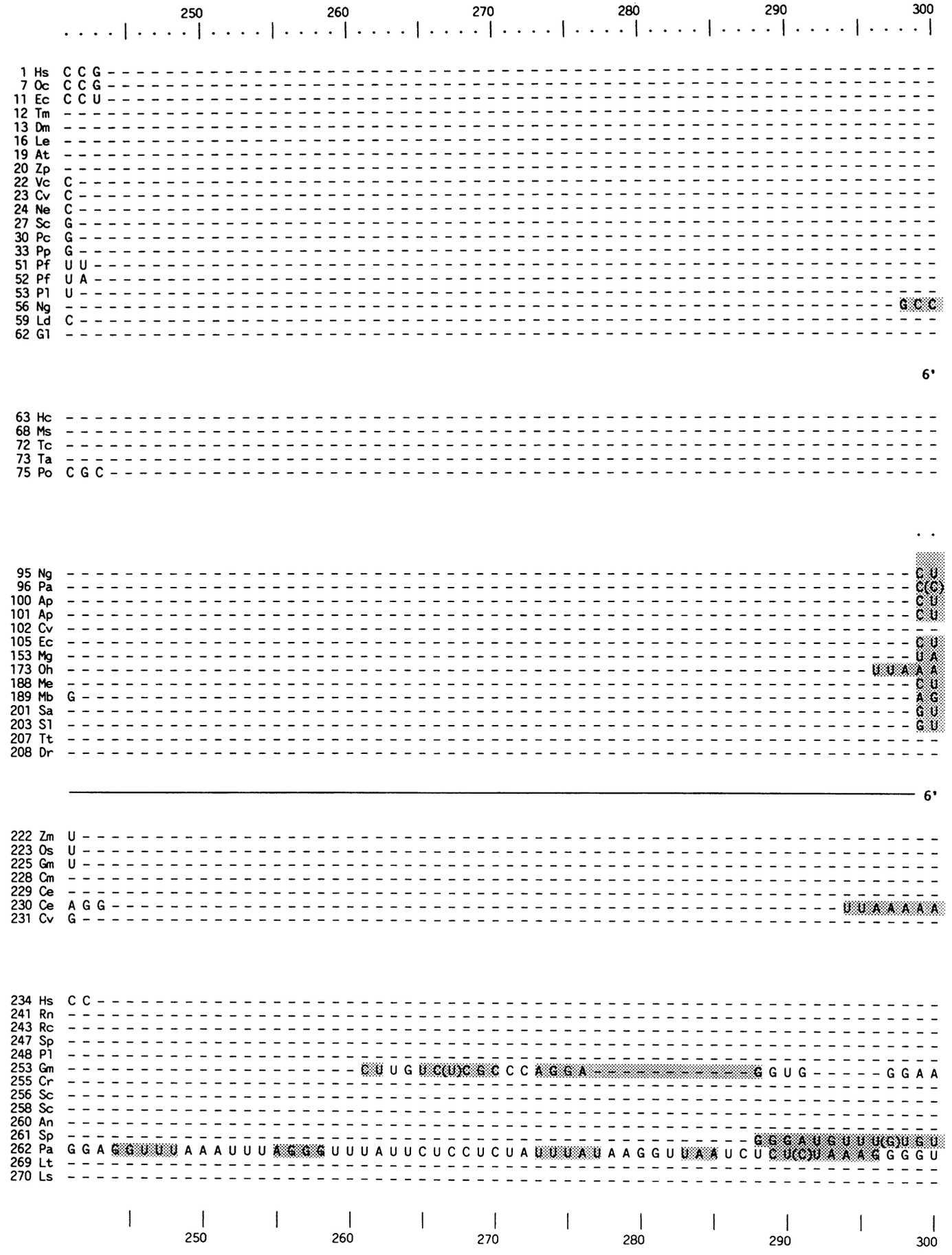
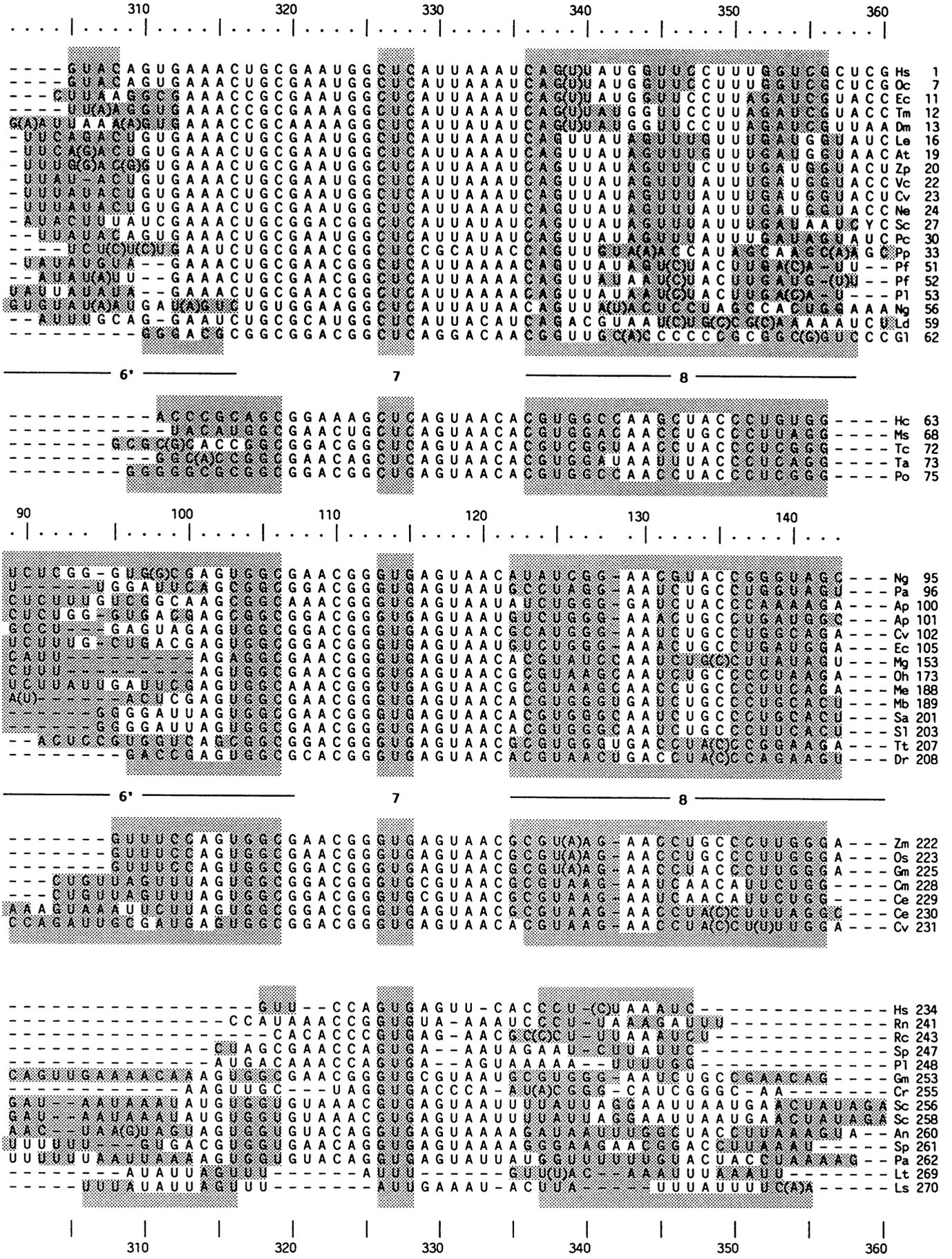
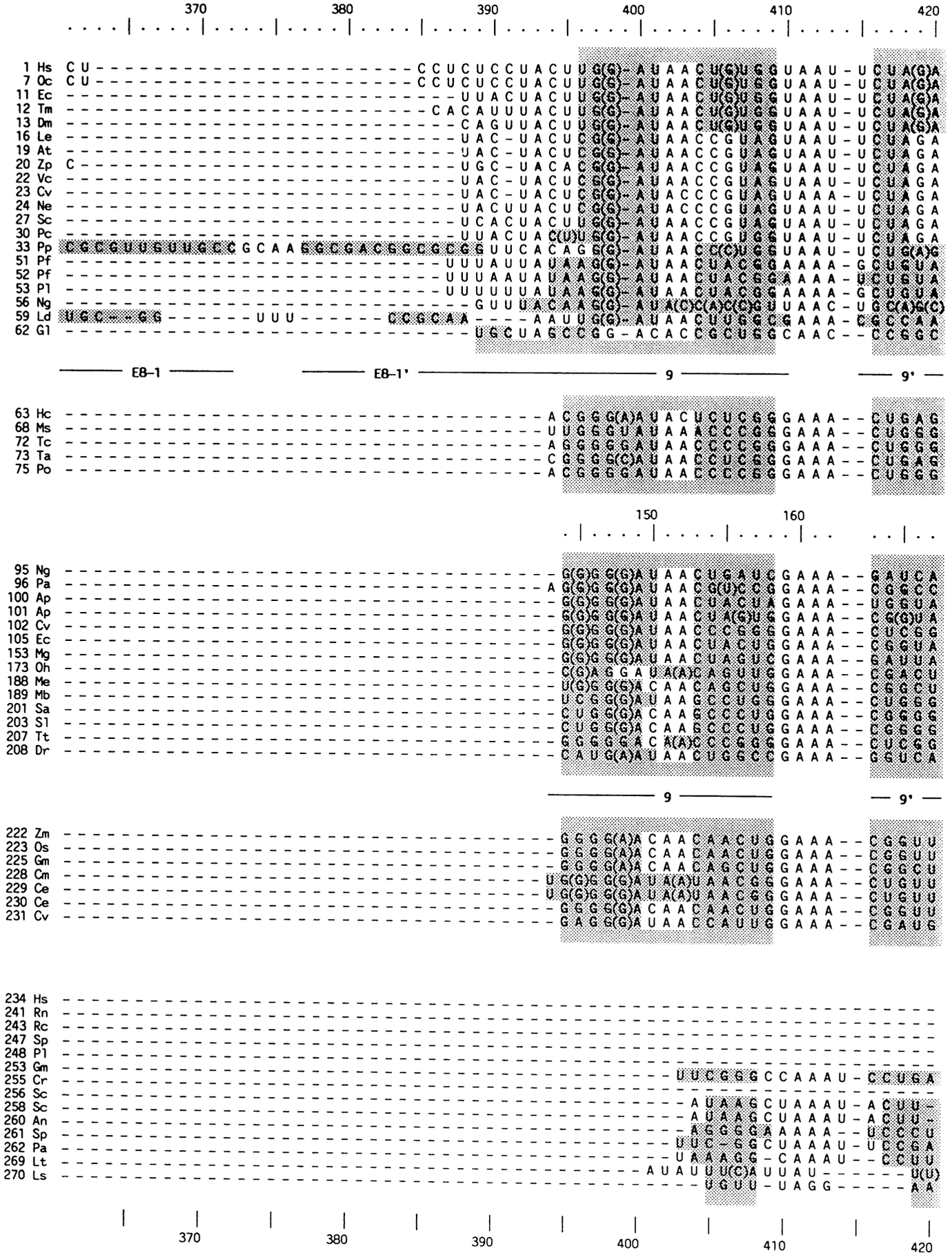
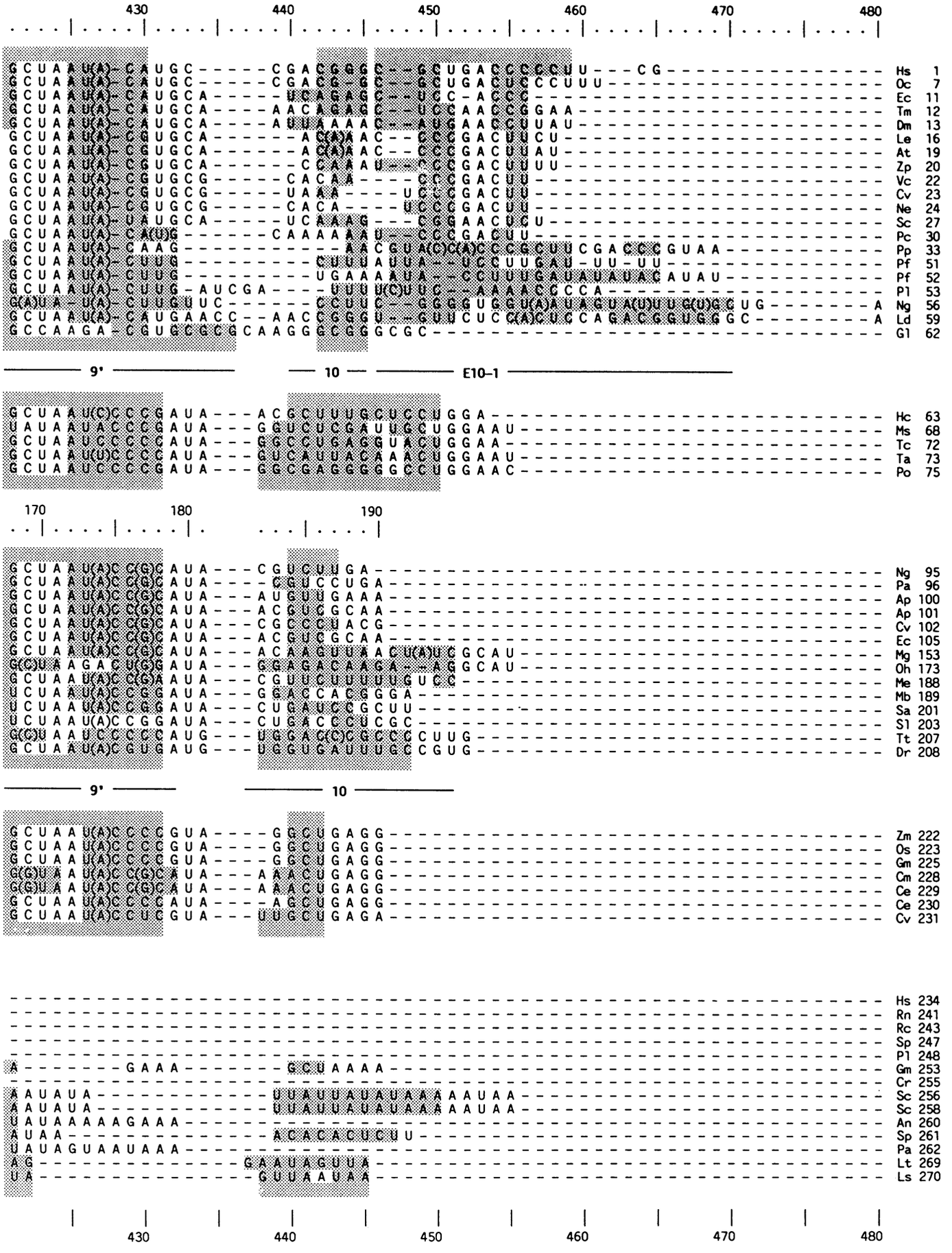
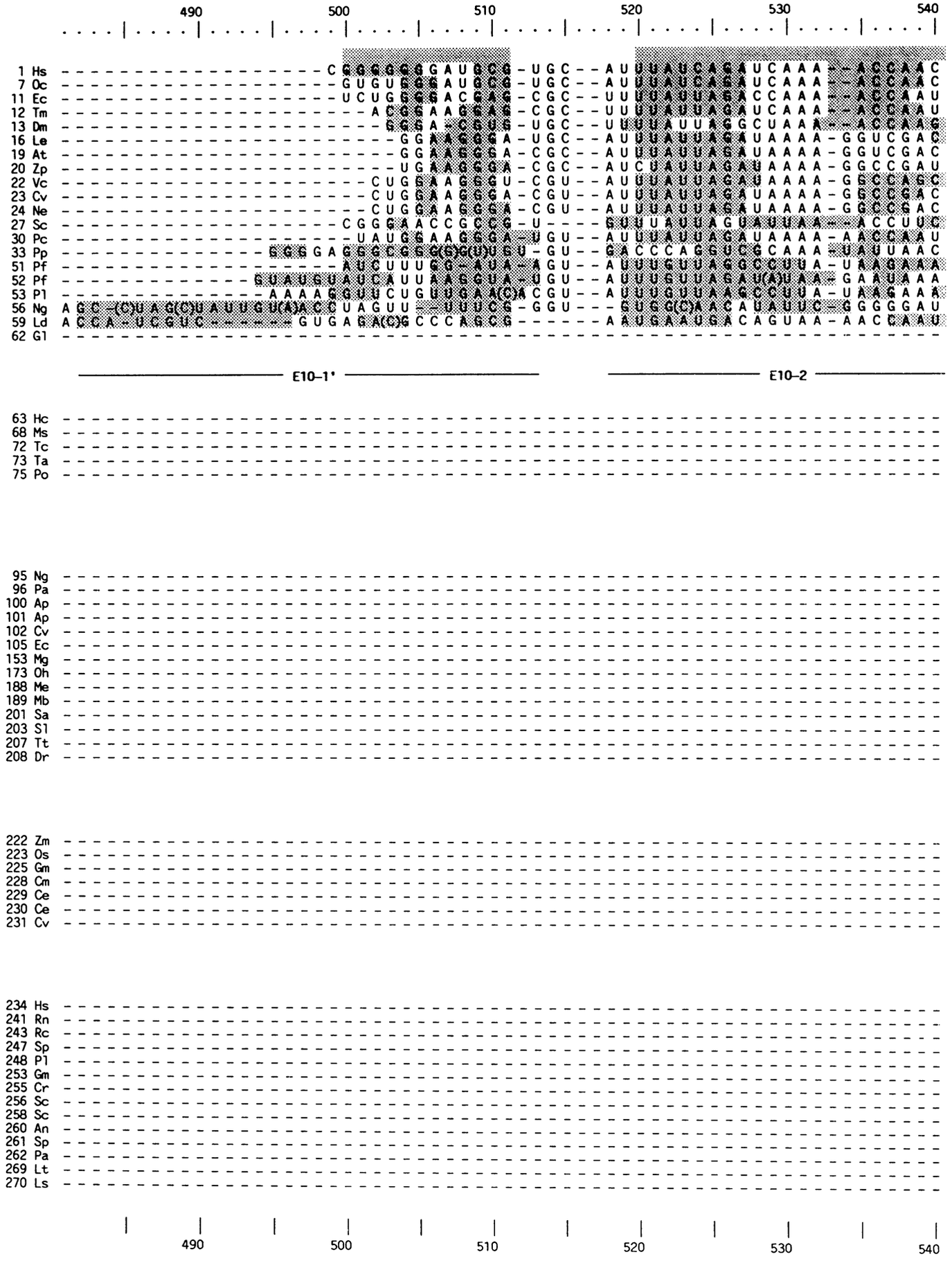
210
220
230
240

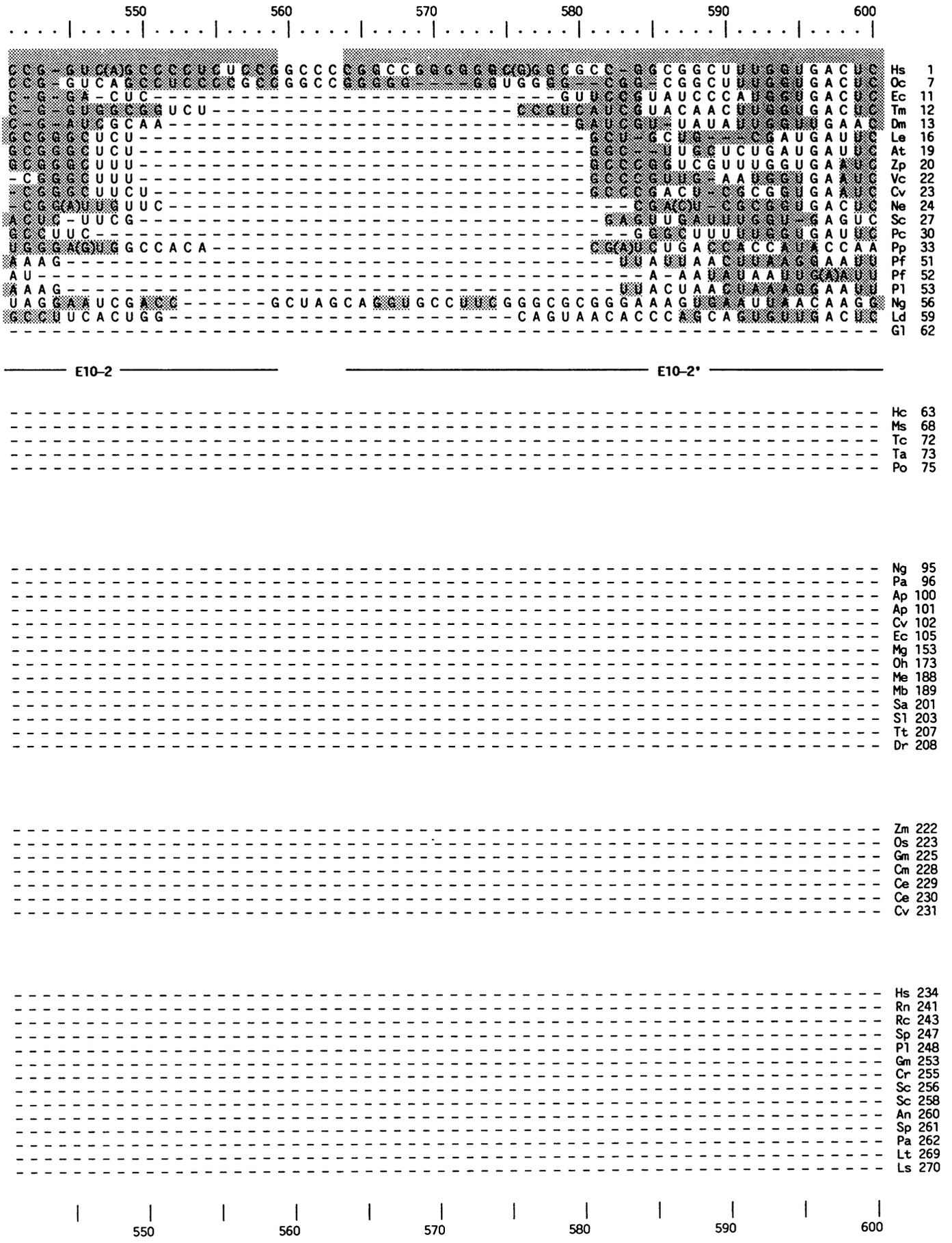

250
260
270
280
290
300
1 Hs C C G
7 Oc C C G
11 Ec C C U
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc C
23 Cv C
24 Ne C
27 Sc G
30 Pc G
33 Pp G
51 Pf U U
52 Pf U A
53 Pl U
56 Ng G C C
59 Ld C
62 Gl
6'
63 Hc
68 Ms
72 Tc
73 Ta
75 Po C G C
95 Ng C U
96 Pa C(C)
100 Ap C U
101 Ap C U
102 Cv
105 Ec C U
153 Mg U A
173 Oh U U A A A
188 Me C U
189 Mb G A G
201 Sa G U
203 Sl G U
207 Tt
208 Dr
6'
222 Zm U
223 Os U
225 Gm U
228 Cm
229 Ce
230 Ce A G G U U A A A A A
231 Cv G
234 Hs C C
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm C U U G U C(U)C G C C C A G G A G G U G G G A A
255 Cr
256 Sc
258 Sc
260 An
261 Sp G G G A U G U U U(G)U G U
262 Pa G G A G G U U U A A A U U U A G G G U U U A U U C U C C U C U A U U U A U A A G G U U A A U C U C U(C)U A A A G G G G U
269 Lt
270 Ls
250
260
270
280
290
300

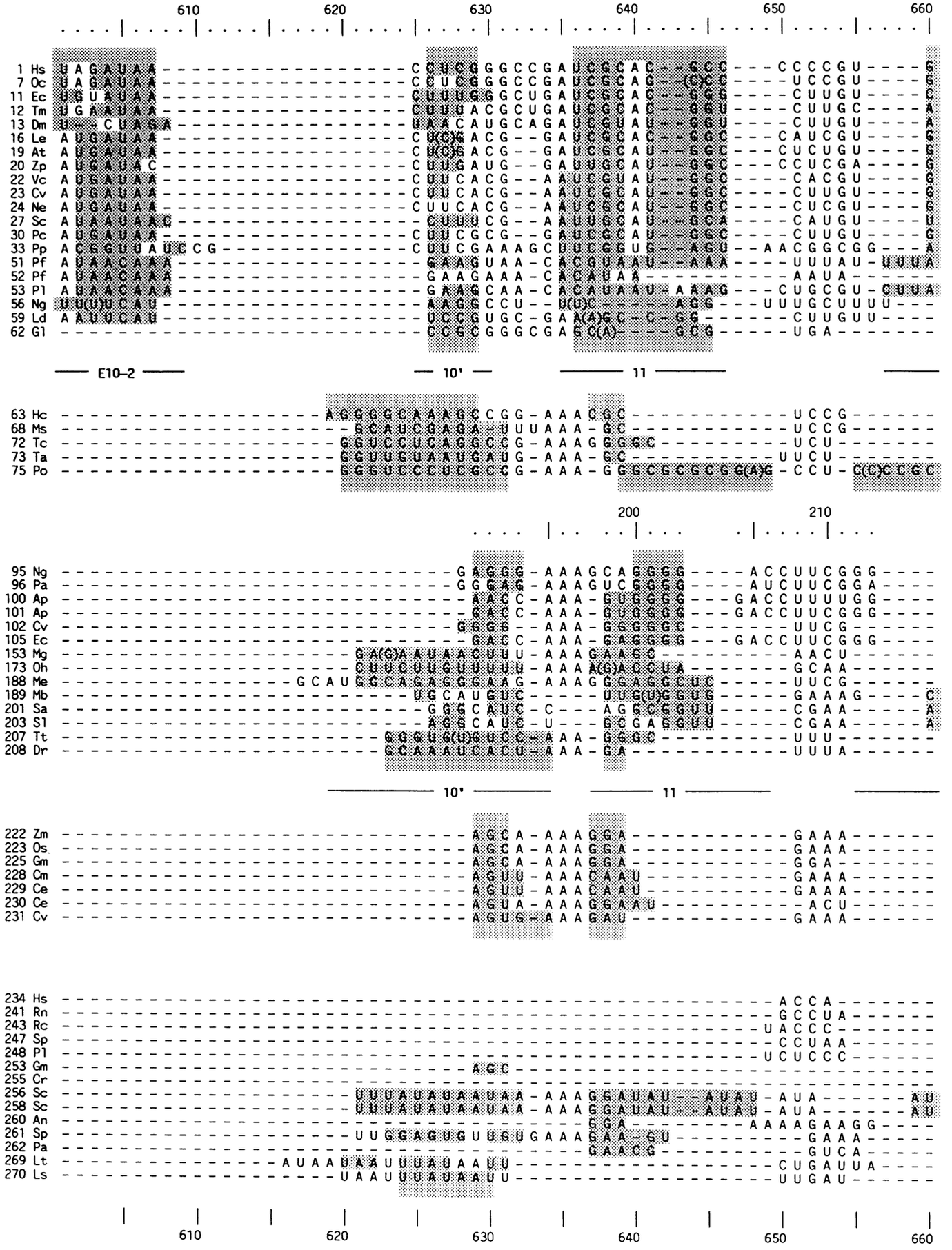

310
320
330
340
350
360
6'
7
8
90
100
110
120
130
140

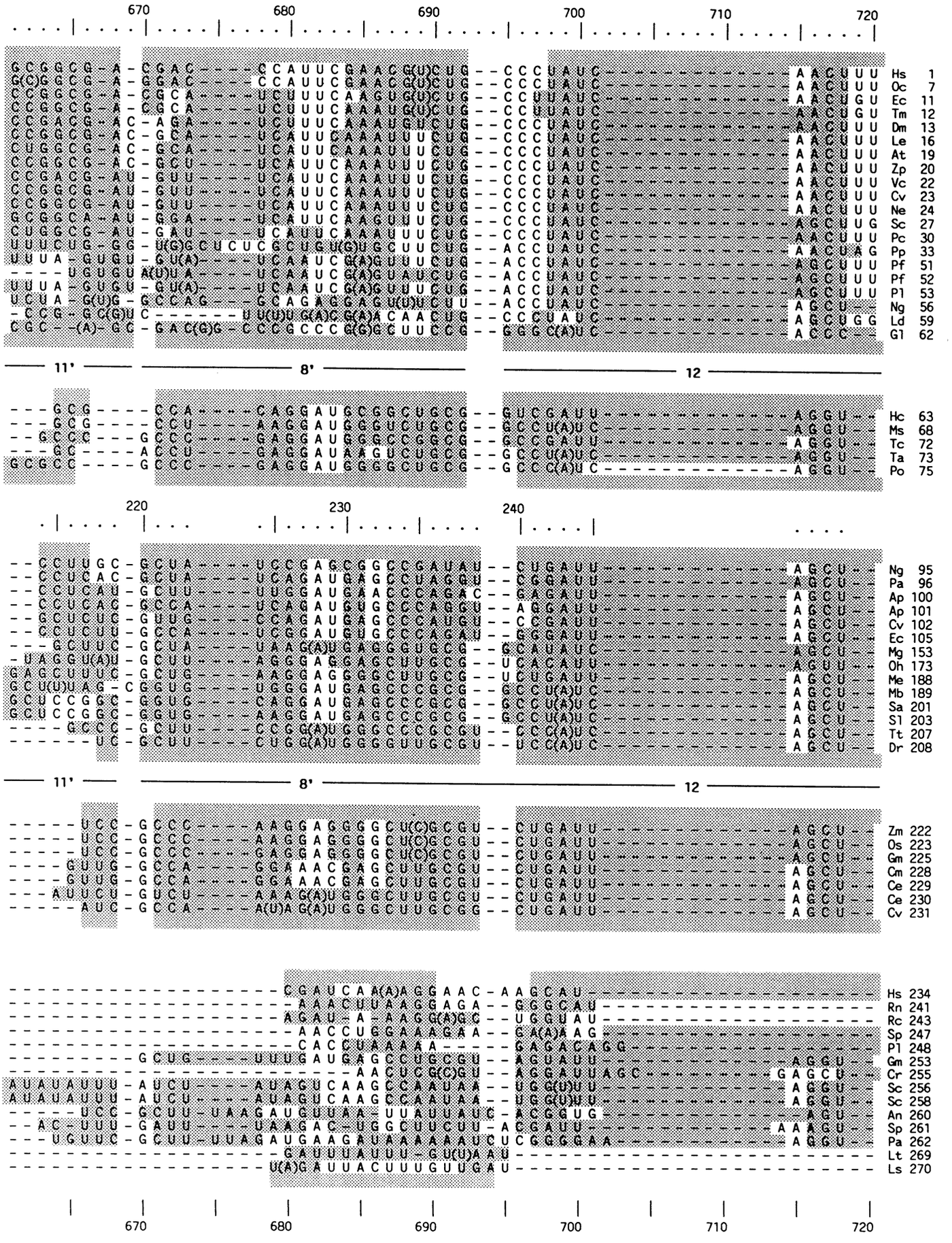

370
380
390
400
410
420
E8-1
E8-1'
9
9'
150
160

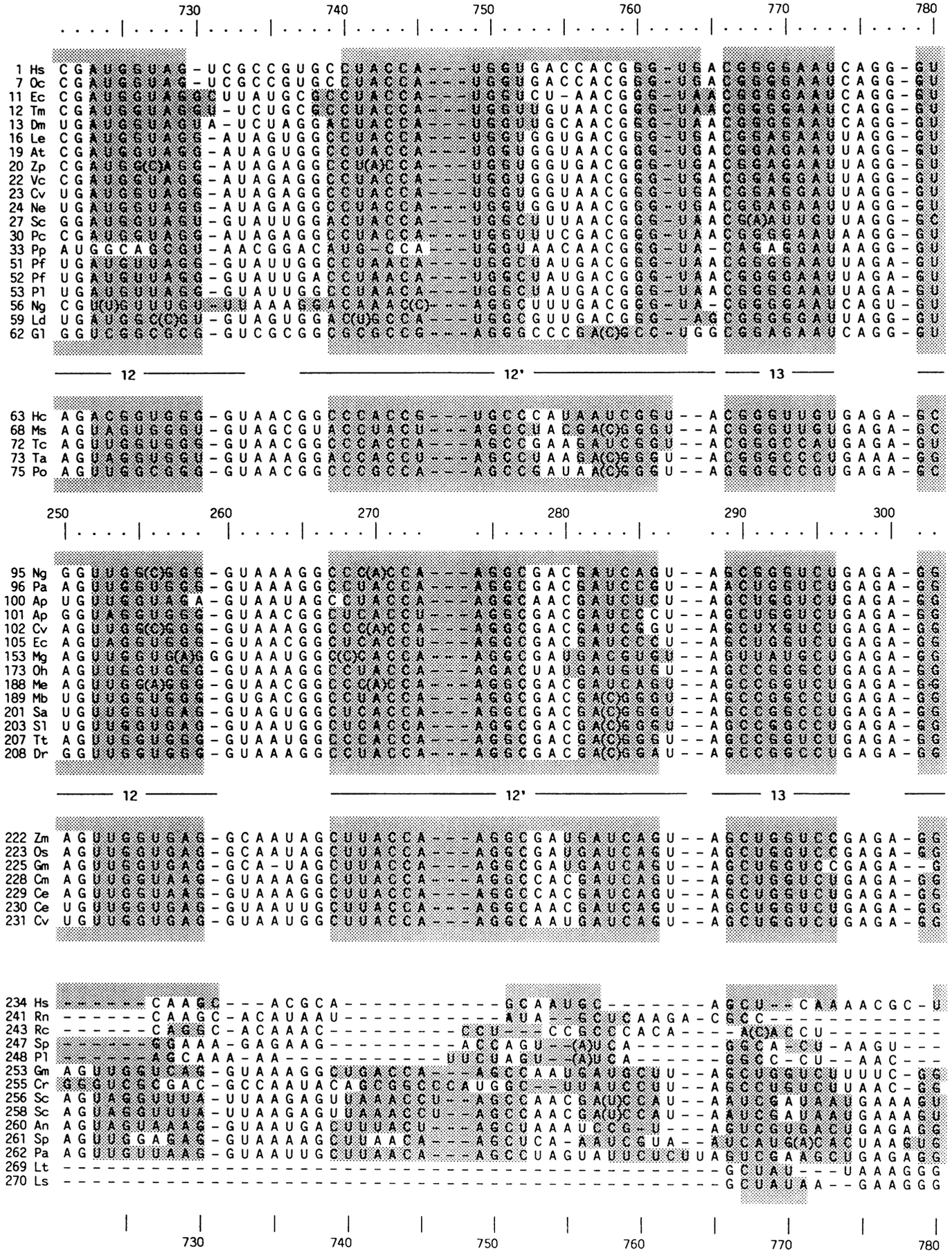

430
440
450
460
470
480
9'
10
E10–1
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
170
180
190
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
9'
10
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
430
440
450
460
470
480

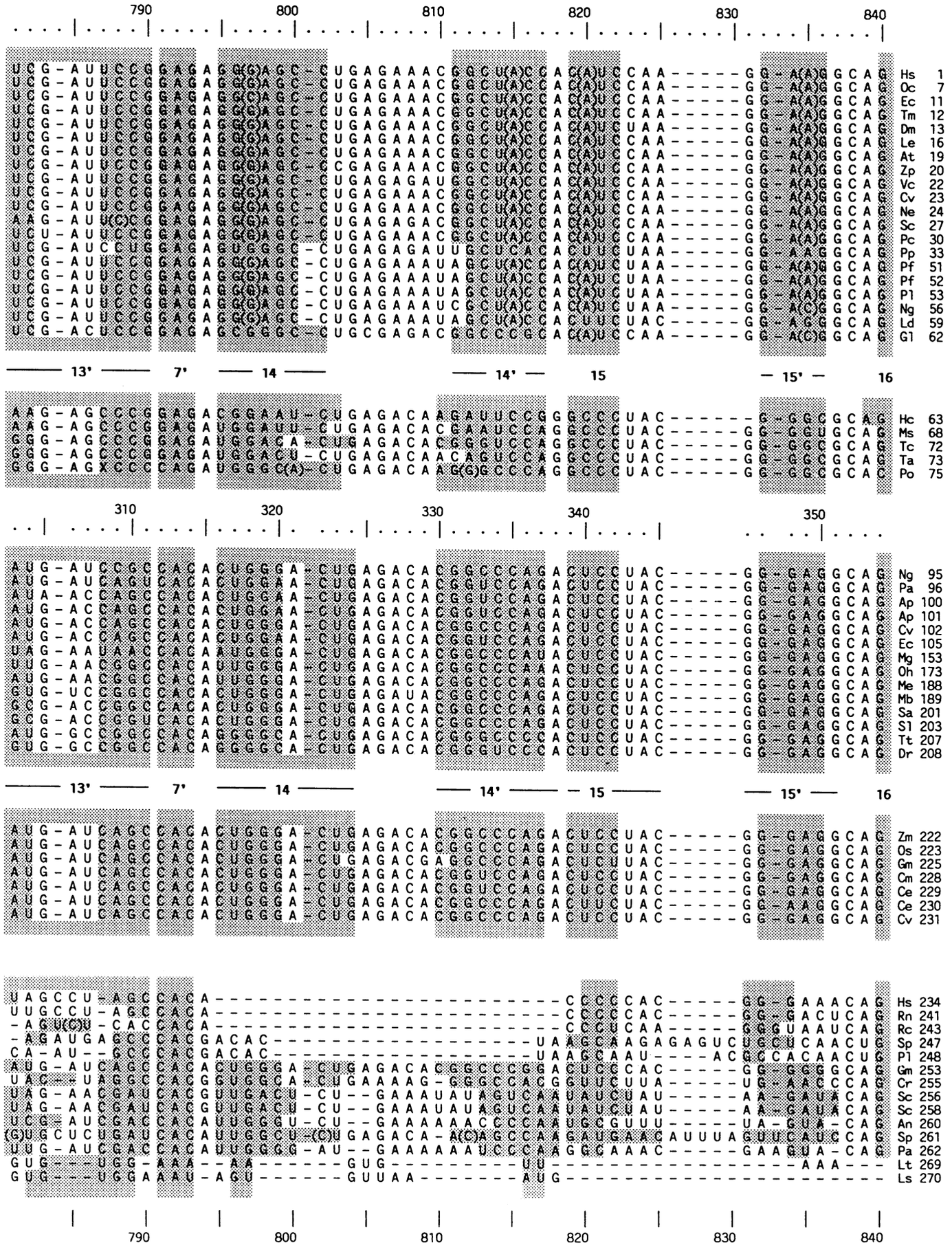

490
500
510
520
530
540
E10–1'
E10–2
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld
62 Gl
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc
258 Sc
260 An
261 Sp
262 Pa
269 Lt
270 Ls

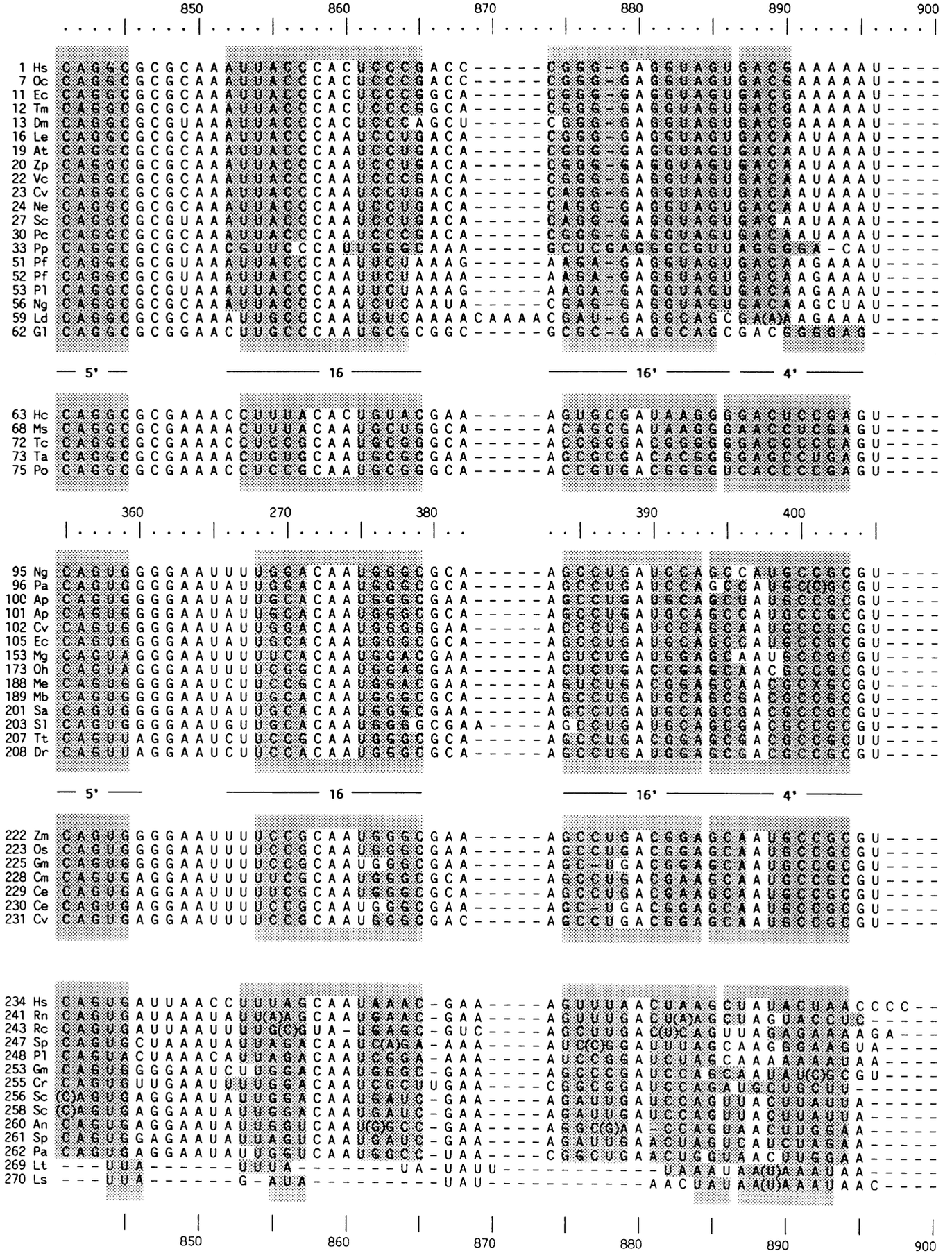

550
560
570
580
590
600
E10–2
E10–2*
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270

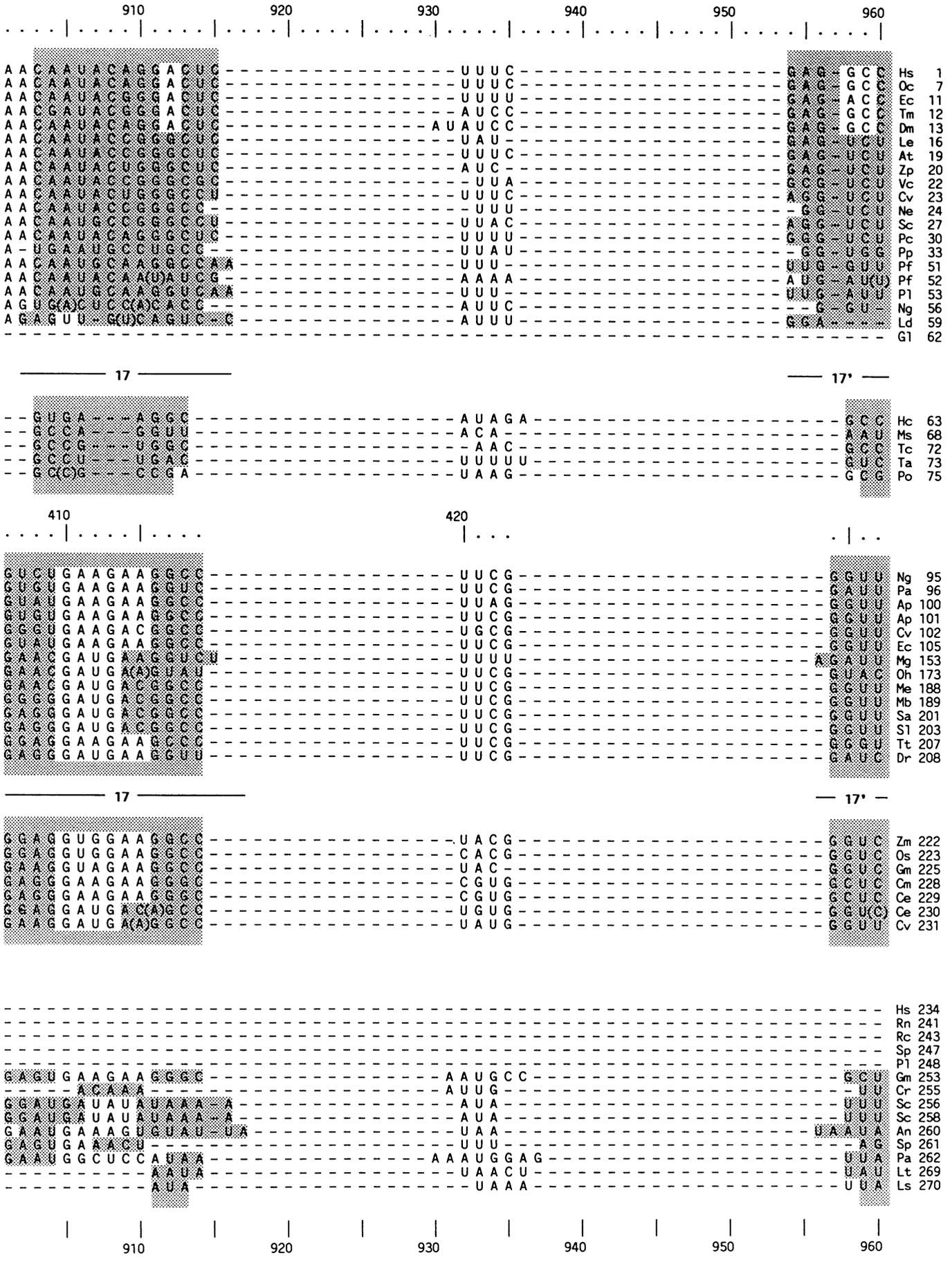

610
620
630
640
650
660
E10–2
10'
11
200
210
10'
11

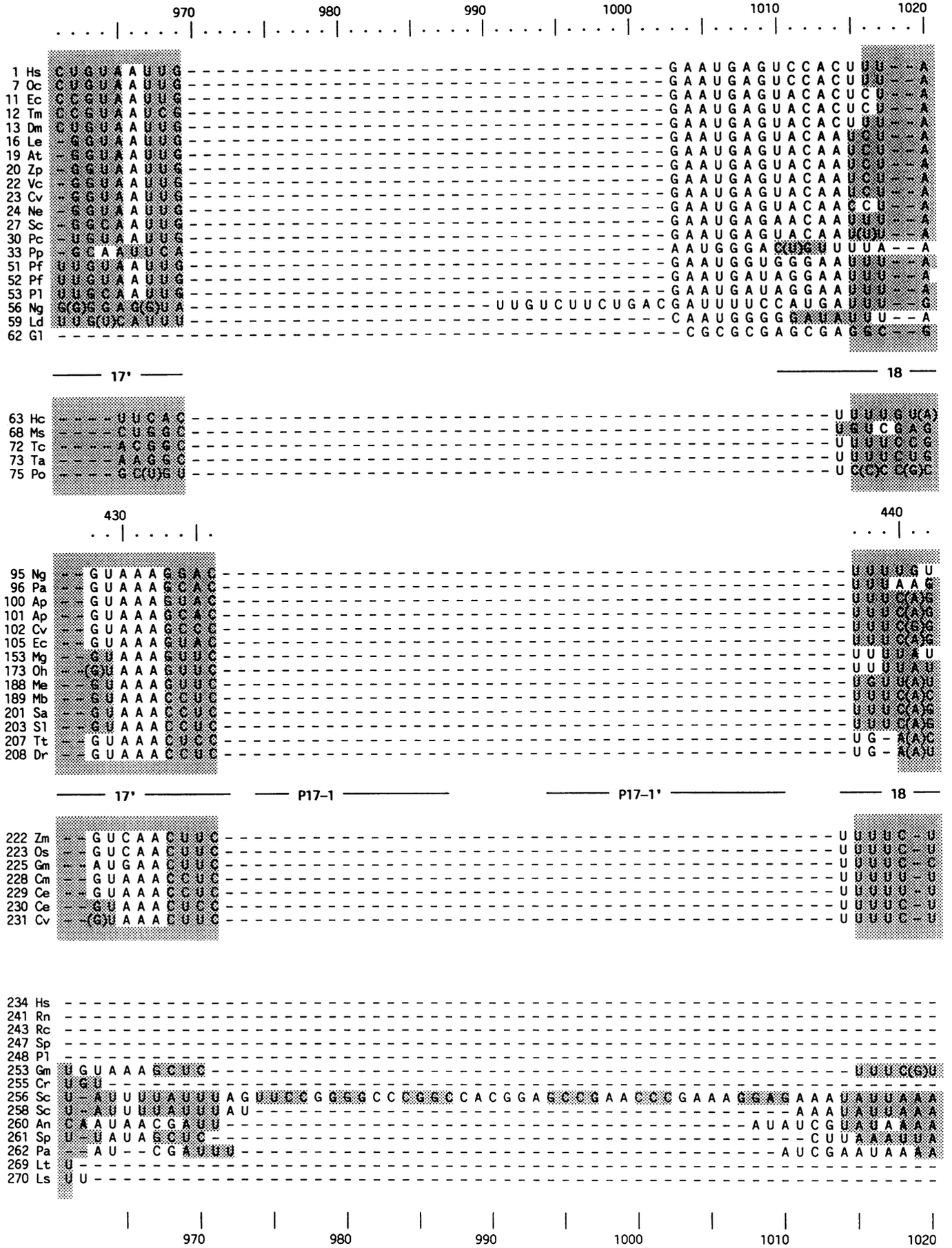

670
680
690
700
710
720
11'
8'
12
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
220
230
240
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270

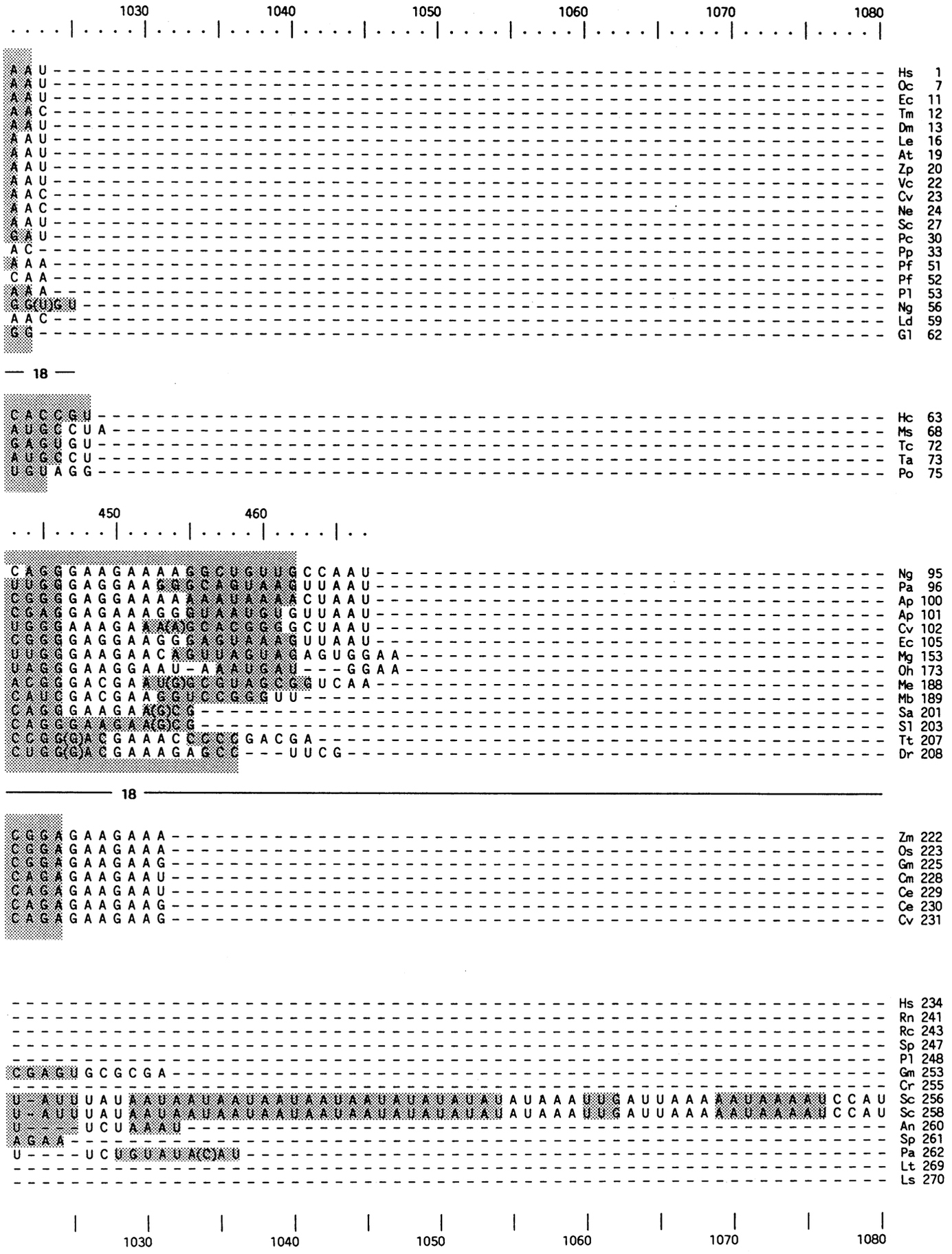

730
740
750
760
770
780
12
12'
13
250
260
270
280
290
300
12
12'
13
730
740
750
760
770
780

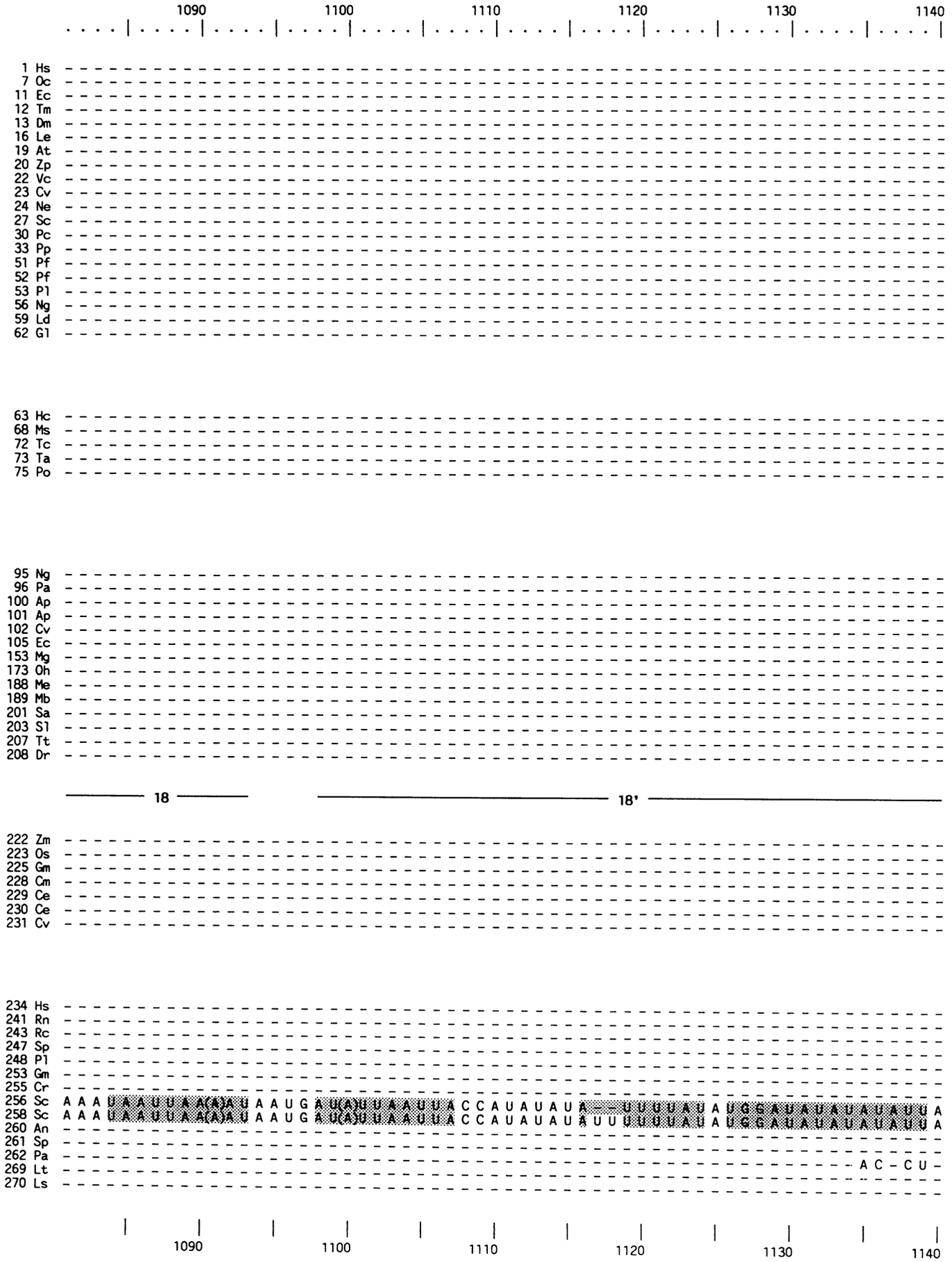

790
800
810
820
830
840
13'
7'
14
14'
15
15'
16
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
310
320
330
340
350
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270


850
860
870
880
890
900
5'
16
16'
4'
360
270
380
390
400


910
920
930
940
950
960
17
17'
410
420
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270


970
980
990
1000
1010
1020
17'
18
430
440
P17–1
P17–1'


1030
1040
1050
1060
1070
1080
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
18
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
450
460
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
18
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
1030
1040
1050
1060
1070
1080


1090
1100
1110
1120
1130
1140
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld
62 Gl
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
18
18'
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc A A A U A A U U A A(A)A U A A U G A U(A)U U A A U U A C C A U A U A U A — — U U U U A U A U G G A U A U A U A U A U U A
258 Sc A A A U A A U U A A(A)A U A A U G A U(A)U U A A U U A C C A U A U A U A U U U U U U A U A U G G A U A U A U A U A U U A
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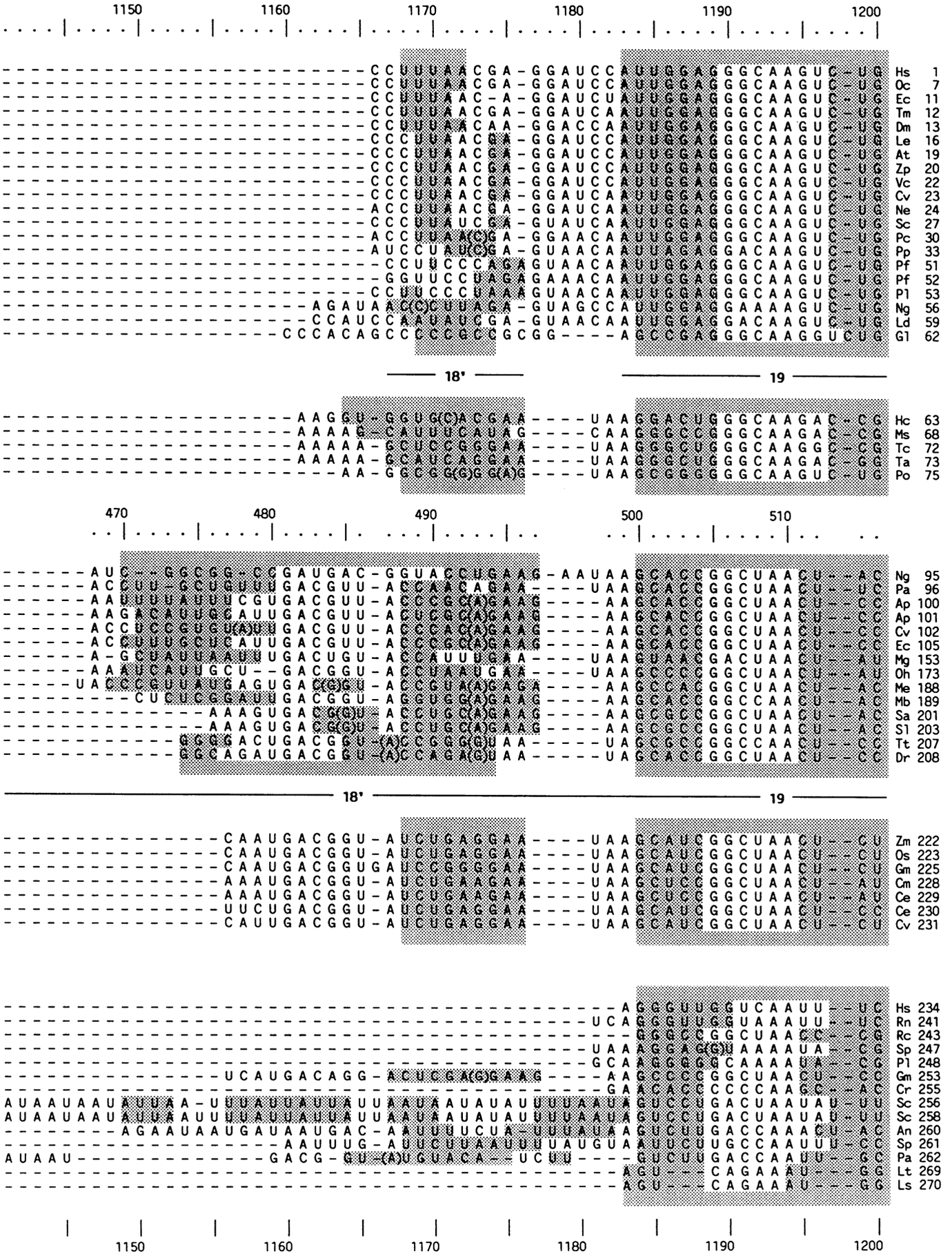
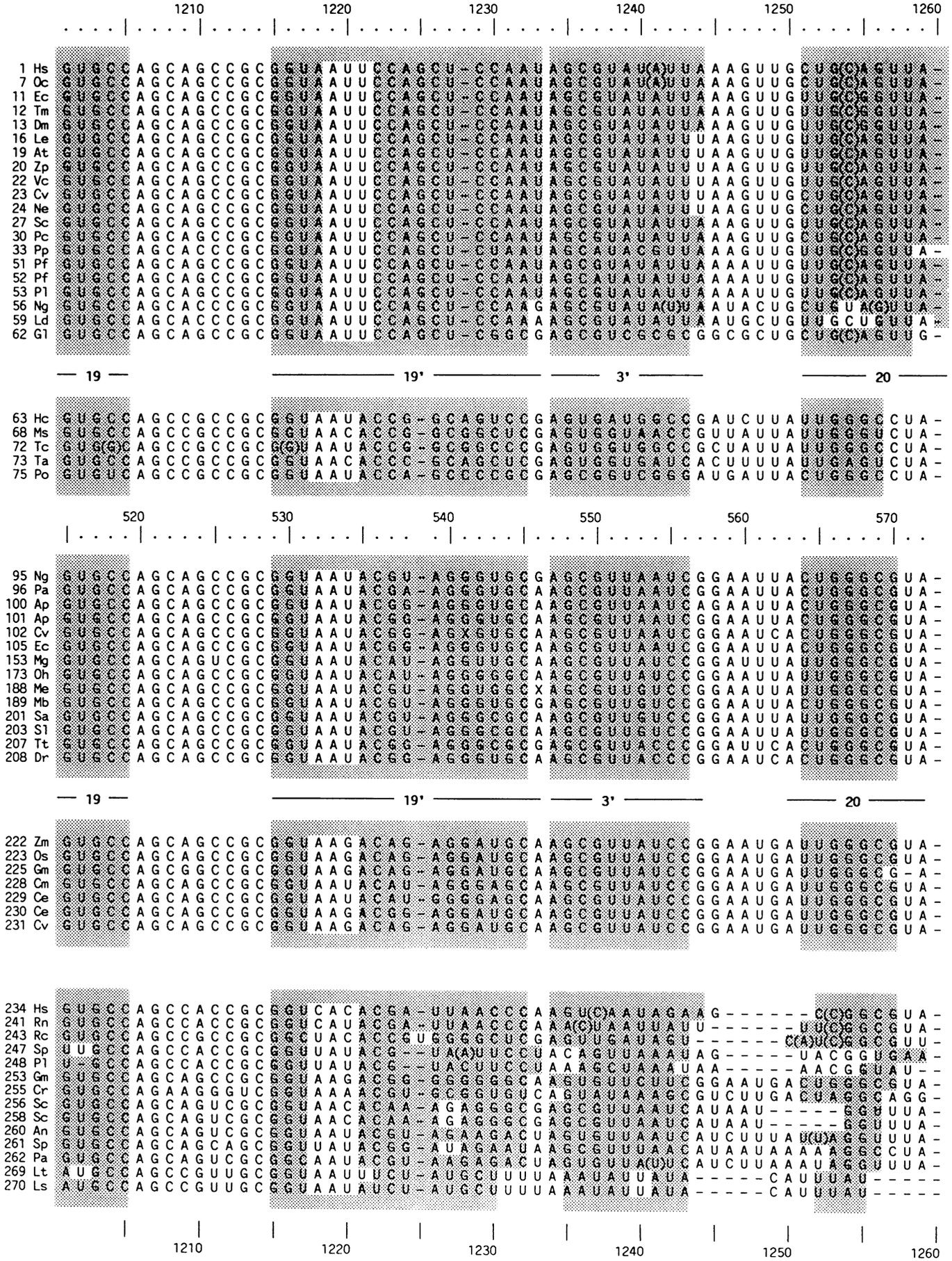
261 Sp
262 Pa
269 Lt A C - C U -
270 Ls
1090
1100
1110
1120
1130
1140


1150
1160
1170
1180
1190
1200
18'
19
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
470
480
490
500
510
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270


1210
1220
1230
1240
1250
1260
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld
62 Gl
— 19 —
19'
3'
20
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
520
530
540
550
560
570
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
— 19 —
19'
3'
20
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc
258 Sc
260 An
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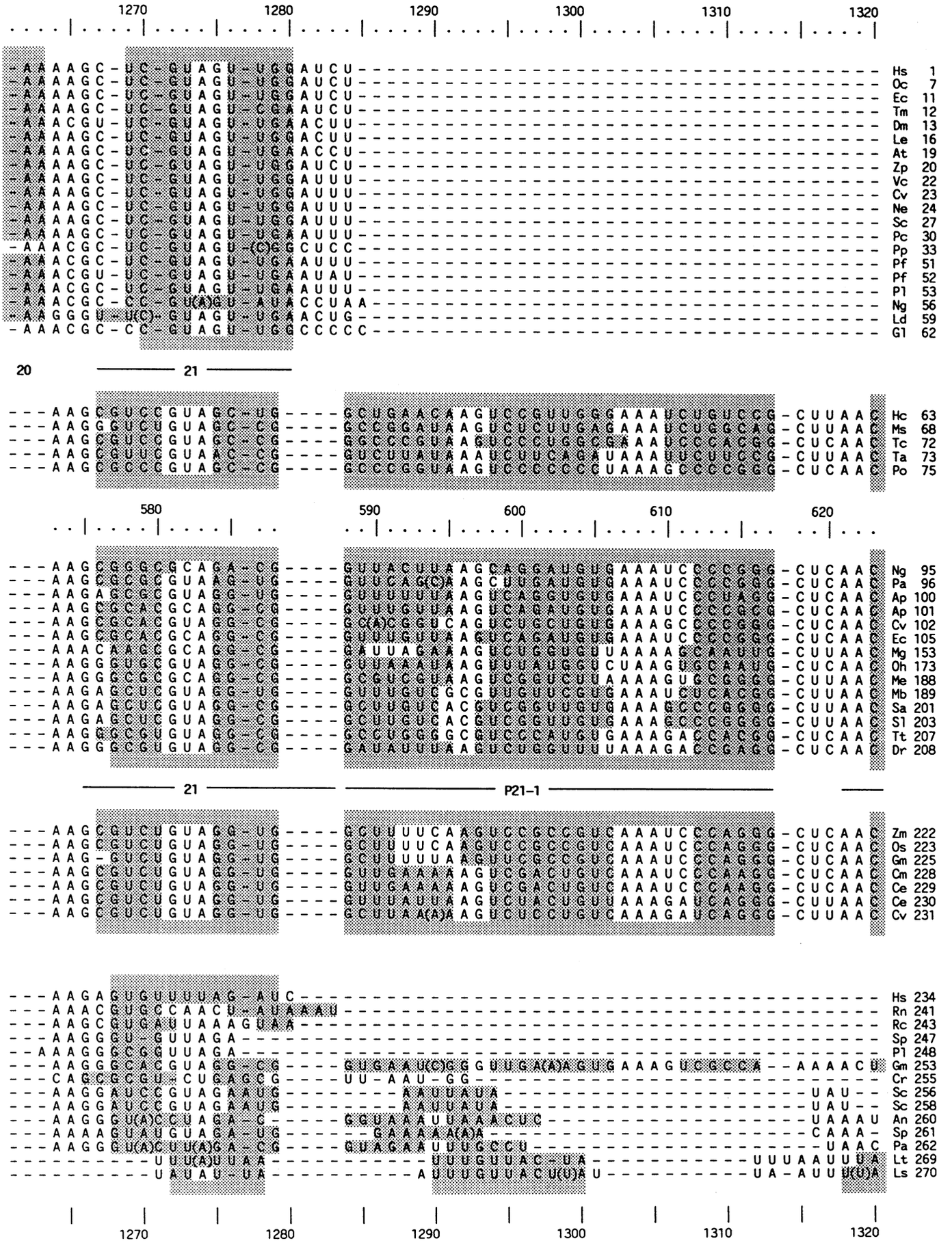
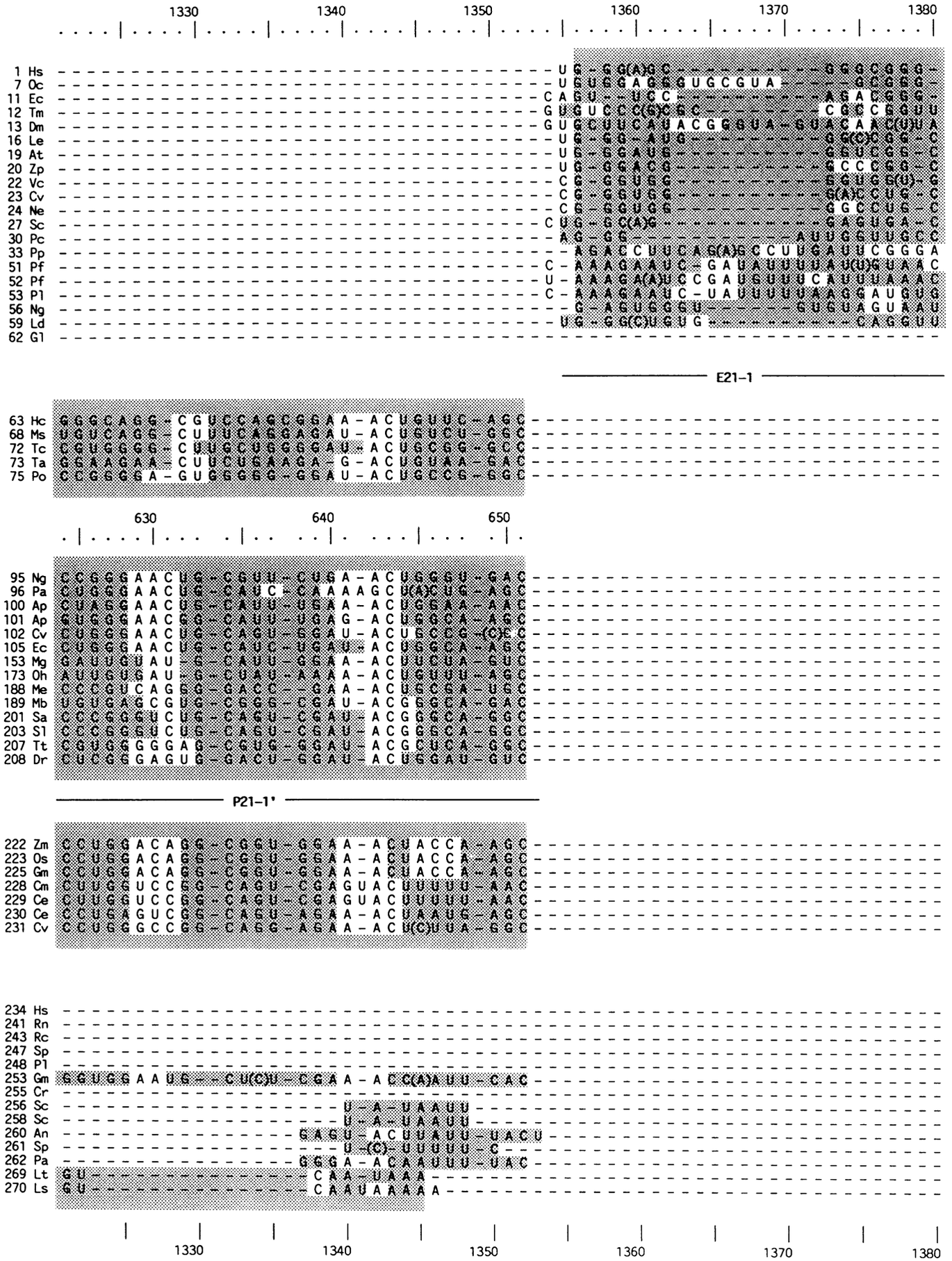
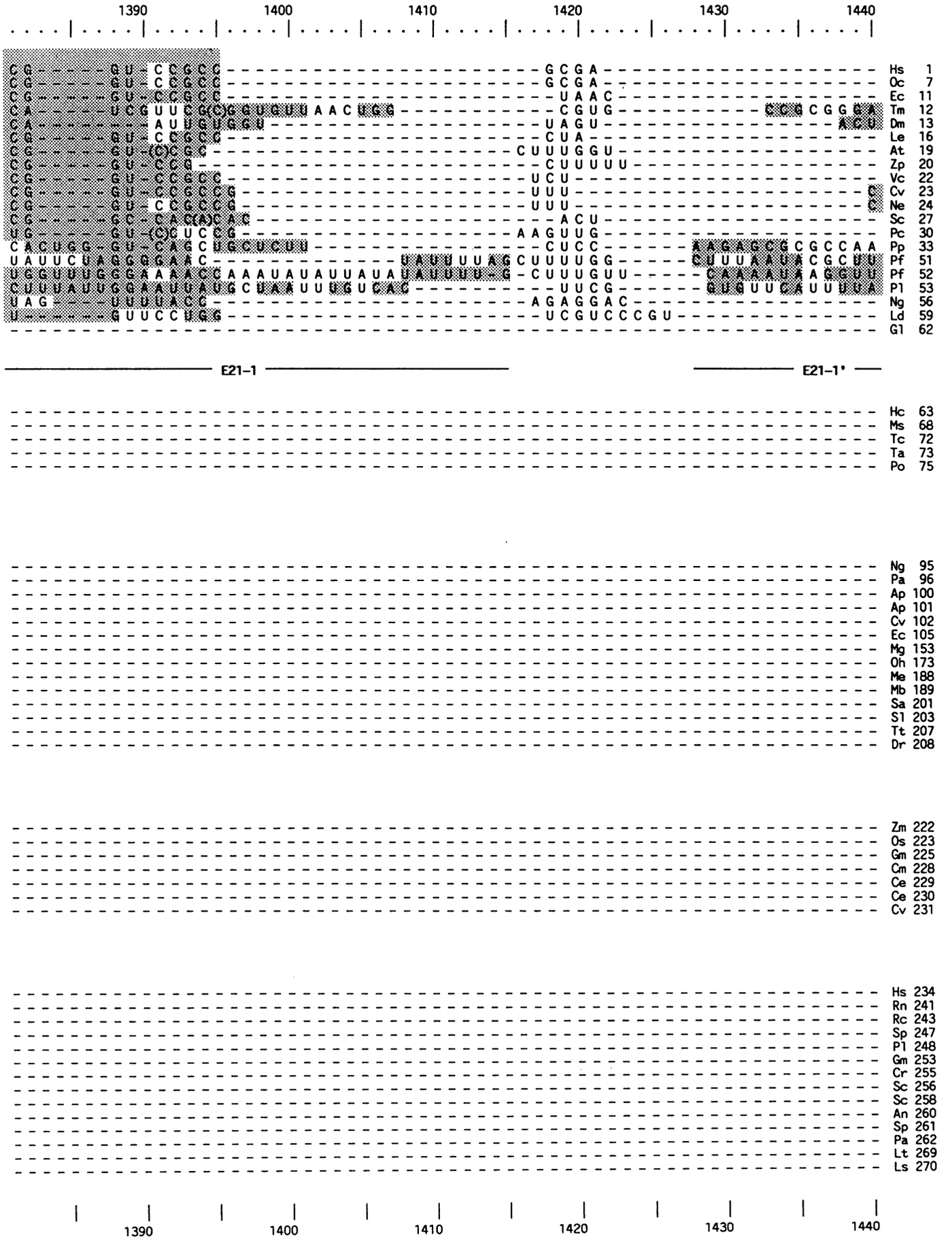
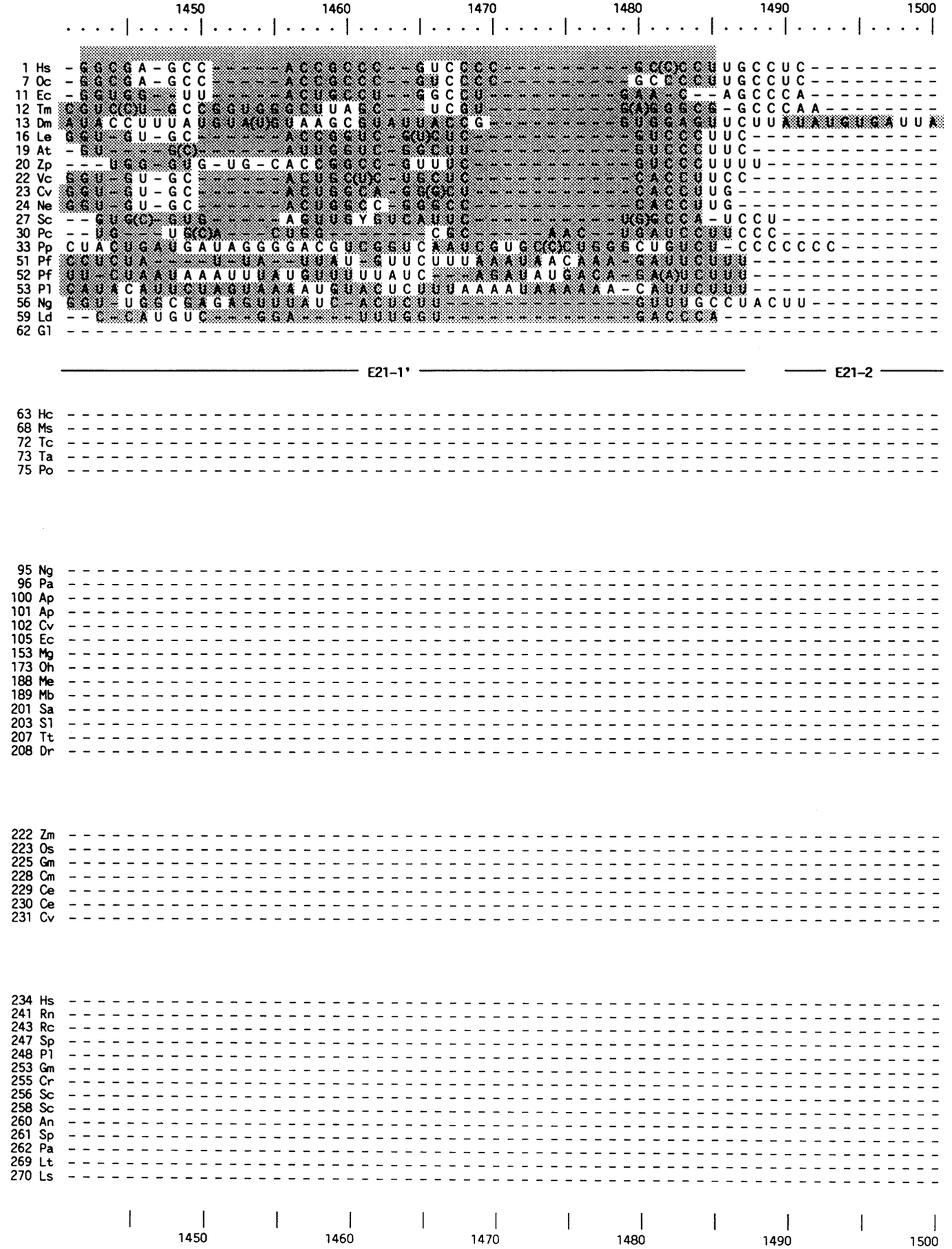
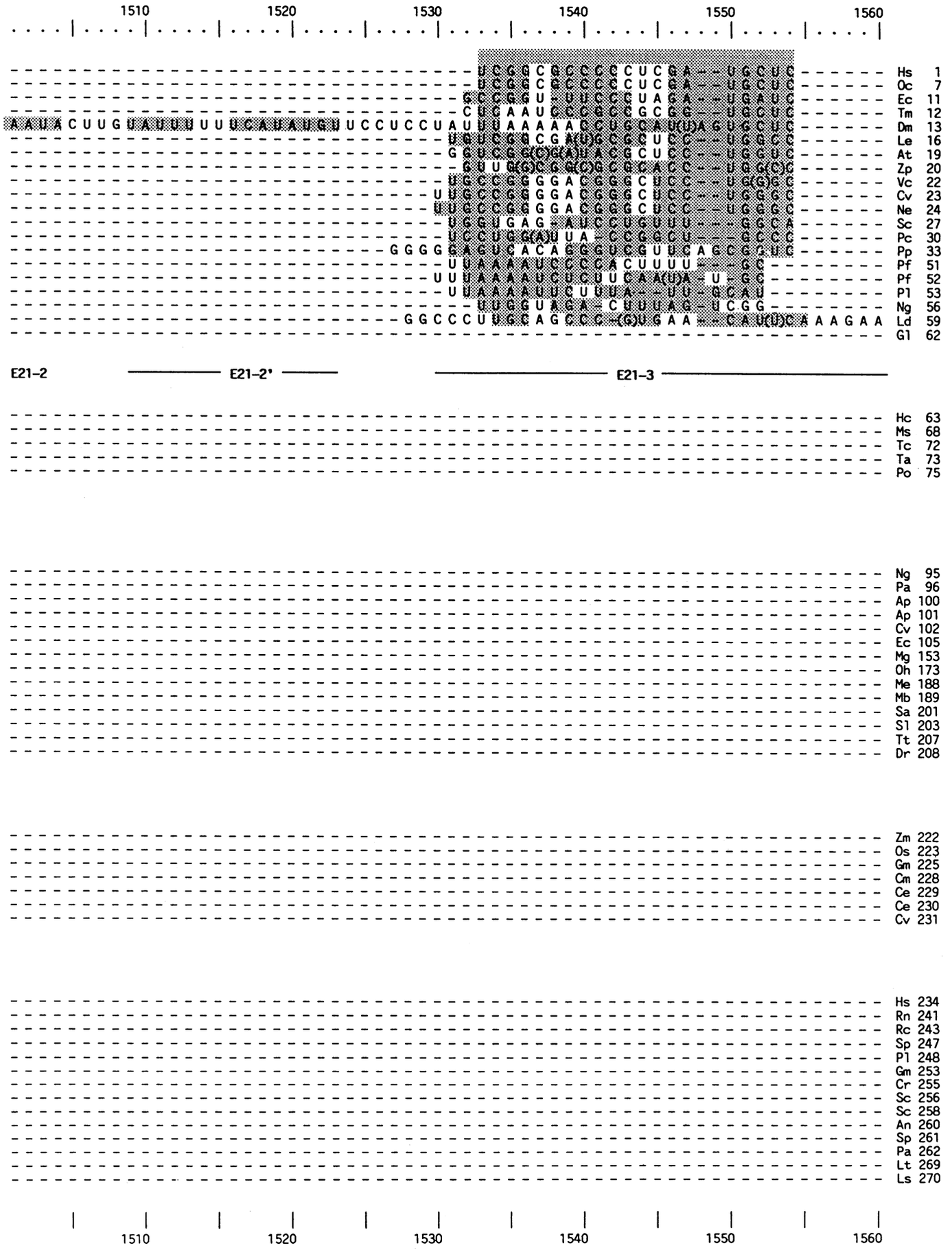
262 Pa
269 Lt
270 Ls
1210
1220
1230
1240
1250
1260


1270
1280
1290
1300
1310
1320
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
20
21
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
580
590
600
610
620
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
21
P21-1
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
1270
1280
1290
1300
1310
1320


1330
1340
1350
1360
1370
1380
E21-1
630
640
650
P21-1'


1390
1400
1410
1420
1430
1440
E21-1
E21-1*
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270


1450
1460
1470
1480
1490
1500
E21-1'
E21-2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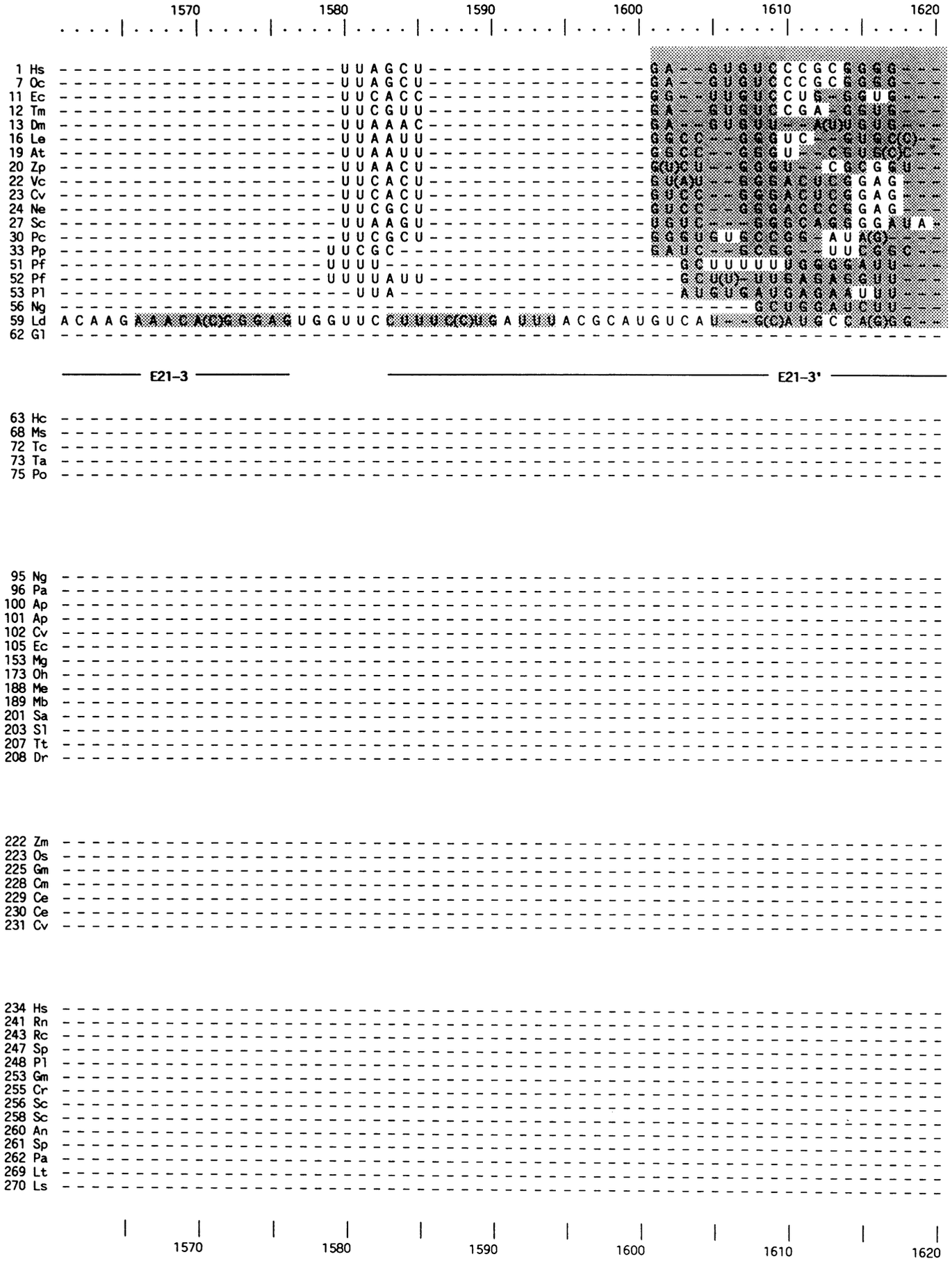
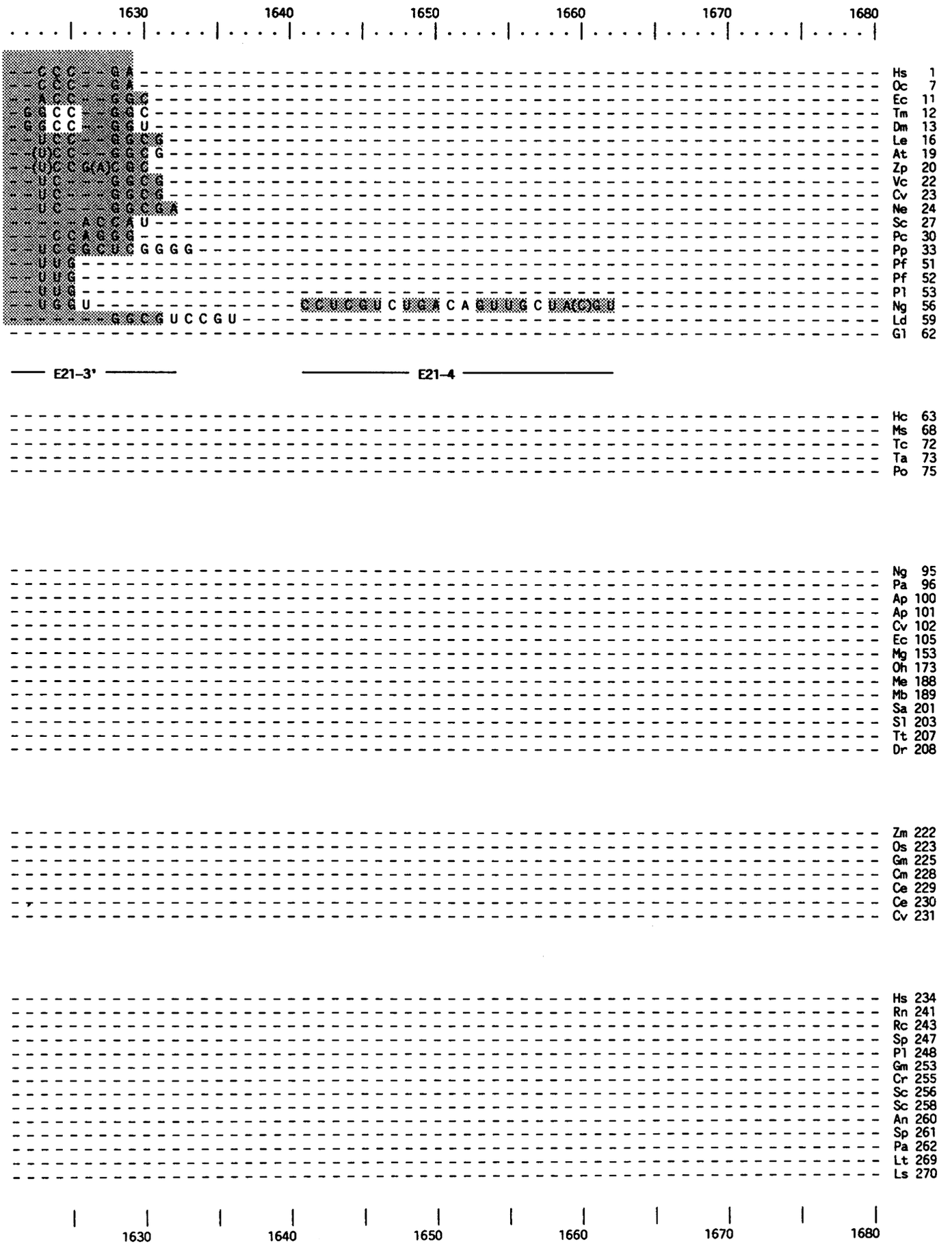
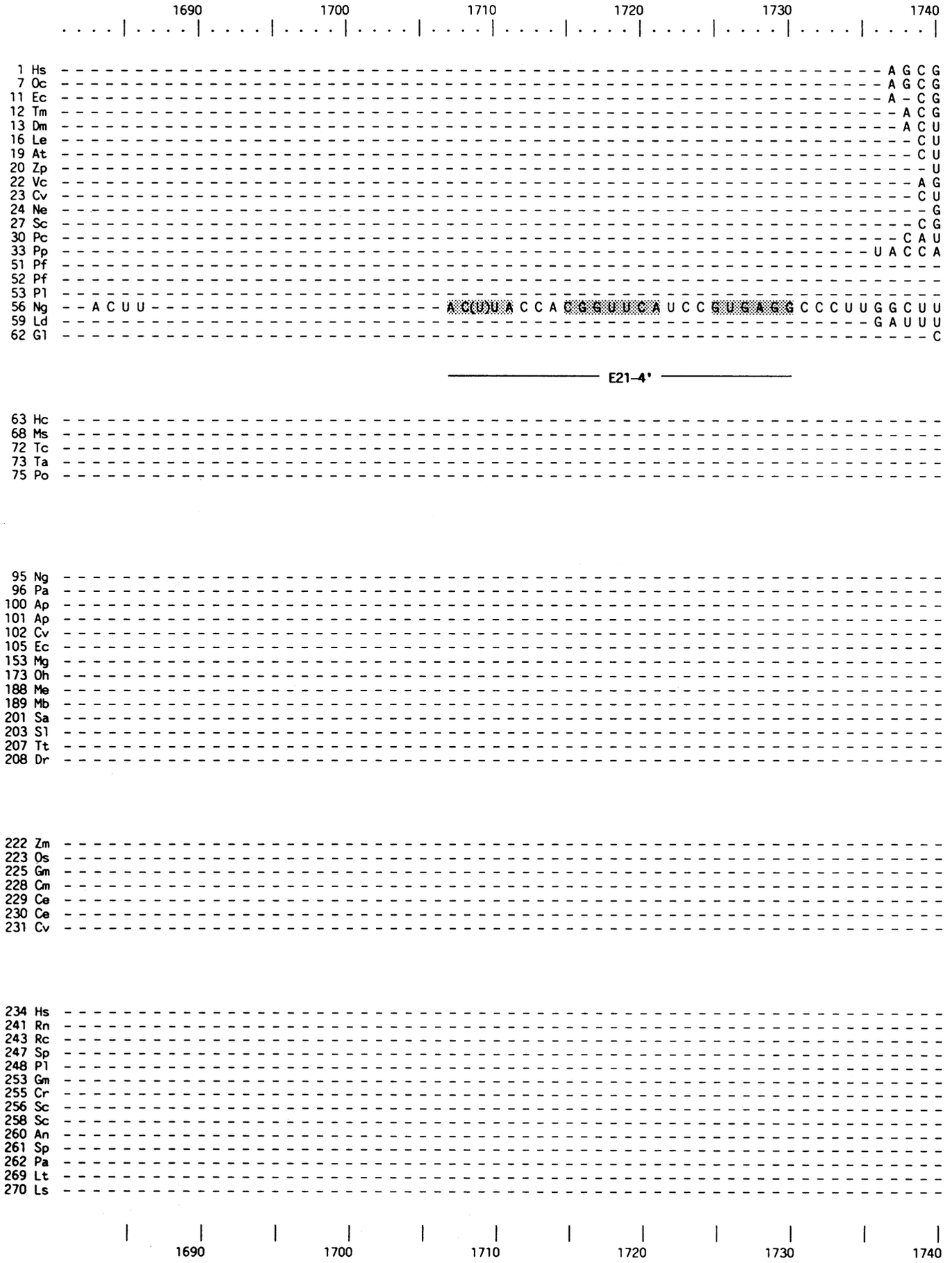
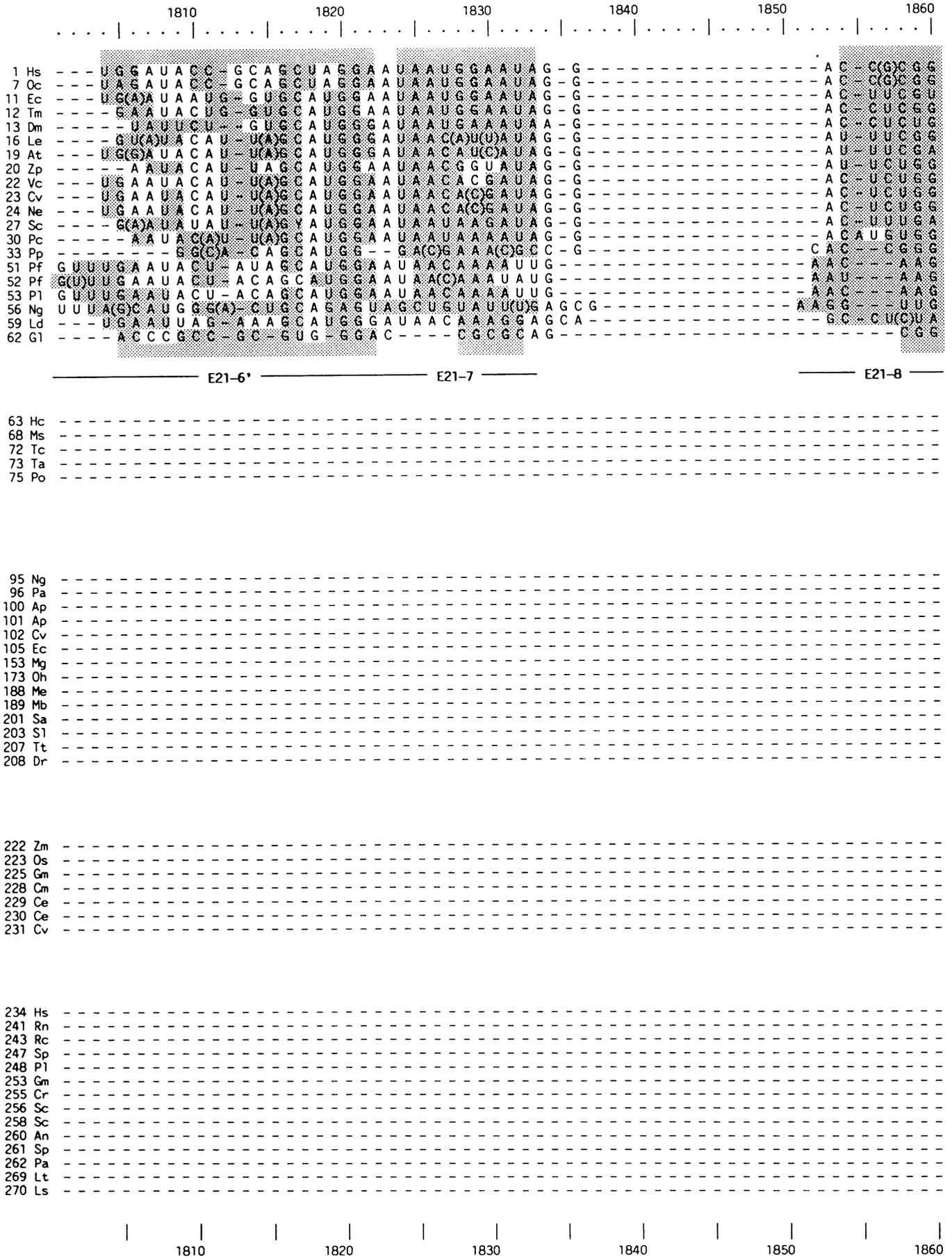
1530
1540
1550
1560
E21-2
E21-2'
E21-3


1570
1580
1590
1600
1610
1620
E21-3
E21-3'

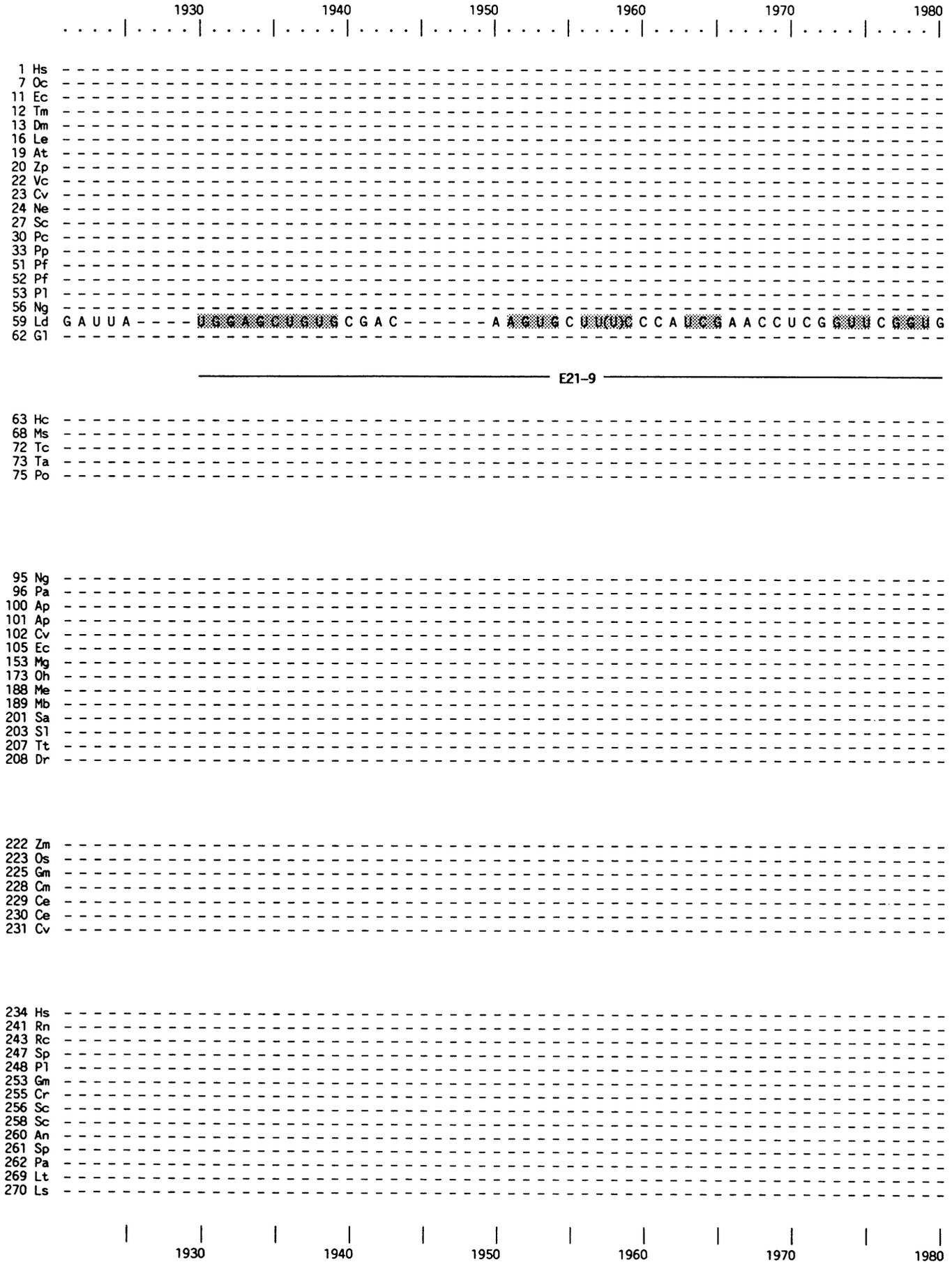

1630
1640
1650
1660
1670
1680
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
E21-3'
E21-4
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270

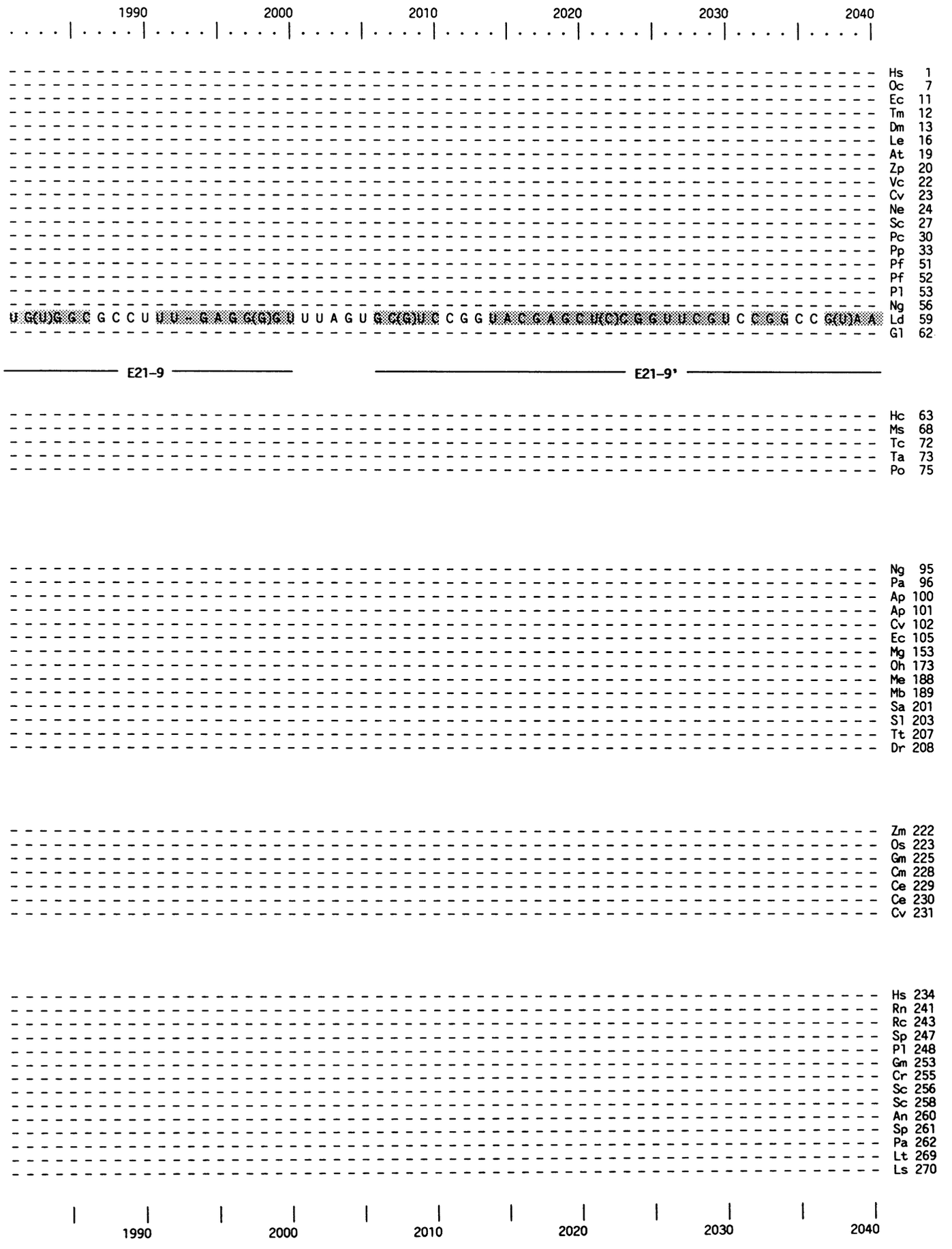

1690
1700
1710
1720
1730
1740
E21-4'

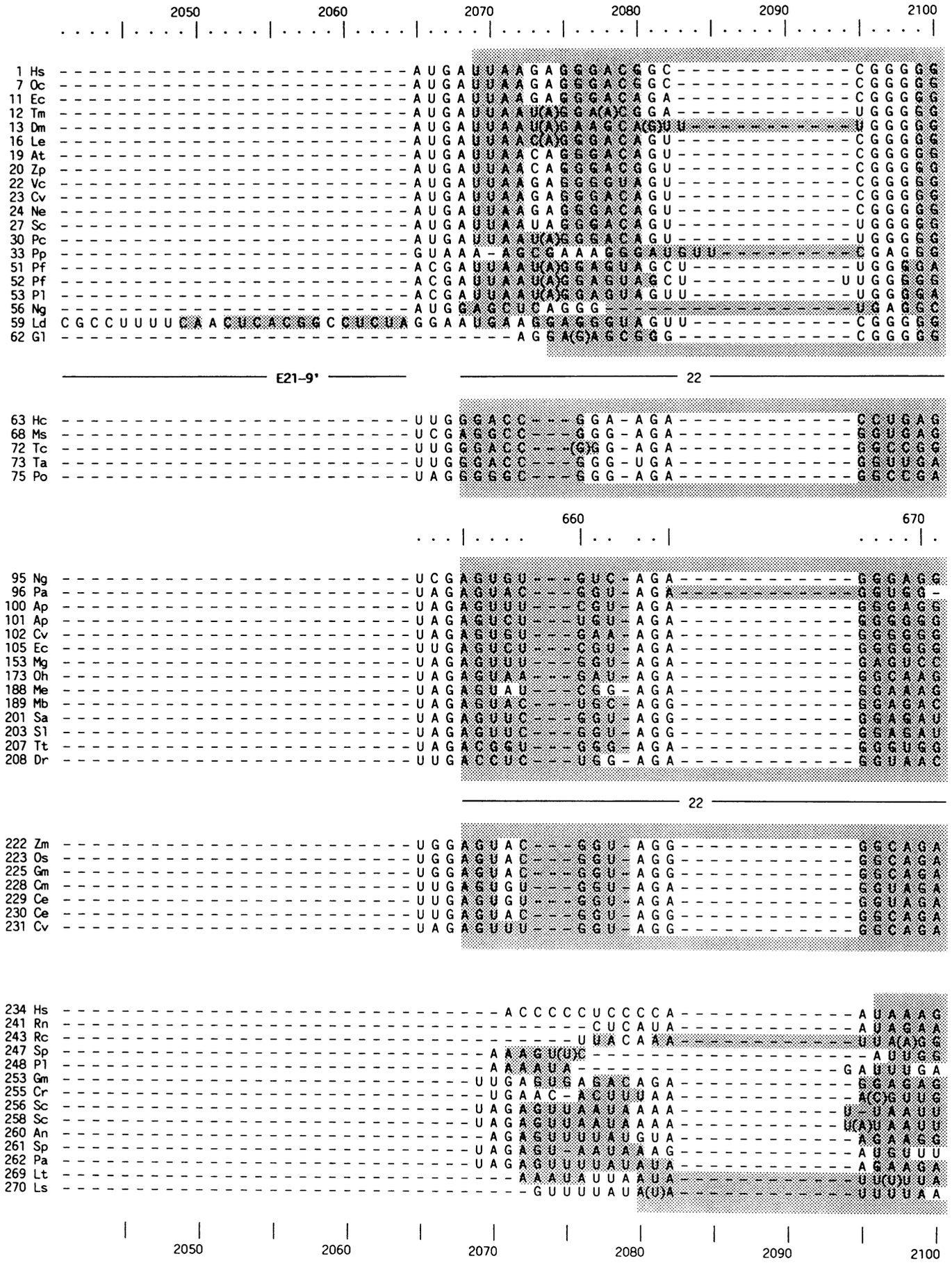

1750
1760
1770
1780
1790
1800
E21-5
E21-5'
E21-6
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270

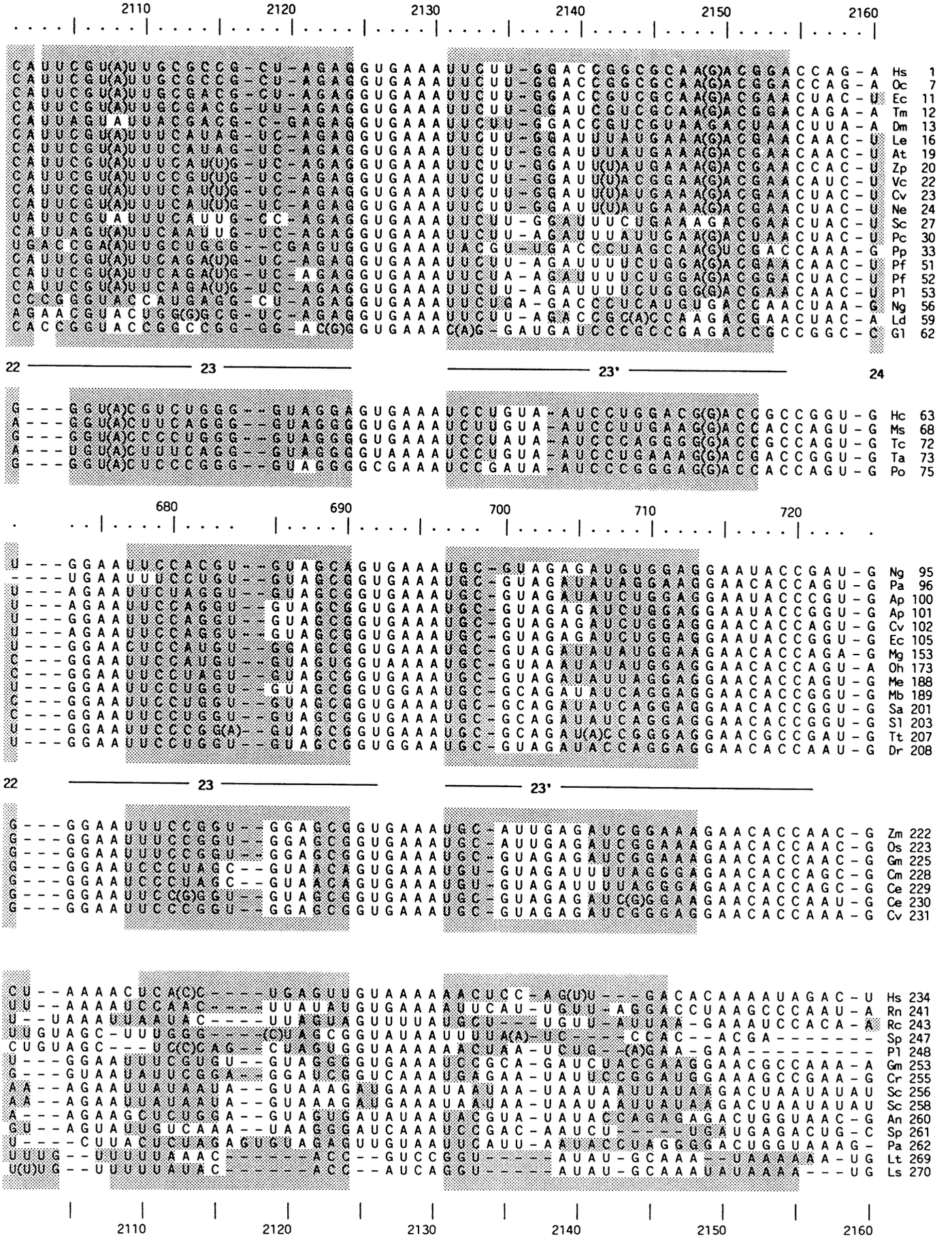

1810
1820
1830
1840
1850
1860
E21-6'
E21-7
E21-8

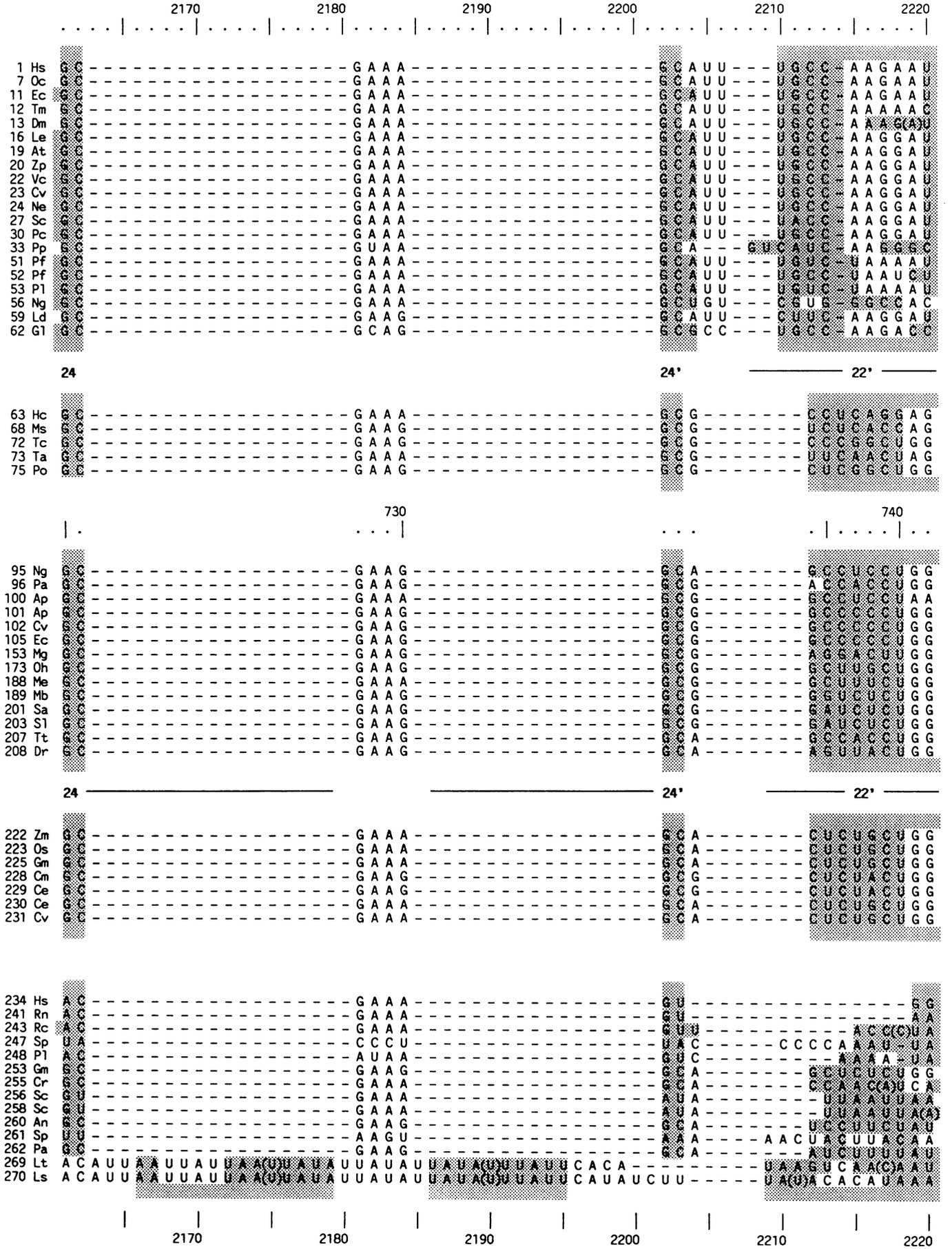

1870
1880
1890
1900
1910
1920
E21-8
E21-7'
E21-8'
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270

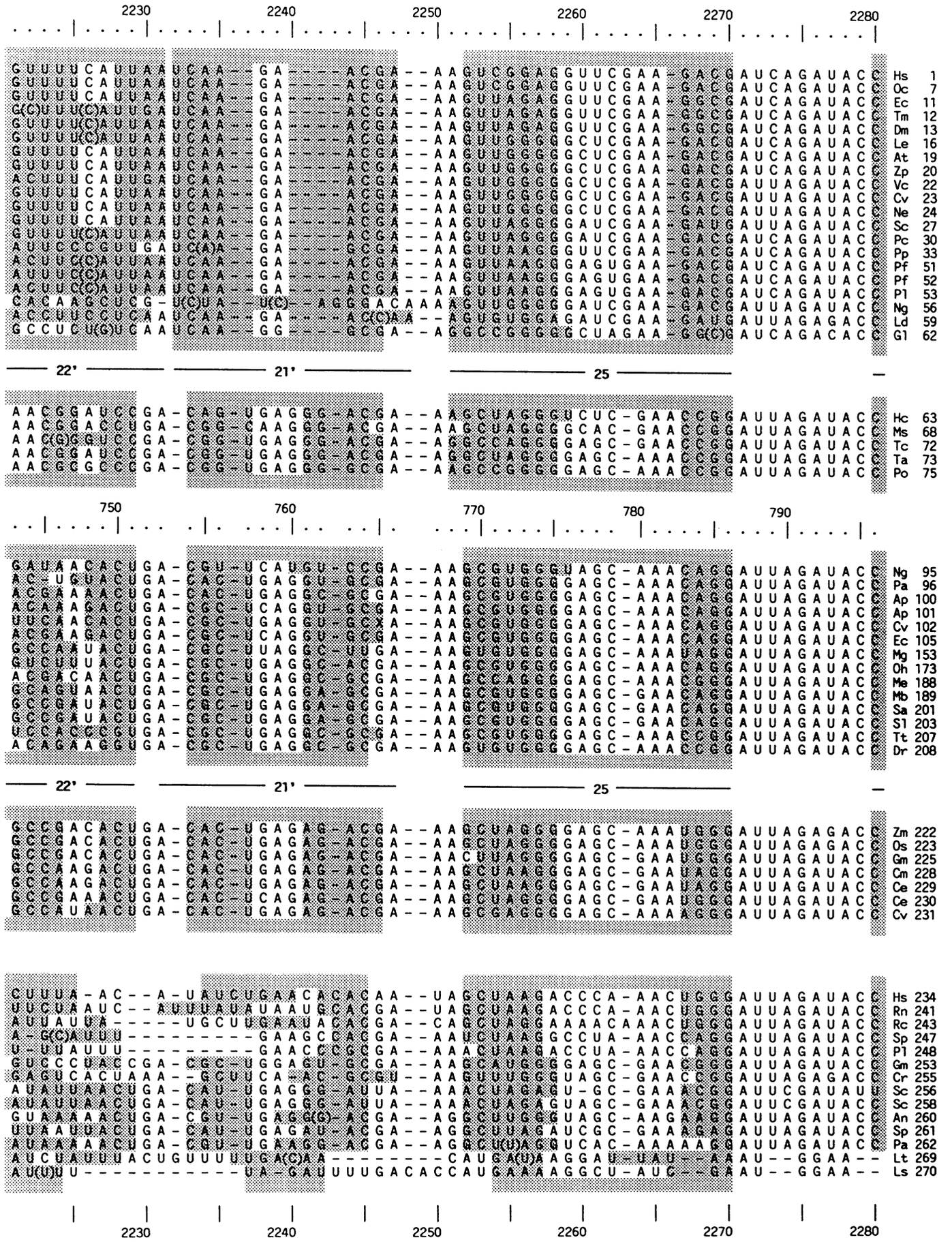

1930
1940
1950
1960
1970
1980
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld G A U U A - - - - U G C A C C U G U G C G A C - - - - - - A A G U G C U U(U)C C C A U C G A A C C U C G G U U C G C U G
62 Gl
E21-9
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc
258 Sc
260 An
261 Sp
262 Pa
269 Lt
270 Ls

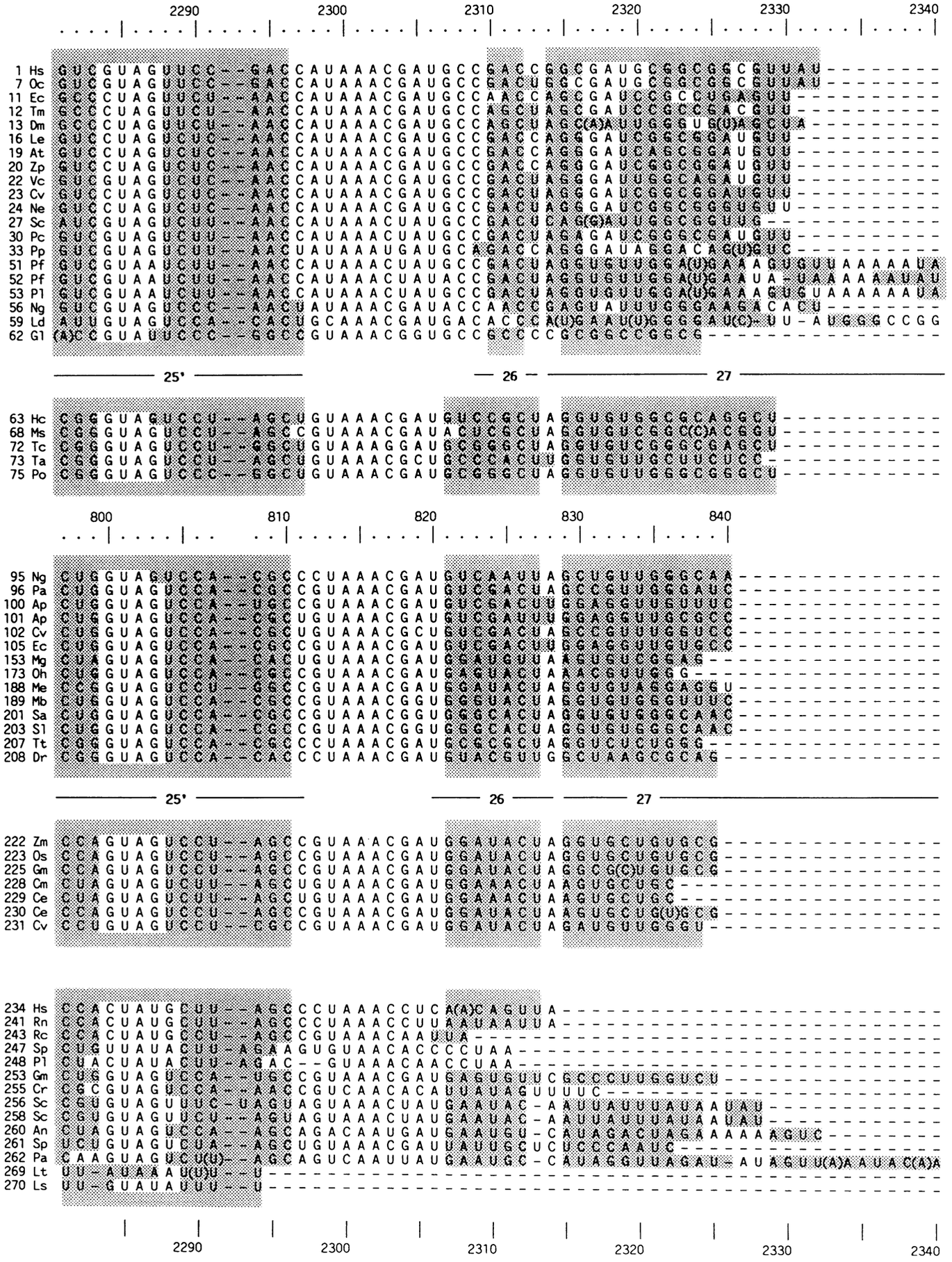

1990
2000
2010
2020
2030
2040
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
E21-9
E21-9'
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270

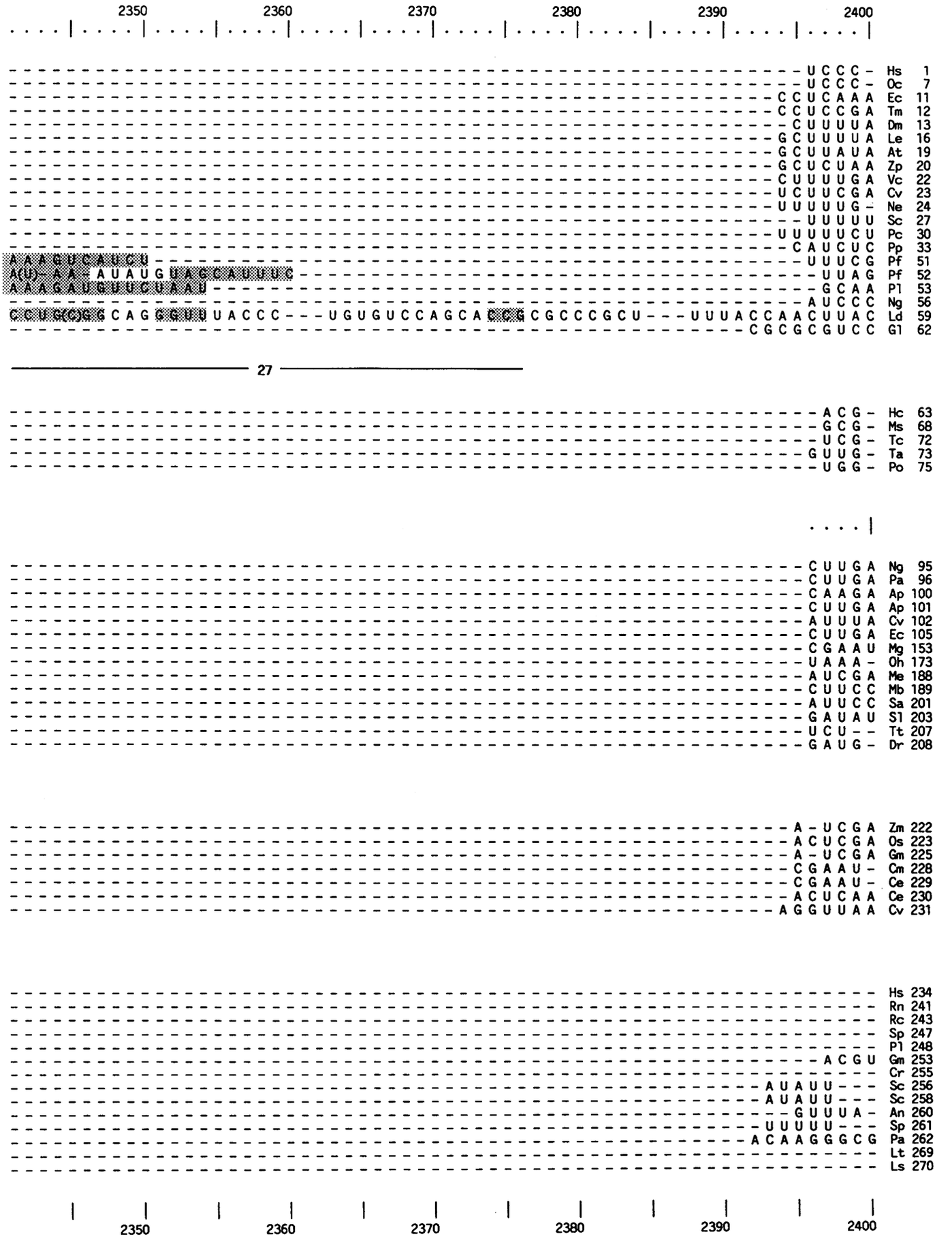

2050
2060
2070
2080
2090
2100
E21-9'
22
660
670
22
2050
2060
2070
2080
2090
2100

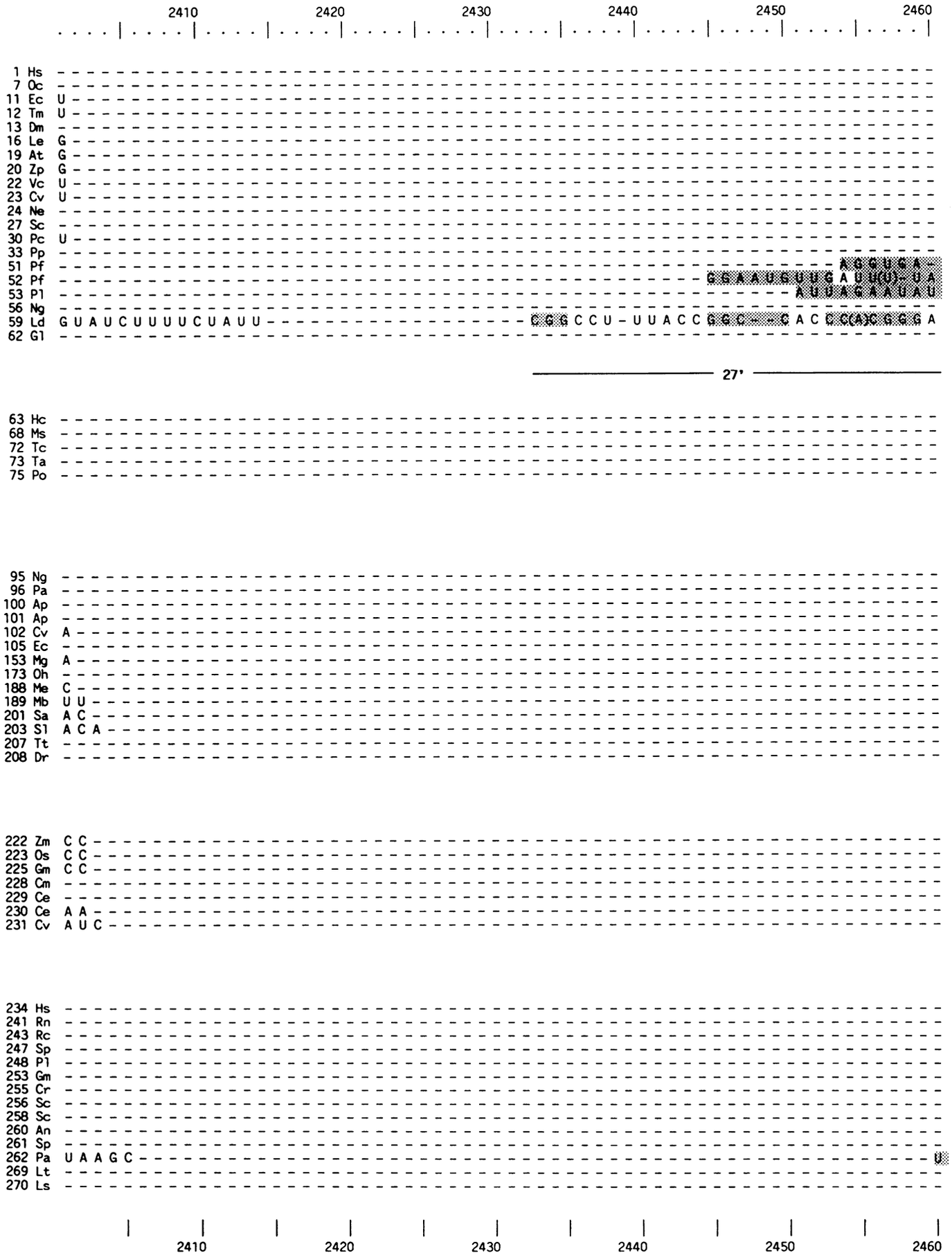

2110
2120
2130
2140
2150
2160
22
23
23'
24
680
690
700
710
720

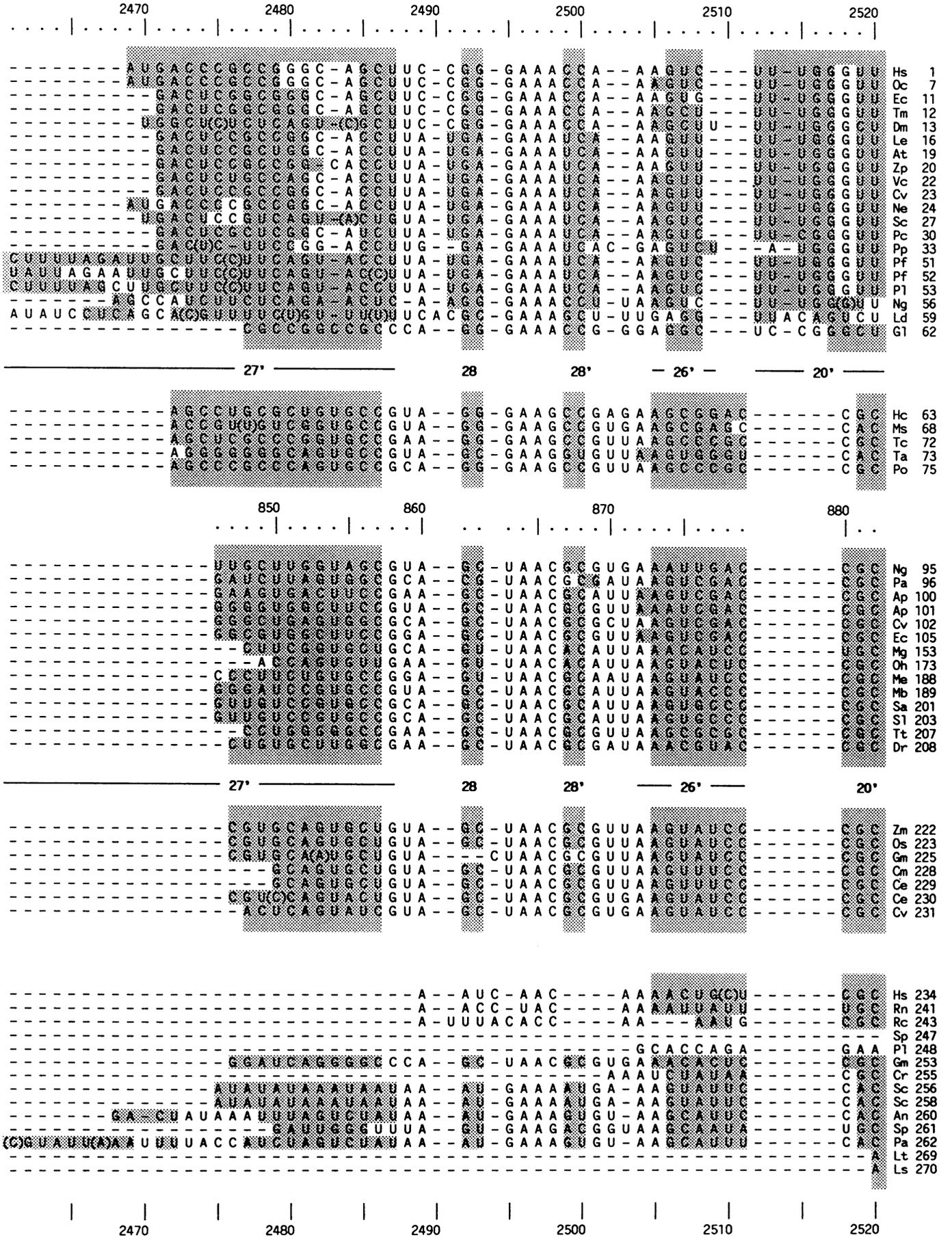

2170
2180
2190
2200
2210
2220
24
24'
22'
730
740

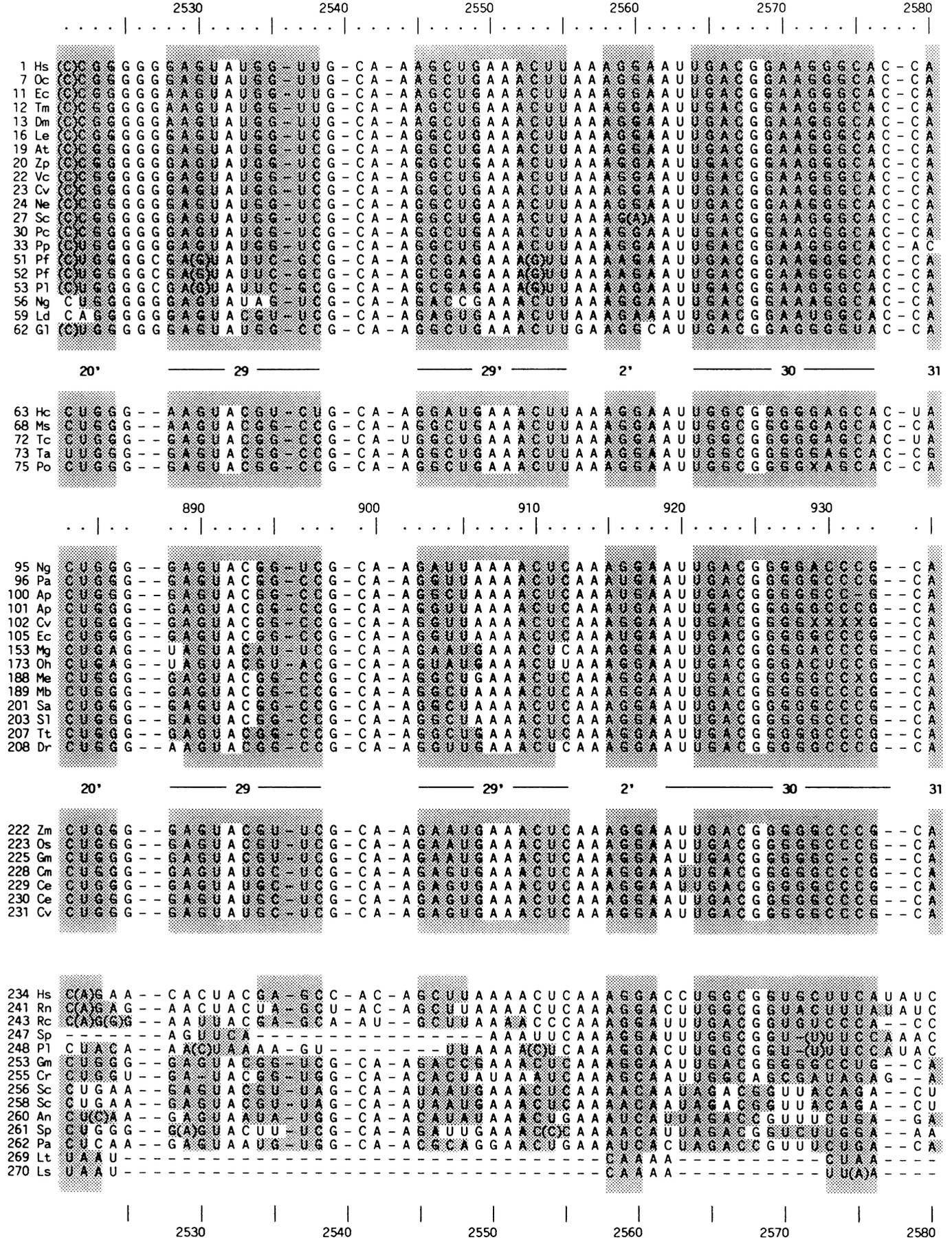

2230
2240
2250
2260
2270
2280
22'
21'
25
750
760
770
780
790

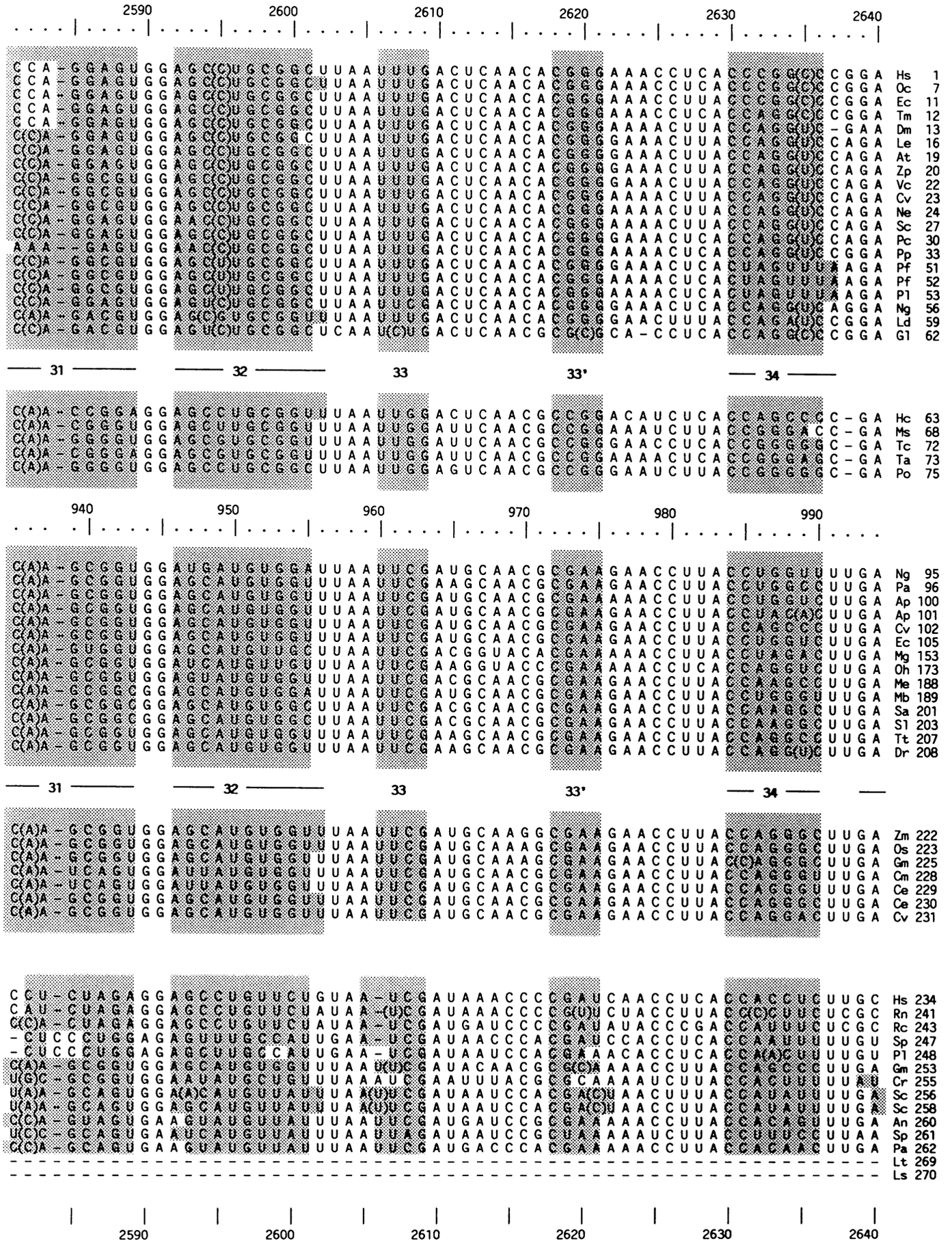

2290
2300
2310
2320
2330
2340
25'
26
27
800
810
820
830
840

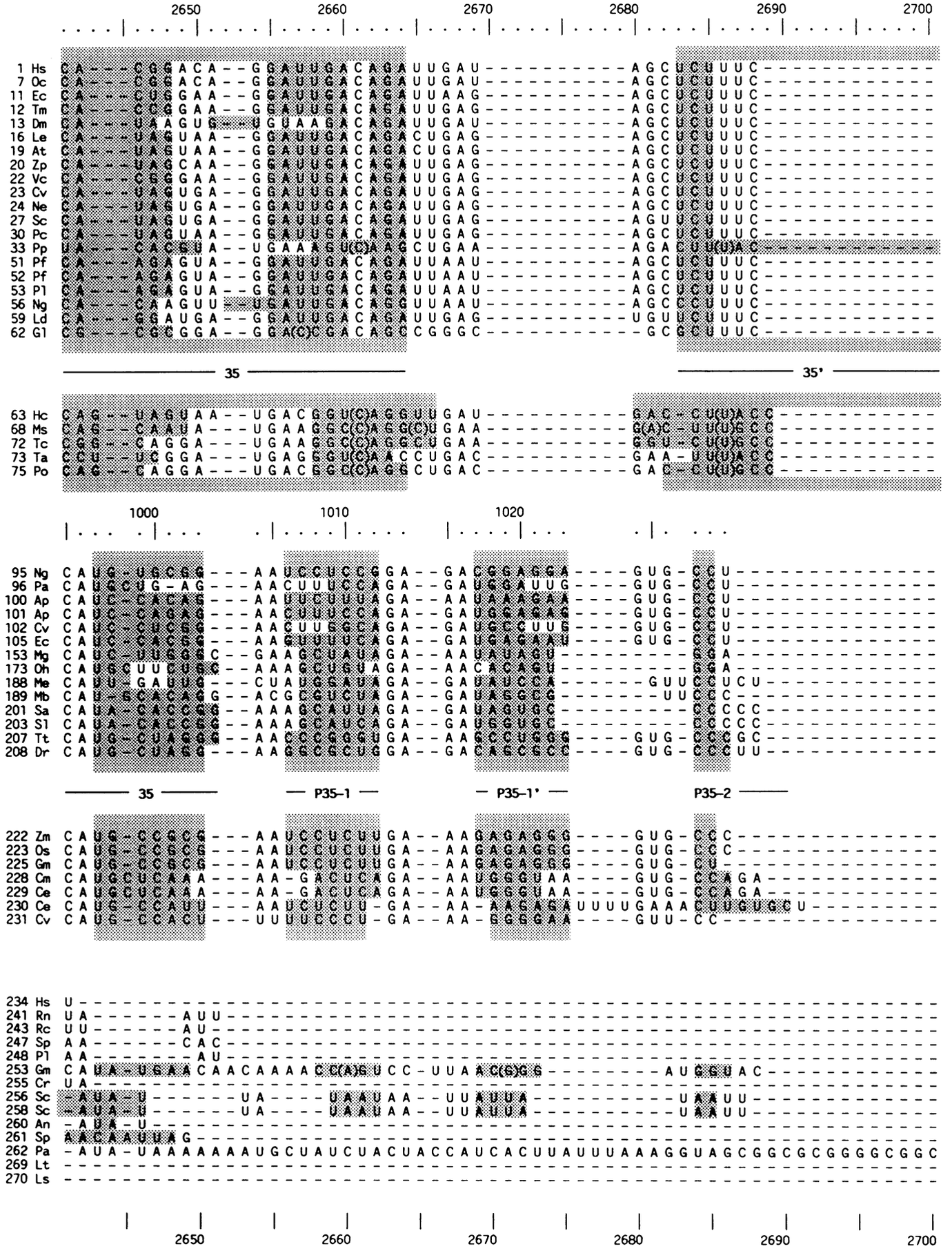

2350
2360
2370
2380
2390
2400
27

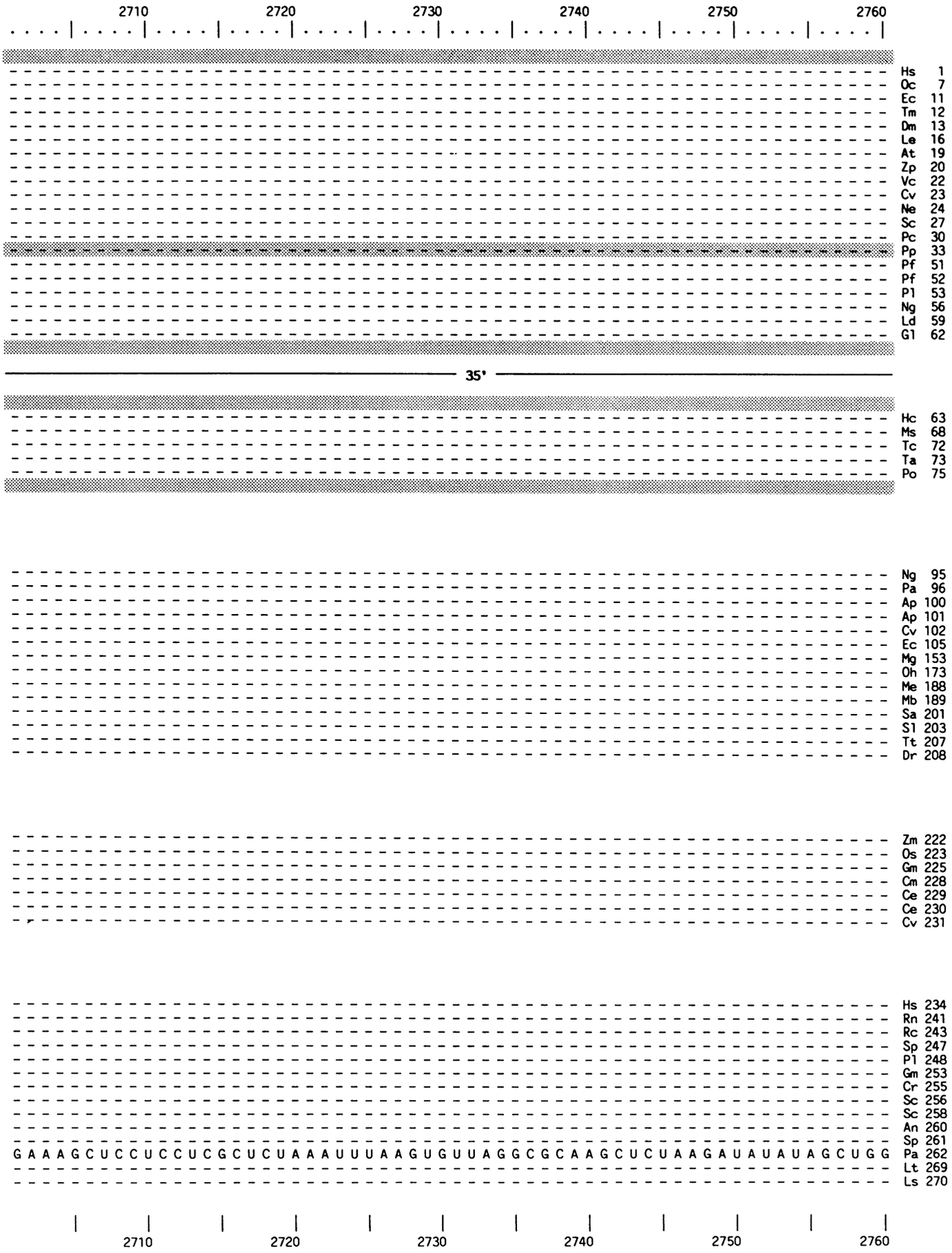

2410
2420
2430
2440
2450
2460
27'

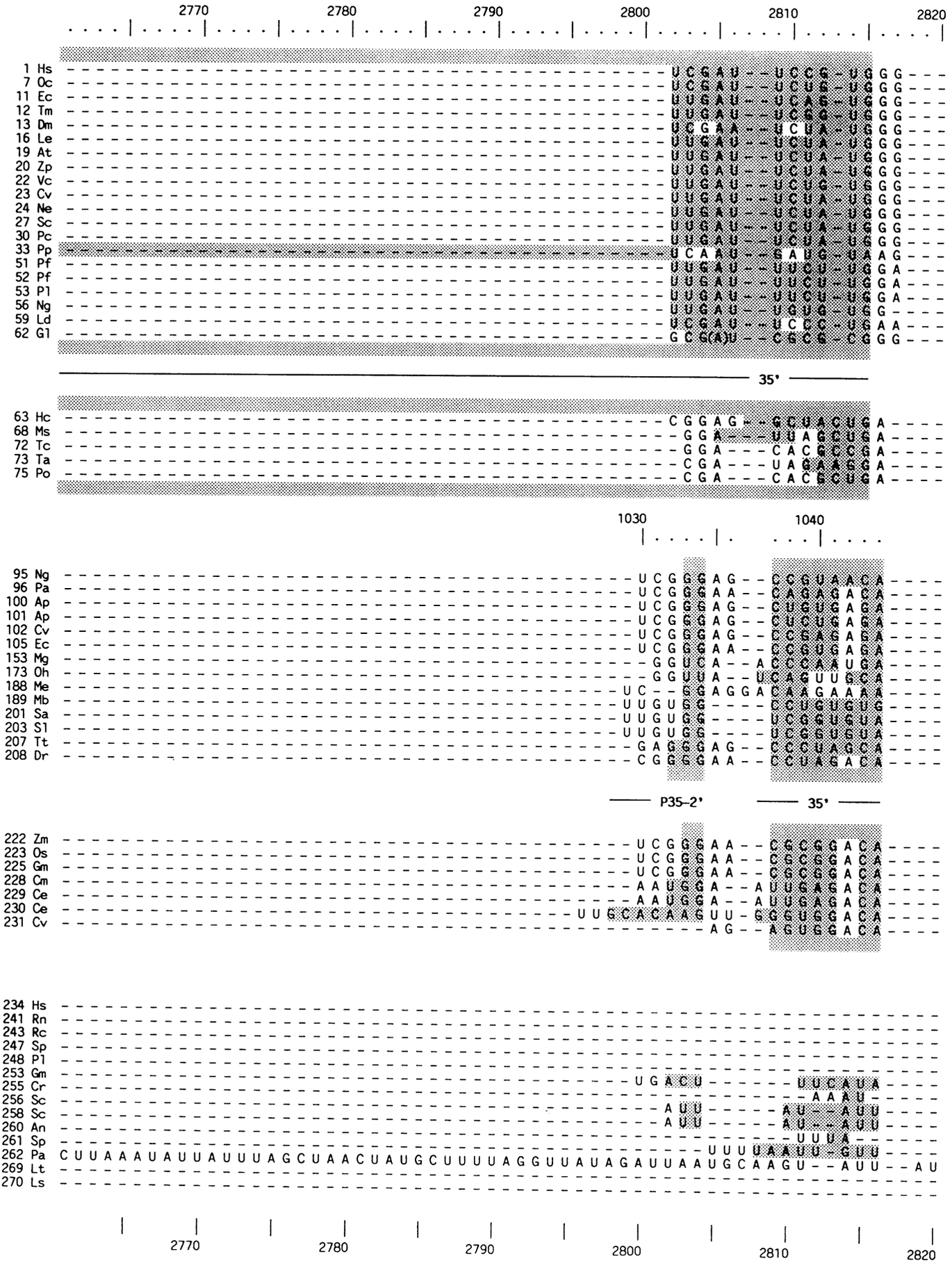

2470
2480
2490
2500
2510
2520
27'
28
28'
26'
20'
850
860
870
880

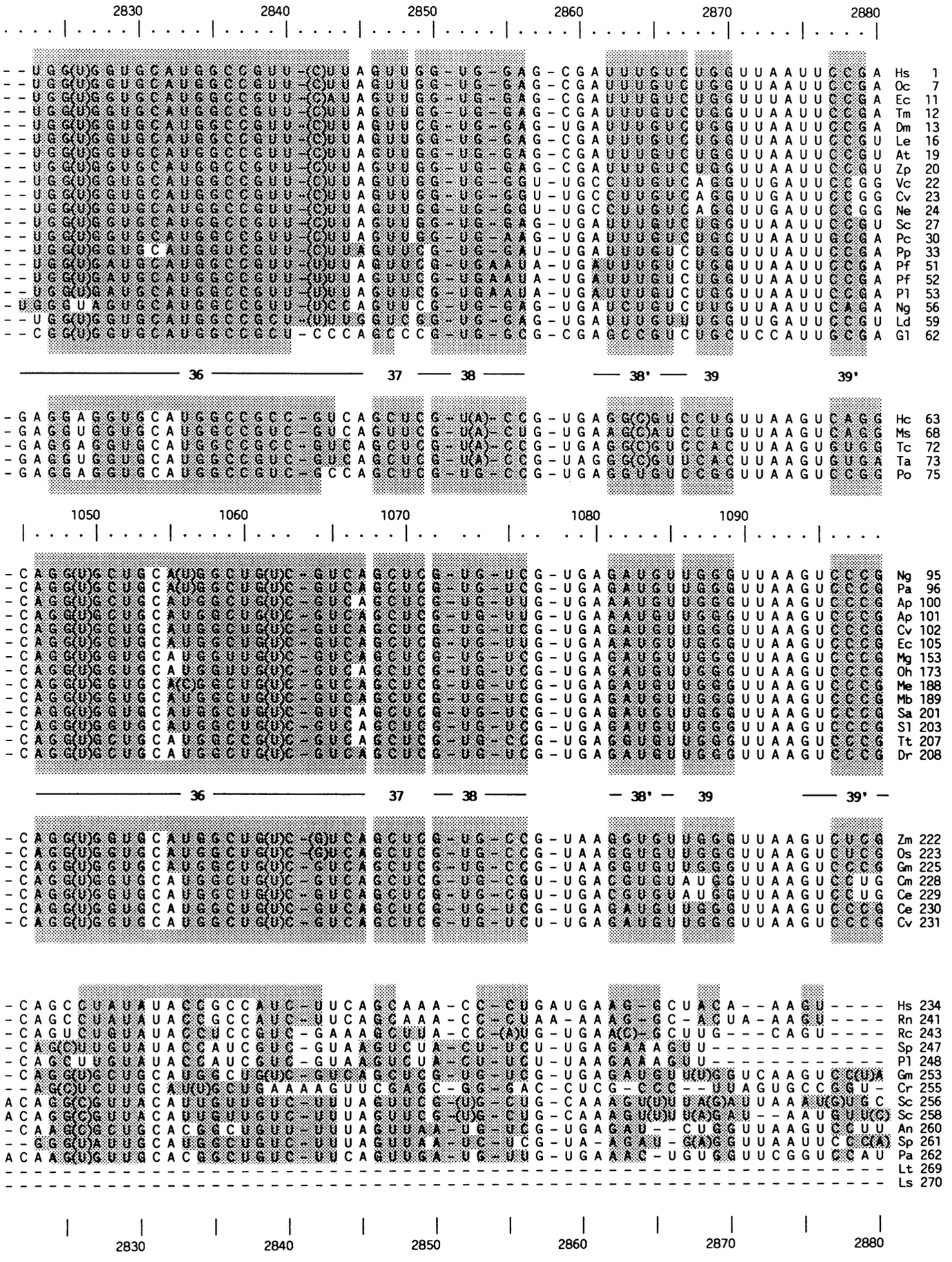

2530
2540
2550
2560
2570
2580
20'
29
29'
2'
30
31
890
900
910
920
930

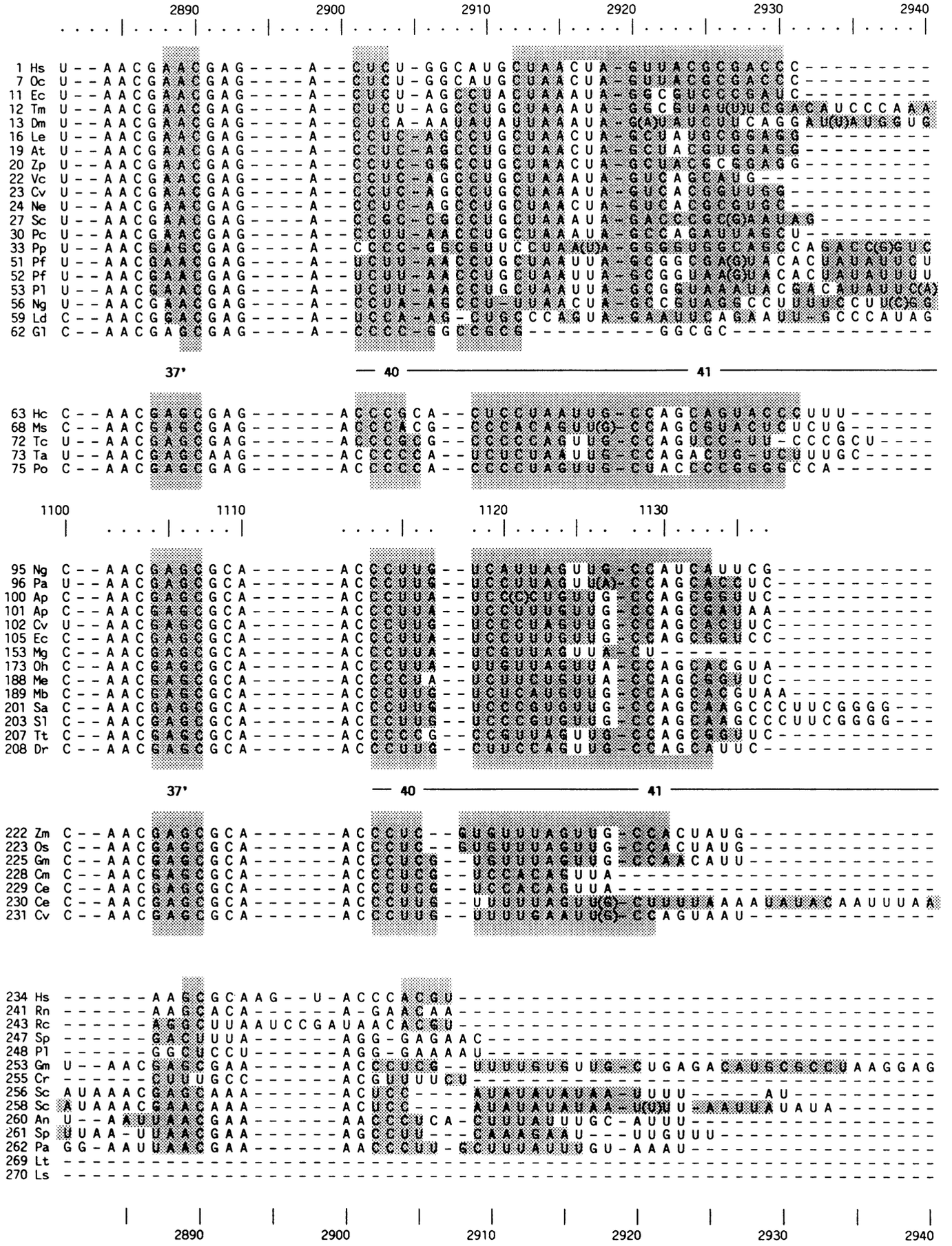

2590
2600
2610
2620
2630
2640
31
32
33
33'
34
940
950
960
970
980
990

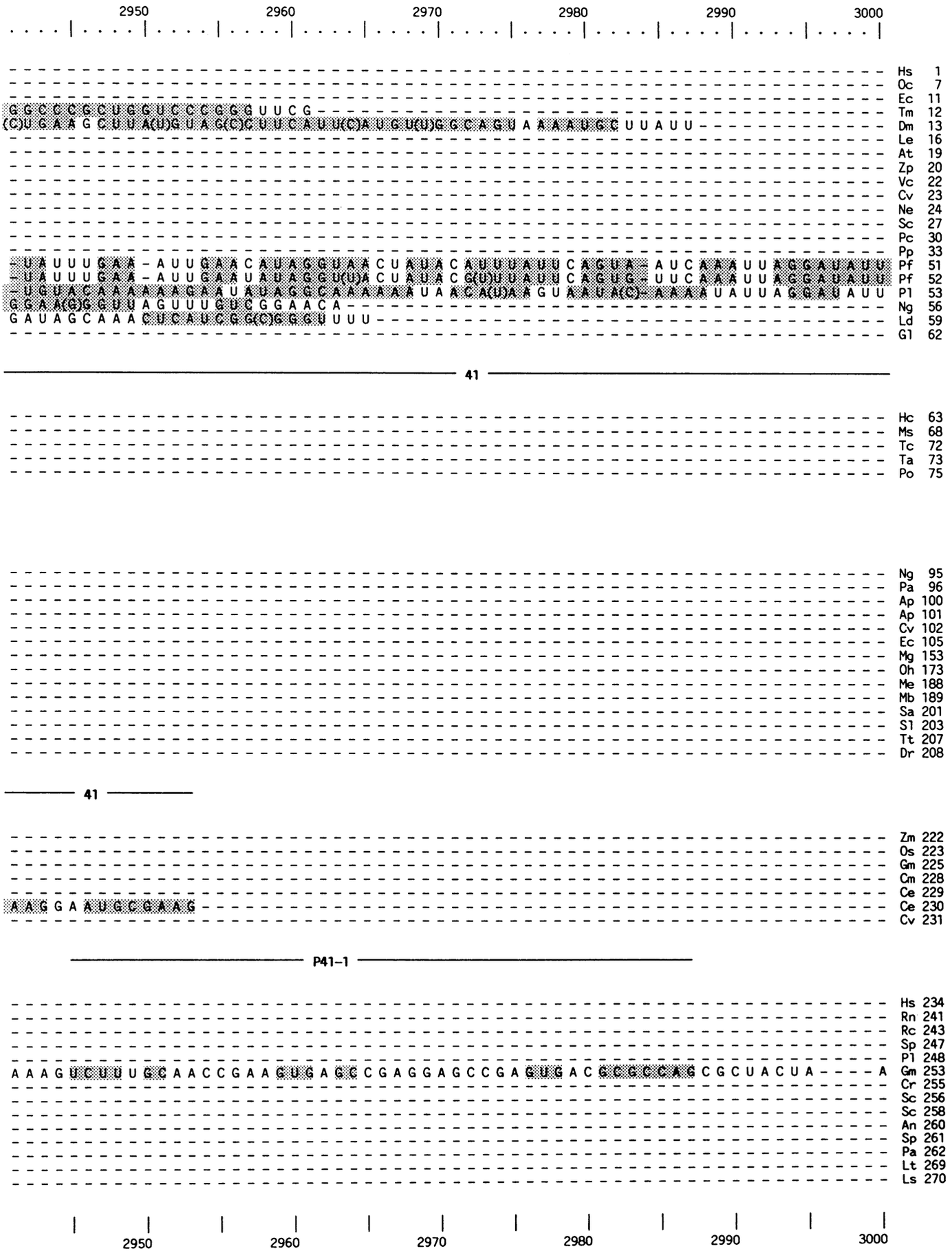

2650
2660
2670
2680
2690
2700
35
35'
1000
1010
1020
35
P35-1
P35-1'
P35-2

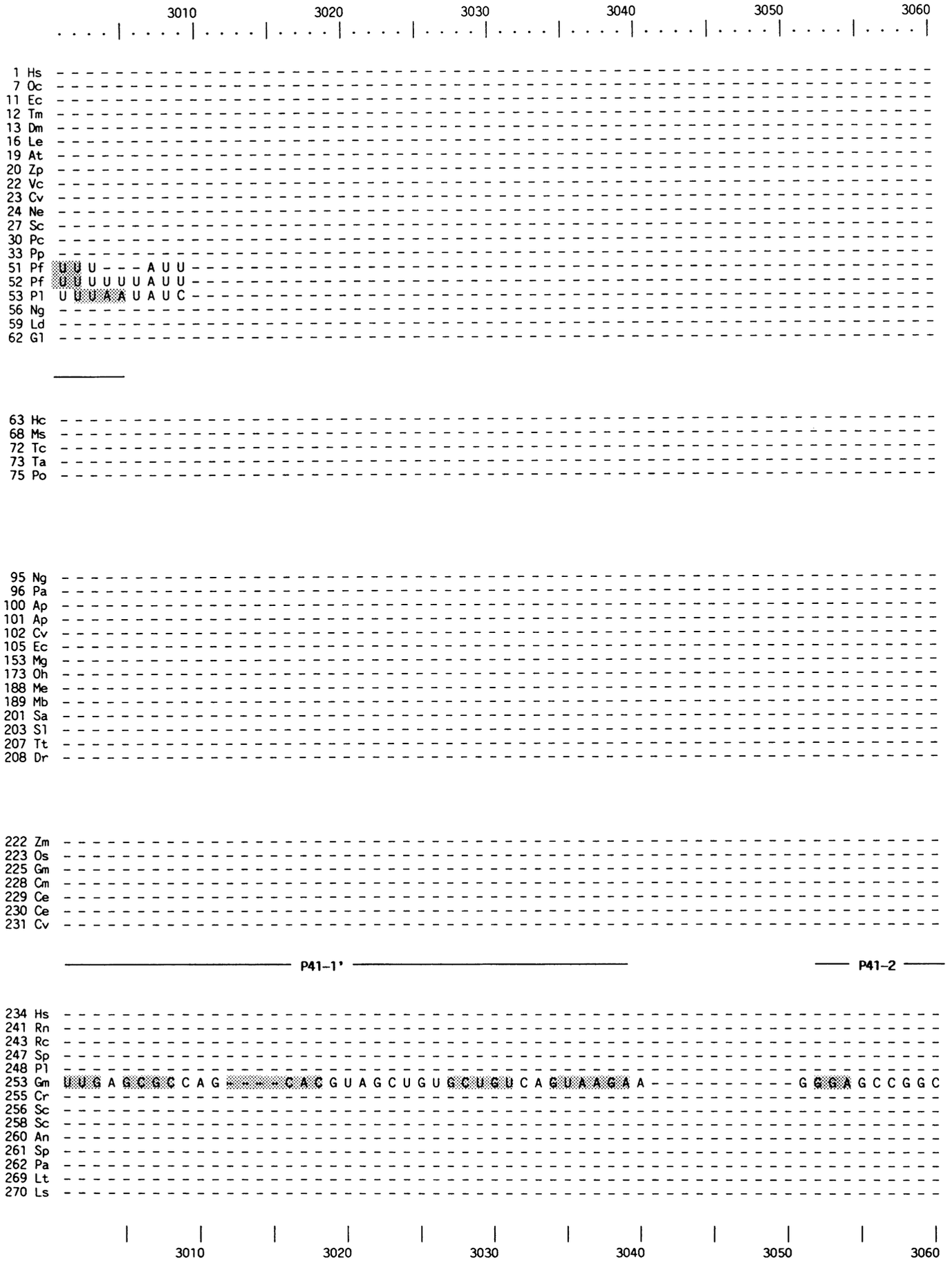

2710
2720
2730
2740
2750
2760
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
35'
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
GAAAGCUCCUCCUCGCUCUAAAUUUAAGUGUUAGGCGCAAGCUCUAAGAUAUAUAGCUGG Pa 262
Lt 269
Ls 270
2710
2720
2730
2740
2750
2760

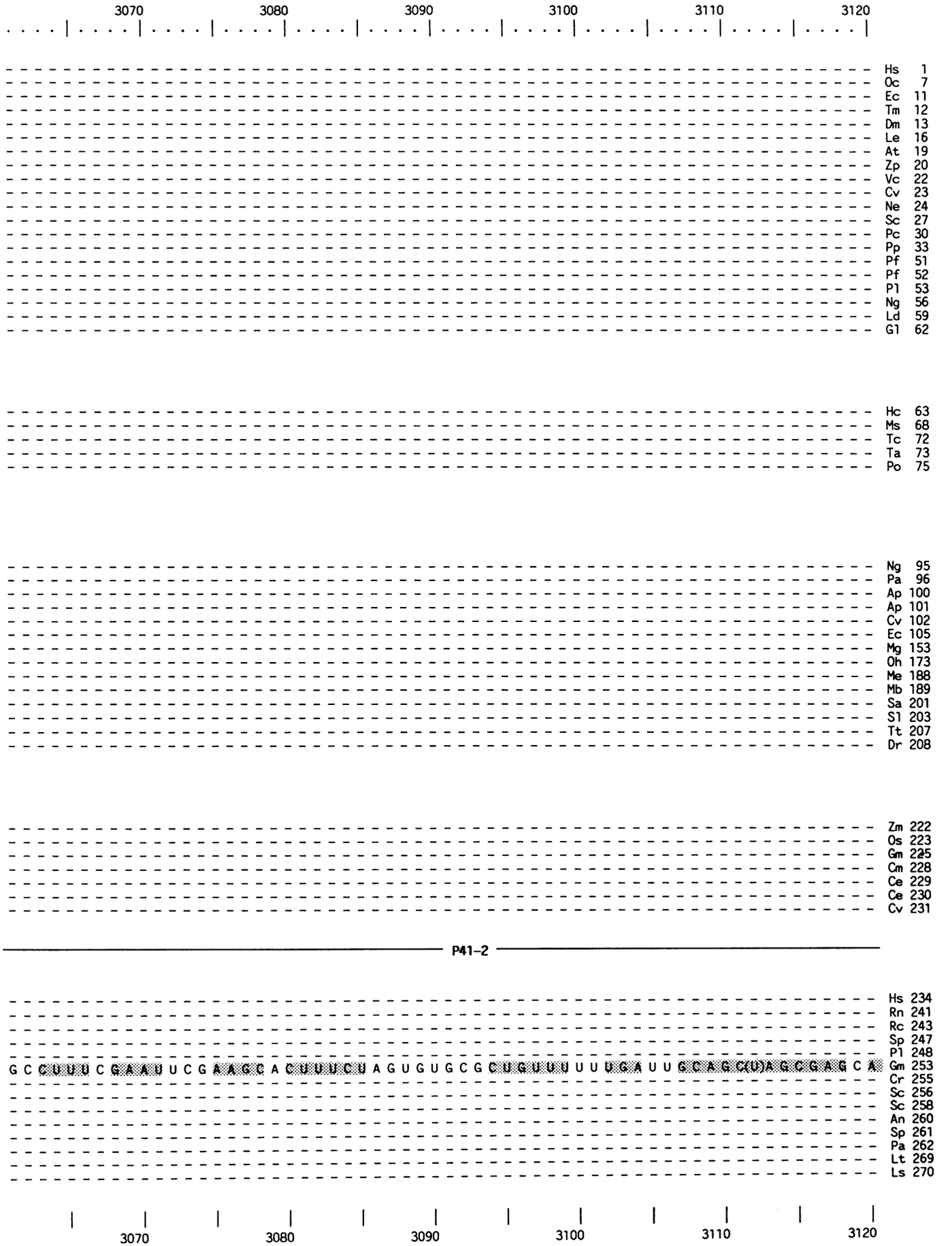

2770
2780
2790
2800
2810
2820
35'
1030
1040
P35-2'
35'

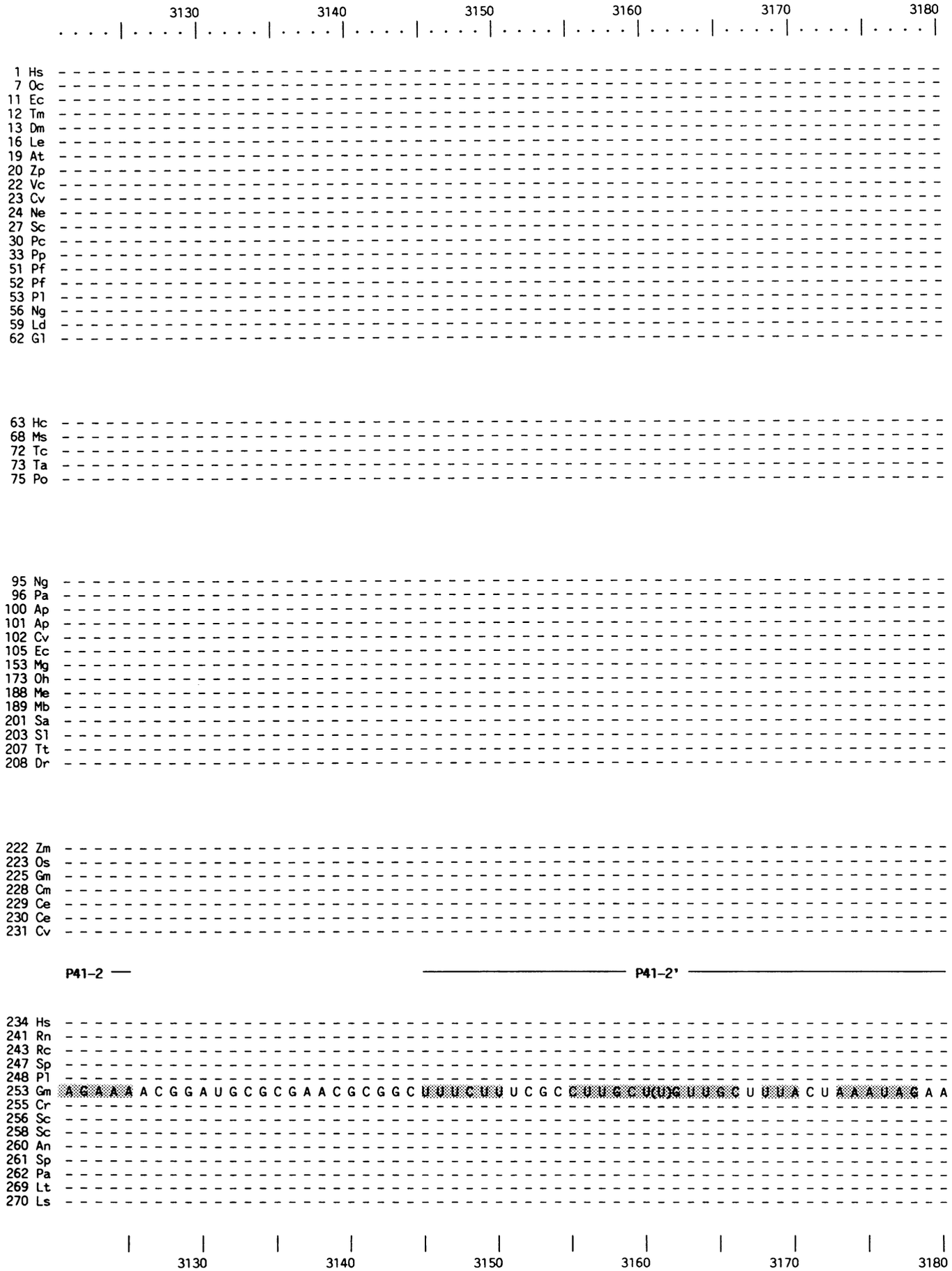

2830
2840
2850
2860
2870
2880
36
37
38
38'
39
39'
1050
1060
1070
1080
1090

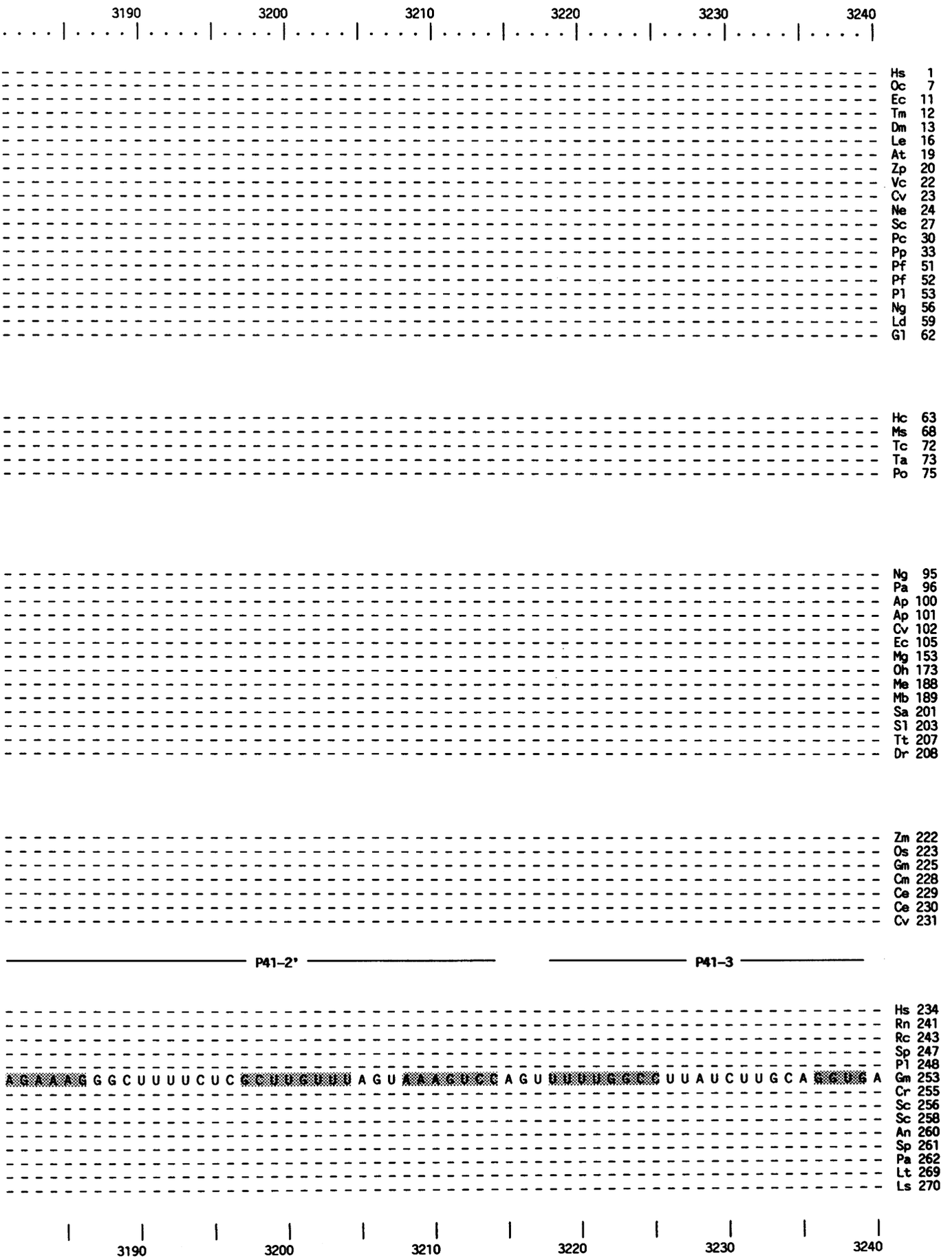

2890
2900
2910
2920
2930
2940
37'
40
41
1100
1110
1120
1130

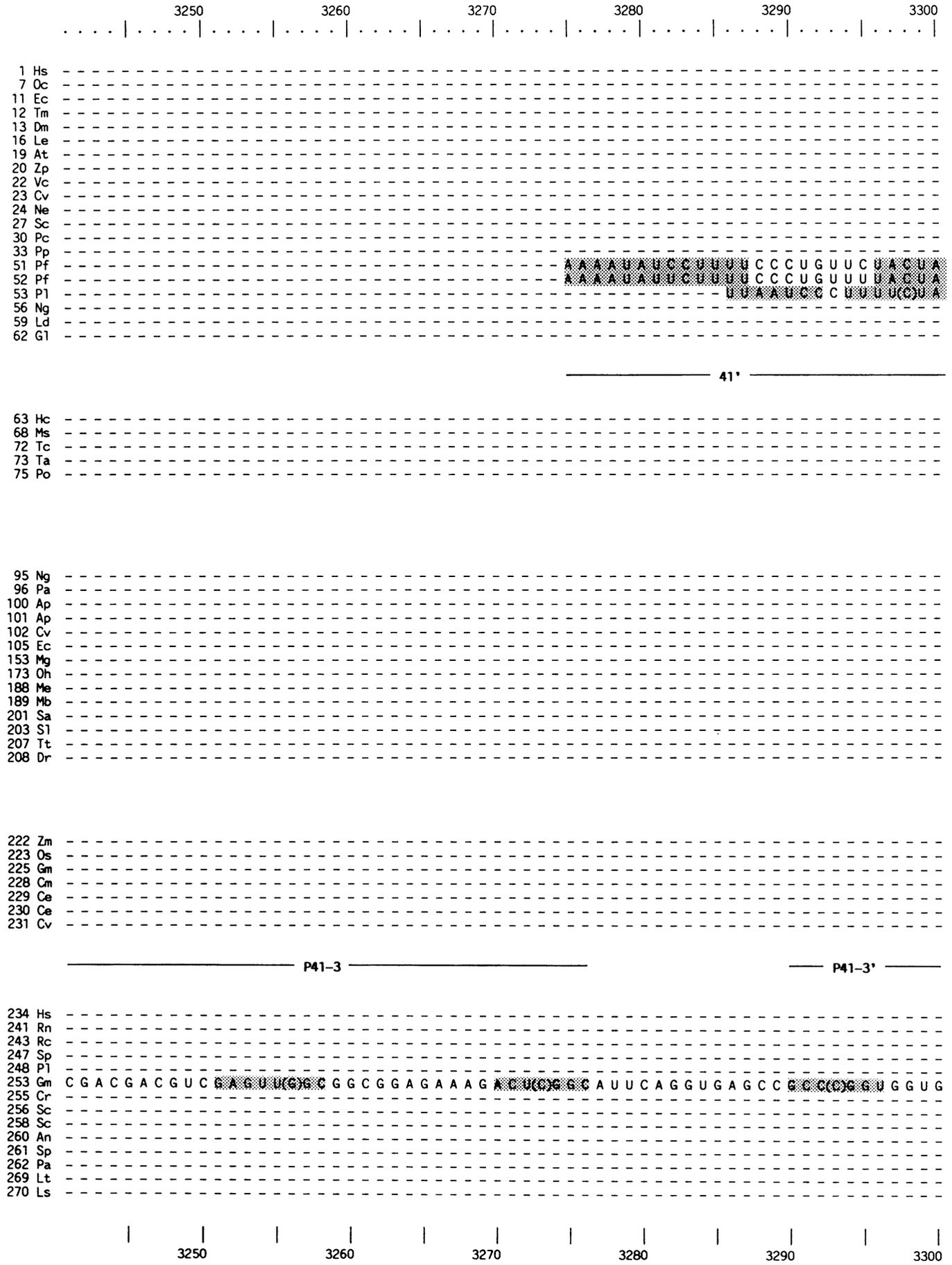

2950
2960
2970
2980
2990
3000
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
41
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
41
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
P41-1
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
2950
2960
2970
2980
2990
3000

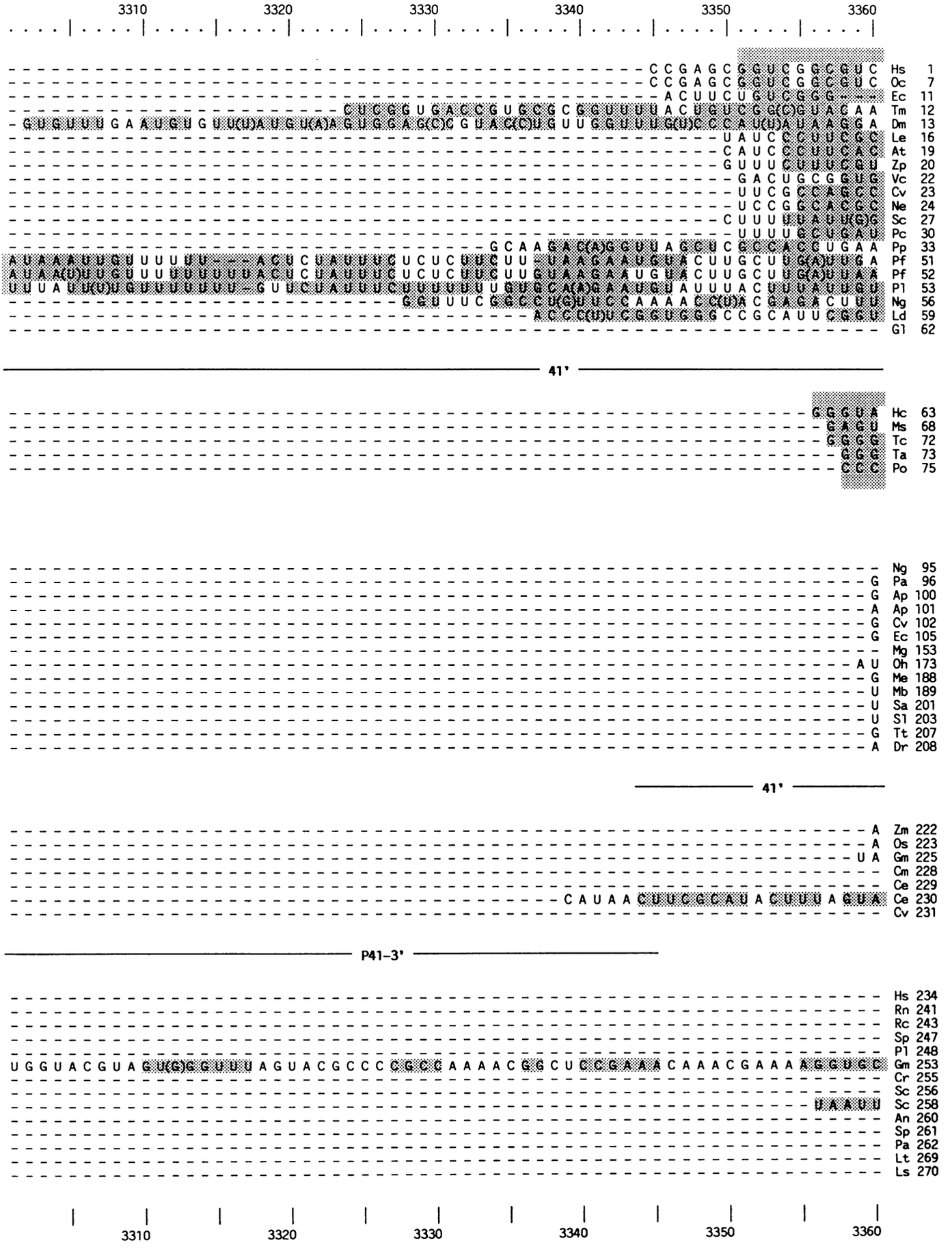

3010
3020
3030
3040
3050
3060
P41–1'
P41–2

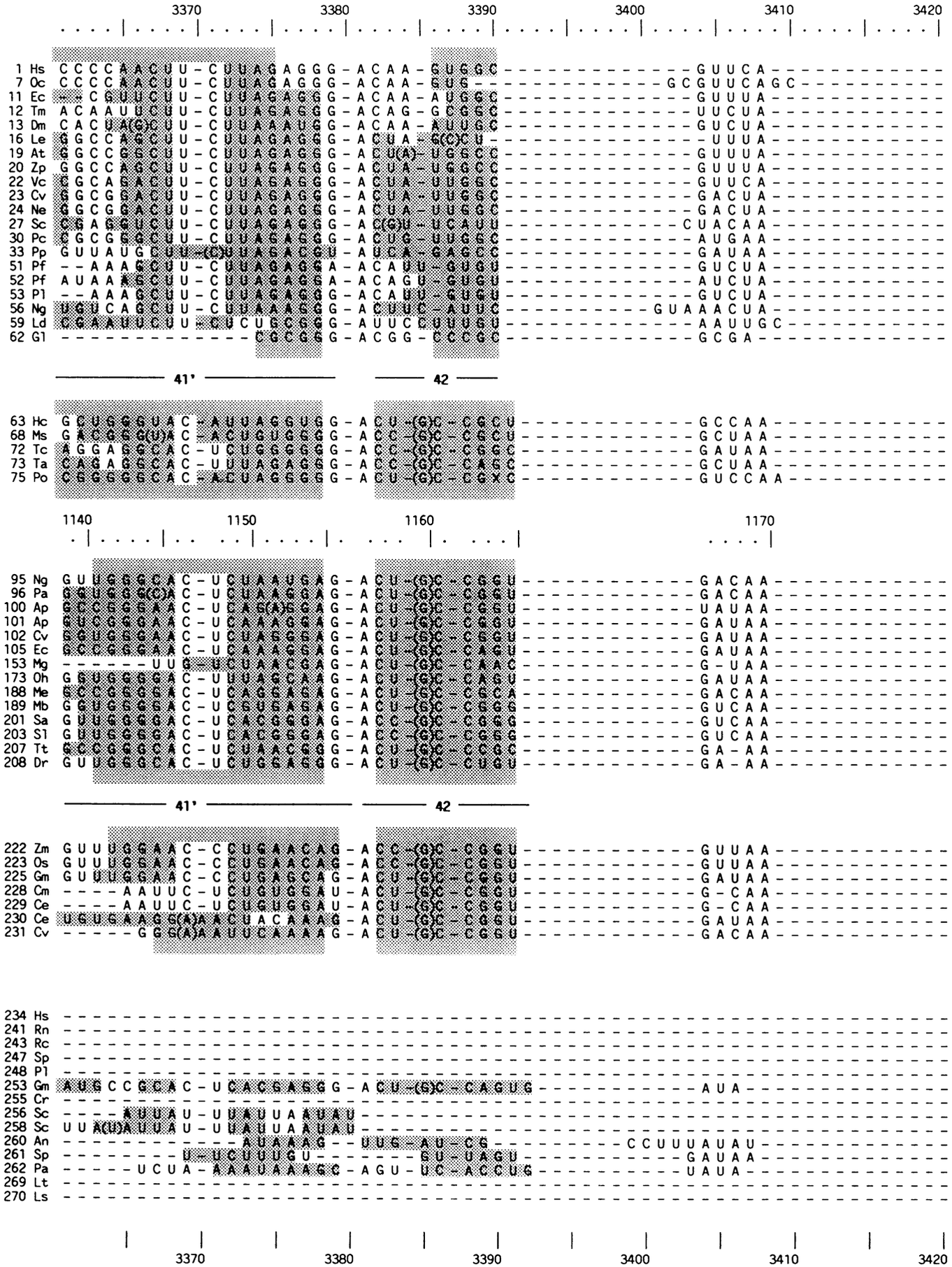

3070
3080
3090
3100
3110
3120
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
P41-2
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
G C C U U U C G A A U U C G A A G C A C U U U C U A G U G U G C G C U G U U U U U U G A U U G C A G C(U)A G C G A G C A Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
3070
3080
3090
3100
3110
3120

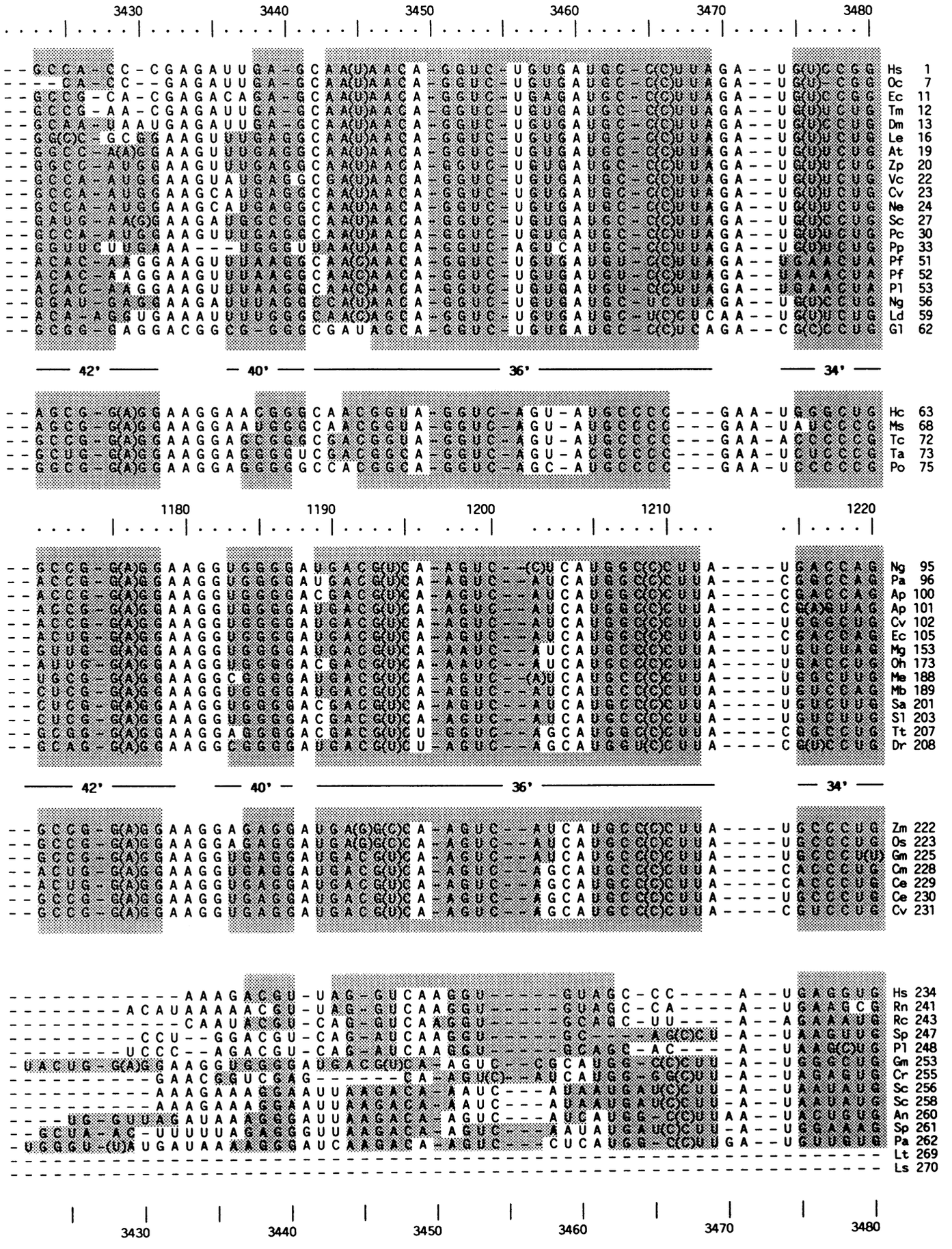

3130
3140
3150
3160
3170
3180
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld
62 Gl
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
P41-2
P41-2'
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc
258 Sc
260 An
261 Sp
262 Pa
269 Lt
270 Ls

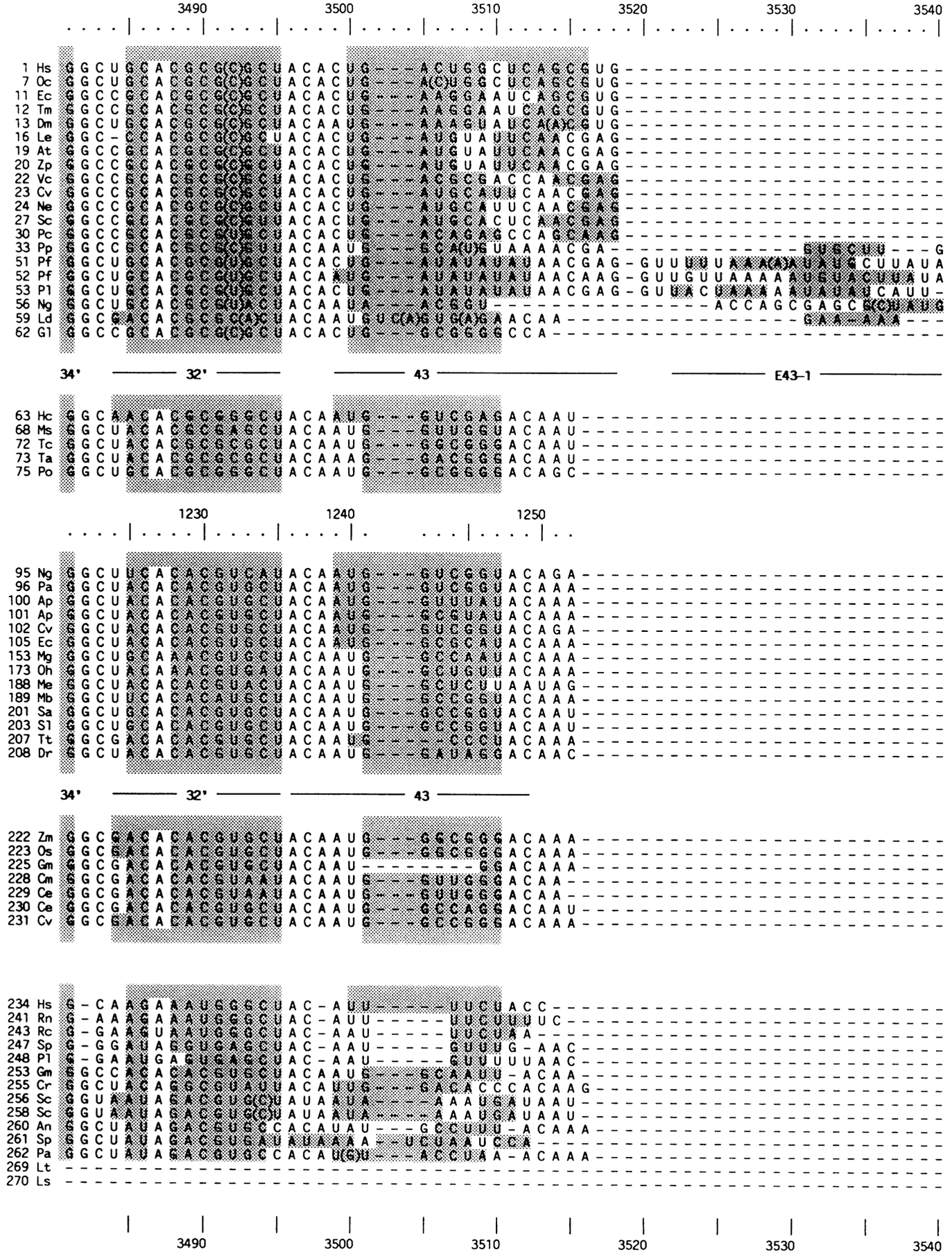

3190
3200
3210
3220
3230
3240
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
P41-2'
P41-3
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
AGAAAGGGCUUUUCUCGCUUGUUUAGUAAAGUCCAGUUUUUGGCCGUUAUCUUGCAGGUGA Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270
3190
3200
3210
3220
3230
3240

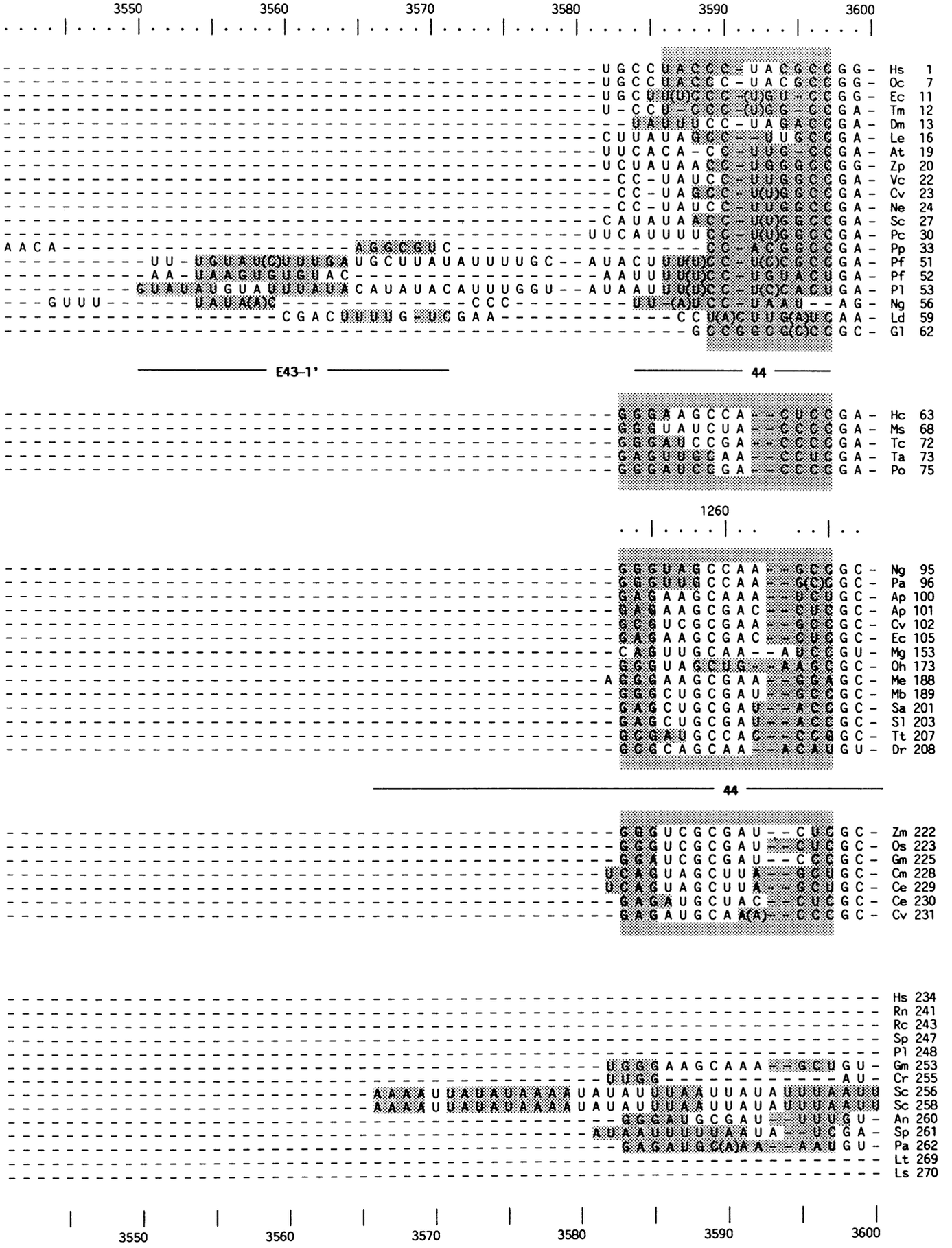

3250
3260
3270
3280
3290
3300
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld
62 Gl
41'
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
P41-3
P41-3'
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc
258 Sc
260 An
261 Sp
262 Pa
269 Lt
270 Ls


3310
3320
3330
3340
3350
3360
41'
41'
P41–3'


3370
3380
3390
3400
3410
3420
41'
42
1140
1150
1160
1170


3430
3440
3450
3460
3470
3480
42'
40'
36'
34'
1180
1190
1200
1210
1220


3490
3500
3510
3520
3530
3540
34'
32'
43
E43-1
1230
1240
1250
34'
32'
43


3550
3560
3570
3580
3590
3600
E43-1'
44
1260
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
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Rc 243
Sp 247
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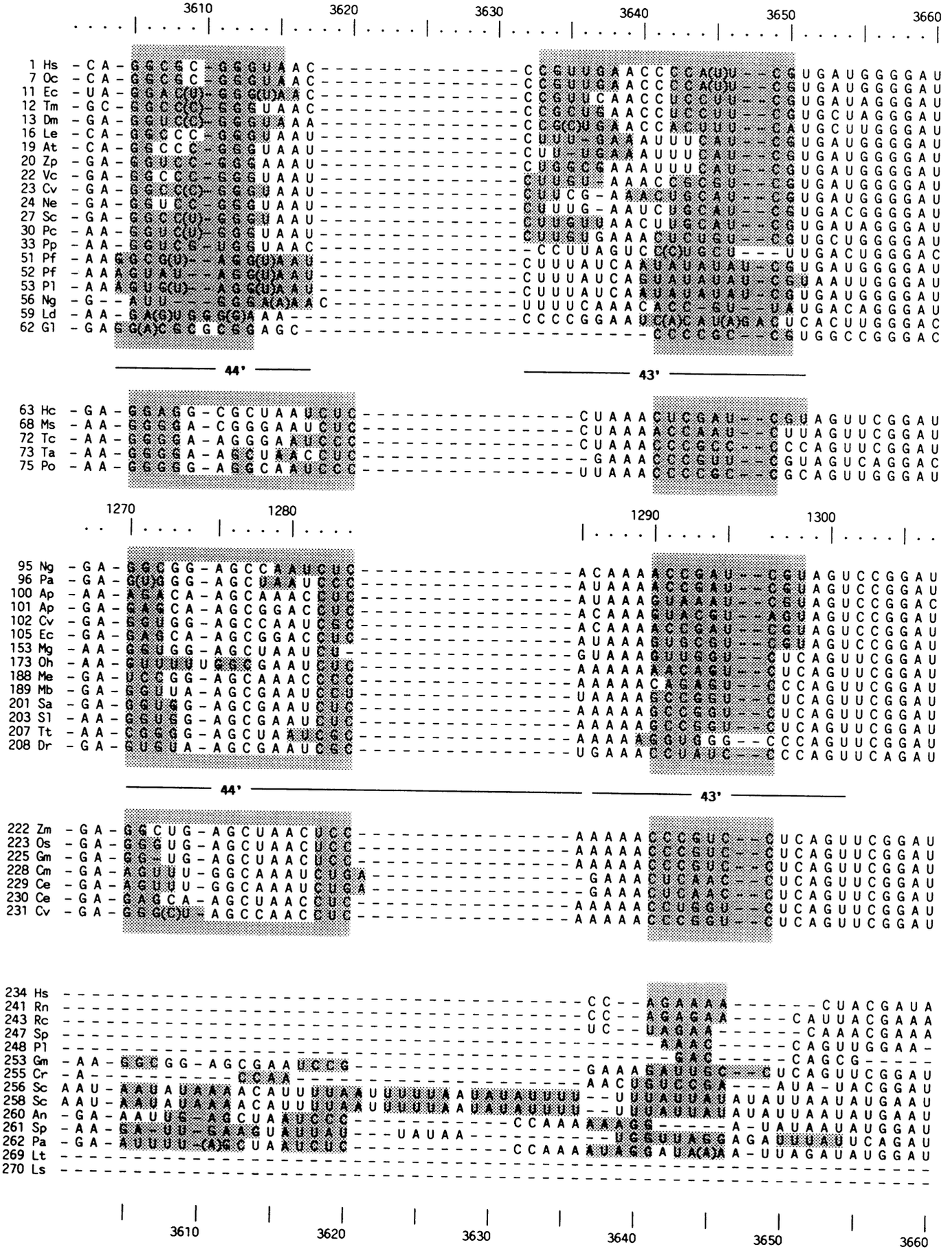
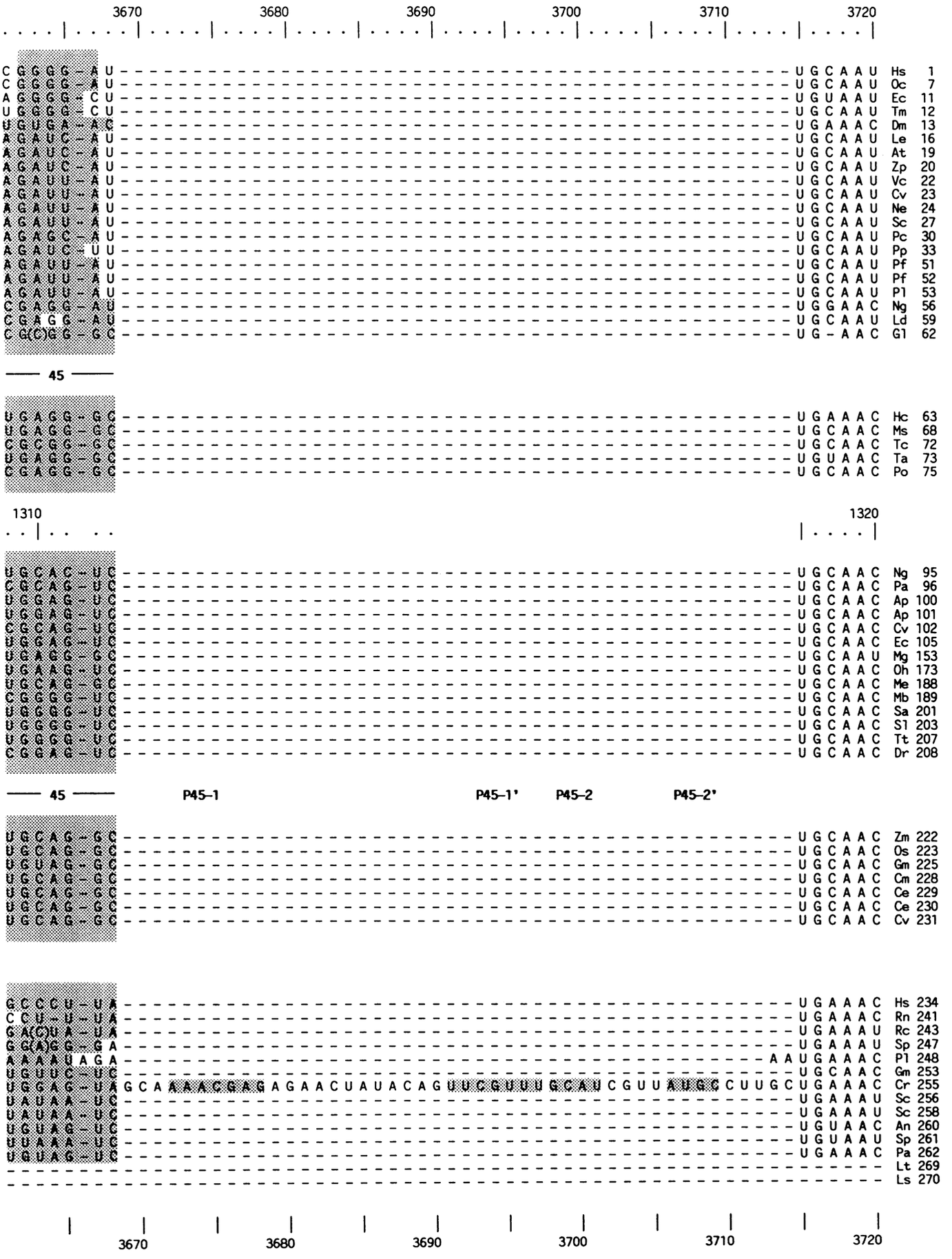
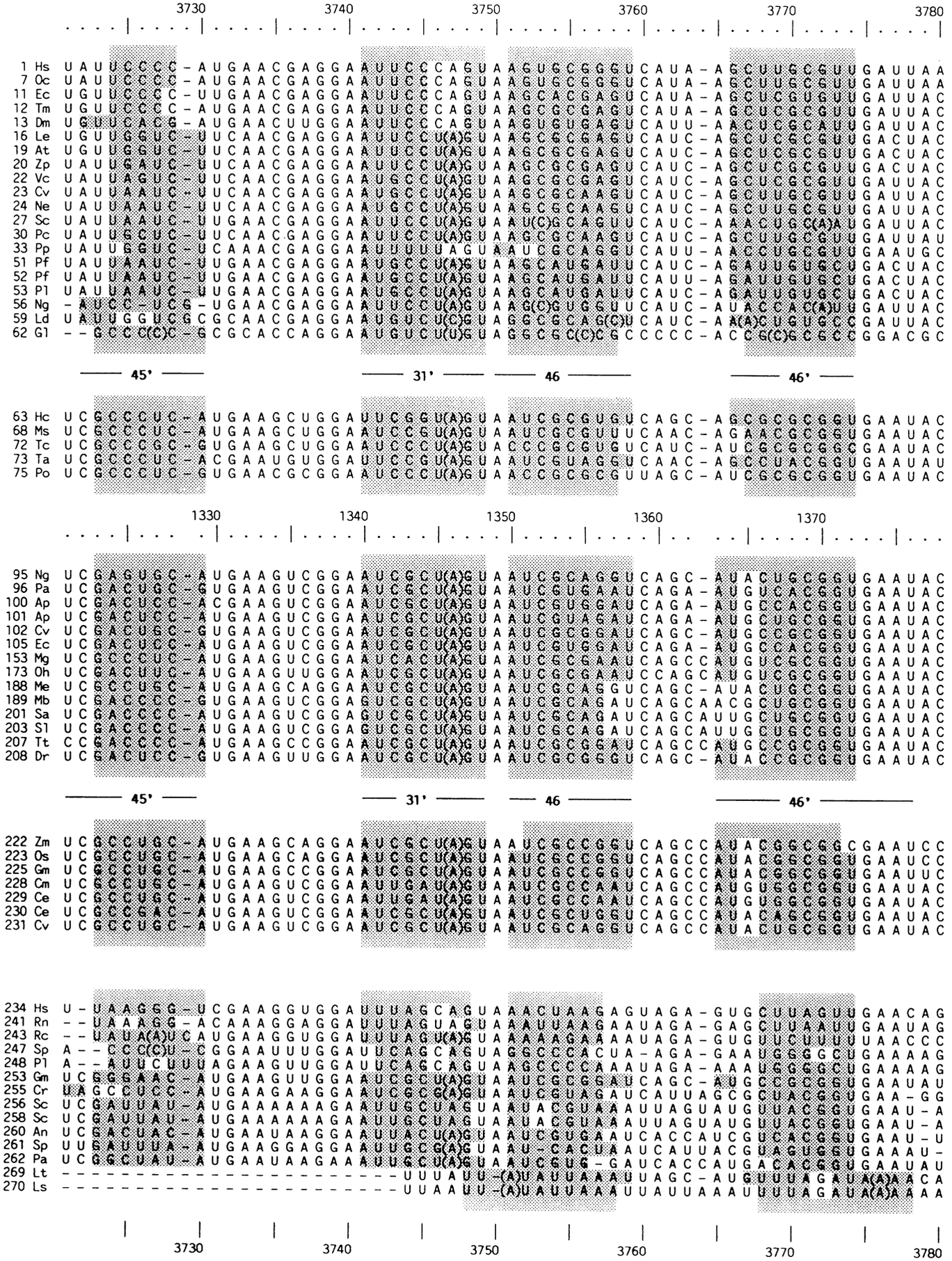
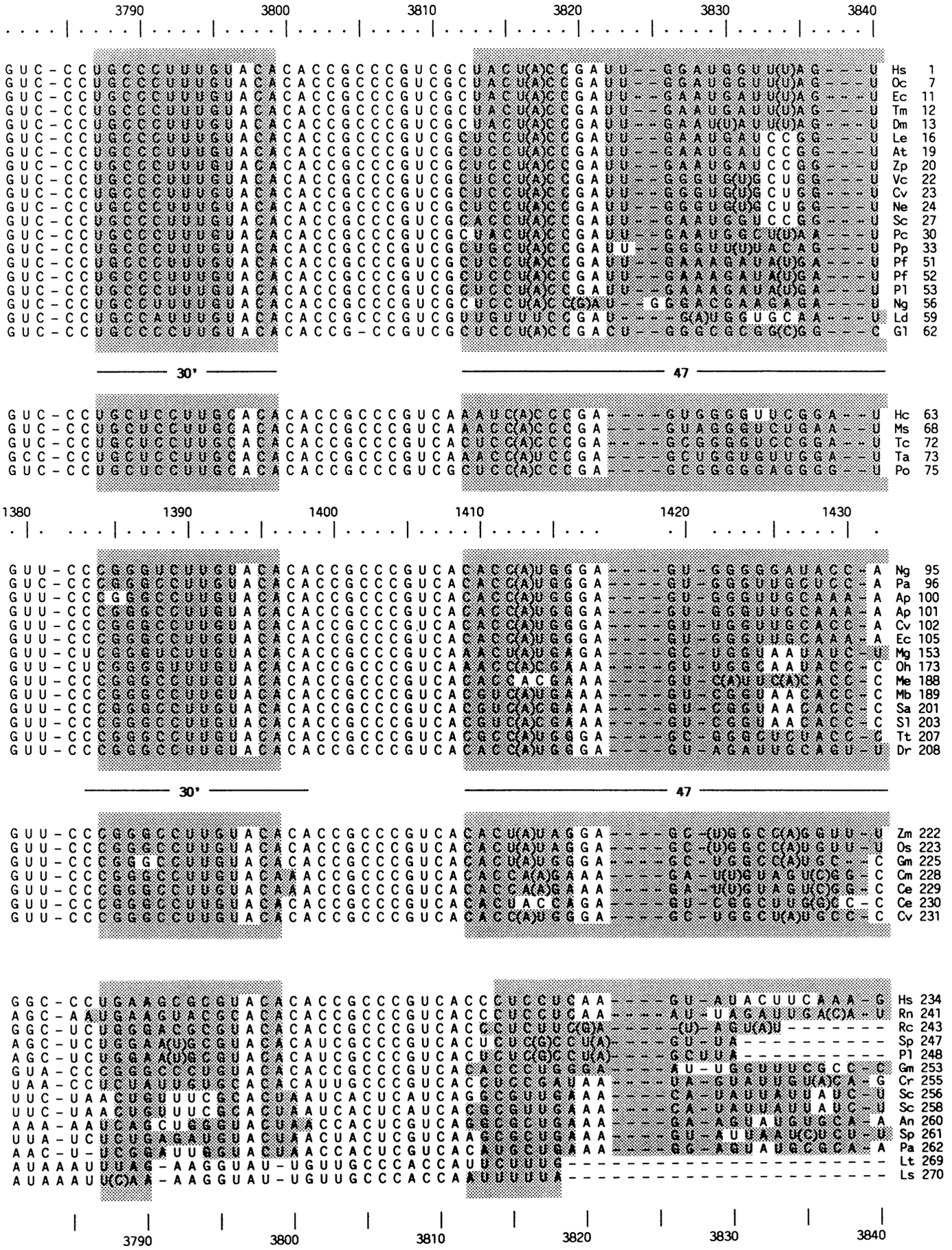
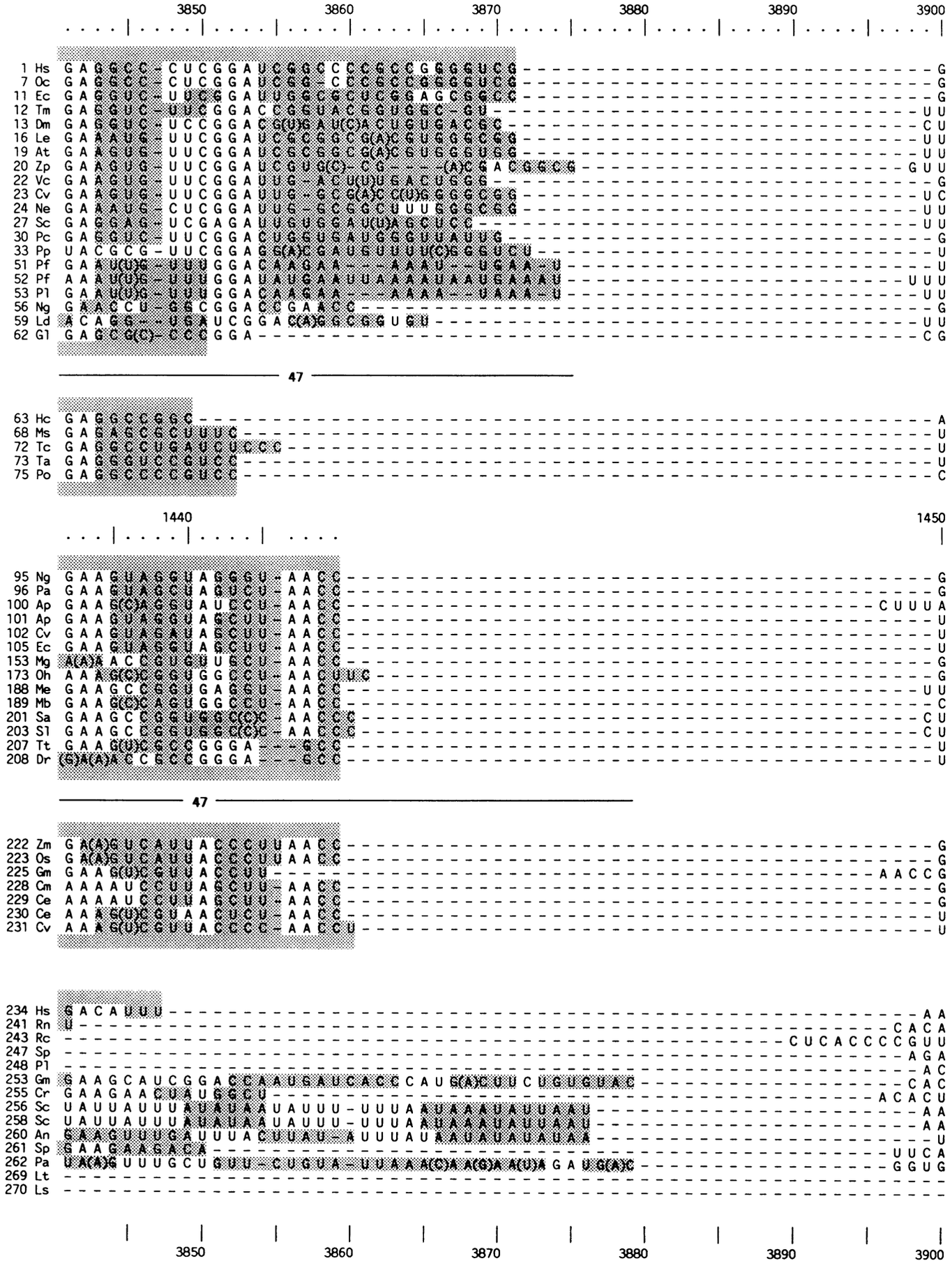
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
Pa 262
Lt 269
Ls 270


3610
3620
3630
3640
3650
3660
44'
43'
1270
1280
1290
1300
44'
43'
3610
3620
3630
3640
3650
3660


3670
3680
3690
3700
3710
3720
45
1310
1320
45
P45-1
P45-1'
P45-2
P45-2'
3670
3680
3690
3700
3710
3720


3730
3740
3750
3760
3770
3780
45'
31'
46
46'
1330
1340
1350
1360
1370


3790
3800
3810
3820
3830
3840
30'
47
1380
1390
1400
1410
1420
1430
30'
47
3790
3800
3810
3820
3830
3840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3850
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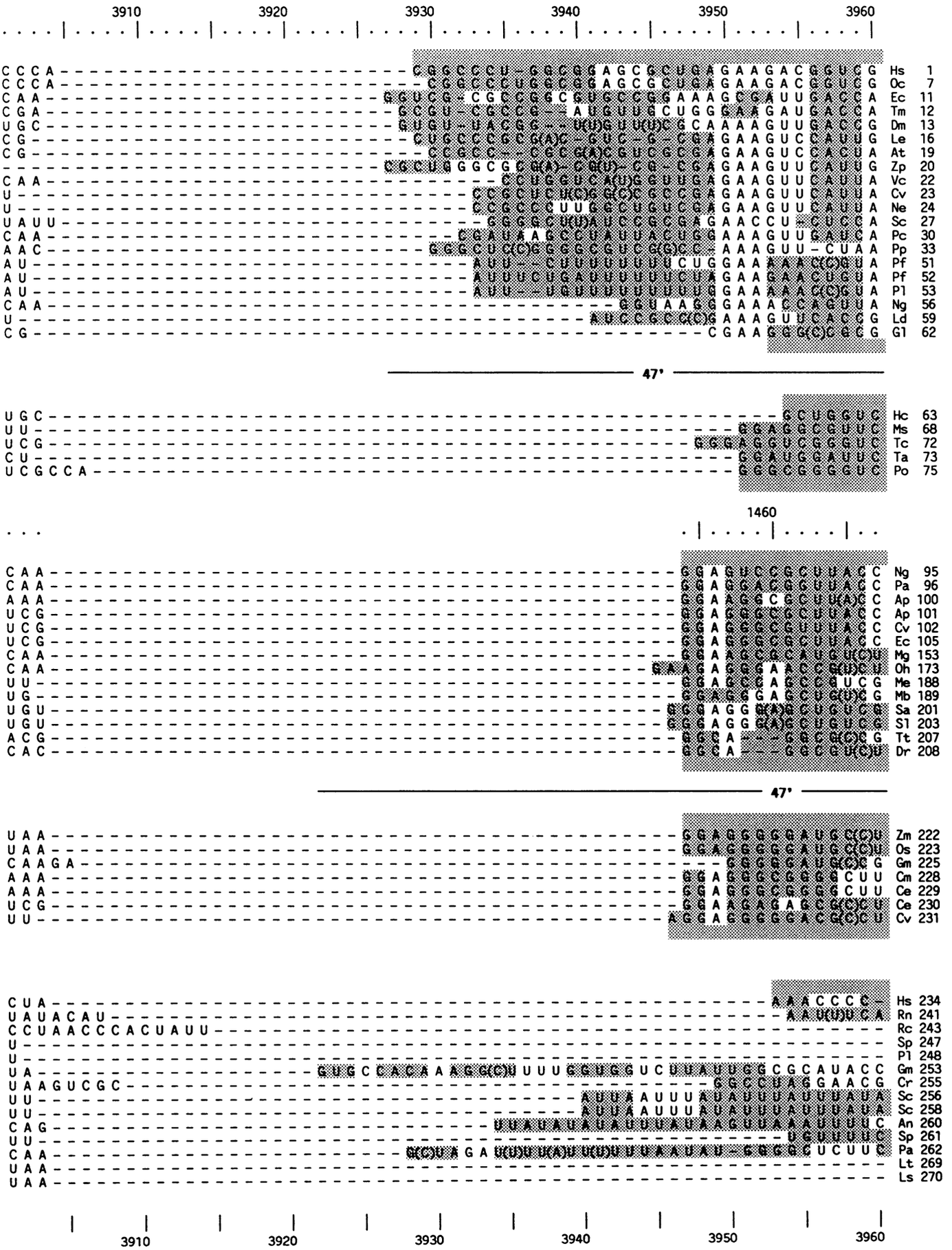
3890
3900


3910
3920
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3950
3960
47'
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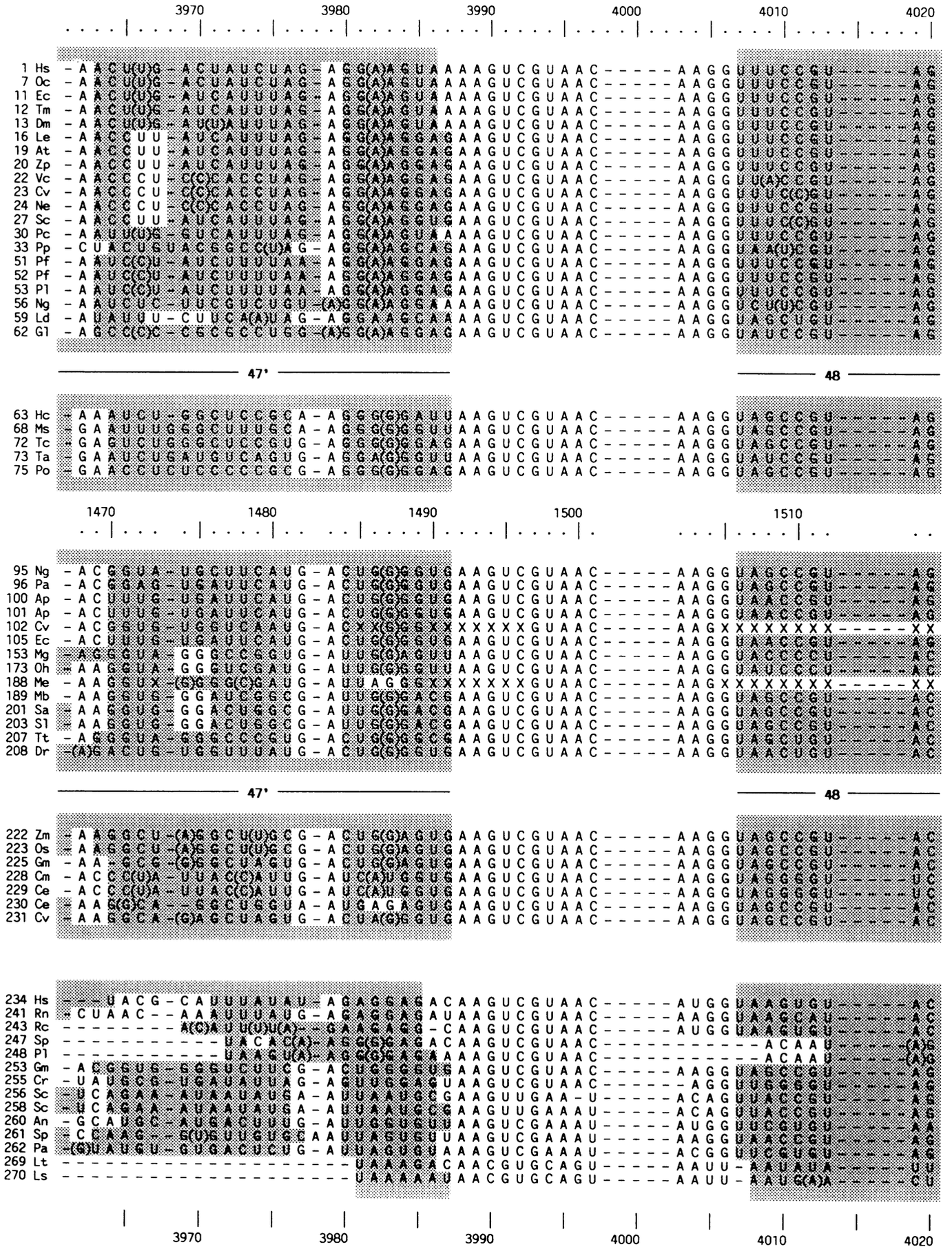
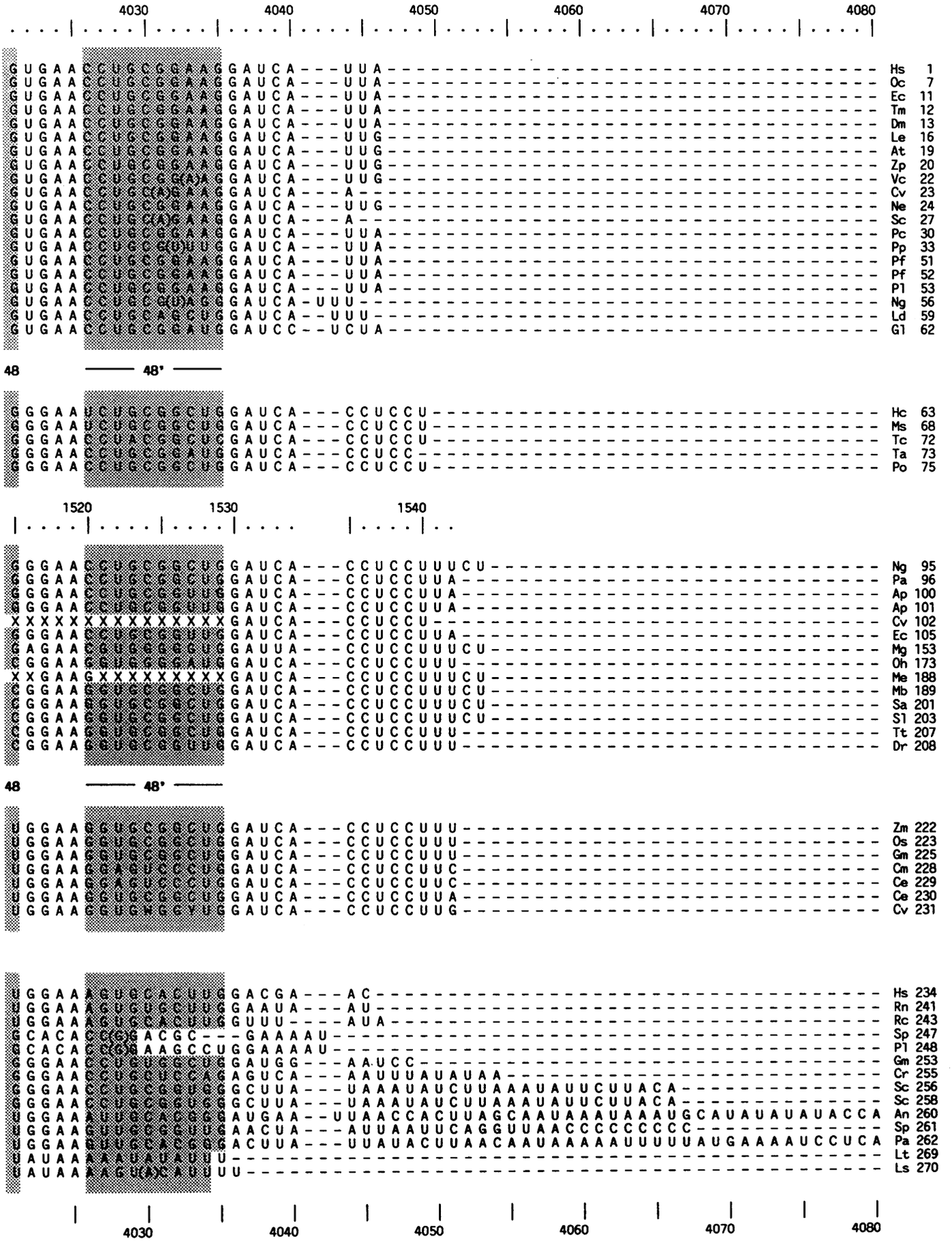
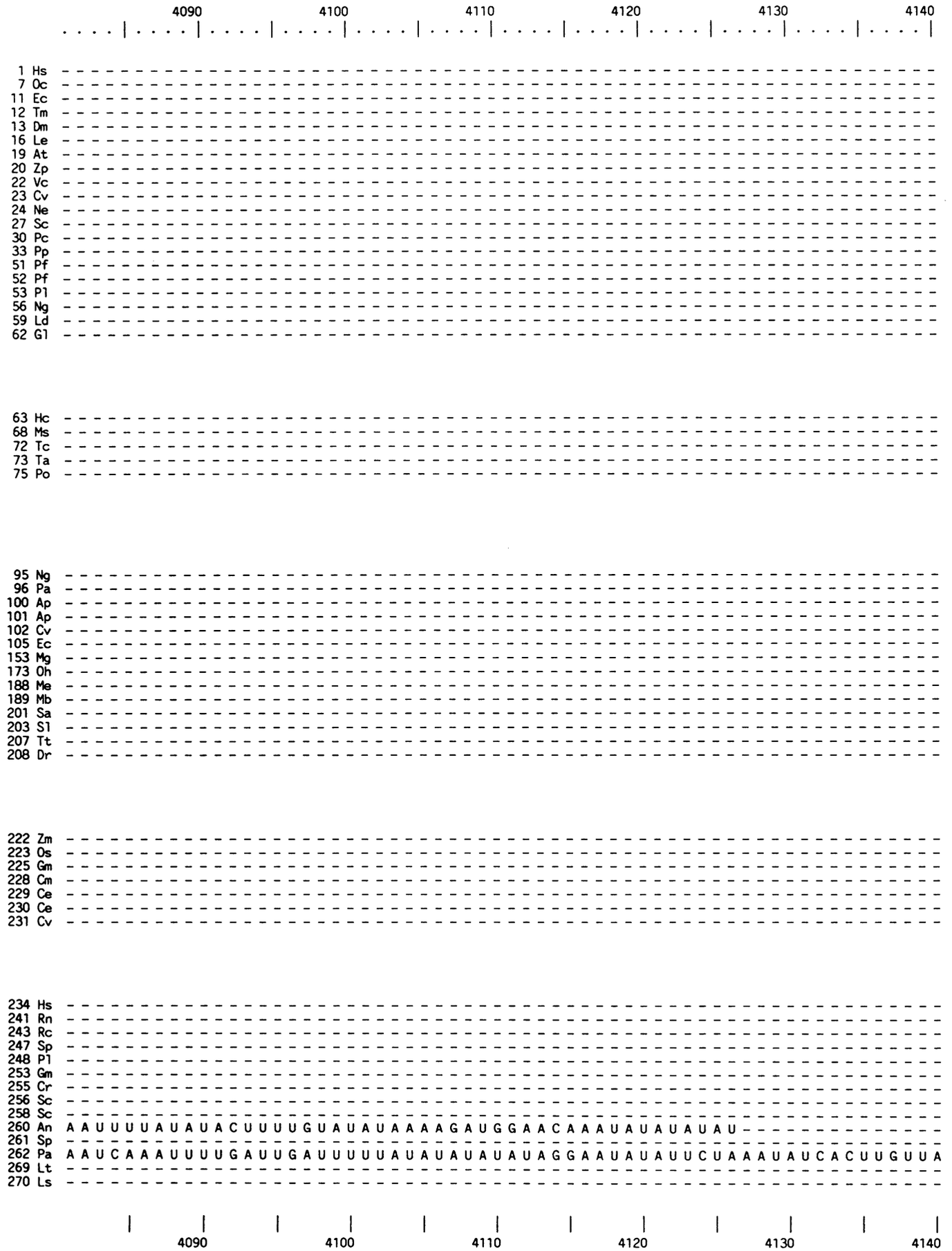
47'
3910
3920
3930
3940
3950
3960


3970
3980
3990
4000
4010
4020
47'
48
1470
1480
1490
1500
1510


4030
4040
4050
4060
4070
4080
48
48'
1520
1530
1540


4090
4100
4110
4120
4130
4140
1 Hs
7 Oc
11 Ec
12 Tm
13 Dm
16 Le
19 At
20 Zp
22 Vc
23 Cv
24 Ne
27 Sc
30 Pc
33 Pp
51 Pf
52 Pf
53 Pl
56 Ng
59 Ld
62 Gl
63 Hc
68 Ms
72 Tc
73 Ta
75 Po
95 Ng
96 Pa
100 Ap
101 Ap
102 Cv
105 Ec
153 Mg
173 Oh
188 Me
189 Mb
201 Sa
203 Sl
207 Tt
208 Dr
222 Zm
223 Os
225 Gm
228 Cm
229 Ce
230 Ce
231 Cv
234 Hs
241 Rn
243 Rc
247 Sp
248 Pl
253 Gm
255 Cr
256 Sc
258 Sc
260 An A A U U U U A U A U A C U U U U G U A U A U A A A A G A U G G A A C A A A U A U A U A U A U
261 Sp
262 Pa A A U C A A A U U U U G A U U G A U U U U U A U A U A U A U A U A G G A A U A U A U U C U A A A U A U C A C U U G U U A
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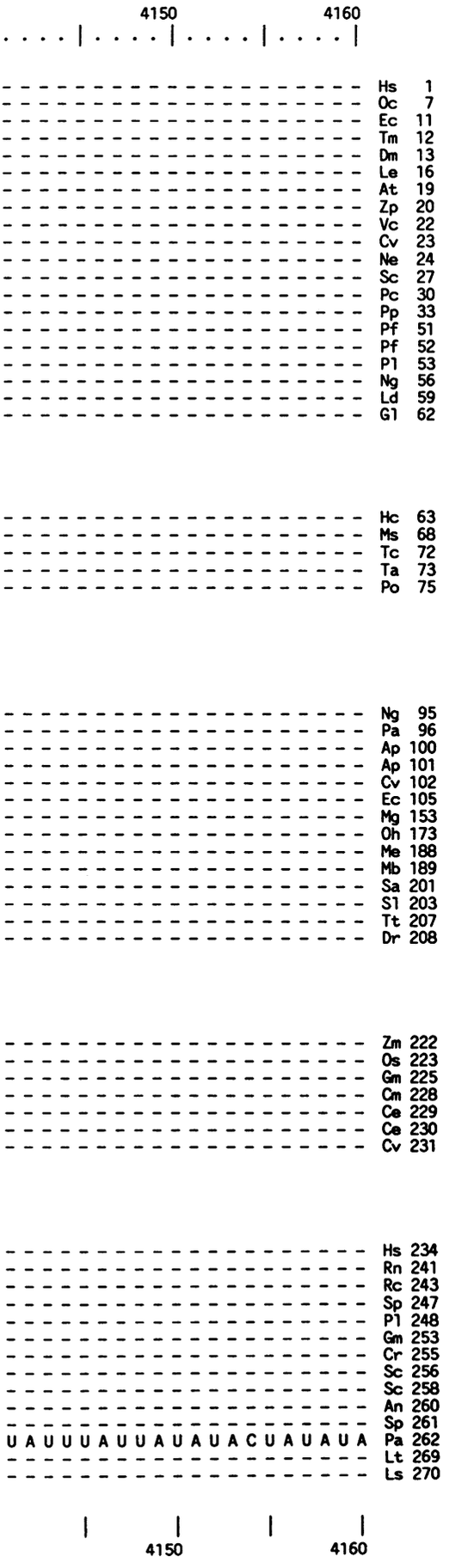
270 Ls
4090
4100
4110
4120
4130
4140


4150
4160
Hs 1
Oc 7
Ec 11
Tm 12
Dm 13
Le 16
At 19
Zp 20
Vc 22
Cv 23
Ne 24
Sc 27
Pc 30
Pp 33
Pf 51
Pf 52
Pl 53
Ng 56
Ld 59
Gl 62
Hc 63
Ms 68
Tc 72
Ta 73
Po 75
Ng 95
Pa 96
Ap 100
Ap 101
Cv 102
Ec 105
Mg 153
Oh 173
Me 188
Mb 189
Sa 201
Sl 203
Tt 207
Dr 208
Zm 222
Os 223
Gm 225
Cm 228
Ce 229
Ce 230
Cv 231
Hs 234
Rn 241
Rc 243
Sp 247
Pl 248
Gm 253
Cr 255
Sc 256
Sc 258
An 260
Sp 261
U A U U U A U U A U A U A C U A U A U A Pa 262
Lt 269
Ls 270
4150
4160