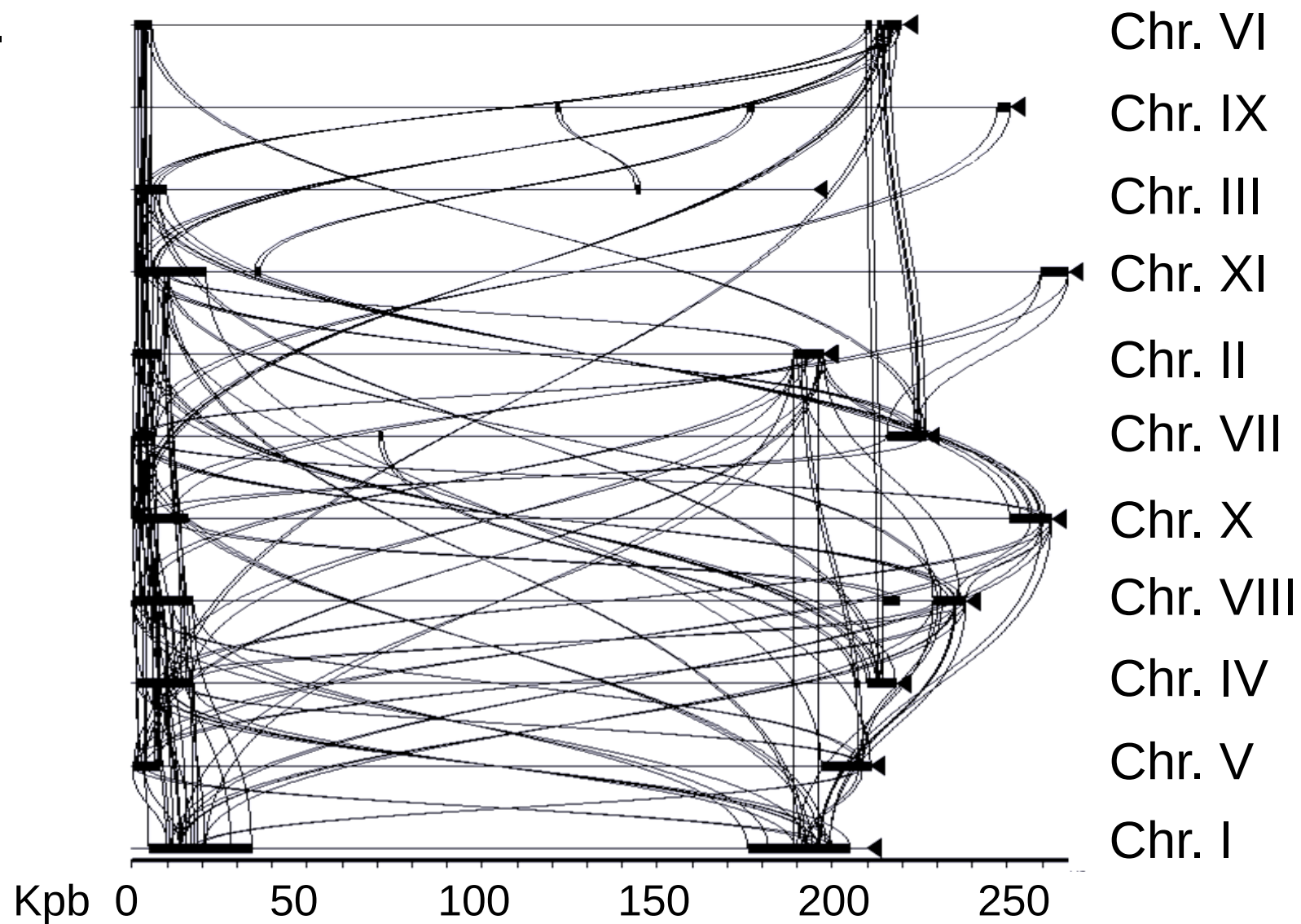
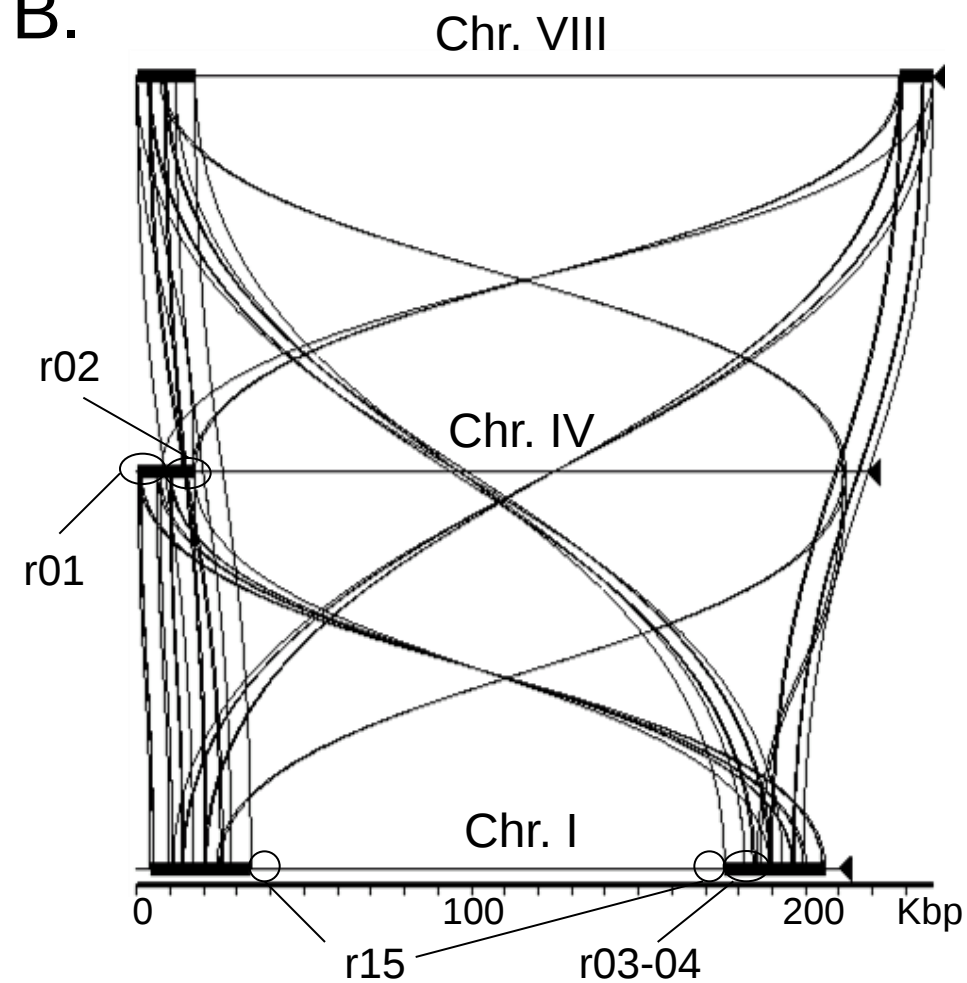
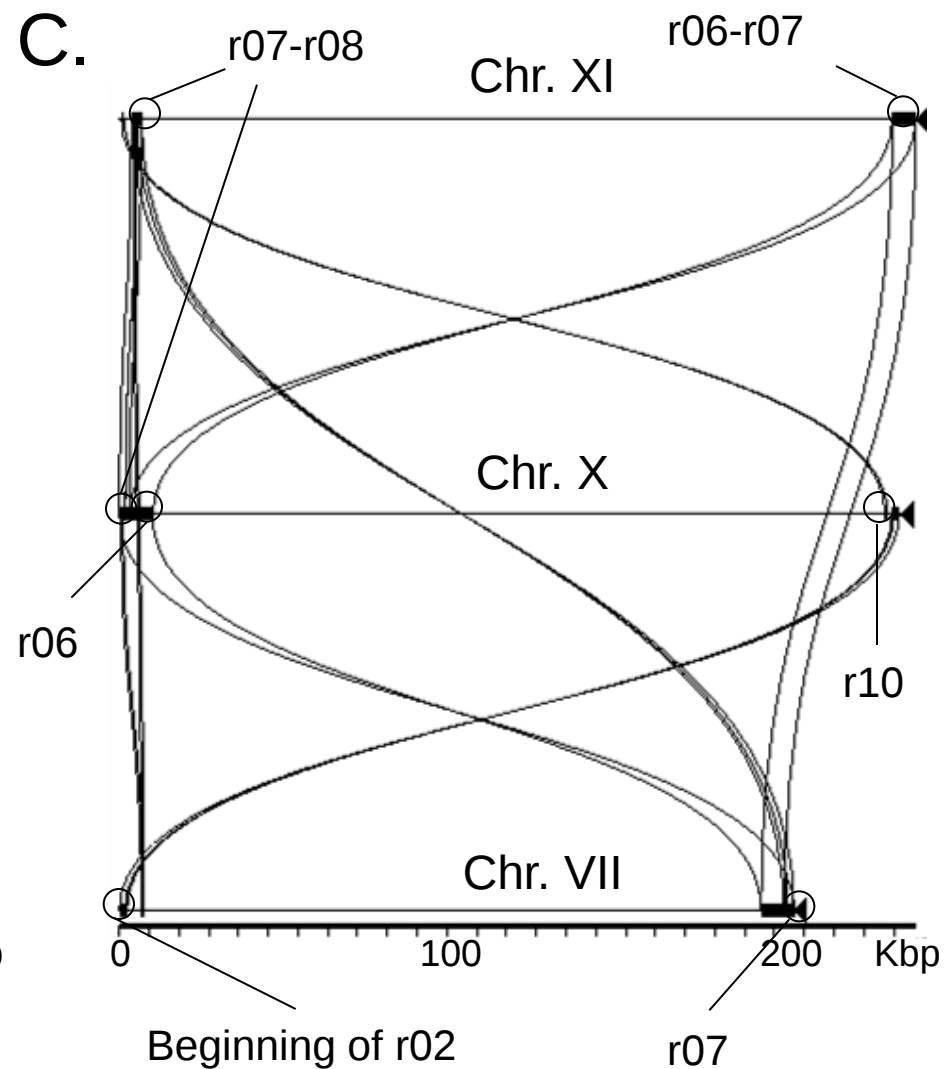
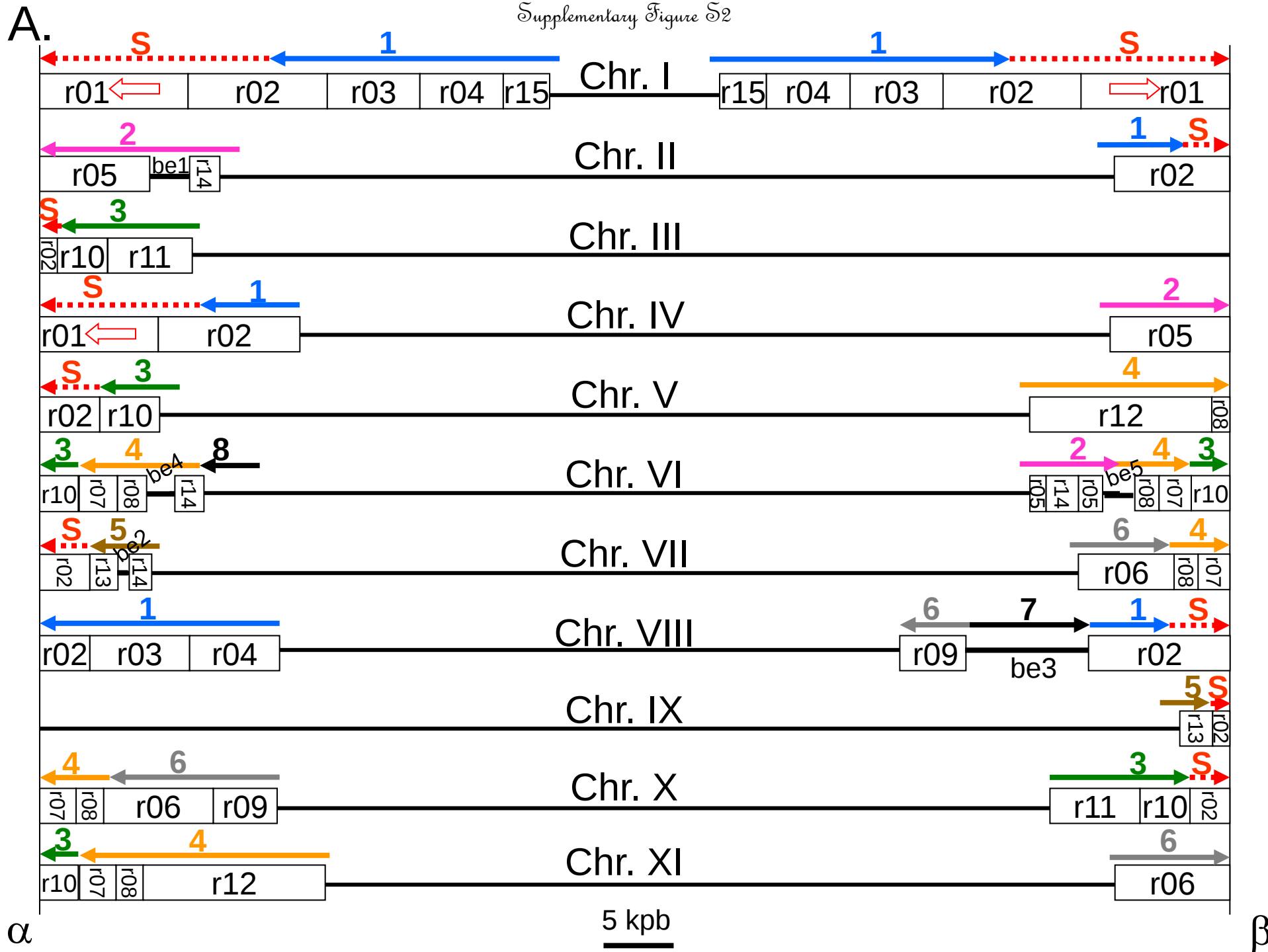


A.

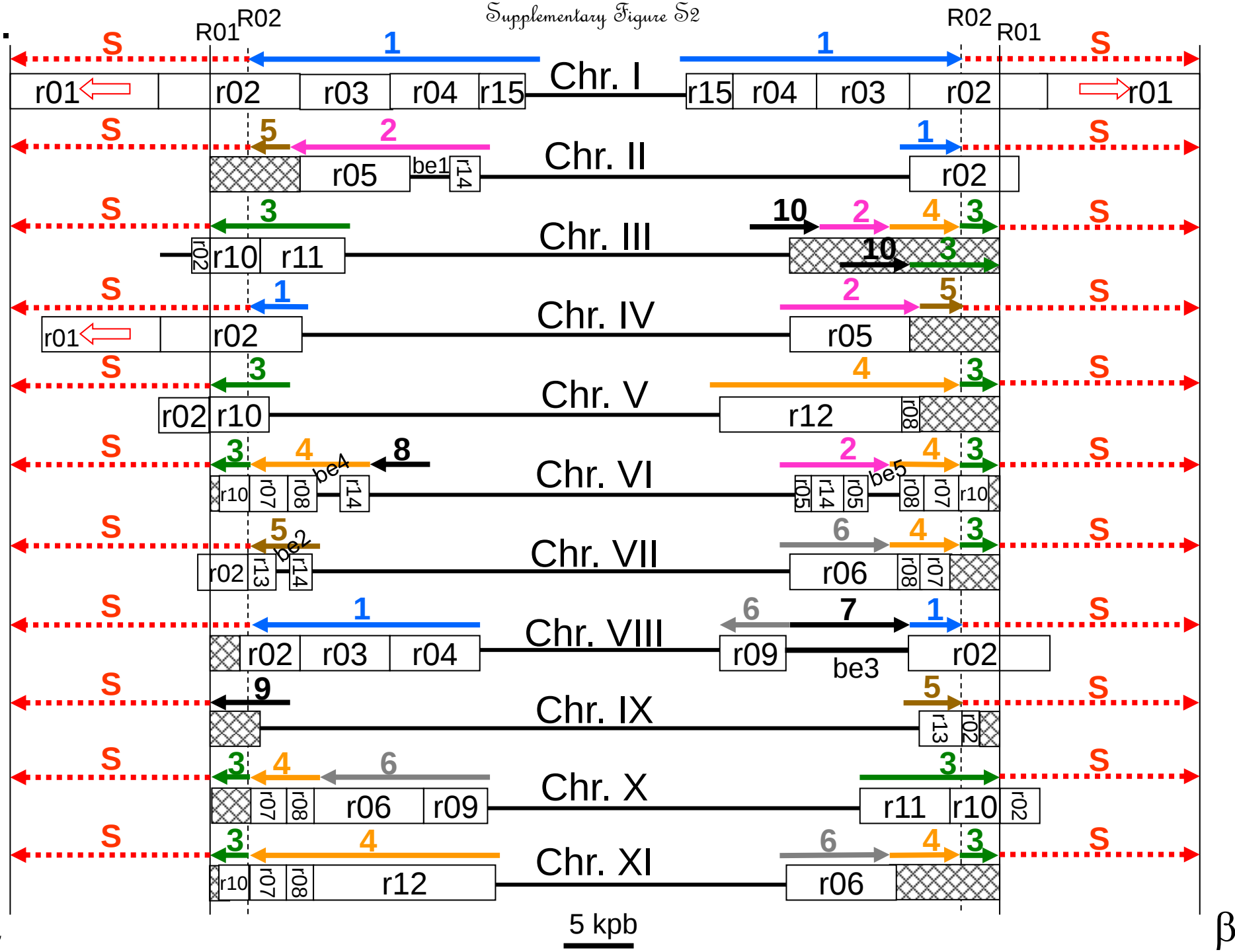


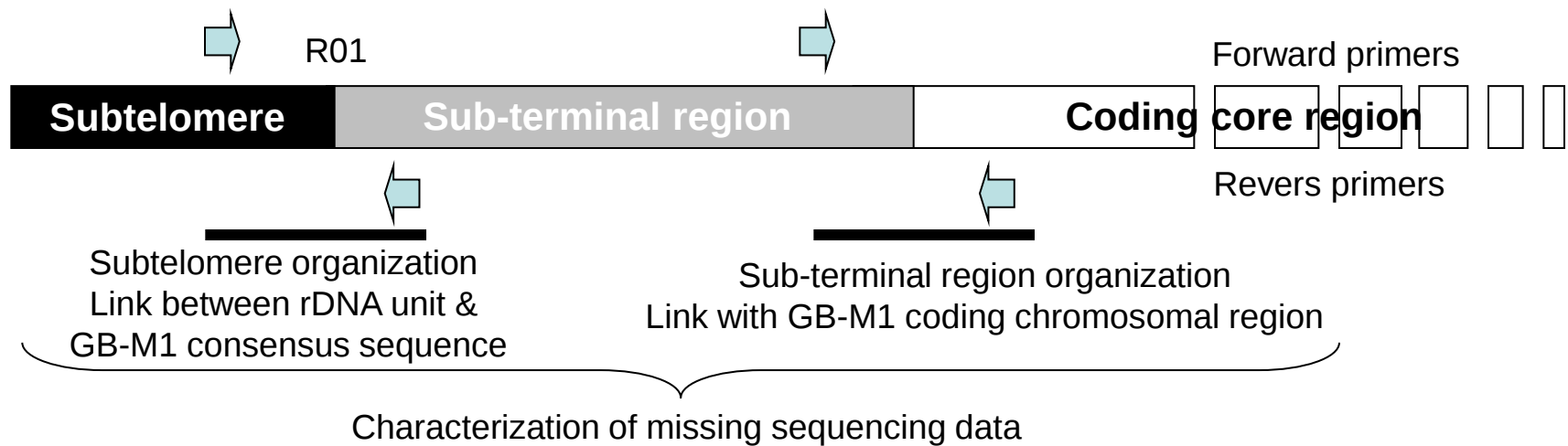
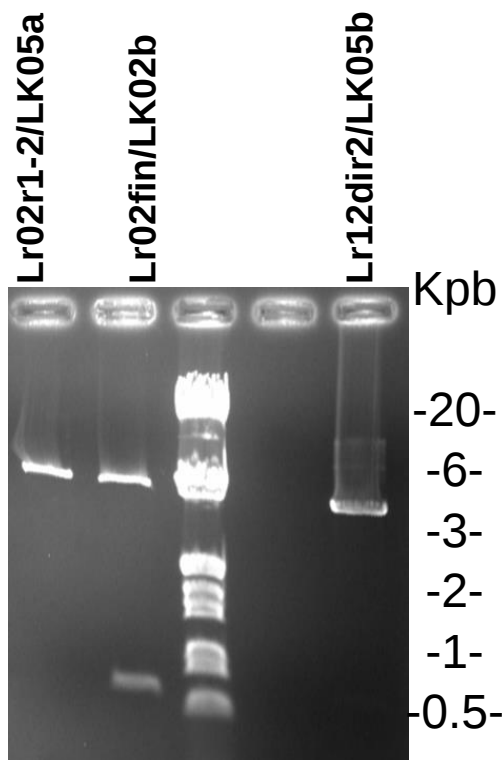
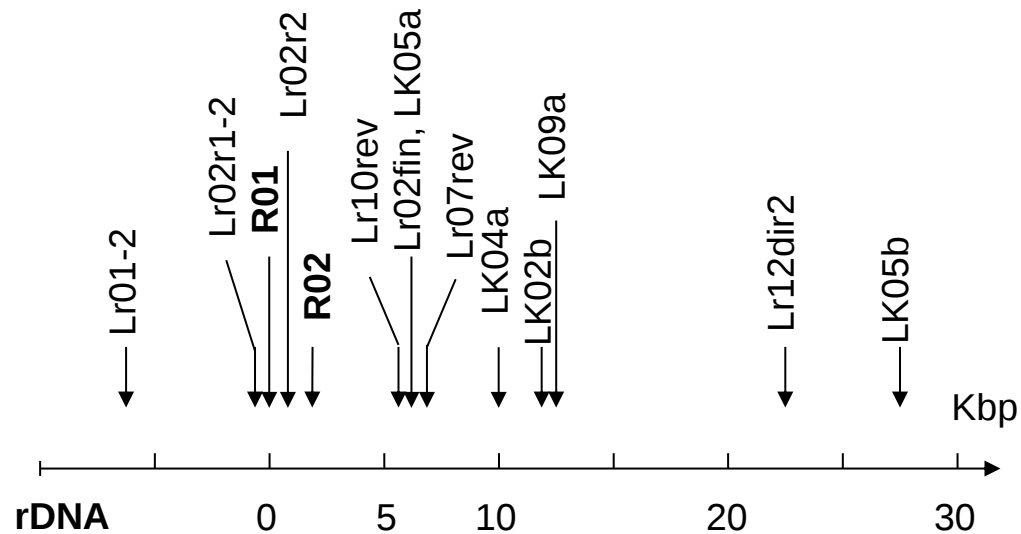
B.**C.**



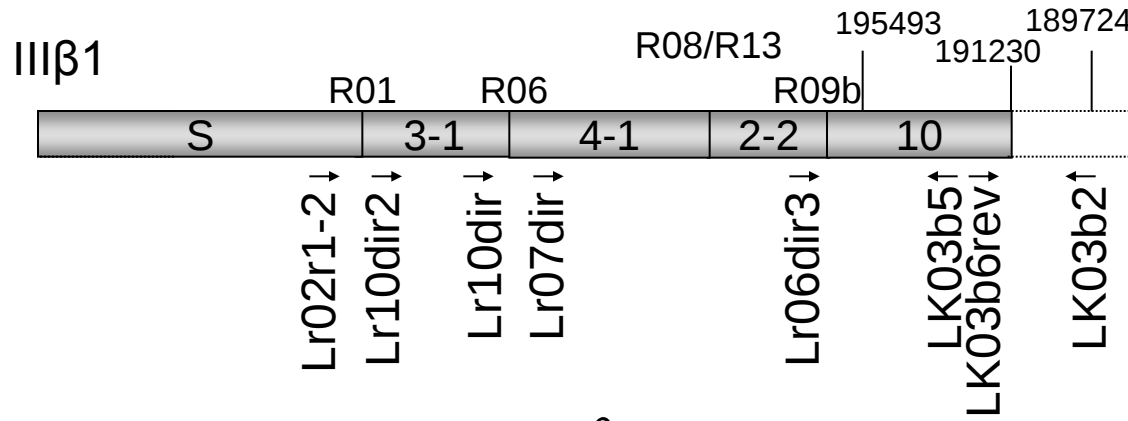
B.

Supplementary Figure S2

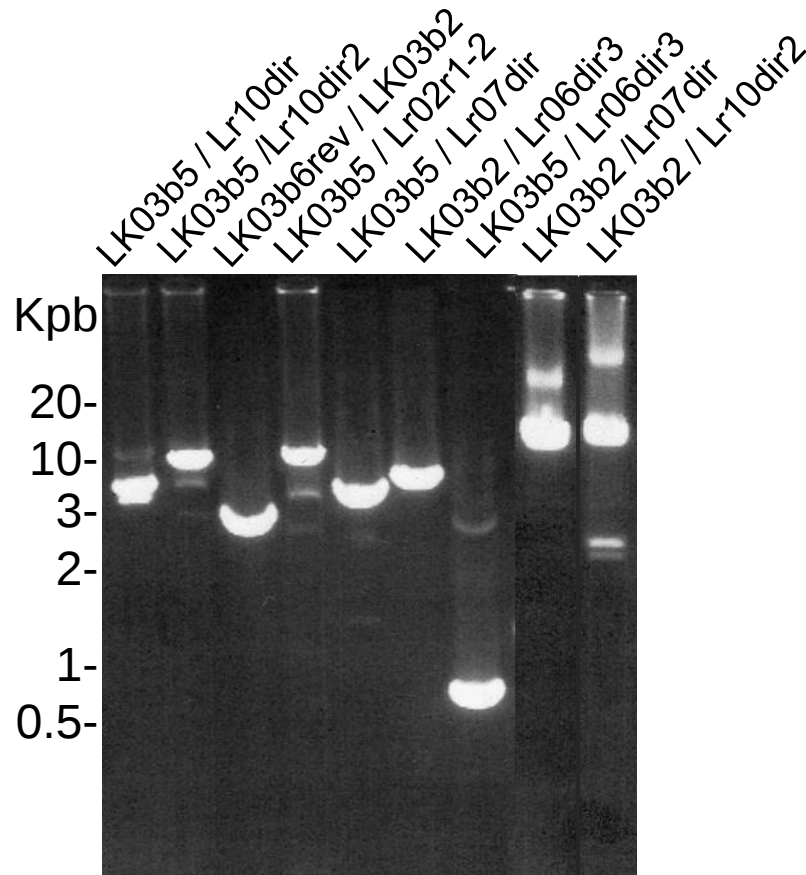


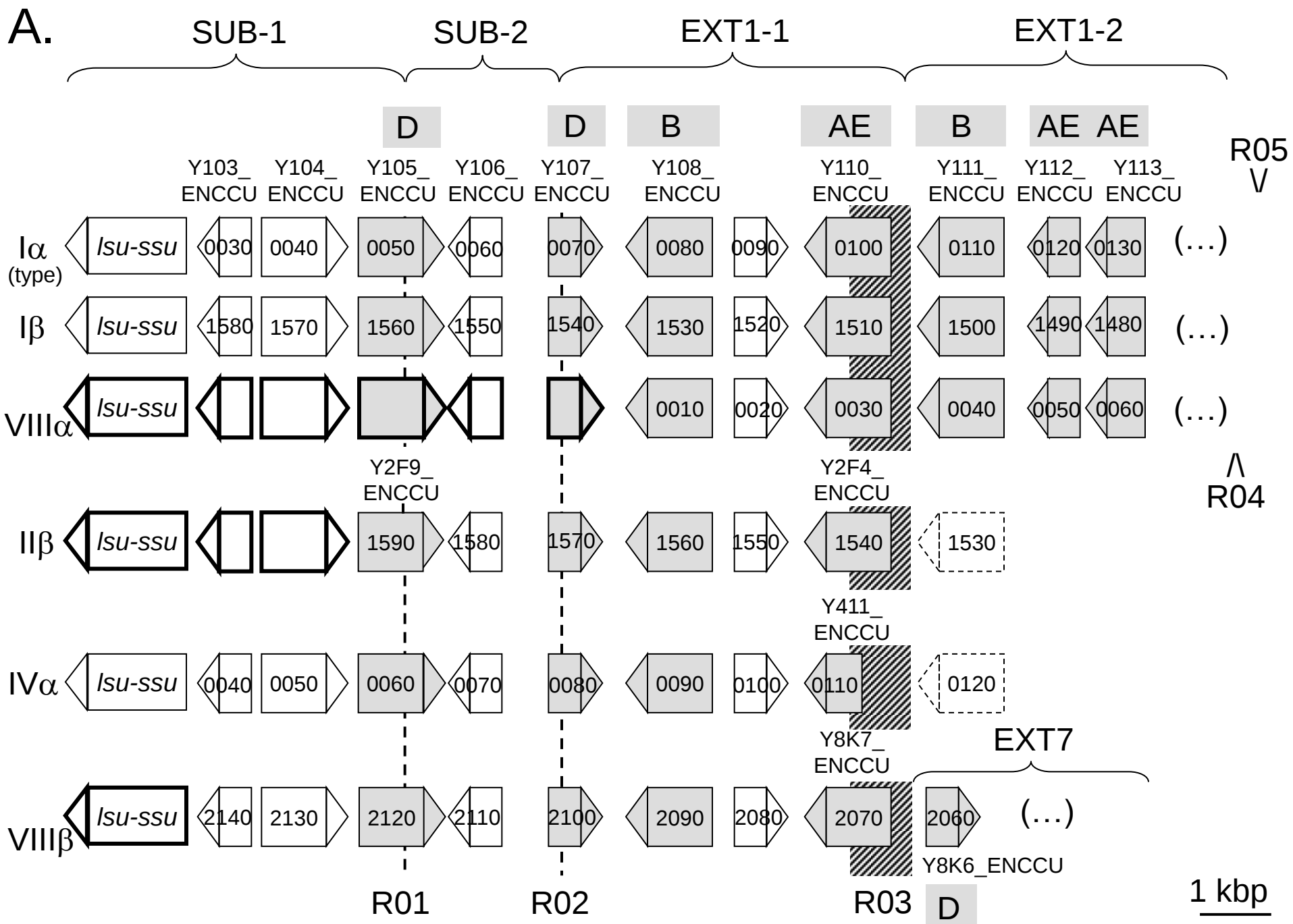
A.**B.****C.**

A.

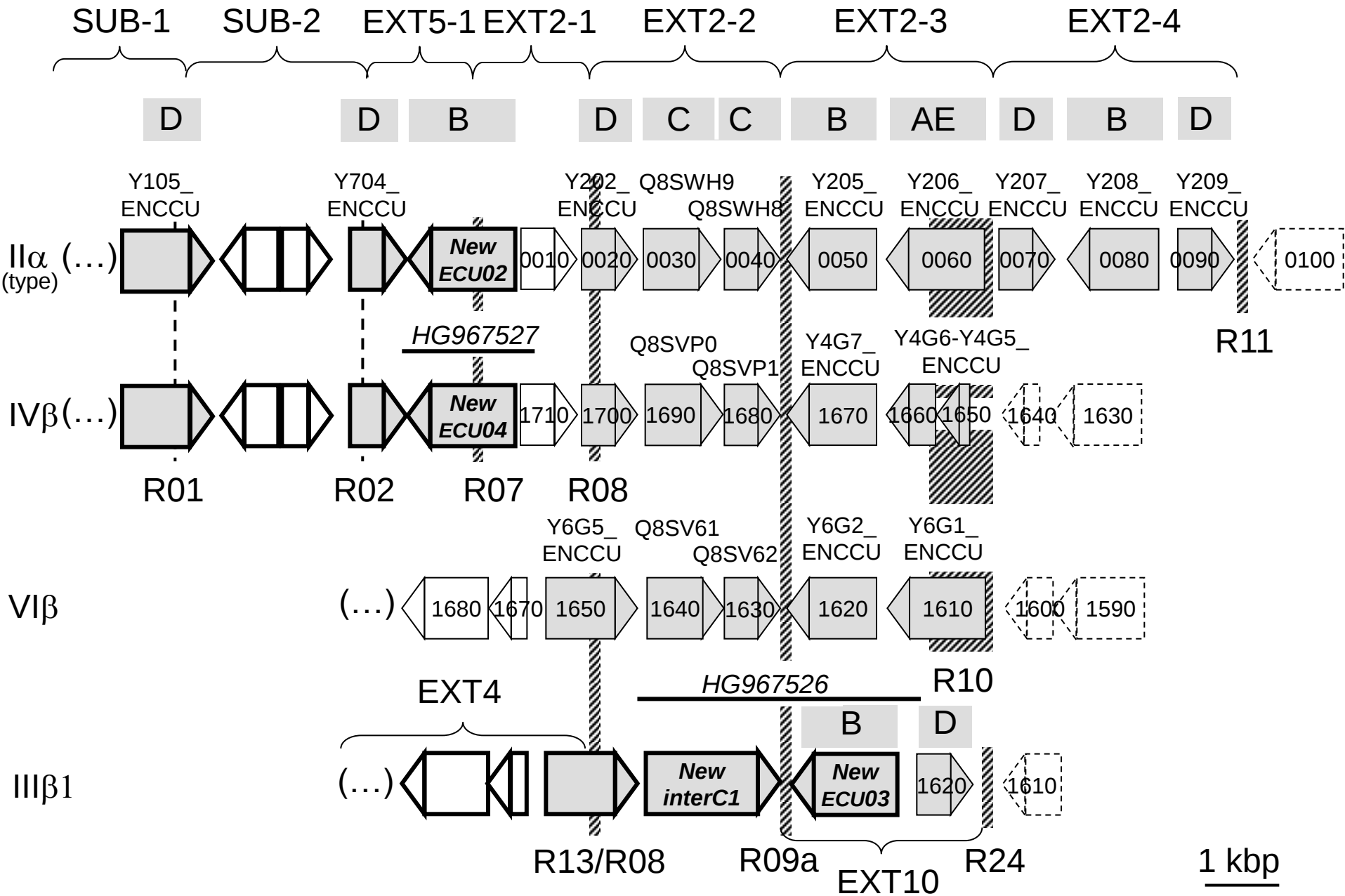


B.

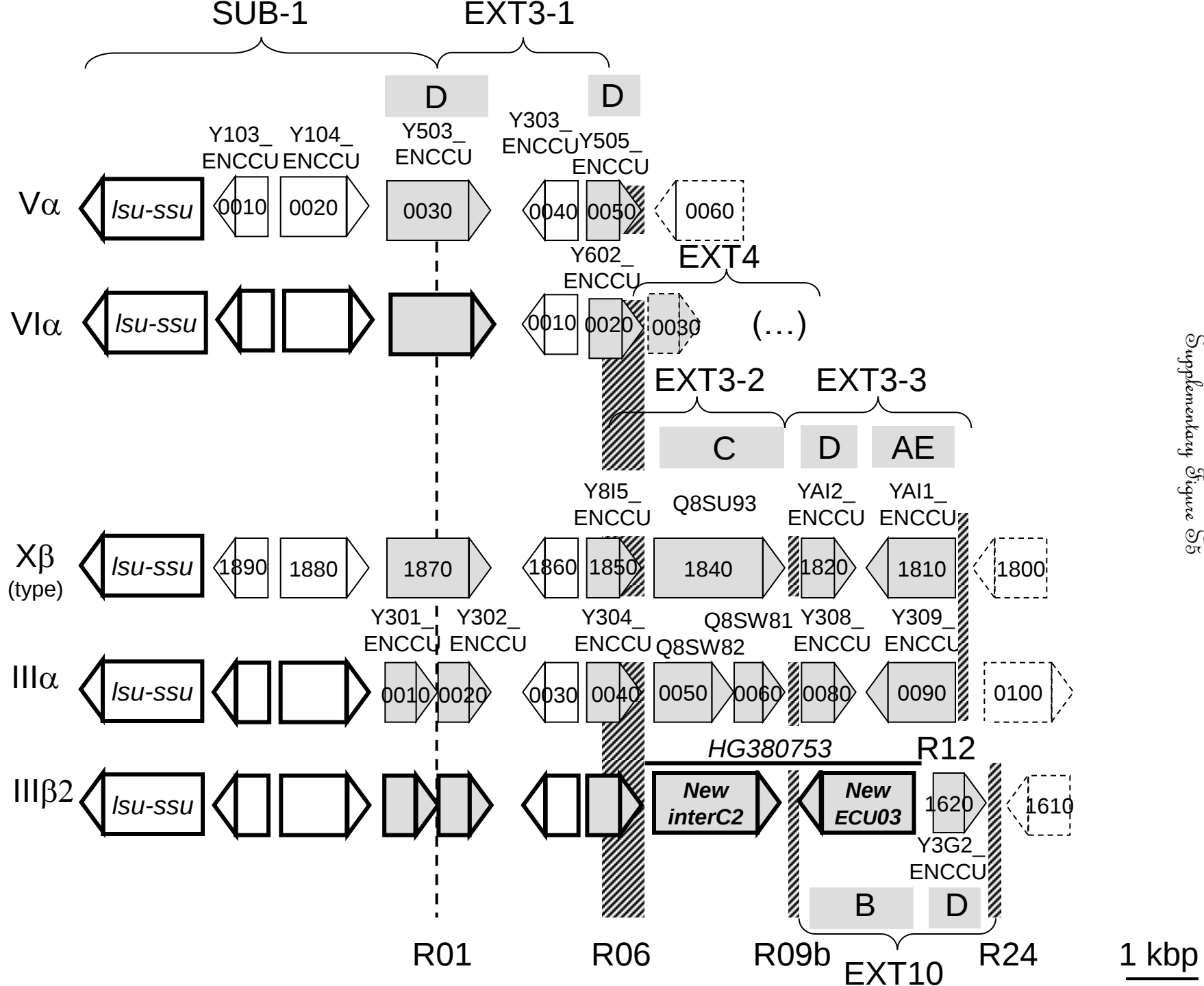


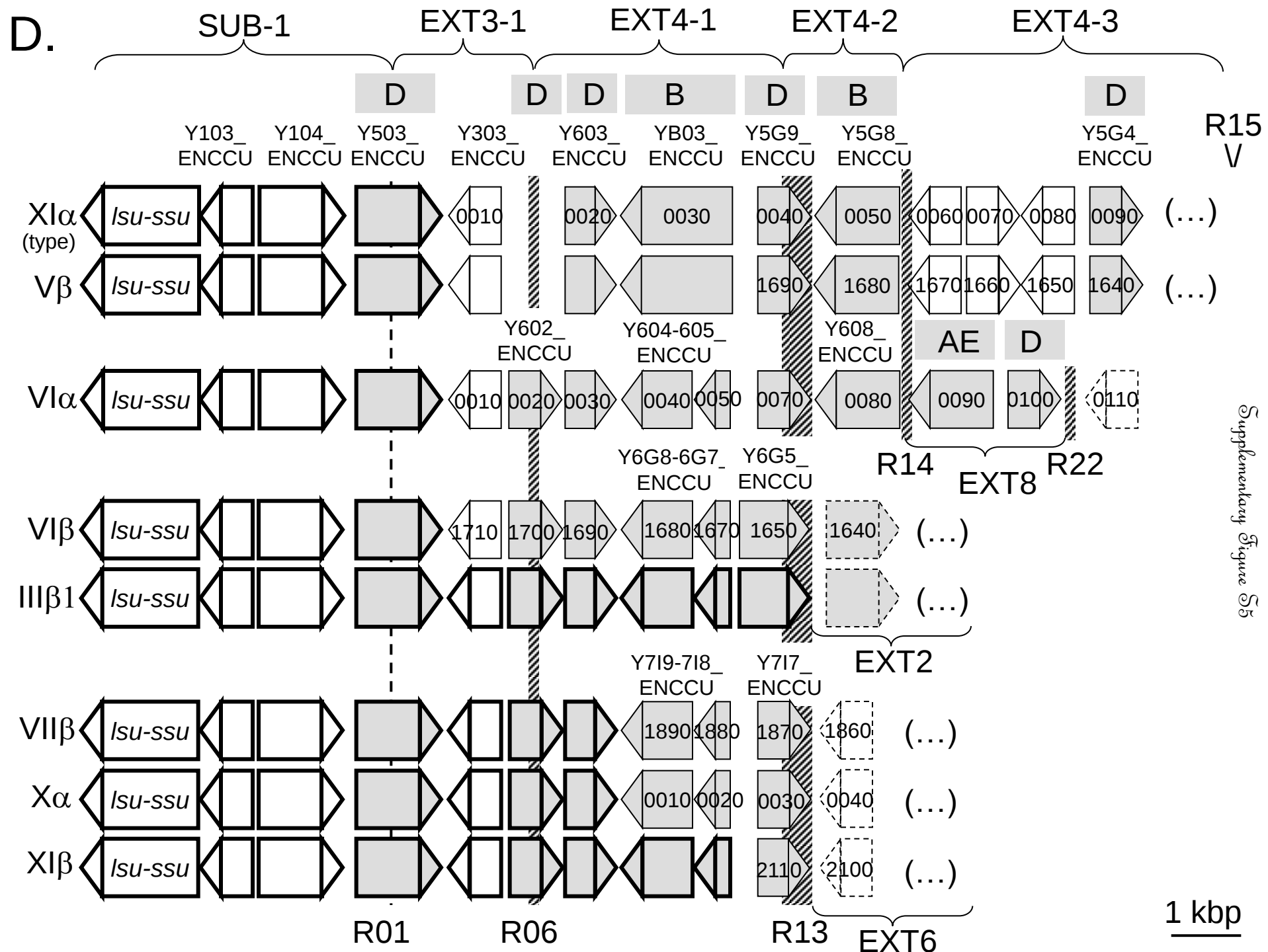


B.

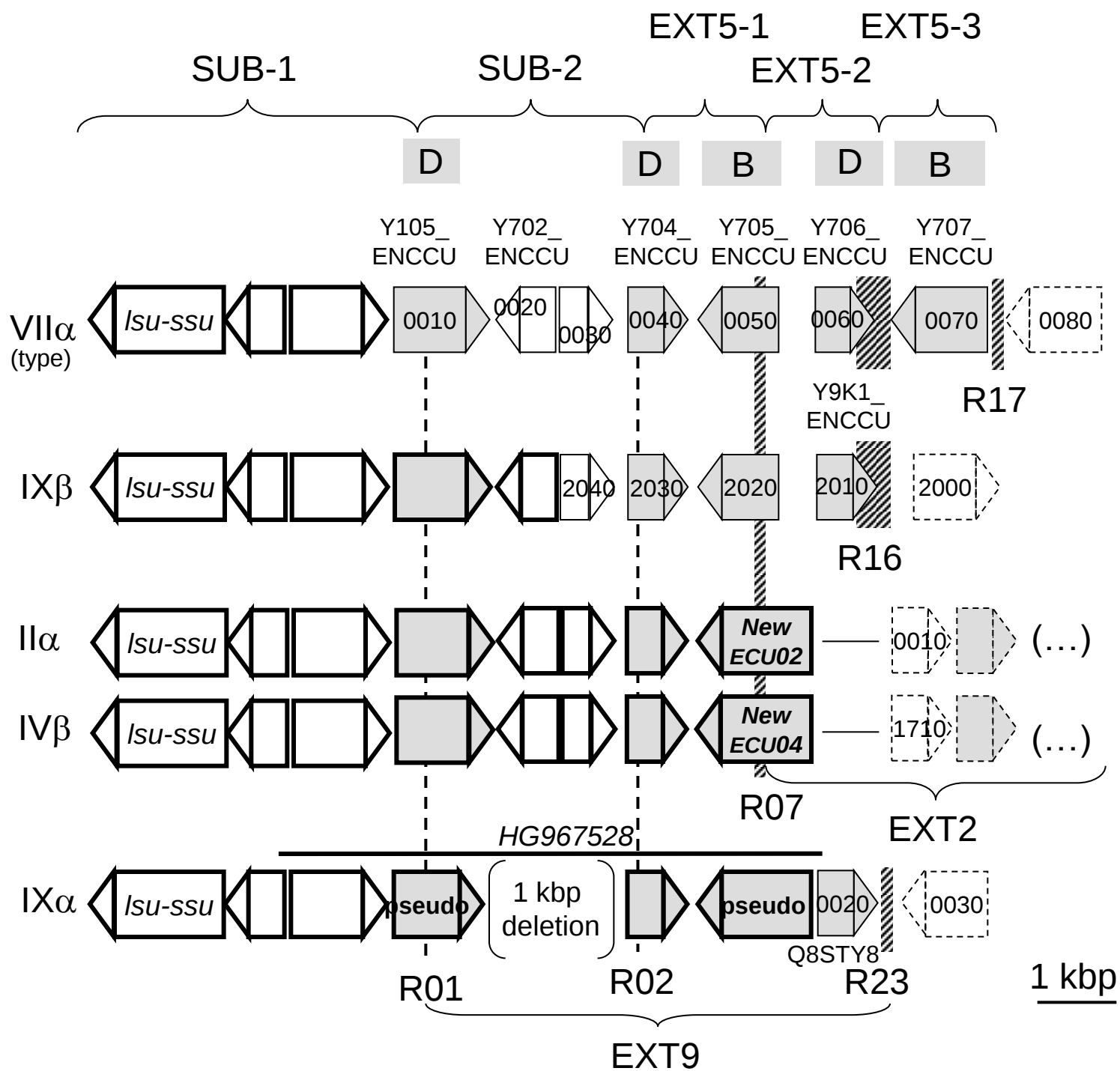


C.

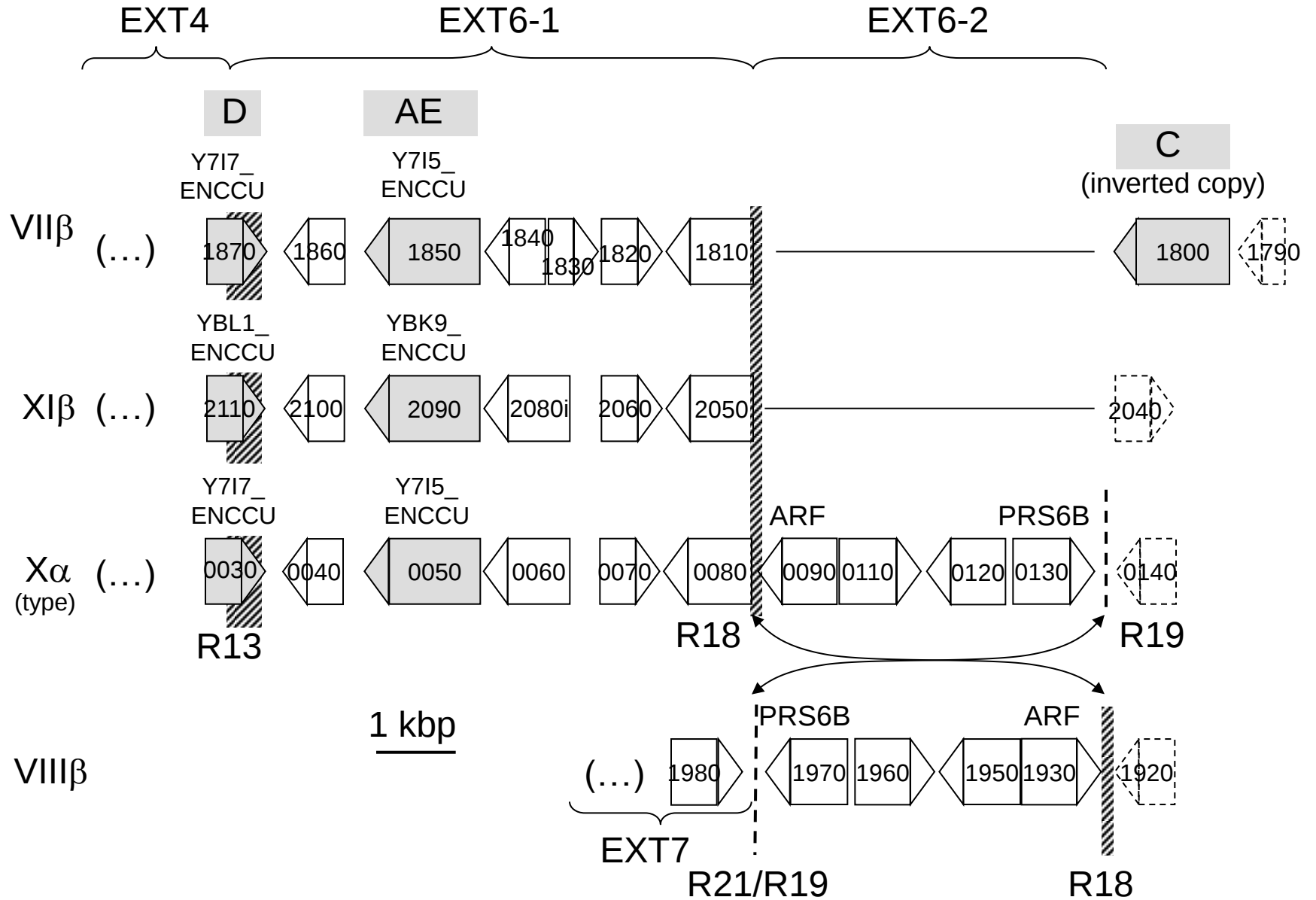




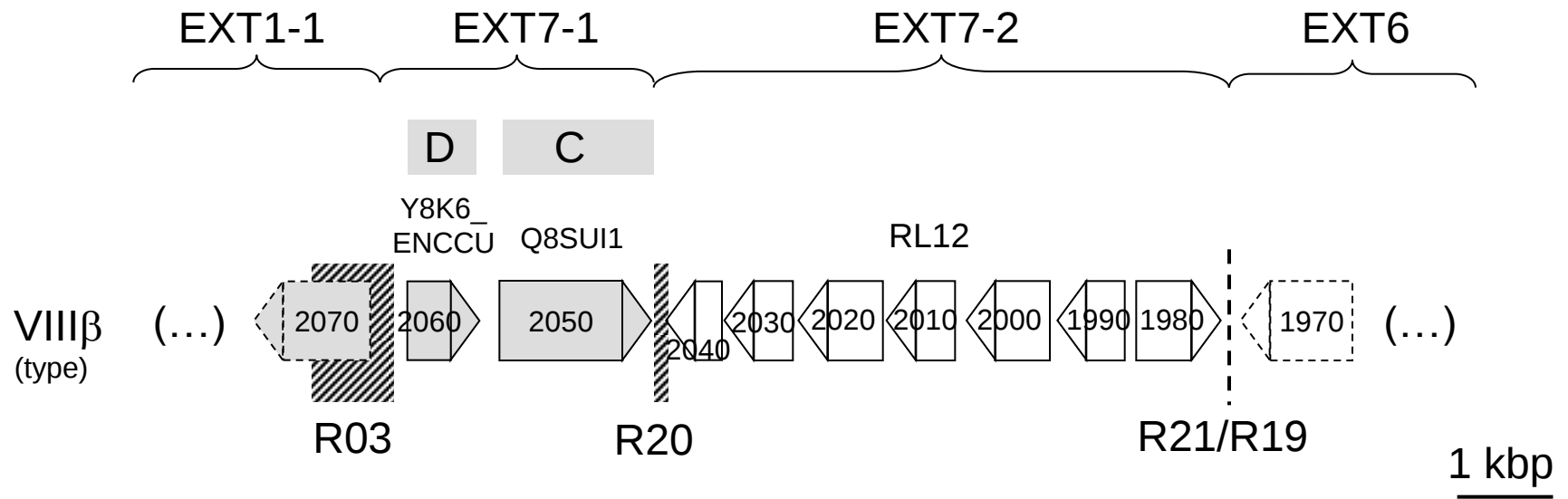
E.

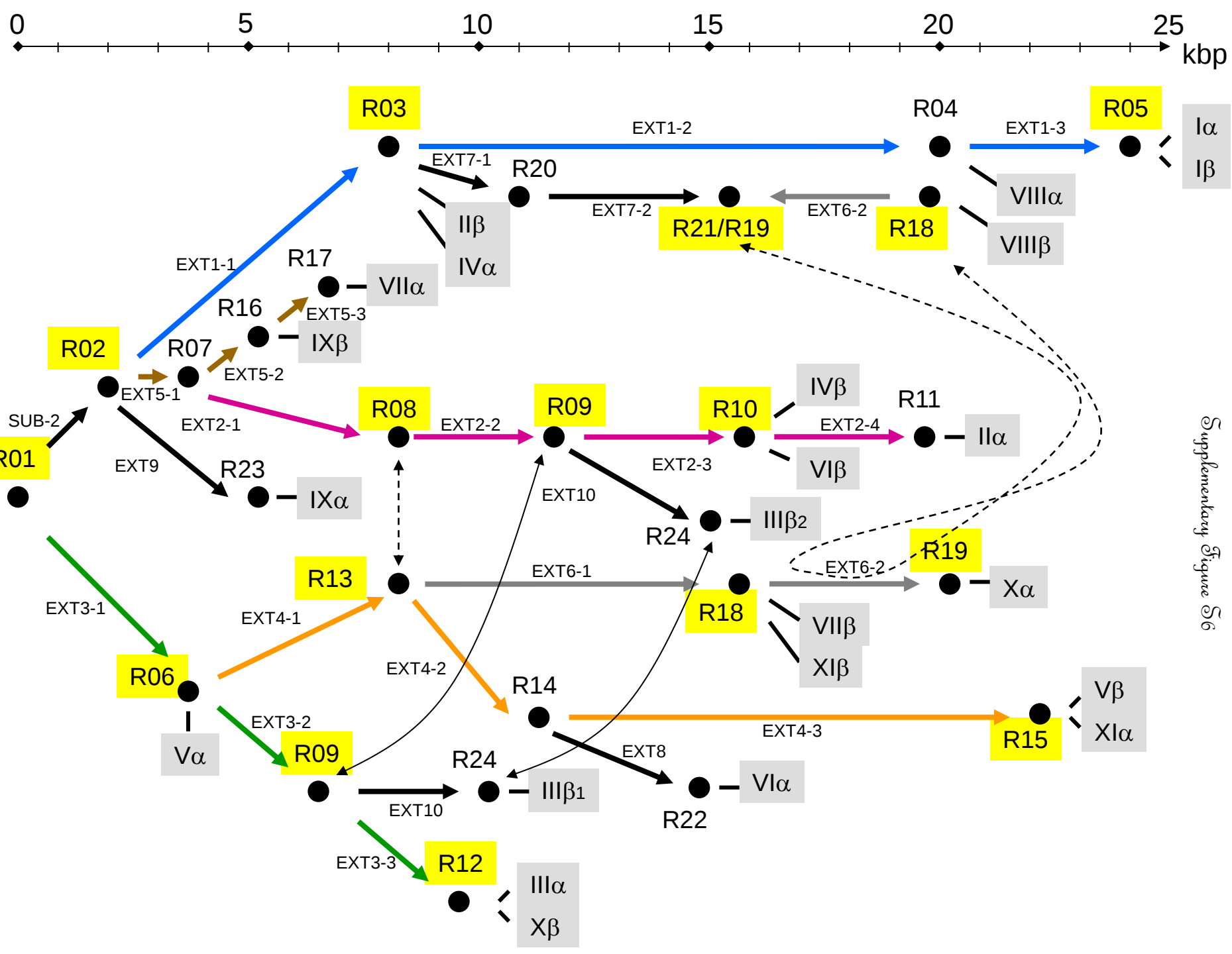


F.



G.

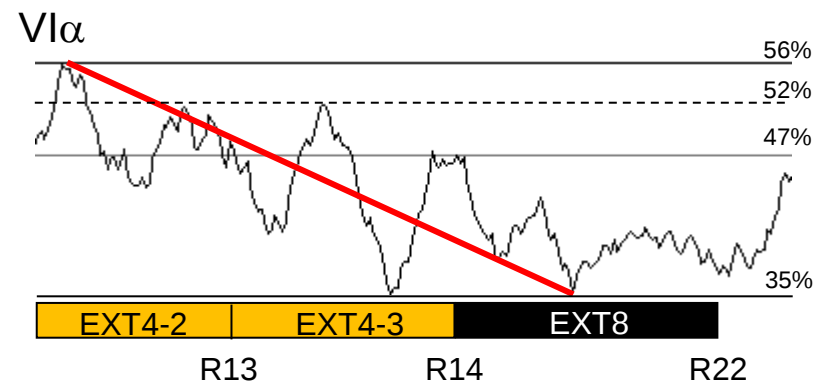
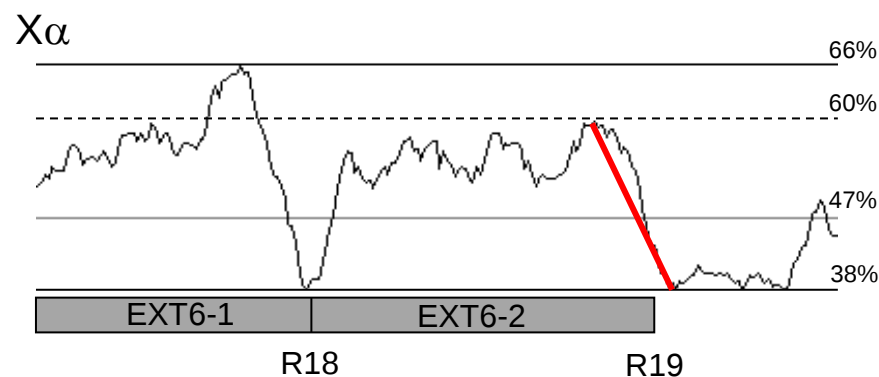
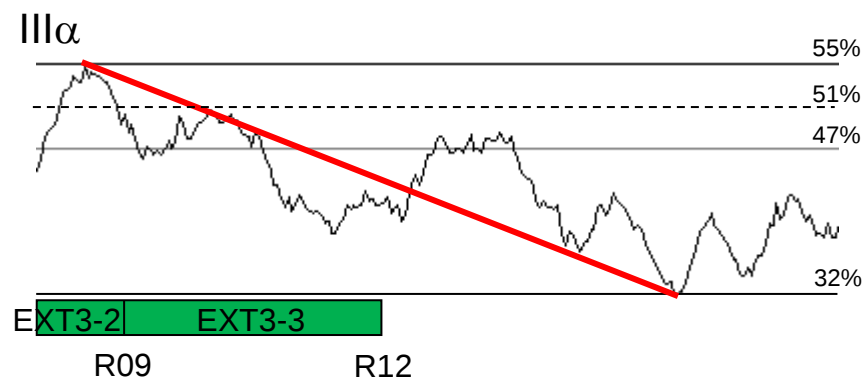
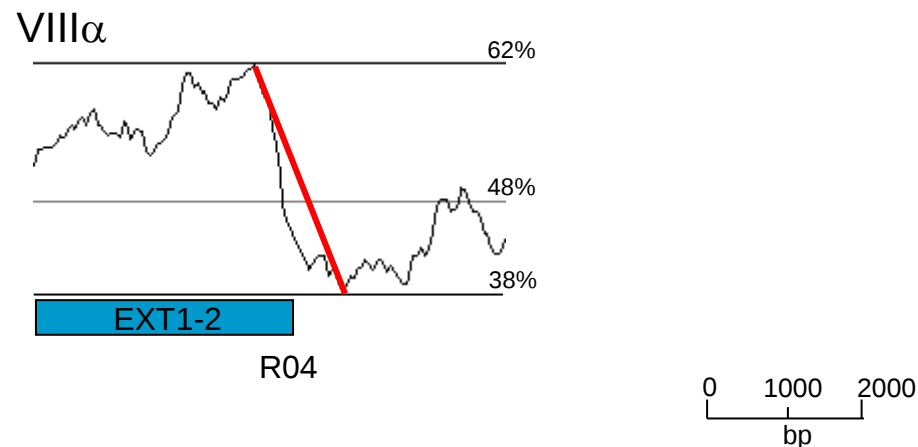




A GC% shift is associated to chromosome ends

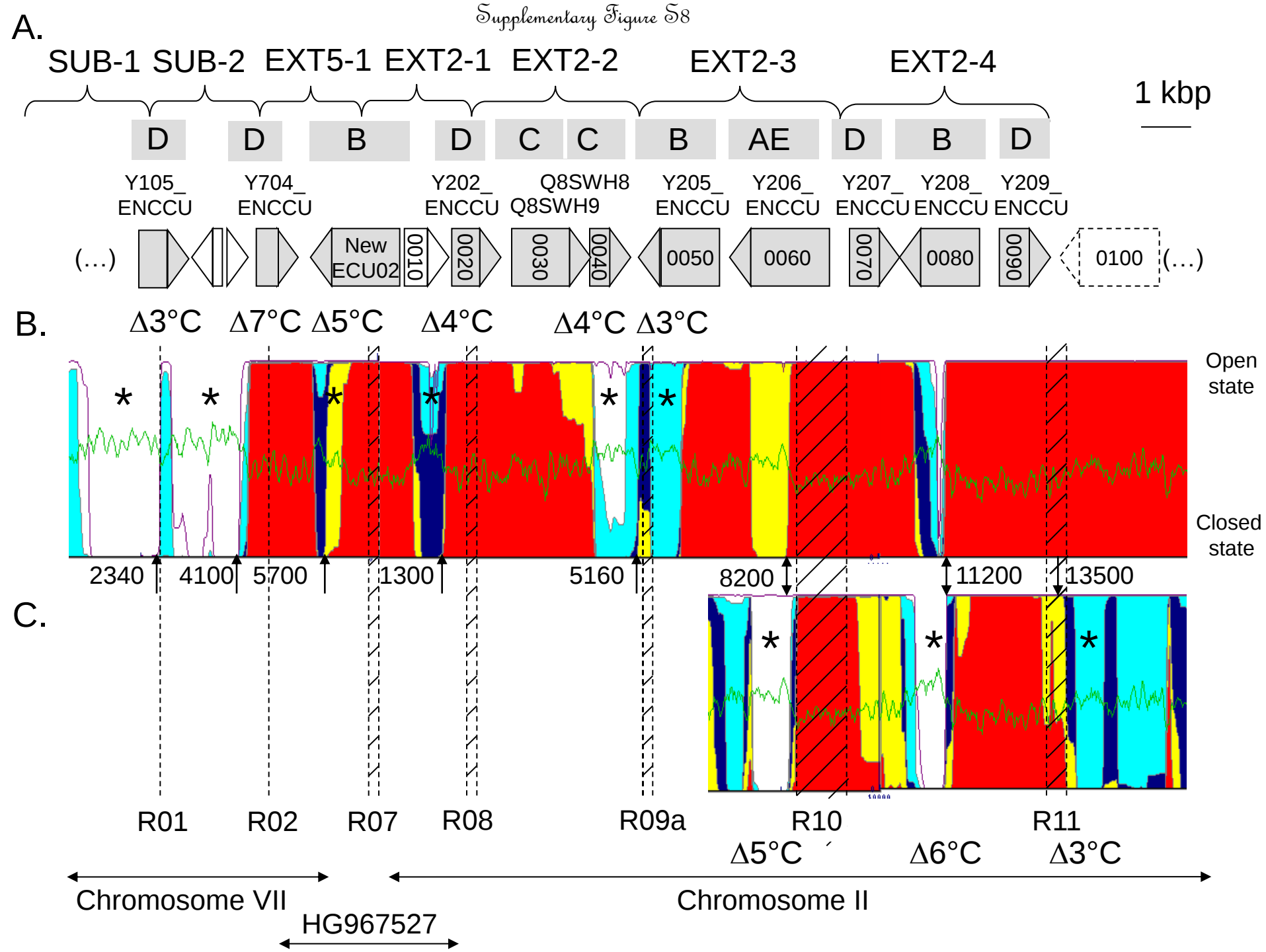
Sudden GC% shift > 2.0% / 100 bp

Slow GC% shift < 0.3% / 100 bp



Telomere <- -> core region

Telomere <- -> core region



InterAE/InterB

ECU04_1670 (586 aa),
Y4G7_ENCCU (Q8SVP2)



Source	Domain	Start	End
sig_p	n/a	1	21
transmembrane	n/a	37	56
low_complexity	n/a	164	180
Pfam A	DUF3654	165	304
disorder	n/a	168	182
low_complexity	n/a	219	233
disorder	n/a	276	280
low_complexity	n/a	305	321
coiled_coil	n/a	312	332
disorder	n/a	315	316
disorder	n/a	326	386
low_complexity	n/a	330	373
Pfam A	DUF1609	357	585
disorder	n/a	409	412
disorder	n/a	417	418
disorder	n/a	451	455
disorder	n/a	525	530

InterC

ECU10_1840 (584 aa),
Q8SU93_ENCCU



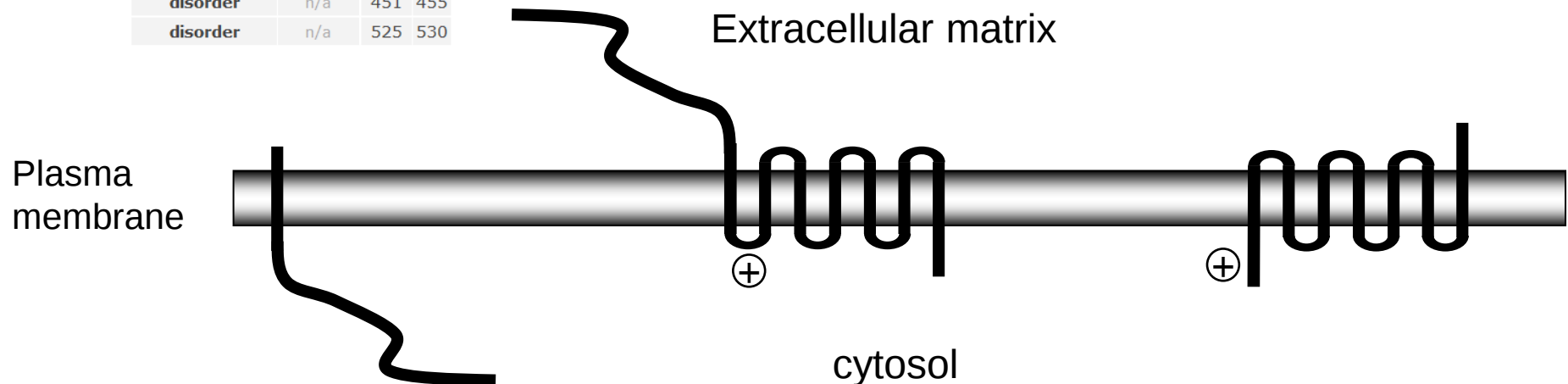
Source	Domain	Start	End
Pfam B	Pfam-B_453445	1	117
Pfam B	Pfam-B_2347	216	277
coiled_coil	n/a	325	345
transmembrane	n/a	357	374
Pfam A	DUF1686	380	566
transmembrane	n/a	386	405
transmembrane	n/a	425	442
transmembrane	n/a	449	468
transmembrane	n/a	474	492
transmembrane	n/a	504	527
low_complexity	n/a	510	524
transmembrane	n/a	539	563
disorder	n/a	582	583

InterD

ECU01_0070/ECU01_1540/ECU02_1570/
ECU04_0080/ECU08_2100 (254 aa),
Y107_ENCCU (Q8ST97)



Source	Domain	Start	End
transmembrane	n/a	26	44
Pfam A	DUF2463	37	231
transmembrane	n/a	56	75
transmembrane	n/a	81	101
low_complexity	n/a	83	104
transmembrane	n/a	113	130
transmembrane	n/a	150	168
low_complexity	n/a	154	168
transmembrane	n/a	175	191
transmembrane	n/a	211	238



A.

Supplementary Figure S10

All Results	Ortholog Groups	Microsporidia																				
		<i>M. Annecalia</i> (nr Genes: 0)		<i>M. Edhazardia</i>	<i>M. Encephalitozoon</i> (nr Genes: 38)				<i>M. Encephalitozoon</i> (nr Genes: 3)		<i>M. Encephalitozoon</i>	<i>M. Encephalitozoon</i>	<i>M. Enterocytozoon</i>	<i>M. Mitosporidium</i>	<i>M. Nematocida</i> (nr Genes: 0)		<i>M. Nematocida</i> (nr Genes: 0)		<i>M. Nosema</i>	<i>M. Nosema</i>	<i>M. Ordospora</i>	<i>M. Spragu</i>
		algerae PRA109	algerae PRA339	aedis USNM 41457	cuniculi EC1	cuniculi EC2	cuniculi EC3	cuniculi GB-M1	hellem ATCC 50504	hellem Swiss	intestinalis ATCC 50506	romaleae SJ-2008	bieneusi H348	daphniae UGP3	parisii ERTm1	parisii ERTm3	sp. 1 ERTm2	sp. 1 ERTm6	bombycis CQ1	ceranae BRL01	colligata OC4	lophii 42_110
66	3	0	0	0	7	8	8	36	3	1	3	0	0	0	0	0	0	0	0	0	0	

Gene ID	Genomic Location
ECU01_0100	AL391737: 20,249 - 22,108 (-)
ECU01_0110	AL391737: 22,867 - 24,645 (-)
ECU01_0120	AL391737: 25,107 - 25,706 (-)
ECU01_1490	AL391737: 184,277 - 184,876 (+)
ECU01_1500	AL391737: 185,338 - 187,116 (+)
ECU01_1510	AL391737: 187,875 - 189,734 (+)
ECU02_0050	AL590442: 5,448 - 7,019 (-)
ECU02_0060	AL590442: 7,441 - 9,249 (-)
ECU02_0080	AL590442: 10,535 - 12,274 (-)
ECU02_1540	AL590442: 187,833 - 189,683 (+)
ECU03_0090	AL590443: 8,576 - 10,444 (-)
ECU04_0110	AL590444: 16,684 - 17,325 (-)
ECU04_1680	AL590444: 209,875 - 210,684 (+)
ECU04_1670	AL590444: 211,107 - 212,867 (+)
ECU05_1680	AL590445: 207,816 - 209,654 (+)
ECU06_0040	AL590446: 4,779 - 6,212 (-)
ECU06_0080	AL590446: 8,293 - 10,035 (-)
ECU06_0090	AL590446: 11,059 - 12,879 (-)
ECU06_1610	AL590446: 205,815 - 207,638 (+)
ECU06_1620	AL590446: 207,962 - 209,701 (+)
ECU06_1680	AL590446: 214,140 - 215,516 (+)
ECU07_0050	AL590447: 5,249 - 5,899 (-)
ECU07_0070	AL590447: 7,406 - 9,253 (-)
ECU07_1850	AL590447: 218,977 - 220,881 (+)
ECU07_1890	AL590447: 224,581 - 225,882 (+)
ECU08_0030	AL590448: 3,463 - 5,322 (-)
ECU08_0040	AL590448: 6,081 - 7,859 (-)
ECU08_0050	AL590448: 8,321 - 8,920 (-)
ECU08_2070	AL590448: 226,792 - 228,651 (+)
ECU09_2020	AL590451: 248,027 - 248,677 (+)
ECU10_0010	AL590449: 695 - 1,996 (-)
ECU10_0050	AL590449: 5,696 - 7,600 (-)
ECU10_1810	AL590449: 250,014 - 251,879 (+)
ECU11_0030	AL590450: 4,681 - 6,606 (-)
ECU11_0050	AL590450: 8,173 - 10,011 (-)
ECU11_2090	AL590450: 263,188 - 265,092 (+)

interAE, interB genes (UPF0329)

GB-M1 11/11 chromosomes

Sequence	Organism	Chromosome	#Genes	Length	Gene Locations
AL391737	Encephalitozoon cuniculi GB-M1	I	6	209982	
AL590442	Encephalitozoon cuniculi GB-M1	II	4	197426	
AL590443	Encephalitozoon cuniculi GB-M1	III	1	194439	
AL590444	Encephalitozoon cuniculi GB-M1	IV	3	218329	
AL590445	Encephalitozoon cuniculi GB-M1	V	1	211018	
AL590446	Encephalitozoon cuniculi GB-M1	VI	6	220294	
AL590447	Encephalitozoon cuniculi GB-M1	VII	4	226576	
AL590448	Encephalitozoon cuniculi GB-M1	VIII	4	238147	
AL590449	Encephalitozoon cuniculi GB-M1	X	3	262797	
AL590450	Encephalitozoon cuniculi GB-M1	XI	3	267509	
AL590451	Encephalitozoon cuniculi GB-M1	IX	1	251002	

EC1 4/11 chromosomes

Sequence	Organism	Chromosome	#Genes	Length	Gene Locations
ECI_CH02	Encephalitozoon cuniculi EC1	2	1	180123	
ECI_CH04	Encephalitozoon cuniculi EC1	4	1	192854	
ECI_CH06	Encephalitozoon cuniculi EC1	6	4	201713	
ECI_CH07	Encephalitozoon cuniculi EC1	7	1	207567	
Sequence	Organism	Chromosome	#Genes	Length	Gene Locations

EC3 5/11 chromosomes

ECIII_CH02	Encephalitozoon cuniculi EC3	2	1	177125	
ECIII_CH03	Encephalitozoon cuniculi EC3	3	1	184824	
ECIII_CH06	Encephalitozoon cuniculi EC3	6	4	201381	
ECIII_CH07	Encephalitozoon cuniculi EC3	7	1	211783	
ECIII_CH08	Encephalitozoon cuniculi EC3	8	1	217589	
Sequence	Organism	Chromosome	#Genes	Length	Gene Locations

B.

Supplementary Figure S10

All Results	Ortholog Groups	Microsporidia																				
		<i>M.Anncaliia</i> (nr Genes: 0)		<i>M.Edhazardia</i>	<i>M.Encephalitozoon</i> (nr Genes: 23)				<i>M.Encephalitozoon</i> (nr Genes: 7)		<i>M.Encephalitozoon</i>	<i>M.Encephalitozoon</i>	<i>M.Enterocytozoon</i>	<i>M.Mitosporidium</i>	<i>M.Nematocida</i> (nr Genes: 0)		<i>M.Nematocida</i> (nr Genes: 0)		<i>M.Nosema</i>	<i>M.Nosema</i>	<i>M.Ordospora</i>	<i>M.Spragu</i>
		algerae PRA109	algerae PRA339	aedis USNM 41457	cuniculi EC1	cuniculi EC2	cuniculi EC3	cuniculi GB-M1	hellem ATCC 50504	hellem Swiss	intestinalis ATCC 50506	romaleae SJ-2008	bieneusi H348	daphniae UGP3	parisii ERTm1	parisii ERTm3	sp. 1 ERTm2	sp. 1 ERTm6	bombycis CQ1	ceranae BRL01	colligata OC4	lophii 42_110
69	4	0	0	0	13	7	8	23	5	4	4	5	0	0	0	0	0	0	0	0	0	

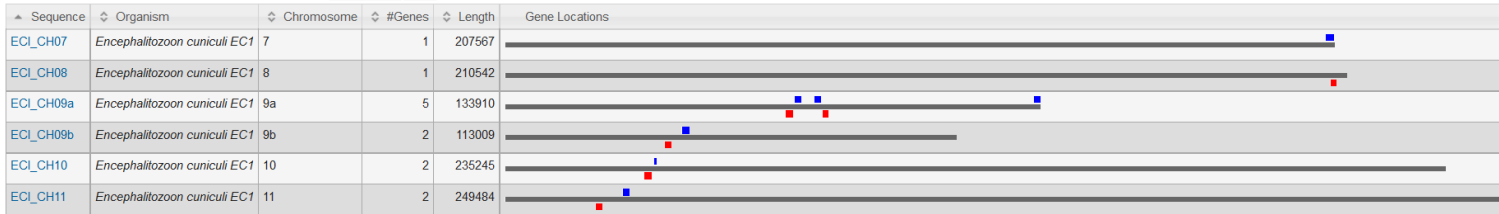
interC genes (UPF0329)

Gene ID	Genomic Location
ECU02_0030	AL590442: 3,287 - 4,384 (+)
ECU02_0040	AL590442: 4,524 - 4,895 (+)
ECU03_0050	AL590443: 5,400 - 6,665 (+)
ECU03_0060	AL590443: 6,782 - 7,153 (+)
ECU04_1680	AL590444: 213,230 - 213,829 (-)
ECU04_1690	AL590444: 213,718 - 214,836 (-)
ECU06_1630	AL590446: 210,069 - 210,440 (-)
ECU06_1640	AL590446: 210,557 - 211,744 (-)
ECU07_1800	AL590447: 213,403 - 215,382 (+)
ECU08_2050	AL590448: 223,792 - 225,192 (-)
ECU09_0530	AL590451: 68,590 - 70,473 (-)
ECU09_0540	AL590451: 70,894 - 72,597 (+)
ECU09_0580	AL590451: 75,755 - 77,383 (+)
ECU09_0590	AL590451: 77,832 - 79,427 (-)
ECU09_1120	AL590451: 130,649 - 132,373 (+)
ECU09_1160	AL590451: 133,647 - 135,251 (-)
ECU09_1530	AL590451: 174,234 - 175,946 (-)
ECU09_1550	AL590451: 178,654 - 180,429 (+)
ECU10_0450	AL590449: 50,646 - 52,472 (-)
ECU10_0460	AL590449: 52,845 - 53,708 (+)
ECU10_1840	AL590449: 253,302 - 255,056 (-)
ECU11_0250	AL590450: 33,269 - 34,918 (-)
ECU11_0290	AL590450: 40,082 - 41,680 (+)

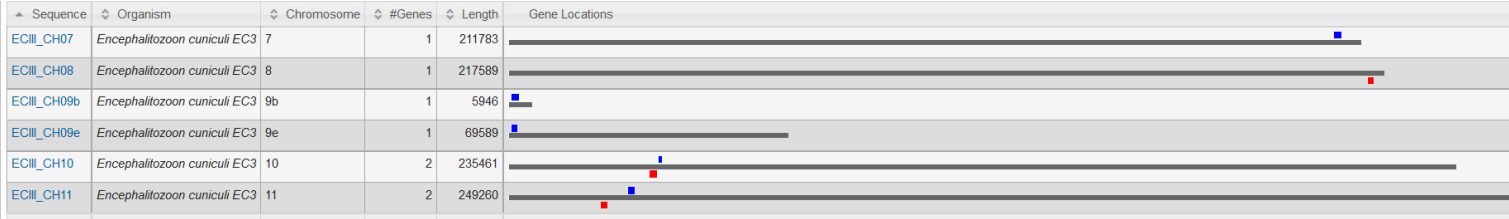
GB-M1 9/11 chromosomes



EC1 5/11 chromosomes



EC3 5/11 chromosomes



All Results	Ortholog Groups	Microsporidia																				
		<i>M.Anncalia</i> (nr Genes: 0)		<i>M.Edhazardia</i>	<i>M.Encephalitozoon</i> (nr Genes: 50)				<i>M.Encephalitozoon</i> (nr Genes: 8)		<i>M.Encephalitozoon</i>	<i>M.Encephalitozoon</i>	<i>M.Enterocytozoon</i>	<i>M.Mitosporidium</i>	<i>M.Nematocida</i> (nr Genes: 0)		<i>M.Nematocida</i> (nr Genes: 0)		<i>M.Nosema</i>	<i>M.Nosema</i>	<i>M.Ordospora</i>	<i>M.Spragu</i>
		algerae PRA109	algerae PRA339	aedis USNM 41457	cuniculi EC1	cuniculi EC2	cuniculi EC3	cuniculi GB-M1	hellem ATCC 50504	hellem Swiss	intestinalis ATCC 50506	romaleae SJ-2008	bieneusi H348	daphniae UGP3	parisii ERTm1	parisii ERTm3	sp. 1 ERTm2	sp. 1 ERTm6	bombicis CQ1	ceranae BRL01	colligata OC4	lophii 42_110
108	8	0	0	0	12	14	12	49	4	7	4	6	0	0	0	0	0	0	0	0	0	

Gene ID	Genomic Location
ECU01_0100	AL391737: 20,249 - 22,108 (-)
ECU01_0110	AL391737: 22,867 - 24,645 (-)
ECU01_0120	AL391737: 25,107 - 25,706 (-)
ECU01_1490	AL391737: 184,277 - 184,876 (+)
ECU01_1500	AL391737: 185,338 - 187,116 (+)
ECU01_1510	AL391737: 187,875 - 189,734 (+)
ECU02_0050	AL590442: 5,448 - 7,019 (-)
ECU02_0060	AL590442: 7,441 - 9,249 (-)
ECU02_0080	AL590442: 10,535 - 12,274 (-)
ECU02_1540	AL590442: 187,833 - 189,683 (+)
ECU03_0090	AL590443: 8,576 - 10,444 (-)
ECU04_0110	AL590444: 16,684 - 17,325 (-)
ECU04_1660	AL590444: 209,875 - 210,684 (+)
ECU04_1670	AL590444: 211,107 - 212,867 (+)
ECU05_1680	AL590445: 207,816 - 209,654 (+)
ECU06_0040	AL590446: 4,779 - 6,212 (-)
ECU06_0080	AL590446: 8,293 - 10,035 (-)
ECU06_0090	AL590446: 11,059 - 12,879 (-)
ECU06_1610	AL590446: 205,815 - 207,638 (+)
ECU06_1620	AL590446: 207,962 - 209,701 (+)
ECU06_1680	AL590446: 214,140 - 215,516 (+)
ECU07_0050	AL590447: 5,249 - 5,899 (-)
ECU07_0070	AL590447: 7,406 - 9,253 (-)
ECU07_1850	AL590447: 218,977 - 220,881 (+)
ECU07_1890	AL590447: 224,581 - 225,882 (+)
ECU08_0040	AL590448: 6,081 - 7,859 (-)
ECU08_0050	AL590448: 8,321 - 8,920 (-)
ECU08_2070	AL590448: 226,792 - 228,651 (+)
ECU09_2020	AL590451: 248,027 - 248,677 (+)
ECU10_0010	AL590449: 695 - 1,996 (-)
ECU10_0050	AL590449: 5,696 - 7,600 (-)
ECU10_1810	AL590449: 250,014 - 251,879 (+)
ECU11_0030	AL590450: 4,681 - 6,606 (-)
ECU11_0050	AL590450: 8,173 - 10,011 (-)
ECU11_2090	AL590450: 263,188 - 265,092 (+)

interD genes (UPF0328)

GB-M1 11/11 chromosomes

Sequence	Organism	Chromosome	#Genes	Length	Gene Locations
AL391737	Encephalitozoon cuniculi GB-M1	I	6	209982	
AL590442	Encephalitozoon cuniculi GB-M1	II	4	197426	
AL590443	Encephalitozoon cuniculi GB-M1	III	1	194439	
AL590444	Encephalitozoon cuniculi GB-M1	IV	3	218329	
AL590445	Encephalitozoon cuniculi GB-M1	V	1	211018	
AL590446	Encephalitozoon cuniculi GB-M1	VI	6	220294	
AL590447	Encephalitozoon cuniculi GB-M1	VII	4	226576	
AL590448	Encephalitozoon cuniculi GB-M1	VIII	4	238147	
AL590449	Encephalitozoon cuniculi GB-M1	X	3	262797	
AL590450	Encephalitozoon cuniculi GB-M1	XI	3	267509	
AL590451	Encephalitozoon cuniculi GB-M1	IX	1	251002	
Sequence	Organism	Chromosome	#Genes	Length	Gene Locations

EC1 4/11 chromosomes

Sequence	Organism	Chromosome	#Genes	Length	Gene Locations
ECI_CH02	Encephalitozoon cuniculi EC1	2	1	180123	
ECI_CH04	Encephalitozoon cuniculi EC1	4	1	192854	
ECI_CH06	Encephalitozoon cuniculi EC1	6	4	201713	
ECI_CH07	Encephalitozoon cuniculi EC1	7	1	207567	
Sequence	Organism	Chromosome	#Genes	Length	Gene Locations

EC3 5/11 chromosomes

Sequence	Organism	Chromosome	#Genes	Length	Gene Locations
ECIII_CH02	Encephalitozoon cuniculi EC3	2	1	177125	
ECIII_CH03	Encephalitozoon cuniculi EC3	3	1	184824	
ECIII_CH06	Encephalitozoon cuniculi EC3	6	4	201381	
ECIII_CH07	Encephalitozoon cuniculi EC3	7	1	211783	
ECIII_CH08	Encephalitozoon cuniculi EC3	8	1	217589	
Sequence	Organism	Chromosome	#Genes	Length	Gene Locations