

Appendix III(b). Table 1B. Diagnostic nucleotide sites from the PAST fragment Pairwise Aggregate Analysis (PAA) of Lepilemur.

	111111111112222222223333333333334555555555555555555666666666677777777777788888888889999999000000000	1111111111
ANAL5	CCCCATAAATCAACCATGAAACAGGCCACACCCCAATGAACACACCACATCACAACAGAAAAATACGTACGACCCACCCACCAATTTTACCATCACAACCACG	
DAR4.7T.....A.....T.....A.....A.....
LOKO4.2A.....T.....A.....A.....
FARY5.1	..G..C...A.G.....TG.AT..C.....GG.A...T.....G...A.....A.....T.....T.....AC.....C	
ANT5.2A.....A.....A.....A.T..T.....AC.....	
LAZA5.1G..A.....A.....T.....T.G.T..A.....AC.....	
BEZ14	..T..C.....T.....AA.....T.....A.G.....T.....G.....T.....TG.....AC.....G.....T.....	
AND65	..T..C.....T.....CA.....A.G.....T.....T..G.....T.....T.AC.....T.....	
MOR117G...A.....AT.....AGG.....T.....G.....AC.....T.....	
ZOMB8T.....A.....T.....A.....GT.....G.....G.....C.....A.....AC.....GG.....C	
BEMA5GT...G...AA.....A.G.....T.....G.....A.T...CAC...T...T...G.TG..	
MAR1C.....A.....A.G.....T.....AC.....C	
HIH21C.....G.....A.GA.....C.....T.....AA.C.....C...T...C	
KIBO22	..T.....A.....G..A..A.....AC.....	
JAM4.27T.....A.....A.G...T..G...T..G...T.....A.....AC.....C.....	
TAD25	..T..T.....AA.....A.G.....C.....A.T..T.....T..A..AC.....G.....T.....	
M83BT.....AA.....A.G.....C.....A.T..T.....T..A..AC.....T.....	
FAN10	G.T.....AA.....A.....C.....A.T..T.....T..A..AC.....T..T.....	
AND20	.TT.....C...T.....AA..T.....CA.G..AC..A.A..C.....C..A.T..T.....T..A..AC.....T.....	
RANO234C.....G.....AA.....A.G.....TG.....TG..AC.....T.....	
KALA24GC.....TA.....AA.....A.G.....C.....G..ACT..T.....T..A..ACG.T.T.....T.....	
JAR2C.....TT..C.....AA.....T.....A.....C.....G..G.A.A..A.....A..AC.....T.....	
NARA8.5C.G.....T.....A.....A.....CG.....A.T..T.....A..AC.....T.....	
MAS6.12A.....T.....A..T.....A.....C.....A.T..T.....T..A..ACC.....A.....	
BIBO7.1C.....G.....G..AA.....A.....A.C.....T.....T.A.....ACC.....GT.....C	

Appendix III(c). Table 4A. Genetic distance matrix for D-Loop fragment sequence data for *Lepilemur* species. The numbers represent the following *Lepilemur* species: [1] *Lepilemur ankaranensis*; [2] *Lepilemur milanoii*; [3] *Lepilemur tymerlachsoni*; [4] *Lepilemur septentrionalis*; [5] *Lepilemur dorsalis*; [6] *Lepilemur sahamalazensis*; [7] *Lepilemur petteri*; [8] *Lepilemur leucopus*; [9] *Lepilemur ruficaudatus*; [10] *Lepilemur hubbardorum*; [11] *Lepilemur randrianasoli*; [12] *Lepilemur edwardsi* [13] *Lepilemur grewcockorum*; [14] *Lepilemur ahmansonorum*; [15] *Lepilemur aeeclis*; [16] *Lepilemur mustelinus*; [17] *Lepilemur jamesorum*; [18] *Lepilemur betsileo*; [19] *Lepilemur fleuretae*; [20] *Lepilemur microdon*; [21] *Lepilemur wrightae*; [22] *Lepilemur seali*; [23] *Lepilemur species nova #2*; [24] *Lepilemur scottorum*; and [25] *Lepilemur otto*. Parsimony information sites between compared species are displayed above the diagonal, and genetic distance based as a percentage is displayed below the diagonal.

	1	2	3	4	5	6	7	8	9	10	11	12
1		20	25	49	45	41	64	63	70	62	65	65
2	2.7±0.7		18	42	39	39	63	61	70	63	67	64
3	4.5±0.9	2.9±0.8		41	32	29	58	58	64	60	62	63
4	7.7±1.2	6.6±1.1	6.7±1.1		48	46	56	61	60	59	57	69
5	6.9±1.1	5.6±1.0	4.9±1.0	6.8±1.1		28	57	61	66	66	67	61
6	6.4±1.1	5.9±1.1	4.6±0.9	7.2±1.2	4.2±0.9		55	58	63	68	67	56
7	11.3±1.5	11.4±1.5	11.0±1.5	10.6±1.5	10.8±1.5	10.6±1.5		22	55	60	45	55
8	10.2±1.5	10.3±1.5	10.2±1.5	10.9±1.5	11.1±1.6	10.7±1.5	3.4±0.8		60	57	43	58
9	11.9±1.5	12.5±1.6	11.9±1.5	11.3±1.5	12.3±1.5	11.4±1.6	9.9±1.4	9.5±1.4		41	46	70
10	10.2±1.5	10.7±1.5	10.8±1.5	10.4±1.4	10.7±1.5	12.6±1.6	9.7±1.4	8.4±1.3	6.6±1.1		39	73
11	10.4±1.5	11.3±1.6	10.9±1.5	10.1±1.6	12.4±1.6	7.0±1.1	7.4±1.2	5.5±1.1	8.9±1.4	6.5±1.1		65
12	8.2±1.3	8.5±1.3	8.9±1.4	10.6±1.4	8.4±1.3	7.4±1.2	8.2±1.3	8.1±1.3	10.6±1.5	10.1±1.5	9.6±1.5	
13	9.6±1.4	8.8±1.4	8.8±1.4	10.8±1.5	7.8±1.3	5.8±1.0	9.7±1.4	9.7±1.4	11.2±1.4	10.2±1.5	10.4±1.5	5.4±1.0
14	6.5±1.1	6.6±1.1	6.2±1.1	8.8±1.4	6.0±1.0	10.4±1.4	11.4±1.6	10.1±1.5	12.5±1.6	10.6±1.5	9.9±1.5	6.9±1.2
15	10.9±1.5	11.1±1.5	11.0±1.5	11.4±1.4	11.4±1.5	15.3±1.8	8.8±1.3	8.6±1.3	8.6±1.3	7.9±1.2	7.2±1.2	8.5±1.3
16	16.5±1.8	15.5±1.7	16.0±1.8	15.2±1.8	16.7±1.8	15.4±1.9	15.0±1.7	15.4±1.7	13.3±1.5	14.4±1.6	15.4±1.7	14.9±1.7
17	15.8±1.8	15.3±1.8	15.6±1.8	14.5±1.8	16.6±1.9	13.2±1.7	16.7±1.9	17.5±2.0	14.1±1.7	14.9±1.7	15.9±1.9	14.6±1.7
18	14.1±1.7	13.5±1.7	13.9±1.7	14.7±1.8	14.8±1.7	14.9±1.8	15.8±1.8	16.0±1.9	14.5±1.7	13.8±1.7	15.4±1.9	13.0±1.6
19	15.1±1.8	14.8±1.7	15.9±1.9	14.6±1.9	16.3±1.9	10.7±1.5	16.2±1.9	16.7±1.9	15.3±1.8	15.9±1.8	15.6±1.8	14.2±1.8
20	11.2±1.5	10.9±1.5	11.6±1.6	12.4±1.6	12.1±1.6	14.5±1.8	10.9±1.4	10.1±1.4	11.6±1.5	12.3±1.6	10.8±1.5	7.7±1.2
21	16.0±1.9	15.0±1.8	14.1±1.7	15.9±1.9	14.5±1.7	15.4±1.9	15.6±1.8	15.9±1.9	16.4±1.9	15.4±1.8	15.3±1.8	13.8±1.7
22	14.5±1.7	14.0±1.7	15.4±1.8	15.2±1.8	16.3±1.9	14.6±1.8	16.5±1.9	17.5±2.0	14.5±1.8	15.0±1.7	15.6±1.9	14.4±1.8
23	14.6±1.8	15.2±1.8	14.3±1.8	14.2±1.8	16.5±1.9	14.3±1.7	16.5±1.9	16.3±1.9	14.6±1.8	15.9±1.9	15.3±2.0	14.8±1.8
24	14.4±1.7	14.1±1.7	15.4±1.8	15.4±1.8	16.3±1.8	14.6±1.8	18.2±2.0	18.6±2.0	17.6±2.0	16.8±1.9	16.6±2.0	14.3±1.7
25	9.5±1.4	10.3±1.5	9.9±1.4	11.8±1.6	9.2±1.4	8.2±1.3	10.2±1.4	9.9±1.4	10.1±1.4	10.3±1.4	11.1±1.5	5.0±0.9

Appendix III(c). Table 4A. (cont.)

	13	14	15	16	17	18	19	20	21	22	23	24	25
1	69	46	74	101	88	83	86	65	98	89	91	89	68
2	63	43	73	97	85	79	85	62	92	86	92	87	70
3	61	39	70	96	85	79	86	62	86	89	85	89	64
4	63	55	72	94	79	80	78	70	90	83	82	85	70
5	56	38	72	104	92	87	91	66	90	97	97	97	63
6	52	33	69	99	88	80	86	57	90	91	88	88	57
7	60	62	63	94	88	86	86	58	93	92	92	98	60
8	63	60	66	102	98	94	94	64	100	102	99	107	66
9	64	73	54	91	81	83	88	63	99	87	90	100	60
10	65	66	59	98	88	83	95	74	106	92	98	104	68
11	60	58	50	100	91	89	89	59	98	96	95	100	66
12	41	57	69	107	96	90	94	51	99	98	100	98	37
13		54	64	103	95	87	86	45	87	85	95	94	36
14	8.4±1.4		68	100	84	83	78	62	84	89	93	87	57
15	9.5±1.4	9.7±1.4		108	105	95	105	67	102	97	102	106	71
16	16.1±1.7	16.7±1.8	14.9±1.6		42	42	26	95	72	67	68	71	105
17	16.6±1.9	15.6±1.8	16.9±1.9	6.4±1.0		37	44	89	58	61	53	57	91
18	14.4±1.7	14.6±1.7	14.3±1.7	5.9±1.0	6.2±1.1		50	79	66	59	58	57	88
19	14.9±1.8	14.1±1.7	17.1±1.9	8.8±1.2	8.3±1.3	9.3±1.4		91	71	57	63	64	92
20	7.4±1.2	10.9±1.5	10.6±1.4	14.7±1.7	15.9±1.8	13.3±1.6	15.6±1.8		93	84	95	95	49
21	13.3±1.6	14.2±1.6	15.2±1.7	10.6±1.4	9.3±1.4	10.3±1.5	11.6±1.6	15.1±1.8		63	64	72	92
22	13.9±1.7	15.4±1.8	14.5±1.8	9.1±1.3	10.1±1.4	9.3±1.3	9.4±1.4	14.0±1.7	10.8±1.5		43	36	96
23	16.0±1.9	17.0±1.9	15.7±1.9	10.9±1.4	9.1±1.3	9.9±1.5	11.0±1.5	15.5±1.8	11.1±1.5	7.5±1.2		39	96
24	16.1±1.9	15.3±1.7	16.8±1.9	10.8±1.4	9.7±1.4	9.8±1.3	11.1±1.5	17.0±1.8	12.8±1.6	6.3±1.1	7.0±1.2		101
25	6.4±1.1	8.4±1.3	10.5±1.4	15.8±1.8	15.0±1.8	14.0±1.7	14.7±1.8	8.4±1.3	13.7±1.7	15.5±1.9	15.3±1.8	16.8±1.9	

Appendix III(d). Table 4B. Genetic distance matrix for PAST fragment sequence data for *Lepilemur* species. The numbers represent the following *Lepilemur* species: [1] *Lepilemur ankaranensis*; [2] *Lepilemur milanoii*; [3] *Lepilemur tymerlachsoni*; [4] *Lepilemur septentrionalis*; [5] *Lepilemur dorsalis*; [6] *Lepilemur sahamalazensis*; [7] *Lepilemur petteri*; [8] *Lepilemur leucopus*; [9] *Lepilemur ruficaudatus*; [10] *Lepilemur hubbardorum*; [11] *Lepilemur randrianasoli*; [12] *Lepilemur edwardsi* [13] *Lepilemur grewcockorum*; [14] *Lepilemur ahmansorum*; [15] *Lepilemur aeeclis*; [16] *Lepilemur mustelinus*; [17] *Lepilemur jamesorum*; [18] *Lepilemur betsileo*; [19] *Lepilemur fleuretae*; [20] *Lepilemur microdon*; [21] *Lepilemur wrightae*; [22] *Lepilemur seali*; [23] *Lepilemur species nova #2*; [24] *Lepilemur scottorum*; and [25] *Lepilemur otto*. Parsimony information sites between compared species are displayed above the diagonal, and genetic distance based as a percentage is displayed below the diagonal.

	1	2	3	4	5	6	7	8	9	10	11	12
1		33	55	197	106	128	282	287	277	271	271	223
2	1.2±0.2		54	196	98	114	272	275	276	272	275	218
3	2.3±0.3	2.4±0.3		202	108	126	281	284	279	272	269	225
4	8.9±0.6	9.0±0.6	9.4±0.6		198	196	310	313	266	257	255	220
5	4.6±0.4	4.3±0.4	4.8±0.5	9.2±0.6		108	275	275	266	264	264	207
6	4.8±0.5	4.6±0.4	5.0±0.5	9.0±0.6	4.7±0.5		280	285	269	273	264	277
7	13.3±0.8	13.0±0.8	13.6±0.8	15.0±0.8	13.1±0.8	13.1±0.9		46	263	257	262	269
8	13.1±0.8	12.7±0.8	13.2±0.8	14.8±0.8	12.7±0.8	12.9±0.8	1.8±0.3		269	257	269	276
9	13.0±0.9	13.1±0.9	13.3±0.8	12.7±0.8	12.6±0.8	12.7±0.8	12.5±0.8	12.4±0.8		85	142	268
10	12.8±0.8	13.0±0.9	13.1±0.8	12.3±0.7	12.6±0.8	12.6±0.8	12.2±0.8	11.9±0.8	3.8±0.4		151	257
11	12.8±0.8	13.2±0.8	12.9±0.8	12.1±0.7	12.6±0.8	12.5±0.8	12.5±0.8	12.5±0.9	6.4±0.5	6.9±0.6		254
12	10.2±0.7	10.0±0.7	10.5±0.7	10.3±0.7	9.6±0.7	9.6±0.7	12.7±0.8	12.7±0.8	12.7±0.8	12.2±0.7	12.0±0.7	
13	10.7±0.6	10.8±0.7	11.2±0.7	10.6±0.7	10.8±0.7	11.0±0.7	13.6±0.8	13.7±0.8	13.3±0.8	12.7±0.7	12.7±0.8	2.9±0.3
14	4.9±0.4	4.8±0.4	5.2±0.4	9.6±0.6	4.7±0.5	2.8±0.3	13.6±0.9	13.2±0.9	13.3±0.8	13.2±0.8	13.3±0.8	10.3±0.7
15	12.9±0.9	13.2±0.8	13.5±0.8	13.5±0.8	12.5±0.8	12.9±0.8	12.0±0.7	11.9±0.7	6.4±0.6	6.9±0.5	5.5±0.5	12.5±0.7
16	18.2±1.0	18.0±1.0	18.2±1.0	19.1±1.0	17.7±1.0	18.0±1.0	20.4±1.2	19.6±1.1	19.8±1.1	19.9±1.1	19.6±1.1	17.6±0.9
17	18.3±1.1	18.2±1.0	18.2±1.0	18.6±1.0	17.6±1.0	17.7±1.0	20.1±1.1	19.4±1.1	20.1±1.1	20.4±1.1	19.7±1.1	17.5±0.9
18	18.1±1.0	17.9±1.0	17.9±1.0	18.7±1.0	17.3±1.0	17.7±0.9	20.4±1.2	19.6±1.2	20.0±1.1	20.1±1.1	19.7±1.1	17.2±1.0
19	18.8±1.0	18.7±1.0	18.7±1.0	19.7±1.0	18.2±1.0	18.7±1.0	20.8±1.2	20.0±1.2	20.6±1.1	20.7±1.1	19.9±1.0	18.6±1.0
20	10.3±0.6	10.4±0.7	10.6±0.7	10.7±0.7	10.3±0.7	10.7±0.7	13.7±0.8	13.7±0.8	12.7±0.8	12.4±0.7	12.7±0.8	7.8±0.6
21	17.4±0.9	17.5±0.9	17.5±0.9	17.6±0.9	17.4±0.9	17.9±0.9	19.6±1.1	19.4±1.1	18.6±1.0	18.6±1.0	18.5±1.0	17.3±0.9
22	18.7±1.1	18.6±1.1	18.9±1.0	18.6±1.0	18.8±1.1	18.7±1.0	20.3±1.1	20.0±1.1	19.7±1.1	19.9±1.1	20.0±1.2	17.6±1.0
23	18.3±1.2	18.1±1.2	18.0±1.1	18.9±1.2	18.2±1.2	18.0±1.1	20.0±1.2	19.7±1.2	18.8±1.2	19.2±1.1	19.3±1.2	17.4±1.1
24	17.9±1.0	17.8±1.0	17.5±1.0	18.4±1.0	18.1±1.0	18.1±0.9	19.5±1.0	19.1±1.0	18.9±1.0	18.7±1.0	19.2±1.1	17.1±1.0
25	10.7±0.7	10.8±0.7	11.2±0.7	11.1±0.7	10.3±0.7	10.4±0.7	13.2±0.9	13.2±0.9	13.0±0.8	12.7±0.8	12.8±0.8	3.0±0.4

Appendix III(d). Table 4B. (cont.)

	13	14	15	16	17	18	19	20	21	22	23	24	25
1	231	113	278	389	375	364	395	220	359	382	375	379	230
2	232	108	283	384	372	360	387	216	358	378	369	364	233
3	237	114	286	385	370	358	388	218	355	381	365	356	237
4	226	207	286	401	378	373	394	223	359	378	381	372	236
5	230	103	267	376	360	348	370	213	354	380	367	366	221
6	240	71	285	417	372	364	377	230	370	383	366	368	223
7	283	285	259	418	402	401	415	281	391	405	399	391	278
8	291	286	263	413	397	393	410	287	395	407	401	390	285
9	279	278	147	409	401	393	412	261	376	396	379	381	272
10	267	276	156	413	405	394	416	254	375	399	385	377	266
11	266	277	129	408	396	388	398	262	375	400	387	385	267
12	66	220	268	378	359	347	395	157	353	360	355	351	68
13		241	280	382	364	352	376	167	350	363	356	350	76
14	11.4±0.7		281	385	368	354	381	223	368	391	370	373	230
15	13.2±0.8	13.2±0.8		399	386	380	403	277	367	400	387	386	275
16	18.1±1.0	18.1±1.0	18.8±1.0		76	67	41	393	193	274	253	242	399
17	17.9±1.0	18.0±1.0	18.8±1.0	2.3±0.3		41	115	373	172	265	245	235	381
18	17.6±1.0	17.6±1.0	18.9±1.0	2.2±0.3	1.8±0.3		109	368	167	249	225	218	370
19	18.4±1.0	18.6±1.0	19.6±1.0	4.7±0.5	4.4±0.4	4.6±0.4		391	188	262	242	222	388
20	8.2±0.6	10.9±0.7	13.1±0.7	17.3±0.9	17.1±0.9	17.2±0.9	17.8±0.9		351	371	371	358	163
21	17.2±0.9	18.2±0.9	17.8±1.1	8.0±0.6	7.8±0.6	7.9±0.6	8.2±0.7	15.4±0.8		242	233	217	363
22	17.7±1.1	19.5±1.0	19.7±1.2	12.0±0.8	12.4±0.8	11.9±0.7	12.1±0.7	17.3±0.9	11.2±0.7		98	116	369
23	17.5±1.1	18.3±1.1	19.0±1.2	11.0±0.8	11.3±0.8	10.7±0.8	11.3±0.7	17.4±1.0	10.9±0.7	4.2±0.4		95	365
24	17.1±1.0	18.5±0.9	19.0±1.1	10.4±0.7	10.9±0.7	10.3±0.7	10.3±0.7	16.7±0.9	10.0±0.6	5.1±0.5	4.2±0.4		360
25	3.4±0.4	10.8±0.7	12.9±0.8	19.0±1.0	18.8±1.0	18.5±1.0	19.2±1.1	8.0±0.5	17.9±1.0	18.0±1.0	18.0±1.1	17.7±1.1	

*Appendix III(e). Haplotype Table I (Summary of designated haplotypes for the genus *Lepilemur* from all localities for D-loop and PAST fragments).*

Haplotypes for *Lepilemur* D-Loop Sequences

1. ANJZ32, ANJZ33, JOZO4.11
2. TAD25, TAD4.4, TAD4.17, TAD4.19, TAD4.23, TAD4.58, TAD4.59, TAD4.60, TAD4.61, MIZA3, MIZA4.11, MIZA4.15, ANOSIB15
3. ANOSIB18
4. MIZA4.18, TAD4.1
5. SIN26, SIN27
6. BET21
7. ZAH21, ZAH22, ZAH25, ZAH201, ZAH216, ZAH217
8. TSINJ36
9. TSINJ37
10. M83B, M93B, M94B, M95B, M104B, M140, M141, M142, L5
11. M105B
12. FAN10, FAN11
13. FAN4.24
14. AND20
15. JAR2, JAR3, JAR8, JAR3.38, JAR3.39, JAR3.46
16. NARA4.20
17. NARA8.5
18. NARA8.7, NARA8.8, NARA8.11, NARA8.12
19. KALA4.9
20. KALA5.12
21. KALA4.18, KALA4.19
22. KALA4.24
23. KALA4.16
24. FARY5.1, FARY5.2, FARY5.3, FARY5.4, LAVA5.1, LAVA5.2, LAVA5.3, LAVA5.4
25. ANK4, ANK16
26. MAR1, MAR2, MAR18, MAR20, MAR21, MAR22, MAR23, MAR27, MAR36, MAR38
27. HIH21, HIH22, HIH23
28. RANO2.24, RANO2.25, RAN3.1, KEL1
29. RIR02, TOL2.17, VOP2.6
30. RANO234, RANO235, RANO236, PBZT111
31. VOP2.16
32. AND65, AND66
33. AND67, AND78, HAZO5.7
34. AND79, AND93
35. AND68, AND69, AND92, AND94, HAZO5.6, HAZO5.16, HAZO5.17, HAZO5.18, HAZO5.19, HAZO5.20, HAZO5.21, HAZO5.22, HAZO5.23
36. BEZ14, BEZ15, BEZ18, BEZ21, BEZ22
37. BEMA5, BEMA6, BEMA7
38. JAM4.9, JAM4.10, JAM4.12, PBZT119
39. JAM4.8

40. JAM4.11, JAM4.13, JAM4.27
41. MIT16, MIT17, PBZT112
42. MOR117
43. MOR142
44. MOR147
45. ZOMB8, ZOMB15, ZOMB16
46. ZOMB9
47. ZOMB12
48. ZOMB21
49. ZOMB52
50. FIA5.1, FIA5.5, FIA5.9, FIA5.13, ANAL2.29, LAME5.6, LAME5.8, MER26
51. FIA5.12
52. CAR6, CAR11, CAR15, CAR17, CAR43, CAR58, CAR59
53. CAR21, CAR33, CAR45, CAR46, FIA5.6
54. ANAL2.1, ANAL2.2, ANAL2.4, ANAL2.12, ANAL2.13, ANAL5, MER24, LABE5.1, LABE5.2, LABE5.3, LABE5.4, LABE5.17
55. ANAL13
56. FIA5.11
57. DAR4.7, DAR4.17, DAR4.23, DAR4.27, DAR4.28, DAR4.30, DAR4.35
58. DAR4.18
59. DAR4.41
60. DAR4.19
61. FIA5.7, FIA5.8, FIA5.10
62. LOKO4.2, LOKO4.5, LOKO4.19, LOKO4.20, LOKO4.23, LOKO4.32, LOKO4.33, LOKO4.34, LOKO4.35, LOKO4.36
63. KIBO58, KIBO65, KIBO68
64. KIBO22
65. ANT5.2, ANT5.6
66. ANT5.5
67. ANT5.7
68. ANT5.11, GAR1
69. LAZA5.1, LAZA5.10
70. MAS6.12, MAS6.13, MAS6.14, MAS6.15, MAS6.16
71. BIBO7.1
72. BIBO7.3
73. BIBO7.6
74. BIBO7.7

Haplotypes for *Lepilemur* PAST Sequences

1. ANAL5, ANAL2.1
2. ANAL13
3. ANAL2.2
4. ANAL2.4
5. LABE5.1, LABE5.2, LABE5.3, LABE5.4, LABE5.17, MER24, ALA2.12
6. ANAL2.13
7. FIA5.1, FIA5.9, FIA5.13, CAR11, CAR43, ANAL2.29

8. CAR6
9. CAR15
10. CAR21
11. CAR33
12. FIA5.6
13. LAME5.6, LAME5.8, FIA5.5
14. FIA5.11
15. FIA5.12
16. CAR17
17. CAR45
18. CAR46
19. CAR58
20. CAR59
21. MER26
22. DAR4.7
23. DAR4.17, DAR4.23, DAR4.27
24. DAR4.18
25. DAR4.35
26. FIA5.7, FIA5.8
27. FIA5.10
28. DAR4.19
29. DAR4.28
30. DAR4.30
31. DAR4.41
32. LOKO4.2
33. LOKO4.5
34. LOKO4.19, LOKO4.33, LOKO4.36
35. LOKO4.20
36. LOKO4.23
37. LOKO4.32
38. LOKO4.34
39. LOKO4.35
40. FARY5.1, FARY5.2, FARY5.3, FARY5.4
41. LAVA5.1, LAVA5.2, LAVA5.3, LAVA5.4
42. ANT5.2, ANT5.6, ANT5.7, ANT5.11
43. ANT5.5
44. GAR1
45. LAZA5.1, LAZA5.10
46. BEZ14
47. BEZ15
48. BEZ18
49. BEZ21
50. BEZ22
51. AND65
52. AND66
53. AND67, AND69, AND92

54. AND68
55. AND78
56. AND79
57. AND93
58. AND94
59. HAZO5.6, HAZO5.7, HAZO5.16, HAZO5.17, HAZO5.18, HAZO5.19, HAZO5.20, HAZO5.21, HAZO5.22, HAZO5.23
60. MOR117
61. MOR142
62. MOR147
63. ZOMB8
64. ZOMB9
65. ZOMB12, ZOMB21
66. ZOMB15
67. ZOMB16
68. ZOMB52
69. BEMA5, BEMA7
70. BEMA6
71. ANK4
72. ANK16
73. MAR1
74. MAR2
75. MAR18
76. MAR20, MAR21
77. MAR22
78. MAR23
79. MAR27
80. MAR36
81. MAR38
82. HIH21
83. HIH22
84. HIH23
85. KIBO22
86. KIBO58
87. KIBO65
88. KIBO68
89. PBZT119
90. JAM4.8
91. JAM4.9, JAM4.12
92. JAM4.10
93. JAM4.11, JAM4.27
94. JAM4.13
95. MIT16
96. MIT17
97. PBZT112
98. ANOSIB15, ANOSIB18

99. TAD4.4
100. ANJZ32, ANJZ33, TAD4.16, TAD4.17
101. TAD4.19
102. TAD4.23
103. TAD4.58
104. TAD4.59
105. TAD4.60
106. TAD4.61
107. TAD25
108. MIZA3
109. MIZA11
110. MIZA15
111. MIZA18
112. JOZO4.11
113. SIN26
114. SIN27
115. BET21
116. TSINJ36
117. TSINJ37
118. ZAH21
119. ZAH22
120. ZAH25
121. ZAH201
122. ZAH216
123. ZAH217
124. L5
125. M83B
126. M93B
127. M94B
128. M95B
129. M104B, M142
130. M140, M141
131. M105B
132. FAN10, FAN11
133. FAN4.24
134. AND20
135. RANO2.24, RANO234
136. RANO235, RANO236
137. RANO2.25
138. PBZT111
139. TOL2.17
140. VOP2.6
141. VOP2.16
142. KEL1
143. RIR02
144. RAN3.1

145.KALA24
146.KALA4.9
147.KALA4.16
148.KALA4.18
149.KALA4.19
150.KALA5.12
151.JAR2
152.JAR3
153.JAR8
154.JAR3.38
155.JAR3.39
156.NARA4.20, NARA8.5
157.NARA8.7, NARA8.8, NARA8.11, NARA8.12
158.BIBO7.3
159.BIBO7.1, BIBO7.6, BIBO7.7
160.MAS6.12, MAS6.13, MAS6.14, MAS6.15, MAS6.16

MBP