Supplemental Information for:

Comparative population genomics unveils congruent secondary suture zone in Southwest Pacific Hydrothermal Vents

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Tables

Table 1: Sample details for all species used in this study, including the number of replicates. All samples have been collected during the Chubacarc 2019 campaign and a few samples from S.Hourdez (SH) and C.L Van Dover's (CDV) collections from 2009. I. nautilei population information can be found in Tran Lu Y et al., 2022. A hierarchical sampling has been followed with 3 levels of hierarchy: sites, localities and basins. N° samples is the number of individuals processed per site. N° libraries represent the total number of RAD libraries (including replicates) per site. Depth is in meters. Species short names: A_koj = Alviniconcha kojimai; B_m = Bathymodiolus manusensis; B_seg = Branchinotogluma segonzaci; E_ohtai = Eochionelasmus ohtai; L_affschro = Lepetodrilus aff. schrolli; L_schro = Lepetodrilus schrolli; S_toll = Shinkailepas tollmanni.

Basin	Locality	ID_Site	N° sample	N° libraries	Species	Longitude	Latitude	Depth
Futuna	Fati_Ufu	12	19	19	A_koj	W 177 11.082	S 14 45.589	1519
Futuna	Fati_Ufu	14	3	3	A_koj	W 177 11.098	S 14 45.587	1518
Futuna	Fati_Ufu	18	20	23	A_koj	W 177 11.116	S 14 45.597	1519
Futuna	Fatu_Kapa	25	4	4	A_koj	W 177 09.132	S 14 45.109	1562
Futuna	Fatu_Kapa	30	14	14	A_koj	W 177 09.960	S 14 44.245	1547
Lau	Mangatolo	46	3	3	A_koj	W 174 39.210	S 15 24.875	2031
Lau	Mangatolo	51	18	18	A_koj	W 174 39.331	S 15 24.961	2039
Lau	Abe	6	2	2	A_koj	W 176 11.481	S 20 45.785	2149
Lau	Tow_Cam	74	21	23	A_koj	W 176 08.257	S 20 19.074	2716
Lau	Tow_Cam	77	19	21	A_koj	W 176 08.264	S 20 19.085	2711
Lau	Tui_Malila	78	20	21	A_koj	W 176 34.070	S 21 59.254	1899
Lau	Tui_Malila	83	12	12	A_koj	W 176 34.091	S 21 59.356	1884
Lau	Tui_Malila	86	16	18	A_koj	W 176 34.099	S 21 59.354	1886
Manus	Suzette	139	18	18	A_koj	E 152 05.783	S 03 47.368	1505
Manus	North_Su	144	13	15	A_koj	E 152 06.046	S 03 47.933	1218
Manus	South_Su	158	16	16	A_koj	E 152 06.299	S 03 48.530	1300
North-Fiji	Phoenix	53	16	16	A_koj	E 173 55.078	S 16 56.963	1973
North-Fiji	Phoenix	59	18	22	A_koj	E 173 55.127	S 16 57.000	1961
Woodlark	Scala	164	1	3	A_koj	E 155 03.117	S 09 47.939	3344
Woodlark	Scala	171	23	23	A_koj	E 155 03.160	S 09 47.945	3388
Manus	Fenway	102	24	24	B_m	E 151 40.360	S 03 43.675	1696
Manus	Fenway	105	15	16	B_m	E 151 40.370	S 03 43.681	1698
Manus	Solwara_6	126	13	16	B_m	E 151 40.867	S 03 43.649	1725
Manus	Desmos	127	5	5	B_m	E 151 51.933	S 03 41.528	1896
Manus	North_Su	146	16	16	B_m	E 152 06.060	S 03 47.942	1210
Manus	North_Su	148	16	16	B_m	E 152 06.089	S 03 47.957	1195
Manus	South_Su	160	19	19	B_m	E 152 06.300	S 03 48.482	1360
Manus	South_Su	162	13	16	B_m	E 152 06.310	S 03 48.582	1353
Futuna	Fati_Ufu	21	2	2	B_m	W 177 11.301	S 14 45.921	1520
Futuna	Fati_Ufu	22	5	5	B_m	W 177 11.303	S 14 45.920	1500
Futuna	Kulo_Lasi	36	12	12	B_m	W 177 15.004	S 14 56.537	1412

Futuna	Kulo_Lasi	37	3	3	B_m	W 177 15.007	S 14 56.539	1414
Futuna	Kulo_Lasi	38	1	1	B_m	W 177 15.551	S 14 56.468	1371
Futuna	Kulo_Lasi	41	13	13	B_m	W 177 15.565	S 14 56.384	1407
Lau	Mangatolo	45	7	7	B_m	W 174 39.209	S 15 24.878	2031
Manus	Snowcap	88	22	24	B_m	E 151 40.213	S 03 43.691	1640
Futuna	Fati_Ufu	11	3	5	B_seg	W 177 11.082	S 14 45.587	1520
Manus	Solwara_7	110	3	3	B_seg	E 151 40.377	S 03 43.033	1765
Manus	Solwara_8	114	1	1	B_seg	E 151 40.452	S 03 43.820	1737
Manus	Romans_Ruins	118	3	3	B_seg	E 151 40.463	S 03 43.287	1666
Futuna	Fati_Ufu	13	24	30	B_seg	W 177 11.093	S 14 45.590	1520
Manus	Suzette	137	17	17	B_seg	E 152 05.733	S 03 47.348	1497
Manus	Suzette	141	2	2	B_seg	E 152 05.794	S 03 47.345	1503
Woodlark	Scala	164	3	3	B_seg	E 155 03.117	S 09 47.939	3344
Woodlark	Scala	170	17	20	B_seg	E 155 03.160	S 09 47.935	3374
Manus	South_Su	174	1	3	B_seg	E 152 06.314	S 03 48.556	1331
Futuna	Fati_Ufu	19	2	2	B_seg	W 177 11.149	S 14 45.576	1519
Futuna	Fati_Ufu	20	7	7	B_seg	W 177 11.180	S 14 45.486	1527
Futuna	Fatu_Kapa	28	5	5	B_seg	W 177 09.257	S 14 45.165	1545
Futuna	Fatu_Kapa	32	20	20	B_seg	W 177 09.964	S 14 44.236	1547
Futuna	Kulo_Lasi	39	2	2	B_seg	W 177 15.554	S 14 56.468	1371
Lau	Mangatolo	43	11	18	B_seg	W 174 39.205	S 15 24.867	2027
North-Fiji	Phoenix	54	6	9	B_seg	E 173 55.080	S 16 56.951	1973
North-Fiji	Phoenix	60	4	6	B_seg	E 173 55.127	S 16 57.001	1961
Lau	Tow_Cam	67	10	10	B_seg	W 176 08.205	S 20 18.981	2716
Lau	Tow_Cam	68	9	9	B_seg	W 176 08.207	S 20 18.982	2716
Lau	Tow_Cam	72	5	6	B_seg	W 176 08.245	S 20 19.074	2717
Lau	Abe	8	11	11	B_seg	W 176 11.526	S 20 45.762	2127
Lau	Tui_Malila	82	14	23	B_seg	W 176 34.089	S 21 59.375	1873
Manus	Suzette	87	1	1	B_seg	E 152 05.412	S 03 47.412	1579
Lau	Abe	9	11	11	B_seg	W 176 11.530	S 20 45.766	2129
Manus	Big_Papi	95	17	26	B_seg	E 151 40.334	S 03 43.729	1709
Manus	Big_Papi	96	9	9	B_seg	E 151 40.335	S 03 43.731	1708
Kermadec	Haungaroa	SH	20	20	B_seg	W 179°37.12	S 32°37.264	NA
Manus	Solwara_8	113	24	28	E_ohtai	E 151 40.451	S 03 43.825	1736
Manus	North_Su	143	24	24	E_ohtai	E 152 06.045	S 03 47.936	1215
Futuna	Fatu_Kapa	23	16	17	E_ohtai	W 177 09.096	S 14 45.110	1567
Futuna	Fatu_Kapa	29	7	7	E_ohtai	W 177 09.960	S 14 44.243	1548
Lau	Abe	3	24	27	E_ohtai	W 176 11.479	S 20 45.786	2151
Futuna	Fatu_Kapa	31	24	26	E_ohtai	W 177 09.961	S 14 44.243	1548
Futuna	Kulo_Lasi	37	24	26	E_ohtai	W 177 15.007	S 14 56.539	1414
Lau	Mangatolo	45	24	26	E_ohtai	W 174 39.209	S 15 24.878	2031
Lau	Mangatolo	52	24	24	E_ohtai	W 174 39.335	S 15 24.963	2039
North-Fiji	Phoenix	61	24	29	E_ohtai	E 173 55.127	S 16 57.002	1961

Lau	Tow_Cam	70	24	24	E_ohtai	W 176 08.212	S 20 19.051	2965
Lau	Tui_Malila	80	24	24	E_ohtai	W 176 34.077	S 21 59.280	1892
Futuna	Fati_Ufu	16	24	24	L_aff_schro	W 177 11.113	S 14 45.601	1519
Lau	Abe	2	24	26	L_aff_schro	W 176 11.479	S 20 45.784	2153
Futuna	Fatu_Kapa	26	4	4	L_aff_schro	W 177 09.133	S 14 45.110	1562
Futuna	Fatu_Kapa	29	20	20	L_aff_schro	W 177 09.960	S 14 44.243	1548
Futuna	Kulo_Lasi	37	10	12	L_aff_schro	W 177 15.007	S 14 56.539	1414
Futuna	Kulo_Lasi	38	24	26	L_aff_schro	W 177 15.551	S 14 56.468	1371
Lau	Mangatolo	45	12	12	L_aff_schro	W 174 39.209	S 15 24.878	2031
Lau	Mangatolo	52	12	12	L_aff_schro	W 174 39.335	S 15 24.963	2039
North-Fiji	Phoenix	56	18	18	L_aff_schro	E 173 55.111	S 16 56.936	1974
North-Fiji	Phoenix	62	18	20	L_aff_schro	E 173 55.133	S 16 57.005	1961
Lau	Tow_Cam	73	16	24	L_aff_schro	W 176 08.250	S 20 19.074	2711
Lau	Tow_Cam	76	16	16	L_aff_schro	W 176 08.263	S 20 19.084	2711
Lau	Tui_Malila	80	16	16	L_aff_schro	W 176 34.077	S 21 59.280	1892
Lau	Tui_Malila	84	16	16	L_aff_schro	W 176 34.094	S 21 59.354	1877
Manus	Fenway	103	8	8	L_schro	E 151 40.367	S 03 43.665	1699
Manus	Fenway	105	8	8	L_schro	E 151 40.370	S 03 43.681	1698
Manus	Solwara_7	107	16	18	L_schro	E 151 40.374	S 03 43.042	1769
Manus	Solwara_8	111	23	25	L_schro	E 151 40.441	S 03 43.825	1739
Manus	Solwara_6	123	15	15	L_schro	E 151 40.854	S 03 43.654	1729
Manus	Desmos	132	24	44	L_schro	E 151 51.985	S 03 41.542	1912
Manus	South_Su	135	24	24	L_schro	E 152 06.310	S 03 48.582	1353
Manus	Suzette	140	15	15	L_schro	E 152 05.783	S 03 47.368	1506
Manus	North_Su	145	16	16	L_schro	E 152 06.046	S 03 47.935	1216
Manus	North_Su	146	8	10	L_schro	E 152 06.060	S 03 47.942	1210
Manus	North_Su	147	12	12	L_schro	E 152 06.084	S 03 47.957	1194
Manus	North_Su	148	8	16	L_schro	E 152 06.089	S 03 47.957	1195
Woodlark	Scala	172	19	31	L_schro	E 155 03.161	S 09 47.945	3388
Manus	Fenway	98	8	8	L_schro	E 151 40.342	S 03 43.707	1703
Manus	Fenway	99	6	6	L_schro	E 151 40.344	S 03 43.704	1701
Manus	Solwara_1	CDV	12	12	L_schro	NA	NA	NA
Manus	Solwara_8	CDV	8	8	L_schro	NA	NA	NA
Kermadec	Haungaroa	SH	24	24	L_schro	W 179°37.12	S 32°37.264	NA
Lau	Abe	2	20	28	S_toll	W 176 11.479	S 20 45.784	2153
Futuna	Fati_Ufu	10	6	18	S_toll	W 177 10.968	S 14 45.325	1516
Futuna	Fati_Ufu	16	6	21	S_toll	W 177 11.113	S 14 45.601	1519
Futuna	Fatu_Kapa	24	11	13	S_toll	W 177 09.103	S 14 45.113	1564
Futuna	Fatu_Kapa	29	14	14	S_toll	W 177 09.960	S 14 44.243	1548
Futuna	Kulo_Lasi	38	23	25	S_toll	W 177 15.551	S 14 56.468	1371
Lau	Mangatolo	46	12	12	S_toll	W 174 39.210	S 15 24.875	2031
Lau	Mangatolo	52	12	12	S_toll	W 174 39.335	S 15 24.963	2039
Fidjien	Phoenix	56	23	25	S_toll	E 173 55.111	S 16 56.936	1974

Fidjien	Phoenix	62	20	28	S_toll	E 173 55.133	S 16 57.005	1961
Lau	Tow_Cam	73	12	12	S_toll	W 176 08.250	S 20 19.074	2711
Lau	Tow_Cam	76	11	13	S_toll	W 176 08.263	S 20 19.084	2711
Lau	Tui_Malila	80	10	16	S_toll	W 176 34.077	S 21 59.280	1892
Lau	Tui_Malila	84	12	12	S_toll	W 176 34.094	S 21 59.354	1877
Manus	Fenway	98	11	17	S_toll	E 151 40.342	S 03 43.707	1703
Manus	Solwara_7	107	12	12	S_toll	E 151 40.374	S 03 43.042	1769
Manus	Solwara_8	116	12	12	S_toll	E 151 40.460	S 03 43.820	1737
Manus	Romans_Ruins	119	3	21	S_toll	E 151 40.469	S 03 43.287	1659
Manus	Solwara_6	123	13	15	S_toll	E 151 40.854	S 03 43.654	1729
Manus	South_Su	135	12	12	S_toll	E 152 06.310	S 03 48.582	1353
Manus	Suzette	140	14	14	S_toll	E 152 05.783	S 03 47.368	1506
Manus	North_Su	145	14	14	S_toll	E 152 06.046	S 03 47.935	1216
Woodlark	Scala	172	10	10	S_toll	E 155 03.161	S 09 47.945	3388
Manus_CDV	CDV	NA	41	41	S_toll	0	NA	NA
Lau_JUV	Tui_Malila_JUV	NA	50	52	S_toll	NA	NA	NA

Table 2: Summary table of table S1 per basin, locality and species. The first number represents the number of sites sampled and the second the total number of samples sampled per locality. Species short names: A_koj = Alviniconcha kojimai; B_m = Bathymodiolus manusensis; B_seg = Branchinotogluma segonzaci; E_ohtai = Eochionelasmus ohtai; L_affschro = Lepetodrilus aff. schrolli; L_schro = Lepetodrilus schrolli; S_toll = Shinkailepas tollmann. SUM= SUM for all species of total sites used (ID_sites) and total number of samples used.

Basin	**Locality**	***S_toll***	***A_koj***	***B_m***	***B_seg***	***E_ohtai***	***L_schro & aff schro***
North-Fiji	Phoenix	2 / 53	2 / 38	0 / 0	2 / 15	1 / 29	2 / 38
Futuna	Fati_Ufu	2 / 39	3 / 45	2 / 7	4 / 44	0 / 0	1 / 24
Futuna	Fatu_Kapa	2 / 27	2 / 18	0 / 0	2 / 25	3 / 50	2 / 24
Futuna	Kulo_Lasi	1 / 25	0 / 0	4 / 29	1 / 2	1 / 26	2 / 38
Kermadec	Haungaroa	0 / 0	0 / 0	0 / 0	1 / 20	0 / 0	1 / 24
Lau	Abe	1 / 28	1 / 2	0 / 0	2 / 22	1 / 27	1 / 26
Lau	Mangatolo	2 / 24	2 / 21	1 / 7	1 / 18	2 / 50	2 / 24
Lau	Tow_Cam	2 / 25	2 / 44	0 / 0	3 / 25	1 / 24	2 / 40
Lau	Tui_Malila	2 / 28	3 / 51	0 / 0	1 / 23	1 / 24	2 / 32
Lau_JUV	Tui_Malila_JUV	1 / 52	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
Manus	Big_Papi	0 / 0	0 / 0	0 / 0	2 / 35	0 / 0	0 / 0
Manus	Desmos	0 / 0	0 / 0	1 / 5	0 / 0	0 / 0	1 / 44

Manus	Fenway	1 / 17	0 / 0	2 / 40	0 / 0	0 / 0	4 / 30
Manus	North_Su	1 / 14	1 / 15	2 / 32	0 / 0	1 / 24	4 / 54
Manus	Romans_Ruins	1 / 21	0 / 0	0 / 0	1 / 3	0 / 0	0 / 0
Manus	Snowcap	0 / 0	0 / 0	1 / 24	0 / 0	0 / 0	0 / 0
Manus	Solwara_1	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0	1 / 12
Manus	Solwara_6	1 / 15	0 / 0	1 / 16	0 / 0	0 / 0	1 / 15
Manus	Solwara_7	1 / 12	0 / 0	0 / 0	1 / 3	0 / 0	1 / 18
Manus	Solwara_8	1 / 12	0 / 0	0 / 0	1 / 1	1 / 28	2 / 33
Manus	South_Su	1 / 12	1 / 16	2 / 35	1 / 3	0 / 0	1 / 24
Manus	Suzette	1 / 14	1 / 18	0 / 0	3 / 20	0 / 0	1 / 15
Manus_CDV	CDV	1 / 41	0 / 0	0 / 0	0 / 0	0 / 0	0 / 0
Woodlark	Scala	1 / 10	2 / 26	0 / 0	2 / 23	0 / 0	1 / 31
SUM		25 / 469	20 / 294	16 / 195	28 / 282	12 / 282	18 / 546

Table 3: Description of all filtering steps to obtain the VCF files. HWE (step10) test (performed with snpgdsHWE function from SNPRelate R package V.1.21.7*), was performed independently within each genetic unit depicted by the PCA and loci were excluded if they deviated from HWE in any populations (genetic cluster) with a p-value threshold of 0.05.*

Filtering criteria	STEP
Assembled data	1
Replicate and samples with more 20 % miss data	2
SNPs with heterozygosity > 0.6	3
max missing data per SNPs 10%	4
max missing data per sample 10 % (15 % S. tollmanni)	5
Max Read Depth (DP) > 80	7
Minor allele frequency > 0.05	8
Max missing data par sample 10 % (15 % S. tollmanni)	9
Out of Hardy-Weinberg equibrium *p*-value < 0.05	10
1 SNPs per RADtag	11

Table 4: Filtering steps for each species with their number of variants (SNPs), radtags and samples.

	A. kojimai			***S. tollmanni***		
Filtering step	**N° SNPs**	**N° radtag**	**N° samples**	**N° SNPs**	**N° radtag**	**N° samples**
1	286,975	39,931	294	1,142,237	21,424	384
2	286,975	39,931	259	1,142,237	21,424	347
3	286,975	39,931	259	1,142,237	21,424	347
4	164,171	24,375	259	174,914	4,920	347

5	164,144	24,363	259	174,914	4,920	347
6	164,077	24,349	212	174,853	4,907	356
7	32,031	13,728	212	15,413	3,395	347
8	32,031	13,728	212	15,413	3,395	347
9	28,330	12,957	212	11,059	3,074	347
10	12,957	12,957	212	3,074	3,074	347

	E. ohtai			***B. manusensis***		
Filtering step	**N° SNPs**	**N° radtag**	**N° samples**	**N° SNPs**	**N° radtag**	**N° samples**
1	2,144,137	103,097	282	84,281	11,665	186
2	2,144,137	103,097	256	84,281	11,665	168
3	2,143,451	103,077	256	84,281	11,665	168
4	1,407,227	74,794	256	43,222	6,393	168
5	1,407,227	74,794	240	43,222	6,393	161
6	1,407,110	74,773	240	43,222	6,393	161
7	118,173	48,486	240	6,783	3,356	161
8	118,173	48,486	224	6,783	3,356	159
9	104,892	45,984	224	5,358	2,904	159
10	45,984	45,984	224	2904	2904	159

	B. segonzaci			***L. schrolli & L. aff. schrolli***		
Filtering step	**N° SNPs**	**N° radtag**	**N° samples**	**N° SNPs**	**N° radtag**	**N° samples**
1	899,488	93,006	262	1,463,969	35,025	522
2	899,488	93,006	233	1,463,969	35,025	451
3	899,488	93,006	233	1,463,969	35,025	451
4	640691	69106	233	1,161,506	27,853	451
5	640691	69106	233	1,161,506	27,853	423
6	640673	69101	233	1,107,329	26,695	423
7	147128	50221	233	87,258	22,147	423
8	147128	50221	204	87,258	22,147	423
9	127888	47547	204	48,979	14,297	423
10	47547	47547	204	14,297	14,297	423

NB: In addition, a filter specific to L. schrolli (& L. affschro) was applied before the last step 10, to remove radtags and variants potentially linked to some genomic architecture or sex determism. To achieve this, markers contributing more than 50% to the PC1 of the separation in Manus BAB were removed from the total dataset.

Table 5: Stacks parameters for de novo assembly of bi-allelic loci between individuals and number of SNPs and individuals for each dataset at one SNP per ddRADtag/loci. n.SNPs: number of SNPs structure analysis; n.SNPs dadi dataset: number of SNPs dadi analysis; n.Ind: total number of individuals. (Ifremeria nautilei data from Tran Lu Y et al. 2022). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

Species	***m***	***M***	***n***	***n.SNPs***	***n.SNPs dadi dataset***	***n.Ind***
Ifremeria nautilei	5	6	6	10,570	17,365	362
Alviniconcha kojimai	6	7	7	12,957	39,669	212
Shinkailepas tollmanni	5	11	11	3,074	12,953	347
Eochionelasmus ohtai	4	7	7	45,984	74,773	224
Bathymodiolus manusensis	5	5	5	2,904	6,340	159
Branchinotogluma segonzaci	4	4	4	47,547	69,101	195
Lepetodrilus schrolli & aff. schrolli	4	5	5	14,297	26,627	414

Table 6: Pairwise F_{st} matrix between BABs for each species calculated with arlequin (V.3.5.2.2). Significativity threshold for 10000 permutations (:0.05, **:0.01, ***:<0.001). For the species L. schrolli/aff. schrolli and B. segonzaci, one additional population has been sampled and processed from the Kermadec BAB (display in red). For coherence between species and readability, these results from Kermadec have not been reported and discussed in the main part of the paper*

A. kojimai					
	Manus	Woodlark	North Fiji	Lau	Futuna
Manus	0.00000				
Woodlark	-0.00079	0.00000			
North Fiji	**0.01651*****	**0.01668*****	0.00000		
Lau	**0.01888*****	**0.01911*****	**0.00317*****	0.00000	
Futuna	**0.01868*****	**0.01881*****	**0.00324*****	-0.00044	0.00000

E. ohtai				
	Manus	Lau	North Fiji	Futuna
Manus	0.00000			
Lau	**0.20507*****	0.00000		
North Fiji	**0.21365*****	**-0.00008****	0.00000	
Futuna	**0.20765*****	-0.00022	**0.00008****	0.00000

B. manusensis			
	Manus	Lau	Futuna
Manus	0.00000		
Lau	**0.19262*****	0.00000	
Futuna	**0.20663*****	-0.00315	0.00000

S. tollmanni						
	Manus	Woodlark (M)	Woodlark (NFFL)	North Fiji	Lau	Futuna
Manus	0.00000					
Woodlark_M	**0.00695****	0.00000				
Woodlark_NFFL	**0.26753*****	**0.21692****	0.00000			
North Fiji	**0.27114*****	**0.23451*****	0.00146*	0.00000		
Lau	**0.27280*****	**0.23649*****	-0.00248	-0.00103	0.00000	
Futuna	**0.27256*****	**0.23492*****	-0.00212	-0.00049	-0.00057	0.00000

B. segonzaci						
	Manus	Woodlark	North Fiji	Futuna	Lau	Kermadec
Manus	0.00000					
Woodlark	**0.00921*****	0.00000				
North Fiji	**0.04145*****	**0.03551*****	0.00000			
Futuna	**0.04132*****	**0.03658*****	**0.00099*****	0.00000		
Lau	**0.04087*****	**0.03640*****	**0.00076*****	**-0.00021***	0.00000	
Kermadec	0.03695***	0.03071***	-0.00318	-0.00334	-0.00332	0.00000

L. schrolli & L. aff. schrolli						
	Manus	Woodlark	Lau	Futuna	North Fiji	Kermadec
Manus	0.00000					
Woodlark	**0.18480*****	0.00000				
Lau	**0.36353*****	**0.15474*****	0.00000			
Futuna	**0.36170*****	**0.15610*****	**0.00992*****	0.00000		
North Fiji	**0.35485*****	**0.14153*****	**0.02855*****	**0.02557*****	0.00000	
Kermadec	**0.41578*****	**0.30053*****	**0.18267*****	**0.18120*****	0.27850**	0.00000

Table 7: All dadi parameters for the best model and each species. Species are by column and row is the parameter value under the best model. All parameters are scaled by Nref which is scaled by theta. Nu1 and Nu2 represent population size. b1 and b2 represent the growth factor over time. hrf represents the hill-robertson factor. Ts represents the divergence time without migration for AM, SC and SI and with migration for IM model. Tsc represents the time of secondary contact between the two populations. m12, represents the unrestricted migration rate from population 2 towards population 1; me12, the restricted migration rate (e.g., barrier loci) from population 2 towards population 1. Q represents the proportion of loci affected by the linked selection (hill-robertson effect) and P the proportion of loci that show unconstrained gene flow (m12 and m21).

	A. kojimai	***S. tollmanni***	***S. tollmanni***	***E. ohtai***	***B. segonzaci***	***B. manusensis***	***B. manusensis***	***B. manusensis***	***L. schrolli & L. aff. schrolli***

Model	SC2N2mG	SC2N2m	SC2N2mG	SC2mG	SC2N2mG	IM2N	SC2N2m	SC2N	SC2N2mG
Nu1 (NFFL)	0.694	16.057	1.752	1.343	2.757	10.896	6.052	9.524	1.077
Nu2 (M/W)	2.750	1.527	3.568	1.203	0.605	10.691	5.282	10.809	1.018
b1	57.949		4.378	31.559	2.191				5.581
b2	7.981		0.524	4.080	4.082				39.899
hrf	0.381	0.042	0.039	0.656	0.064	0.075	0.013	0.080	0.089
Ts	0.627	1.037	1.004	1.000	0.467	2.156	1.486	1.216	1.041
Tsc	0.252	0.089	0.103		0.394		0.105	0.818	1.470
m12	4.741	0.321	0.445	0.364	0.579	0.436	3.989	0.520	0.878
m21	4.389	3.314	2.887	1.386	6.489	0.566	4.891	0.537	0.308
me12	0.384	4.334	4.747	0.013	2.195		0.227		0.009
me21	0.841	13.866	14.381	0.124	5.412		0.646		0.007
P	0.851	0.014	0.039	0.508	0.000		0.323		0.180
Q	0.005	0.434	0.416		0.232	0.580	0.699	0.531	0.569
Theta	860.782	107.227	109.056	1 268.530	1 714.163	140.211	81.495	137.803	136.458
Nref	23 243.21	30 529.04	31 049.58	28 403.58	19 491.165	23 594.133	13 713.680	23 188.985	23 243.207

NB: in main text table 3, for S. tollmanni and B. segonzaci, the purpose of understanding and displaying the main gene flow value, m and me have been switch, as well for P (switch to 1-P).

Table S8: all Standard deviation (SD) parameters for the best model and each species, estimated with Fisher Information Matrix (FIM) from dadi and from SI Table 7 value.

	A. kojimai	***S. tollmanni***	***S. tollmanni***	***E. ohtai***	***B. segonzaci***	***B. manusensis***	***B. manusensis***	***B. manusensis***	***L. schrolli & L. aff. schrolli***
	SC2N2mG	SC2N2m	SC2N2mG	SC2mG	SC2N2mG	IM2N	SC2N2m	SC2N	SC2N2mG
Nu1 (NFFL)	0.091	3.519	3.493	0.160	1.755	2.792	0.855	1.957	0.527
Nu2 (M/W)	0.181	0.322	0.342	0.157	0.287	3.253	1.115	2.881	0.054
b1	15.152		0.380	4.124	4.401				13.586
b2	1.707		2.349	0.438	2.324				0.526
hrf	1.883	0.009	0.007		0.024	0.008	0.006	0.009	0.018
Ts	0.073	0.135	0.122	0.103	0.533	0.481	0.239	0.302	0.410
Tsc	0.016	0.022	0.074	0.051	0.064		0.047	0.202	0.085
m12	0.502	0.113	0.090	0.057	0.376	0.130	1.911	0.105	0.197
m21	0.540	0.973	0.227	0.142	5.379	0.171	2.419	0.134	0.112
me12	0.082	1.492	3.020	0.002	0.858		0.156		0.004

me21	0.011	4.009	3.968	0.011	4.475		0.308		0.008
P	0.014	0.147	0.086	0.013	0.530		0.085		0.123
Q	0.078	0.090	0.068		0.129	0.042	0.071	0.044	0.253
Theta	35.588	7.896	8.253	71.235	341.493	21.664	8.309	17.119	23.705

Figures

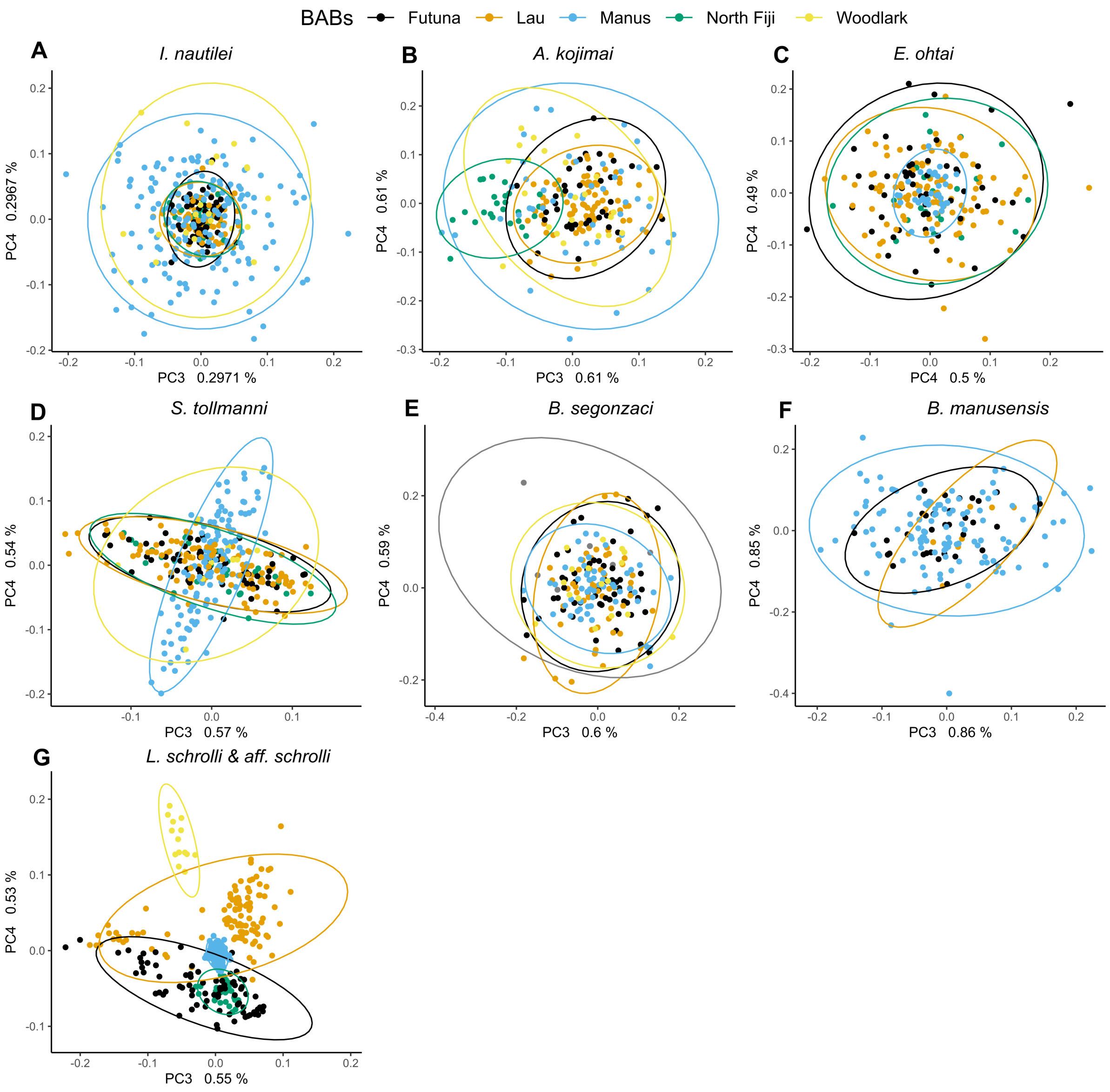


Figure 1: All PCA plots for Principal Component 3 and 4 for each species. Open ellipses represent the multivariate normal distribution of each group at 95%, here BABs. Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022

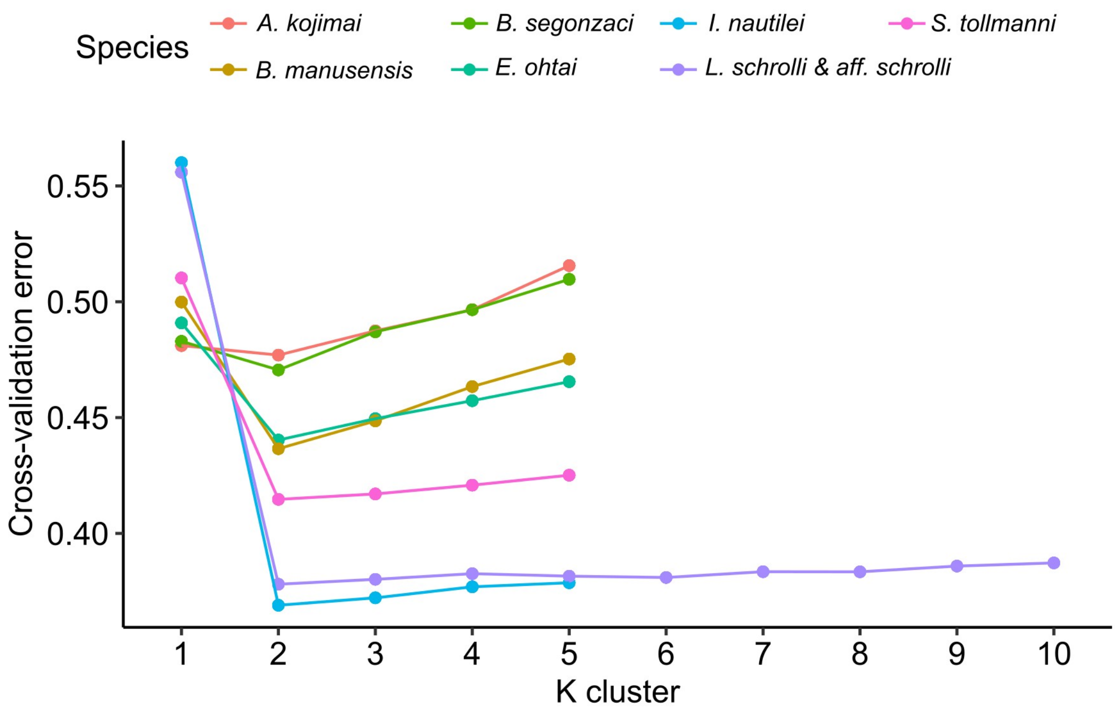


Figure 2: Cross-validation error for each K value for all species and runs of Admixture analysis. Color represents species. Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022

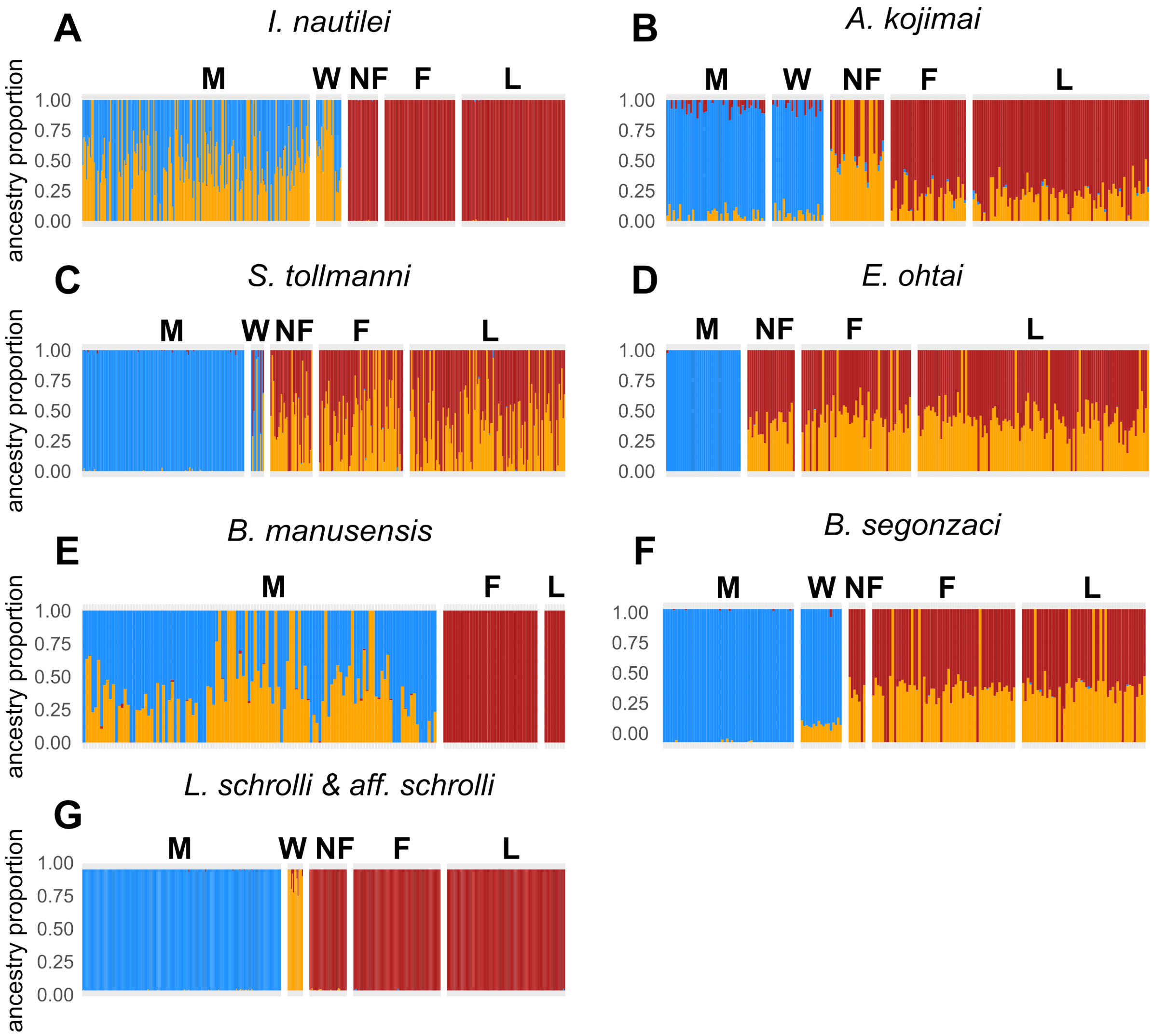


Figure 3 : Bar Plot of K=3 Admxiture analysis for each species. Each color represents a genetic cluster and each bar represents an individual. All individuals are grouped by geographic zone. Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022

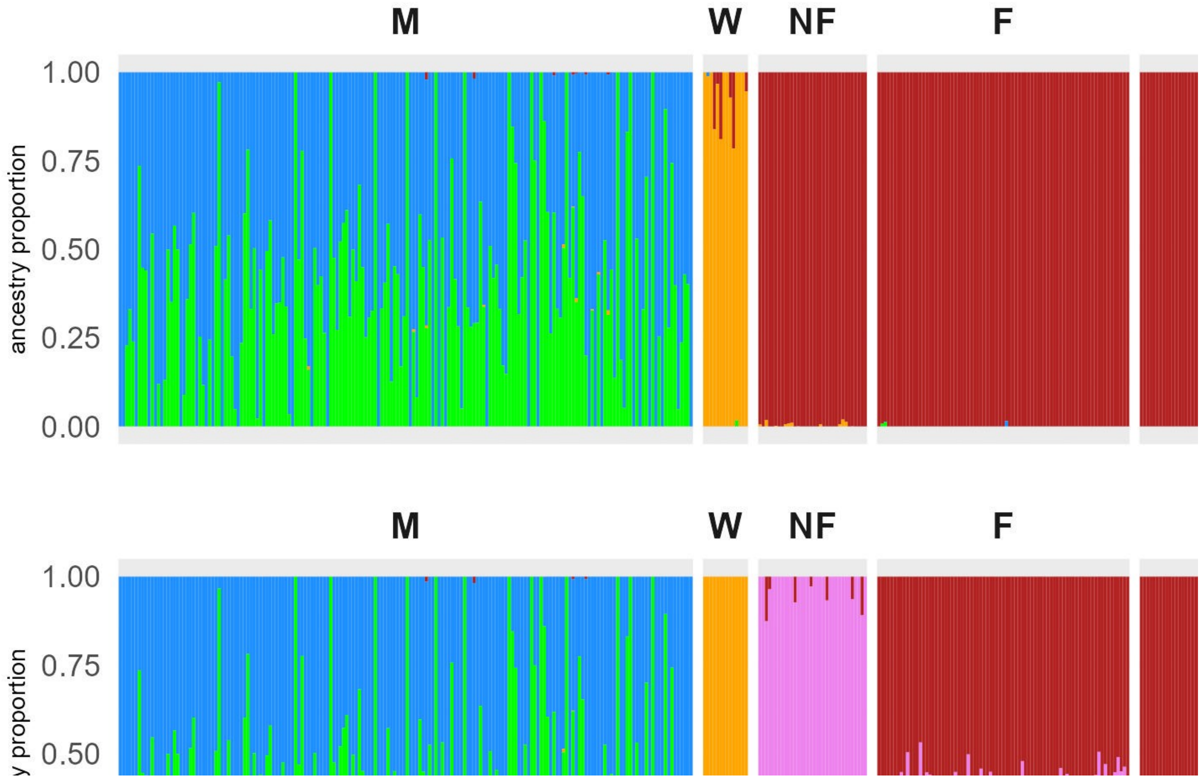


Figure 4 : Barplot of K=4 and K=5 Admture analysis for L. schrolli & aff schrolli. Each color represents a genetic cluster and each bar represents an individual. All individuals are grouped by geographic zone.

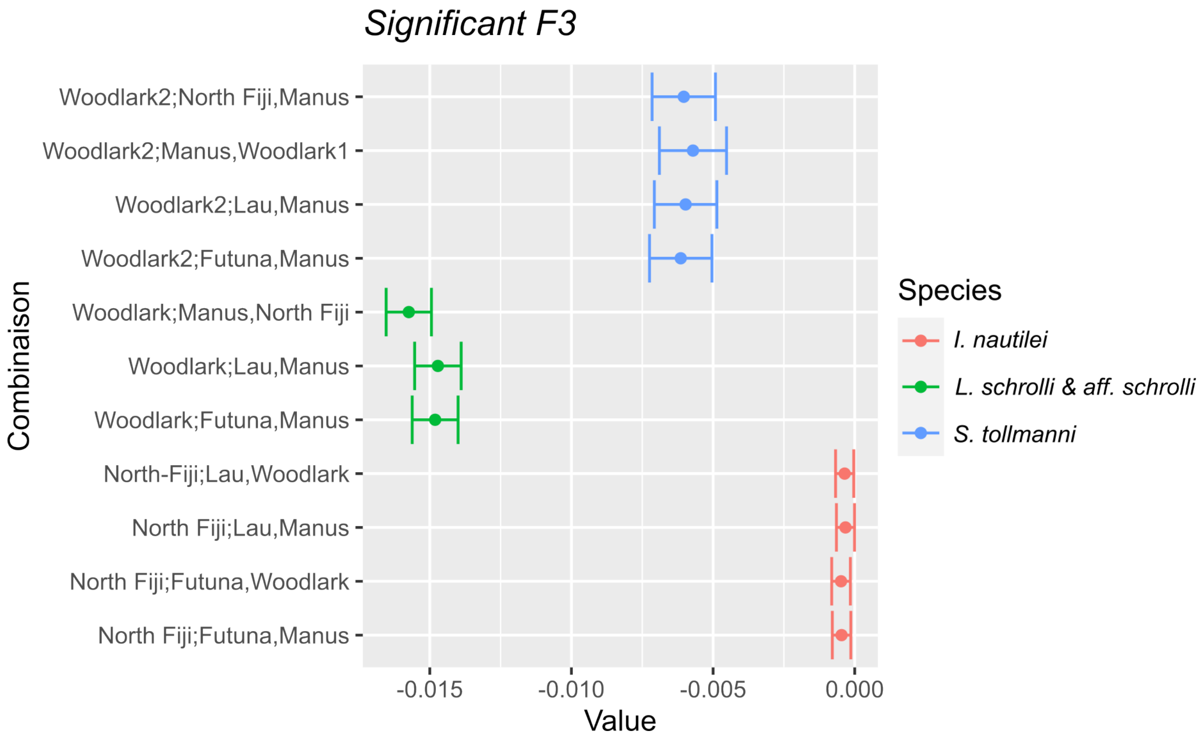


Figure 5 : Plot of f3 statistics and the confidence interval at 95%. Combinaison represent, first the focal population and then the two source populations. Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022

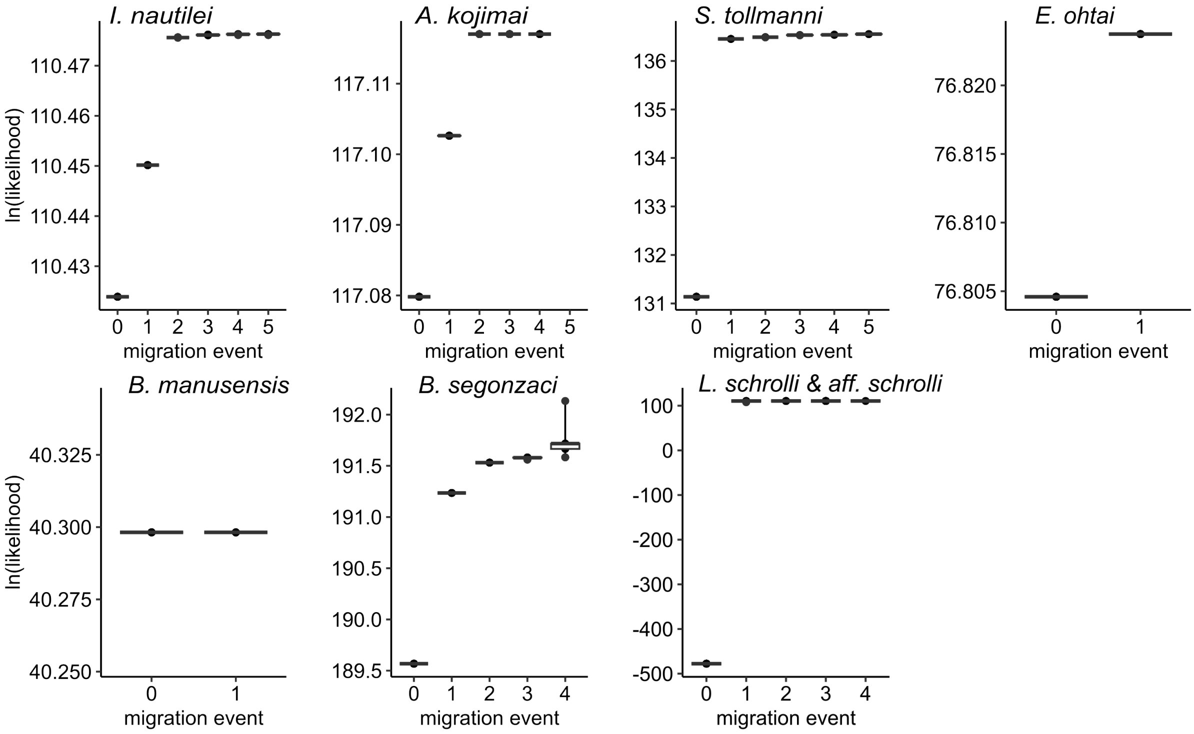

I. nautilei
110.47
110.46
110.45
110.44
110.43
ln(likelihood)
0 1 2 3 4 5
migration event
A. kojimai
117.11
117.10
117.09
117.08
0 1 2 3 4 5
migration event
S. tollmanni
136
135
134
133
132
131
0 1 2 3 4 5
migration event
E. ohtai
76.820
76.815
76.810
76.805
0 1
migration event
B. manusensis
40.325
40.300
40.275
40.250
ln(likelihood)
0 1
migration event
B. segonzaci
192.0
191.5
191.0
190.5
190.0
189.5
0 1 2 3 4
migration event
L. schrolli & aff. schrolli
100
0
-100
-200
-300
-400
-500
0 1 2 3 4
migration event

Figure 6 : Log likelihood for each species and each migration event for 10 independent runs . Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022

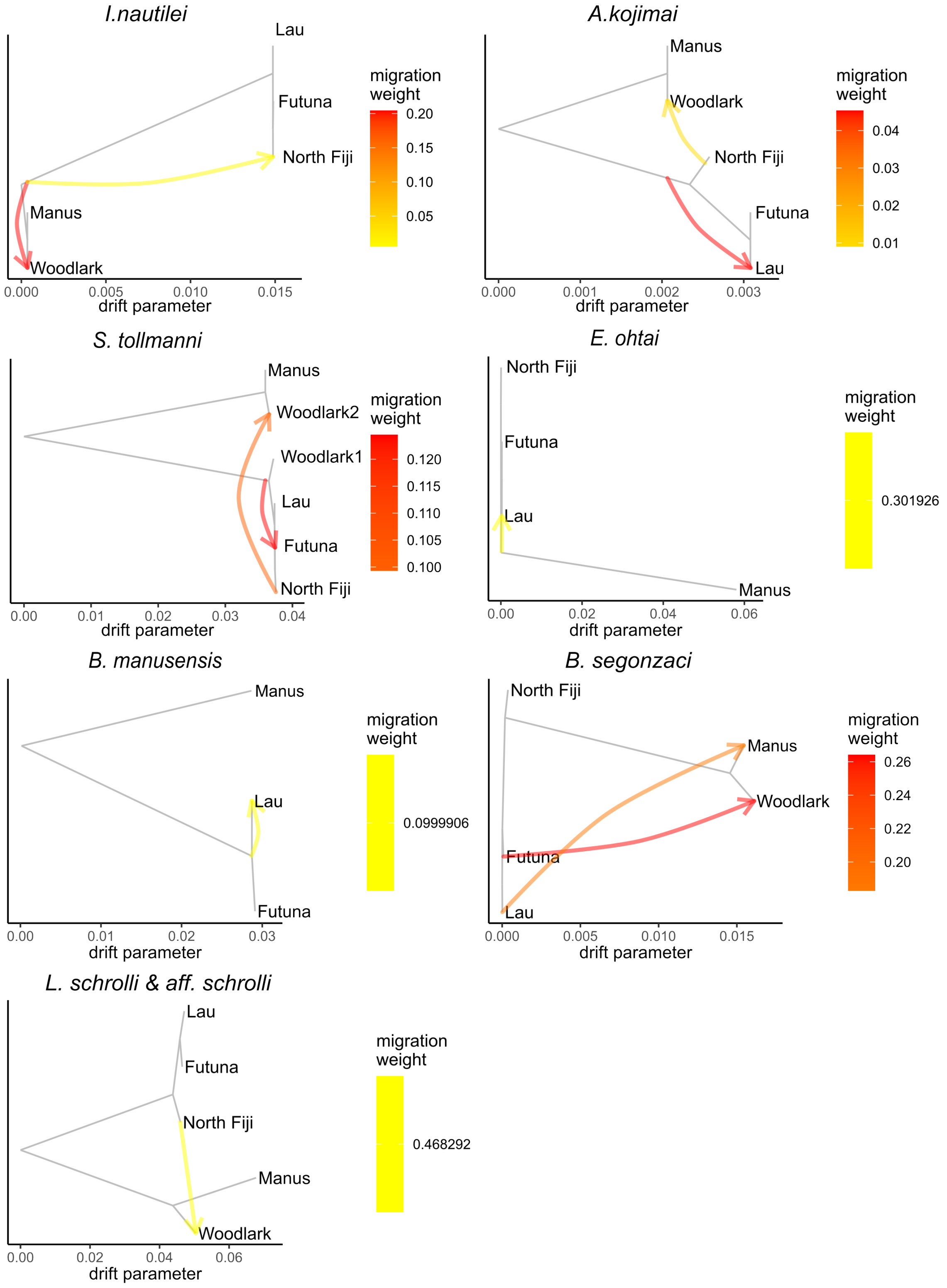


Figure 7 : Treemix plot for each species and the optimal number of migration events. Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022

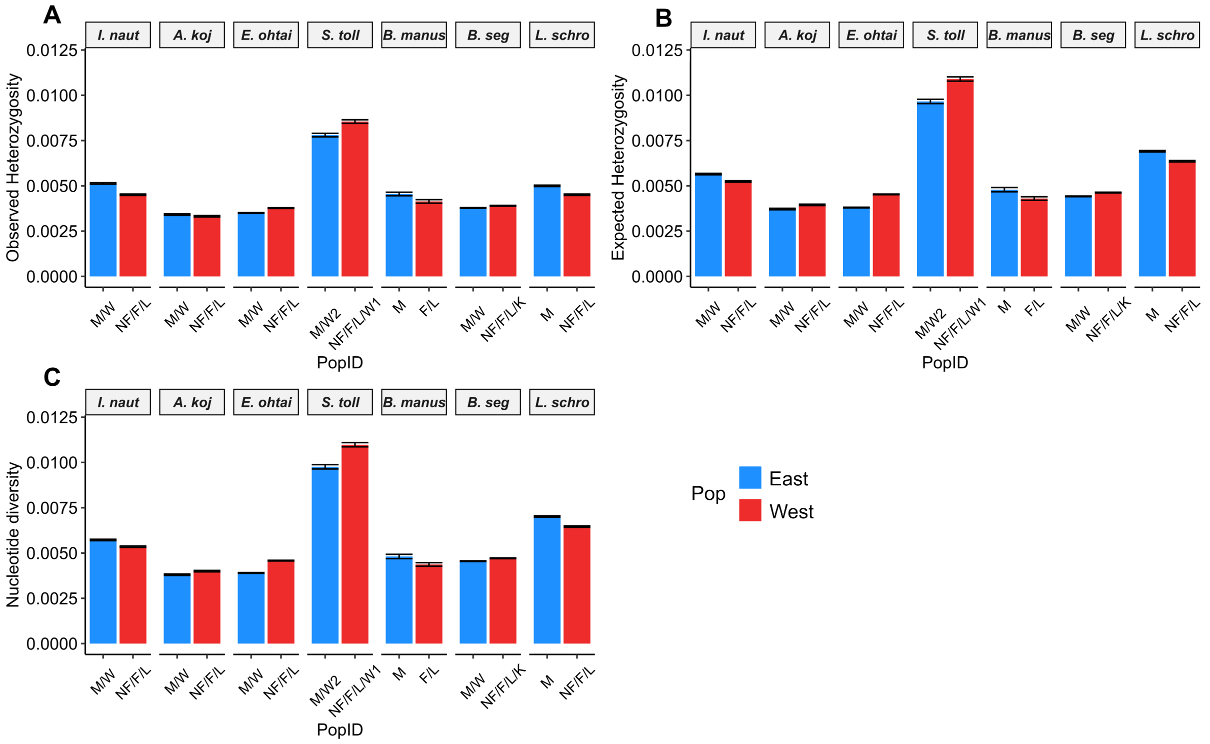


Figure 8: Observed (Ho) and expected (He) heterozygosities and nucleotide diversity (π) calculated with Stacks2 on the final dataset including all sites (variant and non variant). Error bars represent the confidence interval (CI) estimated at 95%. Colors identify the two main metapopulations (lineages). Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022. I. naut : I. nautilei, A. koj: A. kojimai, S. toll: S. tollmanni; B. manus:B. manusensis, B. seg: B. segonzaci, L. schro: L. schrolli & aff schrolli

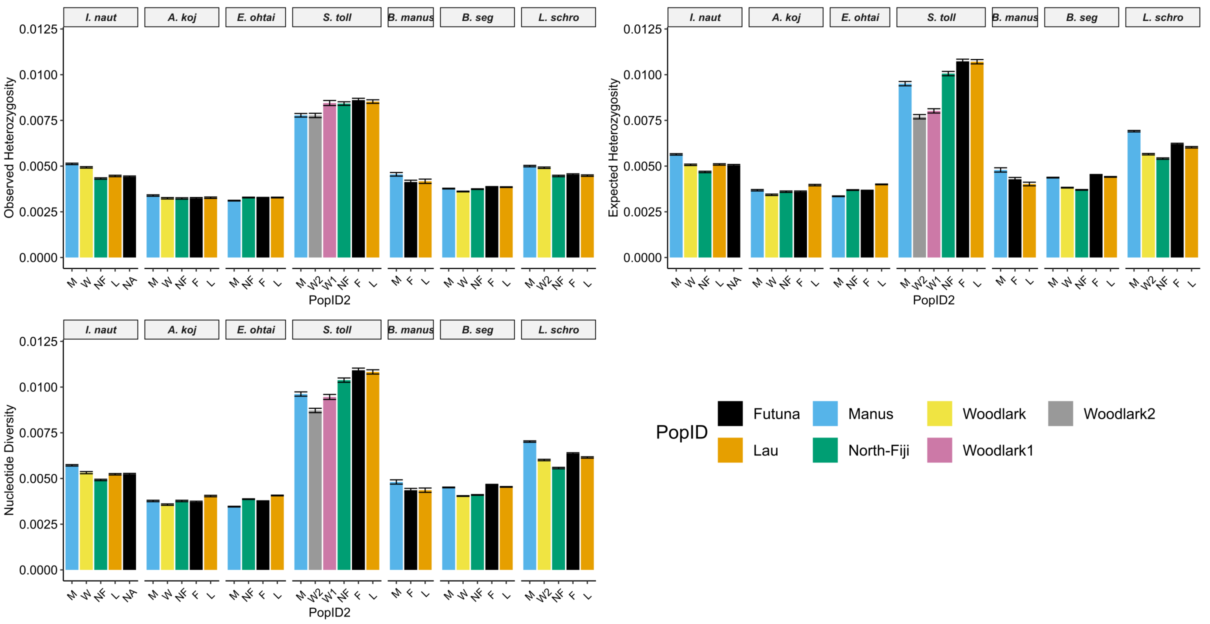


Figure 9: Observed (Ho) and expected (He) heterozygosities and nucleotide diversity (π) calculated with Stacks2 on the final dataset including all sites (variant and non variant). Error bars represent the confidence interval (CI) estimated at 95%. Colors

identify each BAB. Ifremeria nautilei data are directly taken from Tran Lu Y et al., 2022. I. nautilei, A. koj: A. kojimai, S. toll: S. tollmanni; B. manus:B. manusensis, B. seg: B. segonzaci, L. schro: L. schrolli & aff schrolli

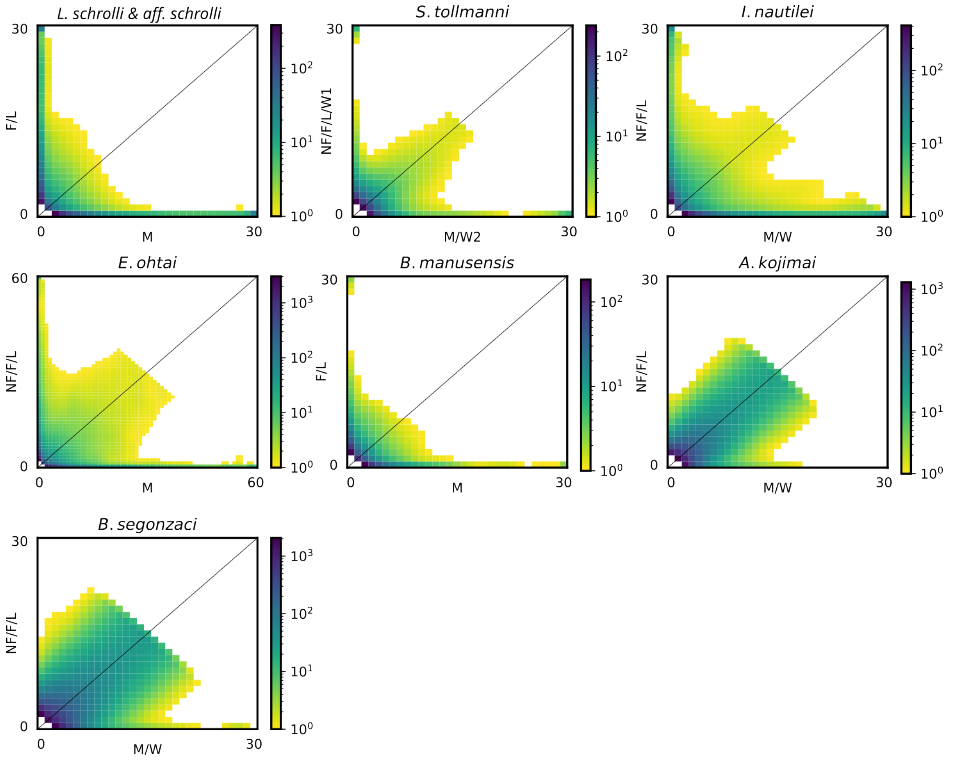


Figure 10:. For each plot Observed Joint allele frequency spectrum (JAFS) between lineages East and West per species. Color gradients display the frequency of each SNPs class between populations. Population abbreviation for NF: North Fiji, F: Futuna, L: Lau, M: Manus, W: Woodlark.

Figure 11 : Heatmap of AIC values on the best runs for all models and parameters per species. The lowest value represents the best model fit. Ifremeria nautilei data from Tran Lu Y et al. (2022).

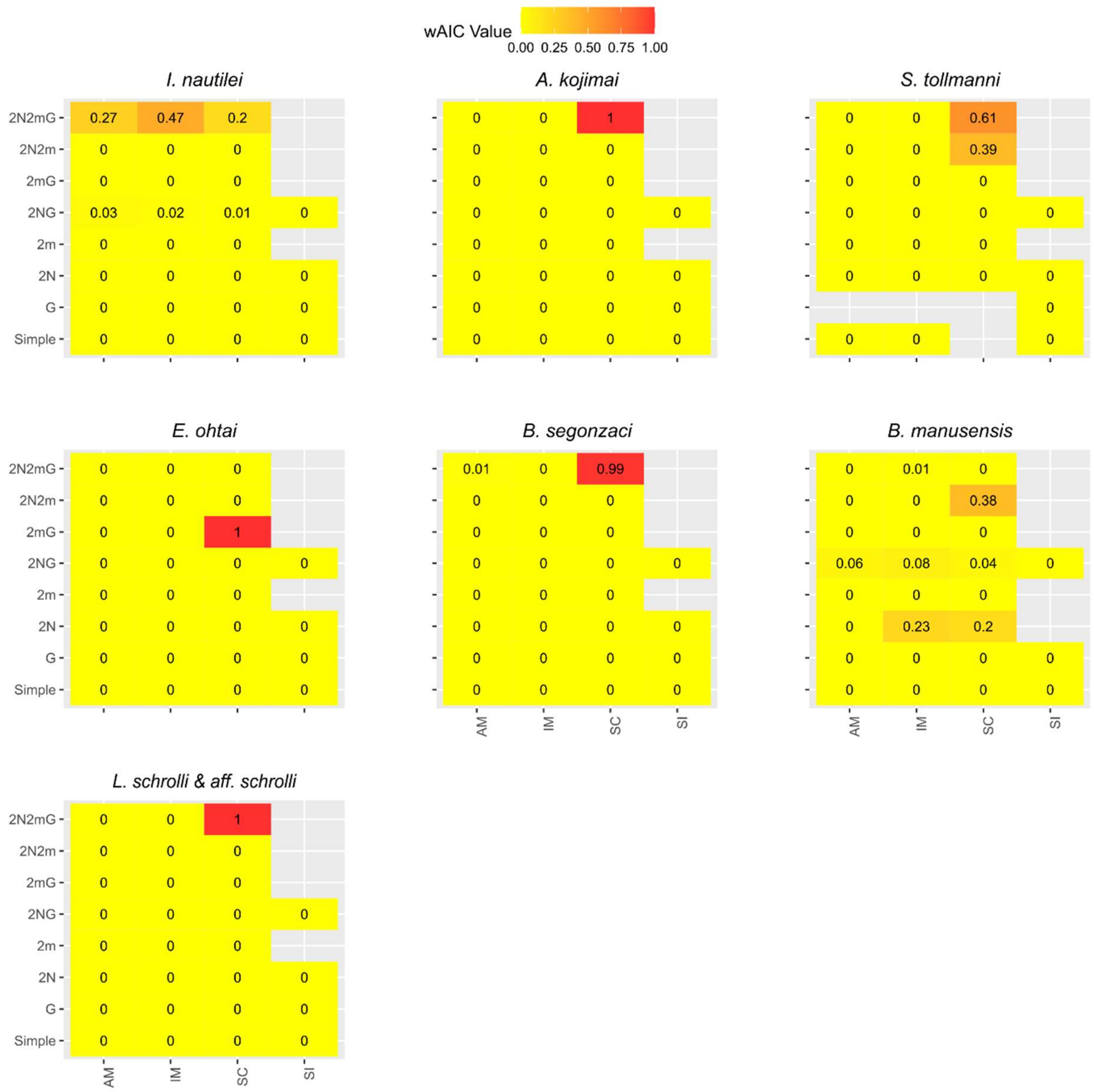
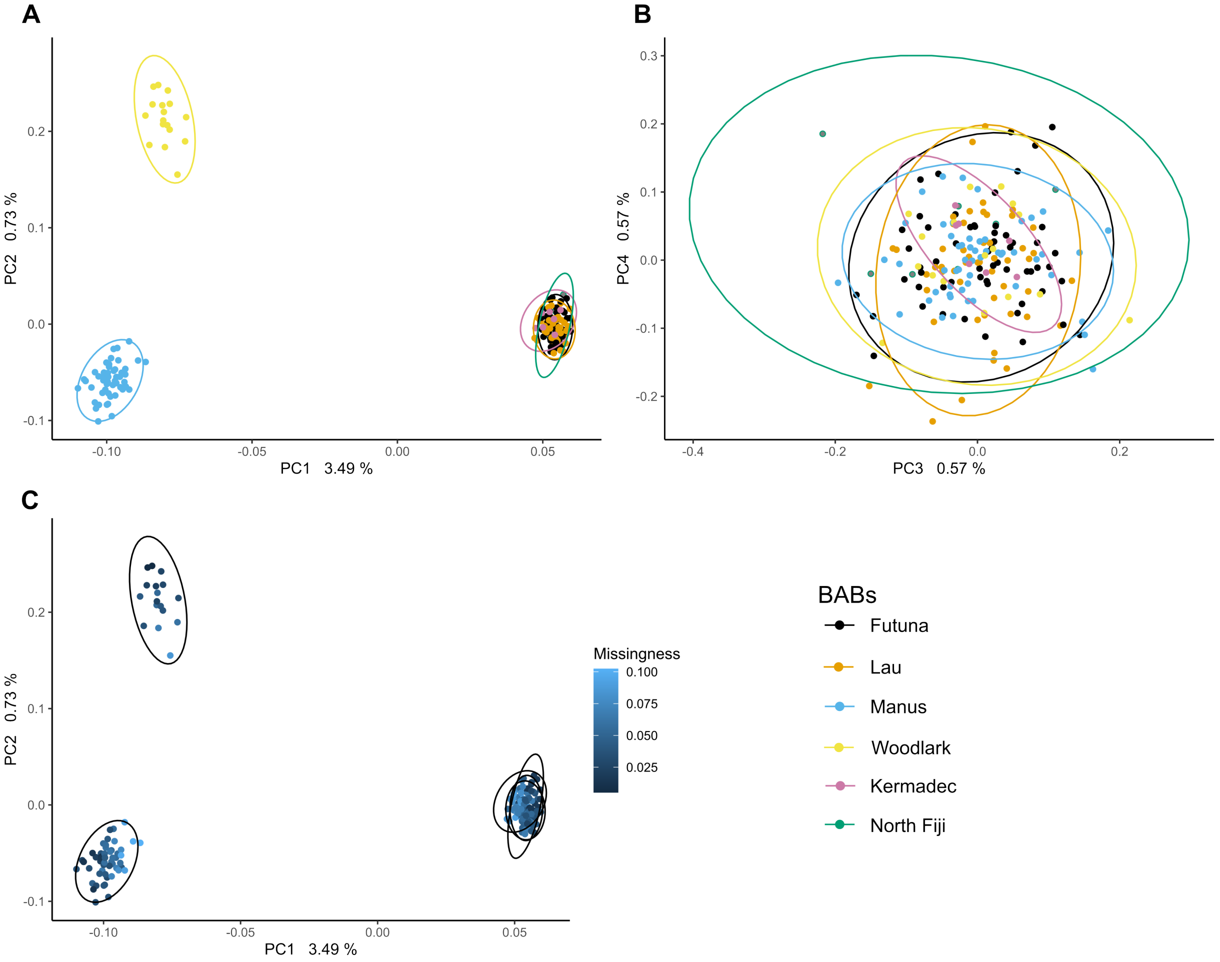
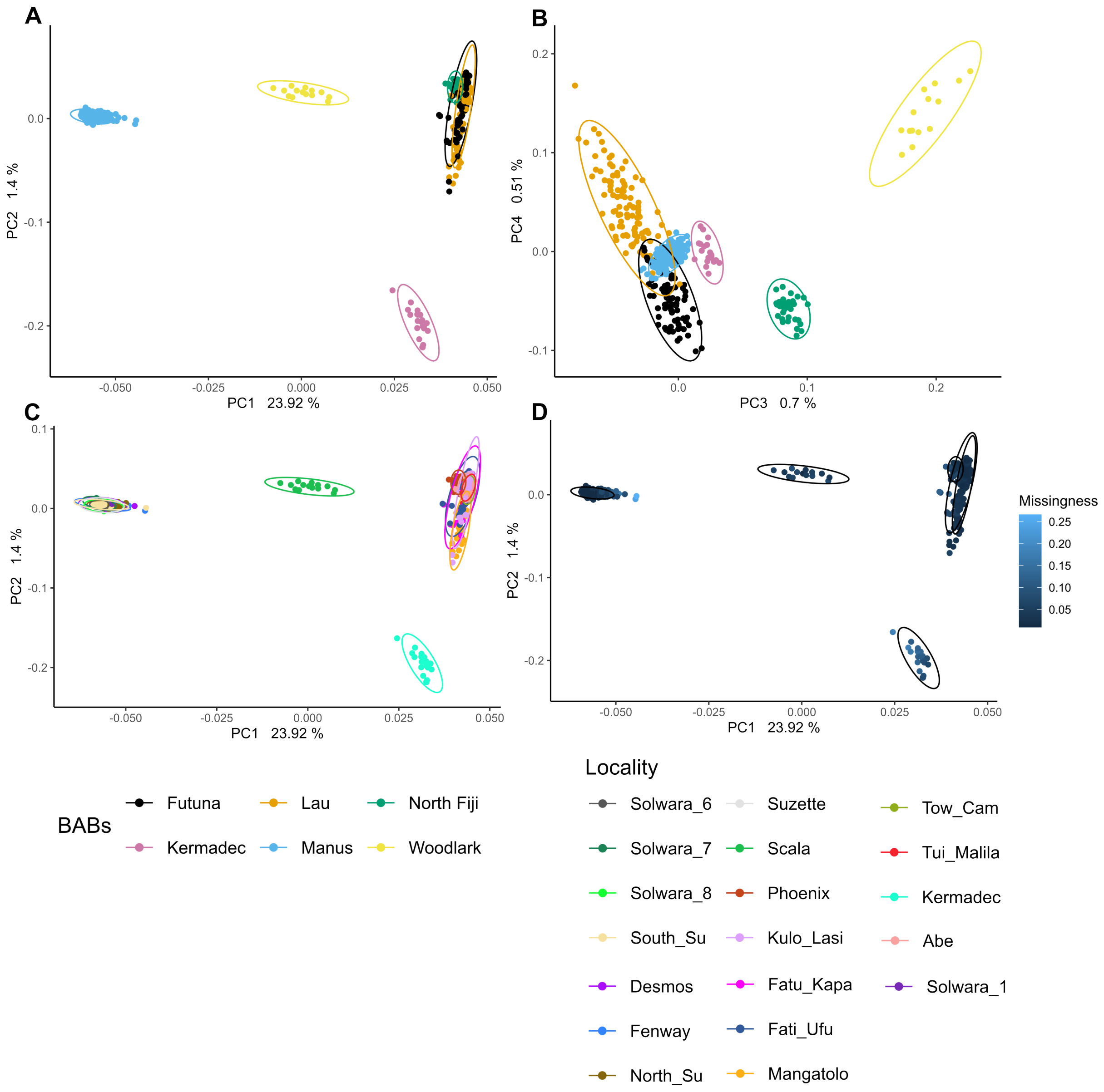


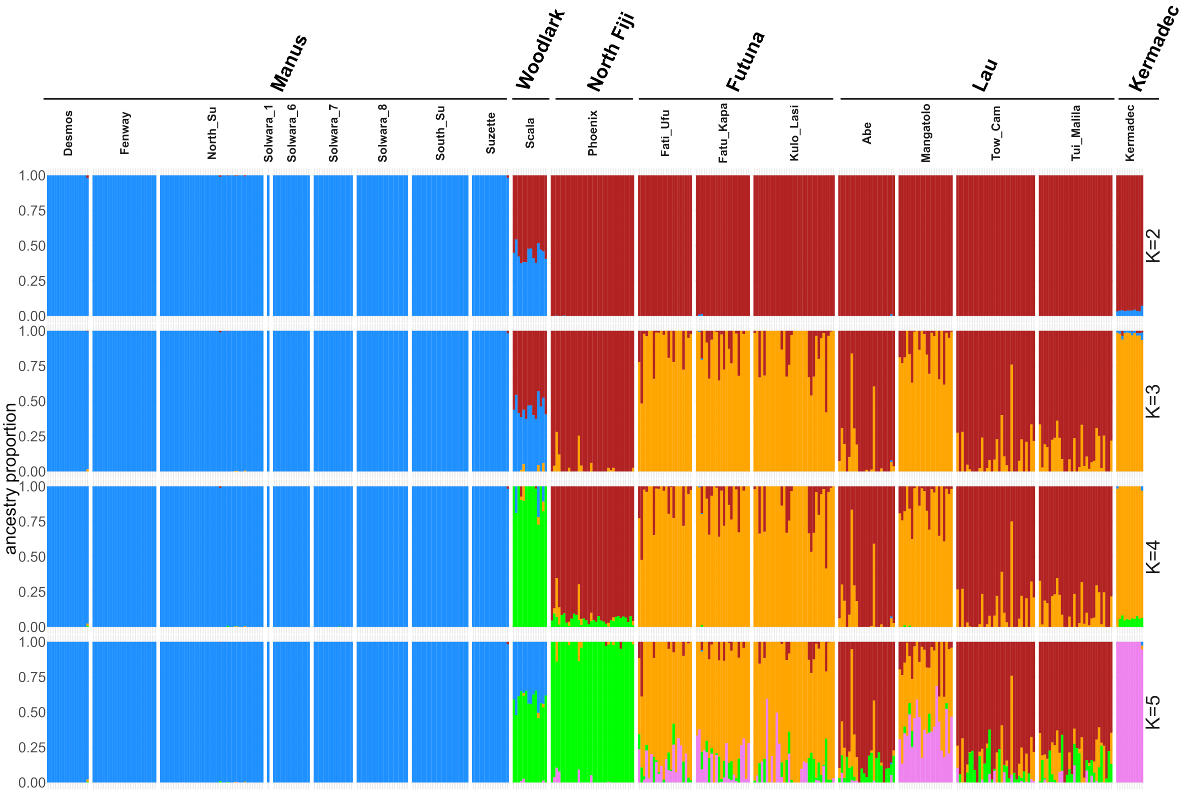
Figure 12 : Weighted AIC value on the best runs for all models and parameters per species. Highest value represents the best model fit (the lowest AIC value). Ifremeria nautilei data are derived from Tran Lu Y et al. (2022).



Figures 13 : PCA plots for B. segonzaci with Kermadec individuals (in black) for first four components and missingness data per individual. In plot A, B colors represents basin and C, the percent of missing data per sample.



Figures 14 : PCA plots for L. schrolli & aff schrolli, with Kermadec individuals (in pink) for first four components and missingness data per individual. In plot A, B colors represents basin. In C colors represents localities and D the percent of missing data per sample.



Figures 15 : Barplot of K=2 to K=5 of Admxiture analysis for L. schrolli &L. aff. schrolli ***Including Kermadec samples.*** *Each color represents a genetic cluster and each bar represents an individual. All individuals are grouped by geographic zone.*

Figure 16: Histogram of pairwise Fst between all localities. Colors represent species. Ak: A. kojimai, Bm: B. manusensis, Bs: B. segonzaci. Eo: E. ohtai, In: I. nautilei, Ls: L. schrolli & L. aff. schrolli. St: S. tollmanni

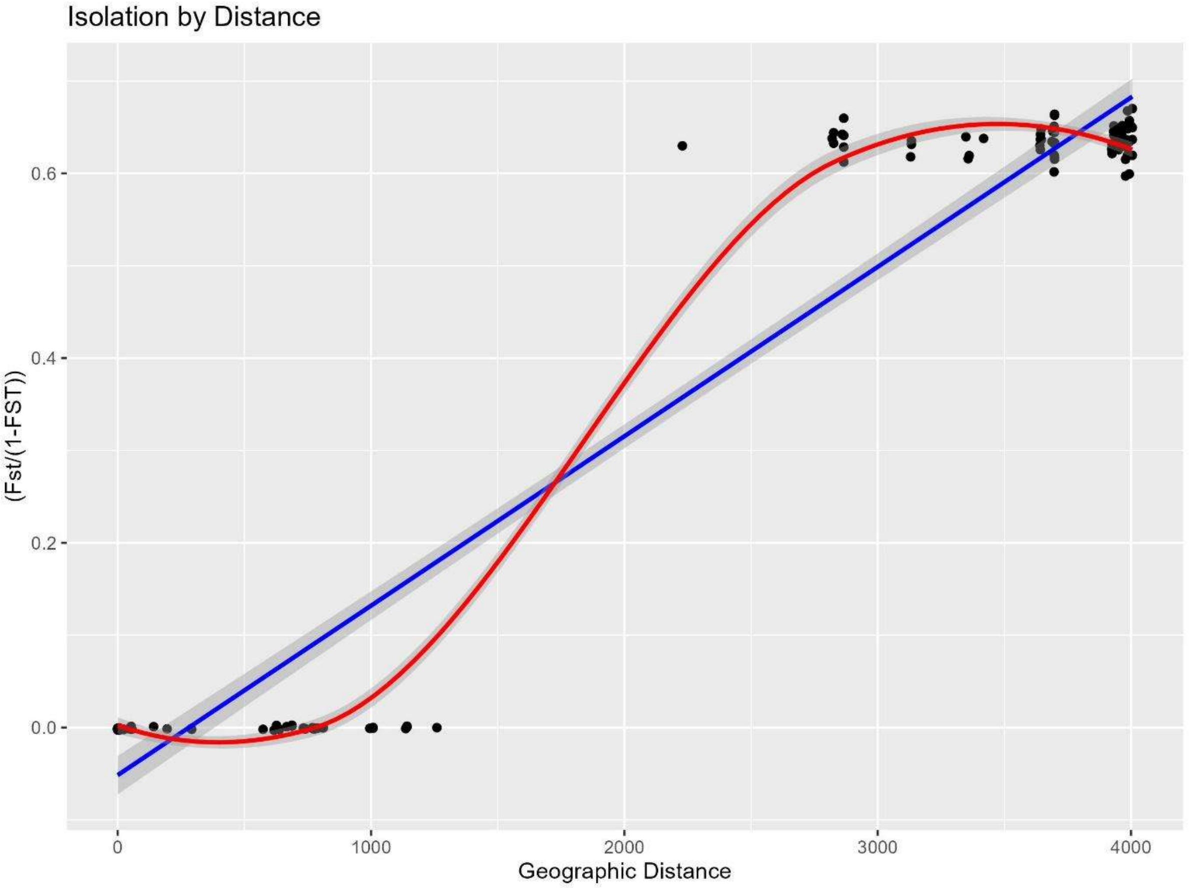


*Figure 17: Relationship between genetic differentiations measured as Linearized Fst and geographic distance in km for **Ifremeria nautilei**. Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and the red line the model of polynomial regression (Loess). Grey band represents standart deviations (se) of the model at 95%.*

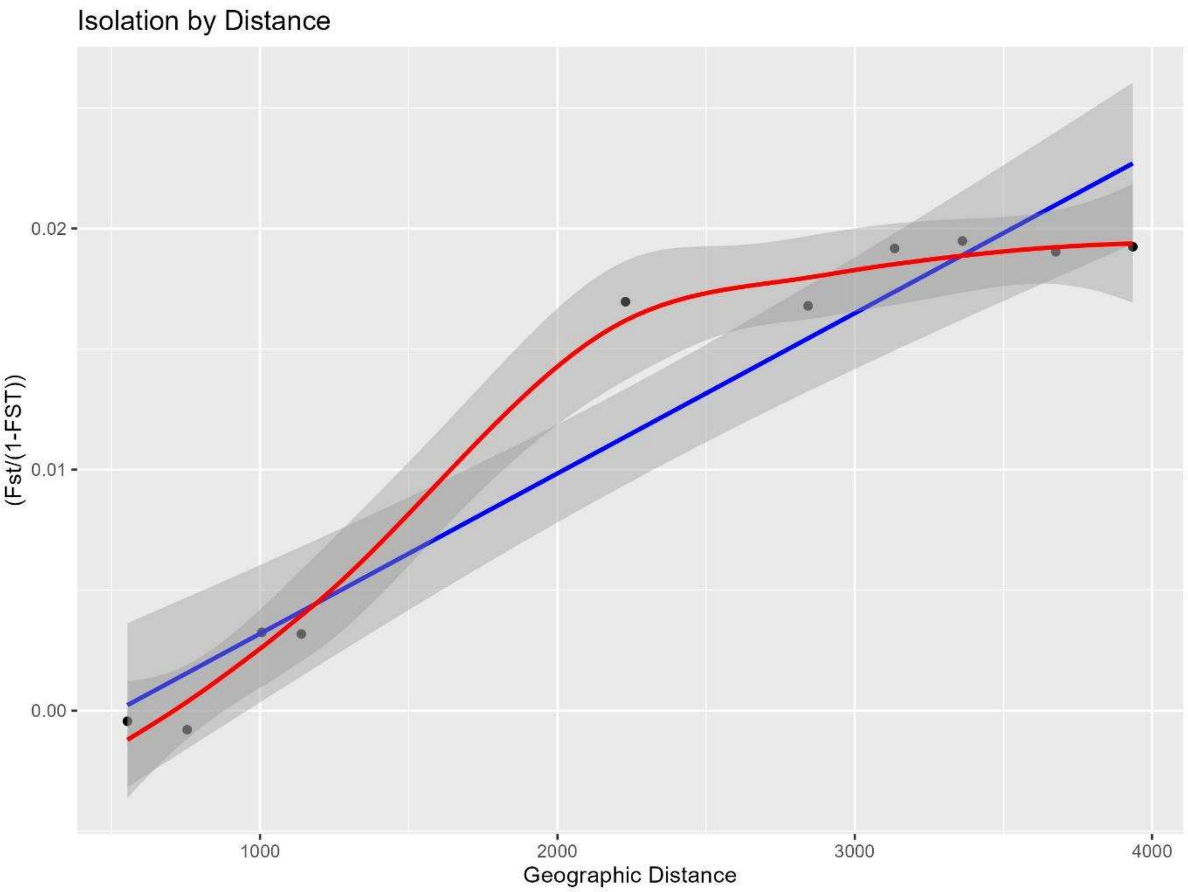


Figure 18: Relationship between genetic differentiations measured Linearized Fst and geographic distance in Km for ***Alviniconcha kojimai****. Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and the red line the model of polynomial regression (Loess). Grey band represents of standart deviations (se) of the model at 95%.*

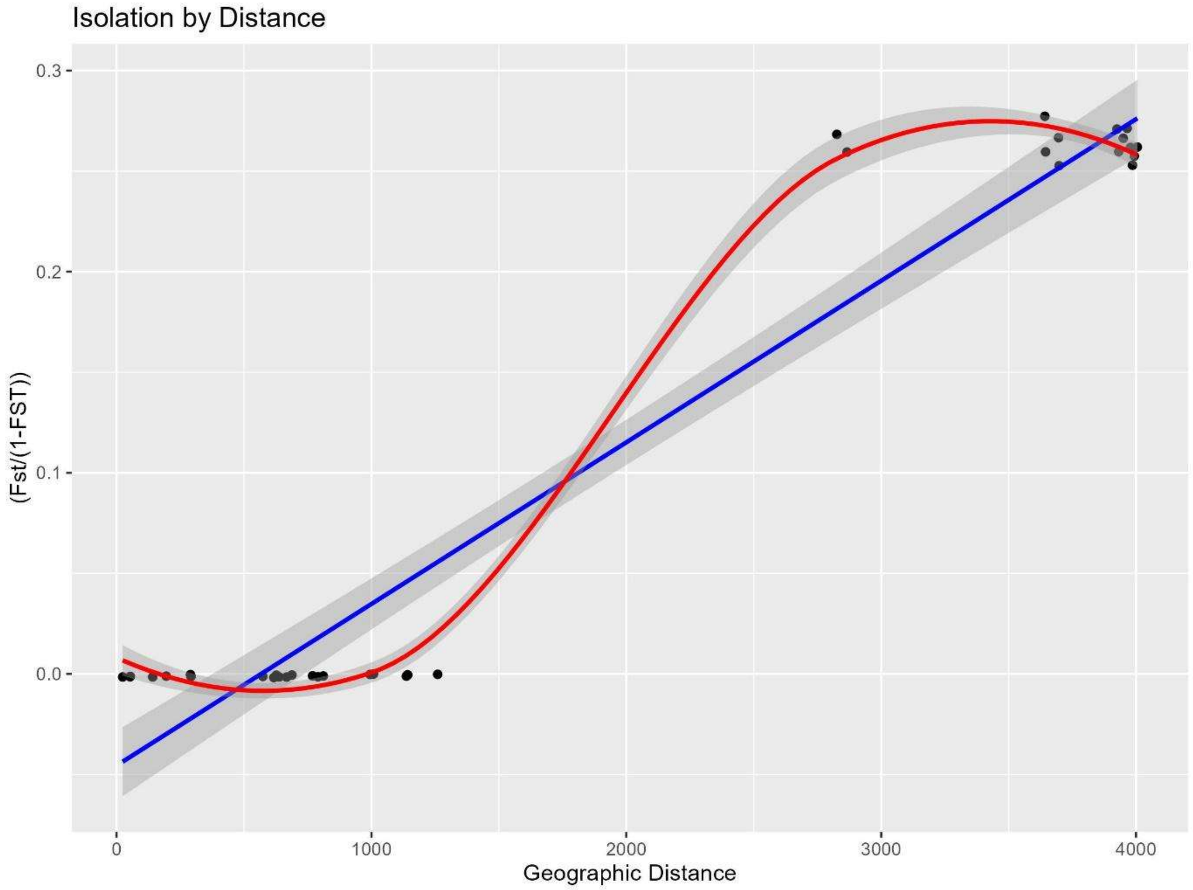


Figure 19: Relationship between genetic differentiations measured as Linearized Fst and geographic distance in km for ***Eochionelasmus ohtai****. Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and the red line the model of polynomial regression (Loess). Grey band represents of standart deviations (se) of the model at 95%.*

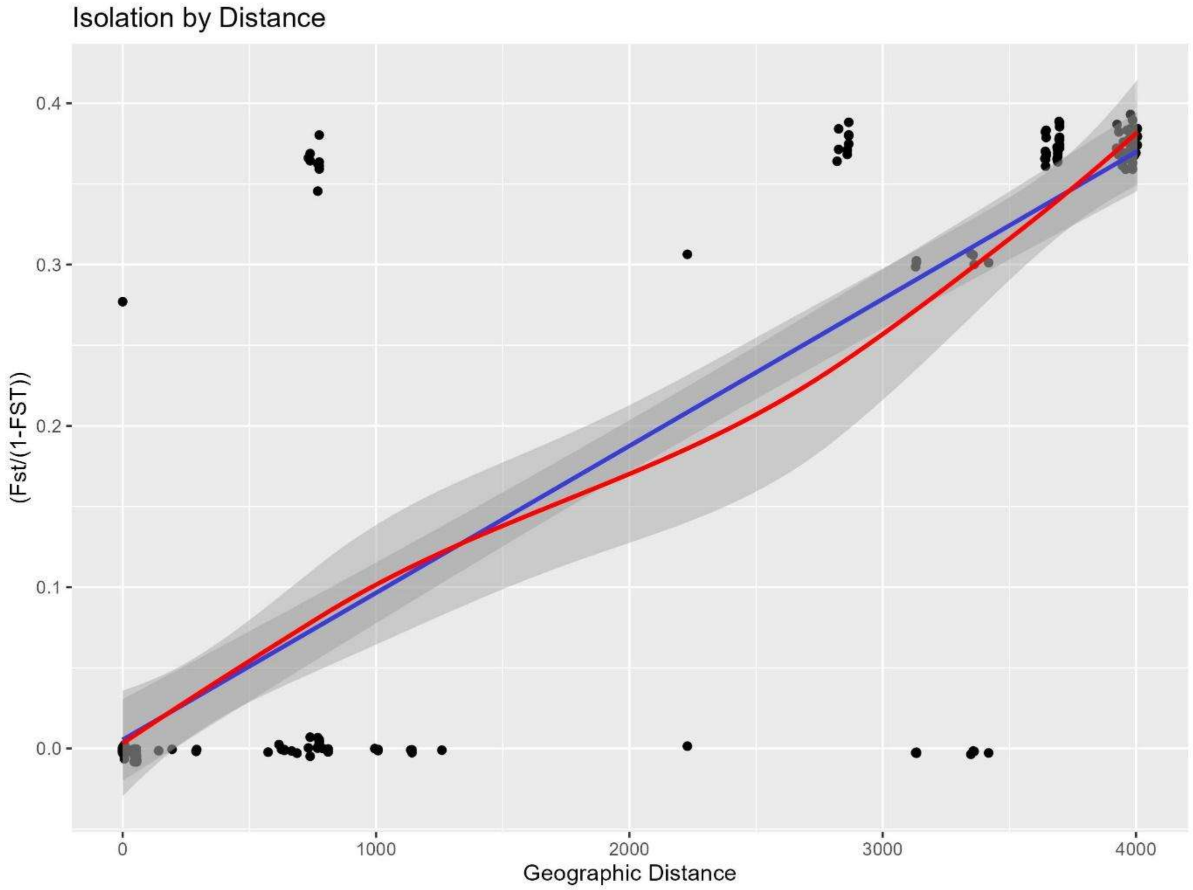


Figure 20: Relationship between genetic differentiations measured as Linearized Fst and geographic distance in km for ***S. tollmanni****. Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and the red line the model of polynomial regression (Loess). Grey band represents of standart deviations (se) of the model at 95%.*

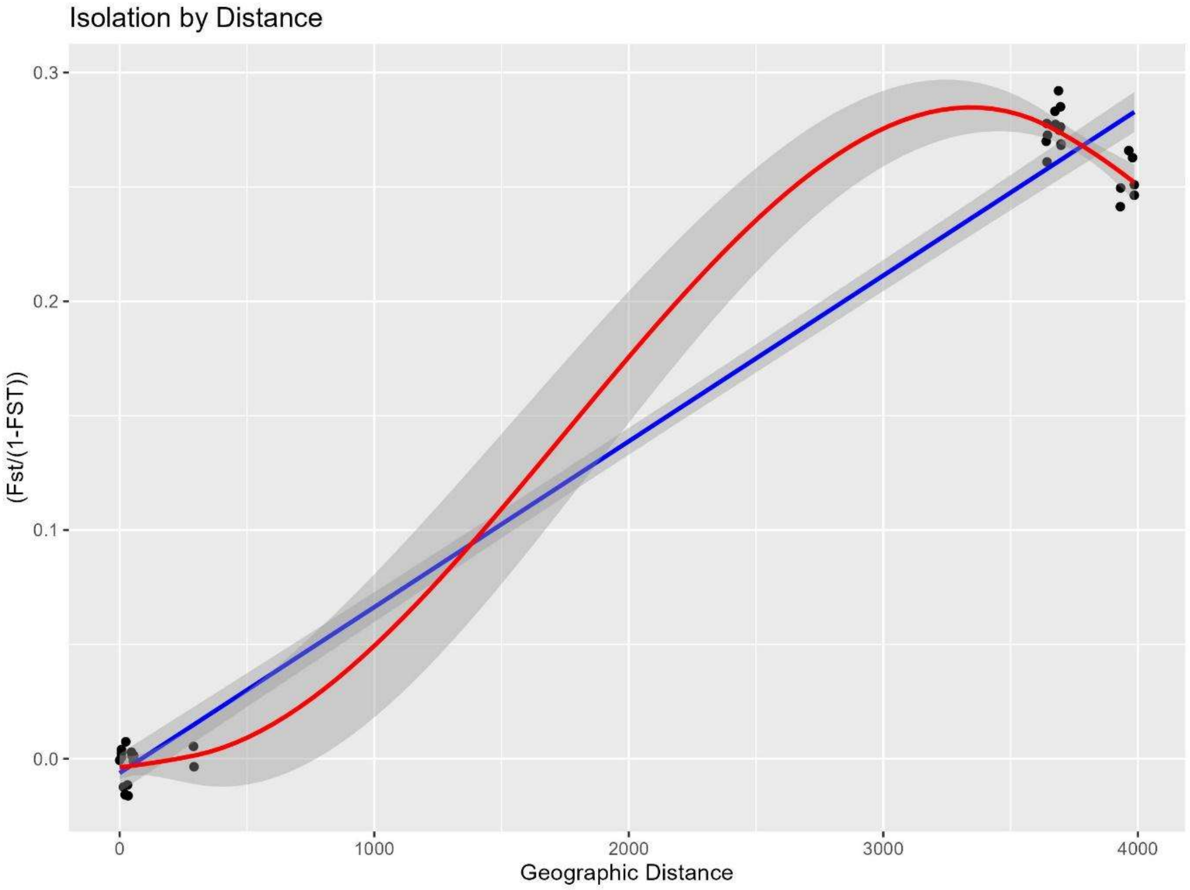


Figure 21: Relationship between genetic differentiations measured as Linearized Fst and geographic distance in km for ***Bathymodiolus manusensis****. Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and the red line the model of polynomial regression (Loess). Grey band represents of standart deviations (se) of the model at 95%.*

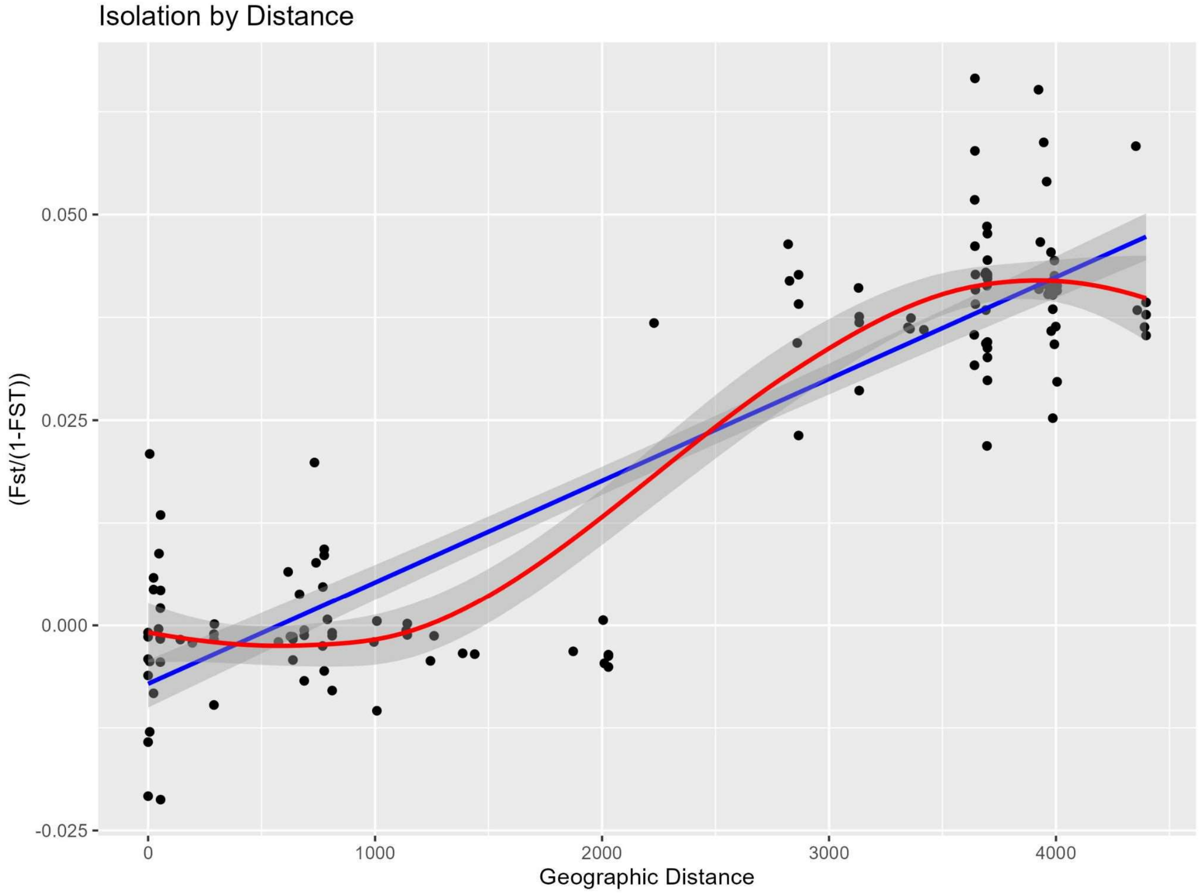


*Figure 22: Relationship between genetic differentiations measured as Linearized Fst and geographic distance in km for **Branchinotogluma segonzaci**. Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and the red line the model of polynomial regression (Loess). Grey band represents of standart deviations (se) of the model at 95%.*

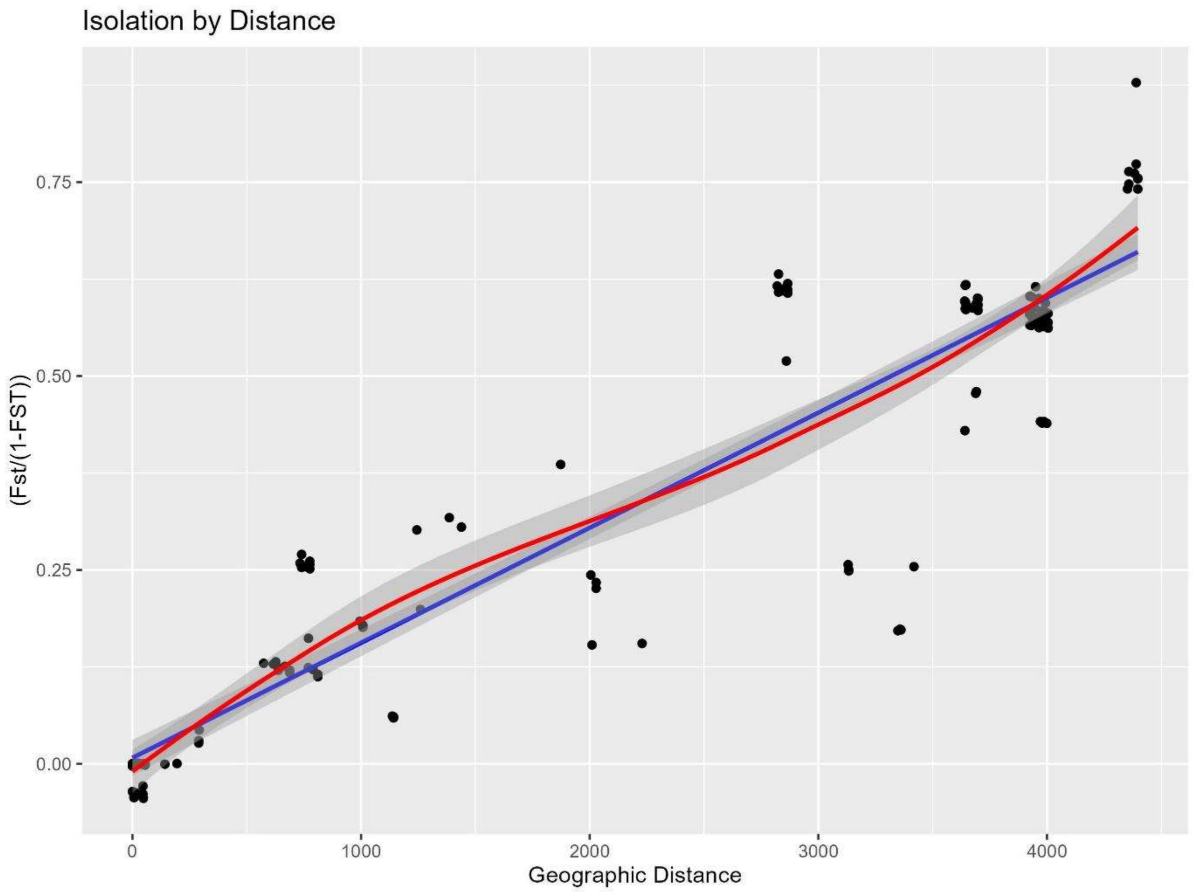
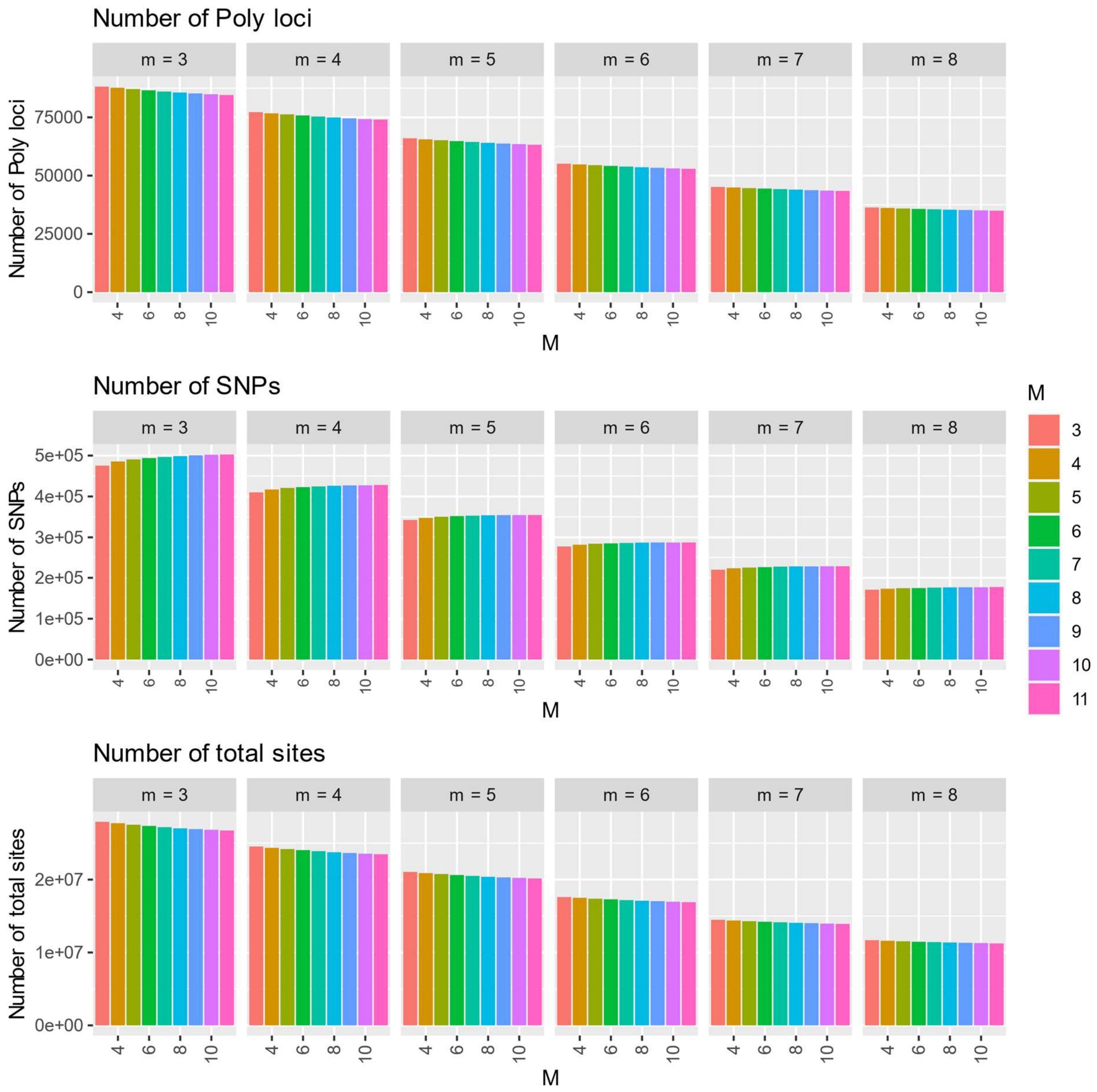


Figure 23: Relationship between genetic differentiations measured as Linearized Fst and geographic distance in km for ***L. schrolli & L. aff. schrolli.*** *Each point represents a pairwise comparison between localities. Blue line is the model of linear regression (Lm) and red line the model of polynomial regression (Loess). Grey band represents of standart deviations (se) of the model at 95%.*

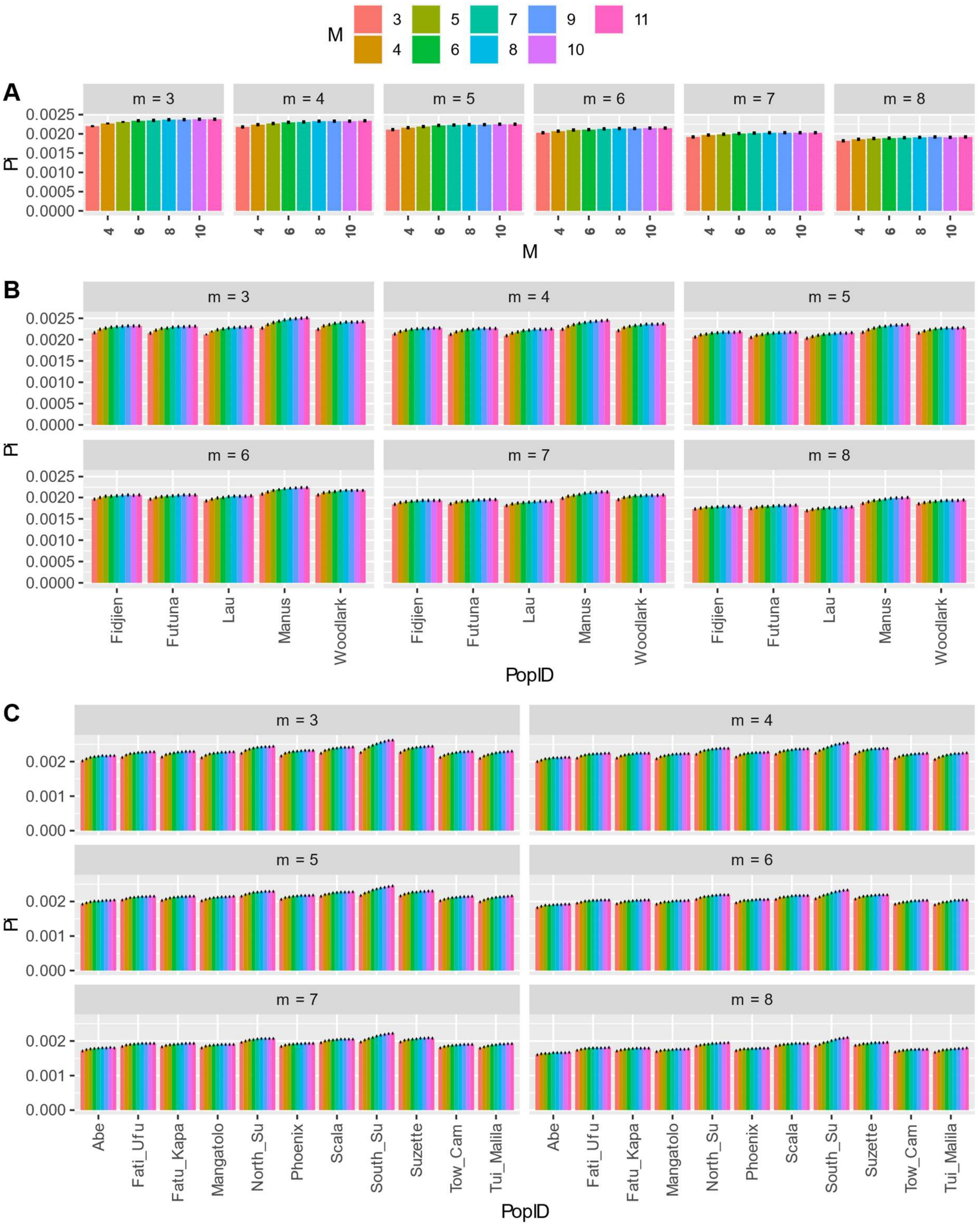
Calibration of «*De novo*» Assembly

De novo assembly of raw reads was performed independently for each species using Stacks2. For each species, we apply the same calibration protocol as described in Tran Lu Y et al. (2022), where the assembly and calibration parameter protocol are described in the supplementary information. Briefly, this protocol used the guidelines proposed by Paris et al. (2017) and Mastretta Yanes et al. (2015). These guidelines evaluate various statistics such as the number of assembled loci, the number of polymorphic loci, the number of SNPs, the total number of assembled sites, and the nucleotide diversity to monitor assembly. In addition, genotyping error was investigated using DNA sequencing replicates (the same DNA sample sequenced twice or more, independently). To perform this last step, genotyping error was calculated by measuring the genotyping differences between replicates of the same individual.

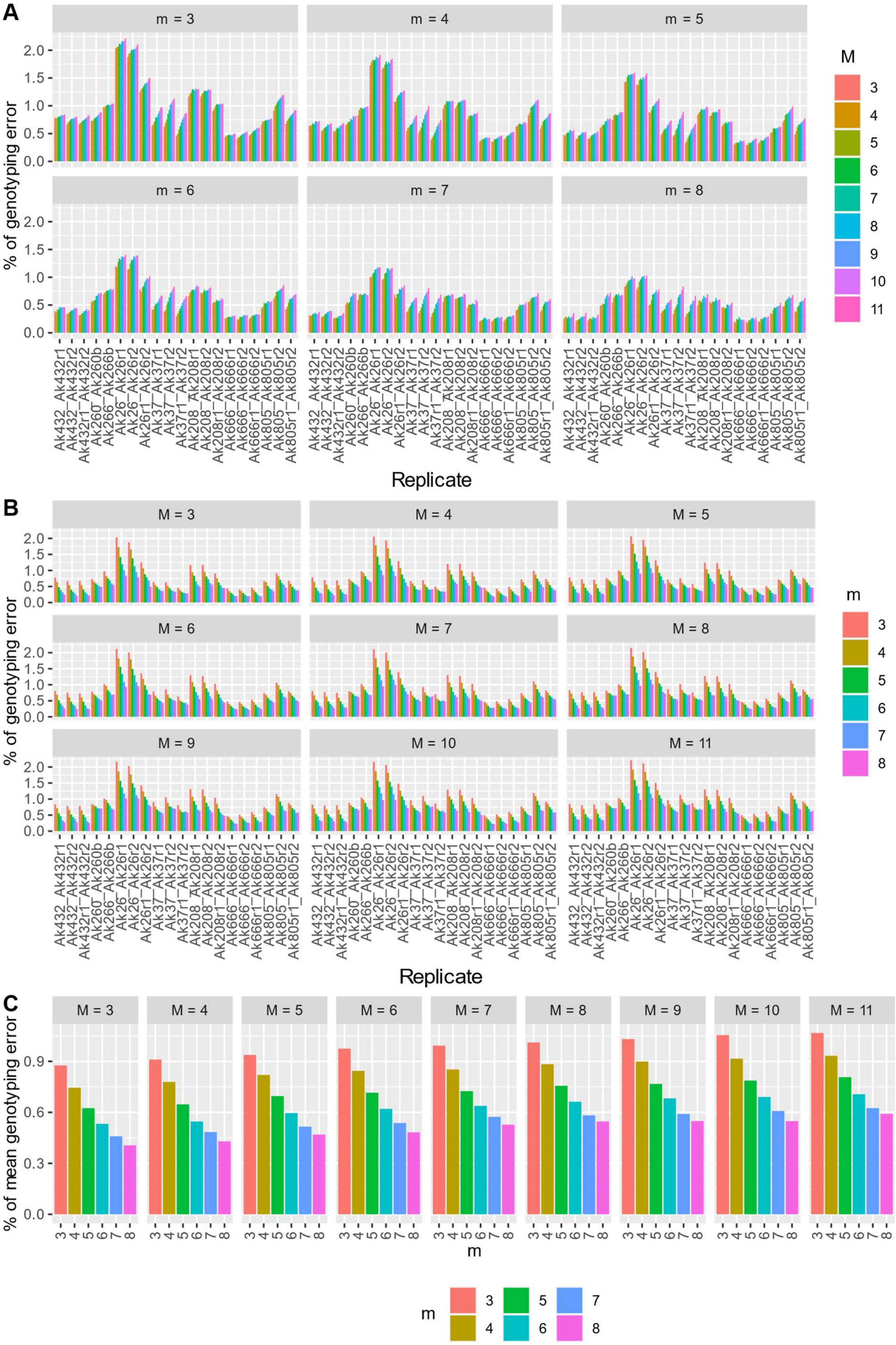
Alviniconcha kojimai



Figures 1 calibration : Calibration statistics for m (each small box represents a value of m) and M (n=M), representing the number of Polymorphic loci (radtag), number of variants (SNPs) and the total number of sites assembled (variant and non-variant). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

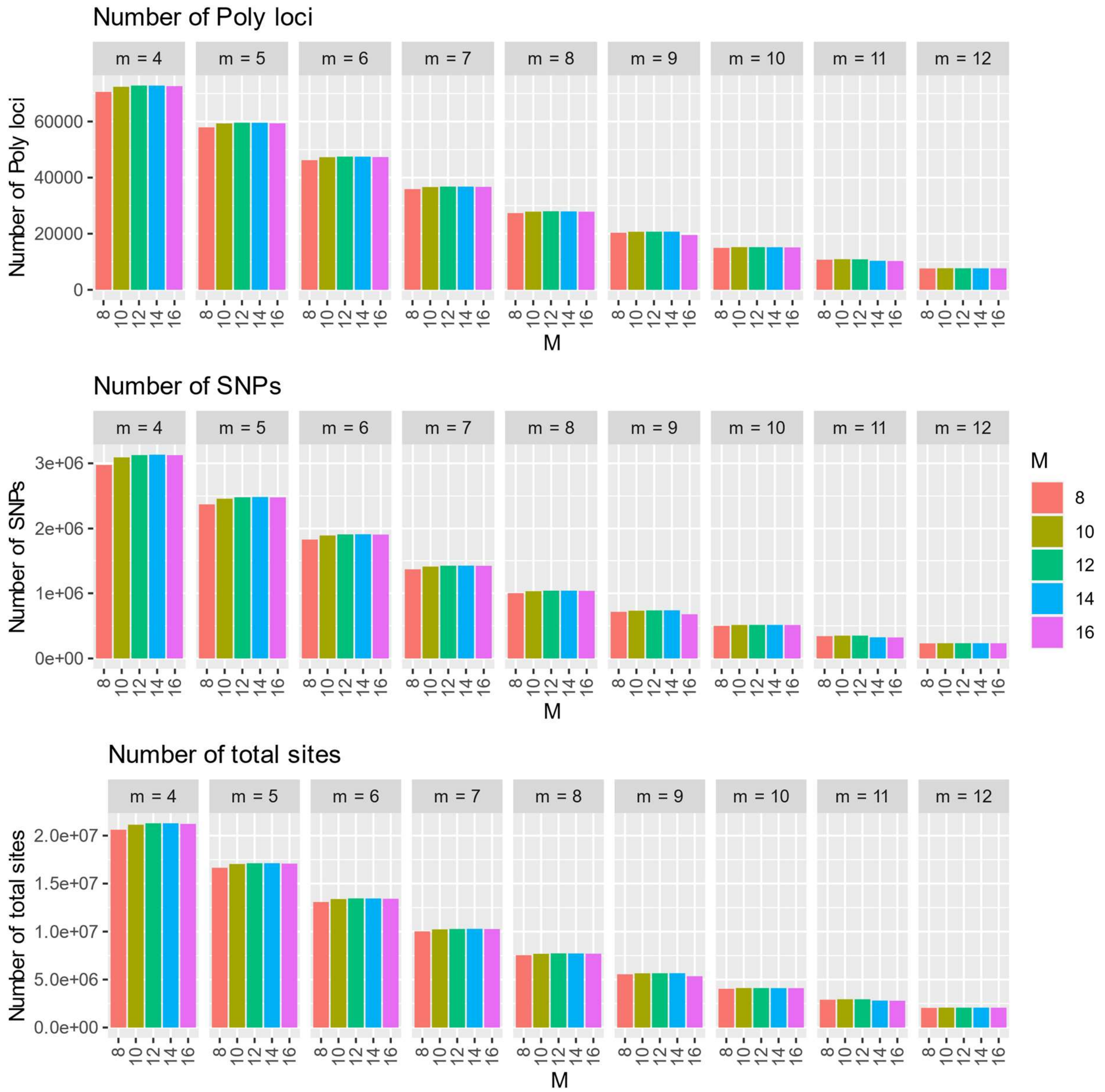

M
3
4
5
6
7
8
9
10
11
A
m = 3
m = 4
m = 5
m = 6
m = 7
m = 8
Pi
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
4
6
8
10
M
B
m = 3
m = 4
m = 5
m = 6
m = 7
m = 8
Pi
0.0025
0.0020
0.0015
0.0010
0.0005
0.0000
Fidjien
Futuna
Lau
Manus
Woodlark
PopID
C
m = 3
m = 4
m = 5
m = 6
m = 7
m = 8
Pi
0.002
0.001
0.000
Abe
Fati_Ufu
Fatu_Kapa
Mangatolo
North_Su
Phoenix
Scala
South_Su
Suzette
Tow_Cam
Tui_Malila
PopID

Figures 2 calibration : Nucleotide diversity (pi) for m (each small box represents a value of m) and M (n=M), estimated with Stacks V2.52 and considering all samples as one population (A), per back-arc-basin (B) and per locality (C). Estimation was performed without replicate. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

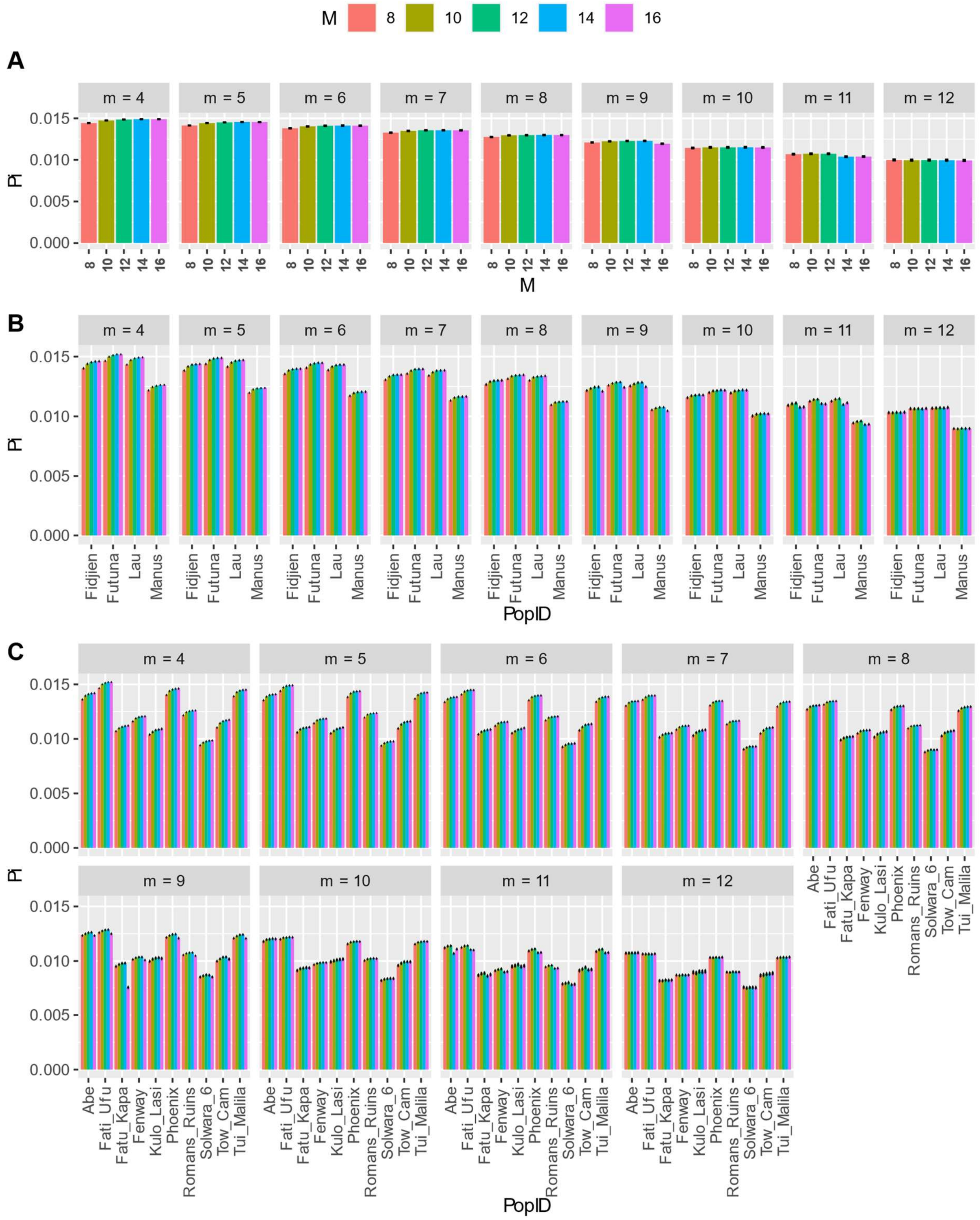

A
m = 3
m = 4
m = 5
m = 6
m = 7
m = 8
% of genotyping error
0.0
0.5
1.0
1.5
2.0
Replicate
Ak432_Ak432r1
Ak432_Ak432r2
Ak432r1_Ak432r2
Ak260_Ak260b
Ak266_Ak266b
Ak26_Ak26r1
Ak26_Ak26r2
Ak26r1_Ak26r2
Ak37_Ak37r1
Ak37_Ak37r2
Ak37r1_Ak37r2
Ak208_Ak208r1
Ak208_Ak208r2
Ak208r1_Ak208r2
Ak666_Ak666r1
Ak666_Ak666r2
Ak666r1_Ak666r2
Ak805_Ak805r1
Ak805_Ak805r2
Ak805r1_Ak805r2
M
3
4
5
6
7
8
9
10
11
B
M = 3
M = 4
M = 5
M = 6
M = 7
M = 8
M = 9
M = 10
M = 11
% of genotyping error
Replicate
m
3
4
5
6
7
8
C
% of mean genotyping error
0.0
0.3
0.6
0.9
m
3 4 5 6 7 8

Figures 3 calibration : Percent of genotyping error between pairs of replicates for each parameter m and M (n=M). (A) plot of M in function of m. (B) m in function of M. (C) mean genotyping error over all pairs of replicate for each value of M and m. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

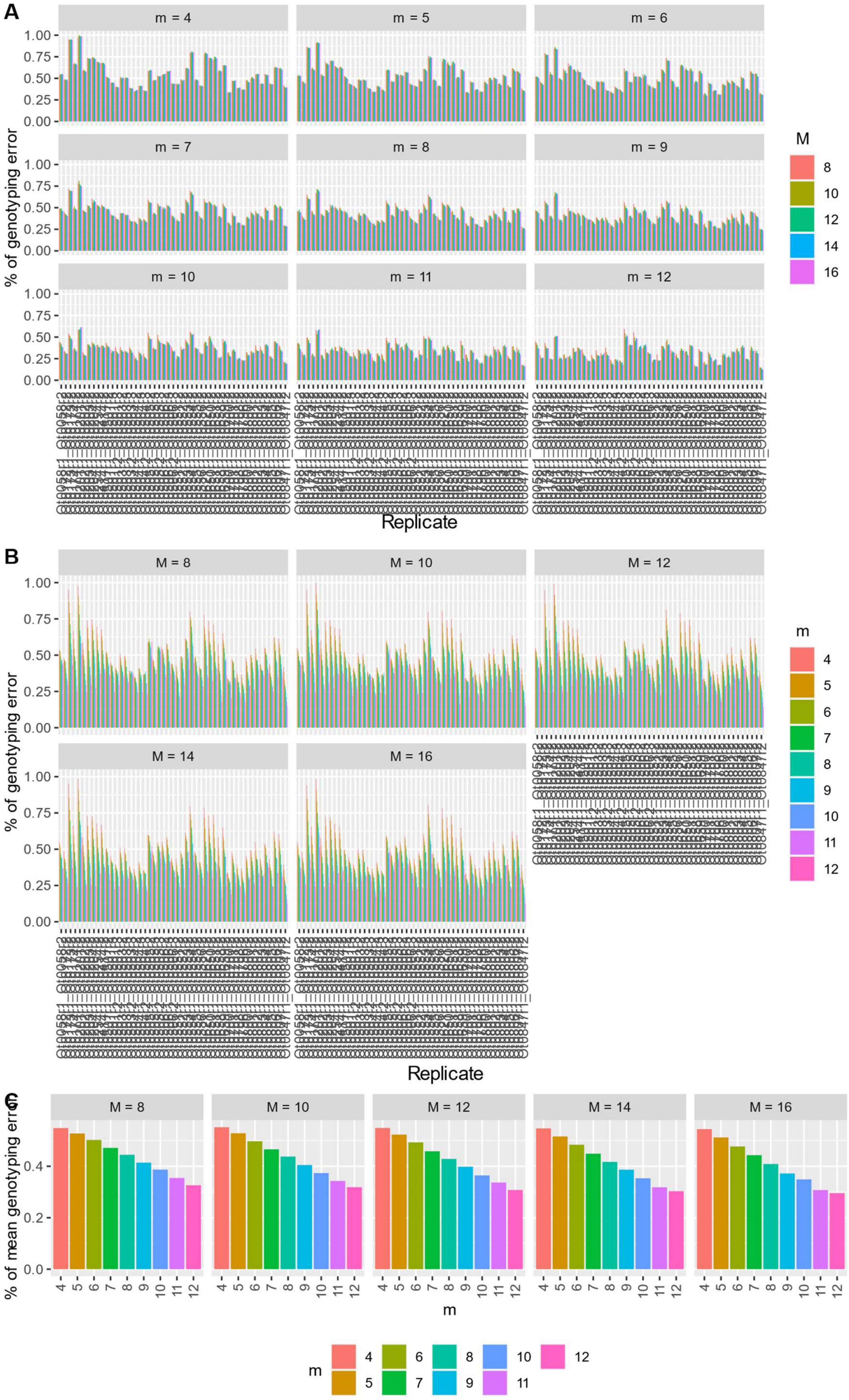
Shinkailepas tollmanni



Figures 4 calibration : Calibration statistics for m (each small box represents a value of m) and M (n=M), representing the number of Polymorphic loci (radtag), number of variants (SNPs) and the total number of sites assembled (variant and non-variant). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

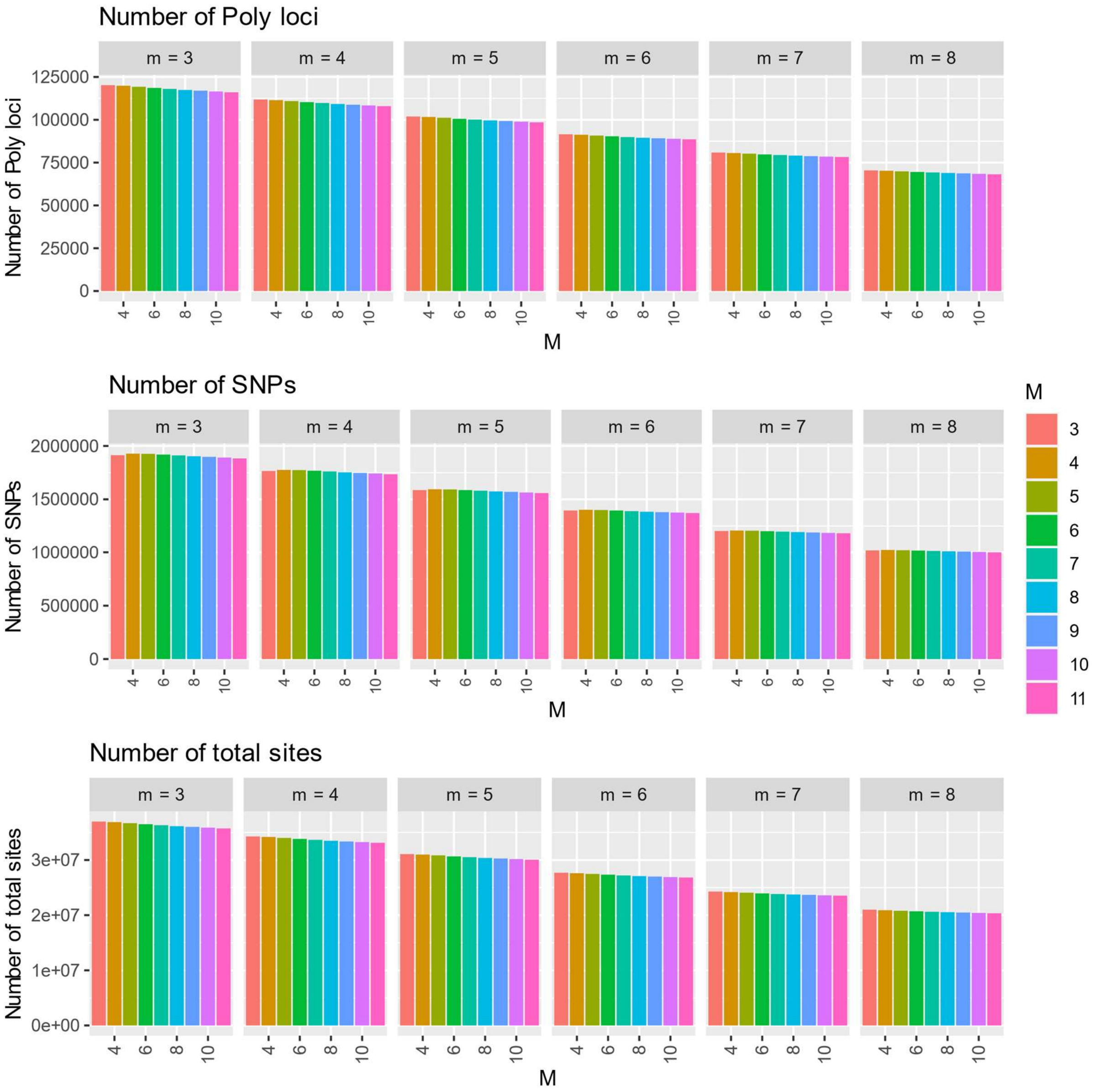


Figures 5 calibration : Nucleotide diversity (pi) for m (each small box represents a value of m) and M (n=M), estimated with Stacks V2.52 and considering all samples as one population (A), per back-arc-basin (B) and per locality (C). Estimation was performed without replicate. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

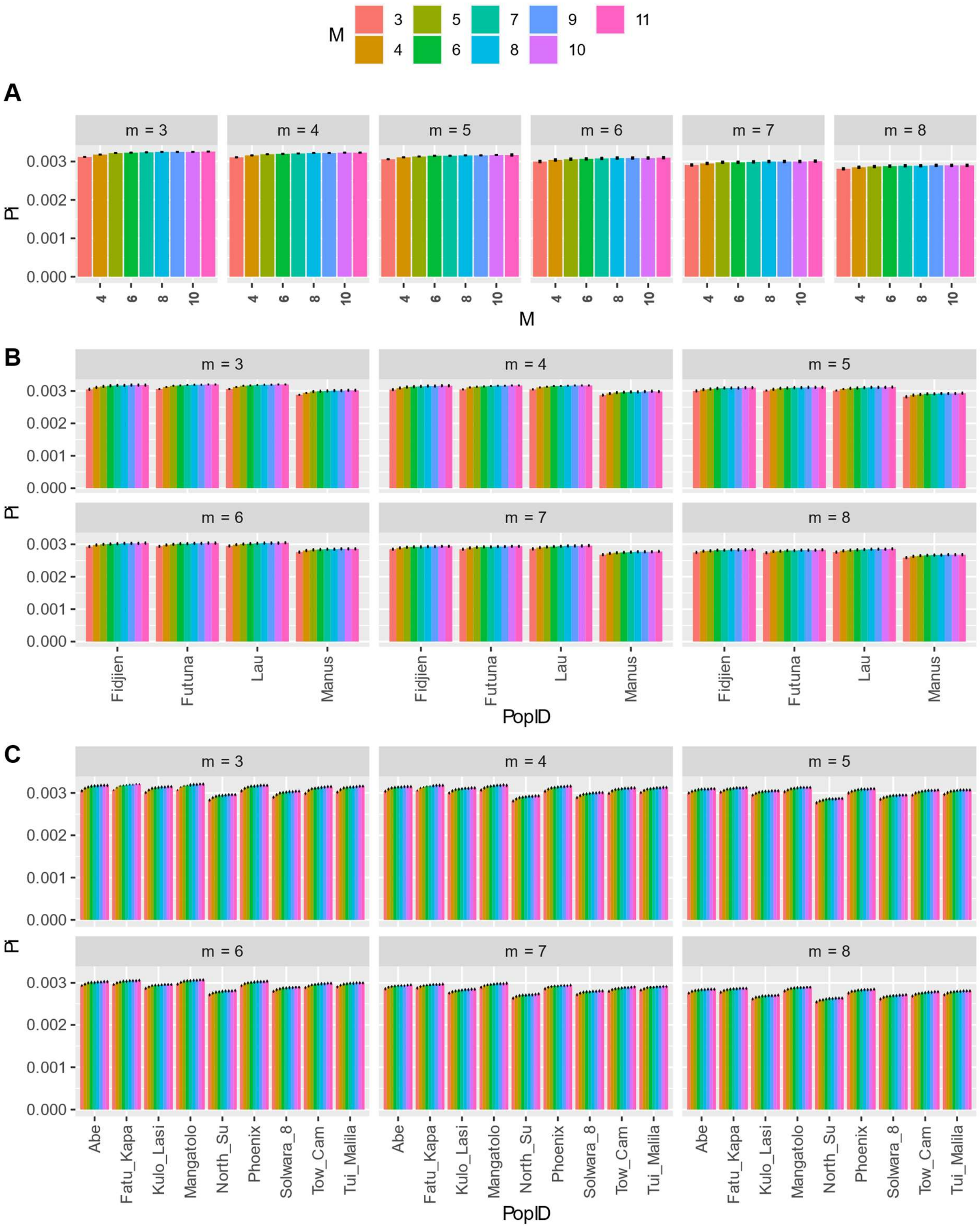

A
m = 4
m = 5
m = 6
m = 7
m = 8
m = 9
m = 10
m = 11
m = 12
1.00
0.75
0.50
0.25
0.00
% of genotyping error
Replicate
M
8
10
12
14
16
B
M = 8
M = 10
M = 12
M = 14
M = 16
% of genotyping error
Replicate
m
4
5
6
7
8
9
10
11
12
C
M = 8
M = 10
M = 12
M = 14
M = 16
% of mean genotyping error
0.0
0.2
0.4
4
5
6
7
8
9
10
11
12
m

Figures 6 calibration: Percent of genotyping error between pairs of replicates for each parameter m and M (n=M). (A) plot of M in function of m. (B) m in function of M. (C) mean genotyping error over all pairs of replicate for each value of M and m. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

Eochionelasmus ohtai

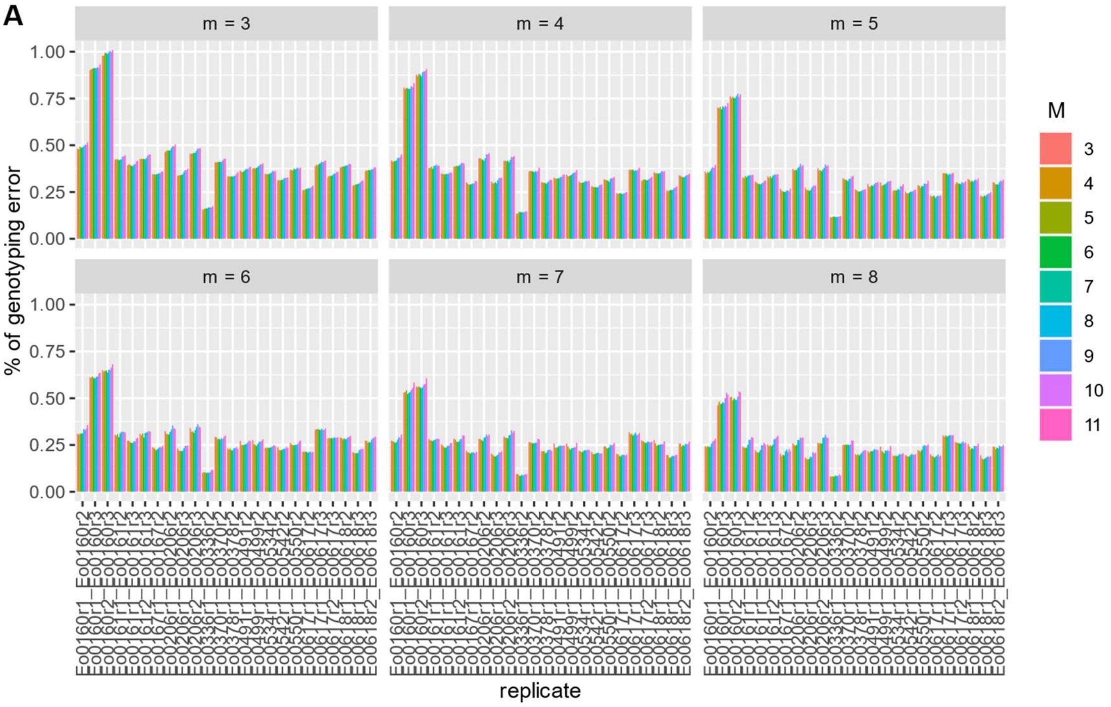


Figures 7 calibration: Calibration statistics for m (each small box represents a value of m) and M (n=M), representing the number of Polymorphic loci (radtag), number of variants (SNPs) and the total number of sites assembled (variant and non-variant). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

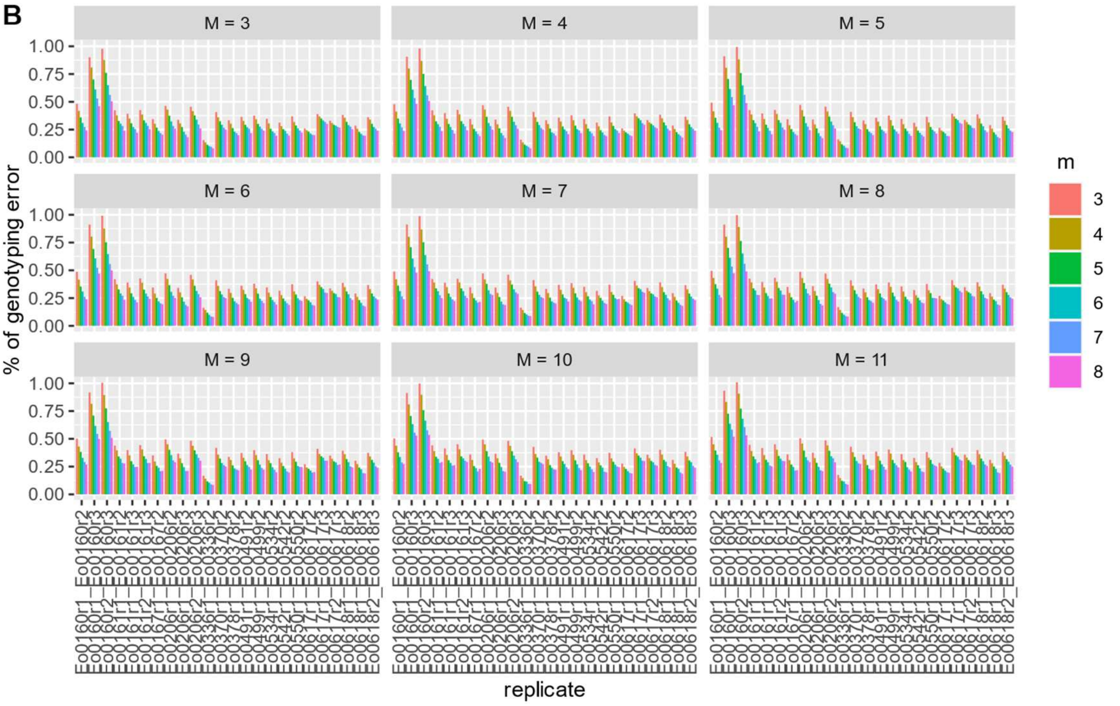


Figures 8 calibration : Nucleotide diversity (pi) for m (each small box represents a value of m) and M (n=M), estimated with Stacks (V2.52) and considering all samples as one population (A), per back-arc-basin (B) and per locality (C). Estimation was performed without replicate. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

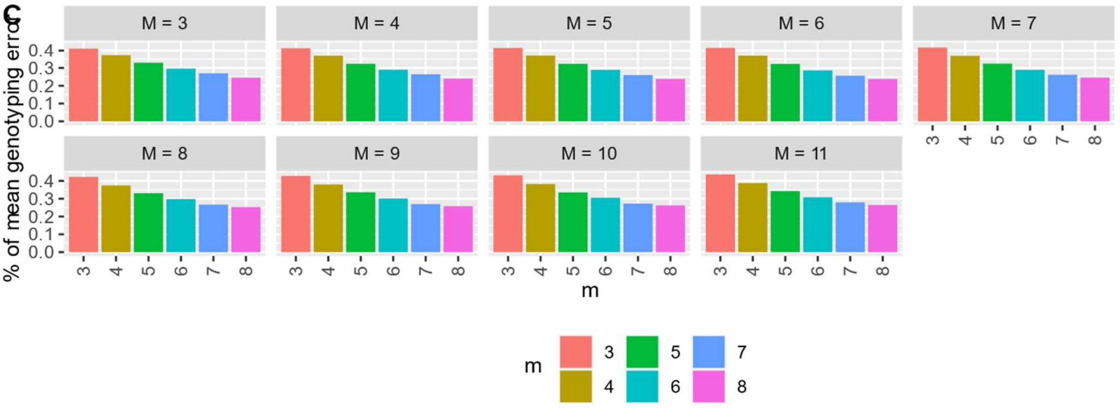
A


m = 3
m = 4
m = 5
m = 6
m = 7
m = 8
% of genotyping error
1.00
0.75
0.50
0.25
0.00
replicate
Eo0160r1_Eo0160r2
Eo0160r1_Eo0160r3
Eo0160r2_Eo0160r3
Eo0161r1_Eo0161r2
Eo0161r1_Eo0161r3
Eo0161r2_Eo0161r3
Eo0167r1_Eo0167r2
Eo0206r1_Eo0206r2
Eo0206r1_Eo0206r3
Eo0206r2_Eo0206r3
Eo0336r1_Eo0336r2
Eo0370r1_Eo0370r2
Eo0378r1_Eo0378r2
Eo0491r1_Eo0491r2
Eo0499r1_Eo0499r2
Eo0534r1_Eo0534r2
Eo0542r1_Eo0542r2
Eo0550r1_Eo0550r2
Eo0617r1_Eo0617r2
Eo0617r1_Eo0617r3
Eo0617r2_Eo0617r3
Eo0618r1_Eo0618r2
Eo0618r1_Eo0618r3
Eo0618r2_Eo0618r3
M
3
4
5
6
7
8
9
10
11

B

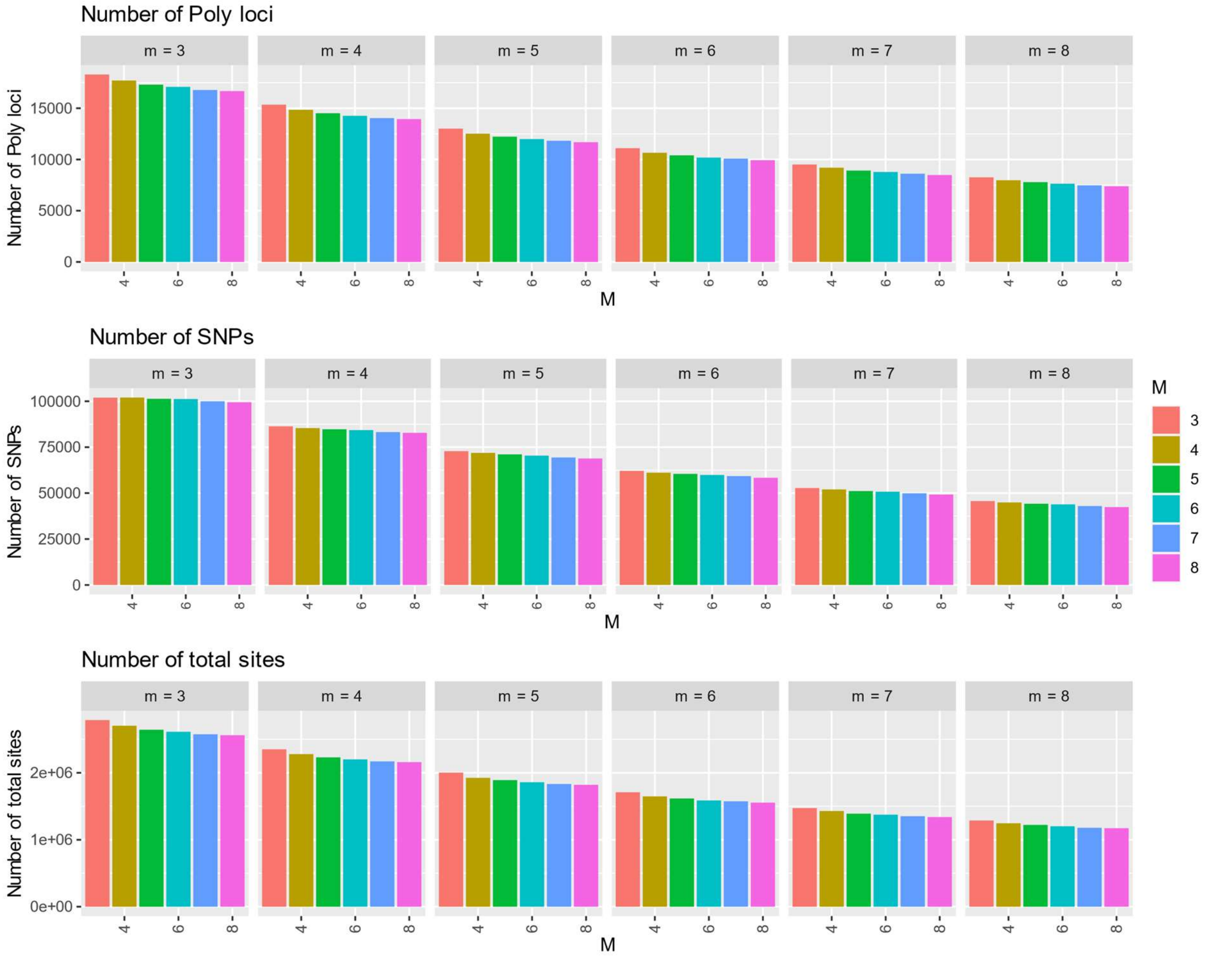

M = 3
M = 4
M = 5
M = 6
M = 7
M = 8
M = 9
M = 10
M = 11
% of genotyping error
1.00
0.75
0.50
0.25
0.00
replicate
Eo0160r1_Eo0160r2
Eo0160r1_Eo0160r3
Eo0160r2_Eo0160r3
Eo0161r1_Eo0161r2
Eo0161r1_Eo0161r3
Eo0161r2_Eo0161r3
Eo0167r1_Eo0167r2
Eo0206r1_Eo0206r2
Eo0206r1_Eo0206r3
Eo0206r2_Eo0206r3
Eo0336r1_Eo0336r2
Eo0370r1_Eo0370r2
Eo0378r1_Eo0378r2
Eo0491r1_Eo0491r2
Eo0499r1_Eo0499r2
Eo0534r1_Eo0534r2
Eo0542r1_Eo0542r2
Eo0550r1_Eo0550r2
Eo0617r1_Eo0617r2
Eo0617r1_Eo0617r3
Eo0617r2_Eo0617r3
Eo0618r1_Eo0618r2
Eo0618r1_Eo0618r3
Eo0618r2_Eo0618r3
m
3
4
5
6
7
8

C

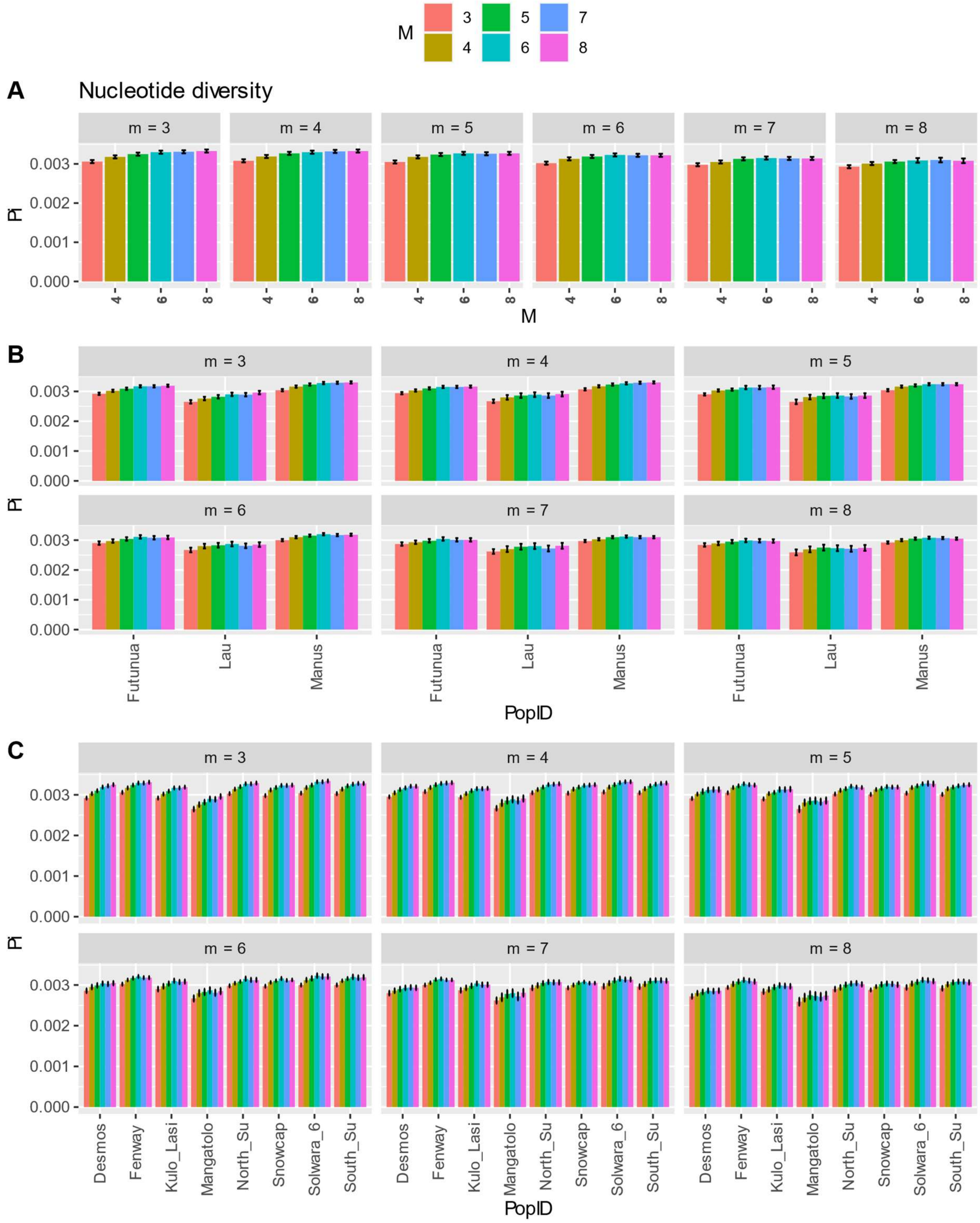

M = 3
M = 4
M = 5
M = 6
M = 7
M = 8
M = 9
M = 10
M = 11
% of mean genotyping error
0.4
0.3
0.2
0.1
0.0
3
4
5
6
7
8
m
m
3
4
5
6
7
8

Figures 9 calibration : Percent of genotyping error between pairs of replicates for each parameter m and M (n=M). (A). Plot of M in function of m. (B) m in function of M. (C) mean genotyping error over all pairs of replicate for each value of M and m. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

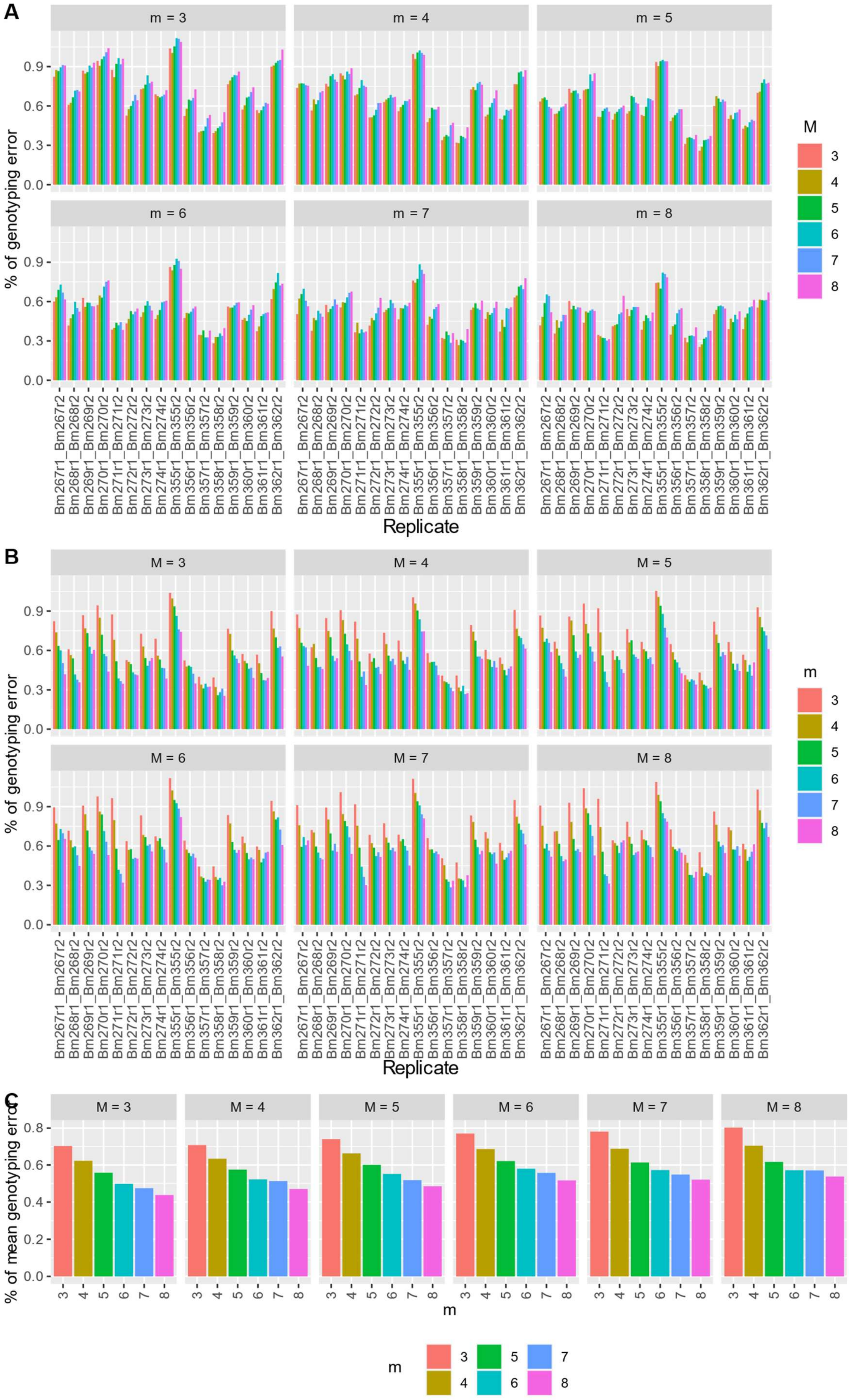
Bathymodiolus manusensis



Figures 10 calibration: Calibration statistics for m (each small box represents a value of m) and M (n=M), representing the number of Polymorphic loci (radtag), number of variants (SNPs) and the total number of sites assembled (variant and non-variant). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

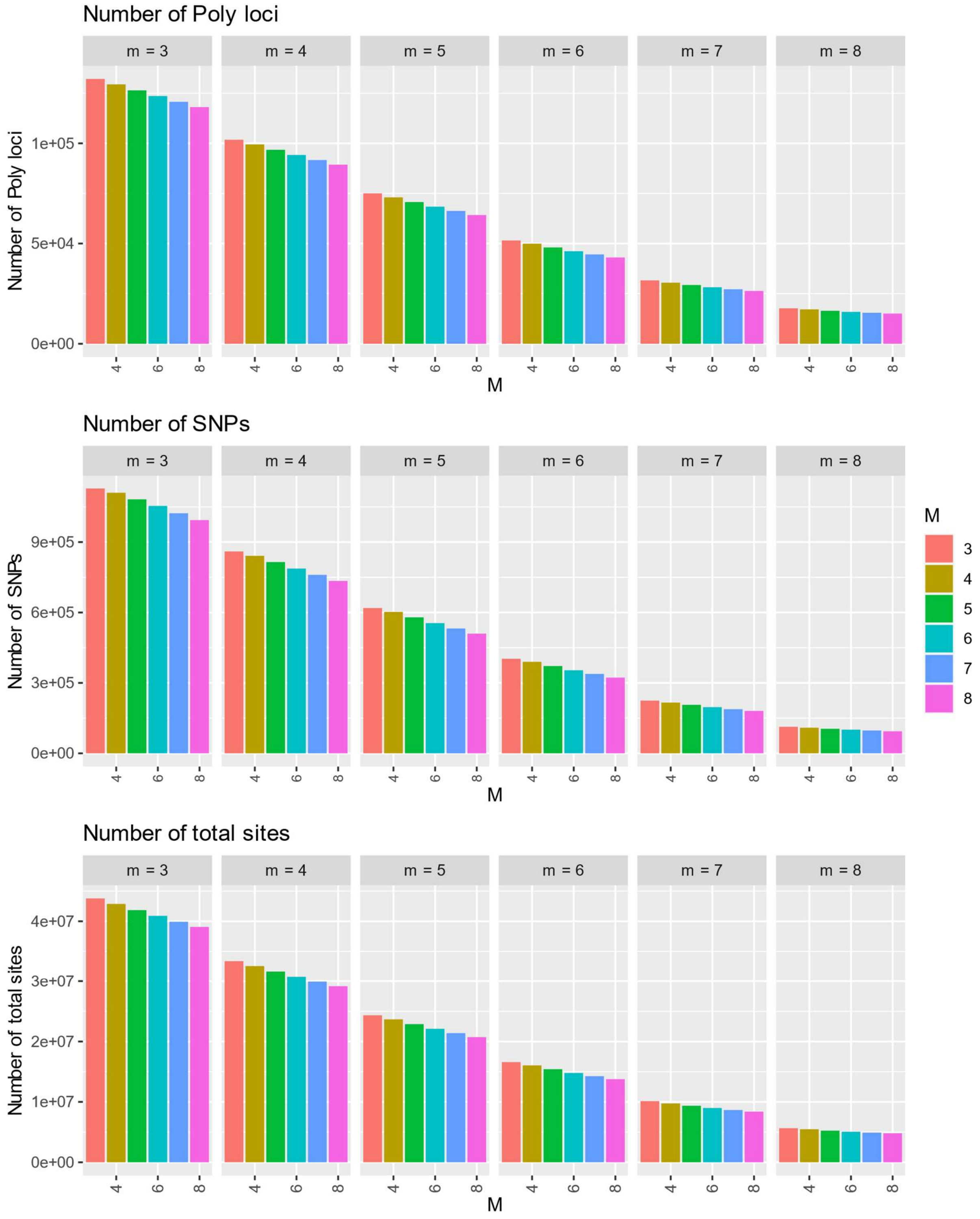


Figures 11 calibration: Nucleotide diversity (pi) for m (each small box represents a value of m) and M (n=M), estimated with Stacks V2.52 and considering all samples as one population (A), per back-arc-basin (B) and per locality (C). estimation was performed without replicate. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

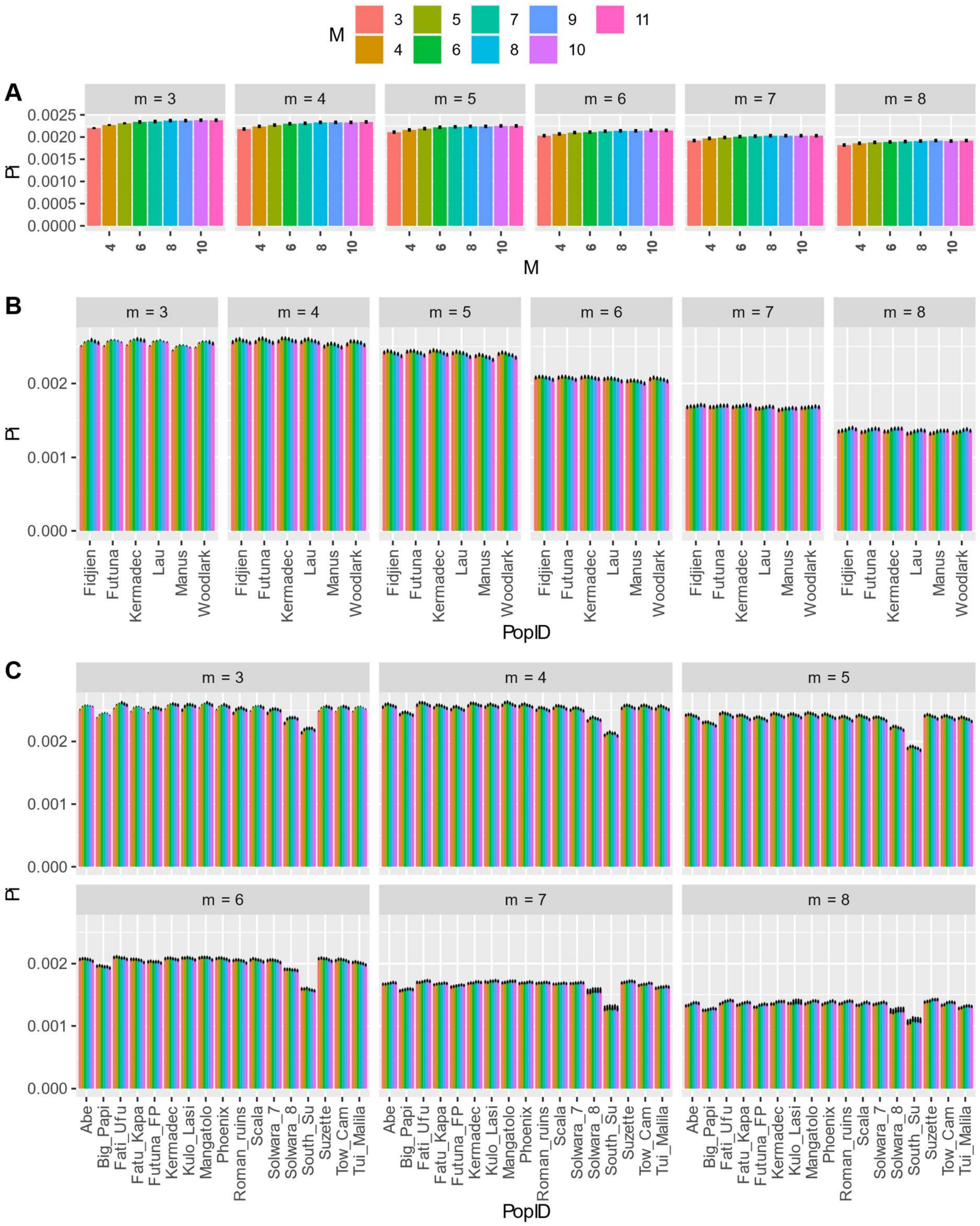

A
m = 3
m = 4
m = 5
m = 6
m = 7
m = 8
% of genotyping error
0.0
0.3
0.6
0.9
Bm267r1_Bm267r2
Bm268r1_Bm268r2
Bm269r1_Bm269r2
Bm270r1_Bm270r2
Bm271r1_Bm271r2
Bm272r1_Bm272r2
Bm273r1_Bm273r2
Bm274r1_Bm274r2
Bm355r1_Bm355r2
Bm356r1_Bm356r2
Bm357r1_Bm357r2
Bm358r1_Bm358r2
Bm359r1_Bm359r2
Bm360r1_Bm360r2
Bm361r1_Bm361r2
Bm362r1_Bm362r2
Replicate
M
3
4
5
6
7
8
B
M = 3
M = 4
M = 5
M = 6
M = 7
M = 8
% of genotyping error
Replicate
m
C
% of mean genotyping error
0.0
0.2
0.4
0.6
0.8
m

Figures 12 calibration: Percent of genotyping error between pairs of replicates for each parameter m and M (n=M). (A) plot of M in function of m. (B) m in function of M. (C) mean genotyping error over all pairs of replicate for each value of M and m. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

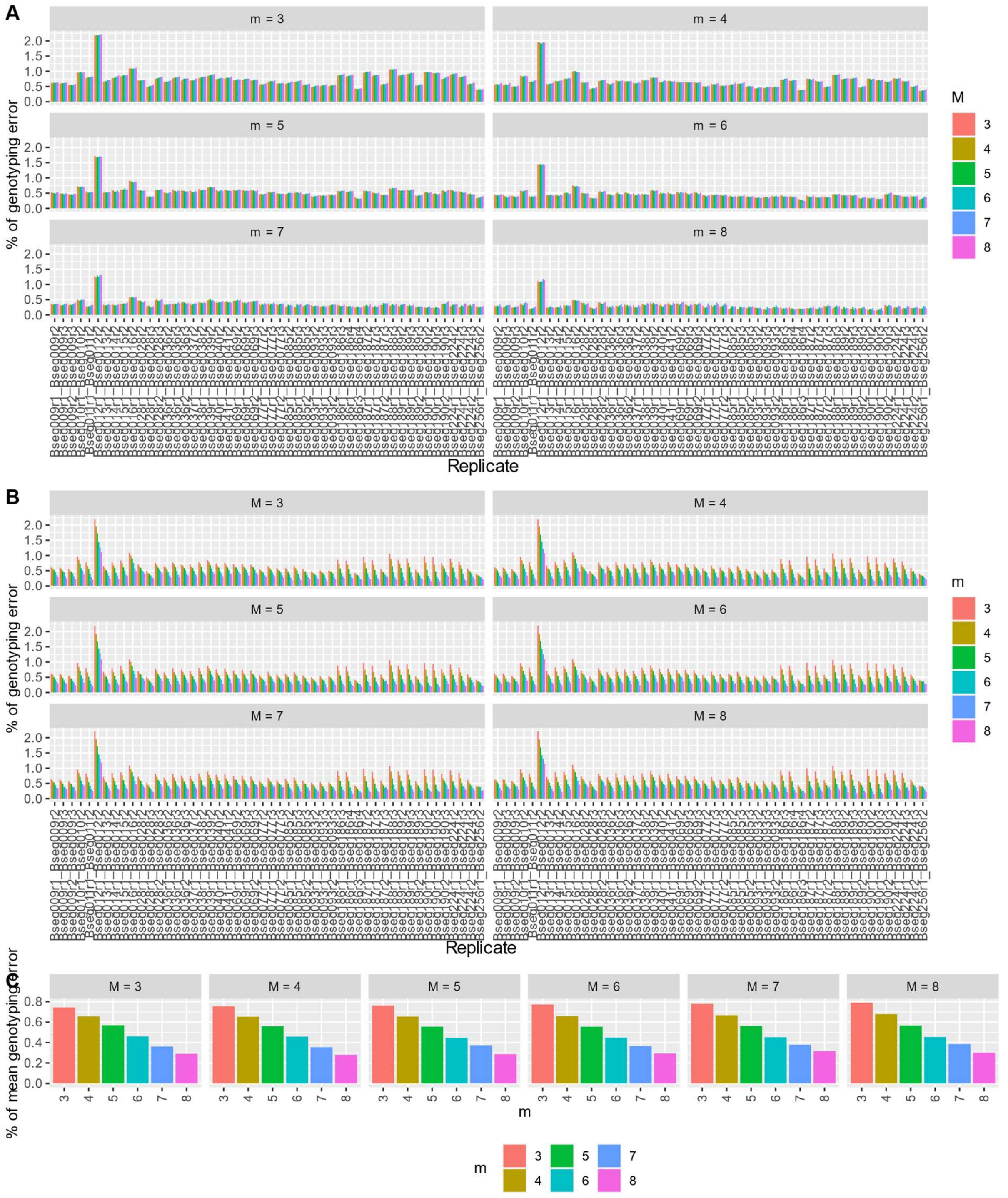
Branchinotogluma segonzaci



Figures 13 calibration: Calibration statistics for m (each small box represents a value of m) and M (n=M), representing the number of Polymorphic loci (radtag), number of variants (SNPs) and the total number of sites assembled (variant and non-variant). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.



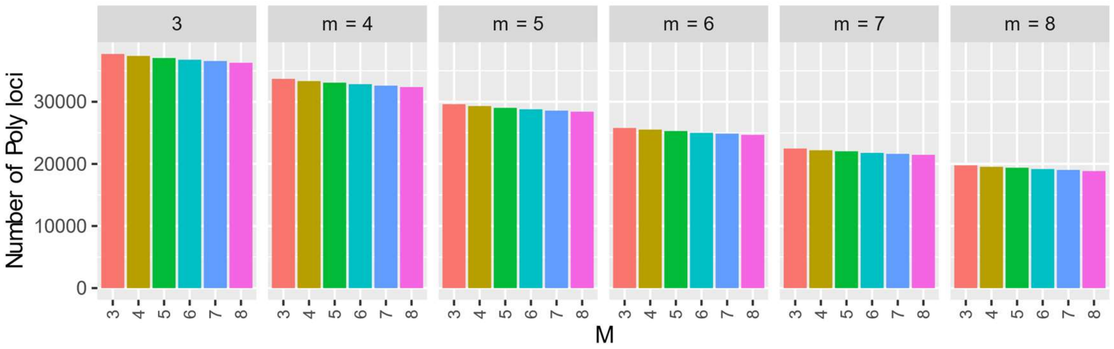
Figures 14 calibration : Nucleotide diversity (pi) for m (each small box represents a value of m) and M (n=M), estimated with Stacks V2.52 and considering all samples as one population (A), per back-arc-basin (B) and per locality (C). estimation was performed without replicate. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.



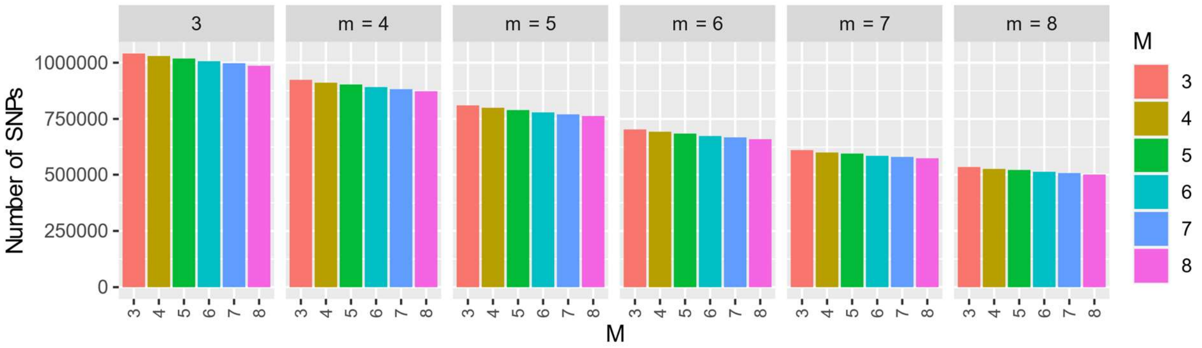
Figures 15 calibration : Percent of genotyping error between pairs of replicates for each parameter m and M (n=M). (A) plot of M in function of m. (B) m in function of M. (C) mean genotyping error over all pairs of replicate for each value of M and m. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.

Lepetodrillus schrolli & L. aff. schrolli

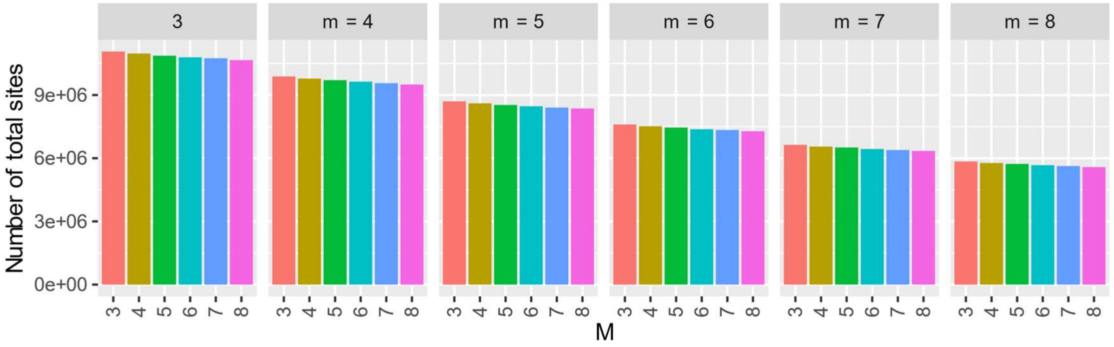
Number of Poly loci



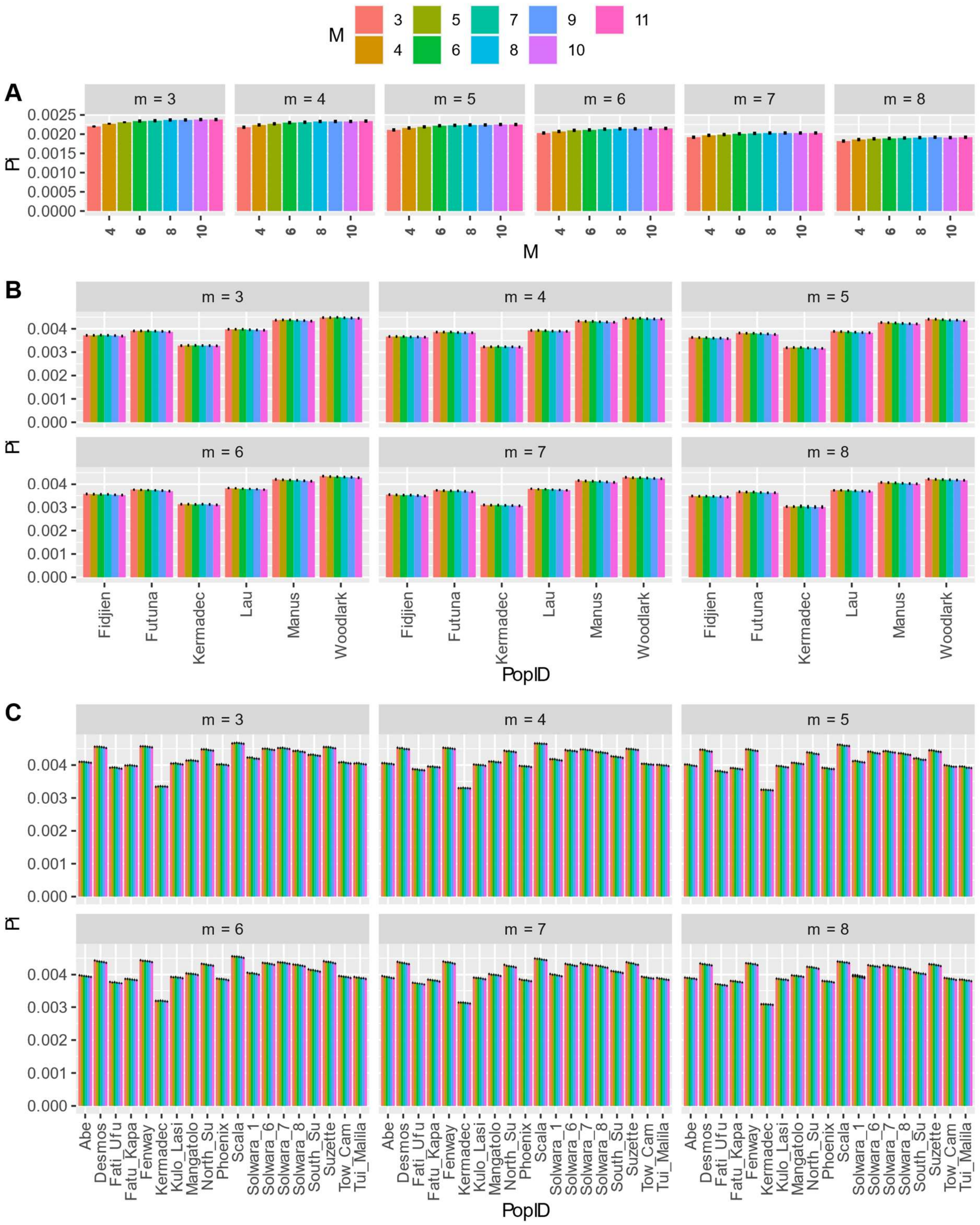
Number of SNPs



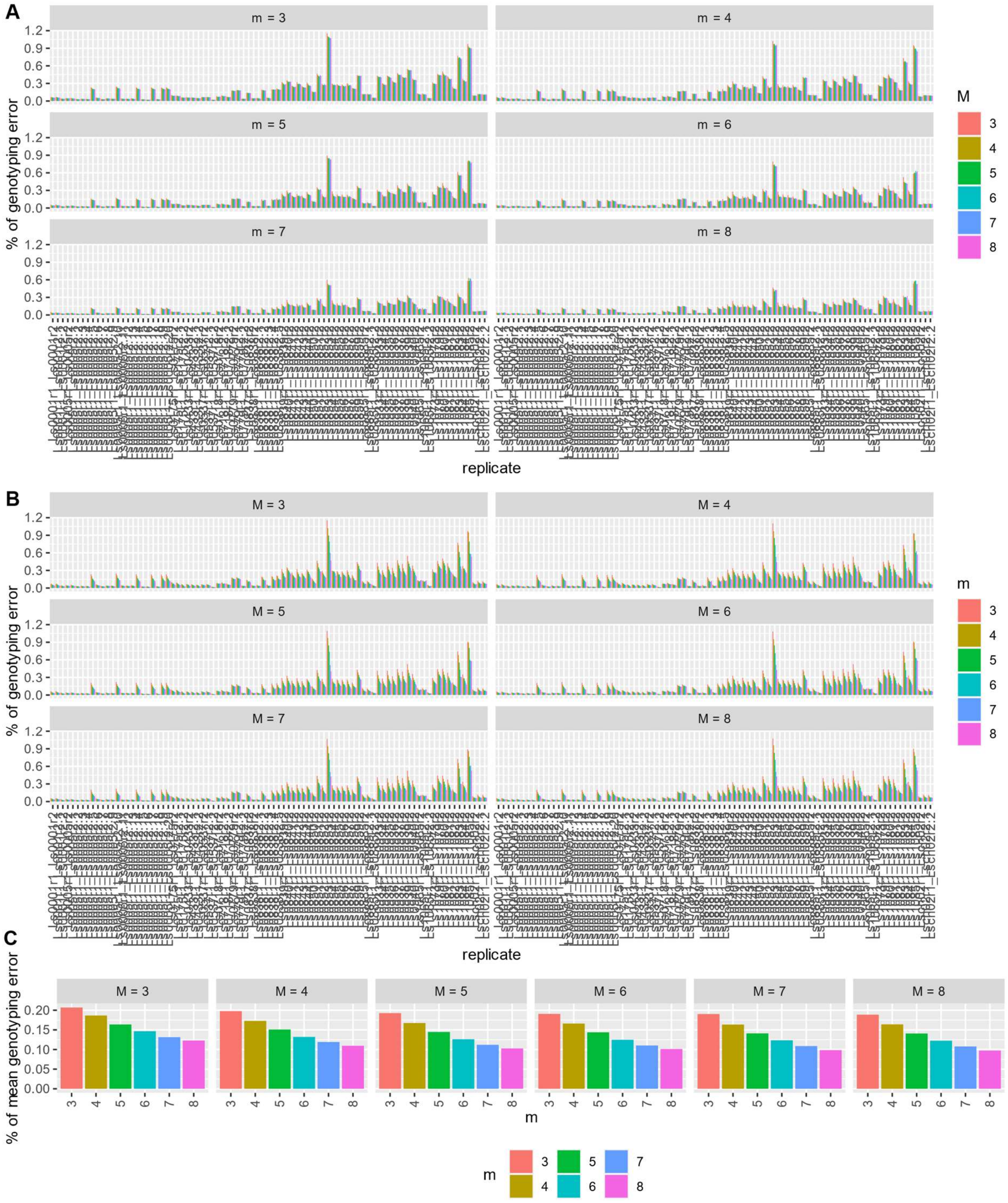
Number of total sites



Figures 16 calibration: Calibration statistics for m (each small box represents a value of m) and M (n=M), representing the number of Polymorphic loci (radtag), number of variants (SNPs) and the total number of sites assembled (variant and non-variant). m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.



Figures 17 calibration : Nucleotide diversity (pi) for m (each small box represents a value of m) and M (n=M), estimated with Stacks V2.52 and considering all samples as one population (A), per back-arc-basin (B) and per locality (C). Estimation was *calculated without replicate. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.*



Figures 18 calibration: Percent of genotyping error between pairs of replicates for each parameter m and M (n=M). (A) plot of M in function of m. (B) m in function of M. (C) mean genotyping error over all pairs of replicate for each value of M and m. m is the Minimum stack depth, M the Distance allowed between stacks and n the Distance allowed between catalog loci.