

Con	feature	size	dist	from	to	chr	Homology	top sim. in	%id	%sim
A	R9170	9170		1	9170	5				
A	R9170-1>>rB1	0	-9168	2	1	5				
A	R9170-2>>A1	2	9168	9169	9170	5				
A	R203	203	173	9343	9545	5				
A	rA3>>rF2	2	-1	9544	9545	5				
A	x462	462	9	9554	10015	5	< COX15-ctaA, fragments	<i>Rickettsia</i> spp.	59%	71%
A	x984	984	277	10292	11275	5	< Polyprenyl synthase family protein, full CDS	<i>Rickettsia</i> spp.	60	77
A	x327	225	856	12131	12355	5	< VirB4 secretion protein, fragment	<i>Rickettsia</i> spp.	83	90
A	x1464	2223	571	12926	15148	5	> FtsK DNA translocase, full CDS	<i>Rickettsia</i> spp.	67	78
A	x185	185	650	15798	15982	5				
A	x1269	1269	527	16509	17777	5	> NuoF, full CDS	<i>Rickettsia</i> spp.	85	91
A	cp455	455	82	17859	18313	5	rrnL (IR)	<i>Antrophyum</i>	98	
A	cp97	97	-4	18309	18405	5	chlB	<i>Haplopteris</i>	90	
A	ms (gaaaa)7	35	240	18645	18679	5				
A	cp103	103	616	19295	19397	5	psaA	<i>Asplenium</i>	99	
A	tatC	888	2153	21550	22437	5				
A	ms (T)10	10	-555	21882	21891	5				
A	ms (T)10	10	179	22070	22079	5				
A	R6899-1	6899	220	22299	29197	5				
A	rA4>>rK1	2	-6848	22349	22350	5				
A	cp1693	1693	1134	23484	25176	5	ndhC-ndhK-ndhJ	<i>Asplenium</i>	99	
A	trnR-UCG(cm)-1<	74	658	25834	25907	5				
A	cp114	114	1443	27350	27463	5	psbA	<i>Neolepisorus</i>	93	
A	ms (CCTCT)16	80	37	27500	27579	5				
A	trnY-GUA-1	83	558	28137	28219	5				
A	cp555	555	110	28329	28883	5	IR	<i>Pteris</i>	86	
A	cp275	286	17	28900	29185	5	IR	<i>Jamesonia</i>	90	
A	cp1301	1301	35	29220	30520	5	rrnL-rrn4.5-rrn5	<i>Haplopteris</i>	88	
A	ms (CT)7	14	-782	29738	29751	5				
A	x1292	1691	3546	33297	34987	5	> Serine tRNA ligase, pseudo	<i>Caedimonas</i> spp.	85	93
A	rA5>>rL1	2	0	34987	34988	5				
A	cp375	375	1	34989	35363	5	rrnL-rrn4.5 (IR)	<i>Vaginularia</i>	98	
A	cp69	69	862	36225	36293	5	rpoC1			
A	cp98	98	1	36294	36391	5	rpoC1			

A	cp314	314	1	36392	36705	5	psbB		
A	R114	114	531	37236	37349	5			
A	cp397	383	1521	38870	39252	5	IR	<i>Histiopteris</i>	79
A	R203	203	271	39523	39725	5			
A	rA2>>R9170-2	2	171	39896	39897	5			
A	R9170	9170	1	39898	49067	5			
A	rrnS	1693	-9167	39900	41592	5			
A	rrn5	127	1646	43238	43364	5			
A	cp247	247	596	43960	44206	5	rrnS	<i>Pteris</i>	97
A	rrnL, 5' part	2049	129	44335	46383	5			
A	cp327	327	26	46409	46735	5	psbD	<i>Pteris</i>	82
A	trnMi-CAU	74	259	46994	47067	5			
A	cp272	272	827	47894	48165	5	chlB	<i>Adiantum</i>	85
A	cp297	297	-4	48161	48457	5	rbcL	<i>Adiantum</i>	91
A	R9170-1>>rB1	2	-1	48456	48457	5			
A	end of contig A	2	0	48457	48457	5			
B	start of contig B			48458	48458	5			
B	rB1>>R9170	0		48459	48458	5			
B	rB5>>rG2	2	3266	51724	51725	5			
B	R180-1	180	-1	51724	51903	5			
B	cp157	157	-44	51859	52015	5	rpl16	<i>Adiantum</i>	82
B	R137-1	140	392	52407	52546	5			
B	nad9<	1365	1	52547	53911	5			
B	x1749	1749	1522	55433	57181	5	Bact-ORF1 RNA pol	<i>bacterial Magnetovibrio sp.</i>	
B	x1912	1913	1053	58234	60146	5	Bact-ORF2 DNA pol	<i>bacterial Zoogloea sp</i>	
B	R114	114	1177	61323	61436	5			
B	nad1<	7067	2684	64120	71186	5			
B	x888	888	1482	72668	73555	5	OMBB	<i>Rickettsia spp.</i>	
B	R180-2	180	2537	76092	76271	5			
B	x1623	1623	-53	76218	77840	5	HscA ,RmuC , pseudo	<i>Caedimonas spp.</i>	
B	cp232a	269	2087	79927	80195	5	morffo 1 fragment	<i>Antrophyum</i>	70
B	cp103	110	113	80308	80417	5	IR	<i>Pteris</i>	85
B	cp2126	2126	250	80667	82792	5	morffo		
B	cp291	291	60	82852	83142	5	IR	<i>Haplopteris</i>	96

B	cp51	51	1	83143	83193	5	IR	<i>Haplopteris</i>	100	
B	ms (GGAAA)6	30		83659	83688	5				
B	R513-1	513	2800	86488	87000	5				
B	x384	1092	-398	86602	87693	5	orf	<i>Corynebacterium spj</i>	37	55
B	R232-1	232	1407	89100	89331	5				
B	pseudo atp1	2193	-143	89188	91380	5				
B	ms (C)14	14		91530	91543	5				
B	cp2442	2442	2475	94018	96459	5	chlN-chlL-trnN	<i>Antrophyum</i>	91	
B	trnN-GUU(cp)<	72	-2237	94222	94293	5				
B	rB3>>rJ2	2	2185	96478	96479	5				
B	R309	309	1	96480	96788	5				
B	cp420	420	-133	96655	97074	5	ndhH	<i>Adiantum</i>	81	
B	R407-1	407	63	97137	97543	5				
B	cp284	284	2342	99885	100168	5		<i>Adiantum</i>	93	
B	trnD-GUC<	74	254	100422	100495	5				
B	trnH-GUG-1<	73	3935	104430	104502	5				
B	trnL-UAA-1<	84	155	104657	104740	5				
B	R239	239	199	104939	105177	5				
B	cp241	231	1844	107021	107251	5	rmS (IR)	<i>Brainea</i>	96	
B	cp50	50	1	107252	107301	5	IR	<i>Acrostichum</i>	98	
B	rB4>>rC2	2	553	107854	107855	5				
B	cp55	59	2258	110113	110171	5	rbcL	<i>Haplopteris</i>	100	
B	cp232b	232	695	110866	111097	5	psbl-trnS-gcu	<i>Haplopteris</i>	96	
B	trnS-GCU(cp)<	75	-76	111021	111095	5				
B	trnK-UUU>	73	1097	112192	112264	5				
B	trnY-GUA-2>	83	1280	113544	113626	5				
B	pseudo nad5	236	423	114049	114284	5				
B	cp265	265	238	114522	114786	5	atpE-trnM	<i>Adiantum</i>	80	
B	trnMe-CAU(cp)	73	-74	114712	114784	5				
B	rps14>	2066	2693	117477	119542	5				
B	trnC-GCA>	71	163	119705	119775	5				
B	trnH-GUG-2<	75	819	120594	120668	5				
B	ms (CCCTT)17	85		120687	120771	5				
B	trnL-UAA-2<	84	117	120888	120971	5				
B	trnA-UGC-1>	73	1711	122682	122754	5				

B	cp68	68	54	122808	122875	5	rmS (IR)	<i>Sphaeropteris</i>	89
B	cp1063	1065	2299	125174	126238	5	rpoA-rps11-rpl36	<i>Haplopteris</i>	88
B	rB2>>rC1	2	28	126266	126267	5			
B	end of contig B	1	0	126267	126267	5			
B	start of contig C	1	1	126268	126268	5			
C	rC1>>	0	1	126269	126268	5			
C	cp3288	3288	129	126397	129684	5	petA-psbJ-psbL-psbF-psbE-petL-petG	<i>Haplopteris</i>	93
C	ms (T)10	10		127066	127075	5			
C	rC3>>rL2	2	2610	129685	129686	5			
C	cp282	290	809	130495	130784	5	atpA	<i>Pteris</i>	92
C	trnN-GUU(cm)>	73	27	130811	130883	5			
C	x817	832	440	131323	132154	5	radA -like homolog, CvpA, fragment		
C	rC4>>rL2	2	162	132316	132317	5			
C	nad2<	7858	157	132474	140331	5			
C	sdh3<	396	561	140892	141287	5			
C	trnG-UCC<	71	170	141457	141527	5			
C	R239	239	1409	142936	143174	5			
C	R141	141	316	143490	143630	5			
C	pseudo rps19	74	-68	143562	143635	5			
C	rpl2<	1826	107	143742	145567	5			
C	trnG-GCC<	72	970	146537	146608	5			
C	trnW-CCA<	73	228	146836	146908	5			
C	cp407	412	1770	148678	149089	5	psbB	<i>Asplenium</i>	94
C	pseudo-rps4	566	211	149300	149865	5			
C	ms (AT)9	18		150491	150508	5			
C	ms (T)10	10		152304	152313	5			
C	pseudo-atp1	151	1091	153404	153554	5			
C	R232-2	232	-40	153514	153745	5			
C	cp1645	1677	1	153746	155422	5	trnL-uaa-trnF-gaa	<i>Haplopteris</i>	82
C	ms (A)11	11		154618	154628	5			
C	trnF-GAA(cp)	73		155260	155332	5			
C	atp4>	597	1718	156346	156942	5			
C	trnR-UCG(cm)-2>	74	1453	158395	158468	5			
C	cp142	142	156	158624	158765	5	rps19	<i>Haplopteris</i>	87
C	cp1035	1035	252	159017	160051	5	psaA	<i>Haplopteris</i>	96

C	R309	309	-42	160009	160317	5				
C	cp134	135	-134	160183	160317	5				
C	pseudo-nad9	247	691	161008	161254	5				
C	cp1105	1105	169	161423	162527	5	morffo1	<i>Pteris</i>	76	
C	R513-2	513	371	162898	163410	5				
C	cp135	135	261	163671	163805	5	psbD	<i>Vittaria</i>	87	
C	cp85	85	1	163806	163890	5	rpoB	<i>Vittaria</i>	94	
C	cp792	792	-12	163878	164669	5	psaB	<i>Vittaria</i>	93	
C	nad3>	384	397	165066	165449	5				
C	cob>	1569	133	165582	167150	5				
C	rC5>>rE1	2	-965	166185	166186	5				
C	nad7<	4251	1515	167701	171951	5				
C	cp213	213	353	172304	172516	5				
C	cp412	200	0	172516	172715	5				
C	rC2>>rB4	2	196	172911	172912	5				
C	end of contig C	1	0	172912	172912	5				
D	start of contig D	1		27959	27959	1				
D	rD1>>R9170-1	0	1	27960	27959	1				
D	rD3>>rK2	0	415	28374	28373	1				
D	cp219	219	93	28466	28684	1	trnP-UGG	<i>Adiantum</i>	84	
D	trnP-UGG(cp)	74	-77	28607	28680	1				
D	cp224	224	931	29611	29834	1	ycf2 (IR)	<i>Pteris</i>	94	
D	x394	394	189	30023	30416	1				
D	x923	924	-224	30192	31115	1	lytic transglycolase with SLT domain, fragment	<i>Caedimonas spp.</i>	38	56
D	cp131	131	1274	32389	32519	1	rbcL	<i>Haplopteris</i>	97	
D	cp273	273	191	32710	32982	1	rmS (IR)	<i>Dicranopteris</i>	73	
D	rps1>	1571	647	33629	35199	1				
D	cp294	294	388	35587	35880	1	trnA-UGC (IR)	<i>Pteris</i>	97	
D	R180	180	836	36716	36895	1				
D	trnL-UAG>	86	1431	38326	38411	1				
D	trnS-UGA>	87	306	38717	38803	1				
D	ms(gcaa)68	271	57	38860	39130	1				
D	trnV-UAC>	73	159	39289	39361	1				
D	trnE-UUC>	72	617	39978	40049	1				
D	trnP-UGG>	74	378	40427	40500	1				

D	cp280	280	1363	41863	42142	1	IR	<i>Myriopteris</i>	77
D	trnQ-UUG>	72	353	42495	42566	1			
D	ms (G)14	14	-20	42546	42559	1			
D	trnI-CAU>	74	114	42673	42746	1			
D	trnR-UCU<	74	755	43501	43574	1	rrnL-trnA-ugc (IR)	<i>Pteris</i>	96
D	cp370	370	532	44106	44475	1			
D	pseudo-nad9	556	125	44600	45155	1			
D	cp566	566	643	45798	46363	1			
D	R407-2	407	3084	49447	49853	1	rpoB	<i>Asplenium</i>	97
D	cp436	436	2582	52435	52870	1			
D	trnR-UCG(cm)-3<	74	300	53170	53243	1			
D	trnS-GGA(cp)	87	1539	54782	54868	1			
D	cp153	153	555	55423	55575	1	trnI-GAU (IR)	<i>Scoliosorus</i>	94
D	trnS-GCU<	87	144	55719	55805	1			
D	cp485	486	13	55818	56303	1			
D	ms (GCAA)34(AA	272	282	56585	56856	1			
D	rD6>>rH1	0	-114	56742	56741	1	psaB-psaA	<i>Cryptogramma</i>	86
D	R295-1	295	1	56742	57036	1			
D	ms (GGAA)5	20	1394	58430	58449	1			
D	cp202	202	1669	60118	60319	1			
D	cp145	145	-144	60175	60319	1	matK	<i>Adiantum</i>	78
D	ms (A)11	11	307	60626	60636	1			
D	trnA-UGC-2>	73	146	60782	60854	1			
D	rD5>>rI2	2	10	60864	60865	1			
D	rps2	1557	87	60952	62508	1	IR	<i>Lygodium</i>	82
D	rD4>>rH2	2	668	63176	63177	1			
D	R141-1	-139	1	63178	63038	1			
D	sdh4>	264	1285	64323	64586	1			
D	nad6<	615	477	65063	65677	1	k		
D	cox3>	939	323	66000	66938	1			
D	rps12<	381	239	67177	67557	1			
D	rD2>>rF3	2	198	67755	67756	1			
D	end of contig D	1	0	67756	67756	1			
E	start of contig E	1		107715	107715	6			
E	rE1>>rC1	0	1	107716	107715	6			

E	x2170	2235	206	107921	110155	6	XpsD, prepilin peptidase, pseudo	<i>Caedimonas spp.</i>	90	93
E	nad4L<	303	782	110937	111239	6				
E	rps11<	468	1892	113131	113598	6				
E	rps13<	453	12	113610	114062	6				
E	rpl6<	300	4	114066	114365	6				
E	cp101	101	79	114444	114544	6	petD	<i>Antrophyum</i>	83	
E	cp387	387	-2	114542	114928	6	ycf3	<i>Antrophyum</i>	90	
E	cp1213	1213	3	114931	116143	6	rps4	<i>Haplopteris</i>	82	
E	R151-1	151	291	116434	116584	6				
E	atp9<	225	-4	116580	116804	6				
E	cp600	600	687	117491	118090	6	rpoC1	<i>Histiopteris</i>	95	
E	cp67	67	945	119035	119101	6	rpoC1	<i>Adiantum</i>	96	
E	rE3>>rJ1	2	676	119777	119778	6				
E	cp354	354	1651	121429	121782	6	IR	<i>Asplenium</i>	76	
E	cp667	667	342	122124	122790	6		<i>Antrophyum</i>	70	
E	cp140	144	197	122987	123130	6	IR	<i>Pteris</i>	77	
E	atp8>	501	488	123618	124118	6				
E	R6899-2	6899	-138	123980	130878	6				
E	rE4>>rG1	0	-6897	123981	123980	6				
E	ms (CCTCT)16	80	5201	129181	129260	6				
E	x1920	1920	1909	131169	133088	6	mfd - rimM - trmD - rpl19, pseudo	<i>Caedimonas spp.</i>	88	94
E	rps4>	915	142	133230	134144	6				
E	cp357	357	1	134145	134501	6	tRNA-UGC(IR)	<i>Haplopteris</i>	86	
E	cp645	645	-1	134500	135144	6	atpF-atpH	<i>Haplopteris</i>	95	
E	cp1039	1039	3	135147	136185	6	atpA-atpF	<i>Haplopteris</i>	98	
E	pseudo-cob	769	264	136449	137217	6				
E	rE2>>rC5	2		136612	136613	6				
E	end of contig E	1	0	136613	136613	6				
F	start of contig F	1	-127208	9405	9405	2				
F	rF1>>rA1	0	0	9405	9404	2				
F	R203	203	1	9405	9607	2				
F	rrnL, 3'-part<	4569	925	10532	15100	2				
F	R596	596	-1367	13733	14328	2				
F	x643	643	2277	16605	17247	2	rmuC	<i>Caedimonas spp.</i>	94	96
F	cp416	431	2	17249	17679	2	clpP	<i>Pellaea</i>	74	

F	cox2>	1763	183	17862	19624	2							
F	pseudo-tatC	56	425	20049	20104	2							
F	rpl16<	408	139	20243	20650	2							
F	rps3<	3553	-53	20597	24149	2							
F	rps19<	237	19	24168	24404	2							
F	R163-1	163	-6	24398	24560	2							
F	trnF-GAA<	74	-88	24472	24545	2							
F	cp1558	1558	324	24869	26426	2	ycf2 (IR)	Haplopteris	96				
F	rps7<	411	1034	27460	27870	2							
F	pseudo-nad5	52	89	27959	28010	2							
F	rF3>>rD2	0	-44	27966	27965	2							
F	x306	359	1011	28976	29334	2	artM	Caedimonas spp.	82	92			
F	x2293	2360	193	29527	31886	2	mrcA	Caedimonas spp.	87	93			
F	x1435	1436	475	32361	33796	2	CafA / Rnase E Aminopeptidase						
F	x210	210	1162	34958	35167	2	rps21	Rickettsia spp.	94	96			
F	x633	633	133	35300	35932	2	COQ9 family protein	Rickettsia spp.	51	71			
F	x3215	3216	15	35947	39162	2	Isoleucine tRNA ligase	Rickettsia spp.	72	84			
F	x1066	1067	168	39330	40396	2	IS481 family transposase	Rickettsia spp.					
F	rF2>>rA3	2	627	41023	41024	2							
F	end of contig F	1	0	41024	41024	2							
G	start of contig G	1		192745	192745	8							
G	R151-2	151	0	192745	192895	8							
G	rG1>>rE4	0	-149	192746	192745	8							
G	atp1>	1542	219	192964	194505	8							
G	x300	300	216	194721	195020	8	IS481 family transposase	Rickettsia spp.	76	85			
G	x1993	1998	228	195248	197245	8	acetyl/propionyl/methylcrotonyl-CoA carboxylase a	Rickettsia spp.	86	94			
G	x1442	1545	30	197275	198819	8	acyl-CoA carboxylase b	Rickettsia spp.	88	94			
G	x1246	1278	225	199044	200321	8	murA	Rickettsia spp.	69	83			
G	x458	458	235	200556	201013	8	SIMPL domain-containing protein	Rickettsia spp.	43	61			
G	x1378	741	499	201512	202252	8	P-type conjugative transfer protein VirB9	Rickettsia spp.	54	67			
G	x695	696	-11	202241	202936	8	virB8 family protein <	Rickettsia spp.	60	75			
G	R137-2	140	645	203581	203720	8							
G	rG2>>rB5	2	-1	203719	203720	8							
G	end contig G	1	0	203720	203720	8							
H	start of contig H	1		81514	81514	4							

H	rH1>>rD6	0	1	81515	81514	4			
H	nad5<	5923	293	81807	87729	4			
H	R596-2	596	-2879	84850	85445	4			
H	cp364	364	2746	88191	88554	4		<i>Vittaria</i>	67
H	cp749	749	724	89278	90026	4		<i>Asplenium</i>	66
H	cp686	686	258	90284	90969	4	psbD	<i>Haplopteris</i>	73
H	cp219	219	493	91462	91680	4	psbC	<i>Haplopteris</i>	85
H	cp1271	1271	172	91852	93122	4	rrnL	<i>Haplopteris</i>	99
H	cp4165	4165	-3	93119	97283	4	ndhH-ndhE	<i>Haplopteris</i>	99
H	ms (A)12	12	-1525	95758	95769	4			
H	R141-2	141	6227	101996	102136	4			
H	rH2>>rD4	2	-1	102135	102136	4			
H	end of contig H	1	0	102136	102136	4			
I	ms (CCCTT)17	85		120687	120771	9			
I	start of contig I	1	5468	126239	126239	9			
I	rl1>>rC4	2	0	126239	126240	9			
I	ms (T)10	10		127066	127075	9			
I	nad4<	6618	6254	132493	139110	9			
I	cp510	511	373	139483	139993	9	ndhH	<i>Vittaria</i>	91
I	cp281	283	2348	142341	142623	9	psbB	<i>Tectaria</i>	99
I	cp524	524	3492	146115	146638	9	morffo 2	<i>Histiopteris</i>	70
I	pseudo-rps10	309	275	146913	147221	9			
I	R163-2	163	342	147563	147725	9			
I	rl2>>rD5	2	-1	147724	147725	9			
I	end of contig I	1	0	147725	147725	9			
J	ms (AGGAG)16	80	32341	180066	180145	7			
J	start of contig J	1		185209	185209	7			
J	R137-3	140	0	185209	185348	7			
J	rJ>>rE3	0	-138	185210	185209	7			
J	atp6<	756	53	185262	186017	7			
J	rps10<	333	284	186301	186633	7			
J	rpl5>	573	450	187083	187655	7			
J	pseudo-atp8	135	85	187740	187874	7			
J	pseudo-atp1	1205	5	187879	189083	7			
J	R232-3	232	-143	188940	189171	7			

J	rJ2>>rB3	2	-1	189170	189171	7
J	end of contig J	1	0	189171	189171	7
K	start of contig K	1		22353	22353	3
K	rK1>>rA4	0	1	22354	22353	3
K	cox1>	2265	1160	23513	25777	3
K	cp63	63	85	25862	25924	3
K	ms (gaaaa)12	60	1608	27532	27591	3
K	rK2>>rD3	2	121	27712	27713	3
K	end of contig K	1	0	27713	27713	3
L	start of contig L	1	38754	66467	66467	2
L	R295-2	295	0	66467	66761	2
L	rL1>>rA5	2	-6062	60699	60700	2
L	cp763	1301	-1	60699	61999	2
L	x1850	1850	2777	64776	66625	2
L	R295	295	-158	66467	66761	2
L	R151	151	1625	68386	68536	2
L	cp1456	1712	407	68943	70654	2
L	cp1063	1067	25	70679	71745	2
L	rL2>>rB2	2	-1	71744	71745	2
L	end of contig	1	0	71745	71745	2

ndhJ

Adiantum

78

rrn23, rrn4.5, rrn5 region *Haplopteris elongata*

serS-surE-nlpD

Caedibacter varicae

81%

morfo 2, specific, twice in *H. elongata*

rpoA-rps11-rpl36

Haplopteris

97

xDNA Acronyms

artM: Arginine ABC transporter permease

CafA: ribonuclease E/G

COQ9: Ubiquinone biosynthesis protein

HscA: Fe-S cluster biosynthesis chaperone

mfd: transcription repair coupling factor

mrcA: peptidoglycan glycosyltransferase/peptidoglycan DD-transpeptidase

OMBB: autotransporter outer membrane beta-barrel domain-containing protein

rimM: ribosome maturation factor

RmuC: DNA recombination protein

rpl19: ribosomal protein L19

rps21: ribosomal protein S21

trmD: tRNA (guanosine(37)-N1)-methyltransferase

XpsD: Type II secretion system protein D precursor

virB: secretion/conjugal transfer ATPase family type

CvpA: Uncharacterized membrane protein, required for colicin V production

NuoF: NADH-quinone oxidoreductase subunit

COX15-ctaA: Cytochrome oxidase assembly protein

serS: serine--tRNA ligase

surE: 5'/3' nucleotidase

nlpD: murein hydrolase activator

murA; UDP-N-acetylglucosamine 1-carboxyvinyltransferase