

Table S1 : Genome assemblies used in the comparative phylogenomic analysis.

Species	Sections	Code	N° accession GenBank	Sequencing method	Genome size (Mb)	Contigs	Contig N50	GC%
<i>Alternaria chlamydospora</i>	<i>Phragmosporae</i>	SC11	GCA 047302185.1	Oxford Nanopore ; Illumina NovaSeq	36.4	19	3.3 Mb	51.5
<i>Alternaria rosae</i>	<i>Pseudoalternaria</i>	BMP 2777	GCA 024043135.1	Illumina HiSeq	32.8	203	794.6 kb	52
<i>Alternaria metachromatica</i>	<i>Infectoriae</i>	BMP 0045	GCF 023757995.1	Illumina HiSeq	37.3	12	1 Mb	50
<i>Alternaria ethzedia</i>	<i>Infectoriae</i>	BMP 0044	GCF 023757985.1	Illumina HiSeq	36	13	863.8 kb	50.5
<i>Alternaria conjuncta</i>	<i>Infectoriae</i>	BMP 0040	GCF 024043145.1	Illumina HiSeq	36.1	179	1.9 Mb	50.5
<i>Alternaria guansuensis</i>	<i>Undifilum</i>	LYZ1412	GCA 009289805.1	Illumina	75.1	1,034	163.8 kb	37
<i>Alternaria consortialis</i>	<i>Ulocladioides</i>	JCM 1940	GCA 001950455.1	HiSeq 2500	34.2	105	1 Mb	50.5
<i>Alternaria brassicicola</i>	<i>Brassicicola</i>	Abra43	GCA 002796735.1	PacBio	31	29	2.1 Mb	51
<i>Alternaria brassicae</i>	/	PNT	GCA 036768465.1	PacBio	33.8	10	3.5 Mb	51
<i>Alternaria panax</i>	<i>Panax</i>	BNCC115425	GCA 019702505.1	PacBio ; Illumina HiSeq	34.8	42	2.8 Mb	51
<i>Alternaria radicina</i>	<i>Radicina</i>	CBR2	GCA 050230835.1	Illumina NovaSeq ; Oxford Nanopore	34.6	6	6.5 Mb	49.5
<i>Alternaria solani</i>	<i>Porri</i>	NL03003	GCA 002952155.1	PacBio	32.8	10	2.9 Mb	51.5
<i>Alternaria dauci</i>	<i>Porri</i>	A2016	GCF 042100115.1	PacBio Sequel II ; Illumina NovaSeq	34.9	10	3.4 Mb	50.5
<i>Alternaria alternata</i>	<i>Alternaria</i>	SRC1lrK2f	GCF 001642055.1	Illumina	33	91	1.1 Mb	51.5
<i>Alternaria arborescens</i>	<i>Alternaria</i>	FERA 675	GCF 004154835.1	Illumina MiSeq	33.9	328	862.6 kb	51
<i>Stemphylium lycopersici</i>	/	CIDEFI 212	GCA 003268315.1	Illumina HiSeq	34.1	633	236.5 kb	51.5

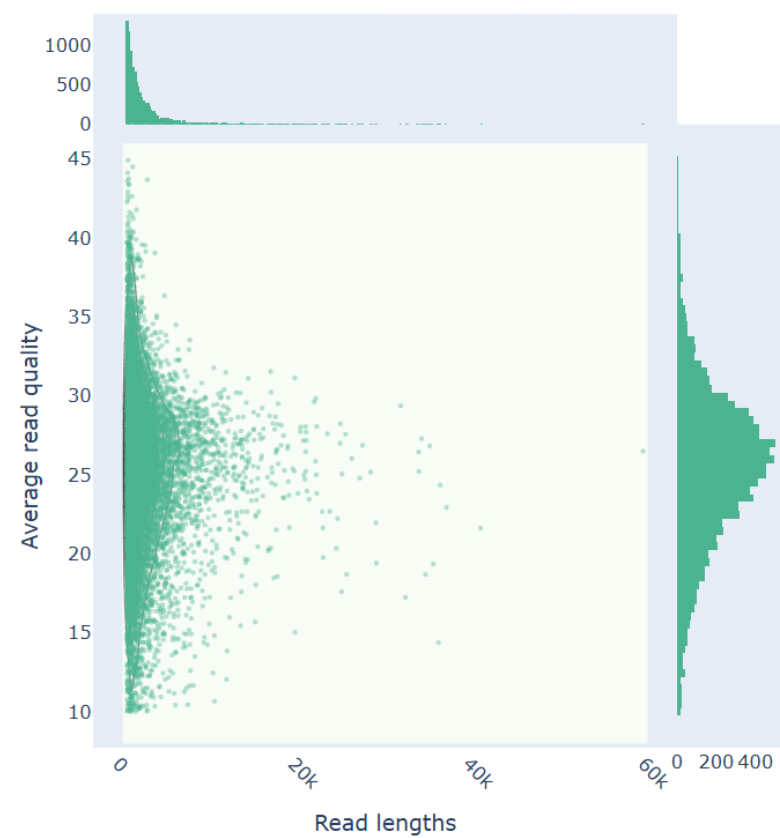
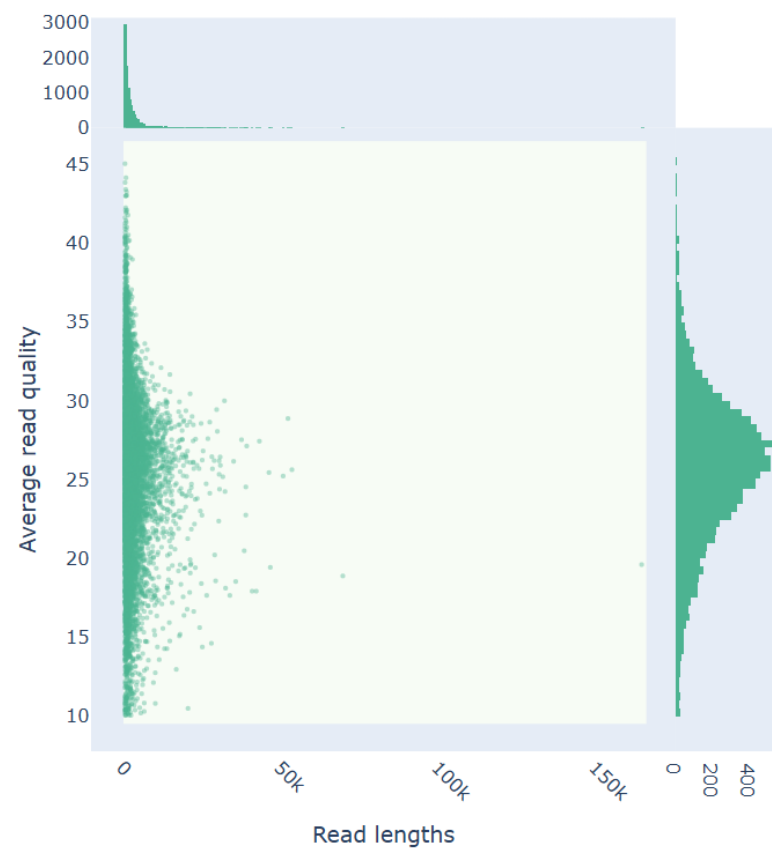


Figure S1 Scatter plot of Nanopore readings for *A. telliensis* strain CBS145643^T (left) and *A. japonica* strain CBS118390^T (right), showing reading length as a function of quality score, generated with NanoPlot (kde graph).