

Table S4. Summary of the alignments analyzed in this study.

Orthologue name	amino acid positions subjected to phylogenetic analyses	Number of sequences	Substitution model
MgCH (ChlD)	608	68	LG + Γ
MgCH (ChlH)	1095	96	LG + Γ
MgPMT	209	65	WAG + Γ
POR	285	132	WAG + Γ
N-DVR	290	63	WAG + Γ
F-DVR	358	37	WAG + Γ
CS	294	67	Blosum62 + Γ
GTR	361	83	WAG + Γ
GSAT	415	72	WAG + Γ
ALAD	300	114	LG + Γ
PBGD	267	109	WAG + Γ
UROS	176	76	WAG + Γ
UROD	302	206	WAG + Γ
CPOX	251	134	WAG + Γ
PPOX	300	87	LG + Γ
FeCH	214	129	WAG + Γ
DXS	604	57	LG + Γ
DXR	358	55	WAG + Γ
IspD	201	58	WAG + Γ
IspE	227	55	WAG + Γ
IspF	133	63	LG + Γ
IspG	595	55	WAG + Γ
IspH	328	68	WAG + Γ