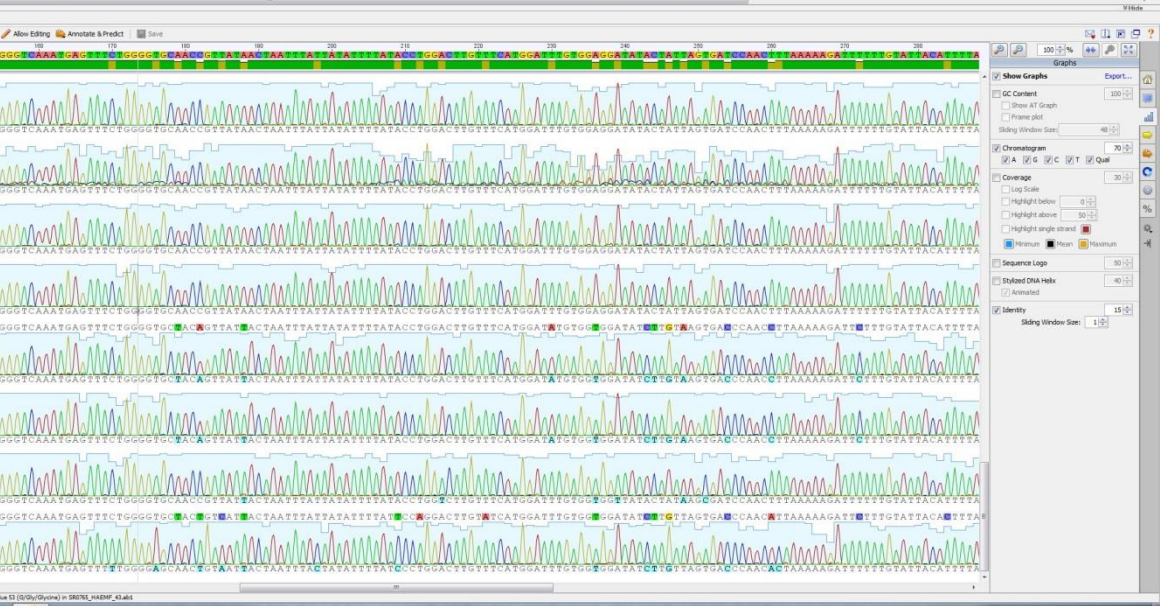


Path	Species	Tree builder	FCN	Sequence Le...	Post-trim	%GC	Topology	Molecule Type	# Sequences	% Pairwise E...	% Identical ...	En	Acc...
K:Glaucoparis...SR1022_H4EM...	-	-	95.8%	455	455	27.3%	linear	DNA	-	-	-	High	-
K:Glaucoparis...SR1091_H4EM...	-	-	93.8%	455	455	27.3%	linear	DNA	-	-	-	High	-
K:Glaucoparis...SR1124_H4EM...	-	-	94.1%	455	455	27.3%	linear	DNA	-	-	-	High	-
K:Glaucoparis...SR1196_H4EM...	-	-	95.4%	455	455	27.3%	linear	DNA	-	-	-	High	-
...	-	-	-	503	-	27.6%	linear	-	2	100.0%	100.0%	-	-
...	-	-	-	478	-	26.8%	linear	-	3	92.4%	88.5%	-	-
...	-	-	-	478	-	27.3%	linear	-	3	90.4%	85.6%	-	-
...	-	-	-	478	-	27.0%	linear	-	4	91.8%	86.0%	-	-
...	-	-	-	478	-	27.2%	linear	-	7	100.0%	100.0%	-	-
...	-	-	-	478	-	27.0%	linear	-	7	94.7%	88.7%	-	-
...	-	-	-	478	-	27.3%	linear	-	7	100.0%	100.0%	-	-
...	-	-	-	478	-	27.3%	linear	-	9	100.0%	100.0%	-	-
...	-	-	-	478	-	27.2%	linear	-	9	100.0%	99.8%	-	-
...	-	-	-	478	-	27.2%	linear	-	12	100.0%	100.0%	-	-
...	-	-	-	478	-	26.4%	linear	-	26	92.9%	77.0%	-	-
...	-	-	-	478	-	27.1%	linear	-	48	97.2%	81.4%	-	-
...	-	-	-	478	-	26.4%	linear	-	36	87.4%	77.0%	-	-



Using 303 / 6114 MB memory

Cursor before base 64 (original base 41). Mouse over base 179 (G - quality 42), nucleid 63 (G/Gly/Gly) in SR0785\_H4EM\_43.ab1

- PlasMapper Features (314)
  - Plasmids from MB (27)
  - Proteins (12)
  - Protein Documents (8)
  - Tree Documents (4)
- Shared Databases (212)
  - Operations
    - Gene
    - Genome
    - Nucleotide
    - Protein
    - PubMed
    - SNP
    - Structure
    - Taxonomy
    - UniProt

▷ 32. SR0722\_H4EM\_41.ab1  
 ▷ 33. SR0729\_H4EM\_42.ab1  
 ▷ 34. SR0785\_H4EM\_43.ab1  
 ▷ 35. Plasmodium ICTCAV01  
 ▷ 36. SR0340\_H4EM\_32.ab1  
 ▷ 37. SR0373\_H4EM\_12.ab1  
 ▷ 38. SR0845\_H4EM-correctR.ab1  
 ▷ 39. Plasmodium PADM01 (Plasm H)  
 ▷ 40. SR0847\_H4EM-correctR.ab1















Local (0)	Name	Description	Path (Import...)	Filename (Im...)	Tree builder	HQ%	Sequence Le...	Post-Trim	%GC	Topology	Molecule Type	# Sequences	% Pairwise ...	% Identical ...	Bin	Act...
AK_P1_FC_MDB_1_2014-08-21 (97)	SR1027_HAEMF_24.ab1	-	K:\Sauvegarde...SR1027_HAEM...	-	-	95.8%	455	455	27.3%	linear	DNA	-	-	-	High	-
IB_ZF_Cross plasm (14)	SR1091_HAEMF_25.ab1	-	K:\Sauvegarde...SR1091_HAEM...	-	-	93.8%	455	455	27.3%	linear	DNA	-	-	-	High	-
IB_ZF_PA_1sur2 (94)	SR1134_HAEMF_26.ab1	-	K:\Sauvegarde...SR1134_HAEM...	-	-	94.1%	455	455	27.3%	linear	DNA	-	-	-	High	-
IB_ZF_PA_2sur2 (97)	SR1146_HAEMF_46.ab1	-	K:\Sauvegarde...SR1146_HAEM...	-	-	95.4%	455	455	27.3%	linear	DNA	-	-	-	High	-
IB_ZF_PB (97)	Align SR209 with LOXPOR01	Alignment of 2 sequences: SR209_HAEMF_47.ab1, Parahaemophilus LOXPOR01	-	-	-	-	-	-	27.6%	linear	-	2	100.0%	100.0%	-	-
IB_ZF_PC (97)	Align SR39 with saouches ref	Alignment of 3 sequences: SR99_HAEMF_1.ab1, Plasmodium ICTCA101, Parahaemophilus LOXPOR01	-	-	-	-	-	-	26.8%	linear	-	3	92.4%	88.5%	-	-
IB_ZF_PD_1sur2 (96)	Align SR845 & SR847	Alignment of 3 sequences: SR0845_HAEMF-correctedR.ab1, SR0847_HAEMF-correctedR.ab1, Parahaemophilus LOXPOR01	-	-	-	-	-	-	27.3%	linear	-	3	90.4%	85.6%	-	-
IB_ZF_PD_2sur2 (96)	Align SR210 with LOXPOR01	Alignment of 8 sequences: SR0210_HAEMF_27.ab1, Parahaemophilus LOXPOR01, Plasmodium ICTCA101, Plasmodium PADM11 (Plasm H)	-	-	-	-	-	-	27.0%	linear	-	4	91.5%	86.0%	-	-
IB_ZF_PE_1sur2 (96)	Align SR216 to SR317 with LOXPOR01	Alignment of 7 sequences: SR0216_HAEMF_28.ab1, SR0235_HAEMF_10.ab1, SR0261_HAEMF_11.ab1, SR0310_HAEMF_29.ab1, SR0312_HAEMF_30.ab1, SR0...	-	-	-	-	-	-	27.3%	linear	-	7	100.0%	100.0%	-	-
IB_ZF_PE_2sur2 (96)	Align SR340 to SR401 with LOXPOR01	Alignment of 7 sequences: SR0340_HAEMF_32.ab1, SR0352_HAEMF_33.ab1, SR0373_HAEMF_12.ab1, SR0397_HAEMF_34.ab1, SR0399_HAEMF_35.ab1, SR0...	-	-	-	-	-	-	27.0%	linear	-	7	94.7%	88.7%	-	-
IB_ZF_PF_1sur2 (96)	Align SR785 to SR1146 with LOXPOR01	Alignment of 7 sequences: SR0785_HAEMF_34.ab1, SR1021_HAEMF_23.ab1, SR1027_HAEMF_24.ab1, SR1091_HAEMF_25.ab1, SR1134_HAEMF_26.ab1, SR1...	-	-	-	-	-	-	27.3%	linear	-	7	100.0%	100.0%	-	-
IB_ZF_PF_2sur2 (96)	Align SR412 to SR474 with LOXPOR01	Alignment of 9 sequences: SR0412_HAEMF_36.ab1, SR0429_HAEMF_37.ab1, SR0492_HAEMF_38.ab1, SR0498_HAEMF_13.ab1, SR0498_HAEMF_14.ab1, SR0...	-	-	-	-	-	-	27.3%	linear	-	9	100.0%	100.0%	-	-
IB_ZF_PG_1sur3 (96)	Align SR544 to SR765 with LOXPOR01	Alignment of 9 sequences: SR0544_HAEMF_17.ab1, SR0547_HAEMF_18.ab1, SR0574_HAEMF_19.ab1, SR0687_HAEMF_20.ab1, SR0710_HAEMF_21.ab1, SR0...	-	-	-	-	-	-	27.2%	linear	-	9	100.0%	99.8%	-	-
IB_ZF_PG_2sur3 (96)	Align SR626 to SR631 with LOXPOR01	Alignment of 12 sequences	-	-	-	-	-	-	27.3%	linear	-	12	100.0%	100.0%	-	-
IB_ZF_PG_3sur3 (96)	Align SR845 & SR847 with refs	Alignment of 36 sequences	-	-	-	-	-	-	26.4%	linear	-	26	92.9%	77.0%	-	-
IB_ZF_PH_1sur3 (96)	Align 40 seq plasmap F&B	Alignment of 40 sequences	-	-	-	-	-	-	22.1%	linear	-	40	97.2%	81.4%	-	-
IB_ZF_PH_2sur3 (96)	Align SR845 & SR847 with refs tree	Neighbour-joining tree: Align SR845 & SR847 with refs	-	-	Geneious Tree ...	-	-	-	26.4%	linear	-	26	92.9%	77.0%	-	-

