

Material supplementary 2

The seven new assembled regions lost during *Leishmania major* Friedlin strain genome assembly. The sequence headers include current genome coordinates (1-based) where the new sequences must be inserted in between. Additionally, 100 nt upstream and downstream sequences are provided in red to help to localize the insertion place (these sequences are not part of the new assembled regions). CDS within the new assembled region are indicated in bold.

>H150:LmjF.15:598566-601599

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