



3 **Supplementary figure 1** – Complete genome synteny analysis containing
 4 different *Marseilleviridae* isolates representing each lineage. Each line
 5 represents the sequence of a different virus, which are identified in the legend
 6 on the left. The letters A, B, C, D and E indicate the respective phylogenetic
 7 lineages of each analyzed virus. Blocks of the same color indicate similar
 8 regions between sequences. The areas without any colored blocks represent
 9 regions exclusive to that virus, that is, which do not show similarity with the
 10 other viruses used in the analysis. Note: As they have a circular topology, the
 11 sequences were adjusted to start from the main capsid protein (MCP) aiming to
 12 facilitate interpretation of this figure. *Marseillevirus marseillevirus* was the
 13 sequence used as the reference genome.

| Lineage | Virus | Aragorn | | |
|-----------|-------------------|-------------------------------------|------------------------------|--|
| | | Allowing intron | Not allowing intron | tRNA scan SE |
| Lineage A | MsV cajuinensis | tRNA-Gln (CTG) | - | - |
| | Tokyovirus | tRNA-His(GTG), tRNA-Leu(TAA) | tRNA-His(GTG), tRNA-Leu(TAA) | tRNA-His(GTG), tRNA-Leu (TAA), tRNA-Tyr (GTA) |
| | MsV MsV (T19) | tRNA-Glu(CTC), tRNA-Leu(AAG) | - | - |
| | Cannes8 virus | - | - | - |
| | MsV Shanghai | - | - | - |
| | Melbourne virus | tRNA-Glu(CTC) | - | - |
| | Kurlavirus | - | - | - |
| Lineage B | Lausannevirus | - | - | - |
| | Noumeavirus | - | - | - |
| | Port-miou virus | - | - | - |
| Lineage C | Insectomime virus | tRNA-Ile(TAT) | - | - |
| | Tunisvirus | tRNA-Ile(TAT) | - | - |
| Lineage D | Brazilian Msv | - | - | - |
| Lineage E | Golden Msv | tRNA-Lys(TTT), tRNA-Ala(GGC) | - | - |

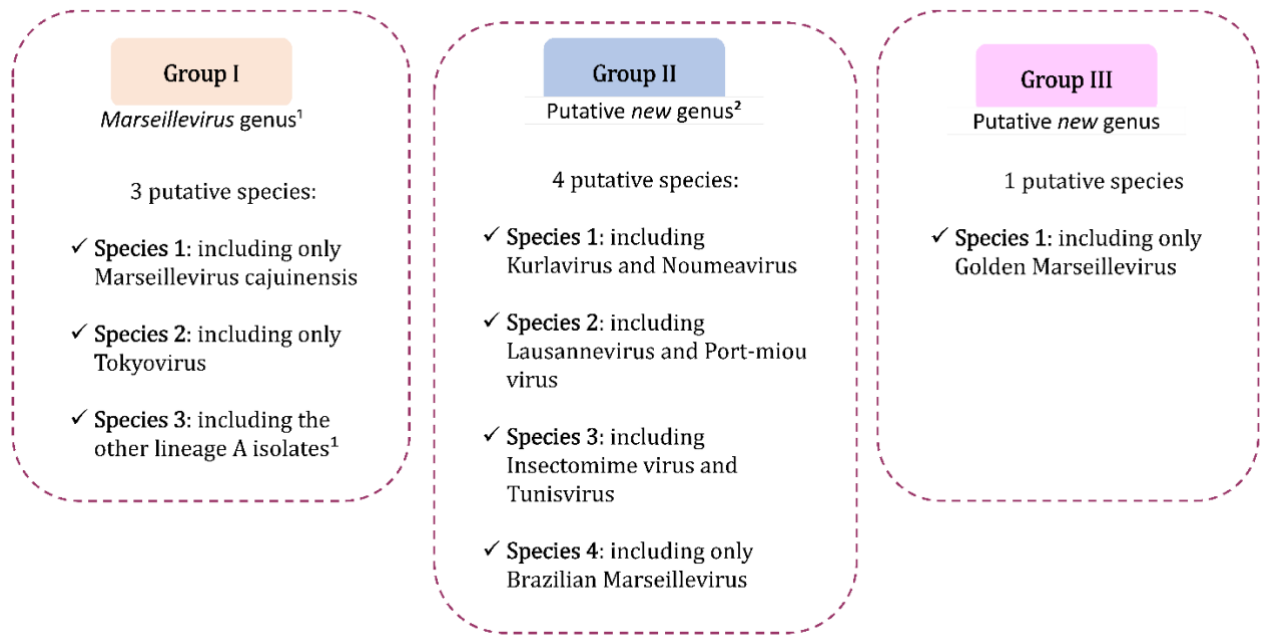
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17 **Supplementary figure 2** - List of transfer RNAs (tRNA) detected among
18 viruses of the five classical *Marseilleviridae* lineages. tRNAs labeled in bold are
19 those that, to our knowledge, have not yet been described previously. MsVs:
20 Marseillevirus.

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24 **Supplementary figure 3** – Current and proposed organization of
 25 *Marseilleviridae* in three genera and eight species suggest by Relative
 26 Evolutionary Distance and Average Amino acid/Nucleotide Identities.

27 Notes: ¹ *Marseillevirus* genus is already an official taxon, as well as one of the
 28 proposed species (species 3). ² the second genus was recently proposed by the
 29 ICTV subcommittee (*Losanna* genus), as well as two of the four proposed
 30 species (species 2 and 3). They are under publishing. In exception to the notes
 31 mentioned before, the other genus and species proposed represent only a
 32 suggestion based on the analyses from this work and was not officially analyzed
 33 or recognized by the ICTV.

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