* There were queries on the low % ID of the Zot and CoaB proteins used to compare against the new taxa.

In the table, each newly identified species is highlighted in bold and assigned a specific color, with members of the same genus sharing the same color. Phages included for comparison were selected based on their closest phylogenetic relationship to the newly defined taxa, and this information has been added to the table legends. The number of related phages varies depending on the availability of closely related genomes. The low percentage identity observed in the Zot and CoaB proteins further supports the designation of these phages as novel species and representatives of a new genus, in line with current criteria for species and genus demarcation. Additional explanations have been incorporated into the text.

* Repetition of phages used for comparisons within the tables, were these the closest relatives to the new taxa?

Yes, the phages listed multiple times represent the closest known relatives of the analyzed taxa. Their repeated appearance results from conducting separate comparisons for each phage strain or group of closely related strains. This strategy was employed to avoid constructing overly large and complex tables involving all analyzed taxa.

* Provide a more extensive/complete phylogenetic tree comprising all new genera and some existing genera to enable comparisons. Alternatively it could be explained why this was not achievable in the text.

A phylogenetic tree based on the amino acid sequences of the assembly proteins is provided. It includes representatives of all newly proposed genera, along with representative members of existing genera for comparison. The tree places the defined species and genera into a broader phylogenetic context and supports the conclusions drawn from the comparative analyses.