

|                                     |   | 1     | 2     | 3     | 4     | 5     | 6     | 7    |
|-------------------------------------|---|-------|-------|-------|-------|-------|-------|------|
| 06-08_Blauer_Limberger_GVF          | 1 |       | 6601  | 6966  | 6074  | 6094  | 6094  | 6089 |
| 33-05_Tempranillo_GVF               | 2 | 87,55 |       | 7063  | 5726  | 5733  | 5735  | 5739 |
| 45-07_Red_Globe_GVF                 | 3 | 92,39 | 93,76 |       | 6057  | 6060  | 6068  | 6070 |
| 11-05_Delight_GVF                   | 4 | 80,56 | 75,94 | 80,33 |       | 6896  | 6882  | 6886 |
| 14-14_Gamay_Hatif_des_Vosges_GVF    | 5 | 80,82 | 76,03 | 80,37 | 91,47 |       | 7434  | 7457 |
| 22-10_Muscadelle_GVF                | 6 | 80,82 | 76,06 | 80,48 | 91,29 | 98,61 |       | 7487 |
| 24-10_Noir_Hatiff_de_Marseilles_GVF | 7 | 80,76 | 76,18 | 80,58 | 91,34 | 98,91 | 99,31 |      |

Figure S10: Average nucleotide identity comparisons between the complete/near complete genomes of grapevine virus F variants from this study. The x-axis values express average nucleotide variability between variants as a percentage, while the y-axis values present the total number of nucleotide differences between each variant.