Table S2

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Network1 | Participants2 | Network measure | Phylogeny measure | Tau c correlation coefficient | p-value3 | Mean4 | SD5 |
| Baseline |  |  |  |  |  |  |  |
|  | *HCV infected* | *geodesic distance* | *MCL distance* | *-0.016* | *0.021* | *0.000* | *0.008* |
|  | HCV infected excluding genotype 6 | geodesic distance | MCL distance | -0.0060 | 0.448 | 0.000 | 0.044 |
| Flattened |  |  |  |  |  |  |  |
|  | *HCV infected* | *geodesic distance* | *MCL distance* | *-0.046* | *0.005* | *-0.000* | *0.019* |
|  | HCV infected excluding genotype 6 | geodesic distance | MCL distance | -0.028 | 0.124 | -0.001 | 0.023 |