**Table S3. Significant predictors of viral structural gene substitution rates** **using** **one rate per viral species**. For each multiple regression analysis, the overall adjusted *R*2 () of the model is given along with significant predictor variables (*P*<0.01) and their standardized coefficients (β) with 95% confidence intervals (CIs). In the first regression, the base levels were epithelial target cells, fecal-oral/respiratory transmission route, acute/persistent infection, species-specific host range, and dsRNA genome architecture. In the second regression, the base levels were neural target cells, bites/scratches transmission route, persistent infection, order-specific host range, and (-)ssRNA genome architecture. In the third regression, the base levels were leukocyte target cells, respiratory/vertical transmission route, acute infection, family-specific host range, and (+)ssRNA genome architecture.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | Predictor | β (95% CI) | Significance |
| 1 | 0.65 | Neurons | -0.76 (-1.14, -0.38) | <0.0001 |
|
|
| 2 | 0.65 | Epithelial cells | 1.01 (0.50, 1.51) | <0.0001 |
| Leukocytes | 0.51 (0.14, 0.89) | 0.009 |
| 3 | 0.65 | Neurons | -0.39 (-0.10, -0.68) | 0.009 |
| Epithelial cells | 0.49 (0.18, 0.69) | 0.009 |