

	1	2	3	4	5	6	7	8	9
1 NP_001358344.1_Homo_sapiens									
2 XP_023104564.1_Felis_catus	0.206								
3 NP_001158732.1_Canis_lupus_familiaris	0.265	0.049							
4 XP_002719891.1_Oryctolagus_cuniculus	0.207	0.098	0.109						
5 XP_004597549.2_Ochotona_princeps	0.209	0.204	0.224	0.099					
6 XP_003503283.1_Cricetulus_griseus	0.103	0.263	0.289	0.154	0.155				
7 XP_005074266.1_Mesocricetus_auratus	0.103	0.263	0.289	0.154	0.155	0			
8 NP_081562.2_Mus_musculus	0.549	0.639	0.695	0.494	0.53	0.433	0.433		
9 NP_001012006.1_Rattus_norvegicus	0.494	0.615	0.669	0.473	0.509	0.336	0.336	0.242	
10 NP_001297119.1_Mustela_putorius_furo	0.392	0.154	0.103	0.227	0.315	0.424	0.424	0.765	0.801

Estimates of Evolutionary Divergence between Sequences. Only 22 residues corresponding to the sites of contact between SARS-CoV-2 RBD and ACE2 were considered. The number of amino acid substitutions per site from between sequences are shown. Analyses were conducted using the JTT matrix-based model. The rate variation among sites was modeled with a gamma distribution (shape parameter = 5).