

Adebali, O.; Bircan, A.; Circi, D.; Islek, B.; Kilinc, Z.; Selcuk, B. & Turhan, B. (2020), 'Phylogenetic Analysis of SARS-CoV-2 Genomes in Turkey', *bioRxiv*, 2020.05.15.095794.

Ae, C.; Parra, B.; Tapia, P.; Acevedo, A.; Lagos, J.; Andrade, W.; Arata, L.; Leal, G.; Barra, G.; Tambley, C.; Tognarelli, J.; Bustos, P.; Ulloa, S.; Fasce, R. & Fernández, J. (2020), 'Phylogenetic analysis of the first four SARS-CoV-2 cases in Chile.', *Journal of Medical Virology*.

Alexander, M. R.; Schoeder, C. T.; Brown, J. A.; Smart, C. D.; Moth, C. W.; Wikswa, J. P.; Capra, J. A.; Meiler, J.; Chen, W. & Madhur, M. S. (2020), 'Which animals are at risk? Predicting species susceptibility to Covid-19', *bioRxiv*, 2020.07.09.194563.

Alm, E.; Broberg, E. K.; Connor, T.; Hodcroft, E. B.; Komissarov, A. B.; Maurer-Stroh, S.; Melidou, A.; Neher, R. A.; O'Toole, Á.; Pereyaslov, D.; Group, T. W. E. R. s. l. & EpiCoV, G. I. S. A. I. D. (2020), 'Geographical and temporal distribution of SARS-CoV-2 clades in the WHO European Region, January to June 2020', *Eurosurveillance* **25**(32), 2001410.

Andres, C.; Garcia-Cehic, D.; Gregori, J.; Pinana, M.; Rodriguez-Frias, F.; Guerrero, M.; Esperalba, J.; Rando, A.; Gotteris, L.; Codina, M. G.; Quer, S.; Martin, M. C.; Campins, M.; Ferrer, R.; Almirante, B.; Esteban, J. I.; Pumarola, T.; Anton, A. & Quer, J. (2020), 'Naturally occurring SARS-CoV-2 gene deletions close to the spike S1/S2 cleavage site in the viral quasispecies of COVID19 patients', *bioRxiv*, 2020.06.03.129585.

Andres, C.; Garcia-Cehic, D.; Gregori, J.; Piñana, M.; Rodriguez-Frias, F.; Guerrero-Murillo, M.; Esperalba, J.; Rando, A.; Gotteris, L.; Codina, M. G.; Quer, S.; Martín, M. C.; Campins, M.; Ferrer, R.; Almirante, B.; Esteban, J. I.; Pumarola, T.; Antón, A. & Quer, J. (2020), 'Naturally occurring SARS-CoV-2 gene deletions close to the spike S1/S2 cleavage site in the viral quasispecies of COVID19 patients', *Emerging Microbes & Infections* **0**(ja), 1--48.

Anwar, A. M. & Khodary, S. M. (2020), 'Insights into The Codon Usage Bias of 13 Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Isolates from Different Geo-locations', *bioRxiv*, 2020.04.01.019463.

Arévalo, S. J.; Sifuentes, D. Z.; Robles, C. H.; Bianchi, G. L.; Chávez, A. C.; Casas, R. G.-S.; Uceda-Campos, G. & Chavarría, R. P. (2020), 'Global Geographic and Temporal Analysis of SARS-CoV-2 Haplotypes Normalized by COVID-19 Cases during the First Seven Months of the Pandemic', *bioRxiv*, 2020.07.12.199414.

Artesi, M.; Bontems, S.; Gobbels, P.; Franckh, M.; Boreux, R.; Meex, C.; Melin, P.; Hayette, M.-P.; Bours, V. & Durkin, K. (2020), 'Failure of the cobas® SARS-CoV-2 (Roche) E-gene assay is associated with a C-to-T transition at position 26340 of the SARS-CoV-2 genome', *medRxiv*, 2020.04.28.20083337.

Awoyelu, E. H.; Oladipo, E. K.; Adetuyi, B. O.; Senbadejo, T. Y.; Oyawoye, O. M. & Oloke, J. K. (2020), 'Phylogenetic analysis of SARS-CoV-2 in Nigeria', *New Microbes and New Infections* **36**, 100717.

Ayub, M. I. (2020), 'Reporting Two SARS-CoV-2 Strains Based on A Unique Trinucleotide-Bloc Mutation and Their Potential Pathogenic Difference', .

Badaoui, B.; Sadki, K.; Talbi, C.; Tazi, L. & Salah, D. (2020), 'Genetic Diversity and Genomic Epidemiology of SARS-COV-2 in Morocco', *bioRxiv*, 2020.06.23.165902.

Bai, Y.; Jiang, D.; Lon, J. R.; Chen, X.; Hu, M.; Lin, S.; Chen, Z.; Wang, X.; Meng, Y. & Du, H. (2020), 'Evolution and molecular characteristics of SARS-CoV-2 genome', *bioRxiv*, 2020.04.24.058933.

Baker, D. J.; Kay, G. L.; Aydin, A.; Le-Viet, T.; Rudder, S.; Tedim, A. P.; Kolyva, A.; Diaz, M.; Martins, L. d. O.; Alikhan, N.-F.; Meadows, L.; Bell, A.; Gutierrez, A. V.; Trotter, A. J.; Thomson, N. M.; Gilroy, R.; Griffith, L.; Adriaenssens, E. M.; Stanley, R.; Charles, I. G.; Elumogo, N.; Wain, J.; Prakash, R.; Meader, E.; Mather, A. E.; Webber, M. A.; Dervisevic, S.; Page, A. J. & O'Grady, J. (2020), 'CoronaHiT: large scale multiplexing of SARS-CoV-2 genomes using Nanopore sequencing', *bioRxiv*, 2020.06.24.162156.

Bal, A.; Destras, G.; Gaymard, A.; Bouscambert-Duchamp, M.; Valette, M.; Escuret, V.; Frobert, E.; Billaud, G.; Trouillet-Assant, S.; Cheynet, V.; Brengel-Pesce, K.; Morfin, F.; Lina, B. & Josset, L. (2020), 'Molecular characterization of SARS-CoV-2 in the first COVID-19 cluster in France reveals an amino acid deletion in nsp2 (Asp268del)', *Clinical Microbiology and Infection*.

Banerjee, A.; Doxey, A. C.; Tremblay, B. J.-M.; Mansfield, M. J.; Subudhi, S.; Hirota, J. A.; Miller, M. S.; McArthur, A. G.; Mubareka, S. & Mossman, K. (2020), 'Predicting the recombination potential of severe acute respiratory syndrome coronavirus 2 and Middle East respiratory syndrome coronavirus', *Journal of General Virology* (**published online**).

Banerjee, R.; Basak, K.; Ghosh, A.; Rajachandran, V.; Sureka, K.; Ganguly, D. & Chattopadhyay, S. (2020), 'Spike protein mutational landscape in India: Could Mullers ratchet be a future game-changer for COVID-19?', *bioRxiv*, 2020.08.18.255570.

Banerjee, S.; Seal, S.; Dey, R.; Mondal, K. K. & Bhattacharjee, P. (2020), 'Mutational spectra of SARS-CoV-2 orf1ab polyprotein and Signature mutations in the United States of America', *bioRxiv*, 2020.05.01.071654.

Banu, S.; Jolly, B.; Mukherjee, P.; Singh, P.; Khan, S.; Zaveri, L.; Shambhavi, S.; Gaur, N.; Mishra, R. K.; Scaria, V. & Sowpati, D. T. (2020), 'A distinct phylogenetic cluster of Indian SARS-CoV-2 isolates', *bioRxiv*, 2020.05.31.126136.

Bartolini, B.; Rueca, M.; Gruber, C. E. M.; Messina, F.; Carletti, F.; Giombini, E.; Lalle, E.; Bordi, L.; Matusali, G.; Colavita, F.; Castilletti, C.; Vairo, F.; Ippolito, G.;

Capobianchi, M. R. & Caro, A. D. (2020), 'Early Release - SARS-CoV-2 Phylogenetic Analysis, Lazio Region, Italy, February–March 2020 - Volume 26, Number 8—August 2020 - Emerging Infectious Diseases journal - CDC', **26**(8), 1842-1845.

Bartoszewski, R.; Dabrowski, M.; Jakiela, B.; Matalon, S.; Harrod, K. S.; Sanak, M. & Collawn, J. F. (2020), 'SARS-CoV-2 may regulate cellular responses through depletion of specific host miRNAs', *American Journal of Physiology-Lung Cellular and Molecular Physiology* **319**(3), L444--L455.

Bauer, D. C.; Tay, A. P.; Wilson, L. O. W.; Reti, D.; Hosking, C.; McAuley, A. J.; Pharo, E.; Todd, S.; Stevens, V.; Neave, M. J.; Tachedjian, M.; Drew, T. W. & Vasan, S. S. (2020), 'Supporting pandemic response using genomics and bioinformatics: a case study on the emergent SARS-CoV-2 outbreak', *Transboundary and Emerging Diseases* **n/a**(n/a).

Becker, D.; Albery, G. F.; Sjodin, A. R.; Poisot, T.; Dallas, T.; Eskew, E. A.; Farrell, M. J.; Guth, S.; Han, B. A.; Simmons, N. B. & Carlson, C. J. (2020), 'Predicting wildlife hosts of betacoronaviruses for SARS-CoV-2 sampling prioritization', *bioRxiv*, 2020.05.22.111344.

Bedford, T. (2020), 'Twitter Thread by @trvr: We now have enough #SARSCoV2 genomic data from different states to make some broad conclusions about how the #COVID19 epidemic has unfolded...', Technical report, Fred Hutchinson Cancer Research Center, S0118.

Bedford, T.; Greninger, A. L.; Roychoudhury, P.; Starita, L. M.; Famulare, M.; Huang, M.-L.; Nalla, A.; Pepper, G.; Reinhardt, A.; Xie, H.; Shrestha, L.; Nguyen, T. N.; Adler, A.; Brandstetter, E.; Cho, S.; Giroux, D.; Han, P. D.; Fay, K.; Frazar, C. D.; Ilcisin, M.; Lacombe, K.; Lee, J.; Kiavand, A.; Richardson, M.; Sibley, T. R.; Truong, M.; Wolf, C. R.; Nickerson, D. A.; Rieder, M. J.; Englund, J. A.; Investigators, t. S. F. S.; Hadfield, J.; Hodcroft, E. B.; Huddleston, J.; Moncla, L. H.; Müller, N. F.; Neher, R. A.; Deng, X.; Gu, W.; Federman, S.; Chiu, C.; Duchin, J.; Gautom, R.; Melly, G.; Hiatt, B.; Dykema, P.; Lindquist, S.; Queen, K.; Tao, Y.; Uehara, A.; Tong, S.; MacCannell, D.; Armstrong, G. L.; Baird, G. S.; Chu, H. Y. & Jerome, K. R. (2020), 'Cryptic transmission of SARS-CoV-2 in Washington State', *medRxiv*, 2020.04.02.20051417.

Benedetti, F.; Snyder, G. A.; Giovanetti, M.; Angeletti, S.; Gallo, R. C.; Ciccozzi, M. & Zella, D. (2020), 'Emerging of a SARS-CoV-2 viral strain with a deletion in nsp1', *Journal of Translational Medicine* **18**(1), 329.

Benvenuto, D.; Angeletti, S.; Giovanetti, M.; Bianchi, M.; Pascarella, S.; Cauda, R.; Ciccozzi, M. & Cassone, A. (2020), 'Evolutionary analysis of SARS-CoV-2: how mutation of Non-Structural Protein 6 (NSP6) could affect viral autophagy', *The Journal of Infection* **81**(1), e24--e27.

Benvenuto, D.; Demir, A. B.; Giovanetti, M.; Bianchi, M.; Angeletti, S.; Pascarella, S.;

Cauda, R.; Ciccozzi, M. & Cassone, A. (2020), 'Evidence for mutations in SARS-CoV-2 Italian isolates potentially affecting virus transmission', *Journal of Medical Virology* **n/a**(n/a).

Bhadra, S.; Maranhao, A. C. & Ellington, A. (2020), 'One enzyme reverse transcription qPCR using Taq DNA polymerase', *bioRxiv*, 2020.05.27.120238.

Bhattacharyya, C.; Das, C.; Ghosh, A.; Singh, A. K.; Mukherjee, S.; Majumder, P. P.; Basu, A. & Biswas, N. K. (2020), 'Global Spread of SARS-CoV-2 Subtype with Spike Protein Mutation D614G is Shaped by Human Genomic Variations that Regulate Expression of TMPRSS2 and MX1 Genes', *bioRxiv*, 2020.05.04.075911.

Bhojar, R. C.; Jain, A.; Sehgal, P.; Divakar, M. K.; Sharma, D.; Imran, M.; Jolly, B.; Ranjan, G.; Rophina, M.; Sharma, S.; Siwach, S.; Pandhare, K.; Sahoo, S.; Sahoo, M.; Nayak, A.; Mohanty, J. N.; Das, J.; Bhandari, S.; Mathur, S. K.; Kumar, A.; Sahlot, R.; Rojarani, P.; Lakshmi, J. V.; Surekha, A.; Sekhar, P. C.; Mahajan, S.; Masih, S.; Singh, P.; Kumar, V.; Jose, B.; Mahajan, V.; Gupta, V.; Gupta, R.; Arumugam, P.; Singh, A.; Nandy, A.; P.v, R.; Jha, R. M.; Kumari, A.; Gandotra, S.; Rao, V.; Faruq, M.; Kumar, S.; Betsy Reshma, G.; Varma, N. G.; Roy, S. S.; Sengupta, A.; Chattopadhyay, S.; Singhal, K.; Pradhan, S.; Tyagi, N.; Wadhwa, S.; Jha, D.; Naushin, S.; Poojary, M.; Scaria, V. & Sivasubbu, S. (2020), 'High throughput detection and genetic epidemiology of SARS-CoV-2 using COVIDSeq next generation sequencing', *bioRxiv*, 2020.08.10.242677.

Bindayna, K. M. & Crinion, S. (2020), 'Variant analysis of SARS-CoV-2 strains in Middle Eastern countries', *bioRxiv*, 2020.06.18.156810.

Biswas, S.; Saha, S.; Bandyopadhyay, S. & Bhattacharyya, M. (2020), 'Tracing Back the Temporal Change of SARS-Cov-2 with Genomic Signatures', *bioRxiv*, 2020.04.24.057380.

Blomberg, N. & Lauer, K. B. (2020), 'Connecting data, tools and people across Europe: ELIXIR's response to the COVID-19 pandemic', *European journal of human genetics: EJHG* **28**(6), 719--723.

Bluhm, A.; Christandl, M.; Gesmundo, F.; Klausen, F. R.; Mancinska, L.; Steffan, V.; Franca, D. S. & Werner, A. (2020), 'SARS-CoV-2 transmission chains from genetic data: a Danish case study', *bioRxiv*, 2020.05.29.123612.

Böhmer, M. M.; Buchholz, U.; Corman, V. M.; Hoch, M.; Katz, K.; Marosevic, D. V.; Böhm, S.; Woudenberg, T.; Ackermann, N.; Konrad, R.; Eberle, U.; Treis, B.; Dangel, A.; Bengs, K.; Fingerle, V.; Berger, A.; Hörmansdorfer, S.; Ippisch, S.; Wicklein, B.; Grahl, A.; Pörtner, K.; Müller, N.; Zeitlmann, N.; Boender, T. S.; Cai, W.; Reich, A.; Heiden, M. a. d.; Rexroth, U.; Hamouda, O.; Schneider, J.; Veith, T.; Mühlemann, B.; Wölfel, R.; Antwerpen, M.; Walter, M.; Protzer, U.; Liebl, B.; Haas, W.; Sing, A.; Drosten, C. & Zapf, A. (2020), 'Investigation of a COVID-19 outbreak in Germany resulting from a single travel-associated primary case: a case series', *The Lancet Infectious Diseases*

20(8), 920-928.

Bolyen, E.; Dillon, M.; Bokulich, N.; Ladner, J.; Larsen, B.; Hepp, C.; Lemmer, D.; Sahl, J.; Sanchez, A.; Holdgraf, C.; Sewell, C.; Choudhury, A.; Stachurski, J.; McKay, M.; Engelthaler, D.; Worobey, M.; Keim, P. & Caporaso, G. (2020), 'Reproducibly sampling SARS-CoV-2 genomes across time, geography, and viral diversity', *F1000Research*.

Boni, M. F.; Lemey, P.; Jiang, X.; Lam, T. T.-Y.; Perry, B.; Castoe, T.; Rambaut, A. & Robertson, D. L. (2020), 'Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic', *bioRxiv*, 2020.03.30.015008.

Boni, M. F.; Lemey, P.; Jiang, X.; Lam, T. T.-Y.; Perry, B. W.; Castoe, T. A.; Rambaut, A. & Robertson, D. L. (2020), 'Evolutionary origins of the SARS-CoV-2 sarbecovirus lineage responsible for the COVID-19 pandemic', *Nature Microbiology*, <https://doi.org/10.1038/s41564-020-0771-4>.

Boskova, V. & Stadler, T. (2020), 'PIQMEE: Bayesian phylodynamic method for analysis of large datasets with duplicate sequences', *Molecular Biology and Evolution*.

Brainard, J. (2020), 'Scientists are drowning in COVID-19 papers. Can new tools keep them afloat?', *Science AAAS* **368**(6491).

Brintnell, E.; Gupta, M. & Anderson, D. W. (2020), 'Detailed phylogenetic analysis of SARS-CoV-2 reveals latent capacity to bind human ACE2 receptor', *bioRxiv*, 2020.06.22.165787.

Brito, A. (2020), 'Update 3 | 2020.04.14 - Yale SARS-CoV-2 Genome Surveillance Initiative', *GitHub*, S0036.

Cagliani, R.; Forni, D.; Clerici, M. & Sironi, M. (2020), 'Computational inference of selection underlying the evolution of the novel coronavirus, SARS-CoV-2', *Journal of Virology*.

Cagliani, R.; Forni, D.; Clerici, M. & Sironi, M. (2020), 'Coding potential and sequence conservation of SARS-CoV-2 and related animal viruses', *Infection, Genetics and Evolution* **83**, 104353.

Cai, H. Y.; Cai, K. K. & Li, J. (2020), 'Identification of Novel Missense Mutations in a Large Number of Recent SARS-CoV-2 Genome Sequences', *Preprints* **2020040482**.

Caly, L.; Druce, J.; Roberts, J.; Bond, K.; Tran, T.; KostECKI, R.; Yoga, Y.; Naughton, W.; Taiaroa, G.; Seemann, T.; Mb, S.; Bp, H.; Tm, K.; Sr, L.; Da, W. & Mg, C. (2020), 'Isolation and rapid sharing of the 2019 novel coronavirus (SARS-CoV-2) from the first patient diagnosed with COVID-19 in Australia.', *The Medical Journal of Australia* **212**(10), 459-462.

Canakoglu, A.; Pinoli, P.; Bernasconi, A.; Alfonsi, T.; Melidis, D. P. & Ceri, S. (2020), 'Virusurf: an integrated database to investigate viral sequences', *bioRxiv*, 2020.08.10.244624.

Candido, D. d. S.; Claro, I. M.; Jesus, J. G. d.; Souza, W. M. d.; Moreira, F. R. R.; Dellicour, S.; Mellan, T. A.; Plessis, L. d.; Pereira, R. H. M.; Sales, F. C. d. S.; Manuli, E. R.; Theze, J.; Almeida, L.; Menezes, M. T. d.; Voloch, C. M.; Fumagalli, M. J.; Coletti, T. d. M.; Silva, C. A. M.; Ramundo, M. S.; Amorim, M. R.; Hoeltgebaum, H.; Mishra, S.; Gill, M.; Carvalho, L. M.; Buss, L. F.; Prete, C. A.; Ashworth, J.; Nakaya, H.; Peixoto, P. d. S.; Brady, O. J.; Nicholls, S. M.; Tanuri, A.; Rossi, A. D.; Braga, C. K. V.; Gerber, A. L.; Guimaraes, A. P.; Gaburo, N.; Alencar, C. S.; Ferreira, A. C. d. S.; Lima, C. X.; Levi, J. E.; Granato, C.; Ferreira, G. M.; Francisco, R. d. S.; Granja, F.; Garcia, M. T.; Moretti, M. L.; Perroud, M. W.; Castineiras, T. M. P. P.; Lazari, C. D. S.; Hill, S. C.; Santos, A. A. d. S.; Simeoni, C. L.; Forato, J.; Sposito, A. C.; Schreiber, A. Z.; Santos, M. N. N.; Sa, C. Z.; Souza, R. P.; Moreira, L. C. R.; Teixeira, M. M.; Hubner, J.; Leme, P. A. F.; Moreira, R. G.; Nogueira, M. L.; Ferguson, N.; Costa, S. F.; Proenca-Modena, J. L.; Vasconcelos, A. T.; Bhatt, S.; Lemey, P.; Wu, C.-H.; Rambaut, A.; Loman, N. J.; Aguiar, R. S.; Pybus, O. G.; Sabino, E. C. & Faria, N. R. (2020), 'Evolution and epidemic spread of SARS-CoV-2 in Brazil', *medRxiv*, 2020.06.11.20128249.

Candido, D. S.; Claro, I. M.; Jesus, J. G. d.; Souza, W. M.; Moreira, F. R. R.; Dellicour, S.; Mellan, T. A.; Plessis, L. d.; Pereira, R. H. M.; Sales, F. C. S.; Manuli, E. R.; Thézé, J.; Almeida, L.; Menezes, M. T.; Voloch, C. M.; Fumagalli, M. J.; Coletti, T. M.; Silva, C. A. M. d.; Ramundo, M. S.; Amorim, M. R.; Hoeltgebaum, H. H.; Mishra, S.; Gill, M. S.; Carvalho, L. M.; Buss, L. F.; Prete, C. A.; Ashworth, J.; Nakaya, H. I.; Peixoto, P. S.; Brady, O. J.; Nicholls, S. M.; Tanuri, A.; Rossi, Á. D.; Braga, C. K. V.; Gerber, A. L.; Guimarães, A. P. d. C.; Gaburo, N.; Alencar, C. S.; Ferreira, A. C. S.; Lima, C. X.; Levi, J. E.; Granato, C.; Ferreira, G. M.; Francisco, R. S.; Granja, F.; Garcia, M. T.; Moretti, M. L.; Perroud, M. W.; Castiñeiras, T. M. P. P.; Lazari, C. S.; Hill, S. C.; Santos, A. A. d. S.; Simeoni, C. L.; Forato, J.; Sposito, A. C.; Schreiber, A. Z.; Santos, M. N. N.; Sá, C. Z. d.; Souza, R. P.; Resende-Moreira, L. C.; Teixeira, M. M.; Hubner, J.; Leme, P. A. F.; Moreira, R. G.; Nogueira, M. L.; Brazil-UK Centre for Arbovirus Discovery, D.; Ferguson, N. M.; Costa, S. F.; Proenca-Modena, J. L.; Vasconcelos, A. T. R.; Bhatt, S.; Lemey, P.; Wu, C.-H.; Rambaut, A.; Loman, N. J.; Aguiar, R. S.; Pybus, O. G.; Sabino, E. C. & Faria, N. R. (2020), 'Evolution and epidemic spread of SARS-CoV-2 in Brazil', *Science*.

Cavallo, L. & Oliva, R. (2020), 'D936Y and Other Mutations in the Fusion Core of the SARS-Cov-2 Spike Protein Heptad Repeat 1 Undermine the Post-Fusion Assembly', *bioRxiv*, 2020.06.08.140152.

Ceraolo, C. & Giorgi, F. M. (2020), 'Genomic variance of the 2019-nCoV coronavirus', *Journal of Medical Virology* **92**(5), 522--528.

Chan, A. P.; Choi, Y. & Schork, N. J. (2020), 'Conserved Genomic Terminals of SARS-CoV-2 as Co-evolving Functional Elements and Potential Therapeutic Targets', *bioRxiv*,

2020.07.06.190207.

Chan, Y. A. & Zhan, S. H. (2020), 'Single source of pangolin CoVs with a near identical Spike RBD to SARS-CoV-2', *bioRxiv*, 2020.07.07.184374.

Chand, G. B. & Azad, G. K. (2020), 'Identification of novel mutations in RNA-dependent RNA polymerases of SARS-CoV-2 and their implications', *bioRxiv*, 2020.05.05.079939.

Chavarria-Miró, G.; Anfruns-Estrada, E.; Guix, S.; Paraira, M.; Galofré, B.; Sáanchez, G.; Pintó, R. & Bosch, A. (2020), 'Sentinel surveillance of SARS-CoV-2 in wastewater anticipates the occurrence of COVID-19 cases', *medRxiv*, 2020.06.13.20129627.

Chechetkin, V. R. & Lobzin, V. V. (2020), 'Ribonucleocapsid assembly/packaging signals in the genomes of the coronaviruses SARS-CoV and SARS-CoV-2: detection, comparison and implications for therapeutic targeting', *Journal of Biomolecular Structure and Dynamics* **0**(0), 1--15.

Chen, C.; Li, J.; Di, L.; Jing, Q.; Du, P.; Song, C.; Li, J.; Li, Q.; Cao, Y.; Xie, S.; Wu, A. R.; Zeng, H.; Huang, Y. & Wang, J. (2020), 'MINERVA: A facile strategy for SARS-CoV-2 whole genome deep sequencing of clinical samples', *bioRxiv*, 2020.04.25.060947.

Chen, N.; Li, X.; Li, S.; Xiao, Y.; Ye, M.; Yan, X. & Li, X. (2020), 'How related is SARS-CoV-2 to other coronaviruses?', *Veterinary Record* **186**(15), 496--496.

Chen, W.; Feng, P.; Liu, K.; Wu, M. & Lin, H. (2020), 'Computational Identification of Small Interfering RNA Targets in SARS-CoV-2', *Virologica Sinica*.

Cheng, M. H.; Zhang, S.; Porritt, R. A.; Arditì, M. & Bahar, I. (2020), 'An insertion unique to SARS-CoV-2 exhibits superantigenic character strengthened by recent mutations', *bioRxiv*, 2020.05.21.109272.

Chiara, M.; Horner, D. S.; Gissi, C. & Pesole, G. (2020), 'Comparative genomics provides an operational classification system and reveals early emergence and spatio-temporal', *bioRxiv*, 2020.06.26.172924.

Chiara, M.; Horner, D. S. & Pesole, G. (2020), 'Comparative genomics suggests limited variability and similar evolutionary patterns between major clades of SARS-Cov-2', *bioRxiv*, 2020.03.30.016790.

Chong, Y. M.; Sam, I.-C.; Chong, J.; Bador, M. K.; Ponnampalavanar, S.; Omar, S. F. S.; Kamarulzaman, A.; Munusamy, V.; Wong, C. K.; Jamaluddin, F. H. & Chan, Y. F. (2020), 'SARS-CoV-2 lineage B.6 is the major contributor to transmission in Malaysia', *bioRxiv*, 2020.08.27.269738.

Chrisman, B.; Paskov, K.; Stockham, N.; Tabatabaei, K.; Jung, J.-Y.; Washington, P.; Varma, M.; Sun, M. W.; Maleki, S. & Wall, D. P. (2020), 'Structural Variants in SARS-

CoV-2 Occur at Template-Switching Hotspots', *bioRxiv*, 2020.09.01.278952.

Ciccolella, S.; Denti, L.; Bonizzoni, P.; Vedova, G. D.; Pirola, Y. & Previtali, M. (2020), 'MALVIRUS: an integrated web application for viral variant calling', *bioRxiv*, 2020.05.05.076992.

Cluzel, N.; Lambert, A.; Maday, Y.; Turinici, G. & Danchin, A. (2020), 'Biochemical and mathematical lessons from the evolution of the SARS-CoV-2 virus: paths for novel antiviral warfare', *bioRxiv*, 2020.07.31.230607.

Colavizza, G.; Costas, R.; Traag, V. A.; Eck, N. J. v.; Leeuwen, T. v. & Waltman, L. (2020), 'A scientometric overview of COVID-19', *bioRxiv*, 2020.04.20.046144.

Colson, P.; Lagier, J.-C.; Baudoin, J.-P.; Bou Khalil, J.; La Scola, B. & Raoult, D. (2020), 'Ultrarapid diagnosis, microscope imaging, genome sequencing, and culture isolation of SARS-CoV-2', *European Journal of Clinical Microbiology & Infectious Diseases* **39**(8), 1601--1603.

Comandatore, F.; Chiodi, A.; Gabrieli, P.; Biffignandi, G. B.; Perini, M.; Ramazzotti, M.; Ricagno, S.; Rimoldi, S. G.; Gismondo, M.; Micheli, V.; Bandi, C. & Brillì, M. (2020), 'Identification of variable sites in Sars-CoV-2 and their abundance profiles in time', *bioRxiv*, 2020.04.30.071027.

Comandatore, F.; Chiodi, A.; Gabrieli, P.; Biffignandi, G. B.; Perini, M.; Ricagno, S.; Mascolo, E.; Petazzoni, G.; Ramazzotti, M.; Rimoldi, S. G.; Gismondo, M.; Micheli, V.; Sasserà, D.; Gaiarsa, S.; Bandi, C. & Brillì, M. (2020), 'Insurgence and worldwide diffusion of genomic variants in SARS-CoV-2 genomes', *bioRxiv*, 2020.04.30.071027.

Consortium, C.-19. G. U. (C.-U. (2020), 'COVID-19 Genomics UK (COG-UK) Consortium Report #9 -25th June 2020', online, S0294.

Conway, M. J. (2020), 'Identification of coronavirus sequences in carp cDNA from Wuhan, China', *Journal of Medical Virology* **n/a**(n/a).

Coppée, F.; Lechien, J. R.; Declèves, A. E.; Tafforeau, L. & Saussez, S. (2020), 'Severe acute respiratory syndrome coronavirus 2: virus mutations in specific European populations', *New Microbes and New Infections* **36**, 100696.

Cortey, M.; Li, Y.; Diaz, I.; Clilverd, H.; Darwich, L. & Mateu, E. (2020), 'SARS-CoV-2 amino acid substitutions widely spread in the human population are mainly located in highly conserved segments of the structural proteins', *bioRxiv*, 2020.05.16.099499.

Crits-Christoph, A. (2020), 'Reproducible analyses for rejecting rare genomic inversions in SARS-CoV-2', S0010.

Das, D. & Akkipeddi, V. S. S. N. R. (2020), 'Population genetic analysis of Indian SARS-

CoV-2 isolates reveals a unique phylogenetic cluster', *bioRxiv*, 2020.07.19.197129.

Dash, P.; Turuk, J.; Behera, S. K.; Palo, S. K.; Raghav, S.; Ghosh, A.; Sabat, J.; Rath, S.; Subhadra, S.; Bhattacharya, D.; Kanungo, S.; Kshatri, J.; Mishra, B. k.; Dash, S.; Mahapatra, N.; Parida, A. & Pati, S. (2020), 'Sequence analysis of Indian SARS-CoV-2 isolates shows a stronger interaction of mutated receptor binding domain with ACE2 receptor', *bioRxiv*, 2020.08.28.271601.

Davda, J. N.; Frank, K.; Prakash, S.; Purohit, G.; Vijayashankar, D. P.; Vedagiri, D.; Tallapaka, K. B.; Harshan, K. H.; Siva, A. B.; Mishra, R. K.; Dhawan, J. & Siddiqi, I. (2020), 'An Inexpensive RT-PCR Endpoint Diagnostic Assay for SARS-CoV-2 Using Nested PCR: Direct Assessment of Detection Efficiency of RT-qPCR Tests and Suitability for Surveillance', *bioRxiv*, 2020.06.08.139477.

Day, T.; Gandon, S.; Lion, S. & Otto, S. P. (2020), 'On the evolutionary epidemiology of SARS-CoV-2', *Current Biology* **30**(15), R849--R857.

Dearlove, B.; Lewitus, E.; Bai, H.; Li, Y.; Reeves, D. B.; Joyce, M. G.; Scott, P. T.; Amare, M. F.; Vasan, S.; Michael, N. L.; Modjarrad, K. & Rolland, M. (2020), 'A SARS-CoV-2 vaccine candidate would likely match all currently circulating strains', *bioRxiv*, 2020.04.27.064774.

Dellicour, S.; Durkin, K.; Hong, S. L.; Vanmechelen, B.; Martí-Carreras, J.; Gill, M. S.; Meex, C.; Bontems, S.; André, E.; Gilbert, M.; Walker, C.; Maio, N. D.; Hadfield, J.; Hayette, M.-P.; Bours, V.; Wawina-Bokalanga, T.; Artesi, M.; Baele, G. & Maes, P. (2020), 'A phylodynamic workflow to rapidly gain insights into the dispersal history and dynamics of SARS-CoV-2 lineages', *bioRxiv*, 2020.05.05.078758.

DeMaio, N.; Walker, C.; Borges, R.; Weilguny, L.; Slodkowitz, G. & Goldman, N. (2020), 'Issues with SARS-CoV-2 sequencing data', *Virological*, S0085.

Deng, X.; Achari, A.; Federman, S.; Yu, G.; Somasekar, S.; Bártolo, I.; Yagi, S.; Mbala-Kingebeni, P.; Kapetshi, J.; Ahuka-Mundeke, S.; Muyembe-Tamfum, J.-J.; Ahmed, A. A.; Ganesh, V.; Tamhankar, M.; Patterson, J. L.; Ndembi, N.; Mbanya, D.; Kaptue, L.; McArthur, C.; Muñoz-Medina, J. E.; Gonzalez-Bonilla, C. R.; López, S.; Arias, C. F.; Arevalo, S.; Miller, S.; Stone, M.; Busch, M.; Hsieh, K.; Messenger, S.; Wadford, D. A.; Rodgers, M.; Cloherty, G.; Faria, N. R.; Thézé, J.; Pybus, O. G.; Neto, Z.; Morais, J.; Taveira, N.; R Hackett, J. & Chiu, C. Y. (2020), 'Metagenomic sequencing with spiked primer enrichment for viral diagnostics and genomic surveillance', *Nature Microbiology* **5**(3), 443--454.

Deng, X.; Gu, W.; Federman, S.; Plessis, L. D.; Pybus, O.; Faria, N.; Wang, C.; Yu, G.; Pan, C.-Y.; Guevara, H.; Sotomayor-Gonzalez, A.; Zorn, K.; Gopez, A.; Servellita, V.; Hsu, E.; Miller, S.; Bedford, T.; Greninger, A.; Roychoudhury, P.; Famulare, M.; Chu, H. Y.; Shendure, J.; Starita, L.; Anderson, C.; Gangavarapu, K.; Zeller, M.; Spencer, E.; Andersen, K.; MacCannell, D.; Tong, S.; Armstrong, G.; Paden, C.; Li, Y.; Zhang, Y.;

Morrow, S.; Willis, M.; Matyas, B.; Mase, S.; Kasirye, O.; Park, M.; Chan, C.; Yu, A.; Chai, S.; Villarino, E.; Bonin, B.; Wadford, D. & Chiu, C. Y. (2020), 'A Genomic Survey of SARS-CoV-2 Reveals Multiple Introductions into Northern California without a Predominant Lineage', *medRxiv*, 2020.03.27.20044925.

Deng, X.; Gu, W.; Federman, S.; Plessis, L. d.; Pybus, O. G.; Faria, N.; Wang, C.; Yu, G.; Bushnell, B.; Pan, C.-Y.; Guevara, H.; Sotomayor-Gonzalez, A.; Zorn, K.; Gopez, A.; Servellita, V.; Hsu, E.; Miller, S.; Bedford, T.; Greninger, A. L.; Roychoudhury, P.; Starita, L. M.; Famulare, M.; Chu, H. Y.; Shendure, J.; Jerome, K. R.; Anderson, C.; Gangavarapu, K.; Zeller, M.; Spencer, E.; Andersen, K. G.; MacCannell, D.; Paden, C. R.; Li, Y.; Zhang, J.; Tong, S.; Armstrong, G.; Morrow, S.; Willis, M.; Matyas, B. T.; Mase, S.; Kasirye, O.; Park, M.; Masinde, G.; Chan, C.; Yu, A. T.; Chai, S. J.; Villarino, E.; Bonin, B.; Wadford, D. A. & Chiu, C. Y. (2020), 'Genomic surveillance reveals multiple introductions of SARS-CoV-2 into Northern California', *Science* **369**(6503), 582-587.

Devaux, C. A.; Pinault, L.; Osman, I. O. & Raoult, D. (2020), 'Can ACE2 receptor polymorphism predicts species susceptibility to SARS-CoV-2?', *Research Square* **rs-25753**.

Didelot, X.; Siveroni, I. & Volz, E. M. (2020), 'Additive uncorrelated relaxed clock models for the dating of genomic epidemiology phylogenies', *Molecular Biology and Evolution*.

Digard, P.; Lee, H.-M.; Sharp, C.; Grey, F. & Gaunt, E. R. (2020), 'Intra-genome variability in the dinucleotide composition of SARS-CoV-2', *bioRxiv*, 2020.05.08.083816.

Dilucca, M.; Forcelloni, S.; Giansanti, A.; Georgakilas, A. & Pavlopoulou, A. (2020), 'Temporal evolution and adaptation of SARS-COV 2 codon usage', *bioRxiv*, 2020.05.29.123976.

Doddapaneni, H. V.; Cregeen, S. J.; Sucgang, R.; Meng, Q.; Qing, X.; Avadhanula, V.; Chao, H.; Menon, V.; Nicholson, E.; Henke, D.; Piedra, F.-A.; Rajan, A.; Momin, Z.; Kottapalli, K.; Hoffman, K. L.; Sedlazeck, F. J.; Metcalf, G.; Piedra, P. A.; Muzny, D. M.; Petrosino, J. F. & Gibbs, R. A. (2020), 'Oligonucleotide capture sequencing of the SARS-CoV-2 genome and subgenomic fragments from COVID-19 individuals', *bioRxiv*, 2020.07.27.223495.

van Dorp, L.; Acman, M.; Richard, D.; Shaw, L. P.; Ford, C. E.; Ormond, L.; Owen, C. J.; Pang, J.; Tan, C. C. S.; Boshier, F. A. T.; Ortiz, A. T. & Balloux, F. (2020), 'Emergence of genomic diversity and recurrent mutations in SARS-CoV-2', *Infection, Genetics and Evolution* **83**, 104351.

Dorp, L. v.; Richard, D.; Tan, C. C. S.; Shaw, L. P.; Acman, M. & Balloux, F. (2020), 'No evidence for increased transmissibility from recurrent mutations in SARS-CoV-2',

bioRxiv, 2020.05.21.108506.

Douglas, J.; Mendes, F. K.; Bouckaert, R.; Xie, D.; Jimenez-Silva, C. L.; Swanepoel, C.; Ligt, J. d.; Ren, X.; Storey, M.; Hadfield, J.; Simpson, C. R.; Geoghegan, J. L.; Welch, D. & Drummond, A. J. (2020), 'Phylodynamics reveals the role of human travel and contact tracing in controlling COVID-19 in four island nations', *medRxiv*, 2020.08.04.20168518.

Duchene, S.; Featherstone, L.; Haritopoulou-Sinanidou, M.; Rambaut, A.; Lemey, P. & Baele, G. (2020), 'Temporal signal and the phylodynamic threshold of SARS-CoV-2', *bioRxiv*, 2020.05.04.077735.

Eskier, D.; Karakūlah, G.; Suner, A. & Oktay, Y. (2020), 'RdRp mutations are associated with SARS-CoV-2 genome evolution', *bioRxiv*, 2020.05.20.104885.

Eskier, D.; Suner, A.; Karakūlah, G. & Oktay, Y. (2020), 'Mutation density changes in SARS-CoV-2 are related to the pandemic stage but to a lesser extent in the dominant strain with mutations in spike and RdRp', *bioRxiv*, 2020.06.15.153239.

Eskier, D.; Suner, A.; Oktay, Y. & Karakūlah, G. (2020), 'Mutations of SARS-CoV-2 nsp14 exhibit strong association with increased genome-wide mutation load', *bioRxiv*, 2020.08.12.248732.

Fahmi, M.; Kubota, Y. & Ito, M. (2020), 'Nonstructural proteins NS7b and NS8 are likely to be phylogenetically associated with evolution of 2019-nCoV', *Infection, Genetics and Evolution* **81**, 104272.

Fang, B.; Liu, L.; Yu, X.; Li, X.; Ye, G.; Xu, J.; Zhang, L.; Zhan, F.; Liu, G.; Pan, T.; Shu, Y. & Jiang, Y. (2020), 'Genome-wide data inferring the evolution and population demography of the novel pneumonia coronavirus (SARS-CoV-2)', *bioRxiv*, 2020.03.04.976662.

Fauver, J. R.; Petrone, M. E.; Hodcroft, E. B.; Shioda, K.; Ehrlich, H. Y.; Watts, A. G.; Vogels, C. B. F.; Brito, A. F.; Alpert, T.; Muyombwe, A.; Razeq, J.; Downing, R.; Cheemarla, N. R.; Wyllie, A. L.; Kalinich, C. C.; Ott, I.; Quick, J.; Loman, N. J.; Neugebauer, K. M.; Greninger, A. L.; Jerome, K. R.; Roychoudhury, P.; Xie, H.; Shrestha, L.; Huang, M.-L.; Pitzer, V. E.; Iwasaki, A.; Omer, S. B.; Khan, K.; Bogoch, I.; Martinello, R. A.; Foxman, E. F.; Landry, M.-L.; Neher, R. A.; Ko, A. I. & Grubaugh, N. D. (2020), 'Coast-to-coast spread of SARS-CoV-2 in the United States revealed by genomic epidemiology', *medRxiv*, 2020.03.25.20043828.

Firth, A. E. (2020), 'A putative new SARS-CoV protein, 3a*, encoded in an ORF overlapping ORF3a', *bioRxiv*, 2020.05.12.088088.

Forcelloni, S.; Benedetti, A.; Dilucca, M. & Giansanti, A. (2020), 'Identification of conserved epitopes in SARS-CoV-2 spike and nucleocapsid protein.', *bioRxiv*, 2020.05.14.095133.

Forster, P.; Forster, L.; Renfrew, C. & Forster, M. (2020), 'Phylogenetic network analysis of SARS-CoV-2 genomes', *Proceedings of the National Academy of Sciences of the United States of America*.

Fountain-Jones, N. M.; Appaw, R. C.; Carver, S.; Didelot, X.; Volz, E. M. & Charleston, M. (2020), 'Emerging phylogenetic structure of the SARS-CoV-2 pandemic', *bioRxiv*, 2020.05.19.103846.

Freed, N. E.; Vlkova, M.; Faisal, M. B. & Silander, O. K. (2020), 'Rapid and Inexpensive Whole-Genome Sequencing of SARS-CoV2 using 1200 bp Tiled Amplicons and Oxford Nanopore Rapid Barcoding', *bioRxiv*, 2020.05.28.122648.

Fuertes, F. D.; Caballero, M. I.; Monzón, S.; Jiménez, P.; Varona, S.; Cuesta, I.; Zaballos, Á.; Thomson, M. M.; Jiménez, M.; Pérez, J. G.; Pozo, F.; Olmeda, M. P.; Alcamí, J. & Casas, I. (2020), 'Phylodynamics of SARS-CoV-2 transmission in Spain', *bioRxiv*, 2020.04.20.050039.

Gallaher, W. R. (2020), 'A palindromic RNA sequence as a common breakpoint contributor to copy-choice recombination in SARS-COV-2', *Archives of Virology*.

Galson, J. D.; Schaetzle, S.; Bashford-Rogers, R. J. M.; Raybould, M. I. J.; Kovaltsuk, A.; Kilpatrick, G. J.; Minter, R.; Finch, D. K.; Dias, J.; James, L.; Thomas, G.; Lee, W.-Y. J.; Betley, J.; Cavlan, O.; Leech, A.; Deane, C. M.; Seoane, J.; Caldas, C.; Pennington, D.; Pfeffer, P. & Osbourn, J. (2020), 'Deep sequencing of B cell receptor repertoires from COVID-19 patients reveals strong convergent immune signatures', *bioRxiv*, 2020.05.20.106294.

Gambaro, F.; Baidaliuk, A.; Behillil, S.; Donati, F.; Albert, M.; Alexandru, A.; Vanpeene, M.; Bizard, M.; Brisebarre, A.; Barbet, M.; Derrar, F.; Werf, S. v. d.; Enouf, V. & Simon-Loriere, E. (2020), 'Introductions and early spread of SARS-CoV-2 in France', *bioRxiv*, 2020.04.24.059576.

Garcés-Ayala, F.; Araiza-Rodríguez, A.; Mendieta-Condado, E.; Rodríguez-Maldonado, A. P.; Wong-Arámbula, C.; Landa-Flores, M.; del Mazo-López, J. C.; González-Villa, M.; Escobar-Escamilla, N.; Fragoso-Fonseca, D. E.; Esteban-Valencia, M. d. C.; Lloret-Sánchez, L.; Arellano-Suarez, D. S.; Nuñez-García, T. E.; Contreras-González, N. B.; Cruz-Ortiz, N.; Ruiz-López, A.; Fierro-Valdez, M. Á.; Regalado-Santiago, D.; Martínez-Velázquez, N.; Mederos-Michel, M.; Vázquez-Pérez, J.; Martínez-Orozco, J. A.; Becerril-Vargas, E.; Salas, J.; Hernández-Rivas, L.; López-Martínez, I.; Alomía-Zegarra, J. L.; López-Gatell, H.; Barrera-Badillo, G. & Ramírez-González, J. E. (2020), 'Full genome sequence of the first SARS-CoV-2 detected in Mexico', *Archives of Virology* **165**(9), 2095--2098.

Geoghegan, J. L.; Ren, X.; Storey, M.; Hadfield, J.; Jelley, L.; Jefferies, S.; Sherwood, J.; Paine, S.; Huang, S.; Douglas, J.; Mendes, F. K. L.; Sporle, A.; Baker, M. G.; Murdoch,

D. R.; French, N.; Simpson, C. R.; Welch, D.; Drummond, A. J.; Holmes, E. C.; Duchene, S. & Ligt, J. d. (2020), 'Genomic epidemiology reveals transmission patterns and dynamics of SARS-CoV-2 in Aotearoa New Zealand', *medRxiv*, 2020.08.05.20168930.

Ghanchi, N. K.; Masood, K. I.; Nasir, A.; Khan, W.; Abidi, S. H.; Shahid, S.; Mahmood, S. F.; Kanji, A. R.; Razzak, S. A.; Ansar, Z.; Islam, N.; Dharejo, M. B.; Hasan, Z. & Hasan, R. (2020), 'SARS-CoV-2 genome analysis of strains in Pakistan reveals GH, S and L clade strains at the start of the pandemic', *bioRxiv*, 2020.08.04.234153.

Giandhari, J.; Pillay, S.; Wilkinson, E.; Tegally, H.; Sinayskiy, I.; Schuld, M.; Lourenço, J.; Chimukangara, B.; Lessells, R. J.; Moosa, Y.; Gazy, I.; Fish, M.; Singh, L.; Khanyile, K. S.; Fonseca, V.; Giovanetti, M.; Alcantara, L. C. J.; Petruccione, F. & Oliveira, T. d. (2020), 'Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report', *medRxiv*, 2020.05.29.20116376.

Gioacchino, A. D.; Sulc, P.; Komarova, A. V.; Greenbaum, B. D.; Monasson, R. & Cocco, S. (2020), 'The heterogeneous landscape and early evolution of pathogen-associated CpG dinucleotides in SARS-CoV-2', *bioRxiv*, 2020.05.06.074039.

Giorgio, S. D.; Martignano, F.; Torcia, M. G.; Mattiuz, G. & Conticello, S. G. (2020), 'Evidence for host-dependent RNA editing in the transcriptome of SARS-CoV-2', *Science Advances*, eabb5813.

Gohl, D. M.; Garbe, J.; Grady, P.; Daniel, J.; Watson, R. H. B.; Auch, B.; Nelson, A.; Yohe, S. & Beckman, K. B. (2020), 'A Rapid, Cost-Effective Tailed Amplicon Method for Sequencing SARS-CoV-2', *bioRxiv*, 2020.05.11.088724.

Gomez-Carballa, A.; Bello, X.; Pardo-Seco, J.; Martinon-Torres, F. & Salas, A. (2020), 'The impact of super-spreaders in COVID-19: mapping genome variation worldwide', *bioRxiv*, 2020.05.19.097410.

Gomez-Carballa, A.; Bello, X.; Pardo-Seco, J.; Martinon-Torres, F. & Salas, A. (2020), 'Mapping genome variation of SARS-CoV-2 worldwide highlights the impact of COVID-19 super-spreaders', *Genome Research*, gr.266221.120.

Goncalves, R. L.; Leite, T. C. R.; Dias, B. d. P.; Caetano, C. C. d. S.; Souza, A. C. G. d.; Batista, U. d. S.; Barbosa, C. C.; Reyes-Sandoval, A.; Coelho, L. F. L. & Silva, B. d. M. (2020), 'SARS-CoV-2 mutations and where to find them: An in silico perspective of structural changes and antigenicity of the Spike protein', *bioRxiv*, 2020.05.21.108563.

Gong, Y.-N.; Tsao, K.-C.; Hsiao, M.-J.; Huang, C.-G.; Huang, P.-N.; Huang, P.-W.; Lee, K.-M.; Liu, Y.-C.; Yang, S.-L.; Kuo, R.-L.; Chen, K.-F.; Liu, Y.-C.; Huang, S.-Y.; Huang, H.-I.; Liu, M.-T.; Yang, J.-R.; Chiu, C.-H.; Yang, C.-T.; Chen, G.-W. & Shih, S.-R. (2020), 'SARS-CoV-2 genomic surveillance in Taiwan revealed novel ORF8-deletion mutant and clade possibly associated with infections in Middle East', *Emerging Microbes & Infections* **0**(ja), 1--37.

Gong, Y.-N.; Tsao, K.-C.; Hsiao, M.-J.; Huang, C.-G.; Huang, P.-N.; Huang, P.-W.; Lee, K.-M.; Liu, Y.-C.; Yang, S.-L.; Kuo, R.-L.; Liu, M.-T.; Yang, J.-R.; Chiu, C.-H.; Yang, C.-T.; Shih, S.-R. & Chen, G.-W. (2020), 'Sequence variation among SARS-CoV-2 isolates in Taiwan', *bioRxiv*, 2020.03.29.014290.

Gonzalez-Reiche, A. S.; Hernandez, M. M.; Sullivan, M.; Ciferri, B.; Alshammary, H.; Obla, A.; Fabre, S.; Kleiner, G.; Polanco, J.; Khan, Z.; Albuquerque, B.; Guchte, A. v. d.; Dutta, J.; Francoeur, N.; Melo, B. S.; Oussenko, I.; Deikus, G.; Soto, J.; Sridhar, S. H.; Wang, Y.-C.; Twyman, K.; Kasarskis, A.; Altman, D. R.; Smith, M.; Sebra, R.; Aberg, J.; Krammer, F.; Garcia-Sarstre, A.; Luksza, M.; Patel, G.; Paniz-Mondolfi, A.; Gitman, M.; Sordillo, E. M.; Simon, V. & Bakel, H. v. (2020), 'Introductions and early spread of SARS-CoV-2 in the New York City area', *medRxiv*, 2020.04.08.20056929.

Gonzalez-Reiche, A. S.; Hernandez, M. M.; Sullivan, M. J.; Ciferri, B.; Alshammary, H.; Obla, A.; Fabre, S.; Kleiner, G.; Polanco, J.; Khan, Z.; Albuquerque, B.; van de Guchte, A.; Dutta, J.; Francoeur, N.; Melo, B. S.; Oussenko, I.; Deikus, G.; Soto, J.; Sridhar, S. H.; Wang, Y.-C.; Twyman, K.; Kasarskis, A.; Altman, D. R.; Smith, M.; Sebra, R.; Aberg, J.; Krammer, F.; García-Sastre, A.; Luksza, M.; Patel, G.; Paniz-Mondolfi, A.; Gitman, M.; Sordillo, E. M.; Simon, V. & van Bakel, H. (2020), 'Introductions and early spread of SARS-CoV-2 in the New York City area', *Science (New York, N.Y.)* **369**(6501), 297--301.

Gordenin, D. A.; Klimczak, L. J.; Randall, T. A.; Saini, N. & Li, J.-L. (2020), 'Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic', *bioRxiv*, 2020.08.03.234005.

Graudenzi, A.; Maspero, D.; Angaroni, F.; Piazza, R. & Ramazzotti, D. (2020), 'Mutational signatures and heterogeneous host response revealed via large-scale characterization of SARS-CoV-2 genomic diversity', *bioRxiv*, 2020.07.06.189944.

Lab, G. (2020), 'Update 5 | 2020.04.28 (Yale SARS-CoV-2 Genomic Surveillance Initiative)', *CovidTracker*, S0056.

Grubaugh, N. D.; Hanage, W. P. & Rasmussen, A. L. (2020), 'Making Sense of Mutation: What D614G Means for the COVID-19 Pandemic Remains Unclear', *Cell* **182**(4), 794--795.

Gudbjartsson, D. F.; Helgason, A.; Jonsson, H.; Magnusson, O. T.; Melsted, P.; Norddahl, G. L.; Saemundsdottir, J.; Sigurdsson, A.; Sulem, P.; Agustsdottir, A. B.; Eiriksdottir, B.; Fridriksdottir, R.; Gardarsdottir, E. E.; Georgsson, G.; Gretarsdottir, O. S.; Gudmundsson, K. R.; Gunnarsdottir, T. R.; Gylfason, A.; Holm, H.; Jensson, B. O.; Jonasdottir, A.; Jonsson, F.; Josefsdottir, K. S.; Kristjansson, T.; Magnusdottir, D. N.; le Roux, L.; Sigmundsdottir, G.; Sveinbjornsson, G.; Sveinsdottir, K. E.; Sveinsdottir, M.; Thorarensen, E. A.; Thorbjornsson, B.; Löve, A.; Masson, G.; Jonsdottir, I.; Möller, A. D.; Gudnason, T.; Kristinsson, K. G.; Thorsteinsdottir, U. & Stefansson, K. (2020), 'Spread of SARS-CoV-2 in the Icelandic Population', *New England Journal of Medicine*

0(0), null.

Guo, L.; Boocock, J.; Tome, J. M.; Chandrasekaran, S.; Hilt, E. E.; Zhang, Y.; Sathe, L.; Li, X.; Luo, C.; Kosuri, S.; Shendure, J. A.; Arboleda, V. A.; Flint, J.; Eskin, E.; Garner, O. B.; Yang, S.; Bloom, J. S.; Kruglyak, L. & Yin, Y. (2020), 'Rapid cost-effective viral genome sequencing by V-seq', *bioRxiv*, 2020.08.15.252510.

Gupta, R.; Charron, J.; Stenger, C.; Painter, J.; Steward, H.; Cook, T.; Faber, W.; Frisch, A.; Lind, E.; Bauss, J.; Li, X.; Sirpilla, O.; Soehnen, X.; Underwood, A.; Hinds, D.; Morris, M.; Lamb, N.; Carcillo, J.; Bupp, C.; Uhal, B.; Rajasekaran, S. & Prokop, J. W. (2020), 'SARS-CoV2 (COVID-19) Structural/Evolution Dynamicome: Insights into functional evolution and human genomics.', *bioRxiv*, 2020.05.15.098616.

Gussow, A. B.; Auslander, N.; Faure, G.; Wolf, Y. I.; Zhang, F. & Koonin, E. V. (2020), 'Genomic determinants of pathogenicity in SARS-CoV-2 and other human coronaviruses', *Proceedings of the National Academy of Sciences*.

Habib, P.; Alsamman, A. M.; Saber-Ayad, M.; Hassanein, S. E. & Hamwiah, A. (2020), 'COVIDier: A Deep-learning Tool For Coronaviruses Genome And Virulence Proteins Classification', *bioRxiv*, 2020.05.03.075549.

Hadfield, J. (2020), 'RAMPART v1.1.0 released', *ARTIC Real-time Genomic Surveillance*, S0022.

Hahn, G.; Cho, M. H.; Weiss, S. T.; Silverman, E. K. & Lange, C. (2020), 'Unsupervised cluster analysis of SARS-CoV-2 genomes indicates that recent (June 2020) cases in Beijing are from a genetic subgroup that consists of mostly European and South(east) Asian samples, of which the latter are the most recent', *bioRxiv*, 2020.06.22.165936.

Hahn, G.; Lee, S.; Weiss, S. & Lange, C. (2020), 'Unsupervised cluster analysis of SARS-CoV-2 genomes reflects its geographic progression and identifies distinct genetic subgroups of SARS-CoV-2 virus', *bioRxiv*, 2020.05.05.079061.

Hajibabaei, M. & Singer, G. A. C. (2020), 'The Red Queen's Crown: an evolutionary arms race between coronaviruses and mammalian species reflected in positive selection of the ACE2 receptor among many species', *bioRxiv*, 2020.05.14.096131.

Han, G.-Z. (2020), 'Pangolins Harbor SARS-CoV-2-Related Coronaviruses', *Trends in Microbiology* **28**(7), 515--517.

Harilal, D.; Ramaswamy, S.; Loney, T.; Al Suwaidi, H.; Khansaheb, H.; Alkhaja, A.; Varghese, R.; Deesi, Z.; Nowotny, N.; Alsheikh-Ali, A. & Tayoun, A. A. (2020), 'SARS-CoV-2 Whole Genome Amplification and Sequencing for Effective Population-Based Surveillance and Control of Viral Transmission', *Clinical Chemistry*.

Harilal, D.; Ramaswamy, S.; Loney, T.; Alsuwaidi, H.; Khansaheb, H.; AlKhajeh, A.;

Varghese, R.; Deesi, Z.; Nowotny, N.; Alsheikh-Ali, A. & Tayoun, A. A. (2020), 'SARS-CoV-2 Whole Genome Amplification and Sequencing for Effective Population-Based Surveillance and Control of Viral Transmission', *bioRxiv*, 2020.06.06.138339.

Hasan, M. M.; Das, R.; Rasheduzzaman, M.; Hussain, M. H.; Muzahid, N. H.; Salauddin, A.; Rumi, M. H.; Rashid, S. M. M.; Siddiki, A. Z. & Mannan, A. (2020), 'Global and Local Mutations in Bangladeshi SARS-CoV-2 Genomes', *bioRxiv*, 2020.08.25.267658.

Hasan, S.; Khan, S.; Ahsan, G. U. & Hossain, M. M. (2020), 'Genome Analysis of SARS-CoV-2 Isolate from Bangladesh', *bioRxiv*, 2020.05.13.094441.

Hassan, S. S.; Attrish, D.; Ghosh, S.; Choudhury, P. P. & Roy, B. (2020), 'Pathogenetic Perspective of Missense Mutations of ORF3a Protein of SARS-CoV2', *bioRxiv*, 2020.08.04.236653.

Hassan, S. S.; Choudhury, P. P.; Basu, P. & Jana, S. S. (2020), 'Molecular conservation and differential mutation on ORF3a gene in Indian SARS-CoV2 genomes', *Genomics* **112**(5), 3226--3237.

Hassan, S. S.; Moitrab, A.; Rout, R. K.; Choudhury, P. P.; Pramanik, P. & Jana, S. S. (2020), 'On spatial molecular arrangements of SARS-CoV2 genomes of Indian patients', *bioRxiv*, 2020.05.01.071985.

Haveri, A.; Smura, T.; Kuivanen, S.; Österlund, P.; Hepojoki, J.; Ikonen, N.; Pitkäpaasi, M.; Blomqvist, S.; Rönkkö, E.; Kantele, A.; Strandin, T.; Kallio-Kokko, H.; Mannonen, L.; Lappalainen, M.; Broas, M.; Jiang, M.; Siira, L.; Salminen, M.; Puumalainen, T.; Sane, J.; Melin, M.; Vapalahti, O. & Savolainen-Kopra, C. (2020), 'Serological and molecular findings during SARS-CoV-2 infection: the first case study in Finland, January to February 2020', *Eurosurveillance* **25**(11), 2000266.

Hénaff, E.; Najjar, D.; Perez, M.; Flores, R.; Wobken, C.; Mason, C. E. & Slavin, K. (2020), 'Holobiont Urbanism: sampling urban beehives reveals cities' metagenomes', *bioRxiv*, 2020.05.07.075093.

Hilaire, B. G. S.; Durand, N. C.; Mitra, N.; Pulido, S. G.; Mahajan, R.; Blackburn, A.; Colaric, Z. L.; Theisen, J. W. M.; Weisz, D.; Dudchenko, O.; Gnirke, A.; Rao, S.; Kaur, P.; Aiden, E. L. & Aiden, A. P. (2020), 'A rapid, low cost, and highly sensitive SARS-CoV-2 diagnostic based on whole genome sequencing', *bioRxiv*, 2020.04.25.061499.

Hodcroft, E. B.; Hadfield, J.; Neher, R. A. & Bedford, T. (2020), 'Year-letter Genetic Clade Naming for SARS-CoV-2 on Nextstain.org', *Virological*, S0200.

Holland, L. A.; Kaelin, E. A.; Maqsood, R.; Estifanos, B.; Wu, L. I.; Varsani, A.; Halden, R. U.; Hogue, B. G.; Scotch, M. & Lim, E. S. (2020), 'An 81 nucleotide deletion in SARS-CoV-2 ORF7a identified from sentinel surveillance in Arizona (Jan-Mar 2020)', *Journal of Virology*.

Hu, X.; Li, W. & He, Z. (2020), 'Identification Sus scrofa and Mus musculus as potential hosts of SARS-CoV-2 via phylogenetic and homologous recombination analysis [version 2; peer review: awaiting peer review]', *F1000Research* **9**, 190.

Huong, N. Q.; Nga, N. T. T.; Long, N. V.; Luu, B. D.; Latinne, A.; Pruvot, M.; Phuong, N. T.; Quang, L. T. V.; Hung, V. V.; Lan, N. T.; Hoa, N. T.; Minh, P. Q.; Diep, N. T.; Tung, N.; Ky, V. D.; Robertson, S. I.; Thuy, H. B.; Long, N. V.; Gilbert, M.; Wicker, L.; Mazet, J. A. K.; Johnson, C. K.; Goldstein, T.; Tremeau-Bravard, A.; Ontiveros, V.; Joly, D. O.; Walzer, C.; Fine, A. E. & Olson, S. H. (2020), 'Coronavirus testing indicates transmission risk increases along wildlife supply chains for human consumption in Viet Nam, 2013-2014', *bioRxiv*, 2020.06.05.098590.

Huston, N. C.; Wan, H.; Tavares, R. d. C. A.; Wilen, C. B. & Pyle, A. M. (2020), 'Comprehensive in-vivo secondary structure of SARS-CoV-2 genome reveals novel regulatory motifs and mechanisms', *bioRxiv*, 2020.07.10.197079.

Isabel, S.; Graña-Miraglia, L.; Gutierrez, J. M.; Bundalovic-Torma, C.; Groves, H. E.; Isabel, M. R.; Eshaghi, A.; Patel, S. N.; Gubbay, J. B.; Poutanen, T.; Guttman, D. S. & Poutanen, S. M. (2020), 'Evolutionary and structural analyses of SARS-CoV-2 D614G spike protein mutation now documented worldwide', *Scientific Reports* **10**(10431), 10431.

Isabel, S.; Grana-Miraglia, L.; Gutierrez, J. M.; Bundalovic-Torma, C.; Groves, H. E.; Isabel, M. R.; Eshaghi, A.; Patel, S. N.; Gubbay, J. B.; Poutanen, T.; Guttman, D. S. & Poutanen, S. M. (2020), 'Evolutionary and structural analyses of SARS-CoV-2 D614G spike protein mutation now documented worldwide', *bioRxiv*, 2020.06.08.140459.

Islam, A. B. M. M. K.; Khan, M. A.-A.-K.; Ahmed, R.; Hossain, M. S.; Kabir, S. M. T.; Islam, M. S. & Siddiki, A. M. A. M. Z. (2020), 'Host transcriptional responses and SARS-CoV-2 isolates from the nasopharyngeal samples of Bangladeshi COVID-19 patients', *bioRxiv*, 2020.07.23.218198.

Islam, O. K.; Al Emran, H. M.; Hasan, M. S.; Anwar, A.; Jahid, M. I. K. & Hossain, M. A. (2020), 'Emergence of European and North American mutant variants of SARS-CoV-2 in Southeast Asia', *Transboundary and Emerging Diseases* **n/a**(n/a).

Islam, R. M.; Hoque, M. N.; Rahman, M. S.; Puspo, J. A.; Akhter, M.; Akter, S.; Rubayet-Ul-Alam, A. S. M.; Sultana, M.; Crandall, K. A. & Hossain, M. A. (2020), 'Genome Wide Analysis of Severe Acute Respiratory Syndrome Coronavirus-2 Implicates World-Wide Circulatory Virus Strains Heterogeneity', *Preprints*.

Israeli, O.; Beth-Din, A.; Paran, N.; Stein, D.; Lazar, S.; Weiss, S.; Milrot, E.; Atiya-Nasagi, Y.; Yitzhaki, S.; Laskar, O. & Schuster, O. (2020), 'Evaluating the efficacy of RT-qPCR SARS-CoV-2 direct approaches in comparison to RNA extraction', *bioRxiv*, 2020.06.10.144196.

Issa, E.; Merhi, G.; Panossian, B.; Salloum, T. & Tokajian, S. (2020), 'SARS-CoV-2 and ORF3a: Nonsynonymous Mutations, Functional Domains, and Viral Pathogenesis', *mSystems* 5(3).

Itokawa, K.; Sekizuka, T.; Hashino, M.; Tanaka, R. & Kuroda, M. (2020), 'Disentangling primer interactions improves SARS-CoV-2 genome sequencing by the ARTIC Network's multiplex PCR', *bioRxiv*, 2020.03.10.985150.

Iweriebor, B. C.; Egbule, O. S.; Danso, S. O.; Akujuru, E.; Ibubeleye, V. T.; Oweredaba, C. I.; Ogharanduku, T.; Manu, A. & Longjohn, M. N. (2020), 'Analysis of SARS-CoV-2 genomes from across Africa reveals potentially clinically relevant mutations.', *bioRxiv*, 2020.09.08.287201.

Jaimés, J. A.; André, N. M.; Chappie, J. S.; Millet, J. K. & Whittaker, G. R. (2020), 'Phylogenetic Analysis and Structural Modeling of SARS-CoV-2 Spike Protein Reveals an Evolutionary Distinct and Proteolytically Sensitive Activation Loop', *Journal of Molecular Biology*.

Jain, A.; Rophina, M.; Mahajan, S.; Krishnan, B. B.; Sharma, M.; Mandal, S.; Fernandez, T.; Sultanji, S.; Mathew, S.; Sivasubbu, S. & Scaria, V. (2020), 'Analysis of the potential impact of genomic variants in SARS-CoV-2 genomes from India on molecular diagnostic assays', *bioRxiv*, 2020.08.05.238618.

Jain, S.; Xiao, X.; Bogdan, P. & Bruck, J. (2020), 'Predicting the Emergence of SARS-CoV-2 Clades', *bioRxiv*, 2020.07.26.222117.

Jaroszewski, L.; Iyer, M.; Alisoltani, A.; Sedova, M. & Godzik, A. (2020), 'The interplay of SARS-CoV-2 evolution and constraints imposed by the structure and functionality of its proteins', *bioRxiv*, 2020.08.10.244756.

Jia, Y.; Yang, C.; Zhang, M.; Yang, X.; Li, J.; Liu, J.; Liu, Y.; Yang, X.; Feng, Y.; Dong, X. & Xia, X. (2020), 'Characterization of eight novel full-length genomes of SARS-CoV-2 among imported COVID-19 cases from abroad in Yunnan, China', *Journal of Infection* **81**(2), e96--e98.

Jin, X.; Xu, K.; Jiang, P.; Lian, J.; Hao, S.; Yao, H.; Jia, H.; Zhang, Y.; Zheng, L.; Zheng, N.; Chen, D.; Yao, J.; Hu, J.; Gao, J.; Wen, L.; Shen, J.; Ren, Y.; Yu, G.; Wang, X.; Lu, Y.; Yu, X.; Yu, L.; Xiang, D.; Wu, N.; Lu, X.; Cheng, L.; Liu, F.; Wu, H.; Jin, C.; Yang, X.; Qian, P.; Qiu, Y.; Sheng, J.; Liang, T.; Li, L. & Yang, Y. (2020), 'Virus strain from a mild COVID-19 patient in Hangzhou represents a new trend in SARS-CoV-2 evolution potentially related to Furin cleavage site', *Emerging Microbes & Infections* **0**(ja), 1--74.

Jones, L. R. & Manrique, J. M. (2020), 'Mega-phylogeny sheds light on SARS-CoV-2 spatial phylogenetic structure', *bioRxiv*, 2020.06.05.135954.

Jones, L. R. & Manrique, J. M. (2020), 'Quantitative phylogenomic evidence reveals a spatially structured SARS-CoV-2 diversity', *Virology* **550**, 70--77.

Jones, T. C.; Mühlemann, B.; Schneider, J.; Beheim-Schwarzbach, J.; Veith, T.; Corman, V. M. & Drosten, C. (2020), 'German SARS-CoV-2 sequences', Charité Universitätsmedizin, S0032.

Joshi, A. & Paul, S. (2020), 'Phylogenetic Analysis of the Novel Coronavirus Reveals Important Variants in Indian Strains', *bioRxiv*, 2020.04.14.041301.

Joshi, M.; Puvar, A. C.; Kumar, D.; Ansari, A.; Pandya, M.; Raval, J.; Patel, Z.; Trivedi, P.; Gandhi, M.; Pandya, L.; Patel, K.; Savaliya, N.; Bagatharia, S.; Kumar, S. & Joshi, C. (2020), 'Genomic variations in SARS-CoV-2 genomes from Gujarat: Underlying role of variants in disease epidemiology', *bioRxiv*, 2020.07.10.197095.

Jungreis, I.; Sealfon, R. & Kellis, M. (2020), 'Sarbecovirus comparative genomics elucidates gene content of SARS-CoV-2 and functional impact of COVID-19 pandemic mutations', *bioRxiv*, 2020.06.02.130955.

Junior, I. J. M.; Polveiro, R. C.; Souza, G. M.; Bortolin, D. I.; Sasaki, F. T. & Lima, A. T. M. (2020), 'The global population of SARS-CoV-2 is composed of six major subtypes', *bioRxiv*, 2020.04.14.040782.

Kalinich, C. C.; Jensen, C. G.; Neugebauer, P.; Petrone, M. E.; Peña-Hernández, M.; Ott, I. M.; Wyllie, A. L.; Alpert, T.; Vogels, C. B. F.; Fauver, J. R.; Grubaugh, N. D. & Brito, A. F. (2020), 'Real-time public health communication of local SARS-CoV-2 genomic epidemiology', *PLOS Biology* **18**(8), e3000869.

Kanteh, A.; Manneh, J.; Jabang, S.; Kujabo, M. A.; Sanyang, B.; Oboh, M. A.; Bojang, A.; Jallow, H. S.; Nwakama, D.; Secka, O.; Roca, A.; Amambua-Ngwa, A.; Antonio, M.; Baldeh, I.; Forest, K.; Samateh, A. L.; D'Alessandro, U. & Sesay, A. K. (2020), 'Origin of imported SARS-CoV-2 strains in The Gambia identified from Whole Genome Sequences.', *bioRxiv*, 2020.04.30.070771.

Kapli, P.; Yang, Z. & Telford, M. J. (2020), 'Phylogenetic tree building in the genomic age', *Nature Reviews. Genetics*.

Karamese, M.; Ozgur, D. & Tutuncu, E. E. (2020), 'Molecular Characterization, Phylogenetic and Variation Analyzes of SARS-CoV-2 strains in Turkey', *bioRxiv*, 2020.09.11.293183.

Karamitros, T.; Papadopoulou, G.; Bousali, M.; Mexias, A.; Tsiodras, S. & Mentis, A. (2020), 'SARS-CoV-2 exhibits intra-host genomic plasticity and low-frequency polymorphic quasispecies', *bioRxiv*, 2020.03.27.009480.

Kawano-Sugaya, T.; Yatsu, K.; Sekizuka, T.; Itokawa, K.; Hashino, M.; Tanaka, R. &

Kuroda, M. (2020), 'Haplotype Explorer: an infection cluster visualization tool for spatiotemporal dissection of the COVID-19 pandemic', *bioRxiv*, 2020.07.19.179101.

Kemenesi, G.; Zeghib, S.; Somogyi, B.; Toth, G. E.; Banyai, K.; Solymosi, N.; Szabo, P. M.; Szabo, I.; Balint, A.; Urban, P.; Herczeg, R.; Gyenesei, A.; Nagy, A.; Pereszlenyi, C. I.; Babinszky, G.; Dudas, G.; Terhes, G.; Zoldi, V.; Lovas, R.; Tenczer, S.; Kornya, L. & Jakab, F. (2020), 'Multiple SARS-CoV-2 introductions shaped the early outbreak in Central Eastern Europe: comparing Hungarian data to a worldwide sequence data-matrix', *bioRxiv*, 2020.05.06.080119.

Khailany, R. A.; Safdar, M. & Ozaslan, M. (2020), 'Genomic characterization of a novel SARS-CoV-2', *Gene Reports* **19**, 100682.

Khan, M. I.; Khan, Z. A.; Baig, M. H.; Ahmad, I.; Farouk, A.-E.; Song, Y. G. & Dong, J.-J. (2020), 'Comparative genome analysis of novel coronavirus (SARS-CoV-2) from different geographical locations and the effect of mutations on major target proteins: An in silico insight', *PLOS ONE* **15**(9), e0238344.

Kim, D.; Lee, J.-Y.; Yang, J.-S.; Kim, J. W.; Kim, V. N. & Chang, H. (2020), 'The Architecture of SARS-CoV-2 Transcriptome', *Cell* **181**(4), 914--921.e10.

Kirkland, P. D. & Frost, M. J. (2020), 'The impact of viral transport media on PCR assay results for the detection of nucleic acid from SARS-CoV-2 and other viruses', *bioRxiv*, 2020.06.09.142323.

Korber, B.; Fischer, W.; Gnanakaran, S. G.; Yoon, H.; Theiler, J.; Abfalterer, W.; Foley, B.; Giorgi, E. E.; Bhattacharya, T.; Parker, M. D.; Partridge, D. G.; Evans, C. M.; Silva, T. d.; LaBranche, C. C.; Montefiori, D. C. & Group, S. C. O. V. I. D.-19. G. (2020), 'Spike mutation pipeline reveals the emergence of a more transmissible form of SARS-CoV-2', *bioRxiv*, 2020.04.29.069054.

Korber, B.; Fischer, W. M.; Gnanakaran, S.; Yoon, H.; Theiler, J.; Abfalterer, W.; Hengartner, N.; Giorgi, E. E.; Bhattacharya, T.; Foley, B.; Hastie, K. M.; Parker, M. D.; Partridge, D. G.; Evans, C. M.; Freeman, T. M.; de Silva, T. I.; Angyal, A.; Brown, R. L.; Carrilero, L.; Green, L. R.; Groves, D. C.; Johnson, K. J.; Keeley, A. J.; Lindsey, B. B.; Parsons, P. J.; Raza, M.; Rowland-Jones, S.; Smith, N.; Tucker, R. M.; Wang, D.; Wyles, M. D.; McDanal, C.; Perez, L. G.; Tang, H.; Moon-Walker, A.; Whelan, S. P.; LaBranche, C. C.; Saphire, E. O. & Montefiori, D. C. (2020), 'Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus', *Cell* **182**(4), 812--827.e19.

Kumar, B. K.; Venkatraja, B.; Prithvisagar, K. S.; Rai, P.; Rohit, A.; Hegde, M. N.; Karunasagar, I. & Karunasagar, I. (2020), 'The mutational analysis unveils the distribution of G614 genotype of SARS-CoV-2 in different Indian states and its association with case fatality rate of COVID-19', *bioRxiv*, 2020.07.27.222562.

Kumar, M.; Patel, A. K.; Shah, A. V.; Raval, J.; Rajpara, N.; Joshi, M. & Joshi, C. G. (2020), 'The first proof of the capability of wastewater surveillance for COVID-19 in India through the detection of the genetic material of SARS-CoV-2', *medRxiv*, 2020.06.16.20133215.

Kumar, P.; Pandey, R.; Sharma, P.; Dhar, M.; Vivekanand, A.; Bharathram, U.; Vashistha, H.; Wadhwa, S.; Tyagi, N.; Fatihi, S.; Sharma, U.; Singh, P.; Lall, H.; Datta, M.; Gupta, P.; Saini, N.; Tiwari, A.; Nandi, B.; Kumar, D.; Bag, S.; Deepanshi, D.; Rathore, S.; Jatana, N.; Jaiswal, V.; Gogia, H.; Madan, P.; Singh, S.; Singh, P.; Dash, D.; Bala, M.; Kabra, S.; Singh, S. K.; Mukerji, M.; Thukral, L.; Faruq, M.; Agarwal, A. & Rakshit, P. (2020), 'Integrated genomic view of SARS-CoV-2 in India', *bioRxiv*, 2020.06.04.128751.

Kwon, S. B. & Ernst, J. (2020), 'Single-nucleotide conservation state annotation of SARS-CoV-2 genome', *bioRxiv*, 2020.07.13.201277.

Laamarti, M.; Alouane, T.; Kartti, S.; Chemaou-Elfihri, M. W.; Hakmi, M.; Essabbar, A.; Laamart, M.; Hlali, H.; Allam, L.; Hafidi, N. E. L.; Jaoudi, R. E. L.; Allali, I.; Marchoudi, N.; Fekkak, J.; Benrahma, H.; Nejari, C.; Amzazi, S.; Belyamani, L. & Ibrahimi, A. (2020), 'Large scale genomic analysis of 3067 SARS-CoV-2 genomes reveals a clonal geodistribution and a rich genetic variations of hotspots mutations', *bioRxiv*, 2020.05.03.074567.

Laamarti, M.; Kartti, S.; Alouane, T.; Laamarti, R.; Allam, L.; Ouadghiri, M.; Chemaou-Elfihri, M. W.; Smyej, I.; Rahoui, J.; Benrahma, H.; Diawara, I.; Essabbar, A.; Boumajdi, N.; Bendani, H.; Bouricha, E. M.; Aanniz, T.; Attar, J. E.; Hafidi, N. E.; Jaoudi, R. E.; Sbabou, L.; Nejari, C.; Amzazi, S.; Mentag, R.; Belyamani, L. & Ibrahimi, A. (2020), 'Genetic analysis of SARS-CoV-2 strains collected from North Africa: viral origins and mutational spectrum', *bioRxiv*, 2020.06.30.181123.

Laha, S.; Chakraborty, J.; Das, S.; Biswas, S.; Manna, S. K. & Chatterjee, R. (2020), 'Characterizations of SARS-CoV-2 mutational profile, spike protein stability and viral transmission', *bioRxiv*, 2020.05.03.066266.

Lai, A.; Bergna, A.; Caucci, S.; Clementi, N.; Vicenti, I.; Dragoni, F.; Cattelan, A. M.; Menzo, S.; Pan, A.; Callegaro, A.; Tagliabracci, A.; Caruso, A.; Caccuri, F.; Ronchiadin, S.; Balotta, C.; Zazzi, M.; Vaccher, E.; Clementi, M.; Galli, M. & Zehender, G. (2020), 'Molecular Tracing of SARS-CoV-2 in Italy in the First Three Months of the Epidemic', *Viruses* **12**(8), 798.

Lai, C.-C.; Shih, T.-P.; Ko, W.-C.; Tang, H.-J. & Hsueh, P.-R. (2020), 'Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and coronavirus disease-2019 (COVID-19): The epidemic and the challenges', *International Journal of Antimicrobial Agents* **55**(3), 105924.

Laiton-Donato, K.; Arenas, C. J. V.; Ciro, J. A. U.; Munoz, C. F.; Alvarez-Diaz, D. A.; Villabona-Arenas, L. S.; Echeverria-Londono, S.; Franco-Sierra, N. D.; Cucunuba, Z. M.;

Florez-Sanchez, A. C.; Ferro, C.; Ajami, N. J.; Walteros, D. M.; Prieto-Alvarado, F. E.; Duran-Camacho, C. A.; Ospina-Martinez, M. L. & Mercado-Reyes, M. M. (2020), 'Genomic epidemiology of SARS-CoV-2 in Colombia', *medRxiv*, 2020.06.26.20135715.

Lam, T. T.-Y. (2020), 'Tracking the Genomic Footprints of SARS-CoV-2 Transmission', *Trends in Genetics* **36**(8), 544--546.

Lan, T. C. T.; Allan, M. F.; Malsick, L.; Khandwala, S.; Nyeo, S. S. Y.; Bathe, M.; Griffiths, A. & Rouskin, S. (2020), 'Structure of the full SARS-CoV-2 RNA genome in infected cells', *bioRxiv*, 2020.06.29.178343.

Lanfear, R. (2020), 'What's the best method to get a tree of >>10K SARS-CoV-2 sequences?', *GitHub*, *roblanf/sarscov2phylo*, Github repository, S0088.

Latinne, A.; Hu, B.; Olival, K. J.; Zhu, G.; Zhang, L.; Li, H.; Chmura, A. A.; Field, H. E.; Zambrana-Torrel, C.; Epstein, J. H.; Li, B.; Zhang, W.; Wang, L.-F.; Shi, Z. & Daszak, P. (2020), 'Origin and cross-species transmission of bat coronaviruses in China', *bioRxiv*, 2020.05.31.116061.

Lau, S. K. P.; Luk, H. K. H.; Wong, A. C. P.; Li, K. S. M.; Zhu, L.; He, Z.; Fung, J.; Chan, T. T. Y.; Fung, K. S. C. & Woo, P. C. Y. (2020), 'Possible Bat Origin of Severe Acute Respiratory Syndrome Coronavirus 2 - Volume 26, Number 7—July 2020 - Emerging Infectious Diseases journal - CDC', .

Lau, S.-Y.; Wang, P.; Mok, B. W.-Y.; Zhang, A. J.; Chu, H.; Lee, A. C.-Y.; Deng, S.; Chen, P.; Chan, K.-H.; Song, W.; Chen, Z.; To, K. K.-W.; Chan, J. F.-W.; Yuen, K.-Y. & Chen, H. (2020), 'Attenuated SARS-CoV-2 variants with deletions at the S1/S2 junction', *Emerging Microbes & Infections* **0**(ja), 1--15.

Lazar, M.; Popovici, O.; Muehlemann, B.; Durfeet, T. & Stan, R. (2020), 'Whole-Genome Sequences of the Severe Acute Respiratory Syndrome Coronavirus-2 obtained from Romanian patients between March and June of 2020', *bioRxiv*, 2020.06.28.175802.

Lee, J.; Hughes, T.; Lee, M.-H.; Field, H.; Rovie-Ryan, J. J.; Sitam, F. T.; Sipangkui, S.; Nathan, S. K. S. S.; Ramirez, D.; Kumar, S. V.; Lasimbang, H.; Epstein, J. H. & Daszak, P. (2020), 'No evidence of coronaviruses or other potentially zoonotic viruses in Sunda pangolins (*Manis javanica*) entering the wildlife trade via Malaysia.', *bioRxiv*, 2020.06.19.158717.

Lemey, P.; Hong, S.; Hill, V.; Baele, G.; Poletto, C.; Colizza, V.; O'Toole, A.; McCrone, J. T.; Andersen, K. G.; Worobey, M.; Nelson, M. I.; Rambaut, A. & Suchard, M. A. (2020), 'Accommodating individual travel history, global mobility, and unsampled diversity in phylogeography: a SARS-CoV-2 case study.', *bioRxiv*, 2020.06.22.165464.

Lemoine, F.; Blassel, L.; Voznica, J. & Gascuel, O. (2020), 'COVID-Align: Accurate online alignment of hCoV-19 genomes using a profile HMM', *bioRxiv*,

2020.05.25.114884.

Letko, M.; Seifert, S. N.; Olival, K. J.; Plowright, R. K. & Munster, V. J. (2020), 'Bat-borne virus diversity, spillover and emergence', *Nature Reviews. Microbiology*.

Levasseur, A.; Delerce, J.; Caputo, A.; Brechard, L.; Colson, P.; Lagier, J.-C.; Fournier, P.-E. & Raoult, D. (2020), 'Genomic diversity and evolution of coronavirus (SARS-CoV-2) in France from 309 COVID-19-infected patients', *bioRxiv*, 2020.09.04.282616.

Li, C.; Debruyne, D. N.; Spencer, J.; Kapoor, V.; Liu, L. Y.; Zhou, B.; Pandey, U.; Bootwalla, M.; Ostrow, D.; Maglinte, D. T.; Ruble, D.; Ryutov, A.; Shen, L.; Lee, L.; Feigelman, R.; Burdon, G.; Liu, J.; Oliva, A.; Borcharding, A.; Tan, H.; Urban, A. E.; Gai, X.; Bard, J. D.; Liu, G. & Liu, Z. (2020), 'Highly sensitive and full-genome interrogation of SARS-CoV-2 using multiplexed PCR enrichment followed by next-generation sequencing', *bioRxiv*, 2020.03.12.988246.

Li, C.; Yang, Y. & Ren, L. (2020), 'Genetic evolution analysis of 2019 novel coronavirus and coronavirus from other species', *Infection, Genetics and Evolution* **82**, 104285.

Li, J.; Li, Z.; Cui, X. & Wu, C. (2020), 'Bayesian phylodynamic inference on the temporal evolution and global transmission of SARS-CoV-2', *Journal of Infection* **81**(2), 318--356.

Li, M.; Xu, Y.; Kang, L.; Shen, Z.; Li, X.; Wu, W.; Ma, W.; Fang, C.; Yang, F.; Jiang, X.; Gong, S. & Zhang, L. (2020), 'Hybrid capture-based sequencing enables unbiased recovery of SAR-CoV-2 genomes from fecal samples and characterization of the dynamics of intra-host variants', *bioRxiv*, 2020.07.30.230102.

Li, X.; Giorgi, E. E.; Marichannegowda, M. H.; Foley, B.; Xiao, C.; Kong, X.-P.; Chen, Y.; Gnanakaran, S.; Korber, B. & Gao, F. (2020), 'Emergence of SARS-CoV-2 through recombination and strong purifying selection', *Science Advances*, eabb9153.

Li, X.; Jin, X.; Chen, S.; Wang, L.; Yau, T. O.; Yang, J.; Hong, Z.; Ruan, J.; Duan, G. & Gao, S. (2020), 'The discovery of a recombinant SARS2-like CoV strain provides insights into SARS and COVID-2019 pandemics', *bioRxiv*, 2020.07.22.213926.

Li, X.; Wang, W.; Zhao, X.; Zai, J.; Zhao, Q.; Li, Y. & Chaillon, A. (2020), 'Transmission dynamics and evolutionary history of 2019-nCoV', *Journal of Medical Virology* **92**(5), 501--511.

Li, X.; Zai, J.; Zhao, Q.; Nie, Q.; Li, Y.; Foley, B. T. & Chaillon, A. (2020), 'Evolutionary history, potential intermediate animal host, and cross-species analyses of SARS-CoV-2', *Journal of Medical Virology* **92**(6), 602--611.

Li, Y.; Liu, Q. & Luo, Y. (2020), 'Clustering analysis of single nucleotide polymorphism data reveals population structure of SARS-CoV-2 worldwide', *bioRxiv*,

2020.09.04.283358.

Li, Y.; Wang, Y.; Qiu, Y.; Gong, Z.; Deng, L.; Pan, M.; Yang, H.; Xu, J.; Yang, L. & Li, J. (2020), 'SARS-CoV-2 Spike Glycoprotein Receptor Binding Domain is Subject to Negative Selection with Predicted Positive Selection Mutations', *bioRxiv*, 2020.05.04.077842.

Li, Y.; Yang, X.; Wang, N.; Wang, H.; Yin, B.; Yang, X. & Jiang, W. (2020), 'SNPs or RNA modifications? Concerns on mutation-based evolutionary studies of SARS-CoV-2', *PLOS ONE* **15**(8), e0238490.

Lin, C.-Y.; Wang, W.-H.; Urbina, A. N.; Tseng, S.-P.; Lu, P.-L.; Chen, Y.-H.; Yu, M.-L. & Wang, S.-F. (2020), 'Importation of SARS-CoV-2 infection leads to major COVID-19 epidemic in Taiwan', *International journal of infectious diseases: IJID: official publication of the International Society for Infectious Diseases* **97**, 240--244.

Lin, X.-D.; Wang, W.; Hao, Z.-Y.; Wang, Z.-X.; Guo, W.-P.; Guan, X.-Q.; Wang, M.-R.; Wang, H.-W.; Zhou, R.-H.; Li, M.-H.; Tang, G.-P.; Wu, J.; Holmes, E. C. & Zhang, Y.-Z. (2017), 'Extensive diversity of coronaviruses in bats from China', *Virology* **507**, 1--10.

Liu, B.; Liu, K.; Zhang, H.; Zhang, L. & Huang, L. (2020), 'CoV-Seq: SARS-CoV-2 Genome Analysis and Visualization', *bioRxiv*, 2020.05.01.071050.

Liu, J.; Huang, J. & Xiang, D. (2020), 'Early Release - Large SARS-CoV-2 Outbreak Caused by Asymptomatic Traveler, China - Volume 26, Number 9—September 2020 - Emerging Infectious Diseases journal - CDC', .

Liu, P.; Chen, W. & Chen, J.-P. (2019), 'Viral Metagenomics Revealed Sendai Virus and Coronavirus Infection of Malayan Pangolins (*Manis javanica*)', *Viruses* **11**(11), 979.

Liu, S.; Shen, J.; Yang, L.; Hu, C.-D. & Wan, J. (2020), 'Distinct genetic spectrums and evolution patterns of SARS-CoV-2', *medRxiv*, 2020.06.16.20132902.

Liu, Z.; Zheng, H.; Lin, H.; Li, M.; Yuan, R.; Peng, J.; Xiong, Q.; Sun, J.; Li, B.; Wu, J.; Yi, L.; Peng, X.; Zhang, H.; Zhang, W.; Hulswit, R. J. G.; Loman, N.; Rambaut, A.; Ke, C.; Bowden, T. A.; Pybus, O. G. & Lu, J. (2020), 'Identification of common deletions in the spike protein of SARS-CoV-2', *Journal of Virology*, JVI.00790-20.

Liu, Z.; Zheng, H.; Yuan, R.; Li, M.; Lin, H.; Peng, J.; Xiong, Q.; Sun, J.; Li, B.; Wu, J.; Ke, C.; Hulswit, R. J. G.; Bowden, T. A.; Rambaut, A.; Pybus, O. G.; Loman, N. & Lu, J. (2020), 'Identification of a common deletion in the spike protein of SARS-CoV-2', *bioRxiv*, 2020.03.31.015941.

Long, S. W.; Christensen, P. A.; Bernard, D. W.; Davis, J. R.; Shukla, M.; Nguyen, M.; Saavedra, M. O.; Cantu, C. C.; Yerramilli, P.; Pruitt, L.; Subedi, S.; Hendrickson, H.; Eskandari, G.; Kumaraswami, M.; McLellan, J. S. & Musser, J. M. (2020), 'Molecular

Architecture of Early Dissemination and Evolution of the SARS-CoV-2 Virus in Metropolitan Houston, Texas', *bioRxiv*, 2020.05.01.072652.

Lu, J.; du Plessis, L.; Liu, Z.; Hill, V.; Kang, M.; Lin, H.; Sun, J.; François, S.; Kraemer, M. U. G.; Faria, N. R.; McCrone, J. T.; Peng, J.; Xiong, Q.; Yuan, R.; Zeng, L.; Zhou, P.; Liang, C.; Yi, L.; Liu, J.; Xiao, J.; Hu, J.; Liu, T.; Ma, W.; Li, W.; Su, J.; Zheng, H.; Peng, B.; Fang, S.; Su, W.; Li, K.; Sun, R.; Bai, R.; Tang, X.; Liang, M.; Quick, J.; Song, T.; Rambaut, A.; Loman, N.; Raghwani, J.; Pybus, O. G. & Ke, C. (2020), 'Genomic Epidemiology of SARS-CoV-2 in Guangdong Province, China', *Cell* **181**(5), 997--1003.e9.

Lu, J.; Plessis, L. d.; Liu, Z.; Hill, V.; Kang, M.; Lin, H.; Sun, J.; Francois, S.; Kraemer, M. U. G.; Faria, N. R.; McCrone, J. T.; Peng, J.; Xiong, Q.; Yuan, R.; Zeng, L.; Zhou, P.; Liang, C.; Yi, L.; Liu, J.; Xiao, J.; Hu, J.; Liu, T.; Ma, W.; Li, W.; Su, J.; Zheng, H.; Peng, B.; Fang, S.; Su, W.; Li, K.; Sun, R.; Bai, R.; Tang, X.; Liang, M.; Quick, J.; Song, T.; Rambaut, A.; Loman, N.; Raghwani, J.; Pybus, O. & Ke, C. (2020), 'Genomic epidemiology of SARS-CoV-2 in Guangdong Province, China', *medRxiv*, 2020.04.01.20047076.

Luan, J.; Lu, Y.; Jin, X. & Zhang, L. (2020), 'Spike protein recognition of mammalian ACE2 predicts the host range and an optimized ACE2 for SARS-CoV-2 infection', *Biochemical and Biophysical Research Communications* **526**(1), 165--169.

Lythgoe, K. A.; Hall, M. D.; Ferretti, L.; Cesare, M. d.; MacIntyre-Cockett, G.; Trebes, A.; Andersson, M.; Otecko, N.; Wise, E. L.; Moore, N.; Lynch, J.; Kidd, S.; Cortes, N.; Mori, M.; Justice, A.; Green, A.; Ansari, M. A.; Abeler-Dorner, L.; Moore, C. E.; Peto, T. E. A.; Shaw, R.; Simmonds, P.; Buck, D.; Todd, J. A.; Bonsall, D.; Fraser, C. & Golubchik, T. (2020), 'Shared SARS-CoV-2 diversity suggests localised transmission of minority variants', *bioRxiv*, 2020.05.28.118992.

Maan, H.; Mbareche, H.; Ar, R.; Banerjee, A.; Ja, N.; Ra, K.; Knox, N.; Mubareka, S.; Ag, M. & Wang, B. (2020), 'Genotyping SARS-CoV-2 through an interactive web application.', *The Lancet. Digital Health*.

MacLean, O. A.; Lytras, S.; Singer, J. B.; Weaver, S.; Pond, S. L. K. & Robertson, D. L. (2020), 'Evidence of significant natural selection in the evolution of SARS-CoV-2 in bats, not humans', *bioRxiv*, 2020.05.28.122366.

Mahmud, A. S. M.; Taznin, T.; Sarkar, M. M. H.; Uzzaman, M. S.; Osman, E.; Habib, M. A.; Akter, S.; Banu, T. A.; Goswami, B.; Jahan, I.; Hossain, M. S. & Khan, M. S. (2020), 'The genetic variants analysis of circulating SARS-CoV-2 in Bangladesh.', *bioRxiv*, 2020.07.29.226555.

Maitra, A.; Raghav, S.; Dalal, A.; Ali, F.; Paynter, V. M.; Paul, D.; Biswas, N. K.; Ghosh, A.; Jani, K.; Chinnaswamy, S.; Pati, S.; Sahu, A.; Mitra, D.; Bhat, M. K.; Mayor, S.; Sarin, A.; Consortium, T. P. A. N.-I. 1000. S. A. R. S.-C.-2. R. G. S.; Shouche, Y. S.;

Seshasayee, A. S. N.; Palakodeti, D.; Bashyam, M. D.; Parida, A. & Das, S. (2020), 'PAN-INDIA 1000 SARS-CoV-2 RNA Genome Sequencing Reveals Important Insights into the Outbreak', *bioRxiv*, 2020.08.03.233718.

Malaiyan, J.; Arumugam, S.; Mohan, K. & Radhakrishnan, G. G. (2020), 'An update on origin of SARS-CoV-2: Despite closest identity, bat (RaTG13) and Pangolin derived Coronaviruses varied in the critical binding site and O-linked glycan residues', *Journal of Medical Virology* n/a(n/a).

Marquez, S.; Prado-Vivar, B.; Guadalupe, J. J.; Granja, B. G.; Jibaja, M.; Tobar, M.; Mora, F.; Gaviria, J.; Garcia, M.; Ligna, E.; Espinosa, F.; Reyes, J.; Barragan, V.; Rojas-Silva, P.; Trueba, G.; Grunauer, M. & Cardenas, P. (2020), 'Genome sequencing of the first SARS-CoV-2 reported from patients with COVID-19 in Ecuador.', *medRxiv*, 2020.06.11.20128330.

Mateos, P. A.; Balboa, R. F.; Easteal, S.; Eyras, E. & Patel, H. R. (2020), 'PACIFIC: A lightweight deep-learning classifier of SARS-CoV-2 and co-infecting RNA viruses', *bioRxiv*, 2020.07.24.219097.

Mavian, C.; Marini, S.; Prospero, M. & Salemi, M. (2020), 'A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis', *JMIR public health and surveillance* 6(2), e19170.

May, M.; Rostama, B. & Relich, R. F. (2020), 'Selectomic and Evolvability Analyses of the Highly Pathogenic Betacoronaviruses SARS-CoV-2, SARS-CoV, and MERS-CoV', *bioRxiv*, 2020.05.05.078956.

McAloose, D.; Laverack, M.; Wang, L.; Killian, M. L.; Caserta, L. C.; Mitchell, P. K.; Queen, K.; Mauldin, M. R.; Cronk, B. D.; Bartlett, S. L.; Sykes, J. M.; Zec, S.; Ingerman, K.; Stokol, T.; Frederikson, R.; Delaney, M. A.; Ivancic, M.; Jenkins-Moore, M.; Mazingo, K.; Franzen, K.; Bergeson, N. H.; Goodman, L.; Wang, H.; Wang, S.; Yuan, F.; Fang, Y.; Olmstead, C.; McCann, C.; Thomas, P.; Goodrich, E.; Elvinger, F.; Slavinski, S.; Smith, D. C.; Calle, P. P.; Terio, K.; Torchetti, M. K. & Diel, D. G. (2020), 'From people to Panthera: Natural SARS-CoV-2 infection in tigers and lions at the Bronx Zoo', *bioRxiv*, 2020.07.22.213959.

McIver, D. J.; Silithammavong, S.; Theppangna, W.; Gillis, A.; Douangngeun, B.; Khamvavong, K.; Singhalath, S.; Duong, V.; Buchy, P.; Olson, S. H.; Keatts, L.; Fine, A. E.; Grotorex, Z.; Gilbert, M.; LeBreton, M.; Saylor, K.; Joly, D. O.; Rubin, E. M. & Lange, C. E. (2020), 'Coronavirus surveillance of wildlife in the Lao People's Democratic Republic detects viral RNA in rodents', *Archives of Virology*.

McNamara, R. P.; Caro-Vegas, C.; Landis, J. T.; Moorad, R.; Pluta, L. J.; Eason, A. B.; Thompson, C.; Bailey, A.; Villamor, F. C. S.; Lange, P. T.; Wong, J. P.; Seltzer, T.; Seltzer, J.; Zhou, Y.; Vahrson, W.; Juarez, A.; Meyo, J. O.; Calabre, T.; Broussard, G.; Rivera-Soto, R.; Chappell, D. L.; Baric, R. S.; Damania, B.; Miller, M. B. & Dittmer, D. (2020),

'High-density amplicon sequencing identifies community spread and ongoing evolution of SARS-CoV-2 in the Southern United States', *bioRxiv*, 2020.06.19.161141.

Mercatelli, D. & Giorgi, F. M. (2020), 'Geographic and Genomic Distribution of SARS-CoV-2 Mutations', *Frontiers in Microbiology* **11**.

Mercatelli, D.; Triboli, L.; Fornasari, E.; Ray, F. & Giorgi, F. M. (2020), 'coronapp: a Web Application to Annotate and Monitor SARS-CoV-2 Mutations', *bioRxiv*, 2020.05.31.124966.

Meredith, L. W.; Hamilton, W. L.; Warne, B.; Houldcroft, C. J.; Hosmillo, M.; Jahun, A.; Curran, M. D.; Parmar, S.; Caller, L.; Caddy, S. L.; Khokhar, F. A.; Yakovleva, A.; Hall, G. R.; Feltwell, T.; Forret, S. N.; Sridhar, S.; Weekes, M. p.; Baker, S.; Brown, N.; Moore, E.; Gouliouris, T.; Popay, A.; Roddick, I.; Reacher, M.; Peacock, S.; Dougan, G.; Torok, M. E. & Goodfellow, I. (2020), 'Rapid implementation of real-time SARS-CoV-2 sequencing to investigate healthcare-associated COVID-19 infections', *medRxiv*, 2020.05.08.20095687.

Meredith, L. W.; Hamilton, W. L.; Warne, B.; Houldcroft, C. J.; Hosmillo, M.; Jahun, A. S.; Curran, M. D.; Parmar, S.; Caller, L. G.; Caddy, S. L.; Khokhar, F. A.; Yakovleva, A.; Hall, G.; Feltwell, T.; Forrest, S.; Sridhar, S.; Weekes, M. P.; Baker, S.; Brown, N.; Moore, E.; Popay, A.; Roddick, I.; Reacher, M.; Gouliouris, T.; Peacock, S. J.; Dougan, G.; Török, M. E. & Goodfellow, I. (2020), 'Rapid implementation of SARS-CoV-2 sequencing to investigate cases of health-care associated COVID-19: a prospective genomic surveillance study', *The Lancet Infectious Diseases* **0**(0).

Michaud, W. A.; Boland, G. M. & Rabi, S. A. (2020), 'The SARS-CoV-2 Spike mutation D614G increases entry fitness across a range of ACE2 levels, directly outcompetes the wild type, and is preferentially incorporated into trimers', *bioRxiv*, 2020.08.25.267500.

Michel, C. J.; Mayer, C.; Poch, O. & Thompson, J. D. (2020), 'Characterization of accessory genes in coronavirus genomes', *bioRxiv*, 2020.05.26.118208.

Micheli, V.; Rimoldi, S. G.; Romeri, F.; Comandatore, F.; Mancon, A.; Gigantiello, A.; Perini, M.; Mileto, D.; Pagani, C.; Lombardi, A. & Gismondo, M. R. (2020), 'Geographical reconstruction of the SARS-CoV-2 outbreak in Lombardy (Italy) during the early phase', *Journal of Medical Virology* **n/a**(n/a).

Miladi, M.; Fuchs, J.; Maier, W.; Weigang, S.; Pedrosa, N. D. i.; Weiss, L.; Lother, A.; Nekrutenko, A.; Ruzsics, Z.; Panning, M.; Kochs, G.; Gilsbach, R. & Grüning, B. (2020), 'The landscape of SARS-CoV-2 RNA modifications', *bioRxiv*, 2020.07.18.204362.

Miller, D.; Martin, M. A.; Harel, N.; Kustin, T.; Tirosh, O.; Meir, M.; Sorek, N.; Gefen-Halevi, S.; Amit, S.; Vorontsov, O.; Wolf, D.; Peretz, A.; Shemer-Avni, Y.; Roif-Kaminsky, D.; Kopelman, N.; Huppert, A.; Koelle, K. & Stern, A. (2020), 'Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel', *medRxiv*,

2020.05.21.20104521.

Mishra, A.; Pandey, A. K.; Gupta, P.; Pradhan, P.; Dhamija, S.; Gomes, J.; Kundu, B.; Vivekanandan, P. & Menon, M. B. (2020), 'Mutation landscape of SARS-CoV-2 reveals three mutually exclusive clusters of leading and trailing single nucleotide substitutions', *bioRxiv*, 2020.05.07.082768.

Monahan, L. (2020), 'A protocol for massively parallel diagnosis and genome sequencing of SARS-CoV-2', *protocols.io*.

Morel, B.; Barbera, P.; Czech, L.; Bettisworth, B.; Huebner, L.; Lutteropp, S.; Serdari, D.; Kostaki, E.-G.; Mamais, I.; Kozlov, A.; Pavlidis, P. M.; Paraskevis, D. & Stamatakis, A. (2020), 'Phylogenetic analysis of SARS-CoV-2 data is difficult', *bioRxiv*, 2020.08.05.239046.

Morens, D. M.; Breman, J. G.; Calisher, C. H.; Doherty, P. C.; Hahn, B. H.; Keusch, G. T.; Kramer, L. D.; LeDuc, J. W.; Monath, T. P. & Taubenberger, J. K. (2020), 'The Origin of COVID-19 and Why It Matters', , *tpmd200849*.

Mou, H.; Quinlan, B.; Peng, H.; Guo, Y.; Peng, S.; Zhang, L.; Davis-Gardner, M.; Gardner, M.; Voo, Z. X.; Bailey, C. C.; Alpert, M.; Rader, C.; Choe, H. & Farzan, M. (2020), 'Mutations from bat ACE2 orthologs markedly enhance ACE2-Fc neutralization of SARS-CoV-2', *bioRxiv*, 2020.06.29.178459.

Moustafa, A. M. & Planet, P. (2020), 'Rapid whole genome sequence typing reveals multiple waves of SARS-CoV-2 spread', *bioRxiv*, 2020.06.08.139055.

Munnink, B. B. O.; Sikkema, R. S.; Nieuwenhuijse, D. F.; Molenaar, R. J.; Munger, E.; Molenkamp, R.; Spek, A. v. d.; Tolsma, P.; Rietveld, A.; Brouwer, M.; Bouwmeester-Vincken, N.; Harders, F.; Honing, R. H.-v. d.; Wegdam-Blans, M. C. A.; Bouwstra, R.; GeurtsvanKessel, C.; Eijk, A. v. d.; Velkers, F.; Smit, L.; Stegeman, A.; Poel, W. H. M. v. d. & Koopmans, M. (2020), 'Jumping back and forth: anthrozoootic and zoonotic transmission of SARS-CoV-2 on mink farms', *bioRxiv*, 2020.09.01.277152.

Nabil, B.; Sabrina, B. & Abdelhakim, B. (2020), 'Transmission route and introduction of Pandemic SARS-CoV-2 between China, Italy and Spain', *Journal of Medical Virology* **n/a**(n/a).

Nadeau, S. A.; Vaughan, T. G.; Sciré, J.; Huisman, J. S. & Stadler, T. (2020), 'The origin and early spread of SARS-CoV-2 in Europe', *medRxiv*, 2020.06.10.20127738.

Nagashima, M.; Kumagai, R.; Yoshida, I.; Kawakami, M.; Nagano, M.; Asakura, H.; Kaku, E.; Kitamura, Y.; Hasegawa, M.; Hayashi, Y.; Chiba, T.; Sadamasu, K. & Yoshimura, K. (2020), 'Characteristics of SARS-CoV-2 isolated from asymptomatic carrier in Tokyo', *Japanese Journal of Infectious Diseases* **advpub**.

- Naqvi, A. A. T.; Fatima, K.; Mohammad, T.; Fatima, U.; Singh, I. K.; Singh, A.; Atif, S. M.; Hariprasad, G.; Hasan, G. M. & Hassan, M. I. (2020), 'Insights into SARS-CoV-2 genome, structure, evolution, pathogenesis and therapies: Structural genomics approach', *Biochimica et Biophysica Acta. Molecular Basis of Disease* **1866**(10), 165878.
- Nelson, C. W.; Ardern, Z.; Goldberg, T. L.; Meng, C.; Kuo, C.-H.; Ludwig, C.; Kolokotronis, S.-O. & Wei, X. (2020), 'A previously uncharacterized gene in SARS-CoV-2 illuminates the functional dynamics and evolutionary origins of the COVID-19 pandemic', *bioRxiv*, 2020.05.21.109280.
- Nelson-Sathi, S.; Umashankar Perunthottathu, K.; Easwaran, S.; Nair, R. R.; Joseph, I.; Nori, S. R. C.; Philip, J. S.; Prasad, R.; Kolaparamba, K. V.; Ramesh, S.; Pillai, H.; Gosh, S.; Tr, S. K. & Pillai, M. R. (2020), 'Structural and Functional Implications of Non-synonymous Mutations in the Spike protein of 2,954 SARS-CoV-2 Genomes', *bioRxiv*, 2020.05.02.071811.
- Nemudryi, A.; Nemudraia, A.; Surya, K.; Wiegand, T.; Buyukyoruk, M.; Wilkinson, R. & Wiedenheft, B. (2020), 'Temporal detection and phylogenetic assessment of SARS-CoV-2 in municipal wastewater', *medRxiv*, 2020.04.15.20066746.
- Nguyen, T. T.; Pathirana, P. N.; Nguyen, T.; Nguyen, H.; Bhatti, A.; Nguyen, D. C.; Nguyen, D. T.; Nguyen, N. D.; Creighton, D. & Abdelrazek, M. (2020), 'Genomic Mutations and Changes in Protein Secondary Structure and Solvent Accessibility of SARS-CoV-2 (COVID-19 Virus)', *bioRxiv*, 2020.07.10.171769.
- Nie, Q.; Li, X.; Chen, W.; Liu, D.; Chen, Y.; Li, H.; Li, D.; Tian, M.; Tan, W. & Zai, J. (2020), 'Phylogenetic and phylodynamic analyses of SARS-CoV-2', *Virus Research* **287**, 198098.
- Nielsen, R.; Wang, H. & Pipes, L. (2020), 'Synonymous mutations and the molecular evolution of SARS-Cov-2 origins', *bioRxiv*, 2020.04.20.052019.
- Nomburg, J.; Meyerson, M. & DeCaprio, J. A. (2020), 'Pervasive generation of non-canonical subgenomic RNAs by SARS-CoV-2', *bioRxiv*, 2020.04.28.066951.
- Nour, I.; Alanazi, I. O.; Hanif, A.; Kohl, A. & Eifan, S. A. (2020), 'Insights into molecular evolution recombination of pandemic SARS-CoV-2 using Saudi Arabian sequences', *bioRxiv*, 2020.05.13.093971.
- O'Toole, Á. & McCrone, J. T. (2020), 'hCoV-2019/pangolin', GitHub, S0041.
- Oreshkova, N.; Molenaar, R.-J.; Vreman, S.; Harders, F.; Munnink, B. B. O.; Honing, R. W. H.-v.; Gerhards, N.; Tolsma, P.; Bouwstra, R.; Sikkema, R.; Tacken, M.; Rooij, M. M. T. d.; Weesendorp, E.; Engelsma, M.; Brusckhe, C.; Smit, L. A. M.; Koopmans, M.; Poel, W. H. M. v. d. & Stegeman, J. A. (2020), 'SARS-CoV2 infection in farmed mink, Netherlands, April 2020', *bioRxiv*, 2020.05.18.101493.

Othman, H.; Bouslama, Z.; Brandenburg, J.-T.; Rocha, J. d.; Hamdi, Y.; Ghedira, K.; Abid, N.-S. & Hazelhurst, S. (2020), 'Interaction of the spike protein RBD from SARS-CoV-2 with ACE2: similarity with SARS-CoV, hot-spot analysis and effect of the receptor polymorphism', *bioRxiv*, 2020.03.04.976027.

Ou, X.; Yang, Z.; Zhu, D.; Mao, S.; Wang, M.; Jia, R.; Chen, S.; Liu, M.; Yang, Q.; Wu, Y.; Zhao, X.; Zhang, S.; Huang, J.; Gao, Q.; Liu, Y.; Zhang, L.; Peopplenbosch, M.; Pan, Q. & Cheng, A.-c. (2020), 'Tracing two causative SNPs reveals SARS-CoV-2 transmission in North America population', *bioRxiv*, 2020.05.12.092056.

Pach, S.; Nguyen, T. N.; Trimpert, J.; Kunec, D.; Osterrieder, N. & Wolber, G. (2020), 'ACE2-Variants Indicate Potential SARS-CoV-2-Susceptibility in Animals: An Extensive Molecular Dynamics Study', *bioRxiv*, 2020.05.14.092767.

Pachetti, M.; Marini, B.; Giudici, F.; Benedetti, F.; Angeletti, S.; Ciccozzi, M.; Masciovecchio, C.; Ippodrino, R. & Zella, D. (2020), 'Impact of lockdown on Covid-19 case fatality rate and viral mutations spread in 7 countries in Europe and North America', *Journal of Translational Medicine* **18**(1), 338.

Paden, C. R.; Tao, Y.; Queen, K.; Zhang, J.; Li, Y.; Uehara, A. & Tong, S. (2020), 'Rapid, sensitive, full genome sequencing of Severe Acute Respiratory Syndrome Virus Coronavirus 2 (SARS-CoV-2)', *bioRxiv*, 2020.04.22.055897.

Parag, K. V.; du Plessis, L. & Pybus, O. G. (2020), 'Jointly Inferring the Dynamics of Population Size and Sampling Intensity from Molecular Sequences', *Molecular Biology and Evolution* **37**(8), 2414--2429.

Park, J. J. & Chen, S. (2020), 'Metaviromic identification of genetic hotspots of coronavirus pathogenicity using machine learning', *bioRxiv*, 2020.08.13.248575.

Parvez, M. S. A.; Rahman, M. M.; Morshed, M. N.; Rahman, D.; Anwar, S. & Hosen, M. J. (2020), 'Genetic analysis of SARS-CoV-2 isolates collected from Bangladesh: insights into the origin, mutation spectrum, and possible pathomechanism', *bioRxiv*, 2020.06.07.138800.

Pascall, D. J.; Nomikou, K.; Bréard, E.; Zientara, S.; Filipe, A. d. S.; Hoffmann, B.; Jacquot, M.; Singer, J. B.; Clercq, K. D.; Bøtner, A.; Sailleau, C.; Viarouge, C.; Batten, C.; Puggioni, G.; Ligios, C.; Savini, G.; Rijn, P. A. v.; Mertens, P. P. C.; Biek, R. & Palmarini, M. (2020), "'Frozen evolution" of an RNA virus suggests accidental release as a potential cause of arbovirus re-emergence', *PLOS Biology* **18**(4), e3000673.

Pasquier, C. & Robichon, A. (2020), 'Computational search of hybrid human/ SARS-CoV-2 dsRNA reveals unique viral sequences that diverge from other coronavirus strains', *bioRxiv*, 2020.04.08.031856.

Patro, L. P. P.; Sathyaseelan, C.; Uttamrao, P. P. & Rathinavelan, T. (2020), 'Global variation in the SARS-CoV-2 proteome reveals the mutational hotspots in the drug and vaccine candidates', *bioRxiv*, 2020.07.31.230987.

Paul, D.; Jani, K.; Kumar, J.; Chauhan, R.; Seshadri, V.; Lal, G.; Karyakarte, R.; Joshi, S.; Tambe, M.; Sen, S.; Karade, S.; Anand, K. B.; Shergill, S. P. S.; Gupta, R. M.; Bhat, M. K.; Sahu, A. & Shouche, Y. S. (2020), 'Phylogenomic analysis of SARS-CoV-2 genomes from western India reveals unique linked mutations', *bioRxiv*, 2020.07.30.228460.

Pavesi, A. (2020), 'New insights into the evolutionary features of viral overlapping genes by discriminant analysis', *Virology* **546**, 51--66.

Peccia, J.; Zulli, A.; Brackney, D. E.; Grubaugh, N. D.; Kaplan, E. H.; Casanovas-Massana, A.; Ko, A. I.; Malik, A. A.; Wang, D.; Wang, M.; Weinberger, D. M. & Omer, S. B. (2020), 'SARS-CoV-2 RNA concentrations in primary municipal sewage sludge as a leading indicator of COVID-19 outbreak dynamics', *medRxiv*, 2020.05.19.20105999.

Peddu, V.; Shean, R. C.; Xie, H.; Shrestha, L.; Perchetti, G. A.; Minot, S. S.; Roychoudhury, P.; Huang, M.-L.; Nalla, A.; Reddy, S. B.; Phung, Q.; Reinhardt, A.; Jerome, K. R. & Greninger, A. L. (2020), 'Metagenomic analysis reveals clinical SARS-CoV-2 infection and bacterial or viral superinfection and colonization', *Clinical Chemistry*.

Peñarrubia, L.; Ruiz, M.; Porco, R.; Rao, S. N.; Juanola-Falgarona, M.; Manissero, D.; López-Fontanals, M. & Pareja, J. (2020), 'Multiple assays in a real-time RT-PCR SARS-CoV-2 panel can mitigate the risk of loss of sensitivity by new genomic variants during the COVID-19 outbreak', *International journal of infectious diseases: IJID: official publication of the International Society for Infectious Diseases* **97**, 225--229.

Pereira, F. (2020), 'Evolutionary dynamics of the SARS-CoV-2 ORF8 accessory gene', *Infection, Genetics and Evolution* **85**, 104525.

Pereson, M. J.; Mojsiejczuk, L.; Martinez, A. P.; Flichman, D. M.; Garcia, G. H. & Lello, F. A. D. (2020), 'THE ORIGIN OF A NEW HUMAN VIRUS: PHYLOGENETIC ANALYSIS OF THE EVOLUTION OF SARS-COV-2', *bioRxiv*, 2020.07.21.212860.

Phan, T. (2020), 'Genetic diversity and evolution of SARS-CoV-2', *Infection, Genetics and Evolution* **81**, 104260.

Phelan, J.; Deelder, W.; Ward, D.; Campino, S.; Hibberd, M. L. & Clark, T. G. (2020), 'Controlling the SARS-CoV-2 outbreak, insights from large scale whole genome sequences generated across the world', *bioRxiv*, 2020.04.28.066977.

Picardi, E.; Mansi, L. & Pesole, G. (2020), 'A-to-I RNA editing in SARS-COV-2: real or artifact?', *bioRxiv*, 2020.07.27.223172.

Pillay, S.; Giandhari, J.; Tegally, H.; Wilkinson, E.; Chimukangara, B.; Lessells, R.; Mattison, S.; Moosa, Y.; Gazy, I.; Fish, M.; Singh, L.; Khanyile, K. S.; Fonseca, V.; Giovanetti, M.; Alcantara, L. C. J. & Oliveira, T. d. (2020), 'Whole Genome Sequencing of SARS-CoV-2: Adapting Illumina Protocols for Quick and Accurate Outbreak Investigation During a Pandemic', *bioRxiv*, 2020.06.10.144212.

Pipes, L.; Wang, H.; Huelsenbeck, J. & Nielsen, R. (2020), 'Assessing uncertainty in the rooting of the SARS-CoV-2 phylogeny', *bioRxiv*, 2020.06.19.160630.

Plyusnin, I.; Kant, R.; Jääskeläinen, A. J.; Sironen, T.; Holm, L.; Vapalahti, O. & Smura, T. (2020), 'Novel NGS Pipeline for Virus Discovery from a Wide Spectrum of Hosts and Sample Types', *bioRxiv*, 2020.05.07.082107.

Pollock, D. D.; Castoe, T. A.; Perry, B. W.; Lytras, S.; Wade, K. J.; Robertson, D. L.; Holmes, E. C.; Boni, M. F.; Kosakovsky Pond, S. L.; Parry, R.; Carlton, E. J.; Wood, J. L. N.; Pennings, P. S. & Goldstein, R. A. (2020), 'Viral CpG deficiency provides no evidence that dogs were intermediate hosts for SARS-CoV-2', *Molecular Biology and Evolution*.

Pond, S. (2020), 'Natural selection analysis of SARS-CoV-2/COVID-19', S0019.

Pond, S. (2020), 'Testing recombination in the pandemic SARS-CoV-2 strains', *Virological*, S0175.

Popa, A.; Genger, J.-W.; Nicholson, M.; Penz, T.; Schmid, D.; Aberle, S. W.; Agerer, B.; Lercher, A.; Endler, L.; Colaco, H.; Smyth, M.; Schuster, M.; Grau, M.; Jimenez, F. M.; Pich, O.; Borena, W. T.; Pawelka, E.; Keszei, Z.; Senekowitsch, M.; Laine, J.; Aberle, J.; Redlberger-Fritz, M.; Karolyi, M.; Zoufaly, A.; Maritschnik, S.; Borkovec, M.; Hufnagl, P.; Nairz, M.; Weiss, G.; Wolfinger, M. T.; Laer, D. v.; Superti-Furga, G.; Lopez-Bigas, N.; Puchhammer-Stoeckl, E.; Allerberger, F.; Michor, F.; Bock, C. & Bergthaler, A. (2020), 'Mutational dynamics and transmission properties of SARS-CoV-2 superspreading events in Austria', *bioRxiv*, 2020.07.15.204339.

Portelli, S.; Olshansky, M.; Rodrigues, C. H. M.; D'Souza, E. N.; Myung, Y.; Silk, M.; Alavi, A.; Pires, D. E. V. & Ascher, D. B. (2020), 'COVID-3D: An online resource to explore the structural distribution of genetic variation in SARS-CoV-2 and its implication on therapeutic development', *bioRxiv*, 2020.05.29.124610.

Prasad, P.; Prakash, S.; Sahu, K.; Singh, B.; Shukla, S.; Mishra, H.; Khan, D. N.; Prakash, O.; Bhatt, M. L. B.; Barik, S. K.; Asif, M. H.; Sawant, S. V.; Jain, A. & Bag, S. K. (2020), 'Unique mutational changes in SARS-CoV2 genome of different state of India', *bioRxiv*, 2020.08.24.265827.

Pratas, D. & Silva, J. M. (2020), 'Persistent minimal sequences of SARS-CoV-2', *Bioinformatics*.

Prathiviraj, R.; Kiran, G. S. & Selvin, J. (2020), 'Phylogenomic proximity and comparative proteomic analysis of SARS-CoV-2', *Gene Reports* **20**, 100777.

Pybus, O.; Rambaut, A.; du Plessis, L.; Zarebski, A. E.; Kraemer, M. U. G.; Raghwani, J.; Gutiérrez, B.; Hill, V.; McCrone, J.; Colquhoun, R.; Jackson, B.; O'Toole, Á. & Ashworth, J. (2020), 'Preliminary analysis of SARS-CoV-2 importation & establishment of UK transmission lineages', *Virological*, S0218.

Quick, J. (2020), 'Artic-ncov2019 primer schemes', ARTIC, S0013.

Rad, A. H. & McLellan, A. D. (2020), 'Implications of SARS-CoV-2 mutations for genomic RNA structure and host microRNA targeting', *bioRxiv*, 2020.05.15.098947.

Radhakrishnan, C.; Divakar, M. K.; Jain, A.; Viswanathan, P.; Bhoyar, R. C.; Jolly, B.; Imran, M.; Sharma, D.; Rophina, M.; Ranjan, G.; Jose, B. P.; Raman, R. V.; Kesavan, T. N.; George, K.; Mathew, S.; Poovullathil, J. K.; Govindan, S. K. K.; Nair, P. R.; Vadakkandiyil, S.; Gladson, V.; Mohan, M.; Parambath, F. C.; Mangla, M.; Shamnath, A.; Sivasubbu, S. & Scaria, V. (2020), 'Initial insights into the genetic epidemiology of SARS-CoV-2 isolates from Kerala suggest local spread from limited introductions', *bioRxiv*, 2020.09.09.289892.

Raghav, S.; Ghosh, A.; Turuk, J.; Kumar, S.; Jha, A.; Madhulika, S.; Priyadarshini, M.; Biswas, V. K.; Shyamli, P. S.; Singh, B.; Singh, N.; Singh, D.; Kiran, A.; Smita, S.; Sabat, J.; Bhattacharya, D.; Dash, R.; Senapati, S.; Beuria, T. K.; Swain, R.; Chattopadhyay, S.; Syed, G. H.; Dixit, A.; Prasad, P.; Pati, S. & Parida, A. (2020), 'SARS-CoV2 genome analysis of Indian isolates and molecular modelling of D614G mutated spike protein with TMPRSS2 depicted its enhanced interaction and virus infectivity', *bioRxiv*, 2020.07.23.217430.

Rahman, M. S.; Islam, M. R.; Alam, A. S. M. R. U.; Islam, I.; Hoque, M. N.; Akter, S.; Rahaman, M. M.; Sultana, M. & Hossain, M. A. (2020), 'Evolutionary dynamics of SARS-CoV-2 nucleocapsid protein (N protein) and its consequences', *bioRxiv*, 2020.08.05.237339.

Rahman, M. S.; Islam, M. R.; Hoque, M. N.; Alam, A. S. M. R. U.; Akther, M.; Puspo, J. A.; Akter, S.; Anwar, A.; Sultana, M. & Hossain, M. A. (2020), 'Comprehensive annotations of the mutational spectra of SARS-CoV-2 spike protein: a fast and accurate pipeline', *bioRxiv*, 2020.06.29.177238.

Ramazzotti, D.; Angaroni, F.; Maspero, D.; Gambacorti-Passerini, C.; Antoniotti, M.; Graudenzi, A. & Piazza, R. (2020), 'Characterization of intra-host SARS-CoV-2 variants improves phylogenomic reconstruction and may reveal functionally convergent mutations', *bioRxiv*, 2020.04.22.044404.

Rambaut, A.; Holmes, E. C.; O'Toole, Á.; Hill, V.; McCrone, J. T.; Ruis, C.; du Plessis, L. & Pybus, O. G. (2020), 'A dynamic nomenclature proposal for SARS-CoV-2 lineages

to assist genomic epidemiology', *Nature Microbiology*, <https://doi.org/10.1038/s41564-020-0770-5>.

Rambaut, A.; Holmes, E. C. & Pybus, O. G. (2020), 'A dynamic nomenclature for SARS-CoV-2 to assist genomic epidemiology', *Virological*, S0018.

Ramírez, J. D.; Florez, C.; Muñoz, M.; Hernández, C.; Castillo, A.; Gomez, S.; Rico, A.; Pardo, L.; Barros, E. C.; Castañeda, S.; Ballesteros, N.; Martínez, D.; Vega, L.; Jaimes, J. E.; Cruz Saavedra, L.; Herrera, G.; Patiño, L. H.; Teherán, A. A.; Gonzalez Reiche, A. S.; Hernandez, M. M.; Sordillo, E. M.; Simon, V.; Bakel, H. v. & Paniz Mondolfi, A. (2020), 'The arrival and spread of SARS-CoV2 in Colombia', *Journal of Medical Virology* **Accepted manuscript online**(n/a).

Ramirez, J. D.; Munoz, M.; Hernandez, C.; Florez, C.; Gomez, S.; Rico, A.; Pardo, L.; Barros, E. C. & Paniz-Mondolfi, A. (2020), 'Genetic diversity among SARS-CoV2 strains in South America may impact performance of Molecular detection', *medRxiv*, 2020.06.18.20134759.

Rana, D. R. S. J. B. & Pokhrel, N. (2020), 'Sequence mismatch in PCR probes may mask the COVID-19 detection in Nepal', *Molecular and Cellular Probes* **53**, 101599.

Randazzo, W.; Truchado, P.; Cuevas-Ferrando, E.; Simón, P.; Allende, A. & Sánchez, G. (2020), 'SARS-CoV-2 RNA in wastewater anticipated COVID-19 occurrence in a low prevalence area', *Water Research*, 115942.

Rangan, R.; Zheludev, I. N.; Hagey, R. J.; Pham, E. A.; Wayment-Steele, H. K.; Glenn, J. S. & Das, R. (2020), 'RNA genome conservation and secondary structure in SARS-CoV-2 and SARS-related viruses: a first look', *RNA* **26**(8), 937--959.

Ray, M.; Sarkar, S.; Rath, S. N. & Sable, M. N. (2020), 'Elucidation of Genome Polymorphisms in Emerging SARS-CoV-2', *bioRxiv*, 2020.07.22.215731.

Rayko, M. & Komissarov, A. (2020), 'Quality control of low-frequency variants in SARS-CoV-2 genomes', *bioRxiv*, 2020.04.26.062422.

Resende, P. C.; Delatorre, E.; Graf, T.; Mir, D.; Motta, F. C.; Appolinario, L.; Paixao, A. C. D.; Ogrzewalska, M.; Caetano, B.; Santos, M. C.; Ferreira, J. A.; Junior, E. C. S.; Silva, S. P.; Fernandes, S. B.; Vianna, L. A.; Costa, L.; Ferro, J.; Nardy, V.; Croda, J.; Oliveira, W. K.; Abreu, A. L. d.; Bello, G. & Siqueira, M. M. (2020), 'Genomic surveillance of SARS-CoV-2 reveals community transmission of a major lineage during the early pandemic phase in Brazil', *bioRxiv*, 2020.06.17.158006.

Resende, P. C.; Motta, F. C.; Roy, S.; Appolinario, L.; Fabri, A.; Xavier, J.; Harris, K.; Matos, A. R.; Caetano, B. C.; Garcia, C. C.; Miranda, M. D.; Ogrzewalska, M.; Abreu, A.; Williams, R.; Breuer, J. & Siqueira, M. M. (2020), 'SARS-CoV-2 genomes recovered by long amplicon tiling multiplex approach using nanopore sequencing and applicable to

other sequencing platforms', *bioRxiv*, 2020.04.30.069039.

Rice, A. M.; Morales, A. C.; Ho, A. T.; Mordstein, C.; Mühlhausen, S.; Watson, S.; Cano, L.; Young, B.; Kudla, G. & Hurst, L. D. (2020), 'Evidence for strong mutation bias towards, and selection against, U content in SARS-CoV-2: implications for vaccine design', *Molecular Biology and Evolution*.

Riojas, M. A.; Frank, A. M.; Puthuveetil, N. P.; Flores, B.; Parker, M.; King, S. P.; Peiris, M.; Chu, D. K. W.; Benton, B.; Bradford, R.; Hazbón, M. H. & Rashid, S. (2020), 'A Rare Deletion in SARS-CoV-2 ORF6 Dramatically Alters the Predicted Three-Dimensional Structure of the Resultant Protein', *bioRxiv*, 2020.06.09.134460.

Rojas, C. P.; Chozo, K. V.; Perez, M. G.; Calderon, H. B.; Pari, P. L.; Torres, J. B.; Neyra, D. G.; Nunez, M. H.; Serrano, N. R. & Rey, O. C. (2020), 'Genomic analysis reveals local transmission of SARS-CoV-2 in early pandemic phase in Peru', *bioRxiv*, 2020.09.05.284604.

Ryder, S. P. (2020), 'Analysis of Rapidly Emerging Variants in Structured Regions of the SARS-CoV-2 Genome', *bioRxiv*, 2020.05.27.120105.

Sadykov, M.; Mourier, T.; Guan, Q. & Pain, A. (2020), 'Short sequence motif dynamics in the SARS-CoV-2 genome suggest a role for cytosine deamination in CpG reduction.', *bioRxiv*, 2020.06.19.161687.

Sah, R.; Rodriguez-Morales, A. J.; Jha, R.; Chu, D. K. W.; Gu, H.; Peiris, M.; Bastola, A.; Lal, B. K.; Ojha, H. C.; Rabaan, A. A.; Zambrano, L. I.; Costello, A.; Morita, K.; Pandey, B. D. & Poon, L. L. M. (2020), 'Complete Genome Sequence of a 2019 Novel Coronavirus (SARS-CoV-2) Strain Isolated in Nepal', *Microbiology Resource Announcements* **9**(11).

Saha, O.; Shatadru, R. N.; Rakhi, N. N.; Islam, I.; Hossain, M. S. & Rahaman, M. M. (2020), 'Temporal landscape of mutation accumulation in SARS-CoV-2 genomes from Bangladesh: possible implications from the ongoing outbreak in Bangladesh', *bioRxiv*, 2020.08.20.259721.

Saha, P.; Banerjee, A. K.; Tripathi, P. P.; Srivastava, A. K. & Ray, U. (2020), 'A virus that has gone viral: Amino-acid mutation in S protein of Indian-isolate of Coronavirus COVID-19 might impact receptor-binding, thus infectivity', *Bioscience Reports*.

Saha, S.; Malaker, R.; Sajib, M. S. I.; Hasanuzzaman, M.; Rahman, H.; Ahmed, Z. B.; Islam, M. S.; Islam, M.; Hooda, Y.; Ahyong, V.; Vanaerschot, M.; Batson, J.; Hao, S.; Kamm, J.; Kistler, A.; Tato, C. M.; DeRisi, J. L. & Saha, S. K. (2020), 'Complete Genome Sequence of a Novel Coronavirus (SARS-CoV-2) Isolate from Bangladesh', *Microbiology Resource Announcements* **9**(24).

Saif, R.; Mahmood, T. & Ejaz, A. (2020), 'Whole Genome Comparison of Pakistani

Corona Virus with Chinese and US Strains along with its Predictive Severity of COVID-19', *bioRxiv*, 2020.05.01.072942.

Sailleau, C.; Dumarest, M.; Vanhomwegen, J.; Delaplace, M.; Caro, V.; Kwasiborski, A.; Hourdel, V.; Chevaillier, P.; Barbarino, A.; Comtet, L.; Pourquier, P.; Klonjowski, B.; Manuguerra, J. C.; Zientara, S. & Poder, S. L. (2020), 'First detection and genome sequencing of SARS-CoV-2 in an infected cat in France', *Transboundary and Emerging Diseases* n/a(n/a).

Salazar, C.; Diaz-Viraque, F.; Pereira-Gomez, M.; Ferres, I.; Moreno, P.; Moratorio, G. & Iraola, G. (2020), 'Multiple introductions, regional spread and local differentiation during the first week of COVID-19 epidemic in Montevideo, Uruguay', *bioRxiv*, 2020.05.09.086223.

Sallard, E.; Halloy, J.; Casane, D.; Helden, J. v. & Decroly, É. (2020), 'Retrouver les origines du SARS-CoV-2 dans les phylogénies de coronavirus', *médecine/sciences*.

Sanyal, D.; Chowdhury, S.; Uversky, V. N. & Chattopadhyay, K. (2020), 'An exploration of the SARS-CoV-2 spike receptor binding domain (RBD), a complex palette of evolutionary and structural features', *bioRxiv*, 2020.05.31.126615.

Sapoval, N.; Mahmoud, M.; Jochum, M. D.; Liu, Y.; Elworth, R. A. L.; Wang, Q.; Albin, D.; Ogilvie, H.; Lee, M. D.; Villapol, S.; Hernandez, K.; Berry, I. M.; Foox, J.; Beheshti, A.; Ternus, K.; Aagaard, K. M.; Posada, D.; Mason, C.; Sedlazeck, F. J. & Treangen, T. J. (2020), 'Hidden genomic diversity of SARS-CoV-2: implications for qRT-PCR diagnostics and transmission', *bioRxiv*, 2020.07.02.184481.

Sashittal, P.; Luo, Y.; Peng, J. & El-Kebir, M. (2020), 'Characterization of SARS-CoV-2 viral diversity within and across hosts', *bioRxiv*, 2020.05.07.083410.

Sawmya, S.; Saha, A.; Tasnim, S.; Anjum, N.; Toufikuzzaman, M.; Rafid, A. H. M.; Rahman, M. S. & Rahman, M. S. (2020), 'Analyzing hCov genome sequences: Applying Machine Intelligence and beyond', *bioRxiv*, 2020.06.03.131987.

Schuster, N. A. (2020), 'Using the nucleocapsid protein to investigate the relationship between SARS-CoV-2 and closely related bat and pangolin coronaviruses', *bioRxiv*, 2020.06.25.172312.

Seemann, T.; Lane, C.; Sherry, N.; Duchene, S.; Silva, A. G. d.; Caly, L.; Sait, M.; Ballard, S. A.; Horan, K.; Schultz, M. B.; Hoang, T.; Easton, M.; Dougall, S.; Stinear, T.; Druce, J.; Catton, M.; Sutton, B.; Diemen, A. v.; Alpren, C.; Williamson, D. & Howden, B. P. (2020), 'Tracking the COVID-19 pandemic in Australia using genomics', *medRxiv*, 2020.05.12.20099929.

Sekizuka, T.; Itokawa, K.; Kageyama, T.; Saito, S.; Takayama, I.; Asanuma, H.; Naganori, N.; Tanaka, R.; Hashino, M.; Takahashi, T.; Kamiya, H.; Yamagishi, T.;

Kakimoto, K.; Suzuki, M.; Hasegawa, H.; Wakita, T. & Kuroda, M. (2020), 'Haplotype networks of SARS-CoV-2 infections in the Diamond Princess cruise ship outbreak', *medRxiv*, 2020.03.23.20041970.

Sharma, A. K. & Som, A. (2020), 'Deep phylogenetic analysis of Orthocoronavirinae genomes traces the origin, evolution and transmission route of 2019 novel coronavirus', *bioRxiv*, 2020.05.12.091199.

Sharma, G.; Kolte, V.; Shenu Hudson, B. & Khan, A. (2020), 'Dynamic tracking of variant frequencies depicts the evolution of mutation sites amongst SARS-CoV-2 genomes from India', *bioRxiv*, 2020.07.14.201905.

Sheikh, J. A.; Singh, J.; Singh, H.; Jamal, S.; Khubaib, M.; Kohli, S.; Dobrindt, U.; Rahman, S. A.; Ehtesham, N. Z. & Hasnain, S. E. (2020), 'Emerging genetic diversity among clinical isolates of SARS-CoV-2: Lessons for today', *Infection, Genetics and Evolution* **84**, 104330.

Shen, L.; Bard, J. D.; Biegel, J. A.; Judkins, A. R. & Gai, X. (2020), 'Comprehensive variant and haplotype landscapes of 50,500 global SARS-CoV-2 isolates and accelerating accumulation of country-private variant profiles', *bioRxiv*, 2020.07.09.193722.

Shen, L.; Maglinte, D.; Ostrow, D.; Pandey, U.; Bootwalla, M.; Ryutov, A.; Govindarajan, A.; Ruble, D.; Han, J.; Triche, T. J.; Bard, J. D.; Biegel, J. A.; Judkins, A. R. & Gai, X. (2020), 'Children's Hospital Los Angeles COVID-19 Analysis Research Database (CARD) - A Resource for Rapid SARS-CoV-2 Genome Identification Using Interactive Online Phylogenetic Tools', *bioRxiv*, 2020.05.11.089763.

Shishir, T. A.; Naser, I. B. & Faruque, S. M. (2020), 'In silico comparative genomics of SARS-CoV-2 to determine the source and diversity of the pathogen in Bangladesh', *bioRxiv*, 2020.07.20.212563.

Simmonds, P. (2020), 'Rampant C->U hypermutation in the genomes of SARS-CoV-2 and other coronaviruses – causes and consequences for their short and long evolutionary trajectories', *bioRxiv*, 2020.05.01.072330.

Simmonds, P. (2020), 'Pervasive RNA secondary structure in the genomes of SARS-CoV-2 and other coronaviruses – an endeavour to understand its biological purpose', *bioRxiv*, 2020.06.17.155200.

Simmonds, P. (2020), 'Rampant C → U Hypermutation in the Genomes of SARS-CoV-2 and Other Coronaviruses: Causes and Consequences for Their Short- and Long-Term Evolutionary Trajectories', *mSphere* **5**(3).

Singer, J.; Gifford, R.; Cotten, M. & Robertson, D. (2020), 'CoV-GLUE: A Web Application for Tracking SARS-CoV-2 Genomic Variation', **Preprints 2020, 2020060225**.

Siqueira, J.; Goes, L. R.; Alves, B. M.; Carvalho, P. S. d.; Cicala, C.; Arthos, J.; Viola, J. P. B.; Melo, A. C. d.; Soares, M. A. & (names of participants listed in the acknowledgements section), I. C. O. V. I. D.-19. T. F. (2020), 'SARS-CoV-2 genomic and quasispecies analyses in cancer patients reveal relaxed intrahost virus evolution', *bioRxiv*, 2020.08.26.267831.

Sjaarda, C. P.; Rustom, N.; Huang, D.; Perez-Patrigeon, S.; Hudson, M. L.; Wong, H.; Guan, T. H.; Ayub, M.; Soares, C. N.; Colautti, R. I.; Evans, G. A. & Sheth, P. M. (2020), 'Chasing the origin of SARS-CoV-2 in Canada's COVID-19 cases: A genomics study', *bioRxiv*, 2020.06.25.171744.

Song, F.; Zhang, X.; Zha, Y. & Liu, W. (2020), 'COVID-19: Recommended sampling sites at different stage of the disease', *Journal of Medical Virology* **n/a**(n/a).

Song, S.; Ma, L.; Zou, D.; Tian, D.; Li, C.; Zhu, J.; Chen, M.; Wang, A.; Ma, Y.; Li, M.; Teng, X.; Cui, Y.; Duan, G.; Zhang, M.; Jin, T.; Shi, C.; Du, Z.; Zhang, Y.; Liu, C.; Li, R.; Zeng, J.; Hao, L.; Jiang, S.; Chen, H.; Han, D.; Xiao, J.; Zhang, Z.; Zhao, W.; Xue, Y. & Bao, Y. (2020), 'The global landscape of SARS-CoV-2 genomes, variants, and haplotypes in 2019nCoV-R', *bioRxiv*, 2020.08.30.273235.

Soratto, T. A. T.; Darban, H.; Bjerkner, A.; Coorens, M.; Albert, J.; Allander, T. & Andersson, B. (2020), 'SARS-CoV-2 genome sequences from late April in Stockholm, Sweden reveal a novel mutation in the spike protein', *bioRxiv*, 2020.08.03.233866.

Speranskaya, A.; Kaptelova, V.; Valdokhina, A.; Bulanenko, V.; Samoilov, A.; Korneenko, E.; Shipulina, O. & Akimkin, V. (2020), 'SCV-2000bp: a primer panel for SARS-CoV-2 full-genome sequencing', *bioRxiv*, 2020.08.04.234880.

Starr, T. N.; Greaney, A. J.; Hilton, S. K.; Crawford, K. H. D.; Navarro, M. J.; Bowen, J. E.; Tortorici, M. A.; Walls, A. C.; Velesler, D. & Bloom, J. D. (2020), 'Deep mutational scanning of SARS-CoV-2 receptor binding domain reveals constraints on folding and ACE2 binding', *bioRxiv*, 2020.06.17.157982.

Stefanelli, P.; Faggioni, G.; Presti, A. L.; Fiore, S.; Marchi, A.; Benedetti, E.; Fabiani, C.; Anselmo, A.; Ciammaruconi, A.; Fortunato, A.; Santis, R. D.; Fillo, S.; Capobianchi, M. R.; Gismondo, M. R.; Ciervo, A.; Rezza, G.; Castrucci, M. R.; Lista, F. & Group, o. b. o. I. C. O. V. I. D.-19. s. (2020), 'Whole genome and phylogenetic analysis of two SARS-CoV-2 strains isolated in Italy in January and February 2020: additional clues on multiple introductions and further circulation in Europe', *Eurosurveillance* **25**(13), 2000305.

Su, Y. C. F.; Anderson, D. E.; Young, B. E.; Linster, M.; Zhu, F.; Jayakumar, J.; Zhuang, Y.; Kalimuddin, S.; Low, J. G. H.; Tan, C. W.; Chia, W. N.; Mak, T. M.; Octavia, S.; Chavatte, J.-M.; Lee, R. T. C.; Pada, S.; Tan, S. Y.; Sun, L.; Yan, G. Z.; Maurer-Stroh, S.; Mendenhall, I. H.; Leo, Y.-S.; Lye, D. C.; Wang, L.-F. & Smith, G. J. D. (2020), 'Discovery and Genomic Characterization of a 382-Nucleotide Deletion in ORF7b and

ORF8 during the Early Evolution of SARS-CoV-2', *mBio* **11**(4).

Sun, F.; Wang, X.; Tan, S.; Dan, Y.; Lu, Y.; Zhang, J.; Xu, J.; Tan, Z.; Xiang, X.; Zhou, Y.; He, W.; Wan, X.; Zhang, W.; Chen, Y.; Tan, W. & Deng, G. (2020), 'SARS-CoV-2 Quasispecies provides insight into its genetic dynamics during infection', *bioRxiv*, 2020.08.20.258376.

Sun, L.; Li, P.; Ju, X.; Rao, J.; Huang, W.; Zhang, S.; Xiong, T.; Xu, K.; Zhou, X.; Ren, L.; Ding, Q.; Wang, J. & Zhang, Q. C. (2020), 'In vivo structural characterization of the whole SARS-CoV-2 RNA genome identifies host cell target proteins vulnerable to re-purposed drugs', *bioRxiv*, 2020.07.07.192732.

Sun, W. (2020), 'The discovery of gene mutations making SARS-CoV-2 well adapted for humans: host-genome similarity analysis of 2594 genomes from China, the USA and Europe', *bioRxiv*, 2020.09.03.280727.

Suzuki, Y. (2020), 'Methods for making multiple alignment of genomic sequences for severe acute respiratory syndrome coronavirus 2', *Meta Gene* **26**, 100785.

Taboada, B.; Vázquez-Pérez, J. A.; Muñoz-Medina, J. E.; Ramos-Cervantes, P.; Escalera-Zamudio, M.; Boukadida, C.; Sánchez-Flores, A.; Pavel, I.; Mendieta-Condado, E.; Martínez-Orozco, J. A.; Becerril-Vargas, E.; Salas-Hernández, J.; Grande, R.; González-Torres, C.; Gaytán-Cervantes, F. J.; Vázquez, G.; Pulido, F.; Araiza-Rodríguez, A.; Garcés-Ayala, F.; González-Bonilla, C. R.; Grajales-Muñiz, C.; Borja-Aburto, V. H.; Barrera-Badillo, G.; López, S.; Hernández-Rivas, L.; Pérez-Padilla, R.; Martínez, I. L.; Avila-Rios, S.; Ruiz-Palacios, G.; Ramirez-Gonzalez, J. E. & Arias, C. F. (2020), 'Genomic analysis of early SARS-CoV-2 strains introduced in Mexico', *bioRxiv*, 2020.05.27.120402.

Tagliamonte, M. S.; Adid, N.; Ostrov, D. A.; Chillemi, G.; Pond, S. L. K.; Salemi, M. & Mavian, C. N. (2020), 'Recombination and purifying selection preserves covariant movements of mosaic SARS-CoV-2 protein S', *bioRxiv*, 2020.03.30.015685.

Tavares, R. d. C. A.; Mahadeshwar, G. & Pyle, A. M. (2020), 'The global and local distribution of RNA structure throughout the SARS-CoV-2 genome', *bioRxiv*, 2020.07.06.190660.

Tayoun, A. A.; Loney, T.; Khansaheb, H.; Ramaswamy, S.; Harilal, D.; Deesi, Z.; Varghese, R.; Suwaidi, H. A.; Alkhajeh, A.; AlDabal, L.; Uddin, M.; Senok, A.; Hamoudi, R.; Halwani, R.; Hamid, Q.; Nowotny, N. & Alsheikh-Ali, A. (2020), 'Whole genome sequencing and phylogenetic analysis of SARS-CoV-2 strains from the index and early patients with COVID-19 in Dubai, United Arab Emirates, 29 January to 18 March 2020', *bioRxiv*, 2020.05.06.080606.

Teng, S.; Sobotian, A.; Rhoades, R.; Liu, D. & Tang, Q. (2020), 'Systemic Effects of Missense Mutations on SARS-CoV-2 Spike Glycoprotein Stability and Receptor Binding

Affinity', *bioRxiv*, 2020.05.21.109835.

Teng, X.; Li, Q.; Li, Z.; Zhang, Y.; Niu, G.; Zhang, M.; Xiao, J.; Yu, J.; Zhang, Z. & Song, S. (2020), 'Compositional Variability and Mutation Spectra of Monophyletic SARS-CoV-2 Clades', *bioRxiv*, 2020.08.26.267781.

Tengs, T.; Delwiche, C. F. & Jonassen, C. M. (2020), 'A mobile genetic element in the SARS-CoV-2 genome is shared with multiple insect species', *bioRxiv*, 2020.06.29.177030.

Thao, T. T. N.; Labroussaa, F.; Ebert, N.; V'kovski, P.; Stalder, H.; Portmann, J.; Kelly, J.; Steiner, S.; Holwerda, M.; Kratzel, A.; Gultom, M.; Schmied, K.; Laloli, L.; Hüsler, L.; Wider, M.; Pfaender, S.; Hirt, D.; Cippà, V.; Crespo-Pomar, S.; Schröder, S.; Muth, D.; Niemeyer, D.; Corman, V.; Müller, M. A.; Drosten, C.; Dijkman, R.; Jores, J. & Thiel, V. (2020), 'Rapid reconstruction of SARS-CoV-2 using a synthetic genomics platform', *Nature*.

consortium, T. C.-19. G. U. (C.-U. (2020), 'An integrated national scale SARS-CoV-2 genomic surveillance network', *The Lancet Microbe* **1**.

Tillett, R.; Sevinsky, J.; Hartley, P.; Kerwin, H.; Crawford, N.; Gorzalski, A.; Laverdure, C.; Verma, S.; Rossetto, C.; Jackson, D.; Farrell, M.; Van Hooser, S. & Pandori, M. (2020), 'Genomic Evidence for a Case of Reinfection with SARS-CoV-2', *SSRN*(ID 3680955), 3680955.

Tiwari, M. & Mishra, D. (2020), 'Investigating the genomic landscape of novel coronavirus (2019-nCoV) to identify non-synonymous mutations for use in diagnosis and drug design', *Journal of Clinical Virology* **128**, 104441.

To, K. K.-W.; Hung, I. F.-N.; Ip, J. D.; Chu, A. W.-H.; Chan, W.-M.; Tam, A. R.; Fong, C. H.-Y.; Yuan, S.; Tsoi, H.-W.; Ng, A. C.-K.; Lee, L. L.-Y.; Wan, P.; Tso, E.; To, W.-K.; Tsang, D.; Chan, K.-H.; Huang, J.-D.; Kok, K.-H.; Cheng, V. C.-C. & Yuen, K.-Y. (2020), 'COVID-19 re-infection by a phylogenetically distinct SARS-coronavirus-2 strain confirmed by whole genome sequencing', *Clinical Infectious Diseases*.

Tomaszewski, T.; DeVries, R. S.; Dong, M.; Bhatia, G.; Norsworthy, M. D.; Zheng, X. & Caetano-Anolles, G. (2020), 'New Pathways of Mutational Change in SARS-CoV-2 Proteomes Involve Regions of Intrinsic Disorder Important for Virus Replication and Release', *bioRxiv*, 2020.07.31.231472.

Tort, F. L.; Castells, M. & Cristina, J. (2020), 'A COMPREHENSIVE ANALYSIS OF GENOME COMPOSITION AND CODON USAGE PATTERNS OF EMERGING CORONAVIRUSES', *Virus Research*, 197976.

Toyoshima, Y.; Nemoto, K.; Matsumoto, S.; Nakamura, Y. & Kiyotani, K. (2020), 'SARS-CoV-2 genomic variations associated with mortality rate of COVID-19', *Journal*

of *Human Genetics*, 1--8.

Trottier, J.; Darques, R.; Ait Mouheb, N.; Partiot, E.; Bakhache, W.; Deffieu, M. S. & Gaudin, R. (2020), 'Post-lockdown detection of SARS-CoV-2 RNA in the wastewater of Montpellier, France', *One Health* **10**, 100157.

Trucchi, E.; Gratton, P.; Mafessoni, F.; Motta, S.; Cicconardi, F.; Bertorelle, G.; D'Annessa, I. & Marino, D. D. (2020), 'Unveiling diffusion pattern and structural impact of the most invasive SARS-CoV-2 spike mutation', *bioRxiv*, 2020.05.14.095620.

Turakhia, Y.; Thornlow, B.; Gozashti, L.; Hinrichs, A.; Fernandes, J.; Haussler, D. & Corbett-Detig, R. (2020), 'Stability of SARS-CoV-2 Phylogenies', *bioRxiv*, 2020.06.08.141127.

Tyson, J. R.; James, P.; Stoddart, D.; Sparks, N.; Wickenhagen, A.; Hall, G.; Choi, J. H.; Lapointe, H.; Kamelian, K.; Smith, A. D.; Prystajek, N.; Goodfellow, I.; Wilson, S. J.; Harrigan, R.; Snutch, T. P.; Loman, N. J. & Quick, J. (2020), 'Improvements to the ARTIC multiplex PCR method for SARS-CoV-2 genome sequencing using nanopore', *bioRxiv*, 2020.09.04.283077.

Uddin, M. B.; Hasan, M.; Harun-Al-Rashid, A.; Ahsan, M. I.; Imran, M. A. S. & Ahmed, S. S. U. (2020), 'Ancestral origin, antigenic resemblance and epidemiological insights of novel coronavirus (SARS-CoV-2): Global burden and Bangladesh perspective', *Infection, Genetics and Evolution*, 104440.

Valitutto, M. T.; Aung, O.; Tun, K. Y. N.; Vodzak, M. E.; Zimmerman, D.; Yu, J. H.; Win, Y. T.; Maw, M. T.; Thein, W. Z.; Win, H. H.; Dhanota, J.; Ontiveros, V.; Smith, B.; Tremeau-Brevard, A.; Goldstein, T.; Johnson, C. K.; Murray, S. & Mazet, J. (2020), 'Detection of novel coronaviruses in bats in Myanmar', *PLOS ONE* **15**(4), e0230802.

Vanaerschot, M.; Mann, S. A.; Webber, J. T.; Kamm, J.; Bell, S. M.; Bell, J.; Hong, S. N.; Nguyen, M. P.; Chan, L. Y.; Bhatt, K. D.; Tan, M.; Detweiler, A. M.; Espinosa, A.; Wu, W.; Batson, J.; Dynerman, D.; Consortium, C.; Wadford, D. A.; Puschnik, A.; Neff, N.; Ahyong, V.; Miller, S.; Ayscue, P.; Tato, C. M.; Paul, S.; Kistler, A.; DeRisi, J. L. & Crawford, E. D. (2020), 'Identification of a polymorphism in the N gene of SARS-CoV-2 that adversely impacts detection by a widely-used RT-PCR assay', *bioRxiv*, 2020.08.25.265074.

VanInsberghe, D.; Neish, A.; Lowen, A. C. & Koelle, K. (2020), 'Identification of SARS-CoV-2 recombinant genomes', *bioRxiv*, 2020.08.05.238386.

Vankadari, N. (2020), 'Overwhelming mutations or SNPs of SARS-CoV-2: A point of caution', *Gene* **752**, 144792.

Various (2020), 'Expert reaction to new paper making suggestions about stray dogs being a possible origin of SARS-CoV-2, the virus that causes COVID-19, Science Media

Centre', S0042.

Vaughan, T. G.; Leventhal, G. E.; Rasmussen, D. A.; Drummond, A. J.; Welch, D. & Stadler, T. (2019), 'Estimating Epidemic Incidence and Prevalence from Genomic Data', *Molecular Biology and Evolution* **36**(8), 1804--1816.

Velazquez-Salinas, L.; Zarate, S.; Eberl, S.; Gladue, D. P.; Novella, I. & Borca, M. V. (2020), 'Positive selection of ORF3a and ORF8 genes drives the evolution of SARS-CoV-2 during the 2020 COVID-19 pandemic', *bioRxiv*, 2020.04.10.035964.

Villabona-Arenas, C. J.; Hanage, W. P. & Tully, D. C. (2020), 'Phylogenetic interpretation during outbreaks requires caution', *Nature Microbiology*.

Villmann, T.; Kaden, M.; Bohnsack, K. S.; Weber, M.; Kudla, M.; Gutowska, K. & Blazewicz, J. (2020), 'Analysis of SARS-CoV-2 RNA-Sequences by Interpretable Machine Learning Models', *bioRxiv*, 2020.05.15.097741.

Vishnubhotla, R.; Vankadari, N.; Ketavarapu, V.; Amanchy, R.; Avanthi, S.; Bale, G.; Reddy, D. N. & Sasikala, M. (2020), 'Genetic variants in TMPRSS2 and Structure of SARS-CoV-2 spike glycoprotein and TMPRSS2 complex', *bioRxiv*, 2020.06.30.179663.

Vitanyi, P. M. B. & Cilibrasi, R. L. (2020), 'Phylogeny of the COVID-19 Virus SARS-CoV-2 by Compression', *bioRxiv*, 2020.07.22.216242.

Volz, E. M.; Fu, H.; Wang, H.; Xi, X.; Chen, W.; Liu, D.; Yingying, C.; Tian, M.; Tan, W.; Zai, J.; Sun, W.; Li, J.; Li, J.; Li, X. & Nie, Q. (2020), 'Phylodynamic analysis of a densely sampled COVID19 outbreak in Weifang, China', *Virological* , S0005.

Volz, E. M.; Hill, V.; McCrone, J. T.; Price, A.; Jorgensen, D.; O'Toole, A.; Southgate, J. A.; Johnson, R.; Jackson, B.; Nascimento, F. F.; Rey, S. M.; Nicholls, S. M.; Colquhoun, R. M.; Filipe, A. d. S.; Pacchiarini, N.; Bull, M.; Geidelberg, L.; Siveroni, I.; Goodfellow, I. G.; Loman, N. J.; Pybus, O.; Robertson, D. L.; Thomson, E. C.; Rambaut, A.; Connor, T. R. & Consortium, T. C. O. V. I. D.-19. G. U. K. (2020), 'Evaluating the effects of SARS-CoV-2 Spike mutation D614G on transmissibility and pathogenicity', *medRxiv*, 2020.07.31.20166082.

Wada, K.; Wada, Y. & Ikemura, T. (2020), 'Time-series analyses of directional sequence changes in SARS-CoV-2 genomes and an efficient search method for advantageous mutations for growth in human cells', *bioRxiv*, 2020.06.16.151282.

Wada, K.; Wada, Y. & Ikemura, T. (2020), 'Time-series analyses of directional sequence changes in SARS-CoV-2 genomes and an efficient search method for candidates for advantageous mutations for growth in human cells', *Gene: X* **5**, 100038.

Wakida, H.; Kawata, K.; Yamaji, Y.; Hattori, E.; Tsuchiya, T.; Wada, Y.; Ozaki, H. & Akimitsu, N. (2020), 'Stability of RNA sequences derived from the coronavirus genome

in human cells', *Biochemical and Biophysical Research Communications* **527**(4), 993--999.

Walker, A.; Houwaart, T.; Wienemann, T.; Vasconcelos, M. K.; Strelow, D.; Senff, T.; Hülse, L.; Adams, O.; Andree, M.; Hauka, S.; Feldt, T.; Jensen, B.-E.; Keitel, V.; Kindgen-Milles, D.; Timm, J.; Pfeffer, K. & Diltthey, A. T. (2020), 'Genetic structure of SARS-CoV-2 in Western Germany reflects clonal superspreading and multiple independent introduction events', *medRxiv*, 2020.04.25.20079517.

Wang, D.; Wang, Y.; Sun, W.; Zhang, L.; Ji, J.; Zhang, Z.; Cheng, X.; Li, Y.; Xiao, F.; Zhu, A.; Zhong, B.; Ruan, S.; Li, J.; Ren, P.; Ou, Z.; Xiao, M.; Li, M.; Deng, Z.; Zhong, H.; Li, F.; Chen, W.; Zhu, S.; Wang, W.; Zhang, Y.; Xu, X.; Jin, X.; Zhao, J.; Zhong, N.; Zhang, W.; Zhao, J.; Li, J. & Xu, Y. (2020), 'Population Bottlenecks and Intra-host Evolution during Human-to-Human Transmission of SARS-CoV-2', *bioRxiv*, 2020.06.26.173203.

Wang, H.; Li, X.; Li, T.; Zhang, S.; Wang, L.; Wu, X. & Liu, J. (2020), 'The genetic sequence, origin, and diagnosis of SARS-CoV-2', *European Journal of Clinical Microbiology & Infectious Diseases* **39**(9), 1629--1635.

Wang, J.-T.; Lin, Y.-Y.; Chang, S.-Y.; Yeh, S.-H.; Hu, B.-H.; Chen, P.-J. & Chang, S.-C. (2020), 'The role of phylogenetic analysis in clarifying the infection source of a COVID-19 patient', *Journal of Infection* **0**(0).

Wang, L.; Chen, F.; Guo, X.; You, L.; Yang, X.; Yang, F.; Yang, T.; Gao, F.; Hua, C.; Ding, Y.; Cai, J.; Yang, L.; Huang, W.; Xu, Z.; Wan, B.; Tong, J.; Peng, C.; Yang, Y.; Zhang, L.; Liu, K.; Zhou, F.; Zhang, M.; Tan, C.; Zeng, W.; Wang, B. & Wei, X. (2020), 'VirusDIP: Virus Data Integration Platform', *bioRxiv*, 2020.06.08.139451.

Wang, Y.; Wang, D.; Zhang, L.; Sun, W.; Zhang, Z.; Chen, W.; Zhu, A.; Huang, Y.; Xiao, F.; Yao, J.; Gan, M.; Li, F.; Luo, L.; Huang, X.; Zhang, Y.; Wong, S.-s.; Cheng, X.; Ji, J.; Ou, Z.; Xiao, M.; Li, M.; Li, J.; Ren, P.; Deng, Z.; Zhong, H.; Yang, H.; Wang, J.; Xu, X.; Song, T.; Mok, C.; Peiris, M.; Zhong, N.; Zhao, J.; Li, Y.; Li, J. & Zhao, J. (2020), 'Intra-host Variation and Evolutionary Dynamics of SARS-CoV-2 Population in COVID-19 Patients', *bioRxiv*, 2020.05.20.103549.

Ward, D.; Higgins, M.; Phelan, J.; Hibberd, M. L.; Campino, S. & Clark, T. G. (2020), 'An integrated in silico immuno-genetic analytical platform provides insights into COVID-19 serological and vaccine targets', *bioRxiv*, 2020.05.11.089409.

Weisblum, Y.; Schmidt, F.; Zhang, F.; DaSilva, J.; Poston, D.; Lorenzi, J. C. C.; Muecksch, F.; Rutkowska, M.; Hoffmann, H.-H.; Michailidis, E.; Gaebler, C.; Agudelo, M.; Cho, A.; Wang, Z.; Gazumyan, A.; Cipolla, M.; Luchsinger, L.; Hillyer, C. D.; Caskey, M.; Robbiani, D. F.; Rice, C. M.; Nussenzweig, M. C.; Hatziioannou, T. & Bieniasz, P. D. (2020), 'Escape from neutralizing antibodies by SARS-CoV-2 spike

protein variants', *bioRxiv*, 2020.07.21.214759.

Wells, H. L.; Letko, M. C.; Lasso, G.; Ssebide, B.; Nziza, J.; Byarugaba, D. K.; Navarrete-Macias, I.; Liang, E.; Cranfield, M.; Han, B. A.; Tingley, M. W.; Diuk-Wasser, M.; Goldstein, T.; Johnson, C. K.; Mazet, J.; Chandran, K.; Munster, V.; Gilardi, K. & Anthony, S. J. (2020), 'The evolutionary history of ACE2 usage within the coronavirus subgenus Sarbecovirus', *bioRxiv*, 2020.07.07.190546.

Wen, F.; Yu, H.; Guo, J.; Li, Y.; Luo, K. & Huang, S. (2020), 'Identification of the hyper-variable genomic hotspot for the novel coronavirus SARS-CoV-2', *Journal of Infection* **80**(6), 671--693.

Wen, S.; Sun, C.; Zheng, H.; Wang, L.; Zhang, H.; Zou, L.; Liu, Z.; Du, P.; Xu, X.; Liang, L.; Peng, X.; Zhang, W.; Wu, J.; Yang, J.; Lei, B.; Zeng, G.; Ke, C.; Chen, F. & Zhang, X. (2020), 'High-Coverage SARS-CoV-2 Genome Sequences Acquired by Target Capture Sequencing', *Journal of Medical Virology* **n/a**(n/a).

Wen, S. & Zhang, X. (2020), 'A High-Coverage SARS-CoV-2 Genome Sequence Acquired by Target Capture Sequencing', *medRxiv*, 2020.04.11.20061507.

Wenzel, J. (2020), 'Origins of SARS-CoV-1 and SARS-CoV-2 are often poorly explored in leading publications', *Cladistics* **n/a**(n/a).

Worobey, M.; Pekar, J.; Larsen, B. B.; Nelson, M. I.; Hill, V.; Joy, J. B.; Rambaut, A.; Suchard, M. A.; Wertheim, J. O. & Lemey, P. (2020), 'The emergence of SARS-CoV-2 in Europe and the US', *bioRxiv*, 2020.05.21.109322.

Wozniak, A.; Cerda, A.; Ibarra-Henriquez, C.; Sebastian, V.; Armijo, G.; Lamig, L.; Miranda, C.; Lagos, M.; Solari, S.; Guzman, A. M.; Quiroga, T.; Hitschfeld, S.; Riveras, E.; Ferres, M.; Gutierrez, R. A. & Garcia, P. (2020), 'A simple RNA preparation method for SARS-CoV-2 detection by RT-qPCR', *bioRxiv*, 2020.05.07.083048.

Wright, E. S.; Lakdawala, S. S. & Cooper, V. S. (2020), 'SARS-CoV-2 genome evolution exposes early human adaptations', *bioRxiv*, 2020.05.26.117069.

Wu, K. E.; Fazal, F. M.; Parker, K. R.; Zou, J. & Chang, H. Y. (2020), 'RNA-GPS Predicts SARS-CoV-2 RNA Residency to Host Mitochondria and Nucleolus', *Cell Systems* **11**(1), 102--108.e3.

Xavier, J.; Giovanetti, M.; Adelino, T.; Fonseca, V.; da Costa, A. V. B.; Ribeiro, A. A.; Felicio, K. N.; Duarte, C. G.; Silva, M. V. F.; Salgado, Á.; Lima, M. T.; de Jesus, R.; Fabri, A.; Zoboli, C. F. S.; Santos, T. G. S.; Iani, F.; Ciccozzi, M.; de Filippis, A. M. B.; de Siqueira, M. A. M. T.; de Abreu, A. L.; de Azevedo, V.; Ramalho, D. B.; de Albuquerque, C. F. C.; de Oliveira, T.; Holmes, E. C.; Lourenço, J.; Alcantara, L. C. J. & Oliveira, M. A. A. (2020), 'The ongoing COVID-19 epidemic in Minas Gerais, Brazil: insights from epidemiological data and SARS-CoV-2 whole genome sequencing',

Emerging Microbes & Infections, 1--42.

Xia, X. (2020), 'Extreme genomic CpG deficiency in SARS-CoV-2 and evasion of host antiviral defense', *Molecular Biology and Evolution*, msaa094.

Xiao, K.; Zhai, J.; Feng, Y.; Zhou, N.; Zhang, X.; Zou, J.-J.; Li, N.; Guo, Y.; Li, X.; Shen, X.; Zhang, Z.; Shu, F.; Huang, W.; Li, Y.; Zhang, Z.; Chen, R.-A.; Wu, Y.-J.; Peng, S.-M.; Huang, M.; Xie, W.-J.; Cai, Q.-H.; Hou, F.-H.; Chen, W.; Xiao, L. & Shen, Y. (2020), 'Isolation of SARS-CoV-2-related coronavirus from Malayan pangolins', *Nature* **583**, 286-289.

Yang, X.; Dong, N.; Chan, E. W.-C. & Chen, S. (2020), 'Genetic cluster analysis of SARS-CoV-2 and the identification of those responsible for the major outbreaks in various countries', *Emerging Microbes & Infections* **9**(1), 1287--1299.

Yang, Y.; Yan, W.; Hall, B. & Jiang, X. (2020), 'Characterizing transcriptional regulatory sequences in coronaviruses and their role in recombination', *bioRxiv*, 2020.06.21.163410.

Yao, H.; Lu, X.; Chen, Q.; Xu, K.; Chen, Y.; Cheng, L.; Liu, F.; Wu, Z.; Wu, H.; Jin, C.; Zheng, M.; Wu, N.; Jiang, C. & Li, L. (2020), 'Patient-derived mutations impact pathogenicity of SARS-CoV-2', *medRxiv*, 2020.04.14.20060160.

Yap, P. S. X.; Tan, T. S.; Chan, Y. F.; Tee, K. K.; Kamarulzaman, A. & Teh*, C. S. J. (2020), 'An Overview of the Genetic Variations of the SARS-CoV-2 Genomes Isolated in Southeast Asian Countries', **30**(7), 962--966.

Yasumizu, Y.; Hara, A.; Sakaguchi, S. & Ohkura, N. (2020), 'VIRTUS: a pipeline for comprehensive virus analysis from conventional RNA-seq data', *bioRxiv*, 2020.05.08.085308.

Yazar, S. (2020), 'SARS-CoV-2 virus RNA sequence classification and geographical analysis with convolutional neural networks approach', *arXiv:2007.05055 [cs, q-bio]*.

Yin, C. (2020), 'Genotyping coronavirus SARS-CoV-2: methods and implications', *Genomics* **112**(5), 3588--3596.

Yip, C. C.-Y.; Ho, C.-C.; Chan, J. F.-W.; To, K. K.-W.; Chan, H. S.-Y.; Wong, S. C.-Y.; Leung, K.-H.; Fung, A. Y.-F.; Ng, A. C.-K.; Zou, Z.; Tam, A. R.; Chung, T. W.-H.; Chan, K.-H.; Hung, I. F.-N.; Cheng, V. C.-C.; Tsang, O. T.-Y.; Tsui, S. K. W. & Yuen, K.-Y. (2020), 'Development of a Novel, Genome Subtraction-Derived, SARS-CoV-2-Specific COVID-19-nsp2 Real-Time RT-PCR Assay and Its Evaluation Using Clinical Specimens', *International Journal of Molecular Sciences* **21**(7), 2574.

Yu, W.-B.; Tang, G.-D.; Zhang, L. & Corlett, R. T. (2020), 'Decoding the evolution and transmissions of the novel pneumonia coronavirus (SARS-CoV-2 / HCoV-19) using whole genomic data', *Zoological Research* **41**(3), 247--257.

Zehender, G.; Lai, A.; Bergna, A.; Meroni, L.; Riva, A.; Balotta, C.; Tarkowski, M.; Gabrieli, A.; Bernacchia, D.; Rusconi, S.; Rizzardini, G.; Antinori, S. & Galli, M. (2020), 'Genomic Characterisation and Phylogenetic Analysis of Sars-Cov-2 in Italy', *Journal of Medical Virology* (**Short Communication**).

Zhan, S. H.; Deverman, B. E. & Chan, Y. A. (2020), 'SARS-CoV-2 is well adapted for humans. What does this mean for re-emergence?', *bioRxiv*, 2020.05.01.073262.

Zhan, X.-Y.; Zhang, Y.; Zhou, X.; Huang, K.; Qian, Y.; Leng, Y.; Yan, L.; Huang, B. & He, Y. (2020), 'Molecular evolution of SARS-CoV-2 structural genes: evidence of positive selection in spike glycoprotein', *bioRxiv*, 2020.06.25.170688.

Zhang, C.; Jin, X.; Chen, X.; Leng, Q. & Qiu, T. (2020), 'Antigenic evolution on global scale reveals potential natural selection of SARS-CoV-2 by pre-existing cross-reactive T cell immunity', *bioRxiv*, 2020.06.16.154591.

Zhang, J.; Kang, J.; Liu, M.; Han, B.; Li, L.; He, Y.; Yi, Z. & Chen, L. (2020), 'Multi-site co-mutations and 5'UTR CpG immunity escape drive the evolution of SARS-CoV-2', *bioRxiv*, 2020.07.21.213405.

Zhao, J.; Zhai, X. & Zhou, J. (2020), 'Snapshot of the evolution and mutation patterns of SARS-CoV-2', *bioRxiv*, 2020.07.04.187435.

Zhao, Z.; Sokhansanj, B. A.; Malhotra, C.; Zheng, K. & Rosen, G. (2020), 'Characterizing geographical and temporal dynamics of novel coronavirus SARS-CoV-2 using informative subtype markers', *bioRxiv*, 2020.04.07.030759.

Zheng, J.; Zhou, Y.; Zhu, M.; Qiao, M. & Zhang, Z. (2020), 'Spread of SARS-CoV-2 Genomes on Genomic Index Maps of Hierarchy', *Research Square* **10.21203/rs.3.rs-31883/v2**.

Zhou, H.; Chen, X.; Hu, T.; Li, J.; Song, H.; Liu, Y.; Wang, P.; Liu, D.; Yang, J.; Holmes, E. C.; Hughes, A. C.; Bi, Y. & Shi, W. (2020), 'A Novel Bat Coronavirus Closely Related to SARS-CoV-2 Contains Natural Insertions at the S1/S2 Cleavage Site of the Spike Protein', *Current Biology* **30**(11), 2196--2203.e3.

Zhou, Z.-J.; Qiu, Y.; Pu, Y.; Huang, X. & Ge, X.-Y. (2020), 'BioAider: An efficient tool for viral genome analysis and its application in tracing SARS-CoV-2 transmission', *Sustainable Cities and Society* **63**, 102466.

Zhou, Z.-Y.; Liu, H.; Zhang, Y.-D.; Wu, Y.-Q.; Peng, M.-S.; Li, A.; Irwin, D. M.; Li, H.; Lu, J.; Bao, Y.; Lu, X.; Liu, D. & Zhang, Y.-p. (2020), 'Worldwide tracing of mutations and the evolutionary dynamics of SARS-CoV-2', *bioRxiv*, 2020.08.07.242263.