

Addetia, A.; Lin, M. J.; Peddu, V.; Roychoudhury, P.; Jerome, K. R. & Greninger, A. L. (2020), 'Sensitive recovery of complete SARS-CoV-2 genomes from clinical samples using Swift Biosciences' SARS-CoV-2 multiplex amplicon sequencing panel', *Journal of Clinical Microbiology*, JCM.02226-20.

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* **92**, 1562-1566.

Afrasiabi, A.; Alinejad-Rokny, H.; Lovell, N.; Xu, Z. & Ebrahimi, D. (2020), 'Insight into the origin of 5UTR and source of CpG reduction in SARS-CoV-2 genome', *bioRxiv*, 2020.10.23.351353.

Aggarwal, D.; Myers, R.; Hamilton, W. L.; Bharucha, T.; Tumelty, N.; Brown, C.; Meader, E. J.; Connor, T.; Smith, D.; Bradley, D.; Robson, S.; Bashton, M.; Shallcross, L.; Zambon, M.; Goodfellow, I.; Chand, M.; O'Grady, J.; Török, E.; Peacock, S. J. & Page, A. J. (2020), 'The role of genomics in understanding COVID-19 outbreaks in long term care facilities', *OSF Preprints November 23*, doi:10.31219/osf.io/7y9rk.

Alexander, M. R.; Schoeder, C. T.; Brown, J. A.; Smart, C. D.; Moth, C. W.; Wikswo, 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.; sequencing laboratories Group, T. W. E. R. & 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.

Altenhoff, A. M.; Train, C.-M.; Gilbert, K. J.; Mediratta, I.; Mendes de Farias, T.; Moi, D.; Nevers, Y.; Radovkova, H.-S.; Rossier, V.; Warwick Vesztrocy, A.; Glover, N. M. & Dessimoz, C. (2020), 'OMA orthology in 2021: website overhaul, conserved isoforms, ancestral gene order and more', *Nucleic Acids Research*, gkaa1007.

Andersen, K. G.; Rambaut, A.; Lipkin, W. I.; Holmes, E. C. & Garry, R. F. (2020), 'The proximal origin of SARS-CoV-2', *Nature Medicine* **26**(4), 450-452.

Andréoletti, J.; Zwaans, A.; Warnock, R. C. M.; Aguirre-Fernández, G.; Barido-Sottani, J.; Gupta, A.; Stadler, T. & Manceau, M. (2020), 'A skyline birth-death process for inferring the population size from a reconstructed tree with occurrences', *bioRxiv*, 2020.10.27.356758.

Andres, C.; Garcia-Cehic, D.; Gregori, J.; Pinana, M.; Rodriguez-Frias, F.; Guerrero, M.; Esperalba, J.; Rando, A.; Goterris, 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.; Goterris, 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* **9**(1), 1900-1911.

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.

Arevalo, S. J.; Sifuentes, D. Z.; Robles, C. H.; Bianchi, G. L.; Chavez, A. C.; Casas, R. G.-S.; Chavarria, R. P. & Uceda-Campos, G. (2020), 'Analysis of the Dynamics and Distribution of SARS-CoV-2 Mutations and its Possible Structural and Functional Implications', *bioRxiv*, 2020.11.13.381228.

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.

Avanzato, V. A.; Matson, M. J.; Seifert, S. N.; Pryce, R.; Williamson, B. N.; Anzick, S. L.; Barbian, K.; Judson, S. D.; Fischer, E. R.; Martens, C.; Bowden, T. A.; de Wit, E.; Riedo, F. X. & Munster, V. J. (2020), 'Case Study: Prolonged Infectious SARS-CoV-2 Shedding from an Asymptomatic Immunocompromised Individual with Cancer', *Cell*, (In Press, Corrected Proof).

Awoyelu, E. H.; Oladipo, E. K.; Adetuyi, B. O.; Senbadejo, T. Y.; Oyawoye, O. M. & Oloke, J. K. (2020), 'Phyloevolutionary 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', .

Baang, J. H.; Smith, C.; Mirabelli, C.; Valesano, A. L.; Manthei, D. M.; Bachman, M.; Wobus, C. E.; Adams, M.; Washer, L.; Martin, E. T. & Lauring, A. S. (2020), 'Prolonged SARS-CoV-2 replication in an immunocompromised patient', *The Journal of Infectious Diseases*, (accepted manuscript).

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.

Badua, C. L. D. C.; Baldo, K. A. T. & Medina, P. M. B. (2020), 'Genomic and Proteomic Mutation Landscapes of SARS-CoV-2', *Journal of Medical Virology*, (accepted manuscript online).

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.; Shambhani, 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.

Barrs, V. R.; Peiris, M.; Tam, K. W. S.; Law, P. Y. T.; Brackman, C. J.; To, E. M. W.; Yu, V. Y. T.; Chu, D. K. W.; Perera, R. A. P. M. & Sit, T. H. C. (2020), 'SARS-CoV-2 in Quarantined Domestic Cats from COVID-19 Households or Close Contacts, Hong Kong, China', *Emerging Infectious Diseases journal - CDC* **26**(12), 3071-3074.

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.

Bartoszewicz, J. M.; Seidel, A. & Renard, B. Y. (2020), 'Interpretable detection of novel human viruses from genome sequencing data', *bioRxiv*, 2020.01.29.925354.

Bartoszewski, R.; Dabrowski, M.; Jakielka, 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* **67**:1453– 1462.

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 @trvrb: 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.; Frazer, 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.; Gautam, 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.

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.; Fazar, 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. S.; Gautam, 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.; Shendure, J. & Jerome, K. R. (2020), 'Cryptic transmission of SARS-CoV-2 in Washington state', *Science* **370**(6516), 571-575.

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**.

Berrio, A.; Gartner, V. & Wray, G. A. (2020), 'Positive selection within the genomes of SARS-CoV-2 and other Coronaviruses independent of impact on protein function', *bioRxiv*, 2020.09.16.300038.

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.

Bhoyer, 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.

Bindayna, K. M. & Crinion, S. (2020), 'Variant analysis of SARS-CoV-2 genomes in the Middle East', *bioRxiv*, 2020.10.09.332692.

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.

Biswas, S.; Saha, S.; Bandyopadhyay, S. & Bhattacharyya, M. (2020), 'Motif Analysis in k-mer Networks: An Approach towards Understanding SARS-CoV-2 Geographical Shifts', *bioRxiv*, 2020.10.04.325662.

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.

Bluhm, A.; Christandl, M.; Gesmundo, F.; Klausen, F. R.; Mančinska, L.; Steffan, V.; França, D. S. & Werner, A. H. (2020), 'SARS-CoV-2 transmission routes from genetic data: A Danish case study', *PLOS ONE* **15**(10), e0241405.

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.; Mühlmann, 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>.

Borges, V.; Isidro, J.; Cortes-Martins, H.; Duarte, S.; Vieira, L.; Leite, R.; Gordo, I.; Caetano, C. P.; Nunes, B.; Sá, R.; Oliveira, A.; Guiomar, R.; genomics, P. n. f. S. A. R. S.-C.-2. & Gomes, J. P. (2020), 'Massive dissemination of a SARS-CoV-2 Spike Y839 variant in Portugal', *Emerging Microbes & Infections* **0**(ja), 1-58.

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).

Braun, K. M.; Moreno, G. K.; Halfmann, P. J.; Baker, D. A.; Boehm, E. C.; Weiler, A. M.; Haj, A. K.; Hatta, M.; Chiba, S.; Maemura, T.; Kawaoka, Y.; Koelle, K.; O'Connor, D. & Friedrich, T. (2020), 'Transmission of SARS-CoV-2 in domestic cats imposes a narrow bottleneck', *bioRxiv*, 2020.11.16.384917.

Brierley, L. & Fowler, A. (2020), 'Predicting the animal hosts of coronaviruses from compositional biases of spike protein and whole genome sequences through machine learning', *bioRxiv*, 2020.11.02.350439.

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.

Bruce, E. A.; Huang, M.-L.; Perchetti, G. A.; Tighe, S.; Laaguiby, P.; Hoffman, J. J.; Gerrard, D. L.; Nalla, A. K.; Wei, Y.; Greninger, A. L.; Diehl, S. A.; Shirley, D. J.; Leonard, D. G. B.; Huston, C. D.; Kirkpatrick, B. D.; Dragon, J. A.; Crothers, J. W.; Jerome, K. R. & Botten, J. W. (2020), 'Direct RT-qPCR detection of SARS-CoV-2 RNA from patient nasopharyngeal swabs without an RNA extraction step', *PLOS Biology* **18**(10), e3000896.

Bugembe, D. L.; Kayiwa, J.; Phan, M. V. T.; Tushabe, P.; Balinandi, S.; Dhaala, B.; Lexow, J.; Mwebesa, H.; Aceng, J.; Kyobe, H.; Ssemwanga, D.; Lutwama, J.; Kaleebu, P. & Cotten, M. (2020), 'Main Routes of Entry and Genomic Diversity of SARS-CoV-2, Uganda', *Emerging Infectious Diseases journal - CDC* **26**(10).

Bull, R. A.; Adikari, T.; Ferguson, J. M.; Hammond, J. M.; Stevanovski, I.; Beukers, A.

G.; Naing, Z.; Yeang, M.; Verich, A.; Gamaarachichi, H.; Kim, K. W.; Luciani, F.; Stelzer-Braid, S.; Eden, J.-S.; Rawlinson, W. D.; Hal, S. J. v. & Deveson, I. W. (2020), 'Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis', *bioRxiv*, 2020.08.04.236893.

Bull, R. A.; Adikari, T. N.; Ferguson, J. M.; Hammond, J. M.; Stevanovski, I.; Beukers, A. G.; Naing, Z.; Yeang, M.; Verich, A.; Gamaarachchi, H.; Kim, K. W.; Luciani, F.; Stelzer-Braid, S.; Eden, J.-S.; Rawlinson, W. D.; van Hal, S. J. & Deveson, I. W. (2020), 'Analytical validity of nanopore sequencing for rapid SARS-CoV-2 genome analysis', *Nature Communications* **11**(1), 6272.

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* **94**(12):e00411-20

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* **369**(6508), 1255-1260.

Cappello, L. & Palacios, J. A. (2020), 'Adaptive preferential sampling in phylodynamics', *arXiv:2009.02307 [q-bio, stat]*.

Carbo, E. C.; Sidorov, I. A.; Zevenhoven-Dobbe, J. C.; Snijder, E. J.; Claas, E. C.; Laros, J. F. J.; Kroes, A. C. M. & de Vries, J. J. C. (2020), 'Coronavirus discovery by metagenomic sequencing: a tool for pandemic preparedness', *Journal of Clinical Virology: The Official Publication of the Pan American Society for Clinical Virology* **131**, 104594.

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.; Sánchez,

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, A. T.; Altschuler, K.; Zhan, S. H.; Chan, Y. A. & Deverman, B. E. (2020), 'COVID-19 CG: Tracking SARS-CoV-2 mutations by locations and dates of interest', *bioRxiv*, 2020.09.23.310565.

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, S.; He, C.; Li, Y.; Li, Z. & Melançon, C. E. (2020), 'A computational toolset for rapid identification of SARS-CoV-2, other viruses and microorganisms from sequencing data', *Briefings in Bioinformatics*, bbaa231.

Chen, W.; Feng, P.; Liu, K.; Wu, M. & Lin, H. (2020), 'Computational Identification of Small Interfering RNA Targets in SARS-CoV-2', *Virologica Sinica* **35**(3): 359–361.

Chen, Z.; Boon, S. S.; Wang, M. H.; Chan, R. W. Y. & Chan, P. K. S. (2020), 'Genomic and evolutionary comparison between SARS-CoV-2 and other human coronaviruses', *Journal of Virological Methods*, 114032.

Cheng, M. H.; Zhang, S.; Porritt, R. A.; Ardit, 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.; D'Erchia, A. M.; Gissi, C.; Manzari, C.; Parisi, A.; Resta, N.; Zambelli, F.; Picardi, E.; Pavesi, G.; Horner, D. S. & Pesole, G. (2020), 'Next generation sequencing of SARS-CoV-2 genomes: challenges, applications and opportunities', *Briefings in Bioinformatics*(bbaa297), bbaa297.

Chiara, M.; Horner, D. S.; Gissi, C. & Pesole, G. (2020), 'Comparative genomic 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.

Choi, E. M.; Chu, D. K. W.; Cheng, P. K. C.; Tsang, D. N. C.; Peiris, M.; Bausch, D. G.; Poon, L. L. M. & Watson-Jones, D. (2020), 'Early Release - In-Flight Transmission of Severe Acute Respiratory Syndrome Coronavirus 2', *Emerging Infectious Diseases journal - CDC* **26**(11).

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.

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 was the major contributor to early pandemic transmission in Malaysia', *PLOS Neglected Tropical Diseases* **14**(11), e0008744.

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 CORD-19', *bioRxiv*, 2020.04.20.046144.

Colson, P.; Finaud, M.; Levy, N.; Lagier, J.-C. & Raoult, D. (2020), 'Evidence of SARS-CoV-2 re-infection with a different genotype', *Journal of Infection*, (In Press Journal Pre-Proof).

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. & Brilli, 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.; Sassera, D.; Gaiarsa, S.; Bandi, C. & Brilli, M. (2020), 'Insurgence and worldwide diffusion of genomic variants in SARS-CoV-2 genomes', *bioRxiv*, 2020.04.30.071027.

COVID-19 Genomics UK (COG-UK) Consortium, 'COVID-19 Genomics UK (COG-UK) Consortium Report #9 -25th June 2020',
https://www.cogconsortium.uk/news_item/report-12-15th-october-2020/.

Conway, M. J. (2020), 'Identification of coronavirus sequences in carp cDNA from Wuhan, China', *Journal of Medical Virology* **92**(9), 1629-1633.

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.

Cotten, M.; Bugembe, D. L.; Kaleebu, P. & Phan, M. V. T. (2020), 'Alternate primers for whole-genome SARS-CoV-2 sequencing', *bioRxiv*, 2020.10.12.335513.

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.; Slodkowicz, 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.; Ndembí, 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.; Gómez, 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.; Gómez, 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*.

Díez-Fuertes, F.; Iglesias-Caballero, M.; Pérez, J. G.; Monzón, S.; Jiménez, P.; Varona, S.; Cuesta, I.; Zaballos, Á.; Jiménez, M.; Checa, L.; Pozo, F.; Pérez-Olmeda, M.; Thomson, M. M.; Alcamí, J. & Casas, I. (2020), 'A Founder Effect Led Early Sars-CoV-2 Transmission in Spain', *Journal of Virology*, JVI.01583-20.

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.

Dimonaco, N. J.; Salavati, M. & Shih, B. (2020), 'Hacking the diversity of SARS-CoV-2 and SARS-like coronaviruses in human, bat and pangolin populations', *bioRxiv*, 2020.11.24.391763.

Doddapaneni, H.; Cregeen, S. J.; Sucgang, R.; Meng, Q.; Qin, 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*, 2020.12.11.421057.

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.

Domingues, R. B.; Mendes-Correa, M. C.; de Moura Leite, F. B. V.; Sabino, E. C.; Salarini, D. Z.; Claro, I.; Santos, D. W.; de Jesus, J. G.; Ferreira, N. E.; Romano, C. M. & Soares, C. A. S. (2020), 'First case of SARS-CoV-2 sequencing in cerebrospinal fluid of a patient with suspected demyelinating disease', *Journal of Neurology* **267**(11), 3154-3156.

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.

van Dorp, L.; 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', *Nature Communications* **11**(1), 5986.

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.

Dorp, L. v.; Tan, C. C. S.; Lam, S. D.; Richard, D.; Owen, C.; Berchtold, D.; Orengo, C. & Balloux, F. (2020), 'Recurrent mutations in SARS-CoV-2 genomes isolated from mink point to rapid host-adaptation', *bioRxiv*, 2020.11.16.384743.

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.

Douglas, N. M.; Meumann, E. M.; Krause, V. L. & Davies, J. (2020), 'Successful containment to date of SARS-CoV-2 transmission in the Northern Territory', *Medical Journal of Australia*, (Research Letter).

Du, P.; Ding, N.; Li, J.; Zhang, F.; Wang, Q.; Chen, Z.; Song, C.; Han, K.; Xie, W.; Liu, J.; Wang, L.; Wei, L.; Ma, S.; Hua, M.; Yu, F.; Wang, L.; Wang, W.; An, K.; Chen, J.; Liu, H.; Gao, G.; Wang, S.; Huang, Y.; Wu, A. R.; Wang, J.; Liu, D.; Zeng, H. & Chen, C. (2020), 'Genomic surveillance of COVID-19 cases in Beijing', *Nature Communications* **11**(1), 5503.

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.

Duchene, S.; Featherstone, L.; Haritopoulou-Sinanidou, M.; Rambaut, A.; Lemey, P. & Baele, G. (2020), 'Temporal signal and the phylodynamic threshold of SARS-CoV-2', *Virus Evolution* **6**(2), veaa061.

Dunn, C. D. (2020), 'SequenceBouncer: A method to remove outlier entries from a multiple sequence alignment', *bioRxiv*, 2020.11.24.395459.

Dutta, R.; Buragohain, L. & Borah, P. (2020), 'Analysis of codon usage of severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) and its adaptability in dog', *Virus Research* **288**, 198113.

Elizondo, V.; Harkins, G. W.; Mabvakure, B.; Smidt, S.; Zappile, P.; Marier, C.; Maurano, M.; Perez, V.; Mazza, N.; Beloso, C.; Ifran, S.; Fernandez, M.; Santini, A.; Perez, V.; Estevez, V.; Nin, M.; Manrique, G.; Perez, L.; Ross, F.; Boschi, S.; Zubillaga, M. N.; Balleste, R.; Dellicour, S.; Heguy, A. & Duerr, R. (2020), 'SARS-CoV-2 genomic

characterization and clinical manifestation of the COVID-19 outbreak in Uruguay', *Emerging Microbes & Infections* **0**(ja), 1-52.

Eskier, D.; Karakülah, 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.; Karakülah, 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. & Karakülah, 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.

Fang, S.; Li, K.; Shen, J.; Liu, S.; Liu, J.; Yang, L.; Hu, C.-D. & Wan, J. (2020), 'GESS: a database of global evaluation of SARS-CoV-2/hCoV-19 sequences', *Nucleic Acids Research*, gkaa808.

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.

Featherstone, L.; Giallonardo, F. D.; Holmes, E. C.; Vaughan, T. & Duchene, S. (2020), 'Infectious disease phylodynamics with occurrence data', *bioRxiv*, 596700.

Felix, P. T.; Silva, E. D. A. B.; Venancio, D. B. R. & Ramos, R. d. S. (2020), 'Genetic diversity analysis of the D614G mutation in SARS-CoV-2', *bioRxiv*, 2020.10.30.362954.

Fenizia, C.; Biasin, M.; Cetin, I.; Vergani, P.; Mileto, D.; Spinillo, A.; Gismondo, M. R.; Perotti, F.; Callegari, C.; Mancon, A.; Cammarata, S.; Beretta, I.; Nebuloni, M.; Trabattoni, D.; Clerici, M. & Savasi, V. (2020), 'Analysis of SARS-CoV-2 vertical transmission during pregnancy', *Nature Communications* **11**(1), 5128.

Fernandes, J. D.; Hinrichs, A. S.; Clawson, H.; Gonzalez, J. N.; Lee, B. T.; Nassar, L. R.; Raney, B. J.; Rosenbloom, K. R.; Nerli, S.; Rao, A. A.; Schmelter, D.; Fyfe, A.; Maulding, N.; Zweig, A. S.; Lowe, T. M.; Ares, M.; Corbet-Detig, R.; Kent, W. J.; Haussler, D. & Haeussler, M. (2020), 'The UCSC SARS-CoV-2 Genome Browser', *Nature Genetics* **52**(10), 991-998.

Filho, C. B. d. N.; Ramos, R. d. S.; Paulino, A. J.; Venancio, D. B. R. & Felix, P. T. (2020), 'Levels of genetic diversity of SARS-CoV-2 virus: reducing speculations about the genetic variability of the virus in South America', *bioRxiv*, 2020.09.14.296491.

Firestone, M. J.; Wienkes, H.; Garfin, J.; Wang, X.; Vilen, K.; Smith, K. E.; Holzbauer, S.; Plumb, M.; Pung, K.; Medus, C.; Yao, J. D.; Binnicker, M. J.; Nelson, A. C.; Yohe, S.; Como-Sabetti, K.; Ehresmann, K.; Lynfield, R. & Danila, R. (2020), 'COVID-19 Outbreak Associated with a 10-Day Motorcycle Rally in a Neighboring State - Minnesota, August-September 2020', *MMWR. Morbidity and mortality weekly report* **69**(47), 1771-1776.

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. (2020), 'Errors in Tracing Coronavirus SARS-CoV-2 Transmission Using a Maximum Likelihood Tree. Comment on "A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis"', *JMIR Public Health and Surveillance* **6**(4), e23542.

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.

Geller, G.; Duggal, P.; Thio, C. L.; Mathews, D.; Kahn, J. P.; Maragakis, L. L. & Garibaldi, B. T. (2020), 'Genomics in the era of COVID-19: ethical implications for clinical practice and public health', *Genome Medicine* **12**(1), 95.

Geoghegan, J. L.; Ren, X.; Storey, M.; Hadfeild, J.; Jolley, 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.

Geoghegan, J. L.; Ren, X.; Storey, M.; Hadfeild, J.; Jolley, 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', *Nature Communications* **11**(6351), 6351.

Ghafari, M.; du Plessis, L.; Pybus, O. & Katzourakis, A. (2020), 'Time dependence of SARS-CoV-2 substitution rates', *virological.org*, 542.

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.; Lourenco, J.; Chimukangara, B.; Lessells, R.; Moosa, Y.; Gazy, I.; Fish, M.; Singh, L.; Khanyile, K. S.; Fonseca, V.; Giovanetti, M.; Alcantara, L. C. J.; Petruccione, F. & de Oliveira, T. (2020), 'Early transmission of SARS-CoV-2 in South Africa: An epidemiological and phylogenetic report', *International Journal of Infectious Diseases*, (accepted proof online).

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.

Gilman Kit-Hang, S. I. U.; Lam-Kwong, L. E. E.; LEUNG, K. S.-S.; LEUNG, J. S.-L.; Timothy Ting-Leung, N. G.; Chloe Toi-Mei, C. H. A. N.; Kingsley King-Gee, T. A. M.; Hiu-Yin, L. A. O.; Alan Ka-Lun, W. U.; Miranda Chong-Yee, Y. A. U.; Yvette Wai-Man, L. A. I.; Kitty Sau-Chun, F. U. N. G.; Sandy Ka-Yee, C. H. A. U.; Barry Kin-Chung, W. O. N. G.; Wing-Kin, T. O.; Kristine, L. U. K.; Alex Yat-Man, H. O.; Tak-Lun, Q. U. E.; Kam-Tong, Y. I. P.; Wing Cheong, Y. A. M.; David Ho-Keung, S. H. U. M. & Shea Ping, Y. I. P. (2020), 'Will a new clade of SARS-CoV-2 imported into the community spark a fourth wave of the COVID-19 outbreak in Hong Kong?', *Emerging Microbes & Infections* **0**, 1-19.

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.

Githinji, G.; deLaurent, Z. R.; Mohamed, K. S.; Omuoyo, D. O.; Macharia, P. M.; Morobe, J. M.; Otieno, E.; Kinyanjui, S. M.; Agweyu, A.; Maitha, E.; Kitole, B.; Suleiman, T.; Mwakinangu, M.; Nyambu, J.; Otieno, J.; Salim, B.; Kasera, K.; Kiiru, J.; Aman, R.; Barasa, E.; Warimwe, G.; Bejon, P.; Tssofa, B.; Ochola-Oyier, L. I.; Nokes, D. J. & Agoti, C. N. (2020), 'Tracking the introduction and spread of SARS-CoV-2 in coastal Kenya', *medRxiv*, 2020.10.05.20206730.

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.

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', *BMC Genomics* **21**(1), 863.

Gómez-Carballa, A. A.; Bello, X.; Pardo-Seco, J.; Del Molino-Bernal, Luisa, P. M.; Martinón-Torres, F. & Salas, A. (2020), 'Phylogeography of SARS-CoV-2 pandemic in Spain: a story of multiple introductions, micro-geographic stratification, founder effects, and super-spreaders', *Zoological Research*.

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.

Gong, Z.; Zhu, J.; Li, C.; Jiang, S.; Ma, L.; Tang, B.; Zou, D.; Chen, M.; Sun, Y.; Song, S.; Zhang, Z.; Xiao, J.; Xue, Y.; Bao, Y.; Du, Z. & Zhao, W.-M. (2020), 'A coronavirus online analysis platform at the National Genomics Data Center', *Zoological Research*, 1-6 (accepted manuscript).

Gonzalez-Reiche, A. S.; Hernandez, M. M.; Sullivan, M.; Ciferri, B.; Alshammary, H.; Obla, A.; Fabre, S.; Kleiner, G.; Polanco, J.; Khan, Z.; Alburquerque, 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.; Alburquerque, 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.

Gousseff, M.; Penot, P.; Gallay, L.; Batisse, D.; Benech, N.; Bouiller, K.; Collarino, R.; Conrad, A.; Slama, D.; Joseph, C.; Lemaignen, A.; Lescure, F.-X.; Levy, B.; Mahevas, M.; Pozzetto, B.; Vignier, N.; Wyplosz, B.; Salmon, D.; Goehringer, F. & Botelho-Nevers, E. (2020), 'Clinical recurrences of COVID-19 symptoms after recovery: Viral relapse, reinfection or inflammatory rebound?', *Journal of Infection* **81**(5), 816-846.

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.

Greaney, A. J.; Starr, T. N.; Gilchuk, P.; Zost, S. J.; Binshtein, E.; Loes, A. N.; Hilton, S. K.; Huddleston, J.; Eguia, R.; Crawford, K. H. D.; Dingens, A. S.; Nargi, R. S.; Sutton, R. E.; Suryadevara, N.; Rothlauf, P. W.; Liu, Z.; Whelan, S. P. J.; Carnahan, R. H.; Crowe, J. E. & Bloom, J. D. (2020), 'Complete mapping of mutations to the SARS-CoV-2 spike receptor-binding domain that escape antibody recognition', *bioRxiv*, 2020.09.10.292078.

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.; Nordahl, 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.

Günther, T.; Czech-Sioli, M.; Indenbirken, D.; Robitaille, A.; Tenhaken, P.; Exner, M.; Ottinger, M.; Fischer, N.; Grundhoff, A. & Brinkmann, M. M. (2020), 'SARS-CoV-2 outbreak investigation in a German meat processing plant', *EMBO Molecular Medicine* **12**(12), e13296.

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.; Soehnlen, 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.

Gupta, V.; Bhoyar, R. C.; Jain, A.; Srivastava, S.; Upadhayay, R.; Imran, M.; Jolly, B.; Divakar, M. K.; Sharma, D.; Sehgal, P.; Ranjan, G.; Gupta, R.; Scaria, V. & Sivasubbu, S. (2020), 'Asymptomatic reinfection in two healthcare workers from India with genetically distinct SARS-CoV-2', *Clinical Infectious Diseases*.

Guruprasad, L. (2020), 'Evolutionary relationships and sequence-structure determinants in human SARS coronavirus-2 spike proteins for host receptor recognition', *Proteins: Structure, Function, and Bioinformatics* **88**(11), 1387-1393.

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. (2020), 'COVATOR: A Software for Chimeric Coronavirus Identification', *bioRxiv*, 2020.11.14.383075.

Habib, P.; Alsamman, A. M.; Saber-Ayad, M.; Hassanein, S. E. & Hamwieh, 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.

Hadfield, J.; Douglas, J.; Geoghegan, J. L.; Storey, M.; Ren, X.-Y.; Freed, N.; Silander, O.; Jiménez-Silva, C. L.; French, N.; Drummond, A. J.; Welch, D. & de Ligt, J. (2020), 'Re-emergence of community transmission in Aotearoa New Zealand - Genomic overview of the Auckland Outbreak', *nextstrain.org*, online, S0507, (online narrative).

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.

Hahn, G.; Wu, C. M.; Lee, S.; Hecker, J.; Lutz, S. M.; Haneuse, S.; Qiao, D.; Cho, M. H.; Randolph, A.; Laird, N. M.; Weiss, S. T.; Silverman, E. K.; Ribbeck, K. & Lange, C. (2020), 'Mutations in SARS-CoV-2 spike protein and RNA polymerase complex are associated with COVID-19 mortality risk', *bioRxiv*, 2020.11.17.386714.

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.

Hamer, S. A.; Pauvolid-Correa, A.; Zecca, I. B.; Davila, E.; Auckland, L. D.; Roundy, C. M.; Tang, W.; Torchetti, M. K.; Killian, M. L.; Jenkins-Moore, M.; Mozingo, K.; Akpalu, Y.; Ghai, R. R.; Spengler, J. R.; Behravesh, C. B.; Fischer, R. & Hamer, G. L. (2020), 'Natural SARS-CoV-2 infections, including virus isolation, among serially tested cats and dogs in households with confirmed human COVID-19 cases in Texas, USA', *bioRxiv*, 2020.12.08.416339.

Hammer, A. S.; Quaade, M. L.; Rasmussen, T. B.; Fonager, J.; Rasmussen, M.; Mundbjerg, K.; Lohse, L.; Strandbygaard, B.; Jørgensen, C. S.; Alfaro-Núñez, A.; Rosenstierne, M. W.; Boklund, A.; Halasa, T.; Fomsgaard, A.; Belsham, G. J. & Bøtner, A. (2020), 'SARS-CoV-2 Transmission between Mink (*Neovison vison*) and Humans, Denmark - Volume 27, Number 2—February 2021 - Emerging Infectious Diseases journal - CDC', , (Early Release Article).

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

Handrick, S.; Bestehorn-Willmann, M.; Eckstein, S.; Walter, M. C.; Antwerpen, M. H.; Naija, H.; Stoecker, K.; Wölfel, R. & Ben Moussa, M. (2020), 'Whole genome sequencing and phylogenetic classification of Tunisian SARS-CoV-2 strains from patients of the Military Hospital in Tunis', *Virus Genes*, doi:10.1007/s11262-020-01795-9.

Hang, J.; Li, T.; Chung, H. K.; Pireku, P. K.; Beitzel, B.; Sanborn, M. A.; Tang, C.; Hammer, R.; Ritter, D. G.; Wan, X.-F. & Berry, I. M. (2020), 'Rapid High Throughput Whole Genome Sequencing of SARS-CoV-2 by using One-step RT-PCR Amplification with Integrated Microfluidic System and Next-Gen Sequencing', *bioRxiv*,

2020.11.04.369165.

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.

Harper, H.; Burridge, A. J.; Winfield, M.; Finn, A.; Davidson, A. D.; Matthews, D.; Hutchings, S.; Vipond, B.; Jain, N.; Edwards, K. J.; Barker, G. & Consortium, T. C. O. V. I. D.-19. G. U. (C. O. G.-U. (2020), 'Detecting SARS-CoV-2 variants with SNP genotyping', *bioRxiv*, 2020.11.18.388140.

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.; Pitkäpääsi, M.; Blomqvist, S.; Rönkkö, E.; Kantele, A.; Strandin, T.; Kallio-Kokko, H.; Mannonen, L.; Lappalainen, M.; Broas, M.; Jiang, M.; Siira, L.; Salminen, M.; Puimalainen, 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.; Woebken, C.; Mason, C. E. & Slavin, K. (2020), 'Holobiont Urbanism: sampling urban beehives reveals cities' metagenomes', *bioRxiv*, 2020.05.07.075093.

Hernández Huerta, M. T.; Mayoral, L. P.-C.; Díaz, C. R.; Cruz, M. M.; Mayoral Andrade, G.; Navarro, L. M. S.; Canseco, M. d. S. P.; Parada, E. C.; Cruz, R. M.; Mayoral, E. P.-C.; Santiago, A. D. P.; Martínez, G. V.; Pérez Campos, E. & Matias Cervantes, C. A. (2020), 'Analysis of SARS-CoV-2 mutations in Mexico, Belize and isolated regions of Guatemala and its implication in the diagnosis', *Journal of Medical Virology*(n/a), (accepted manuscript).

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 Nextstrain.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*.

Hosie, M. J.; Epifano, I.; Herder, V.; Orton, R.; Stevenson, A.; Johnson, N.; MacDonald, E.; Dunbar, D.; McDonald, M.; Howie, F.; Tennant, B.; Herrity, D.; Filipe, A. C.; Streicker, D. G.; Willett, B. J.; Murcia, P. R.; Jarrett, R. F.; Robertson, D. L.; Weir, W. & the COVID-19 Genomics UK (COG-UK) consortium (2020), 'Respiratory disease in cats associated with human-to-cat transmission of SARS-CoV-2 in the UK', *bioRxiv*, 2020.09.23.309948.

Hossain, M. U.; Ahammad, I.; Emon, M. T. H.; Bhattacharjee, A.; Chowdhury, Z. M.; Mosaib, M. G.; Das, K. C.; Keya, C. A. & Salimullah, M. (2020), 'Whole Genome Sequencing for Revealing the Point Mutations of SARS-CoV-2 Genome in Bangladeshi Isolates and their Structural Effects on Viral Proteins', *bioRxiv*, 2020.12.05.413377.

Hou, Y. J.; Chiba, S.; Halfmann, P.; Ehre, C.; Kuroda, M.; Dinnon, K. H.; Leist, S. R.; Schäfer, A.; Nakajima, N.; Takahashi, K.; Lee, R. E.; Mascenik, T. M.; Edwards, C. E.; Tse, L. V.; Boucher, R. C.; Randell, S. H.; Suzuki, T.; Gralinski, L. E.; Kawaoka, Y. & Baric, R. S. (2020), 'SARS-CoV-2 D614G Variant Exhibits Enhanced Replication ex vivo and Earlier Transmission in vivo', *bioRxiv*, 2020.09.28.317685.

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.

Hufsky, F.; Lamkiewicz, K.; Almeida, A.; Aouacheria, A.; Arighi, C.; Bateman, A.; Baumbach, J.; Beerewinkel, N.; Brandt, C.; Cacciabue, M.; Chuguransky, S.; Drechsel, O.; Finn, R. D.; Fritz, A.; Fuchs, S.; Hattab, G.; Hauschild, A.-C.; Heider, D.; Hoffmann,

M.; Hölzer, M.; Hoops, S.; Kaderali, L.; Kalvari, I.; von Kleist, M.; Kmiecinski, R.; Kühnert, D.; Lasso, G.; Libin, P.; List, M.; Löchel, H. F.; Martin, M. J.; Martin, R.; Matschinske, J.; McHardy, A. C.; Mendes, P.; Mistry, J.; Navratil, V.; Nawrocki, E. P.; O'Toole, Á. N.; Ontiveros-Palacios, N.; Petrov, A. I.; Rangel-Pineros, G.; Redaschi, N.; Reimering, S.; Reinert, K.; Reyes, A.; Richardson, L.; Robertson, D. L.; Sadegh, S.; Singer, J. B.; Theys, K.; Upton, C.; Welzel, M.; Williams, L. & Marz, M. (2020), 'Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research', *Briefings in Bioinformatics*, bbaa232.

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.; Roberton, 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.

Ikemura, T.; Wada, K.; Wada, Y.; Iwasaki, Y. & Abe, T. (2020), 'Unsupervised explainable AI for simultaneous molecular evolutionary study of forty thousand SARS-CoV-2 genomes', *bioRxiv*, 2020.10.11.335406.

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* **00**, 1-9.

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.

Itokawa, K.; Sekizuka, T.; Hashino, M.; Tanaka, R. & Kuroda, M. (2020), 'Disentangling primer interactions improves SARS-CoV-2 genome sequencing by multiplex tiling PCR', *PLOS ONE* 15(9), e0239403.

Iweriebor, B. C.; Egble, 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.

Jaimes, 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.; Mühlmann, 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.; Sassaki, 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.; Kujabi Mariama, A.; Bakary, S.; Oboh Mary, A.; Bojang, A.; Jallow, H.; Nwakanma, D.; Secka, O.; Rocca, A.; Amambua-Ngwa, A.; Antonio, M.; Baldeh, I.; Forrest, 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*, 2020.10.26.354969.

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.

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', *Journal of Clinical Virology* **131**, 104585.

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.; Zeghbib, S.; Somogyi, B.; Toth, G. E.; Banyai, K.; Solymosi, N.; Szabo, P. M.; Szabo, I.; Balint, A.; Urban, P.; Herczeg, R.; Gyenesi, 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.

Kemp, S. A.; Collier, D. A.; Datir, R.; Gayed, S.; Jahun, A.; Hosmillo, M.; Ferreira, I.; Rees-Spear, C.; Mlcochova, P.; Lumb, I. U.; Roberts, D.; Chandra, A.; Temperton, N.; Collaboration, T. C. I. T. I. D.-N. B. C. O. V. I. D.-19.; Consortium, T. C. O. V. I. D.-19. G. U. (C. O. G.-U.); Sharrocks, K.; Blane, E.; Briggs, J. a. G.; Gils, M. v.; Smith, K. G. C.; Bradley, J. R.; Smith, C.; Goldstein, R. A.; Goodfellow, I. G.; Smielewska, A.; Skittrall, J. P.; Gouliouris, T.; Gkrania-Klotsas, E.; Illingworth, C. J. R.; McCoy, L. E. & Gupta, R. K. (2020), 'Neutralising antibodies drive Spike mediated SARS-CoV-2 evasion', *medRxiv*, 2020.12.05.20241927.

Kennedy, D. A. & Read, A. F. (2020), 'Monitor for COVID-19 vaccine resistance evolution during clinical trials', *PLOS Biology* **18**(11), e3001000.

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.

Klimczak, L. J.; Randall, T. A.; Saini, N.; Li, J.-L. & Gordenin, D. A. (2020), 'Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic', *PLOS ONE* **15**(10), e0237689.

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.

Kubik, S.; Marques, A. C.; Xing, X.; Silvery, J.; Bertelli, C.; Maio, F. D.; Pournaras, S.; Burr, T.; Duffourd, Y.; Siemens, H.; Alloui, C.; Song, L.; Wenger, Y.; Saitta, A.; Macheret, M.; Smith, E. W.; Menu, P.; Brayer, M.; Steinmetz, L. M.; Si-Mohammed, A.; Chuisseau, J.; Stevens, R.; Constantoulakis, P.; Sali, M.; Greub, G.; Tiemann, C.; Pelechano, V.; Willig, A. & Xu, Z. (2020), 'Guidelines for accurate genotyping of SARS-CoV-2 using amplicon-based sequencing of clinical samples', *bioRxiv*, 2020.12.01.405738.

Kuipers, J.; Batavia, A. A.; Jablonski, K. P.; Bayer, F.; Borgsmüller, N.; Dondi, A.; Drăgan, M.-A.; Ferreira, P.; Jahn, K.; Lamberti, L.; Pirkl, M.; Posada-Céspedes, S.; Topolsky, I.; Nissen, I.; Santacroce, N.; Burcklen, E.; Schär, T.; Capece, V.; Beckmann, C.; Kobel, O.; Noppen, C.; Redondo, M.; Nadeau, S.; Seidel, S.; Souza, N. S. d.; Beisel, C.; Stadler, T. & Beerenswinkel, N. (2020), 'Within-patient genetic diversity of SARS-

CoV-2', *bioRxiv*, 2020.10.12.335919.

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.

Kumar, S.; Tao, Q.; Weaver, S.; Sanderford, M. D.; Caraballo, M.; Sharma, S.; Pond, S. L. K. & Miura, S. (2020), 'An evolutionary portrait of the progenitor SARS-CoV-2 and its dominant offshoots in COVID-19 pandemic', *bioRxiv*, 2020.09.24.311845.

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.; Chemao-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.; Nejjari, 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.; Alouane, T.; Kartti, S.; Chemao-Elfihri, M. W.; Hakmi, M.; Essabbar, A.; Laamarti, M.; Hlali, H.; Bendani, H.; Boumajdi, N.; Benhrif, O.; Allam, L.; Hafidi, N. E.; Jaoudi, R. E.; Allali, I.; Marchoudi, N.; Fekkak, J.; Benrahma, H.; Nejjari, C.; Amzazi, S.; Belyamani, L. & Ibrahimi, A. (2020), 'Large scale genomic analysis of 3067 SARS-CoV-2 genomes reveals a clonal geo-distribution and a rich genetic variations of hotspots mutations', *PLOS ONE* 15(11), e0240345.

Laamarti, M.; Essabbar, A.; Alouane, T.; Kartti, S.; Bendani, H.; Boumajdi, N.; Laamarti, R.; Allam, L.; Ouadghiri, M.; Chemao-Elfihri, M. W.; Ghrifi, F.; Smyej, I.; Rahoui, J.; Benrahma, H.; Diawara, I.; Aanniz, T.; Hafidi, N. E.; Jaoudi, R. E.; Nejjari, C.; Amzazi, S.; Mentag, R.; Belyamani, L. & Ibrahimi, A. (2020), 'Do the Moroccan SARS-CoV-2 genetic diversity hamper the use of the developed universal vaccines in Morocco?', *bioRxiv*, 2020.06.30.181123.

Ladhani, S. N.; Chow, J. Y.; Janarthanan, R.; Fok, J.; Crawley-Boevey, E.; Vusirikala, A.; Fernandez, E.; Perez, M. S.; Tang, S.; Dun-Campbell, K.; Wynne-Evans, E.; Bell, A.; Patel, B.; Amin-Chowdhury, Z.; Aiano, F.; Paranthaman, K.; Ma, T.; Saavedra-Campos, M.; Myers, R.; Ellis, J.; Lackenby, A.; Gopal, R.; Patel, M.; Chand, M.; Brown, K.; Hopkins, S.; Consortium, C.; Shetty, N.; Zambon, M. & Ramsay, M. E. (2020), 'Increased risk of SARS-CoV-2 infection in staff working across different care homes: enhanced CoVID-19 outbreak investigations in London care Homes', *Journal of Infection* **81**(4), 621-624.

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.; Tagliabruni, A.; Caruso, A.; Caccuri, F.; Ronchiadini, 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.

Laiton-Donato, K.; Villabona-Arenas, C. J.; Usme-Ciro, J. A.; Franco-Muñoz, C.; Álvarez-Díaz, D. A.; Villabona-Arenas, L. S.; Echeverría-Londoño, S.; Cucunubá, Z. M.; Franco-Sierra, N. D.; Flórez, A. C.; Ferro, C.; Ajami, N. J.; Walteros, D. M.; Prieto, F.; Durán, C. A.; Ospina-Martínez, M. L. & Mercado-Reyes, M. (2020), 'Genomic Epidemiology of Severe Acute Respiratory Syndrome Coronavirus 2, Colombia', *Emerging Infectious Diseases journal - CDC* **26**(12), 2854-2862.

Lam, J.-Y.; Yuen, C.-K.; Ip, J. D.; Wong, W.-M.; To, K. K.-W.; Yuen, K.-Y. & Kok, K.-H. (2020), 'Loss of orf3b in the circulating SARS-CoV-2 strains', *Emerging Microbes & Infections* **0**, 1-678.

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.

Larson, D.; Brodniak, S. L.; Voegtle, L. J.; Cer, R. Z.; Glang, L. A.; Malagon, F. J.; Long, K. A.; Potocki, R.; Smith, D. R.; Lanteri, C.; Burgess, T. & Bishop-Lilly, K. A. (2020), 'A Case of Early Re-infection with SARS-CoV-2', *Clinical Infectious Diseases*, ciaa1436.

Latinne, A.; Hu, B.; Olival, K. J.; Zhu, G.; Zhang, L.; Li, H.; Chmura, A. A.; Field, H. E.; Zambrana-Torrelío, 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.

Lee, J.-S.; Kim, S. Y.; Kim, T. S.; Hong, K. H.; Ryoo, N.-H.; Lee, J.; Park, J. H.; Cho, S. I.; Kim, M. J.; Kim, Y.-g.; Kim, B.; Shin, H. S.; Oh, H. S.; Seo, M.-S.; Gwon, T.-R.; Kim, Y.; Park, J.-S.; Chin, B. S.; Park, W. B.; Park, S. S. & Seong, M.-W. (2020), 'Evidence of Severe Acute Respiratory Syndrome Coronavirus 2 Reinfection After Recovery from Mild Coronavirus Disease 2019', *Clinical Infectious Diseases*, ciaa1421.

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.

Lemey, P.; Hong, S. L.; Hill, V.; Baele, G.; Poletto, C.; Colizza, V.; O'Toole, Á.; McCrone, J. T.; Andersen, K. G.; Worobey, M.; Nelson, M. I.; Rambaut, A. & Suchard, M. A. (2020), 'Accommodating individual travel history and unsampled diversity in Bayesian phylogeographic inference of SARS-CoV-2', *Nature Communications* **11**(1), 5110.

Lemieux, J. E.; Siddle, K. J.; Shaw, B. M.; Loreth, C.; Schaffner, S. F.; Gladden-Young, A.; Adams, G.; Fink, T.; Tomkins-Tinch, C. H.; Krasilnikova, L. A.; DeRuff, K. C.; Rudy, M.; Bauer, M. R.; Lagerborg, K. A.; Normandin, E.; Chapman, S. B.; Reilly, S. K.; Anahtar, M. N.; Lin, A. E.; Carter, A.; Myhrvold, C.; Kemball, M. E.; Chaluvadi, S.; Cusick, C.; Flowers, K.; Neumann, A.; Cerrato, F.; Farhat, M.; Slater, D.; Harris, J. B.; Branda, J. A.; Hooper, D.; Gaeta, J. M.; Baggett, T. P.; O'Connell, J.; Gnirke, A.; Lieberman, T. D.; Philippakis, A.; Burns, M.; Brown, C. M.; Luban, J.; Ryan, E. T.; Turbett, S. E.; LaRocque, R. C.; Hanage, W. P.; Gallagher, G. R.; Madoff, L. C.; Smole, S.; Pierce, V. M.; Rosenberg, E.; Sabeti, P. C.; Park, D. J. & MacInnis, B. L. (2020), 'Phylogenetic analysis of SARS-CoV-2 in Boston highlights the impact of superspreading events', *Science*, eabe3261.

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

Lemoine, F.; Bassel, 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.; Maglione, D. T.; Ruble, D.; Ryutov, A.; Shen, L.; Lee, L.; Feigelman, R.; Burdon, G.; Liu, J.; Oliva, A.; Borcherding, 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, Q.; Zheng, X.-S.; Shen, X.-R.; Si, H.-R.; Wang, X.; Wang, Q.; Li, B.; Zhang, W.; Zhu, Y.; Jiang, R.-D.; Zhao, K.; Wang, H.; Shi, Z.-L.; Zhang, H.-L.; Du, R.-H. & Zhou, P. (2020), 'Prolonged shedding of severe acute respiratory syndrome coronavirus 2 in patients with COVID-19', *Emerging Microbes & Infections* **0**(ja), 1-28.

Li, W.; Yang, S.; Xu, P.; Zhang, D.; Tong, Y.; Chen, L.; Jia, B.; Li, A.; Ru, D.; Zhang, B.; Liu, M.; Lian, C.; Chen, C.; Fu, W.; Yuan, S.; Ren, X.; Liang, Y.; Yang, Z.; Li, W.; Wang, S.; Zhang, X.; Lu, H.; Xu, J.; Wang, H. & Yu, W. (2020), 'Human Identical Sequences of SARS-CoV-2 Promote Clinical Progression of COVID-19 by Upregulating Hyaluronan via NamiRNA-Enhancer Network', *bioRxiv*, 2020.11.04.361576.

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.; 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.

Li, Y.; Yang, X.; Wang, N.; Wang, H.; Yin, B.; Yang, X. & Jiang, W. (2020), 'GC usage of SARS-CoV-2 genes might adapt to the environment of human lung expressed genes', *Molecular Genetics and Genomics* **295**(6), 1537-1546.

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.; Bian, Y. & Huang, L. (2020), 'CoV-Seq, a New Tool for SARS-CoV-2 Genome Analysis and Visualization: Development and Usability Study', *Journal of Medical Internet Research* **22**(10), e22299.

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, T.; Chen, Z.; Chen, W.; Chen, X.; Asanjan, M. H.; Yang, Z.; Li, J.; Ho, D.; Turay, D.; Gheorghe, C.; Jones, W. & Wang, C. (2020), 'A benchmarking study of SARS-CoV-2 whole-genome sequencing protocols using COVID-19 patient samples', *bioRxiv*, 2020.11.10.375022.

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.

Lokman, S. M.; Rasheduzzaman, M.; Salauddin, A.; Barua, R.; Tanzina, A. Y.; Rumi, M. H.; Hossain, M. I.; Siddiki, A. M. A. M. Z.; Mannan, A. & Hasan, M. M. (2020), 'Exploring the genomic and proteomic variations of SARS-CoV-2 spike glycoprotein: A computational biology approach', *Infection, Genetics and Evolution* **84**, 104389.

Lon, J. R.; Bai, Y.; Zhong, B.; Cai, F. & Du, H. (2020), 'Prediction and evolution of B cell epitopes of surface protein in SARS-CoV-2', *Virology Journal* **17**(1), 165.

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.

Long, S. W.; Olsen, R. J.; Christensen, P. A.; Bernard, D. W.; Davis, J. J.; Shukla, M.; Nguyen, M.; Saavedra, M. O.; Yerramilli, P.; Pruitt, L.; Subedi, S.; Kuo, H.-C.; Hendrickson, H.; Eskandari, G.; Nguyen, H. A. T.; Long, J. H.; Kumaraswami, M.; Goike, J.; Boutz, D.; Gollihar, J.; McLellan, J. S.; Chou, C.-W.; Javanmardi, K.; Finkelstein, I. J. & Musser, J. M. (2020), 'Molecular Architecture of Early Dissemination and Massive Second Wave of the SARS-CoV-2 Virus in a Major Metropolitan Area', *mBio* **11**(6).

Lopes, L. R.; de Mattos Cardillo, G. & Paiva, P. B. (2020), 'Molecular evolution and phylogenetic analysis of SARS-CoV-2 and hosts ACE2 protein suggest Malayan pangolin as intermediary host', *Brazilian Journal of Microbiology* **51**(4), 1593-1599.

Lopez, E. J.; Tarazona, D.; Guerrero, F. V.; Serrano, N. R.; Carhuaricra, D.; Hernandez, L. M. & Chavez, R. G. (2020), 'Phylogenomic reveals multiple introductions and early spread of SARS-CoV-2 into Peru', *bioRxiv*, 2020.09.14.296814.

Lou, J.; Zhao, S.; Cao, L.; Chen, Z.; Chan, R. W. Y.; Chong, M. K. C.; Zee, B. C. Y.; Chan, P. K. S. & Wang, M. H. (2020), 'Temporal patterns in the evolutionary genetic distance of SARS-CoV-2 during the COVID-19 pandemic', *bioRxiv*, 2020.11.01.363739.

Lu, B.; Yan, Y.; Dong, L.; Han, L.; Liu, Y.; Yu, J.; Chen, J.; Yi, D.; Zhang, M.; Wang, C.; Wang, R.; Wang, D.; Wei, H.; Liu, D. & Yi, C. (2020), 'Integrated characterization of SARS-CoV-2 genome, microbiome, antibiotic resistance and host response from single throat swabs', *bioRxiv*, 2020.10.15.340794.

Lu, J.; du Plessis, L.; 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.; Raghwan, 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.; Raghwan, 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.

Lulla, V.; Wandel, M. P.; Bandyra, K. J.; Dendooven, T.; Yang, X.; Doyle, N.; Oerum, S.; O'Rourke, S.; Randow, F.; Maier, H. J.; Scott, W.; Ding, Y.; Firth, A. E.; Blozneltye, K. & Luisi, B. F. (2020), 'Antisense oligonucleotides target a nearly invariant structural element from the SARS-CoV-2 genome and drive RNA degradation', *bioRxiv*, 2020.09.18.304139.

Luo, R.; Wong, Y.-S. & Lam, T.-W. (2020), 'Tracking cytosine depletion in SARS-CoV-2', *bioRxiv*, 2020.10.26.354787.

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.; Williams, R.; Vernet, G.; Justice, A.; Green, A.; Nicholls, S. M.; Ansari, M. A.; Abeler-Dorner, L.; Moore, C. E.; Peto, T. E. A.; Eyre, D. W.; Shaw, R.; Simmonds, P.; Buck, D.; Todd, J. A.; Connor, T. R.; Filipe, A. d. S.; Shephard, J.; Thomson, E. C.; Consortium, T. C. O. V. I. D.-19. G. U. (C. O. G.-U.; Bonsall, D.; Fraser, C. & Golubchik, T. (2020), 'Within-host genomics of SARS-CoV-2', *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.

Magalis, B. R.; Ramirez-Mata, A.; Zhukova, A.; Mavian, C.; Marini, S.; Lemoine, F.; Prosperi, M.; Gascuel, O. & Salemi, M. (2020), 'Differing impacts of global and regional responses on SARS-CoV-2 transmission cluster dynamics', *bioRxiv*, 2020.11.06.370999.

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).

Manfredonia, I.; Nithin, C.; Ponce-Salvatierra, A.; Ghosh, P.; Wirecki, T. K.; Marinus, T.; Ogando, N. S.; Snijder, E. J.; van Hemert, M. J.; Bujnicki, J. M. & Incarnato, D. (2020), 'Genome-wide mapping of SARS-CoV-2 RNA structures identifies therapeutically-relevant elements', *Nucleic Acids Research*, gkaa1053.

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.

Massacci, A.; Sperandio, E.; D'Ambrosio, L.; Maffei, M.; Palombo, F.; Aurisicchio, L.; Ciliberto, G. & Pallocca, M. (2020), 'Design of a Companion Bioinformatic Tool to detect the emergence and geographical distribution of SARS-CoV-2 Spike protein genetic variants', *bioRxiv*, 2020.06.22.133355.

Mastriani, E.; Rakov, A. V. & Liu, S.-L. (2020), 'An evolutionary analysis of the SARS-CoV-2 genomes from the countries in the same meridian', *bioRxiv*, 2020.11.12.380816.

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.

Maurano, M. T.; Ramaswami, S.; Zappile, P.; Dimartino, D.; Boytard, L.; Ribeiro-dos-Santos, A. M.; Vulpescu, N. A.; Westby, G.; Shen, G.; Feng, X.; Hogan, M. S.; Ragonnet-Cronin, M.; Geidelberg, L.; Marier, C.; Meyn, P.; Zhang, Y.; Cadley, J. A.; Ordoñez, R.; Luther, R.; Huang, E.; Guzman, E.; Arguelles-Grande, C.; Argyropoulos, K. V.; Black, M.; Serrano, A.; Call, M. E.; Kim, M. J.; Belovarac, B.; Gindin, T.; Lytle, A.; Pinnell, J.; Vougiouklakis, T.; Chen, J.; Lin, L. H.; Rapkiewicz, A.; Raabe, V.; Samanovic, M. I.; Jour, G.; Osman, I.; Aguero-Rosenfeld, M.; Mulligan, M. J.; Volz, E. M.; Cotzia, P.; Snuderl, M. & Heguy, A. (2020), 'Sequencing identifies multiple early introductions of SARS-CoV-2 to the New York City Region', *Genome Research*, gr.266676.120.

Mavian, C.; Marini, S.; Prosperi, M. & Salemi, M. (2020), 'Authors' Reply to: Errors in Tracing Coronavirus SARS-CoV-2 Transmission Using a Maximum Likelihood Tree. Comment on "A Snapshot of SARS-CoV-2 Genome Availability up to April 2020 and its Implications: Data Analysis"', *JMIR Public Health and Surveillance* 6(4), e24661.

Mavian, C.; Marini, S.; Prosperi, 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.

Mavrodiel, E. V.; Tursky, M. L.; Mavrodiel, N. E.; Ebach, M. C. & Williams, D. M. (2020), 'On Classification and Taxonomy of Coronaviruses (Riboviria, Nidovirales, Coronaviridae) with the special focus on severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2)', *bioRxiv*, 2020.10.17.343749.

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.; Ingberman, K.; Stokol, T.; Frederikson, R.; Delaney, M. A.; Ivancic, M.; Jenkins-Moore, M.; Mozingo, 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.; Douangngueun, B.; Khammavong, K.; Singhalath, S.; Duong, V.; Buchy, P.; Olson, S. H.; Keatts, L.; Fine, A. E.; Greatorex, Z.; Gilbert, M.; LeBreton, M.; Sailors, 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.

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. P. (2020), 'High-Density Amplicon Sequencing Identifies Community Spread and Ongoing Evolution of SARS-CoV-2 in the Southern United States', *Cell Reports* 33(5).

Medeiros, I. G.; Khayat, A. S.; Stransky, B.; Santos, S. E. B. d.; Assumpção, P. P. & Souza, J. E. S. d. (2020), 'A small interfering RNA (siRNA) database for SARS-CoV-2', *bioRxiv*, 2020.09.30.321596.

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', *Journal of Medical Virology*, (Accepted Author Manuscript).

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* **20**(11), 1263-1272.

Merino, G. A.; Raad, J.; Bugnon, L. A.; Yones, C.; Kamenetzky, L.; Claus, J.; Ariel, F.; Milone, D. H. & Stegmayer, G. (2020), 'Novel SARS-CoV-2 encoded small RNAs in the passage to humans', *Bioinformatics*, btaa1002.

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.; Giltsbach, 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.

Miller, D.; Martin, M. A.; Harel, N.; Tirosh, O.; Kustin, T.; Meir, M.; Sorek, N.; Gefen-Halevi, S.; Amit, S.; Vorontsov, O.; Shaag, A.; Wolf, D.; Peretz, A.; Shemer-Avni, Y.; Roif-Kaminsky, D.; Kopelman, N. M.; Huppert, A.; Koelle, K. & Stern, A. (2020), 'Full genome viral sequences inform patterns of SARS-CoV-2 spread into and within Israel', *Nature Communications* **11**(1), 5518.

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.

Mollentze, N.; Babayan, S. & Streicker, D. (2020), 'Identifying and prioritizing potential human-infecting viruses from their genome sequences', *bioRxiv*, 2020.11.12.379917.

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.

Moreno, G. K.; Braun, K. M.; Riemersma, K. K.; Martin, M. A.; Halfmann, P. J.; Crooks, C. M.; Prall, T.; Baker, D.; Baczenas, J. J.; Heffron, A. S.; Ramuta, M.; Khubbar, M.; Weiler, A. M.; Accola, M. A.; Rehrauer, W. M.; O'Connor, S. L.; Safdar, N.; Pepperell, C. S.; Dasu, T.; Bhattacharyya, S.; Kawaoka, Y.; Koelle, K.; O'Connor, D. H. & Friedrich, T. C. (2020), 'Revealing fine-scale spatiotemporal differences in SARS-CoV-2 introduction and spread', *Nature Communications* **11**(1), 5558.

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.

Motayo, B. O.; Oluwasemowo, O. O. & Akinduti, P. A. (2020), 'Evolutionary Dynamics And Geographic Dispersal Of Beta Coronaviruses In African Bats', *bioRxiv*, 2020.05.14.056085.

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.

Mourier, T.; Sadykov, M.; Carr, M. J.; Gonzalez, G.; Hall, W. W. & Pain, A. (2020), 'Host-directed editing of the SARS-CoV-2 genome', *Biochemical and Biophysical Research Communications*, (accepted manuscript).

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

Muller, N.; Kunze, M.; Steitz, F.; Saad, N. J.; Mühlmann, B.; Beheim-Schwarzbach, J. I.; Schneider, J.; Drosten, C.; Murajda, L.; Kochs, S.; Ruscher, C.; Walter, J.; Zeitlmann, N. & Corman, V. M. (2021), 'Early Release - Severe Acute Respiratory Syndrome Coronavirus 2 Outbreak Related to a Nightclub, Germany', *eid*2702.204443.

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: anthropozoonotic and zoonotic transmission of SARS-CoV-2 on mink farms', *bioRxiv*, 2020.09.01.277152.

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. J.; GeurtsvanKessel, C.; Eijk, A. A. v. d.; Velkers, F. C.; Smit, L. A. M.; Stegeman, A.; Poel, W. H. M. v. d. & Koopmans, M. P. G. (2020), 'Transmission of SARS-CoV-2 on mink farms between humans and mink and back to humans', *Science*, DOI: 10.1126/science.abe5901.

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* 73(4), 320-322.

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.

Navarro Gonzalez, J.; Zweig, A. S.; Speir, M. L.; Schmelter, D.; Rosenbloom, K. R.; Raney, B. J.; Powell, C. C.; Nassar, L. R.; Maulding, N. D.; Lee, C. M.; Lee, B. T.; Hinrichs, A. S.; Fyfe, A. C.; Fernandes, J. D.; Diekhans, M.; Clawson, H.; Casper, J.; Benet-Pagès, A.; Barber, G. P.; Haussler, D.; Kuhn, R. M.; Haeussler, M. & Kent, W. J. (2020), 'The UCSC Genome Browser database: 2021 update', *Nucleic Acids Research*, gkaa1070.

Neches, R. Y.; McGee, M. D. & Kyrpides, N. C. (2020), 'Recombination should not be an afterthought', *Nature Reviews. Microbiology* **18**(11), 606.

Nelson, C. W.; Ardern, Z.; Goldberg, T. L.; Meng, C.; Kuo, C.-H.; Ludwig, C.; Kolokotronis, S.-O. & Wei, X. (2020), 'Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic', *bioRxiv*, 2020.05.21.109280.

Nelson, C. W.; Ardern, Z.; Goldberg, T. L.; Meng, C.; Kuo, C.-H.; Ludwig, C.; Kolokotronis, S.-O. & Wei, X. (2020), 'Dynamically evolving novel overlapping gene as a factor in the SARS-CoV-2 pandemic', *eLife* **9**, e59633.

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.; Buyukyorkut, 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.

Nguyen, T. T.; Pham, T. N.; Van, T. D.; Nguyen, T. T.; Nguyen, D. T. N.; Le, H. N. M.; Eden, J.-S.; Rockett, R. J.; Nguyen, T. T. H.; Vu, B. T. N.; Tran, G. V.; Le, T. V.; Dwyer, D. E.; Doorn, H. R. v. & Group, o. b. o. t. O. C. O. V. I. D.-19. R. (2020), 'Genetic diversity of SARS-CoV-2 and clinical, epidemiological characteristics of COVID-19 patients in Hanoi, Vietnam', *PLOS ONE* **15**(11), e0242537.

Nicholls, S. M.; Poplawski, R.; Bull, M. J.; Underwood, A.; Chapman, M.; Abu-Dahab, K.; Taylor, B.; Jackson, B.; Rey, S.; Amato, R.; Livett, R.; Goncalves, S.; Harrison, E. M.; Peacock, S. J.; Aanensen, D. M.; Rambaut, A.; Connor, T. R.; Loman, N. J. & Consortium (COG-UK), T. C. O. V. I. D.-19. G. U. K. (2020), 'MAJORA: Continuous integration supporting decentralised sequencing for SARS-CoV-2 genomic surveillance', *bioRxiv*, 2020.10.06.328328.

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.

Nomburg, J.; Meyerson, M. & DeCaprio, J. A. (2020), 'Pervasive generation of non-canonical subgenomic RNAs by SARS-CoV-2', *Genome Medicine* **12**(1), 108.

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.; Bruschke, 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.; Peppelenbosch, 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.

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 Coronavirus 2', *Emerging Infectious Diseases journal - CDC* **26**(10).

Pancer, K.; Milewska, A.; Owczarek, K.; Dabrowska, A.; Kowalski, M.; Łabaj, P.; Branicki, W.; Sanak, M. & Pyrc, K. (2020), 'The SARS-CoV-2 ORF10 is not essential in vitro or in vivo in humans', *PLOS Pathogens* **16**(12), e1008959.

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.

Parker, M. D.; Lindsey, B. B.; Leary, S.; Gaudieri, S.; Chopra, A.; Wyles, M.; Angyal, A.; Green, L. R.; Parsons, P.; Tucker, R. M.; Brown, R.; Groves, D.; Johnson, K.; Carrilero, L.; Heffer, J.; Partridge, D.; Evans, C.; Razza, M.; Keeley, A. J.; Smith, N.; Filipe, A. D. S.; Shepherd, J. G.; Davis, C.; Bennett, S.; Kohl, A.; Aranday-Cortes, E.; Tong, L.; Nichols, J.; Thomson, E. C.; Consortium, T. C. O. V. I. D.-19. G. U. (C. O. G.-U.; Wang, D.; Mallal, S. & Silva, T. I. d. (2020), 'periscope: Sub-Genomic RNA Identification in SARS-CoV-2 Genomic Sequencing Data', *bioRxiv*, 2020.07.01.181867.

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.

Pavel, S. T. I.; Yetiskin, H.; Aydin, G.; Holyavkin, C.; Uygut, M. A.; Dursun, Z. B.; Celik, İ.; Cevik, C. & Ozdarendeli, A. (2020), 'Isolation and characterization of severe acute respiratory syndrome coronavirus 2 in Turkey', *PLOS ONE* 15(9), e0238614.

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*.

Pekar, J.; Worobey, M.; Moshiri, N.; Scheffler, K. & Wertheim, J. O. (2020), 'Timing the SARS-CoV-2 Index Case in Hubei Province', *bioRxiv*, 2020.11.20.392126.

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.; Flichman, D.; Martinez, A.; Bare, P.; Garcia, G. & Lello, F. D. (2020), 'Evolutionary analysis of SARS-CoV-2 spike protein for its different clades', *bioRxiv*, 2020.11.24.396671.

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.

Pereson, M. J.; Mojsiejczuk, L.; Martínez, A. P.; Flichman, D. M.; Garcia, G. H. & Lello, F. A. D. (2020), 'Phylogenetic analysis of SARS-CoV-2 IN THE FIRST MONTHS SINCE ITS EMERGENCE', *Journal of Medical Virology*, (accepted manuscript online).

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.

Pipes, L.; Wang, H.; Huelsenbeck, J. P. & Nielsen, R. (2020), 'Assessing uncertainty in the rooting of the SARS-CoV-2 phylogeny', *Molecular Biology and Evolution*, msaa316.

Plessis, L. d.; McCrone, J. T.; Zarebski, A. E.; Hill, V.; Ruis, C.; Gutierrez, B.; Raghwani, J.; Ashworth, J.; Colquhoun, R.; Connor, T. R.; Faria, N. R.; Jackson, B.; Loman, N. J.; O'Toole, A.; Nicholls, S. M.; Parag, K. V.; Scher, E.; Vasylyeva, T. I.; Volz, E. M.; Watts, A.; Bogoch, I. I.; Khan, K.; Consortium, C.-U.; Aanensen, D.; Kraemer, M. U. G.; Rambaut, A. & Pybus, O. (2020), 'Establishment & lineage dynamics of the SARS-CoV-2 epidemic in the UK', *medRxiv*, 2020.10.23.20218446.

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.

Plyusnin, I.; Kant, R.; Jääskeläinen, A. J.; Sironen, T.; Holm, L.; Vapalahti, O. & Smura, T. (2021), 'Novel NGS Pipeline for Virus Discovery from a Wide Spectrum of Hosts and Sample Types', *Virus Evolution*, veaa091.

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.

Popa, A.; Genger, J.-W.; Nicholson, M. D.; Penz, T.; Schmid, D.; Aberle, S. W.; Agerer, B.; Lercher, A.; Endler, L.; Colaço, H.; Smyth, M.; Schuster, M.; Grau, M. L.; Martínez-Jiménez, F.; Pich, O.; Borena, W.; Pawelka, E.; Keszei, Z.; Senekowitsch, M.; Laine, J.; Aberle, J. H.; 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-Stöckl, E.; Allerberger, F.; Michor, F.; Bock, C. & Bergthaler, A. (2020), 'Genomic epidemiology of superspreading events in Austria reveals mutational dynamics and transmission properties of SARS-CoV-2', *Science Translational Medicine*, abe2555.

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.; Raghwan, 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.

Qutob, N.; Salah, Z.; Richard, D.; Darwish, H.; Sallam, H.; Shtayeh, I.; Najjar, O.; Balloux, F. & Dorp, L. v. (2020), 'The genomic epidemiology of SARS-CoV-2 in

Palestine', *bioRxiv*, 2020.10.26.355677.

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.; Vadekkandiyil, 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.

Ragonnet-Cronin, M.; Boyd, O.; Geidelberg, L.; Jorgensen, D.; Nascimento, F. F.; Siveroni, I.; Johnson, R.; Baguelin, M.; Cucunuba, Z. M.; Jauneikaite, E.; Mishra, S.; Thompson, H. A.; Watson, O. J.; Ferguson, N.; Donnelly, C. A. & Volz, E. (2020), 'COVID-19 epidemic severity is associated with timing of non-pharmaceutical interventions', *medRxiv*, 2020.09.15.20194258.

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.

Rahman, S. A.; Singh, J.; Singh, H. & Hasnain, S. E. (2020), 'Mutational signatures in countries affected by SARS-CoV-2: Implications in host-pathogen interactome', *bioRxiv*, 2020.09.17.301614.

Ramazzotti, D.; Angaroni, F.; Maspero, D.; Gambacorti-Passerini, C.; Antoniotti, M.; Graudenzi, A. & Piazza, R. (2020), 'VERSO: a comprehensive framework for the inference of robust phylogenies and the quantification of intra-host genomic diversity of viral samples', *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* **2020**, 1-6.

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*.

Rimoldi, S. G.; Stefani, F.; Gigantiello, A.; Polesello, S.; Comandatore, F.; Mileto, D.; Maresca, M.; Longobardi, C.; Mancon, A.; Romeri, F.; Pagani, C.; Cappelli, F.; Roscioli, C.; Moja, L.; Gismondo, M. R. & Salerno, F. (2020), 'Presence and infectivity of SARS-CoV-2 virus in wastewaters and rivers', *Science of The Total Environment* **744**, 140911.

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.

Rochman, N. D.; Wolf, Y. I.; Faure, G.; Zhang, F. & Koonin, E. V. (2020), 'Ongoing Adaptive Evolution and Globalization of Sars-Cov-2', *bioRxiv*, 2020.10.12.336644.

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.

Rosenthal, S. H.; Kagan, R. M.; Gerasimova, A.; Anderson, B.; Grover, D.; Hua, M.; Owen, R. & Lacbawan, F. (2020), 'Identification of eight SARS-CoV-2 ORF7a deletion variants in 2,726 clinical specimens', *bioRxiv*, 2020.12.10.418855.

Rouchka, E. C.; Chariker, J. H. & Chung, D. (2020), 'Variant analysis of 1,040 SARS-CoV-2 genomes', *PLOS ONE* **15**(11), e0241535.

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.; Hossain, M. S. & Rahaman, M. M. (2020), 'Genomic exploration light on multiple origin with potential parsimony-informative sites of the severe acute respiratory syndrome coronavirus 2 in Bangladesh', *Gene Reports* **21**, 100951.

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.; Klonjkowski, 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.

Satyam, R.; Jha, N. K.; Kar, R.; Jha, S. K.; Sharma, A.; Kumar, D.; Nand, P.; Ruokolainen, J.; Kesari, K. K. & Kamal, M. A. (2020), 'Deciphering the SSR incidences across viral members of Coronaviridae family', *Chemico-Biological Interactions* **331**, 109226.

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.

Segreto, R. & Deigin, Y. (2020), 'The genetic structure of SARS-CoV-2 does not rule out a laboratory origin', *BioEssays* **00**, e2000240.

Sekizuka, T.; Itokawa, K.; Hashino, M.; Kawano-Sugaya, T.; Tanaka, R.; Yatsu, K.; Ohnishi, A.; Goto, K.; Tsukagoshi, H.; Ehara, H.; Sadamasu, K.; Taira, M.; Shibata, S.; Nomoto, R.; Hiroi, S.; Toho, M.; Shimada, T.; Matsui, T.; Sunagawa, T.; Kamiya, H.; Yahata, Y.; Yamagishi, T.; Suzuki, M.; Wakita, T. & Kuroda, M. (2020), 'A Genome Epidemiological Study of SARS-CoV-2 Introduction into Japan', *mSphere* **5**(6), e00786-20.

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.

Sekizuka, T.; Itokawa, K.; Yatsu, K.; Tanaka, R.; Hashino, M.; Kawano-Sugaya, T.; Ohnishi, M.; Wakita, T.; Kuroda, M. & in Japanese Airport Quarantine, C. O. V. I. D.-19. G. S. N. (2020), 'COVID-19 Genome Surveillance at International Airport Quarantine Stations in Japan', *Journal of Travel Medicine*, taaa217.

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.

Sharma, S.; Dash, P. K.; Sharma, S. K.; Srivastava, A.; Kumar, J. S.; Karothia, B. S.; Chelvam, K. T.; Singh, S.; Gupta, A.; Yadav, R. G.; Yadav, R.; Greshma T., S.; Kushwah, P.; Bhushan, R.; Nagar, D. P.; Nandan, M.; Kumar, S.; Thavaselvam, D. & Dubey, D. K. (2020), 'Emergence and expansion of highly infectious spike:D614G mutant SARS-CoV-2 in central India', *bioRxiv*, 2020.09.15.297846.

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.

Sikkema, R. S.; Pas, S. D.; Nieuwenhuijse, D. F.; O'Toole, Á.; Verweij, J.; Linden, A. v. d.; Chestakova, I.; Schapendonk, C.; Pronk, M.; Lexmond, P.; Bestebroer, T.; Overmars, R. J.; Nieuwkoop, S. v.; Bijllaardt, W. v. d.; Bentvelsen, R. G.; Rijen, M. M. L. v.; Buiting, A. G. M.; Oudheusden, A. J. G. v.; Diederens, B. M.; Bergmans, A. M. C.; Eijk, A. v. d.; Molenkamp, R.; Rambaut, A.; Timen, A.; Kluytmans, J. A. J. W.; Munnink, B. B. O.; Bergh, M. F. Q. K. v. d. & Koopmans, M. P. G. (2020), 'COVID-19 in health-care workers in three hospitals in the south of the Netherlands: a cross-sectional study', *The Lancet Infectious Diseases* **20**(11), 1273-1280.

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).

Simmonds, P. (2020), 'Pervasive RNA Secondary Structure in the Genomes of SARS-CoV-2 and Other Coronaviruses', *mBio* 11(6).

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

Soliman, M. S.; AbdelFattah, M.; Aman, S. M. N.; Ibrahim, L. M. & Aziz, R. K. (2020), 'A Gapless, Unambiguous RNA Metagenome-Assembled Genome Sequence of a Unique SARS-CoV-2 Variant Encoding Spike S813I and ORF1a A859V Substitutions', *OMICS: A Journal of Integrative Biology*, omi.2020.0194.

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 2019nCoVR', *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.

Speake, H.; Phillips, A.; Chong, T.; Sikazwe, C.; Levy, A.; Lang, J.; Scalley, B.; Speers, D. J.; Smith, D. W.; Effler, P. & McEvoy, S. P. (2020), 'Flight-Associated Transmission of Severe Acute Respiratory Syndrome Coronavirus 2 Corroborated by Whole-Genome Sequencing', *Emerging Infectious Diseases journal - CDC* 26(12), 2872-2880.

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.; Addetia, A.; Hannon, W. H.; Choudhary, M. C.; Dingens, A. S.; Li, J. Z. & Bloom, J. D. (2020), 'Prospective mapping of viral mutations that escape antibodies used to treat COVID-19', *bioRxiv*, 2020.11.30.405472.

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.; Veesler, 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.

Tabibzadeh, A.; Zamani, F.; Laali, A.; Esghaei, M.; Safarnezhad Tameshkel, F.; Keyvani,

H.; Jamshidi Makiani, M.; Panahi, M.; Motamed, N.; Perumal, D.; Khoonsari, M.; Ajdarkosh, H.; Sohrabi, M.; Ghanbari, B.; Savaj, S.; Mosavi-Jarrahi, A. & Karbalaie Niya, M. H. (2020), 'SARS-CoV-2 Molecular and Phylogenetic analysis in COVID-19 patients: A preliminary report from Iran', *Infection, Genetics and Evolution* **84**, 104387.

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.

Taiwo, I. A.; Adeleye, N.; Anwoju, F. O.; Adeyinka, A.; Uzoma, I. C. & Bankole, T. T. (2020), 'Sequence Analysis for SNP Detection and Phylogenetic Reconstruction of SARS-CoV-2 Isolated from Nigerian COVID-19 Cases', *bioRxiv*, 2020.09.25.310078.

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.

Tayoun, A. A.; Loney, T.; Khansaheb, H.; Ramaswamy, S.; Harilal, D.; Deesi, Z. O.; Varghese, R. M.; Al Suwaidi, H.; Alkhajeh, A.; AlDabal, L. M.; Uddin, M.; Hamoudi, R.; Halwani, R.; Senok, A.; Hamid, Q.; Nowotny, N. & Alsheikh-Ali, A. (2020), 'Multiple early introductions of SARS-CoV-2 into a global travel hub in the Middle East', *Scientific Reports* **10**(1), 17720.

Teng, S.; Sobitian, 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.

Thakur, M.; Singh, A.; Joshi, B. D.; Ghosh, A.; Singh, S. K.; Singh, N.; Sharma, L. K. & Chandra, K. (2020), 'Time-lapse sentinel surveillance of SARS-CoV-2 spread in India', *PLOS ONE* 15(10), e0241172.

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.; Hüser, 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*.

Tomassini, S.; Kotecha, D.; Bird, P. W.; Folwell, A.; Biju, S. & Tang, J. W. (2020), 'Setting the criteria for SARS-CoV-2 reinfection – six possible cases', *Journal of Infection*, (In Press Journal Pre-Proof).

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.; Maio, N. D.; Thornlow, B.; Gozashti, L.; Lanfear, R.; Walker, C. R.; Hinrichs, A. S.; Fernandes, J. D.; Borges, R.; Slodkowicz, G.; Weilguny, L.; Haussler, D.; Goldman, N. & Corbett-Detig, R. (2020), 'Stability of SARS-CoV-2 phylogenies', *PLOS Genetics* **16**(11), e1009175.

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.

Turakhia, Y.; Thornlow, B.; Hinrichs, A. S.; Maio, N. d.; Gozashti, L.; Lanfear, R.; Haussler, D. & Corbett-Detig, R. (2020), 'Ultrafast Sample Placement on Existing Trees (UShER) Empowers Real-Time Phylogenetics for the SARS-CoV-2 Pandemic', *bioRxiv*, 2020.09.26.314971.

Tyson, J. R.; James, P.; Stoddart, D.; Sparks, N.; Wickenhagen, A.; Hall, G.; Choi, J. H.; Lapointe, H.; Kamelian, K.; Smith, A. D.; Prystajecky, 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.

Utro, F.; Levovitz, C.; Rhissorrakrai, K. & Parida, L. (2020), 'A Common Methodological Phylogenomics Framework for intra-patient heteroplasmies to infer SARS-CoV-2 sublineages and tumor clones', *bioRxiv*, 2020.10.14.339986.

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.

Varabyou, A.; Pockrandt, C.; Salzberg, S. L. & Pertea, M. (2020), 'Rapid detection of inter-clade recombination in SARS-CoV-2 with Bolotie', *bioRxiv*, 2020.09.21.300913.

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.

Velasco, J. M.; Chinnawirotisan, P.; Joonlasak, K.; Manasatienkij, W.; Huang, A.; Valderama, M. T.; Diones, P. C.; Leonardia, S.; Timbol, M. L.; Navarro, F. C.; Villa, V.; Tabinas, H.; Chua, D.; Fernandez, S.; Jones, A. & Klungthong, C. (2020), 'Coding-Complete Genome Sequences of 23 SARS-CoV-2 Samples from the Philippines', *Microbiology Resource Announcements* **9**(43), e01031-20.

Velasco, J. M.; Navarro, F. C.; Diones, P. C.; Villa, V.; Valderama, M. T.; Tabinas, H.; Chua, D.; Rosa, R. D.; Turao-Agoncillo, M. M.; Timbol, J. C.; Leonardia, S.; Timbol, M. L.; Klungthong, C.; Chinnawirotisan, P.; Joonlasak, K.; Manasatienkij, W.; Huang, A.; Jones, A. & Fernandez, S. (2021), 'SARS-CoV-2 Among Military and Civilian Patients, Metro Manila, Philippines', *Military Medicine*, usaa525.

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.

Verma, S.; Dwivedy, A.; Kumar, N. & Biswal, B. K. (2020), 'Computational prediction of SARS-CoV-2 encoded miRNAs and their putative host targets', *bioRxiv*, 2020.11.02.365049.

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

Voeten, H. A. C. M.; Sikkema, R. S.; Damen, M.; Oude Munnink, B. B.; Arends, C.; Stobberingh, E.; Hoogervorst, E.; Koopmans, M. P. G. & Fanoy, E. (2020), 'Unravelling the modes of transmission of SARS-CoV-2 during a nursing home outbreak: looking beyond the church super-spread event', *Clinical Infectious Diseases*, (accepted manuscript).

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

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), 'Phylogenetic 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. & Dilthey, 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-2Population 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, H.-L. (2020), 'The emergence of inter-clade hybrid SARS-CoV-2 lineages revealed by 2D nucleotide variation mapping', *bioRxiv*, 2020.10.13.338038.

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, R.; Chen, J.; Hozumi, Y.; Yin, C. & Wei, G.-W. (2020), 'Decoding Asymptomatic COVID-19 Infection and Transmission', *The Journal of Physical Chemistry Letters*, 10007-10015.

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.

Weber, S.; Ramirez, C. & Doerfler, W. (2020), 'Signal hotspot mutations in SARS-CoV-2 genomes evolve as the virus spreads and actively replicates in different parts of the world', *Virus Research* **289**, 198170.

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.; Hatzioannou, T. & Bieniasz, P. D. (2020), 'Escape from neutralizing antibodies by SARS-CoV-2 spike protein variants', *bioRxiv*, 2020.07.21.214759.

Weissberg, D.; Böni, J.; Rampini, S. K.; Kufner, V.; Zaheri, M.; Schreiber, P. W.; Abela, I. A.; Huber, M.; Sax, H. & Wolfensberger, A. (2020), 'Does respiratory co-infection facilitate dispersal of SARS-CoV-2? investigation of a super-spreading event in an open-space office', *Antimicrobial Resistance & Infection Control* **9**(1), 191.

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).

Wolters, F.; Coolen, J. P. M.; Tostmann, A.; Groningen, L. F. J. v.; Bleeker-Rovers, C. P.; Tan, E. C. T. H.; Geest-Blankert, N. v. d.; Hautvast, J. L. A.; Hopman, J.; Wertheim, H. F.

L.; Rahamat-Langendoen, J. C.; Storch, M. & Melchers, W. J. G. (2020), 'Novel SARS-CoV-2 Whole-genome sequencing technique using Reverse Complement PCR enables fast and accurate outbreak analysis', *bioRxiv*, 2020.10.29.360578.

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.; Hirschfeld, 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.

Wruck, W. & Adjaye, J. (2020), 'Transmission of SARS-CoV-2 from China to Europe and West Africa: a detailed phylogenetic analysis.', *bioRxiv*, 2020.10.02.323519.

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.

Wu, N. C.; Yuan, M.; Bangaru, S.; Huang, D.; Zhu, X.; Lee, C.-C. D.; Turner, H. L.; Peng, L.; Yang, L.; Burton, D. R.; Nemazee, D.; Ward, A. B. & Wilson, I. A. (2020), 'A natural mutation between SARS-CoV-2 and SARS-CoV determines neutralization by a cross-reactive antibody', *PLoS pathogens* **16**(12), e1009089.

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* **9**(1), 1824-1834.

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, H.-C.; Chen, C.-h.; Wang, J.-H.; Liao, H.-C.; Yang, C.-T.; Chen, C.-W.; Lin, Y.-C.; Kao, C.-H.; Lu, M.-Y. J. & Liao, J. C. (2020), 'Analysis of genomic distributions of SARS-CoV-2 reveals a dominant strain type with strong allelic associations', *Proceedings of the National Academy of Sciences*, 202007840.

Yang, J.; Li, J.; Lai, S.; Ruktanonchai, C. W.; Xing, W.; Carioli, A.; Wang, P.; Ruktanonchai, N. W.; Li, R.; Floyd, J. R.; Wang, L.; Bi, Y.; Shi, W. & Tatem, A. J. (2020), 'Uncovering two phases of early intercontinental COVID-19 transmission dynamics', *Journal of Travel Medicine*, (accepted manuscript).

Yang, S.; Shan, T.; Xiao, Y.; Zhang, H.; Wang, X.; Shen, Q.; Wang, Y.; Yao, Y.; Liu, Q.; Wang, H. & Zhang, W. (2020), 'Digging metagenomic data of pangolins revealed SARS-CoV-2 related viruses and other significant viruses', *Journal of Medical Virology* n/a(n/a).

Yang, W. & Jin, G. (2020), 'Origin-independent analysis links SARS-CoV-2 local genomes with COVID-19 incidence and mortality', *Briefings in Bioinformatics*.

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, A. B. & Jiang, X. (2020), 'Characterizing transcriptional regulatory sequences in coronaviruses and their role in recombination', *Molecular Biology and Evolution*, msaa281.

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.

Yuan, F.; Wang, L.; Fang, Y. & Wang, L. (2020), 'Global SNP analysis of 11,183 SARS-CoV-2 strains reveals high genetic diversity', *Transboundary and Emerging Diseases*, (Accepted Author Manuscript).

Yuan, J.; Chen, Z.; Gong, C.; Liu, H.; Li, B.; Li, K.; Chen, X.; Xu, C.; Jing, Q.; Liu, G.; Qin, P.; Liu, Y.; Zhong, Y.; Huang, L.; Zhu, B.-P. & Yang, Z. (2020), 'Sewage as a Possible Transmission Vehicle During a Coronavirus Disease 2019 Outbreak in a Densely populated Community: Guangzhou, China, April 2020', *Clinical Infectious Diseases*, (accepted manuscript).

Zarebski, A. E.; Plessis, L. d.; Parag, K. V. & Pybus, O. G. (2020), 'A computationally tractable birth-death model that combines phylogenetic and epidemiological data', *bioRxiv*, 2020.10.21.349068.

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* **92**, 1637–1640.

Zeng, H.-L.; Dichio, V.; Horta, E. R.; Thorell, K. & Aurell, E. (2020), 'Global analysis of more than 50,000 SARS-CoV-2 genomes reveals epistasis between eight viral genes', *Proceedings of the National Academy of Sciences*, 202012331.

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.

Zhang, L.; Richards, A.; Khalil, A.; Wogram, E.; Ma, H.; Young, R. A. & Jaenisch, R. (2020), 'SARS-CoV-2 RNA reverse-transcribed and integrated into the human genome', *bioRxiv*, 2020.12.12.422516.

Zhang, R.-H.; Ai, X.; Liu, Y.; Li, C.-H. & Zhang, H.-L. (2020), 'Genomic characterization and phylogenetic evolution of the SARS-CoV-2', *Acta virologica*, (accepted article online).

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.

Zhao, Z.; Sokhansanj, B. A.; Malhotra, C.; Zheng, K. & Rosen, G. L. (2020), 'Genetic grouping of SARS-CoV-2 coronavirus sequences using informative subtype markers for pandemic spread visualization', *PLOS Computational Biology* **16**(9), e1008269.

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.

Zhu, W.; Yang, J.; Lu, S.; Lan, R.; Jin, D.; Luo, X.-l.; Pu, J.; Wu, S. & Xu, J. (2020), 'Beta- and Novel Delta-Coronaviruses Are Identified from Wild Animals in the Qinghai-Tibetan Plateau, China', *Virologica Sinica*, <https://doi.org/10.1007/s12250-020-00325-z>.

Zhu, X.; Chang, T.-C.; Webby, R. & Wu, G. (2020), 'idCOV: a pipeline for quick clade identification of SARS-CoV-2 isolates', *bioRxiv*, 2020.10.08.330456.

Zhu, Z.; Meng, K.; Liu, G. & Meng, G. (2020), 'A database resource and online analysis tools for coronaviruses on a historical and global scale', *Database* **00**, baaa070.

Zhu, Z.; Meng, K. & Meng, G. (2020), 'Genomic recombination events may reveal the evolution of coronavirus and the origin of SARS-CoV-2', *Scientific Reports* **10**(1), 21617.