Data-driven recombination detection in viral genomes

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Abstract

Recombination is a key molecular mechanism for the evolution and adaptation of viruses[1,2]. The first recombinant SARS-CoV-2 genomes were recognized in 2021[3]; as of today, more than seventy SARS-CoV-2 lineages are designated as recombinant. In the wake of the COVID-19 pandemic, several methods for detecting recombination in SARS-CoV-2 have been proposed; however, none could faithfully reproduce manual analyses by experts in the field.

We hereby present RecombinHunt, a novel, automated method for the identification of recombinant genomes purely based on a data-driven approach. RecombinHunt compares favorably with other state-of-the-art methods and recognizes recombinant SARS-CoV-2 genomes (or lineages) with one or two breakpoints with high accuracy, within reduced turn-around times and small discrepancies with respect to the expert manually-curated standard nomenclature.

Strikingly, applied to the complete collection of viral sequences from the recent monkeypox epidemic, RecombinHunt identifies recombinant viral genomes in high concordance with manually curated analyses by experts, suggesting that our approach is robust and can be applied to any epidemic/pandemic virus.

Although RecombinHunt does not substitute manual expert curation based on phylogenetic analysis, we believe that our method represents a breakthrough for the detection of recombinant viral lineages in pandemic/epidemic scenarios.

Main

Recombination is a key molecular mechanism used by RNA viruses to boost their evolution. Recombination occurs both in viruses with segmented and non-segmented genomes; parental strains to a recombinant virus are referred to as "donor" and "acceptor". Recombination requires co-circulation and co-infection in the same host; the clinical and epidemiological relevance is substantial since recombinant viral strains have been associated with altered viral host tropism, enhanced virulence, host immune evasion, and the development of resistance to antivirals[4,5]. In light of these considerations, and in hindsight from the recent global scale COVID-19 epidemic, the need for the development of novel and rapid methods to identify recombination has been increasingly recognized by international health authorities and researches[6,7]. Phylogenetic analyses are essential to monitoring the spread and evolution of viruses[8]. All phylogeny-based approaches assume that the shared history of pathogens, isolated from different hosts, can be described by a branching phylogenetic tree. Recombination breaks this assumption and impacts the application of phylogenetic methods for the reconstruction of chains of contagion, viral evolution, and ultimately genomic surveillance of pathogens[9,10].

During the COVID-19 pandemic SARS-CoV-2 has accumulated in excess of 130K distinct nucleotide mutations, leading to the emergence of more than 2K lineages. In the first three years of the COVID-19 pandemic, limited levels of recombination were observed, although an increased number of recombinant lineages has been reported more recently[11]. As SARS-CoV-2 evolved and differentiated, several recombination events – involving SARS-CoV-2 variants of concern (VOCs) – have been recognized, highlighting once more the importance of recombination as a molecular mechanism for the generation of genomic and phenotypic diversity in epidemic/pandemic viruses[3,12–18].

More recently, as the Omicron SARS-CoV-2 variant became dominant worldwide, an excess of 60 recombinant lineages have been identified only within Omicron. XE (also known as V-22APR-02 in Public Health England) was considered the most concerning Omicron lineage during 2022 since it had a reported growth advantage over BA.2. None of the recombinants detected until the Autumn of 2022 spread fast enough to become dominant, while greater concern came from sublineages of Omicron 2 and from Omicron 4 and 5 (e.g., XBF). The recombinant XBB lineage, the ancestor of XBB.1.5 and XBB.1.16 is the only Variants Of Interest according to the World Health Organization at the time of writing[19]).

The fast emergence of SARS-CoV-2 viral lineages and their potential epidemiological implications has called for continuous monitoring of viral genome evolution in the last three years. The largest available col-

lection of genomes has been curated by GISAID[20], which reached 15.2 million deposited viral sequences in April 2023. Genomic surveillance efforts initially focused on the monitoring of single amino acid changes. As the COVID-19 pandemic progressed, research interests shifted toward the study of mutational signatures and variants associated with increased transmission rates and reduced antigenicity, and possibly hampering testing, treatment, and vaccine development[21–23]. A number of methods were proposed to allow automatic early detection of variants[24–28]. Instead, interest in the automatic identification of recombination in SARS-CoV-2 started at a later stage.

Recombination in viral genomes is often identified using algorithms implemented in programs such as Simplot[29]; 3SEQ[30] and its improved version[1]; RDP3 (Recombination Detection Program version 3[31], including four previously proposed tools) and its extensions RDP4[32] / RDP5[33]; and RAPR[34] (Recombination Analysis PRogram). In short, these methods apply phylogenetics approaches to identify recombination hotspots and pinpoint patterns of interest with matrix-based visualizations. However, none of these methods was specifically devised to analyze/deal with large amounts of data/genomes. Moreover, some of these algorithms account for all polymorphic sites equally, regardless of phylogenetic information, and hence might be prone to systematic errors if/when applied to a sparse, arbitrary selection of genome sequences.

A number of studies already applied these methods to SARS-CoV-2. For instance, Pollett *et al.*[35] employed RDP4 on 100K sequences (dataset of August 2021); 3SEQ was applied by Boni *et al.*[36] and Jackson *et al.*[37] for analysis of mosaic signals and breakpoint identification; while[11] combined 3SEQ and RDP5 for assigning parent lineages.

Ignatieva *et al.*[38] proposed KwARG, a parsimony-based method to reconstruct possible genealogical histories of SARS-CoV-2 and disentangle recombination based on a statistical framework. Similar to other comparable works[37,39], the method however suffers from a limited resolution and can not fully resolve pairs of recombinant donors/acceptor sequences at the lineage level.

Zhou *et al.*[40] recently introduced VirusRecom, a novel algorithm that uses information theory to infer recombination. A recombination event is modeled as a transmission process of "information" that uses a weighted information content to quantify the contribution of recombination to a given region in the viral genome. The method is applied only to simulated data and a limited selection of recombinant lineages (XD, XE, and XF); these settings cannot be considered a comprehensive evaluation.

The RIPPLES method[9] and related RIVET software[41] are more conceptually similar to the method described in this study and have been recently applied to the complete collection of SARS-CoV-2 genome se-

quences; a detailed comparison between this method and the novel approach developed in this work is reported below.

Novelty: A computational approach to scout recombinations

Currently, the hunt for recombinant SARS-CoV-2 viral lineages is manually performed by experts who report evidence on the Pango designation GitHub repository in the form of issues; they are broadly documented and allow for discussion with other peers[42]. Here we present a new automatic method (RecombinHunt, Fig. 1) for effectively and efficiently detecting recombination by analyzing the complete data corpus of SARS-CoV-2. Our approach relies exclusively on big data-driven methods, as opposed to manual analyses performed and maintained by trained experts[9]; the method produces results that are easily inspectable on simple visual reports (see Supplementary Files 1–4), thus it is completely transparent to its users.

We considered 15,271,031 SARS-CoV-2 genomes, downloaded from the GISAID database[20] on April 1st, 2023. Genome sequences were aligned to the SARS-CoV-2 reference genome and nucleotide mutations were identified by the HaploCoV pipeline[28]. To mitigate the impacts of sequencing and assembly errors, genome sequences of uncertain/low quality were excluded (i.e., records associated with low coverage, percentage of unknown bases $\geq 2\%$, unknown length, and incomplete metadata). We then retained 5,255,228 viral genomes, for which we only considered the assigned Pango lineage and the list of mutations. Overall, a total of 2,345 distinct lineages were represented; previously designated Variants of Concern (VOCs) lineages were associated with the largest number of assigned genome sequences, namely B.1.1.7 (Alpha), BA.2 (Omicron 2), BA.1.1 (Omicron 1), and AY.4 (Delta).

In the dataset, a total of 57 distinct recombinant lineages (denoted according to the Pango convention for labeling recombinant lineages under the letter 'X') with at least one high-quality sequence are present. Mutations frequencies were estimated across the complete collection of Pango lineages and in the complete collection of SARS-CoV-2 genome sequences. For every lineage in the SARS-CoV-2 reference nomenclature, mutations with a frequency above a 75% threshold were denoted as characteristic mutations; the list of characteristic mutations for a lineage is denoted as the lineage mutation space in RecombinHunt.

The approach

RecombinHunt accepts as input a target genome sequence, in the form of a list of mutations. Genome positions with a nucleotide mutation in the target are denoted as the target mutations space. Candidate "donor" and "acceptor" lineages are defined on the basis of the counts of their mutations in the target mutation space, we denote as "donor" the lineage with the higher count. For every lineage, the union of the lineage and target mutation space is denoted as extended target space. A cumulative likelihood ratio score is derived according to the following procedure: at each position of the extended target space, we compute the logarithmic ratio between the frequency of the mutation in the lineage and in the complete collection of SARS-CoV-2 genomes. This score is added if the mutation is shared by the both target and the lineage, it is subtracted if the mutation is observed in the lineage but not in the target.

The workflow is represented in Extended Data Fig. 1. Likelihood ratio values are computed for all possible lineages; the lineage L1 associated with the maximum value is assigned to the target. If L1 mutation space differs from the target mutation space at most in two positions, then the non-recombinant model is selected, and the target is assigned to L1; else, L1 is designated as the candidate donor. Note that L1 covers the majority of the mutations of the target, located in the genome segment that starts from one of the two ends (either 5' or 3') – denoted as L1's end – and reaches its maximum value at a position designated as max-L1. Upon the identification of a candidate donor, the one-breakpoint (1BP, Fig. 1b) and two-breakpoint (2BP, Fig. 1c) models are compared in parallel.

In the 1BP model, we search for a lineage L2, starting at the opposite end of the genome – denoted as $L1^{opp}$ end. We consider the L2 lineage associated with the maximum likelihood ratio value (max-L2); if such lineage is not different from L1 in at least three mutations, we recede to the non-recombination case, else we designate it as a candidate acceptor. The interval between coordinates max-L1 and max-L2, where the donor and acceptor lineages reach their maximum likelihood ratio, define the 'breakpoint range', which is then reduced to a single position (see *Methods* and Extended Data Fig. 2). An example of a 1BP use case is shown in Fig. 1b where a target sequence assigned to the Pango XBE lineage (Pango issue #1246) is correctly recognized to originate from a BA.5.26 donor (with 64 mutations) and a BE.4 acceptor (with 7 mutations).

In the 2BP model, the candidate donor L1 lineage is assigned to both ends of the genome; this case is explored only when the target sequence has at least three mutations of L1 at the $L1^{opp}$ end of the genome. We designate as $L1^{opp}$ the portion of the genome between the $L1^{opp}$ end and the point where $L1^{opp}$'s likelihood

ratio is maximum, denoted as max-L1^{opp}. A candidate acceptor L2 lineage is searched in the space between max-L1^{opp} and max-L1; the lineage L2 with the maximum likelihood ratio is selected, yielding to a breakpoint range, positioned either between max-L1 and max-L2 or between max-L1^{opp} and max-L2; if such breakpoint range is greater than one mutation, it is reduced to a single mutation. In Fig. 1c a target sequence assigned to the XD lineage (according to the issue #444 of Pango) showcases an application of the 2BP model. The target was correctly recognized to be a mosaic of the AY.4 lineage (23 and 15 mutations at both ends) and the BA.1.22 lineage (29 mutations).

The Akaike Information Criterion (AIC) is used to compare the likelihood ratio of 1BP and 2BP models and select the model highest likelihood. A further comparison with a "non-recombinant" model is made to cross-check the consistency of the results.

As illustrated in Fig. 2 RecombinHunt can identify and resolve alternative combinations of donor/acceptor lineages within phylogenetic clades. Given the best candidates for L1 and L2 (reported in the first row of Fig. 2 tables), alternative candidates must fulfill the following conditions: 1) have a limited difference in likelihood ratio scores compared with the best L1/L2 candidate (AIC p-value $\geq 10^{-5}$); 2) reach max-L1 (or max-L2) within a one-mutation distance in the mutation space from the best candidate; and 3) be in the same phylogenetic sub-tree as the best candidate. In the case of XBE (see Fig. 2a), two candidate lineages i.e., BA.5.2.6 and CP.3, are assigned to the 5' terminal end of the genome whereas six equivalent candidates are identified for the 3' terminal portion. In the case of XD, instead, no alternative candidate donors and acceptors are recovered (see Fig. 2b).

Results

Our method was executed on 51 of the 57 lineages designated as recombinant by Pango at the time of the writing. Two lineages were excluded since they had three breakpoints and other four lineages were disregarded since the defining Pango issue was unclear/controversial. The "ground truth", i.e., the description of the recombinant lineage in terms of donor, acceptor, and breakpoint, was reconstructed directly from the corresponding Pango designation issues[42,43].

Recombinant lineages were removed from the list of Pango designations, and an ideal consensus-genome was reconstructed for every lineage by considering the ordered list of nucleotide mutations shared by >75% high-quality genomes assigned to that lineage.

Three main criteria were used to validate RecombinHunt results with respect to the ground truth: (1) the correct model recombinant (1BP or 2BP) represented a statistically significant improvement (p-value $< 10^{-2}$), compared with the other models; (2) designations of both the donor and the acceptor lineages were correct (i.e., all found candidates are the same or descendants of those in the ground truth); and (3) the breakpoint position, as determined by our method, was within the range of genomic positions indicated in the Pango issue.

Results are shown in Table 1, partitioned as follows: (i) cases with 1BP approximately in the middle of the SARS-CoV-2 genome (from XA to XZ); (ii) 5' proximal 1BP cases (from XAA to XW); (iii) 3' proximal 1BP cases (from XAH to XT); (iv) cases with 2BP (from XAC to XD).

Notably, RecombinHunt results were in complete agreement with the ground truth for 40 recombinant lineages (37 with one breakpoint and 3 with two breakpoint recombinations). The remaining 11 lineages – which did not fully agree with the Pango designation – are stratified into three conceptually distinct groups, discussed below; A detailed report illustrating all eleven cases is provided in Supplementary File 5.

(G1) Six lineages (XAV, XAR, XBF, XN, XAK, and XAZ) are not flagged as recombinant by RecombinHunt. For all these lineages, recombination is supported only by a limited number of mutations, i.e., one (XAK and XAZ) or two (XAV, XAR, XBF, and XN) over an average of 67 mutations considered in the respective consensus-genome.

(G2) In two cases (XBH and XBM), RecombinHunt identifies alternative candidate donor/acceptor lineages with a higher likelihood ratio compared with the solutions reported by the ground truth. This result might be partially explained by fluctuations in estimated mutation frequencies at the lineage level, leading to the assignment of a different lineage.

(G3) Three cases (XAW, XAT, and XP) highlight some limitations of our approach. In XAW, while L1 is correctly identified, none of the lineages defined in the Pango nomenclature provides a good match for 46 out of 103 total target mutations characteristic of the XAW lineage; in this case, the parent acceptor lineage might not be defined in the reference nomenclature. In XAT and XP, recombination as defined by the ground truth is supported by a limited number of mutations at the 3' end of the genome. As these mutations have a relatively high frequency (range 0.17–0.34) in the complete collection of SARS-CoV-2 genomes, they contribute to a modest drop in the log-likelihood ratio score. Both XAT and XP lineages are flagged as non-recombinant by RecombinHunt; we speculate that our method loses sensitivity due to attraction to local maxima and limited/insufficient drops in the cumulative likelihood ratio score.

Reproducibility on individual high-quality sequences

To evaluate 1) whether RecombinHunt could systematically flag recombinant viral genomes; and 2) the reproducibility of the results, our method was applied directly to individual genome sequences. For every recombinant lineage, at most one hundred of randomly selected, high-quality sequences were analyzed; when high-quality sequences were fewer than one hundred we considered all of them. Results are shown in Table 2, in the same order and grouping of Table 1 to facilitate the comparison.

As outlined in Table 2 (comparing '%non-rec', '%1BP', and '%2BP' with the 'consensus'), in 46 out of 51 lineages, RecombinHunt's results of the large majority of single genome sequences (value in bold type) are consistent with those obtained on the corresponding lineage-level genome consensus. The most notable exceptions are: XBG/XAZ (consensus 1BP, whereas respectively 69% and 40% of sequences are 2BP); XBH/XBM (consensus 2BP, whereas respectively 86% and 56% of sequences are 1BP); and XAT (consensus is non-recombinant, whereas 57% of sequences are 1BP).

Histograms in Fig. 3 report the observed frequencies of inferred breakpoint genomic positions. In the first three groups of plots (from XA to XT), for 29 lineages the distribution of results obtained on single sequences is in large agreement with the genome consensus level analysis – see that the mode of the blue bar plots is close to the light blue bar, indicating the breakpoint position of the consensus-genome. Some discrepancies however are observed, which can be summarized in two main cases: (1) Additional breakpoints. The consensus-genome analysis indicated one breakpoint, but two breakpoints are detected in single sequences: this occurs in eight lineages, the most evident case is XBG, whose panel in Fig. 3 shows one light-blue bar and a distribution of double breakpoint positions in orange. (2) Missing breakpoints. Two breakpoints were identified based on the consensus-genome analysis, but only one breakpoint is detected in the single sequences: this occurs in two lineages, XBH and XBM, whose panels in Fig. 3 show two light orange bars and several blue bars, representing single sequences with one breakpoint.

Note that in XAC, XAW, XBL, and XD both the consensus-genome and the majority of sequences were recognized as two-breakpoint recombinants, and that all single genome sequences assigned to XAR were flagged as non-recombinant, in agreement with the consensus-genome result.

Comparison with the RIPPLES method

Turakhia *et al.*[9] introduced RIPPLES, an elegant method based on parsimony analyses for the detection of recombination in SARS-CoV-2. Briefly, candidate recombinant sequences are partitioned into discrete genomic segments. Subsequently, each segment is placed on the SARS-CoV-2 global phylogeny by maximum parsimony; inconsistent phylogenetic signals across genome segments are detected and reconciled; finally, the donor and acceptor lineages are identified as the lineages that result in the highest parsimony score improvement relative to the original placement on the global phylogenetic tree.

More recently, the same authors developed RIVET[41] – an extension of RIPPLES that allows the systematic monitoring of SARS-CoV-2 genome sequences, and the flagging of recombinant genomes in real-time. At the time of writing RIVET is probably the most complete method for the detection of novel recombinants in SARS-CoV-2. Applied to over 6.4 million sequences, RIVET detected a total of 1,470 recombination events of which 453 passed all the quality checks implemented by the method. The authors claimed that "RIVET inferences (such as lineages of parent sequences) of known recombinants were largely consistent with those of manual curators", however, a precise assessment was not provided. We accessed RIVET results as based on the March 30th, 2023 release of the Nextstrain[44] curated collection of SARS-CoV-2 genome sequences[45], and performed a comparison with the results obtained by RecombinHunt on the same dataset.

The Nextstrain dataset was processed according to our quality filtering pipeline. Out of a total of 6,983,419 sequences, 3,984,308 sequences and 61 distinct recombinant Pango lineages were retained. After removing the cases with three or more breakpoints and those for which the ground truth is uncertain, we obtained 51 recombinant cases. A consensus genome was computed for these lineages by retaining mutations with a frequency above the 75% threshold. Subsequently, RecombinHunt was applied. Detailed results are reported in Extended Data Table 1.

Consistent with our previous results of the 51 recombinant lineages included in these analyses (based upon the GISAID dataset), RecombinHunt labels 43 cases correctly w.r.t. the ground truth; these include two lineages (XBB, XM) reporting a different (but phylogenetically close) ancestor lineage. A total of eight recombinant lineages (discussed in Supplementary File 6) are not flagged correctly by RecombinHunt; they are in perfect agreement with the categorization in the G1–G3 classes discussed before for the GISAID dataset, yielding to: **(G1)**: XAV, XAR, XN, XAK, XAZ. **(G2)**: XBH. **(G3)**: XAT and XP.

RIVET reports a total of 17 inter-lineage distinct recombination cases on the complete Nextstrain dataset;

out of these, two have more than two breakpoints and cannot be addressed by RecombinHunt; moreover, XBN was not considered due to the uncertainty of the ground truth. Noticeably, RecombinHunt reports 33 cases designated as recombinant in Pango that are not identified as recombinant by RIVET. Only 14 cases are recorded by both methods and allow a direct comparison. The comparison is summarised in Extended Data Table 2. For every lineage, the donor/acceptor candidates and breakpoints positions found by RIVET and RecombinHunt are compared against the ground truth. Note that in the seven cases (XAK, XBB, XBD, XD, XW, XBT, and XBU) RIVET reported donor/acceptor lineages that are not defined in Pango (e.g., miscBA.5BA.2.75 or miscBA1BA2Post17k), thus candidate parent lineages could not be evaluated.

RecombinHunt on monkeypox

The complete collection of viral genome sequences from the recent monkeypox epidemic[46] has 5,402 records. Recombination has been recently reported in monkeypox; by applying an elegant method based on the study of tandem repetitive sequences, Yeh *et al.*[47] identified eight distinct recombinant isolates, defined by an unusual arrangement of tandem repeat elements. Out of them, one had one breakpoint (Italy/FVG-ITA_01_2022), six had one or two breakpoints (ON838178.1, ON609725.2, ON754985.1, ON754986.1, ON754987.1, ON631241.1), and one had two or three breakpoints (ON631963.1). The authors did also propose an original classification system which however was not adopted by the scientific community. The currently WHO-accepted nomenclature for monkeypox[48] includes a total of 26 distinct lineages, with no direct correspondence/equivalence with the custom designations defined by Yeh *et al.*.

Monkeypox genome sequences and associated metadata were accessed through the dedicated Nexstrain resource[49], low-quality genome sequences were discarded according to the same criteria used for SARS-CoV-2, and mutations were identified by applying the HaploCoV workflow[28] on a collection of 2,526 high-quality sequences. A total of 4,932 distinct mutations were detected. Mutations characteristic of each lineage – as defined in the reference nomenclature – were identified. A threshold of 9% was applied, to account for the high levels of intra-lineage diversity observed in monkeypox[50].

A total of 374 1BP and 331 2BP candidate recombinant genomes were identified by RecombinHunt (see Supplementary Table 1). These include five of the eight manually flagged sequences by Yeh *et al.* (see Extended Data Table 3 for details). Sequences ON838178.1, ON609725.2, ON754985.1, ON754986.1, and ON754987.1 – originally designated as lineage B.1.3 – were labeled as 2BP recombinants (B.1.3 + B.1.2 + B.1.3) by Re-

combinHunt. The 1st breakpoint was set at position 31-32 in the target mutation space (∼85k in the genome) for all the sequences, whereas the 2nd breakpoint was set at position 49-50 (∼150k) for ON609725.2 and ON754987.1 and at 55-56 (∼174k) for ON754986.1, ON754985.1, ON838178.1 cases. Importantly, the recombination pattern inferred by RecombinHunt was highly consistent with the description in Yeh *et al.*[47], e.g., a 2BP recombination, U + M + U, in the custom nomenclature system defined by the authors. Interestingly, the three sequences flagged as recombinant by Yeh *et al.* – but identified as non-recombinant by RecombinHunt – were assigned to the B.1 lineage in the reference monkeypox nomenclature system.

Discussion

We introduce RecombinHunt, a method purely based on big data, for the automatic identification of recombinant viral genomes in epidemic/pandemic scenarios. We record the frequency of nucleotide mutations occurring within lineages, as defined by a reference nomenclature (or otherwise determined clusters), and within all the genomes of a given sequence collection. These data are subsequently used to score viral genomes by means likelihood-based approach and detect recombinant sequences of two lineages, respectively labeled as the "donor" and the "acceptor". The method is general and can be applied to all viral species; as demonstrated by its application on distinct collections of SARS-CoV-2 genomes (retrieved from the EpiCov database of GISAID and the GenBank database curated by Nextstrain) and on genomic sequences from the recent monkeypox epidemic (also curated by Nextstrain). In terms of comparison with the Pango ground truth, RecombinHunt outperforms all the other currently available methods and correctly identifies a significantly larger proportion of recombination events flagged by expert manual analysis. In addition, RecombinHunt is rapid, and can be applied to the analysis of pandemic-scale data; the evaluation of the recombinant cases takes about 13 minutes on the GISAID dataset (15M sequences), and 8 minutes on the Nextstrain dataset (6.4M sequences) using a common portable computer.

We thoroughly evaluated our results in comparison with 51 unambiguous recombinant lineages defined by the Pango SARS-CoV-2 nomenclature for which sufficient genome sequences are available. Initially, lineage levels consensus-genomes were reconstructed and evaluated. Strikingly a complete agreement with the ground truth was observed for 40/51 cases. Of the remaining eleven lineages, six were not recognized as recombinant, two had alternative solutions with a higher likelihood, according to RecombinHunt, and three outlined some potential methodological limitations of our approach. Importantly – in the large majority of these cases –

differences in the determinations were based on a relatively low number of target mutations (2 or fewer), a scenario that is not completely incompatible with convergent evolution.

When applied to high-quality individual sequences, with some well-explainable exceptions, the method produced highly consistent results with those recovered at the lineage level, and the same correct outcome was reported in the vast majority of the individual sequences. Moreover, the small discrepancies observed in our analyses might not necessarily reflect errors, and could be suggestive of intra-lineage heterogeneity and/or microevolution in some SARS-CoV-2 recombinant lineages. Interestingly, for a single lineage (XAT), results obtained on single genome sequences were more aligned with the ground truth than the lineage-level consensus.

Strikingly, once applied to the monkeypox virus, our method was able to replicate the classification of viral sequences recently indicated as recombinant by using a sophisticated ad-hoc method based on expert manual annotation. A large number of additional candidate recombinant genomes (705 cumulatively) were also detected, suggesting previously unreported recombination events in monkeypox.

Our results demonstrate that RecombinHunt is highly accurate and reliable, and represents a major breakthrough for the detection of recombinant viruses in large-scale epidemics/pandemics. The method can be applied to any mid-size available collection of nucleotide mutations for viral species (e.g., Zika and Ebola) and facilitates the detection of recombinant viral genomes in current and future viral outbreaks.

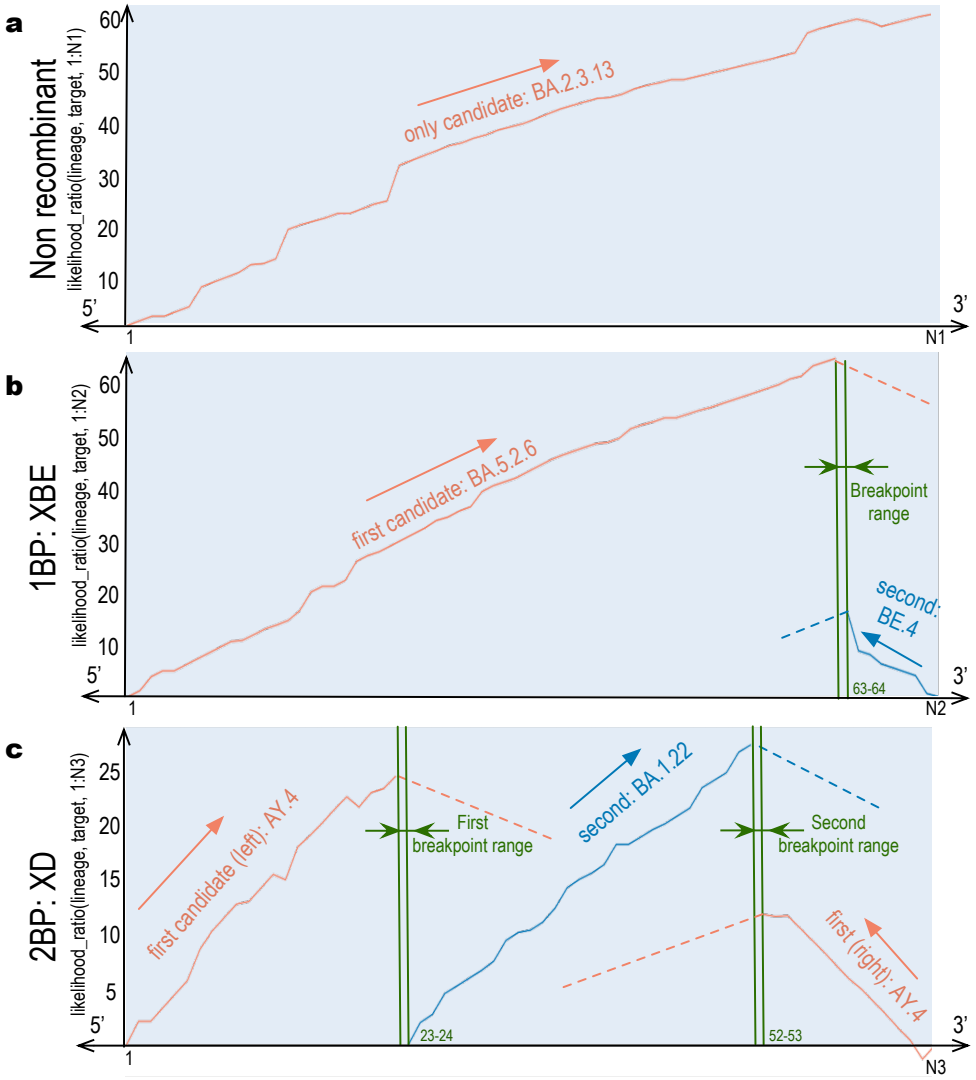
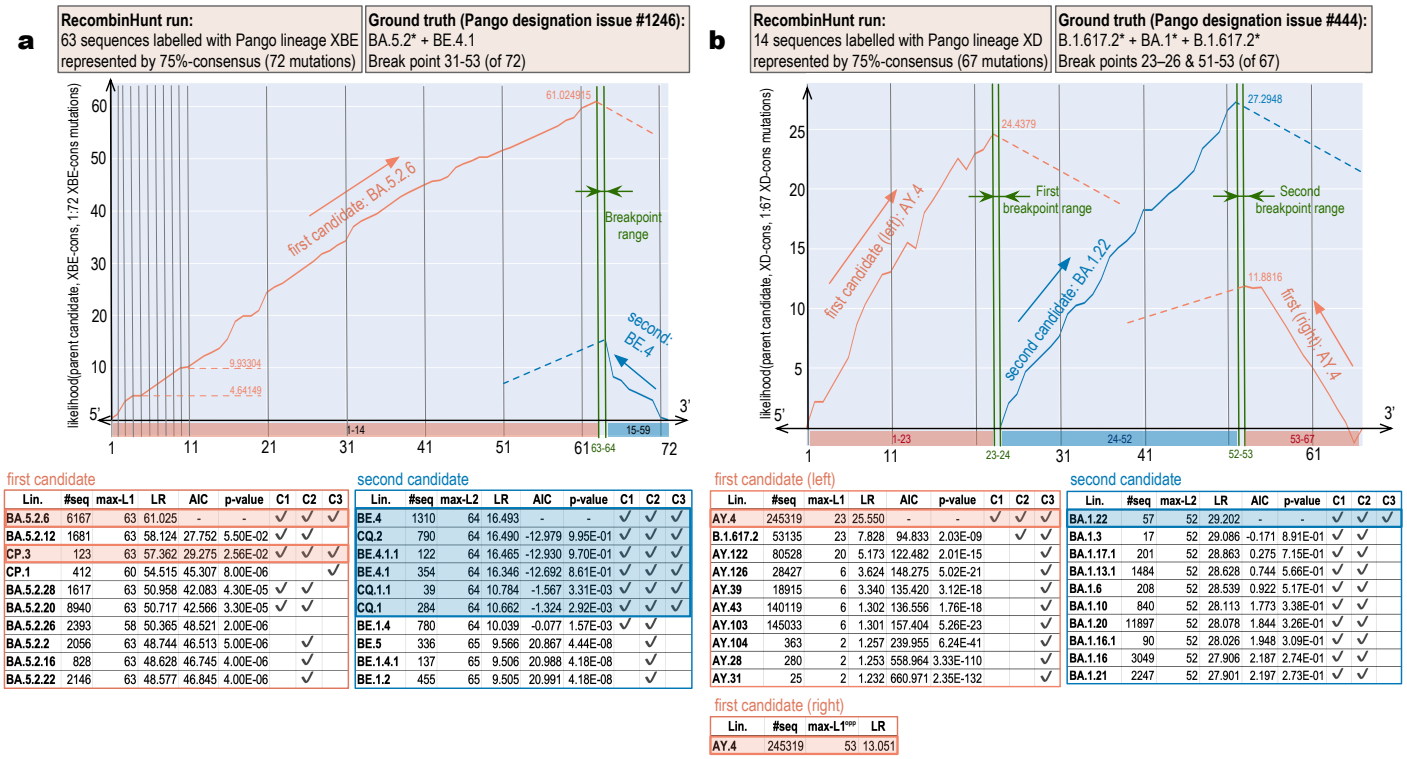


Figure 1 | RecombinHunt has three possible outcomes: no recombination, 1 breakpoint recombination, or 2 breakpoints recombination. **a**, Example of likelihood ratio profile for a non-recombined genome with N1 = 66 mutations, only featuring one donor lineage corresponding to BA.2.3.13. **b**, Example of likelihood ratio profile for a recombined genome assigned to XBE Pango lineage with N2 = 72 mutations, breakpoint at the 63rd mutation, donor lineage BA.5.2.6 (from 5'-end to 63rd mutation), and acceptor lineage BE.4 (from 64th mutation to 3'-end). **c**, Example of likelihood ratio profile for a recombined genome assigned to XD Pango lineage with N3 = 67 mutations, two breakpoints at the 23rd and 52nd mutations, donor lineage AY.4 (from 5'-end to 23rd mutation and from 53rd mutation to 3'-end), and acceptor lineage BA.1.22 (from 24th to 52nd mutation).



first candidate

Lin.	#seq	max-L1	LR	AIC	p-value	C1	C2	C3
BA.5.2.6	6167	63	61.025	-	-	✓	✓	✓
BA.5.2.12	1681	63	58.124	27.752	5.50E-02	✓	✓	
CP.3	123	63	57.362	29.275	2.56E-02	✓	✓	✓
CP.1	412	60	54.515	45.307	8.00E-06			✓
BA.5.2.28	1617	63	50.958	42.083	4.30E-05	✓	✓	
BA.5.2.20	8940	63	50.717	42.566	3.30E-05	✓	✓	
BA.5.2.26	2393	58	50.365	48.521	2.00E-06			
BA.5.2.2	2056	63	48.744	46.513	5.00E-06		✓	
BA.5.2.16	828	63	48.628	46.745	4.00E-06		✓	
BA.5.2.22	2146	63	48.577	46.845	4.00E-06		✓	

second candidate

Lin.	#seq	max-L2	LR	AIC	p-value	C1	C2	C3
BE.4	1310	64	16.493	-	-	✓	✓	✓
CQ.2	790	64	16.490	-12.979	9.95E-01	✓	✓	✓
BE.4.1.1	122	64	16.465	-12.930	9.70E-01	✓	✓	✓
BE.4.1	354	64	16.346	-12.692	8.61E-01	✓	✓	✓
CQ.1.1	39	64	10.784	-1.567	3.31E-03	✓	✓	✓
CQ.1	284	64	10.662	-1.324	2.92E-03	✓	✓	✓
BE.1.4	780	64	10.039	-0.077	1.57E-03	✓	✓	
BE.5	336	65	9.566	20.867	4.44E-08		✓	
BE.1.4.1	137	65	9.506	20.988	4.18E-08		✓	
BE.1.2	455	65	9.505	20.991	4.18E-08		✓	

first candidate (left)

Lin.	#seq	max-L1	LR	AIC	p-value	C1	C2	C3
AY.4	245319	23	25.550	-	-	✓	✓	✓
B.1.617.2	53135	23	7.828	94.833	2.03E-09		✓	✓
AY.122	80528	20	5.173	122.482	2.01E-15			✓
AY.126	28427	6	3.624	148.275	5.02E-21			✓
AY.39	18915	6	3.340	135.420	3.12E-18			✓
AY.43	140119	6	1.302	136.556	1.76E-18			✓
AY.103	145033	6	1.301	157.404	5.26E-23			✓
AY.104	363	2	1.257	239.955	6.24E-41			✓
AY.28	280	2	1.253	558.964	3.33E-110			✓
AY.31	25	2	1.232	660.971	2.35E-132			✓

second candidate

Lin.	#seq	max-L2	LR	AIC	p-value	C1	C2	C3
BA.1.22	57	52	29.202	-	-	✓	✓	✓
BA.1.3	17	52	29.086	-0.171	8.91E-01	✓	✓	
BA.1.17.1	201	52	28.863	0.275	7.15E-01	✓	✓	
BA.1.13.1	1484	52	28.628	0.744	5.66E-01	✓	✓	
BA.1.6	208	52	28.539	0.922	5.17E-01	✓	✓	
BA.1.10	840	52	28.113	1.773	3.38E-01	✓	✓	
BA.1.20	11897	52	28.078	1.844	3.26E-01	✓	✓	
BA.1.16.1	90	52	28.026	1.948	3.09E-01	✓	✓	
BA.1.16	3049	52	27.906	2.187	2.74E-01	✓	✓	
BA.1.21	2247	52	27.901	2.197	2.73E-01	✓	✓	

first candidate (right)

Lin.	#seq	max-L1^{pop}	LR
AY.4	245319	53	13.051

Figure 2 | RecombinHunt recognizes recombination events in one and two-breakpoint cases.

a, Result of RecombinHunt search on the consensus-genome obtained as the set of mutations appearing in 75% of 63 high-quality sequences assigned to the XBE Pango lineage. The Pango designation issue #1246 establishes the ground truth as 1BP recombination of BA.5.2* (i.e., BA.5.2 or its descendants) – contributing the mutations from the genome 5'-end to the 31st, and BE.4.1, contributing the mutations from the 53rd to the genome 3'-end. RecombinHunt exhaustively searches for an L1 candidate and ultimately selects BA.5.2.6 (a child of BA.5.2, see ground truth) starting from the 5'-end of the genome as the one that achieves the highest value of maximum likelihood ratio among all candidates. Maximum likelihood ratio (LR) 61.025 is reached at the 63rd mutation (max-L1) on the consensus-genome. A relevant number of mutations in the consensus-genome (64-72) remain uncovered by L1. RecombinHunt identifies the L2 candidate BE.4, as it achieves the maximum likelihood ratio compared to all other lineages. BA.5.2.6 (left table) and BE.4 (right table) are compared with the following candidates, who scored lower maximum likelihood ratios. For each lineage candidate, tables report the number of sequences; the position max-L1 (resp. max-L2), i.e., the beginning of the breakpoint; and the maximum likelihood ratio value reached on that coordinate. The following columns correspond to the result of the comparison of the row candidate with the first of the table: AIC value (lower values indicate that the row candidate is similar to the first candidate); p-value obtained from the AIC; and three conditions (C1) ✓ if the p-value (comparing the row candidate with the first one) is $\geq 10^{-5}$; (C2) ✓ if pos of the row candidate is at most one mutation apart from the one of the first candidate; (C3) ✓ if the row candidate belongs to the same phylogenetic branch as the first one. Candidates that conjunctively meet all these requirements are incorporated into a group, resulting in BA.5.2.6 and CP.3 (both candidates for L1) and BE.4, CQ.2, BE.4.1.1, BE.4.1, CQ.1.1, CQ.1 (all candidates for L2). Note that the group now includes also BE.4.1, corresponding exactly to the lineage provided in the ground truth.

b, Result of RecombinHunt search on the consensus-genome 75% of 14 high-quality sequences assigned to the XD Pango lineage. The Pango designation issue #444 establishes the ground truth as a 2BP recombination of the lineage B.1.617.2* – contributing the mutations from the genome 5'-end to the 23rd and from the 53rd to the 3'-end, and the lineage BA.1*, contributing the mutations from the 26th to the 52nd. RecombinHunt selects AY.4 as the first L1 candidate, consistently with the ground truth indication (AY.4 is a child of B.1.617.2). Maximum likelihood ratio 25.550 is reached at the 23rd mutation (max-L1) on the consensus-genome. AY.4 is also appropriate for describing the 3'-end portion of the genome, reaching its maximum likelihood ratio at 13.051 at the 53rd position. RecombinHunt identifies the first L2 candidate BA.1.22 (consistent with the ground truth BA.1*). AY.4 (left table) and BA.1.22 (right table) are compared with the following candidates; among these, no one conjunctively meets the three conditions to be included in the alternative candidates' group.

Lin.	#seq	#mut	GT lineages	GT BP	RH lineage candidates	RH BP	RM, LC, BP
XA	7	32	B.1.177 + B.1.1.7	12-14	B.1.177.18 + B.1.1.7	13-14	✓(3.12e-94), ✓, ✓
XAD	70	65	BA.2* + BA.1*	54-56	BA.2 + BA.1.14.1	55-56	✓(7.19e-24), ✓, ✓
XAE	50	67	BA.2* + BA.1*	53-56	BA.2 + BA.1.14	55-56	✓(3.06e-26), ✓, ✓
XAL	72	61	BA.1* + BA.2*	15-17	BA.1.1 + BA.2	15-16	✓(6.09e-76), ✓, ✓,
XAN	123	71	BA.2* + BA.5.1	21-28	BJ.1 + BA.5.1.23	11-12	✓(3.15e-16), ✓, ✗
XAQ	5	64	BA.1* + BA.2*	17-18	BA.1 + BA.2	16-17	✓(3.26e-72), ✓, ✓
XAV	42	70	BA.2* + BA.5*	19-22	BA.5.1.24	non-rec	—— ✗(G1) ——
XBB	1752	85	BJ.1 + BM.1.1.1	49-52	BJ.1 + BM.1.1.1	51-52	✓(2.99e-87), ✓, ✓
XBD	141	82	BA.2.75.2 + BA.5.2.1	52-66	BA.2.75.2 + BF.3	65-66	✓(4.78e-64), ✓, ✓
XBE	63	72	BA.5.2* + BE.4.1	31-53	BA.5.2.6 + BE.4	63-64	✓(5.22e-26), ✓, ✗
XBF	4944	84	BA.5.2 + CJ.1	14-16	BM.1.1.1	non-rec	—— ✗(G3) ——
XBG	86	75	BA.2.76 + BA.5.2	32-41	BA.2.76 + BA.5.2	40-41	✓(3.95e-50), ✓, ✓
XBH	71	78	BA.2.3.17 + BA.2.75.2	19-28	BA.2.75.2 + BA.2.3.17 + BA.2.75.2	4-5, 19-20	—— ✗(G2) ——
XBJ	120	88	BA.2.3.20 + BA.5.2*	59-73	BA.2.3.20 + BA.5.2.36	72-73	✓(8.54e-89), ✓, ✓
XBM	205	77	BA.2.76 + BF.3	33-42	BF.3 + BA.2.76 + BF.3	6-7, 33-34	—— ✗(G2) ——
XE	1009	63	BA.1* + BA.2*	9-11	BA.1.17.2 + BA.2.29	9-10	✓(2.70e-106), ✓, ✓
XJ	47	60	BA.1* + BA.2*	13-16	BA.1.17.2 + BA.2.65	13-14	✓(2.59e-123), ✓, ✓
XK	25	55	BA.1* + BA.2*	15-17	BA.1.7 + BA.2.13	15-16	✓(1.99e-185), ✓, ✓
XM	301	59	BA.1.1* + BA.2*	14-17	BA.1.1.16 + BA.2.33	14-15	✓(2.17e-217), ✓, ✓
XV	27	61	BA.1* + BA.2*	12-14	BA.1.6 + BA.2.25	12-13	✓(1.73e-167), ✓, ✓
XY	44	68	BA.1* + BA.2*	14-16	BA.1.1 + BA.2	14-15	✓(3.43e-67), ✓, ✓
XZ	49	65	BA.2* + BA.1*	55-56	BA.2 + BA.1.1.12	56-57	✓(2.84e-23), ✓, ✓
XAA	33	67	BA.1* + BA.2*	7-8	BA.1.20 + BA.2	7-8	✓(3.56e-37), ✓, ✓
XAB	73	67	BA.1* + BA.2*	6-7	BA.1.1.16 + BA.2	6-7	✓(2.86e-48), ✓, ✓
XAF	64	65	BA.1* + BA.2*	8-10	BA.1.1.16 + BA.2.9	9-10	✓(8.17e-116), ✓, ✓
XAG	227	70	BA.1* + BA.2*	8-9	BA.1.1.14 + BA.2	6-7	✓(1.33e-36), ✓, ✗
XAM	147	69	BA.1.1 + BA.2.9	6-7	BA.1.1.16 + BA.2.9	6-7	✓(4.72e-55), ✓, ✓
XAR	12	64	BA.1* + BA.2*	1-3	BA.2	non-rec	—— ✗(G1) ——
XAU	72	69	BA.1.1* + BA.2.9*	3-5	BA.1.1.2 + BA.2.9	3-4	✓(2.51e-25), ✓, ✓
XF	12	62	B.1.617.2* + BA.1*	6-7	AY.37 + BA.1.16	6-7	✓(2.96e-21), ✓, ✓
XG	272	66	BA.1* + BA.2*	6-7	BA.1.17 + BA.2	6-7	✓(2.82e-29), ✓, ✓
XH	93	65	BA.1* + BA.2*	10-12	BA.1 + BA.2.9	10-11	✓(5.96e-64), ✓, ✓
XL	28	69	BA.1* + BA.2*	8-9	BA.1.17.2 + BA.2	8-9	✓(1.36e-42), ✓, ✓
XN	82	66	BA.1* + BA.2*	2-4	BA.2	non-rec	—— ✗(G1) ——
XQ	43	64	BA.1.1* + BA.2*	4-5	BA.1.1.16 + BA.2.5	4-5	✓(3.77e-61), ✓, ✓
XR	91	66	BA.1.1* + BA.2*	4-5	BA.1.1.16 + BA.2	4-5	✓(8.24e-42), ✓, ✓
XS	15	64	B.1.617.2* + BA.1.1*	10-12	AY.126 + BA.1.1	10-11	✓(8.23e-63), ✓, ✓
XU	4	63	BA.1* + BA.2*	5-6	BA.1.17 + BA.2.37	5-6	✓(8.39e-51), ✓, ✓
XW	88	67	BA.1* + BA.2*	3-5	BA.1.1.2 + BA.2.23	3-4	✓(4.44e-35), ✓, ✓
XAH	141	64	BA.2* + BA.1*	59-61	BA.2 + BA.1.17	56-57	✓(2.49e-13), ✓, ✗
XAP	26	64	BA.2* + BA.1*	54-56	BA.2 + BA.1.1.12	55-56	✓(2.84e-23), ✓, ✓
XAT	28	66	BA.2.3.13 + BA.1*	57-59	BA.2.3.13	non-rec	—— ✗(G3) ——
XC	4	36	AY.29 + B.1.1.7	27-28	AY.29.1 + Q.1	28-29	✓(3.45e-98), ✓, ✓
XP	12	66	BA.1.1* + BA.2*	58-65	BA.1.1	non-rec	—— ✗(G3) ——
XT	11	61	BA.2* + BA.1*	52-54	BA.2 + BA.1.22	53-54	✓(1.67e-29), ✓, ✓
XAC	33	68	BA.2* + BA.1* + BA.2*	56-58, 62-68	BA.2.3 + BA.1.1.16 + BA.2.3	56-57, 62-63	✓(1.38e-19), ✓, ✓
XAK	110	69	BA.2* + BA.1* + BA.2*	20-23, 23-24	BA.2	non-rec	—— ✗(G1) ——
XAW	28	103	AY.122 + BA.2* + AY.122	48-53, 91-93	AY.122 + BQ.1.12 + AY.122	51-52, 97-98	—— ✗(G3) ——
XAZ	1390	69	BA.2.5 + BA.5 + BA.2.5	8-14, 63-64	BQ.1.9 + BA.5	3-4	—— ✗(G1) ——
XBL	153	92	XBB.1 + BA.2.75 + XBB.1	2-7, 12-22	XBB.1.5 + BN.1.3 + XBB.1.5	5-6, 12-13	✓(8.60e-16), ✓, ✓
XD	14	67	B.1.617.2* + BA.1* + B.1.617.2*	23-26, 51-53	AY.4 + BA.1.22 + AY.4	23-24, 52-53	✓(2.21e-170), ✓, ✓

Table 1 | Summary of results on GISAID dataset. Four horizontal sections represent the cases that in the Pango lineage designation ground truth (GT) are defined as i) 1BP, with a breakpoint in the central part of the genome; ii) 1BP, with a breakpoint close to the genome 5'-end; iii) 1BP (with a breakpoint close to the genome 3'-end; and iv) 2BP. The table columns represent, respectively: name of Pango lineage; number of high-quality sequences assigned to Lin. in the database; number of mutations in the 75% consensus-genome for the observed lineage, defining the mutations-space; lineages in the GT; GT breakpoint coordinates in the mutations-space; candidates found by RecombinHunt (RH); RH breakpoint coordinates in the mutations-space; comparison between GT and RH results: (RM) Recombination Model: ✓ when RH selected the same model as GT (non-recombinant, 1BP or 2BP), ✗ otherwise–with the p-value of the AIC comparison between the recombination model and the non-recombination one; (LC) Lineage Candidates: ✓ when all RH candidates are the same or descendants of those in GT, ✗ otherwise; (BP) BreakPoint Range: ✓ when the BP coordinates in RH are included in those of GT with at most 1 mutation of difference, ✗ otherwise. In twelve cases the output of RecombinHunt is considerably different from the GT. These are indicated with ✗ and a discussion code G1–G3, detailed in the text.

Lin.	#seq.	%non-rec	%1BP	%2BP	%p<e-5	consensus	
XA	7	0	**1**	0	1	1BP	
XAD	70	0.13	**0.71**	0.16	0.97	1BP	
XAE	50	0.02	**0.98**	0	1	1BP	
XAL	72	0	**1**	0	1	1BP	
XAN	100	0.28	**0.64**	0.08	0.98	1BP	
XAQ	5	0	**1**	0	1	1BP	
XAV	42	**0.62**	0.26	0.12	0.98	non-rec	
XBB	100	0	**0.92**	0.08	0.99	1BP	
XBD	100	0	**0.8**	0.2	1	1BP	
XBE	63	0	**0.95**	0.05	1	1BP	
XBF	100	**0.91**	0.05	0.04	0.99	non-rec	
XBG	86	0.01	0.3	0.69	1	1BP	*
XBH	71	0	0.86	0.14	1	2BP	*
XBJ	100	0	**1**	0	1	1BP	
XBM	100	0	0.56	0.44	1	2BP	*
XE	100	0.01	**0.99**	0	0.99	1BP	
XJ	47	0.02	**0.98**	0	0.98	1BP	
XK	25	0	**1**	0	1	1BP	
XM	100	0	**1**	0	1	1BP	
XV	27	0	**1**	0	1	1BP	
XY	44	0	**1**	0	1	1BP	
XZ	49	0	**0.98**	0.02	1	1BP	
XAA	33	0	**1**	0	1	1BP	
XAB	73	0.01	**0.99**	0	1	1BP	
XAF	64	0	**1**	0	1	1BP	
XAG	100	0	**1**	0	1	1BP	
XAM	100	0	**1**	0	1	1BP	
XAR	12	**1**	0	0	1	non-rec	
XAU	72	0.03	**0.97**	0	1	1BP	
XF	12	0.08	**0.92**	0	1	1BP	
XG	100	0	**1**	0	1	1BP	
XH	93	0	**0.99**	0.01	1	1BP	
XL	28	0	**1**	0	1	1BP	
XN	82	**0.98**	0.02	0	0.99	non-rec	
XQ	43	0	**1**	0	1	1BP	
XR	91	0.18	**0.82**	0	1	1BP	
XS	15	0	**1**	0	1	1BP	
XU	4	0	**1**	0	1	1BP	
XW	88	0.11	**0.89**	0	0.99	1BP	
XAH	100	0.05	**0.95**	0	0.98	1BP	
XAP	26	0.19	**0.81**	0	1	1BP	
XAT	28	0.43	0.57	0	0.96	non-rec	*
XC	4	0	**1**	0	1	1BP	
XP	12	**0.92**	0.08	0	1	non-rec	
XT	11	0	**1**	0	1	1BP	
XAC	33	0.15	0.21	**0.64**	0.85	2BP	
XAK	100	**0.71**	0.13	0.16	0.06	non-rec	
XAW	28	0.04	0.18	**0.79**	0.93	2BP	
XAZ	100	0.13	0.47	0.4	0.83	1BP	*
XBL	100	0.02	0.03	**0.95**	1	2BP	
XD	14	0	0	**1**	1	2BP	

Table 2 | Summary of reproducibility analysis results on 100 (or less) available genomes for each recombinant lineage. For each Pango lineage, we indicate the number of considered high-quality sequences—100 random ones are selected when more are available. In the following columns, we indicate percentages of sequences with no breakpoint, one breakpoint, or two breakpoints (bold-type for solid majority). The following column reports the percentage of sequences for which the p-value of the most-probable model (for each sequence) is $\leq 10^{-5}$. The last column reports the model chosen for the consensus-genome and * when that model is in contrast with the majority of sequences (underlined).

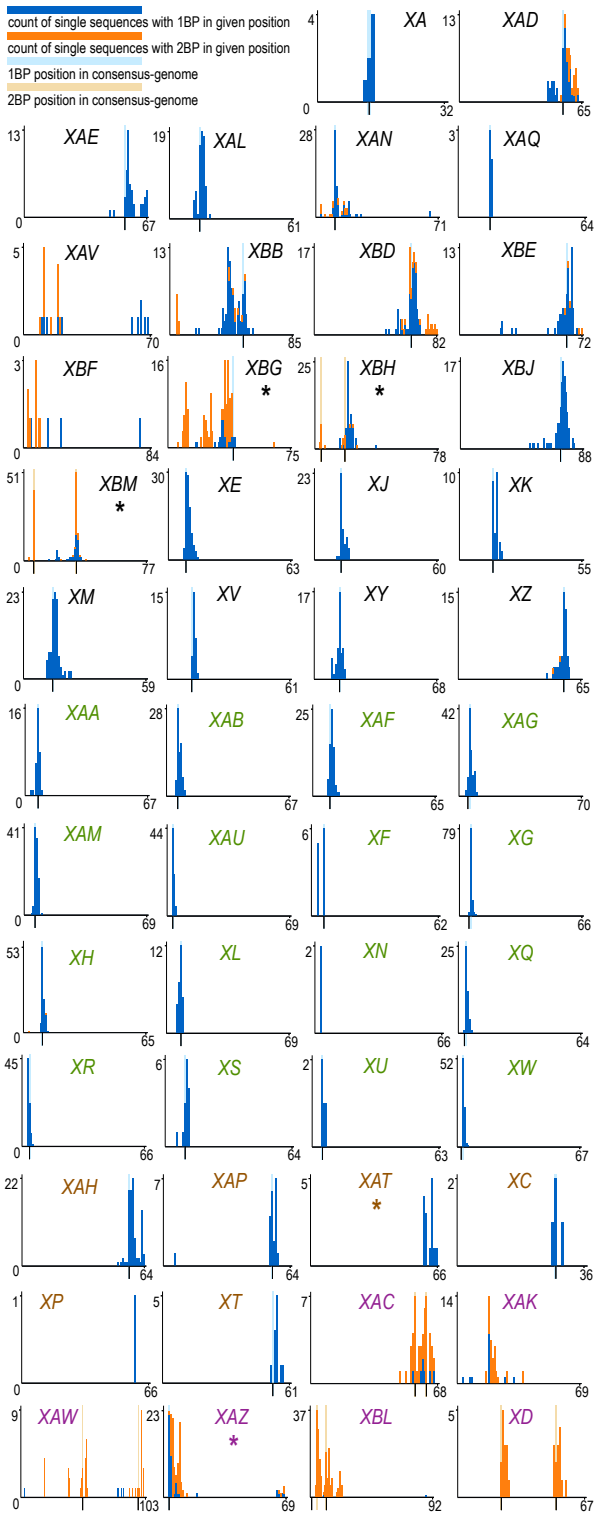


Figure 3 | Barplots of RecombinHunt (RH) outputs for breakpoints positions. Label colors reflect the four groups in Table 2. On the x-axis, the consensus-genome mutations; on the y-axis, the count of single sequences with a breakpoint detected on the x position. A light blue stripe indicates the RH 1BP position; two light orange stripes indicate the RH 2BP positions (see Table 1). Blue bar plots count the sequences whose 1BP is located at a given mutation; orange bar plots count the sequences whose 2BPs are located at given positions (without distinction between the first and the second one).

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Methods

Data collection and genome quality filtering

Since January 5th, 2020, when the first complete genome sequence of SARS-CoV-2 was released on GenBank (Access number: NC_045512.2[51]), viral sequences have been rapidly accumulated. We considered the nucleotide-level mutations of 15,271,031 complete SARS-CoV-2 genome sequences collected from all over the world, downloaded on April 1st, 2023, using EpiCov^{TM} data from the GISAID database[20] available online[52]. The original data included genome sequences in FASTA format and associated metadata (accession ID, collection date, submission date, Pangolin lineage, and collection location). These were processed by the HaploCoV pipeline[28] to derive a large table with the list of mutations and matched metadata for every genome sequence.

Viral genomes identical to the reference sequence or having conflicting lineage assignments according to HaploCoV and GISAID were discarded. Records with incomplete metadata, labeled as low-coverage and/or associated with low-quality sequences (percentage of Ns$\leq$ 2$\%$) were removed by our quality filters. The resulting dataset contains 5,255,228 records (c.a. 34.4% of all the available sequences).

Mutation-lineage probability

We compute the probability of every genomic mutation in the collection of high-quality SARS-CoV-2 genome sequences defined above 1) in the entire database; and 2) in each existing Pango Lineage[53]). Probabilities are approximated with the corresponding frequency, i.e., the ratio between the number of genomes holding the mutation and the total number of genomes (1) or the total number of genomes assigned to a lineage (2). Lineages with less than 10 high-quality sequences (i.e., XA, XAQ, XU, and XC in the GISAID dataset) are excluded – to avoid small denominators.

Screening potential recombinant genomes

The complete workflow of the RecombinHunt method is shown in Extended Data Fig. 1. The input is a sequence (hereon called *target*) represented as an ordered set of nucleotide mutations, either of an existing genome or of a *consensus-genome*, corresponding to the set of mutations with a frequency above a certain threshold in a given lineage.

The search of candidates is based on the computation of the cumulative logarithmic ratio between the probability of a given mutation m to occur in a given lineage L_i and the probability of that mutation to occur in any SARS-CoV-2 genome. More formally, we associate a function $likelihood_ratio$ (see Eq. 1) to each lineage L_i tested on a target genome T in a range R from a *start* to an *end* mutation on T:

$$Likelihood_ratio(L_i, T, R_{start:end}) = \sum_{\forall m \in R} \begin{cases} ln(\frac{P(m \in L_i)}{P(m)}), & \text{if } m \in T \\ -ln(\frac{P(m \in L_i)}{P(m)}), & \text{if } m \notin T \text{ and } m \in L_i \\ 0, & \text{if } m \notin T \text{ and } m \notin L_i \end{cases} \quad (1)$$

The first candidate – denoted as $L1$ – is searched in the whole space of mutations of the genome, both starting from the 5'-genome end and the 3'-genome end. When the high majority of mutations in the target are also included in $L1$ (i.e., all except at most 2) the non-recombinant model is considered as the one that best describes the target. Else, the method evaluates two alternative models, (1) with one breakpoint, separating $L1$ and $L2$, or (2) with double breakpoint, having an $L2$ stretch in between two $L1$ stretches (with a pattern $L1$-$L2$-$L1$).

In both cases, $L1$ is selected as the first candidate contributing to the largest portion of the genome in the space of mutations of the target; it extends from the 5'-end until the breakpoint ($L1$ has the $>>$ direction) or from the 3'-end to the breakpoint ($L1$ has the $<<$ direction). The breakpoint is marked at the mutation where the profile of the $L1$'s $likelihood_ratio$ (computed according to) reaches its maximum.

Then, in the case of a single breakpoint, a second candidate, denoted as $L2$ and different from $L1$, is searched in the space of mutations of the genome that was not already covered by $L1$. This case is only considered when there exists an $L2$ (within the Pango lineages) characterized by at least 3 mutations in that space; else, we recede back to the non-recombinant case. The resulting composition of $L1$ and $L2$ also identifies the position of the breakpoint; when the two candidates cover the entire genome space, the breakpoint corresponds to a pair of adjacent positions. Else, we call *gap* the uncovered portion of the genome and propose a gap-resolution procedure. See the below paragraph, for further details.

In the case of a double breakpoint, $L1$ is considered also from the opposite side of the genome (called $L1^{opp}$); if in this region $L1$ has at least 3 mutations of the target, the model $L1$-$L2$-$L1$ is explored. A second, central candidate $L2$ is then searched between the two stretches of $L1$. After finding $L2$, a gap-resolution procedure may be necessary.

The two models ($L1$-$L2$ and $L1$-$L2$-$L1$) are compared using the Aikake information criterion (AIC). This is framed as follows; we evaluate if $L1$-$L2$ (alternative hypothesis) is better than $L1$-$L2$-$L1$ (null hypothesis). The test obtaining the lowest p-value determines the final output.

Gaps resolution

This procedure is applied when the target positions corresponding to maximum likelihood (i.e., max-$L1$ for $L1$ and max-$L2$ for $L2$) are not adjacent. In such cases, the breakpoint is set as the position p that minimizes the cumulative likelihood loss for both the adjacent regions. The region to the left of the gap is extended up to p, while the positions starting from $p+1$ are assigned to the right-adjacent region. One example of the procedure is shown in Extended Data Fig. 2.

Comparison of recombinant vs non-recombinant models

We finally estimate the error probability of the recombination hypothesis against the non-recombination hypothesis. For each target sequence T, we compute three *global_likelihood* (G) functions, respectively representing the cases where the target is 1) completely explained by lineage L_1 (G_{L_1}); 2) completely explained by L_2 (G_{L_2}); or 3) partially explained by L_1 and by L_2 in different portions (G_{L_1,L_2}) (hence supportive of a recombination). The function cumulatively adds (or subtracts) a contribution for each mutation in the target mutations space, composed by the combination of T with the involved lineages.

Each term of the sum corresponds to the natural logarithm of the probability of the specific mutation to characterize the lineage L_i; the contribution is positive when the mutation occurs on T, and negative when it does not. In Eq. 2, we use the general term L_i to represent L_1 for G_{L_1} and L_2 for G_{L_2}. In the composite case of G_{L_1,L_2}, instead, L_i is composed of portions of L_1 and L_2 according to the best 1BP or 2BP solution.

$$Global_likelihood(L_i, T, R_{start:end}) = \sum_{\forall m \in R, i \in \{T, L_i\}} \begin{cases} ln(P(m \in L_i)), & \text{if } m \in T \text{ and } m \in L_i \\ -ln(P(m \in L_i)), & \text{if } m \notin T \text{ and } m \in L_i. \end{cases} \quad (2)$$

Then, by means of AIC, we compare G_{L_1,L_2} versus G_{L_1} and G_{L_1,L_2} versus G_{L_2}. Small p-values indicate that the recombination model better explains the considered target, as opposed to single lineages. We finally use the smallest p-value for reporting the significance of the recombinant vs. non-recombinant output.

Identification of groups of similar candidates

$L1$ and $L2$ may be represented by additional – similar – candidates. To exhaustively define the group of lineages that are not inconsistent with the roles of, respectively, acceptor and donor, three conditions are checked: 1) the AIC criteria is used to assess how well the stretch of $L1$ (respectively, $L2$) is explained by each of the ten best candidates according to the maximum $likelihood_ratio$ value reached in correspondence of the breakpoint position (see Eq. 1). The candidates from the 2nd to 10th position ones are compared to the first candidate, using the AIC and a hypothesis test with p-values $\geq 10^{-5}$, meaning that they are sufficiently different not to be considered acceptable alternatives for (or be differentiated from) $L1$ (resp. $L2$); 2) candidates that reach the maximum of $likelihood_ratio$ in locations that are apart from the position of the first candidate (i.e., more than one mutation apart) are not to be considered as acceptable alternatives for $L1$ (resp. $L2$); 3) candidates that do not belong to the same phylogenetic branch or sub-tree as the first candidate are not to be considered acceptable alternatives for $L1$ (resp. $L2$). When a candidate meets all of the three requirements, it is incorporated into a group of alternative candidates, equally explaining the recombination model proposed by RecombinHunt.

Collection of ground truth information from Pango designation issues

The hunt for recombinants is manually performed by volunteers who report evidence on the Pango designation GitHub repository in the form of issues, broadly documented and discussed with peers[42]. We extracted from the Pango designation file[43] all the entries whose keys start with 'X' at the first level of nomenclature (i.e., without any dot). Then, we matched them to the `lineage_notes.txt` file[54], retrieving the issues where those designations are discussed. We inspected all the issues present on April 1st, 2023.

Two kinds of information were retrieved: 1) the donor and acceptor lineage candidates of recombination (directly from the `alias_key.json` file[43] and cross-checked withFocosi & Maggi[55], when related information was available); 2) the interval-based position of the breakpoints, manually scouted in the discussions of the issues. As per (1), several candidates[43] are reported with the *name** symbol, indicating that – at the time of designation – it was not possible to assign a precise lineage, but it was possible to assign an entire sub-tree of the phylogeny (with root in *name*). As per (2), sometimes issues' threads reported conflicting intervals; in these cases, we considered the union of such options. For the purposes of RecombinHunt, intervals in genomic coordinates are translated into target mutations space coordinates that depend on the target sequence observed in the given task.

Data availability

Original sequences and metadata are publicly accessible through the GISAID and Nextstrain platforms. The specific sample accessions of the genomes on which RecombinHunt has been applied are reported in Supplementary Tables 2–4.

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Author contributions

T.A. and A.B. conceived the work; T.A., A.B., and S.C. jointly conceptualized and designed the core algorithm; M.C. data preparation, conceptualization of the statistical framework, and data interpretation; T.A. collected

the ground truth information, developed the core algorithm, and performed all the experiments and the reproducibility analysis; A.B. performed state-of-the-art review, created the figures, and drafted the manuscript; all authors revised the final version of the manuscript; S.C. supervised the project.

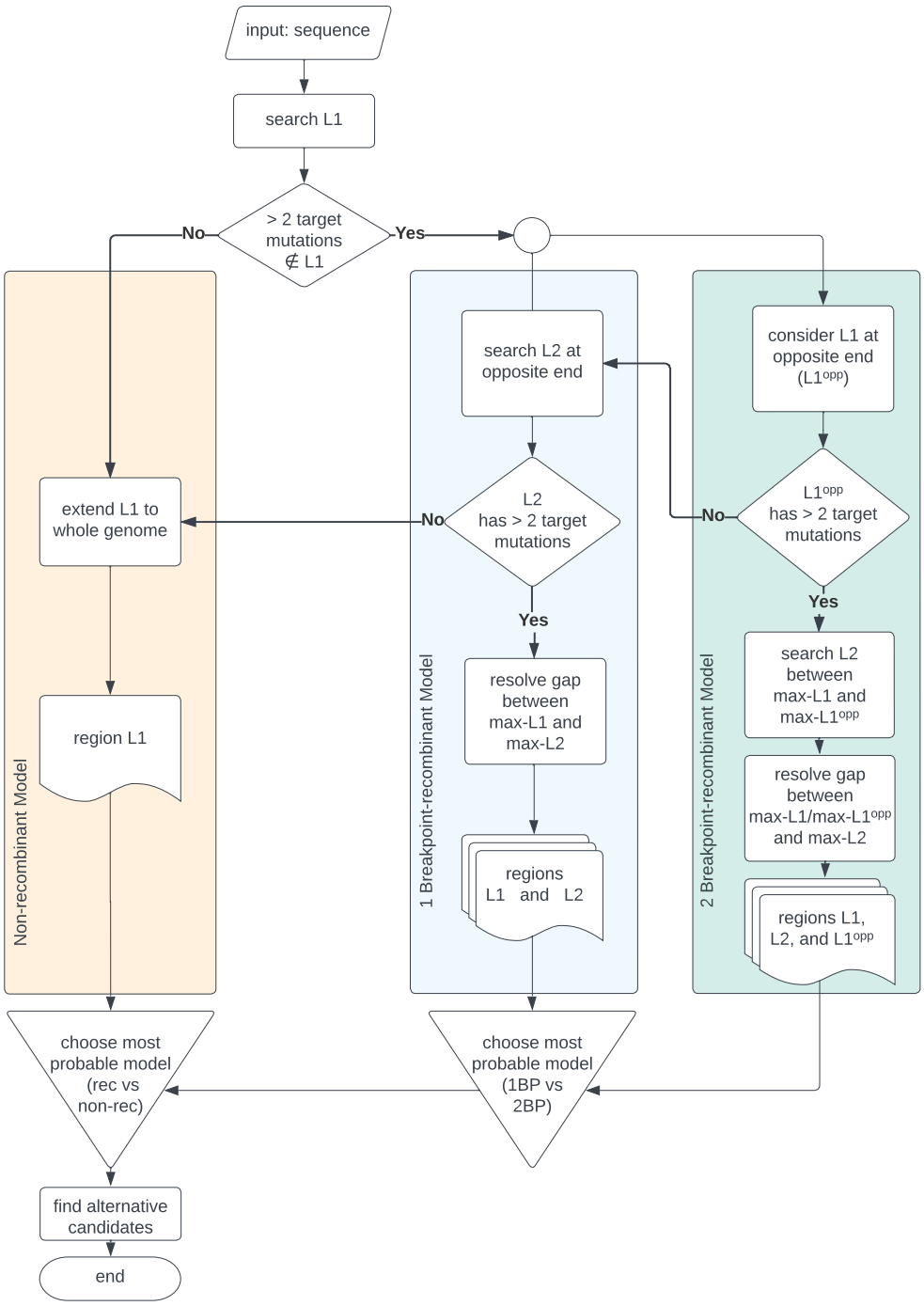
Competing interests

The authors declare no competing interests.

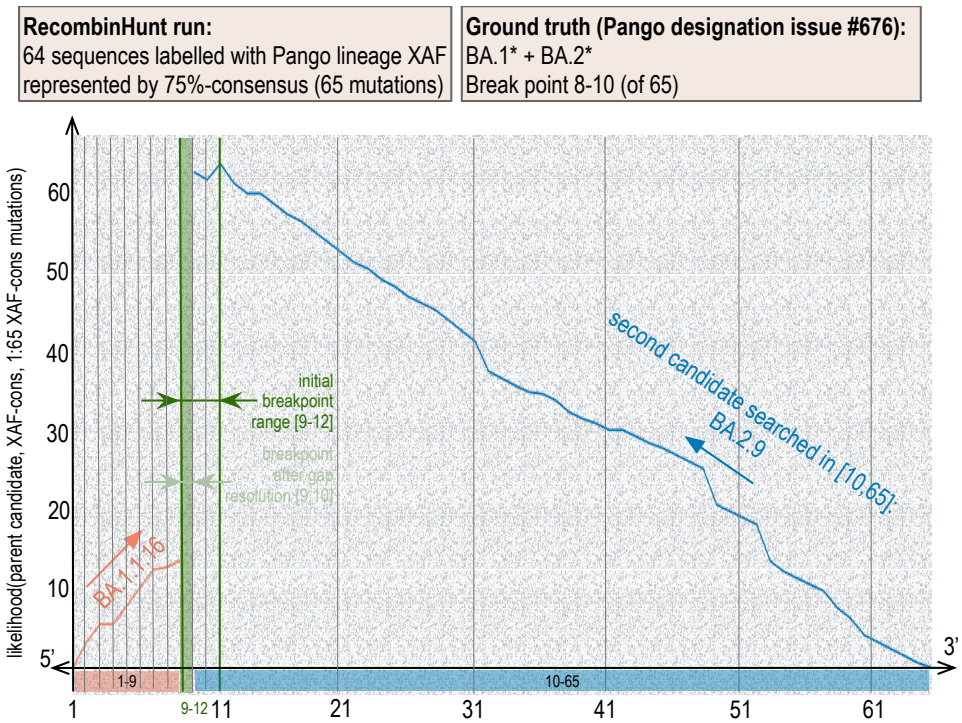
Additional information

Supplementary Information is available for this paper.

Correspondence and requests for materials should be addressed to A.B.



Extended Data Figure 1 | Overall RecombinHunt workflow. An input viral sequence is considered. The donor lineage is searched based on the cumulative likelihood ratio. Then, three branches are considered: non-recombinant model, one-breakpoint recombination model, and two-breakpoint recombination model. The preferred model is chosen using statistical testing, based on the Aikake information criterion.



Extended Data Figure 2 | Reduction of breakpoint range performed by RecombinHunt. The procedure is applied when a precise position of the breakpoint cannot be determined from the likelihood ratio information. Here, the case of running RecombinHunt on the consensus-genome of XAF is shown. The L1 candidate is found to cover positions 1-9, whereas L2 covers 12-65. The initial gap corresponds to a stretch from the 9th and the 12th mutation of the XAF consensus-genome, then resolved to only include the 9th-10th mutations, laying on the [10448, 11288] nucleotides-interval of the SARS-CoV-2 reference genome.

Lin.	#seq	#mut	GT lineages	GT BP	RH lineage candidates	RH BP	RM, LC, BP
XA	33	36	B.1.177 + B.1.1.7	12-14	B.1.177.18 + B.1.1.7	13-14	✓(6.86e-101), ✓, ✓
XAD	11	69	BA.2* + BA.1*	55-57	BA.2 + BA.1	56-57	✓(4.11e-21), ✓, ✓
XAE	18	72	BA.2* + BA.1*	55-58	BA.2 + BA.1	57-58	✓(1.11e-28), ✓, ✓
XAL	13	67	BA.1* + BA.2*	17-19	BA.1.1 + BA.2	17-18	✓(1.96e-86), ✓, ✓
XAN	36	72	BA.2* + BA.5.1	21-28	BA.2 + BA.5.1.23	11-12	✓(4.03e-17), ✓, ✗
XAP	261	65	BA.2* + BA.1*	53-55	BA.2.65 + BA.1.23	54-55	✓(9.79e-70), ✓, ✓
XAT	3	66	BA.2.3.13 + BA.1*	55-57	BA.2.3	non-rec	—— ✗(G3) ——
XAV	19	72	BA.2* + BA.5*	19-22	BA.5.1.24	non-rec	—— ✗(G1) ——
XBB	162	92	BJ.1 + BM.1.1.1	50-54	BA.2.9 + BM.1.1.1	38-39	✓(1.25e-66), ✓*, ✗
XBD	66	86	BA.2.75.2 + BA.5.2.1	53-67	BA.2.75.2 + BF.3	66-67	✓(2.05e-85), ✓, ✗
XBE	134	75	BA.5.2* + BE.4.1	31-53	BA.5.2.6 + BE.4.1.1	63-64	✓(2.32e-38), ✓, ✗
XBF	298	91	BA.5.2 + CJ.1	14-16	BA.5.2.3 + CJ.1.1	11-12	✓(1.27e-56), ✓, ✗
XBG	36	78	BA.2.76 + BA.5.2	32-41	BA.2.76 + BA.5.2	23-24	✓(8.88e-44), ✓, ✗
XBH	10	84	BA.2.3.17 + BA.2.75.2	19-28	BA.2.75.2 + BA.2.3.17 + BA.2.75.2	4-5, 19-20	—— ✗(G2) ——
XBJ	9	92	BA.2.3.20 + BA.5.2*	60-74	BA.2.3.20 + BA.5.2.62	73-74	✓(8.73e-113), ✓, ✓
XBM	49	77	BA.2.76 + BF.3	31-40	BA.2.76 + BF.3.1	31-32	✓(1.40e-69), ✓, ✓
XBP	23	88	BA.2.75* + BQ.1*	40-42	BL.1 + BQ.1.1.3	41-42	✓(1.04e-150), ✓, ✓
XBR	8	94	BA.2.75 + BQ.1	41-42	BN.3.1 + BQ.1.25.1	41-42	✓(4.73e-205), ✓, ✓
XBW	5	95	XBB.1.5 + BQ.1.14	76-80	XBB.1.5 + BQ.1.14	79-80	✓(9.08e-72), ✓, ✓
XJ	24	65	BA.1* + BA.2*	11-14	BA.1.24 + BA.2.1	11-12	✓(1.22e-182), ✓, ✓
XM	145	62	BA.1.1* + BA.2*	13-16	BA.1.24 + BA.2.27	13-14	✓(4.56e-200), ✓*, ✗
XV	25	66	BA.1* + BA.2*	12-14	BA.1.14 + BA.2.52	12-13	✓(5.14e-165), ✓, ✓
XY	62	74	BA.1* + BA.2*	14-16	BA.1.1 + BA.2	14-15	✓(8.66e-77), ✓, ✓
XZ	140	66	BA.2* + BA.1*	54-55	BA.2.34 + BA.1.23	55-56	✓(8.68e-70), ✓, ✓
XAA	52	73	BA.1* + BA.2*	7-8	BA.1.20 + BA.2	7-8	✓(9.03e-37), ✓, ✓
XAB	88	67	BA.1* + BA.2*	4-5	BA.1.6 + BA.2.27	4-5	✓(4.30e-61), ✓, ✓
XAF	51	66	BA.1* + BA.2*	8-10	BA.1.1.9 + BA.2.7	8-9	✓(1.41e-130), ✓, ✓
XAG	15	74	BA.1* + BA.2*	8-9	BA.1.1.14 + BA.2.9	8-9	✓(5.25e-38), ✓, ✓
XAM	67	74	BA.1.1 + BA.2.9	6-7	BA.1.1.9 + BA.2.9	6-7	✓(7.24e-52), ✓, ✓
XAR	65	69	BA.1* + BA.2*	2-4	BA.2.23	non-rec	—— ✗(G1) ——
XAU	17	71	BA.1.1* + BA.2.9*	3-5	BA.1.1.9 + BA.2.9	4-5	✓(1.08e-25), ✓, ✓
XE	1342	67	BA.1* + BA.2*	9-11	BD.1 + BA.2.31	10-11	✓(6.83e-134), ✓, ✓
XF	19	64	B.1.617.2* + BA.1*	6-7	AY.4.2 + BA.1.16	6-7	✓(9.20e-46), ✓, ✓
XG	305	70	BA.1* + BA.2*	6-7	BA.1.17 + BA.2	6-7	✓(4.42e-49), ✓, ✓
XH	102	68	BA.1* + BA.2*	10-12	BA.1 + BA.2.9	10-11	✓(6.81e-61), ✓, ✓
XL	70	74	BA.1* + BA.2*	8-9	BA.1.17.2 + BA.2	8-9	✓(1.83e-39), ✓, ✓
XN	167	71	BA.1* + BA.2*	2-4	BA.2	non-rec	—— ✗(G1) ——
XQ	90	68	BA.1.1* + BA.2*	4-5	BA.1.1.9 + BA.2.23	4-5	✓(1.32e-46), ✓, ✓
XR	24	72	BA.1.1* + BA.2*	4-5	BA.1.1.15 + BA.2.9	5-6	✓(2.23e-32), ✓, ✓
XS	24	68	B.1.617.2* + BA.1.1*	10-12	AY.126 + BA.1.1	10-11	✓(3.01e-68), ✓, ✓
XU	6	71	BA.1* + BA.2*	6-7	BA.1.10 + BA.2	6-7	✓(4.38e-47), ✓, ✓
XW	47	72	BA.1* + BA.2*	3-5	BA.1.1.9 + BA.2	3-4	✓(1.85e-25), ✓, ✓
XAH	1	71	BA.2* + BA.1*	63-65	BA.2 + BA.1.1.18	58-59	✓(1.33e-22), ✓, ✗
XP	56	68	BA.1.1* + BA.2*	58-67	BA.1.1 + BA.5.6.3	59-60	—— ✗(G3) ——
XAC	34	71	BA.2* + BA.1* + BA.2*	56-58, 62-70	BA.2.3 + BA.1.1.9 + BA.2.3	57-58, 62-63	✓(5.84e-46), ✓, ✓
XAK	5	73	BA.2* + BA.1* + BA.2*	20-23, 23-24	BA.2 + BA.2.10	non-rec	—— ✗(G1) ——
XAZ	289	71	BA.2.5 + BA.5 + BA.2.5	8-14, 63-64	BA.5.1.27 + BA.5	non-rec	—— ✗(G1) ——
XBL	5	101	XBB.1 + BA.2.75 + XBB.1	2-7, 12-22	XBB.1.5.24 + BN.1.3 + XBB.1.5.24	3-4, 12-13	✓(1.54e-44), ✓, ✓
XBT	8	86	BA.5.2.34 + BA.2.75 + BA.5.2.34	10-14, 38-50	BA.5.2.34 + BL.1.5 + BA.5.2.34	13-14, 39-40	✓(1.21e-110), ✓, ✓
XBU	5	89	BA.2.75* + BQ.1* + BA.2.75*	40-53, 70-75	BA.2.75.2 + BQ.1.1.19 + BA.2.75.2	51-52, 70-71	✓(7.62e-72), ✓, ✓
XD	10	69	B.1.617.2* + BA.1* + B.1.617.2*	25-27, 53-55	AY.4 + BA.1.15.3 + AY.4	25-26, 54-55	✓(1.93e-166), ✓, ✓

Extended Data Table 1 | Summary of results on Nextstrain dataset. Four horizontal sections and column definitions follow the same criteria as in Table 1. In two cases, XBB and XM, the last column contains ✓* when the lineage candidates (LC) correspond to the ancestor lineage of those in the ground truth.

Lin.	RIVET lineage candidates	RIVET BP	RH lineage candidates	RH BP
XAC	✓	✓	✓	✓
XAK	-	✗	non-recombinant	-
XBB	-	✗	✓*	✗
XBD	-	✓	✓	✓
XBG	✓	✓	✓	✗
XBJ	✓	✓	✓	✓
XBL	✓	✓	✓	✓
XD	-	✗	✓	✓
XH	✓	✗	✓	✓
XM	✓	✓	✓*	✓
XW	-	✗	✓	✓
XBR	✓	✓	✓	✓
XBT	-	✓	✓	✓
XBU	-	✗	✓	✓

Extended Data Table 2 | Comparison between results of RIVET[9,41] and RecombinHunt with respect to the Pango lineage ground truth. For both RIVET and RecombinHunt (RH) we consider the correctness of the proposed donor and acceptor lineages and the correctness of the breakpoint position (BP). The symbol - marks the cases where RIVET lineage candidates are not defined in Pango. The symbol * marks the cases in which RH chooses a close ancestor lineage of those indicated in the Pango designation issue.

Accession ID	Name	Lineage	#BP in Yeh et al.	#BP in RH	LC in RH
ON838178.1	Slovenia/SI2022_S7	B.1.3	1 or 2	2: (31-32, 49-50)	B.1.3 + B.1.2 + B.1.3
ON609725.2	Slovenia/SLO	B.1.3	1 or 2	2: (31-32, 49-50)	B.1.3 + B.1.2 + B.1.3
ON754985.1	Slovenia/SI2022_S4	B.1.3	1 or 2	2: (31-32, 55-56)	B.1.3 + B.1.2 + B.1.3
ON754986.1	Slovenia/SI2022_S5	B.1.3	1 or 2	2: (31-32, 55-56)	B.1.3 + B.1.2 + B.1.3
ON754987.1	Slovenia/SI2022_S1_VERDE6	B.1.3	1 or 2	2: (31-32, 55-56)	B.1.3 + B.1.2 + B.1.3
ON631241.1	Slovenia/2022/2 SLO	B.1	1 or 2	0	B.1
ON755039.1	Italy/FVG-ITA_01_2022	B.1	2	0	B.1
ON631963.1	Australia/VIDRL01/2022	B.1	2 or 3	0	B.1

Extended Data Table 3 | Results of the recombination analysis on eight Mpox sequences. Columns represent the id of sequences and names according to Nextstrain; the lineage assigned by Nextstrain; the information on the number of breakpoints deducible from Yeh *et al.*[47]; and the results of RecombinHunt (RH) in terms of the number of breakpoints (#BP) and acceptor/donor lineage candidates (LC).