

SUPPLEMENTARY MATERIALS

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Supplementary Methods

This analysis included all SARS-CoV-2 RT-PCR tests of nose and throat swabs from 28-September-2020 to 10-January-2021 in the Office for National Statistics (ONS) CIS (ISRCTN21086382, <https://www.ndm.ox.ac.uk/covid-19/covid-19-infection-survey/protocol-and-information-sheets>).

The survey randomly selects private households on a continuous basis from address lists and previous surveys to provide a representative UK sample. Following verbal agreement to participate, a study worker visited each household to take written informed consent, which was obtained from parents/carers for those 2-15 years; those aged 10-15 years provided written assent. Those <2 years were not eligible.

Individuals were asked about demographics, symptoms, contacts and relevant behaviours (<https://www.ndm.ox.ac.uk/covid-19/covid-19-infection-survey/case-record-forms>). To reduce transmission risks, participants ≥ 12 years self-collected nose and throat swabs following study worker instructions. Parents/carers took swabs from children <12 years. At the first visit, participants were asked for (optional) consent for follow-up visits every week for the next month, then monthly for 12 months from enrolment. The study received ethical approval from the South Central Berkshire B Research Ethics Committee (20/SC/0195).

Swabs were analysed at the UK's national Lighthouse Laboratories at Milton Keynes and Glasgow using identical methodology. RT-PCR for three SARS-CoV-2 genes (N protein, S protein and ORF1ab) used the Thermo Fisher TaqPath RT-PCR COVID-19 Kit, and analysed using UgenTec FastFinder 3.300.5, with an assay-specific algorithm and decision mechanism that allows conversion of amplification assay raw data from the ABI 7500 Fast into test results with minimal manual intervention. Samples are called positive if at least a single N-gene and/or ORF1ab are detected (although S-gene cycle threshold (Ct) values are determined, S-gene detection alone is not considered sufficient to call a sample positive). We estimated a single Ct value as the arithmetic

mean of Ct values for genes detected (Spearman correlation >0.98 between each pair of Ct values).

Viral loads were estimated from a linearity curve (Fig.S1 in¹).

The presence of 12 specific symptoms in the previous seven days was elicited at each visit (cough, fever, myalgia, fatigue, sore throat, shortness of breath, headache, nausea, abdominal pain, diarrhoea, loss of taste, loss of smell), as was whether participants thought they had (unspecified) symptoms compatible with COVID-19. Any positive response to any symptom question at the swab-positive visit defined the case as symptomatic at the test; of 1,612,355 visits included in the analysis where no symptom was reported on either question, 27,801 (1.7%) had missing data from both questions and were excluded from analysis based on symptoms. 97,983 (6.1%) reported not having any of the specific symptoms but did not complete the generic symptoms question and 9,485 (0.6%) reported not having any generic symptoms but did not complete the specific symptoms questions; both were included as not self-reporting any symptoms.

We investigated Ct values using median (quantile) regression (as the cycle threshold (Ct) distribution was skewed overall) and finite mixture modelling to decompose the overall Ct distribution into sub-populations, positivity rates at the regional level using multi-level regression and post-stratification (MRP), and growth rates using iterative sequential Poisson regression (ISR)^{2,3}. 95% confidence intervals were derived from estimated standard errors of coefficients for frequentist methods (quantile regression and ISR with Poisson regression) and 95% credible intervals by taking the 2.5th and 97.5th percentile of 6000 draws from the posterior distribution for the Bayesian MRP model implemented using the No-U-Turn samples (a variant of Hamiltonian Monte Carlo). The Bayesian MRP model was used for estimating post-stratified positivity rates and corresponding second derivatives. Cases positive only on a single gene consistently have high Ct values reflecting variable target detection at low viral loads¹. Therefore, we considered only samples positive for ORF1ab+N-gene and negative for S-gene as SGTF, not those positive for the N-gene or ORF1ab alone. We used 5

knot natural cubic splines (knots spaced 10%/25%/50%/75%/90% from the minimum to the maximum) to assess non-linearity in the effect of calendar time on Ct values. As the distribution of Ct values (**Fig.S2**) was a clear mixture distribution, comparing the overall median or mean does not account for different phases of the epidemic; Ct values may vary simply because some strains are increasing in prevalence (so more infections detected are “new”) and others decreasing (so more strains detected are “old”)⁴. In order to compare “like with like” as much as possible, we fitted the same number of sub-distributions in separate mixture models for triple-positives and SGTF, choosing the higher of the two numbers that minimised the BIC for SGTF and triple positives. Analyses of Ct values were conducted in Stata 16.1.

For the primary analysis of positivity rates, we analysed the percentage of the private-residential population testing positive for SARS-CoV-2 from nose and throat swabs over time using Bayesian dynamic multi-level regression and post-stratification (MRP)^{5,6} to correct for any residual non-representativeness in terms of age, sex and region. Several empirical and simulation studies have found MRP to be superior to classical survey weighted and unweighted approaches, including when using small sample sizes at national and regional levels⁵⁻⁷. Partial pooling through the use of random effects in the multilevel model ensures stable estimates can be obtained for subnational levels from relatively small samples that would be problematic using more traditional survey-weighting approaches. Multilevel generalised additive regression was used to model the swab test result as a function of age, sex, time and region. Separate models were fitted for S-gene target failure (SGTF) positives (positive on only ORF1ab and the N-gene) vs other results (negative or non-SGTF positive), triple-positives vs other results, and other positives vs other results. Time, measured in days since 28 September 2020, was modelled using thin-plate splines and allowed to vary by region. We set k , the number of basis functions, to 10 to control the smoothness of the fitted function⁸. We used a normal prior with location set to 4 for the standard deviation of the smooth, as previously⁹. Subsequently, we post-stratified the resulting positivity estimates for each demographic-geographic respondent

type by the percentage of each type in the overall population and in each region. We did not post-stratify for other factors (e.g. ethnicity) because reliable estimates in the target population were not available. We fitted separate models to the nine English regions and each of the three devolved administrations. Because there were very few missing values ($\leq 1\%$) in age and sex, we restricted all analyses to observations with non-missing data. A complementary log-log link was used due to the ability to interpret regression coefficients as arising from an infection process with varying levels of exposure¹⁰. MRP models with random effects for individual participant and/or household nested within region did not converge. Therefore MRP models were run with only a random intercept for region, without a random intercept for participant and/or household. Models with only one participant sampled from each household have given similar results in previous analyses with somewhat wider 95% credible intervals mainly due to the smaller sample size⁹. Analyses were performed using the `rstanarm` package in R version 3.6.1.19.

To estimate current growth rates in SGTF and non-SGTF positives, we used the Iterative Sequential Regression (ISR) algorithm^{2,3} to estimate changepoints in unweighted positivity estimates over calendar time. Growth rates ($-\ln(2)/\ln(\text{rate ratio per day})$) can then be estimated directly from the most recent trend. In summary, ISR looks at the data iteratively, and compares models with one trend with those with 2 trends; if based on some criterion, the one with 2 trends is a better fit, then the “changepoint” is fixed and the process is repeated (i.e. more data is added and new models with this changepoint, but also other potential changepoints after this initial one are fitted). This method enables an unknown number of multiple changes in trend to be estimated efficiently, in contrast to traditional grid search algorithms which require the number of changes in trend to be fixed, and, in addition, also require every possible combination of changepoints to be modelled, making them very computationally intensive even for a small number of changepoints. We considered the binary outcome positive of specific type (1) vs negative or other positive (0) using a log link and poisson regression. The ISR algorithm first modelled the outcome using swab results from the 28 September

to 27 October, and compared a model with one trend over calendar time in the outcome to a model allowing this trend to change on the 12 October (keeping a minimum of 14 days from the last changepoint to the last data included in the model). If the model with two trajectories was not a better fit (determined by a Akaike Information Criterion being lower by at least 6.635 for triple-positives as the outcome and 3.84 for SGTF positives (the critical value corresponding to a significance level of 0.01 or 0.05 with one degree of freedom, respectively, given the very different positivity rates)), then an additional 1 day's observations (to 28 October) were included. The model with one trend was then compared to models with 2 trajectories with changepoints on 12 October or 13 October (keeping a minimum of 14 days of data again to the last data included in the model), again considering whether any model with a change in trend substantially improved model fit. Any changepoint that improved model fit was fixed, and then an additional 28 days of data included (since only changepoints at least 14 days from both the previous changepoint and the last data included in the model were considered). This process was iterated up to the end of the data. Outputs are rate of change per day in the most recent period since the last change in trend was detected (at the last "changepoint") and the current positivity rate (percentage) for each type. Analyses were performed in R version 3.6.1.19.

In order to compare the relative dynamics of SGTF vs triple-positives, we compared growth rates of SGTF vs triple positives within the same region in the two most recent epochs defined by changes in trend in either SGTF/triple positives identified by ISR (as shown in **Figure, Fig.S5**). That is, the most recent epoch was the time period from the most recent change in trend identified in either SGTF/triple positives until the end of the study, and the preceding epoch was the time from the penultimate to the most recent changepoint. Changepoints within 7 days were collapsed in order to exclude small epochs. The average difference between log growth rates for SGTF vs triple positives were estimated using random-effects meta-analysis, assuming independence (i.e. taking the variance

as the sum of the variances of the individual growth rates, since there is no straightforward method of estimating correlations between trends in different outcomes that change at different timepoints).

Analyses of growth rates by age divided the population into those up to and including 15/16 years (up to and including high school age) and older. School years rather than absolute years were used because behaviour is more likely to reflect place of education than numerical age for those 15-17 years.

A recent study estimated that the B.1.1.7 strain is associated with a 43-90% (range of credible intervals 38-130%) higher reproduction number than pre-existing variants. A variety of methods and data sources were used, including fitting a binomial generalised linear mixed model (GLMM) estimating the rate by which the SGTF replaces other positives, directly modelling the proportion of positives that are consistent with SGTF,¹¹ assuming that the growth rate follows a constant logistic growth curve. However, the underlying data did not include information on age, nor positives from asymptomatic individuals as the SGTF estimates originated from non-random symptomatic testing programmes. Here we used an equivalent GLMM to estimate the difference in Malthusian growth rate between SGTF and triple-gene positives¹¹ by directly modelling the proportion of SGTF-positives out of SGTF plus triple-positives, accounting for swab date, region, age and two-way interactions between time and region and time and age. A visit-level random effect was used to account for potential overdispersion. Only SGTF and triple-gene positives were included in this analysis to reduce uncertainty as to whether single gene positives were S-gene positive or negative. We performed separate analyses by age (<17 vs 17+ years of age), and presence of self-reported symptoms (yes/no). Furthermore we also considered restricting to positives with Ct<30 to increase the association between absence of S-gene detection in SGTF and absence of S-gene.

Supplementary Results

381,773 participants from 189,766 households contributed swab test results to the analyses

Supplementary Table 1).

SGTF comprised an increasing, and triple-gene positives a decreasing, percentage of positives from late-November in most English regions and countries within the UK (Wales, Northern Ireland, Scotland), consistent with SGTF representing non-B.1.1.7 H69del/V70del strains, or positives with lower viral load, before this (**Fig.S1**). The timing of rises in SGTF-positives varied strongly across region/country; e.g., rising from 15% early-November to 38% end-November and 81% end-December in London, versus 7%, 13% and 45% respectively in the West Midlands. In parallel, Ct values in SGTF showed a major decrease, being consistently high (~30, ~150 copies/ml) through to mid-November, before dropping sharply to a minimum ~20 (~230,000 copies/ml) at different times depending on region/country (**Fig.S1**), likely reflecting expansion of B.1.1.7 amongst SGTF-positives¹². In contrast, Ct values varied much less in triple-gene positives, remaining ~22-27 (**Fig.S1**), with small increases and decreases consistent with trends in overall positivity^{1,13}. By January 2021, overall median Ct values were similar in SGTF and triple-gene positives in most regions/countries (**Fig.S1**). However, finite mixture modelling showed that SGTF Ct values most likely came from four sub-populations with mean Ct 16.1 (29% of SGTF-positives), 21.6 (17%), 27.7 (25%) and 32.2 (29%). In comparison, identifying four sub-populations in triple-positives suggested higher Cts in those with the greatest viral burden, with mean Ct 17.4 (28% of triple positives), 24.5 (40%), 29.8 (26%) and 32.1 (6%) (**Fig.S2**). The higher percentage of Ct values in the lowest viral burden group for SGTF-positives over this time period (from 28-September-2020 through 10-January-2021) likely reflects the fact that B.1.1.7 comprised an increasing proportion of SGTF only from November onwards (**Fig.S1**).

At a population level, the percentage of individuals with SGTF vs triple positives in different regions/countries varied substantially over time (**Figure, Fig.S3**; showing national restrictions/stay at

home orders for the majority of each region with gray shading). Marked increases in SGTF positivity rates occurred in London, the South East and East of England from late-November despite rates of triple positives remaining stable, suggesting trends were not due to changing behaviour alone. In more northern English regions, increases in SGTF positivity started later, from mid-December, generally on a background of stable rates of triple positives. SGTF positivity increased even later in the South West, Yorkshire and The Humber, Wales, Northern Ireland, and Scotland, furthest from the South East. Importantly, increases in SGTF positivity were similar in those with and without self-reported symptoms (**Fig.S6**).

The relative dynamics of SGTF vs triple-positives varied over time (main **Figure**). Initial increases in growth rates for SGTF occurred at a median positivity rate of 0.21% (range 0.12-0.31%, **Fig.S5**, based on the positivity rate at which the 95% credible interval around the second derivative excluded zero). To assess whether B.1.1.7 was replacing or adding to existing strains, we compared growth rates of SGTF vs triple positives within the same region in the two most recent epochs defined by changes in trend in either SGTF/triple positives identified by ISR (**Figure, Fig.S5, Supplementary Table 3**). SGTF positivity rates increased more rapidly than triple-positive rates in most regions in most epochs (points to the right of the gray line in **Fig.S5**), but particularly strongly in the preceding epoch in London, the South East, the East of England and the West Midlands and in the most recent epoch in the North East, the North West and the South West (doubling times 10 days or less, **Supplementary Table 3**). Further, the rate of growth in SGTF-positives generally exceeded the decline in triple-positives (points above the black line), by an average of 6% (95% CI 4-7%) (**Fig.S5B**), supporting addition rather than replacement with B.1.1.7.

The relative difference in growth rates of SGTF vs triple positives had a similar distribution in those up to high-school age (i.e. $\leq 15/16$ years, 5% excess (95% CI 2-9%)) versus older (6% (4-7%)) (**Fig.S7**,

Supplementary Table 4), with no evidence that SGTF positivity rates were consistently growing faster or slower in those under and over high school age.

When modelling the proportion of SGTF positives among all positives that were either SGTF or triple-positive, SGTF growth rates were higher among those reporting symptoms than those not reporting symptoms (0.052 [95% CI 0.047–0.057] vs. 0.036 [0.033–0.039], **Supplementary Table 2**), potentially as a consequence of the somewhat higher viral load in B.1.1.7 (described above) and greater percentage reporting symptoms¹⁴. This pattern of larger differences in growth rates among those reporting symptoms persisted when restricting to positive tests with Ct<30 (0.094 [0.076–0.112] vs. 0.069 [0.061–0.077] respectively). The multiplicative increase in the reproduction number R_t and hence relative transmissibility can be estimated from these growth rate difference by assuming an equal mean generation time – the time between two subsequent infections - for the variants being compared.¹⁰ There is some uncertainty about the generation time with estimates from the literature varying between 3.6 and 5.5.¹⁰ Thus while restricting to symptomatic infections with a Ct<30 the relative increased transmissibility of SGTF is estimated to be 68% [$1 - e^{0.094 \times 5.5}$] for a generation time of 5.5, 53% for a generation time of 4.5 and 40% for a generation time of 3.6. These estimates are very similar to a recent study based on non-random symptomatic testing¹⁰; however, when also including positive tests with a Ct<30 but no reported symptoms, the relative transmissibility of SGTF is estimated to range between 49% for a generation time of 5.5 and 30% for a generation time of 3.6. It is important to note that these estimates of relative transmissibility of B.1.1.7. are somewhat uncertain and imprecise because we did not correct for the unknown sensitivity and specificity of the SGTF proxy for infections without reported symptoms and due to the uncertainty around the generation time of the B.1.1.7 variant.

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CONFLICTS OF INTEREST

DWE declares lecture fees from Gilead, outside the submitted work. No other author has a conflict of interest to declare.

DATA AVAILABILITY

De-identified study data are available for access by accredited researchers in the ONS Secure Research Service (SRS) for [accredited research purposes](#) under part 5, chapter 5 of the Digital Economy Act 2017. For further information about accreditation, contact Research.Support@ons.gov.uk or visit the [SRS website](#).

CONTRIBUTIONS

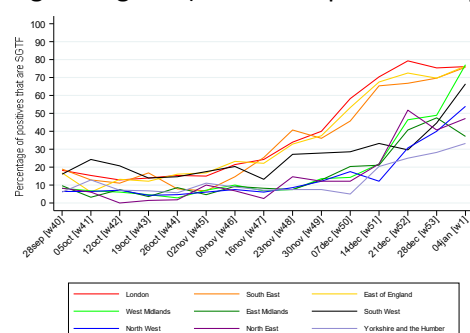
The study was designed and planned by ASW, JF, JB, JN, IB, ID and KBP, and is being conducted by ASW, IB, RS and ER. This specific analysis was designed by ASW, KDV, OG and KBP. ASW, KDV, OG, EP, JJ and KBP contributed to the statistical analysis of the survey data. ASW drafted the manuscript and all authors contributed to interpretation of the data and results and revised the manuscript. All authors approved the final version of the manuscript.

REFERENCES

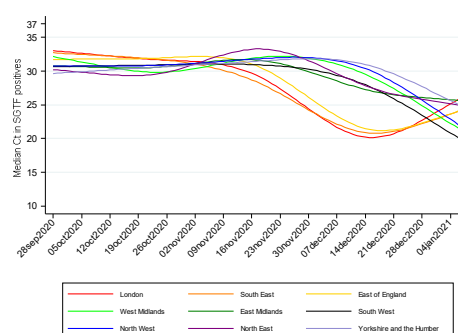
1. Walker AS, Pritchard E, House T, et al. Viral load in community SARS-CoV-2 cases varies widely and temporally MedRxiv 2020;<https://www.medrxiv.org/content/10.1101/2020.10.25.20219048v1>.
2. Schlackow I, Walker AS, Dingle K, et al. Surveillance of infection severity: a registry study of laboratory diagnosed *Clostridium difficile*. PLoS Med 2012;9:e1001279.
3. Vihta KD, Stoesser N, Llewelyn MJ, et al. Trends over time in *Escherichia coli* bloodstream infections, urinary tract infections, and antibiotic susceptibilities in Oxfordshire, UK, 1998-2016: a study of electronic health records. Lancet Infect Dis 2018;18:1138-49.
4. Hay JA, Kennedy-Shaffer L, Kanjilal S, et al. Estimating epidemiologic dynamics from cross-sectional viral load distributions. Science 2021.
5. Gelman A, Lax J, Phillips J, Gabry J, Trangucci R. Using multilevel regression and poststratification to estimate dynamic public opinion ([http://www.stat.columbia.edu/~gelman/research/unpublished/MRT\(1\).pdf](http://www.stat.columbia.edu/~gelman/research/unpublished/MRT(1).pdf); accessed 12 November 2020)2018.
6. Gelman A, Little TC. Poststratification into Many Categories Using Hierarchical Logistic Regression. Survey Methodology 1997;23:127-35.
7. Downes M, Carlin JB. Multilevel regression and poststratification as a modeling approach for estimating population quantities in large population health studies: a simulation study. Biom J 2020;62:479-91.
8. Wood SN. Thin plate regression splines. J R Stat Soc Series B 2003;65:95–114.
9. Pouwels KB, House T, Pritchard E, et al. Community prevalence of SARS-CoV-2 in England from April to November, 2020: results from the ONS Coronavirus Infection Survey. Lancet Public Health 2020;6:E30-8.
10. McCullagh P. Regression models for ordinal data. Journal of the Royal Statistical Society B 1980;42:109-42.
11. Davies NG, Abbott S, Barnard RC, et al. Estimated transmissibility and impact of SARS-CoV-2 lineage B.1.1.7 in England. Science 2021.
12. Public Health England. Investigation of novel SARS-CoV-2 variant: Variant of Concern 202012/01; Technical briefing 2 (https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/948152/Technical_Briefing_VOC202012-2_Briefing_2_FINAL.pdf) 2020.
13. Hay JA, Kennedy-Shaffer L, Kanjilal S, Lipsitch M, Mina MJ. Estimating epidemiologic dynamics from single crosssectional viral load distributions MedRxiv 2020;<https://doi.org/10.1101/2020.10.08.20204222>.
14. Coronavirus (COVID-19) Infection Survey: characteristics of people testing positive for COVID-19 in England, 27 January 2021 (<https://www.ons.gov.uk/peoplepopulationandcommunity/healthandsocialcare/conditionsanddiseases/articles/coronaviruscovid19infectionsinthecommunityinengland/characteristicsofpeopletestingpositiveforcovid19inengland27january2021>). 2021.

Fig.S1 Percentage of positives and Ct values over time for SGTF and triple positives, by English region and country

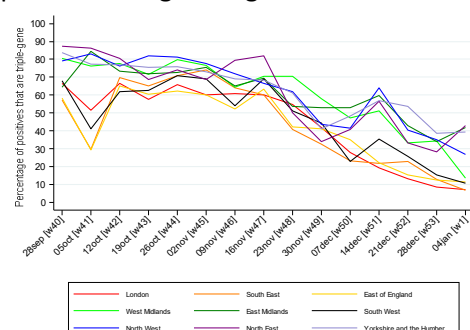
A Percentage of positives that were SGTF in English regions (ORF1ab+N positive only)



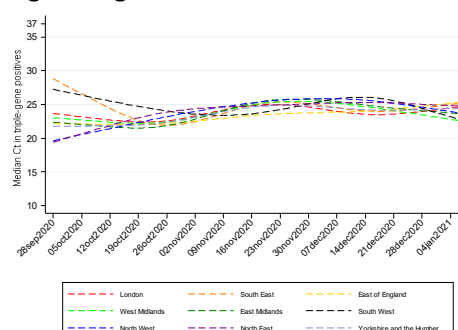
B Median Ct values in SGTF in English regions *



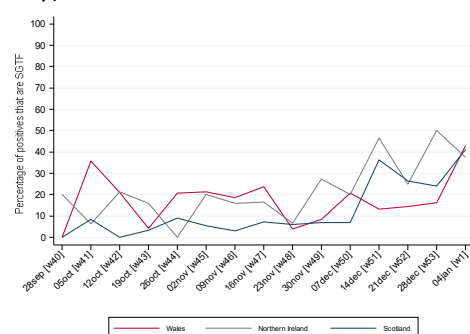
C Percentage of positives that were triple-gene positive in English regions



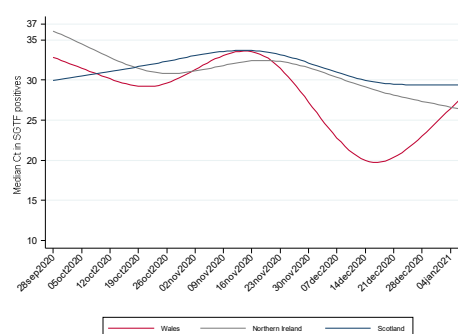
D Median Ct values in triple-gene positives in English regions



E Percentage of positives that were SGTF in Devolved Administrations (ORF1ab+N positive only)



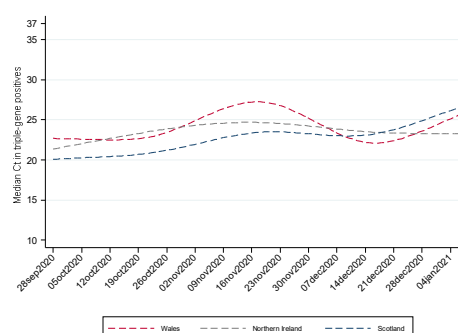
F Median Ct values in SGTF in Devolved Administrations



G Percentage of positives that were triple-gene positive in Devolved Administrations

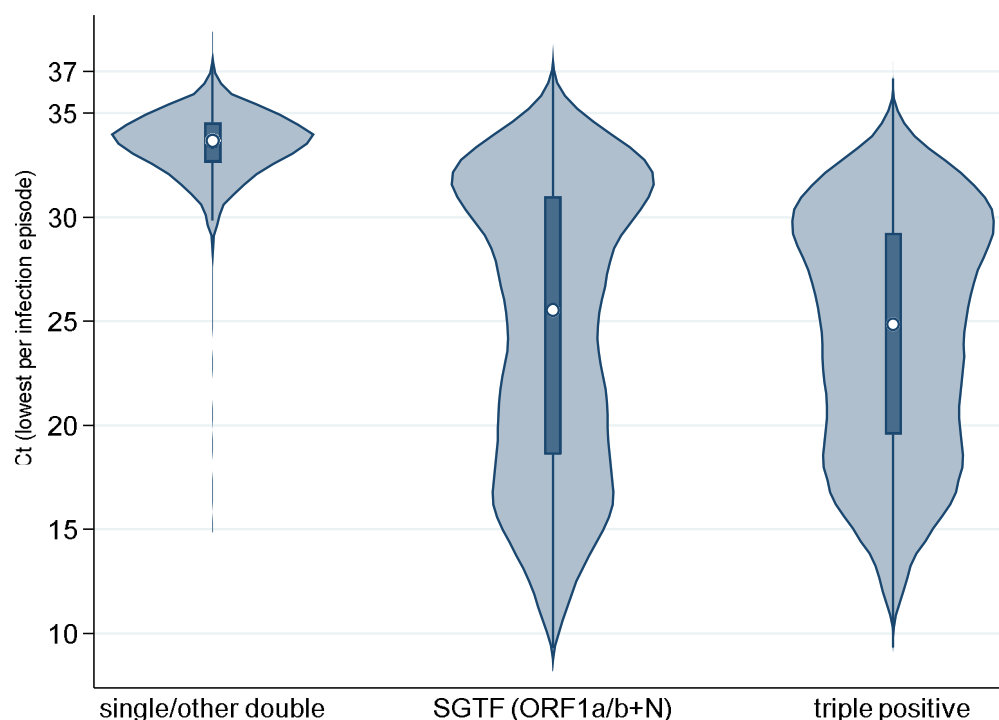


H Median Ct values in triple-gene positives in Devolved Administrations



* whole genome sequencing of community symptomatic testing samples in England showed that 3% samples with H69del/V70del were B.1.1.7 mid-October (N=116), rising to 64% at the start of November (N=398), 88% mid-November (N=602) and 98% at the start of December (N=2,007)¹².
Note: Ct 30 ~150 copies/ml, 25 ~5500 copies/ml, 20 ~230,000 copies/ml based on linearity curves (in ¹ Fig.S1)

Fig.S2 Distribution of cycle threshold (Ct) values in SGTF (ORF1ab+N positive, compatible with B.1.1.7), triple positive and other positives 28-September-2020 through 10-January-2021



Note: for each group, the dot shows the median, the box the 25-75th percentiles and the shaded area the distribution of the data. Finite mixture modelling was used to decompose the overall non-normally distributed Ct values separately for SGTF and triple positive into four separate sub-populations which were normally distributed. Four sub-populations were chosen because this minimised the Bayesian information criterion for SGTF and ensured comparability.

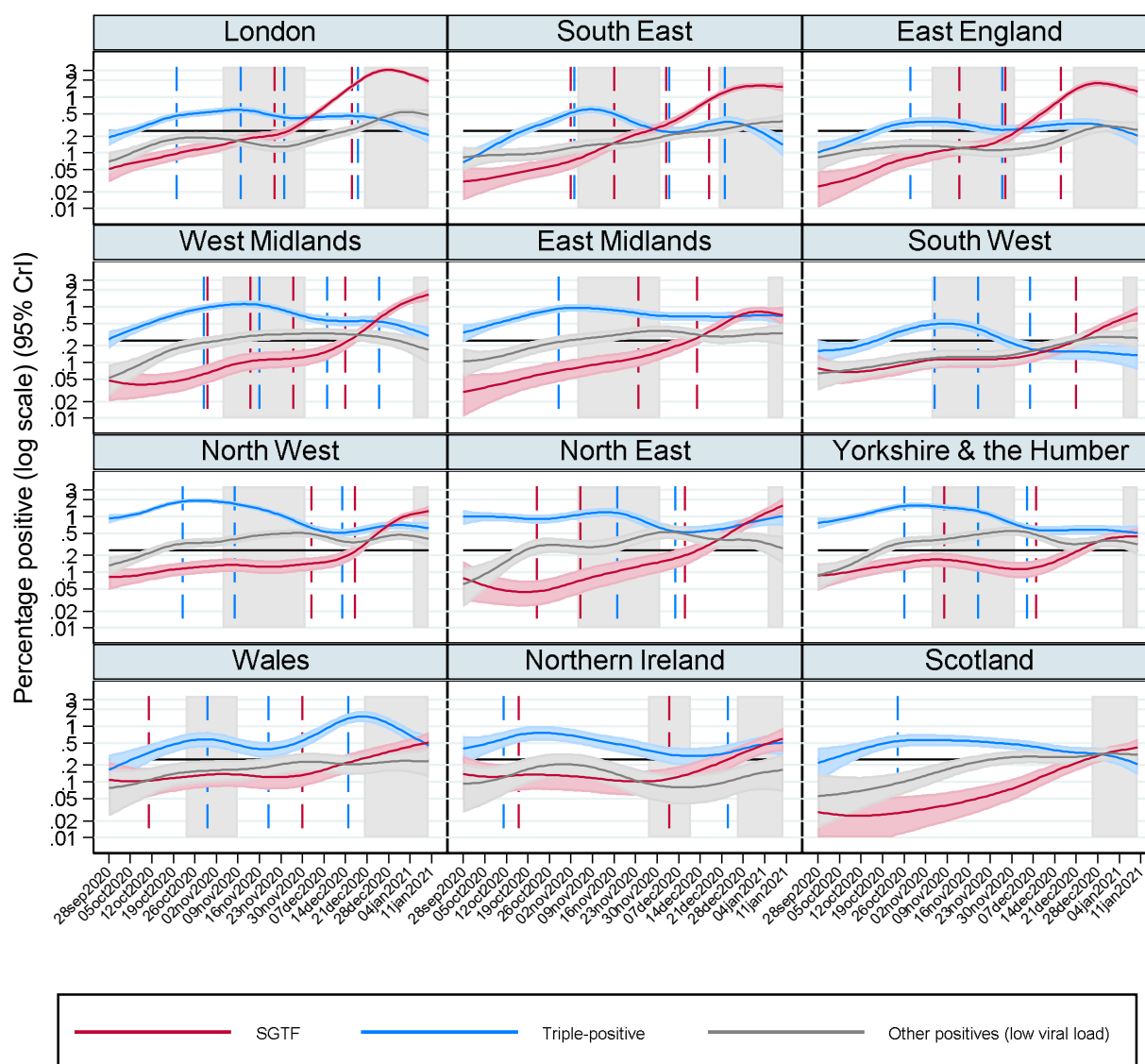
Fitted sub-population*	SGTF (ORF1a/b+N)		Triple-positive	
	Percentage in sub-population	Mean Ct (95% CI)	Percentage in sub-population	Mean Ct (95% CI)
Highest viral burden	29%	16.1 (15.1-17.1)	28%	17.4 (16.9-18.0)
Next highest viral burden	17%	21.6 (20.8-22.3)	40%	24.5 (23.5-25.4)
Moderate viral burden	25%	27.7 (26.7-28.7)	26%	29.8 (29.1-30.4)
Lowest viral burden	29%**	32.2 (32.0-32.4)	6%*	32.1 (31.6-32.7)

* four sub-populations fitted separately to each group of positives, to decompose the distributions shown in the Figure above into the same number of underlying sub-populations for comparison.

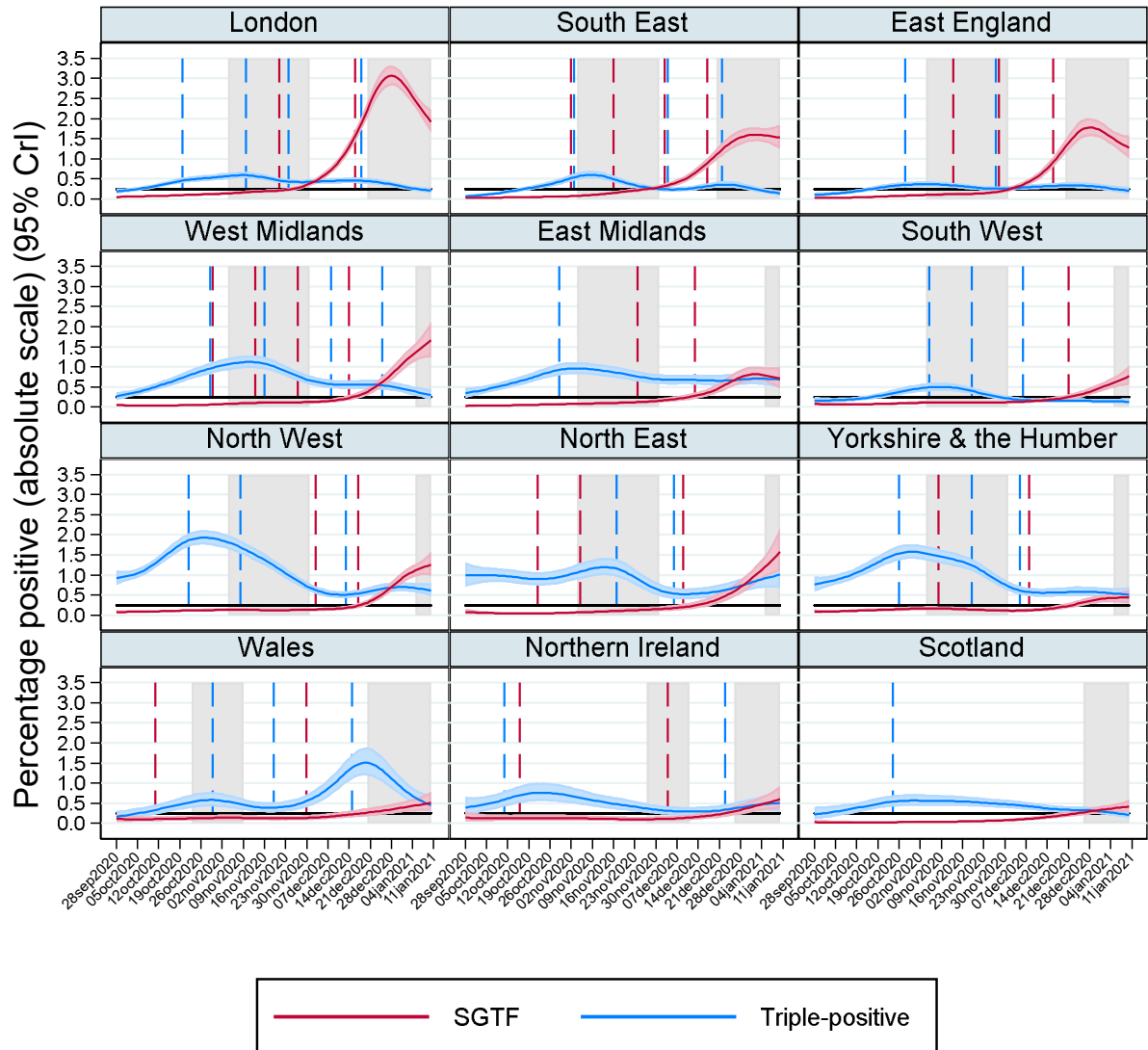
** higher percentage of Ct values in the lowest viral burden group for SGTF from 28-September-2020 through 10-January-2021 reflects the fact that B.1.1.7 comprised an increasing proportion of SGTF from November onwards, see **Supplementary Figure 1**.

Fig.S3 Percentage of the population positive with SGTF (ORF1ab+N positive, compatible with B.1.1.7), triple positive and other positives

(A) log scale

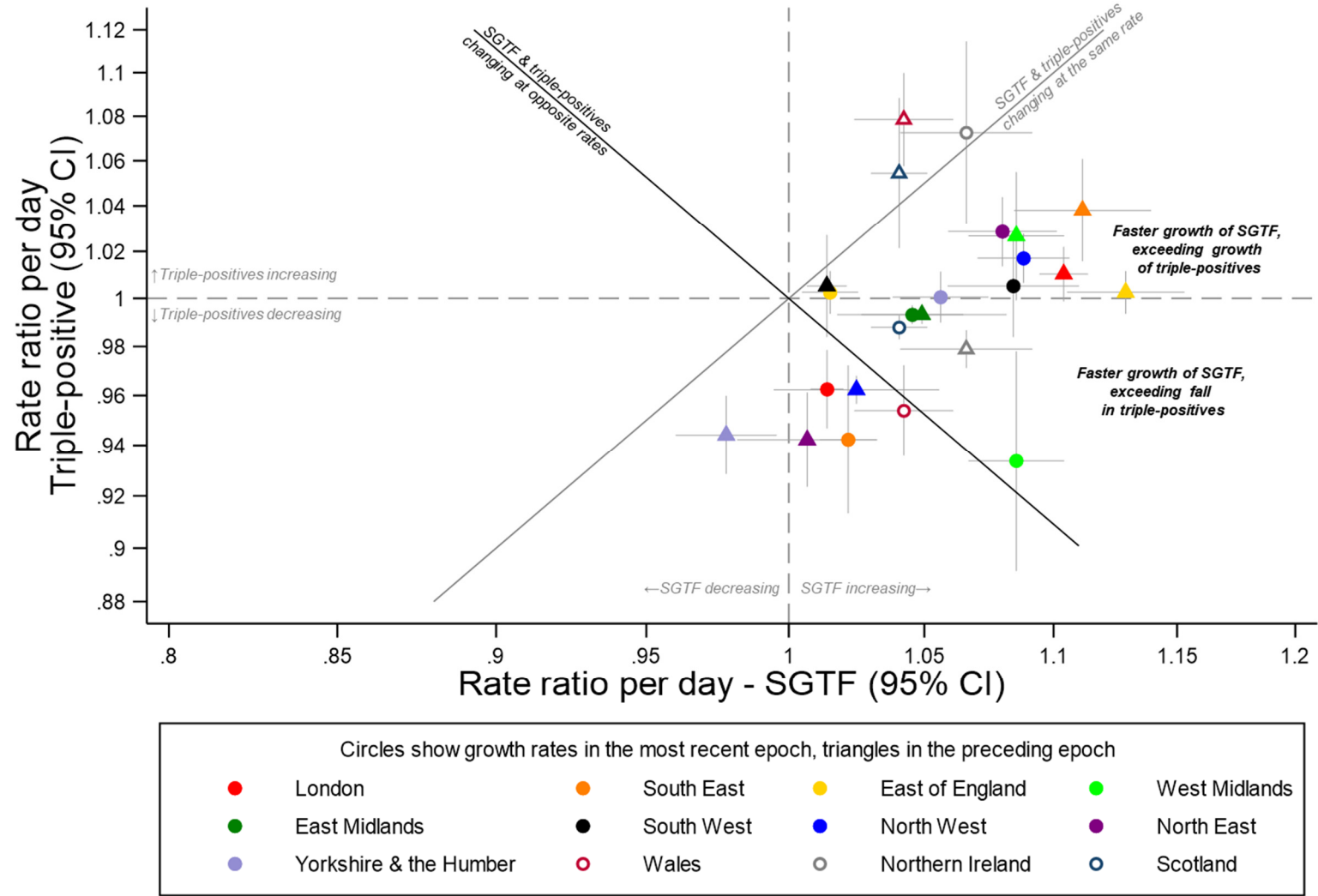


(B) absolute scale for SGTF and triple positive

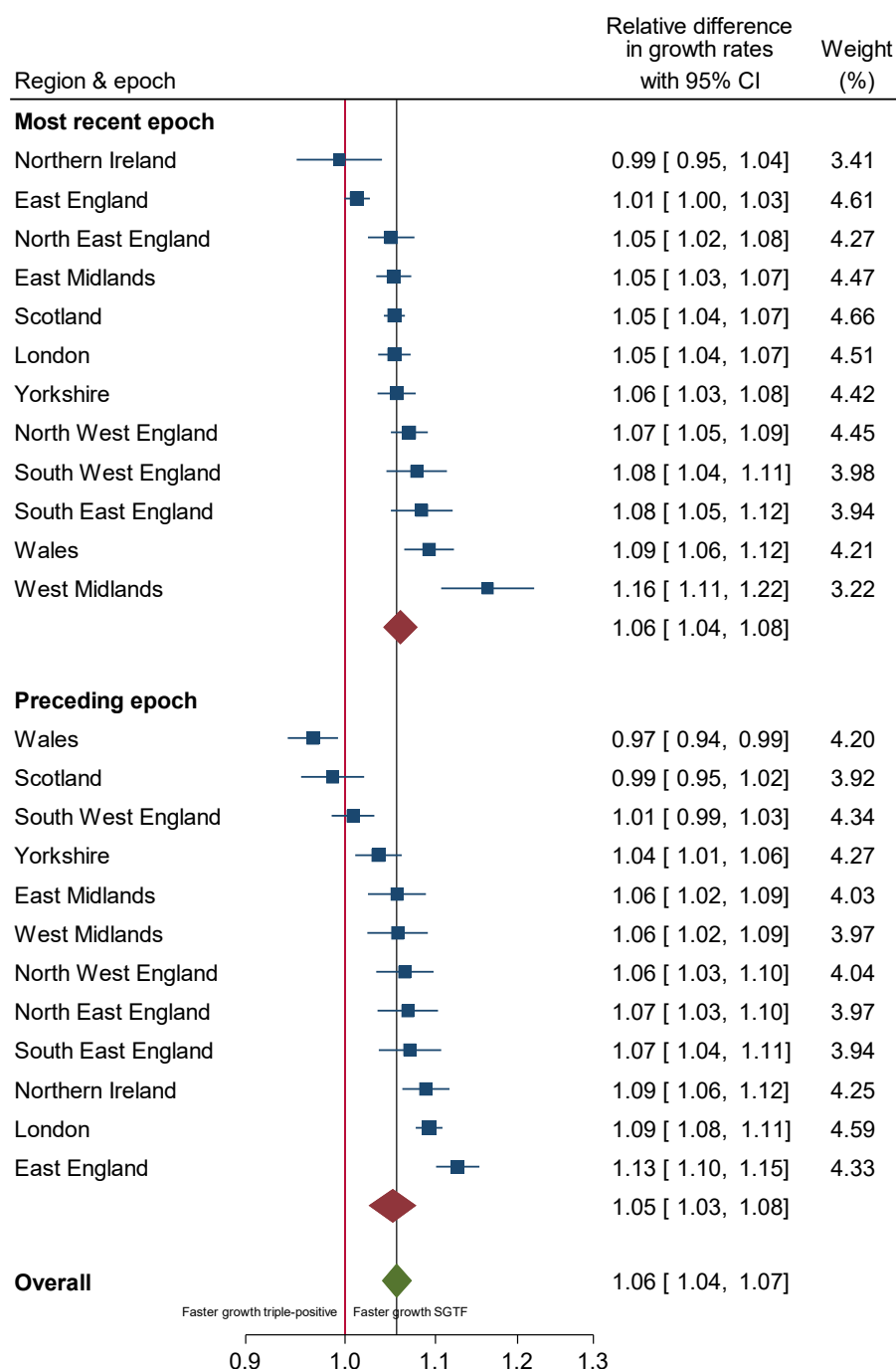


Note: truncating lower 95% CrI at 0.01. Gray shading shows national restrictions/stay at home orders for the majority of the region. Black horizontal line at 0.25%. Dashed lines show changes in trend from ISR algorithm fitted from 1 September (no dashed line means no change in trend with $p < 0.01$ (triple) or $p < 0.05$ (SGTF) detected). See main **Figure** for probabilities on the log scale for SGTF and triple-positive cases.

Fig.S4 Growth rates of SGTF and triple-positives in two most recent epochs defined by ISR
(A) growth rates

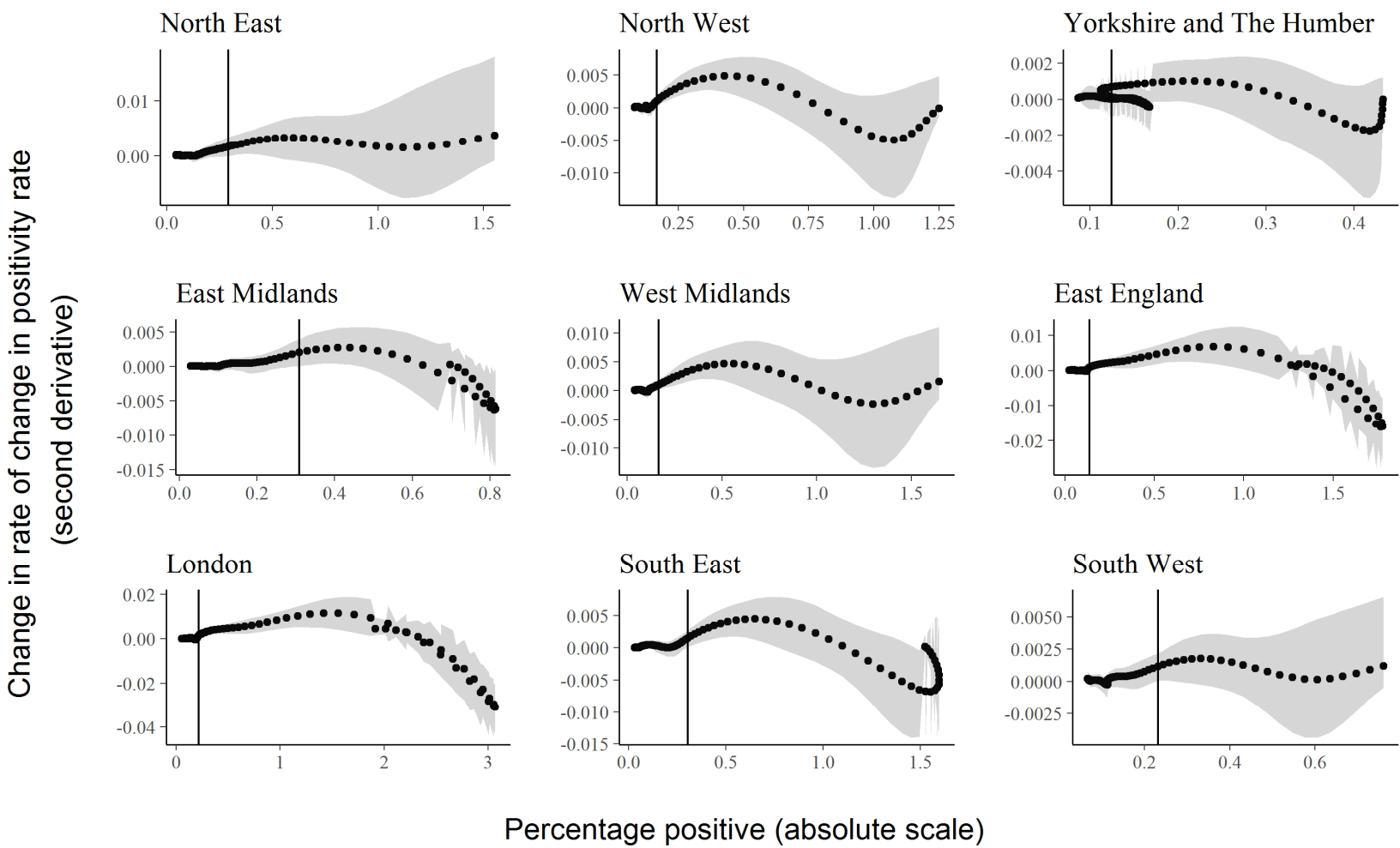


(B) Difference in growth rates (SGTF minus triple-positives)



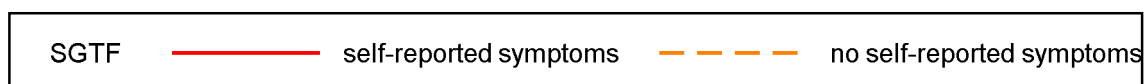
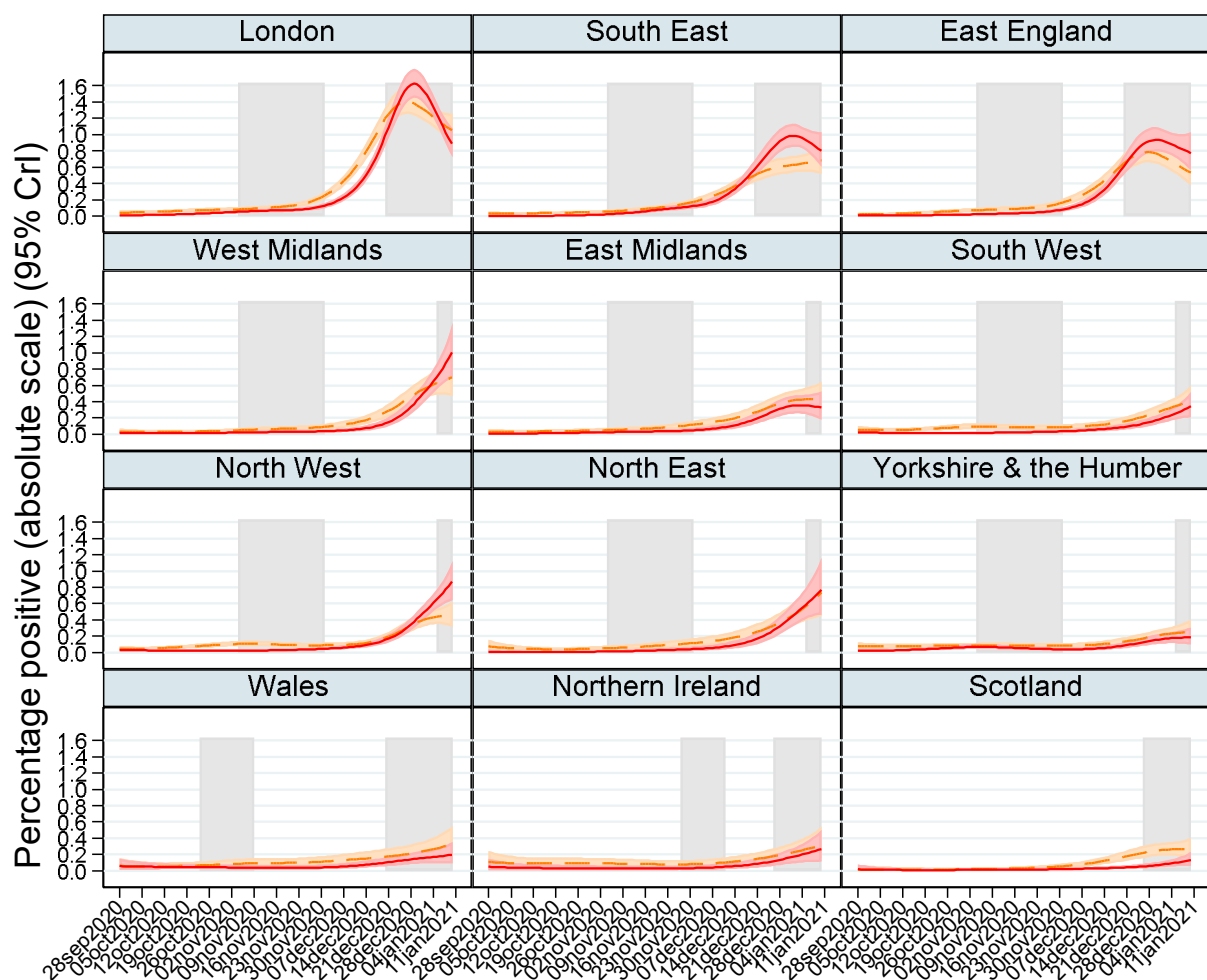
Note: panel (A) shows growth rates (rate ratio (RR) per day) of SGTF (x-axis) and triple (y-axis) positives within the same region in epochs defined by changepoints (change in trend) identified by ISR and shown in main **Figure** and **Supplementary Table 3**. 95% CI are truncated at 0.8 and 1.2. $RR > 1$ mean positivity rates are increasing, < 1 that they are decreasing. Points to the right of the gray diagonal line are periods of time where, within one region, SGTF positives are increasing faster than triple positives; and points on/around the gray line where SGTF and non-positives are changing at similar rates within a region. The black diagonal line indicates opposite growth rates, that is SGTF are increasing at the same rate triple-positives are decreasing or vice versa within a region, consistent with replacement. Points above the black line are consistent with addition. Panel B shows difference between growth rates in SGTF and triple-positives from panel A, combined using random effects meta-analysis.

Fig.S5 Rate of change in growth by absolute percentage positive in SGTF-positives



Note: showing the second derivative of the positivity rate estimated in main **Figure** by the estimated positivity rate. Shaded areas represent 95% credible intervals. The vertical line represents the lowest prevalence at which the lower limit of the credible interval for the second derivative is above zero. Higher values mean growth is accelerating faster, so values above zero provide some indication of when SGTF was increasing fastest.

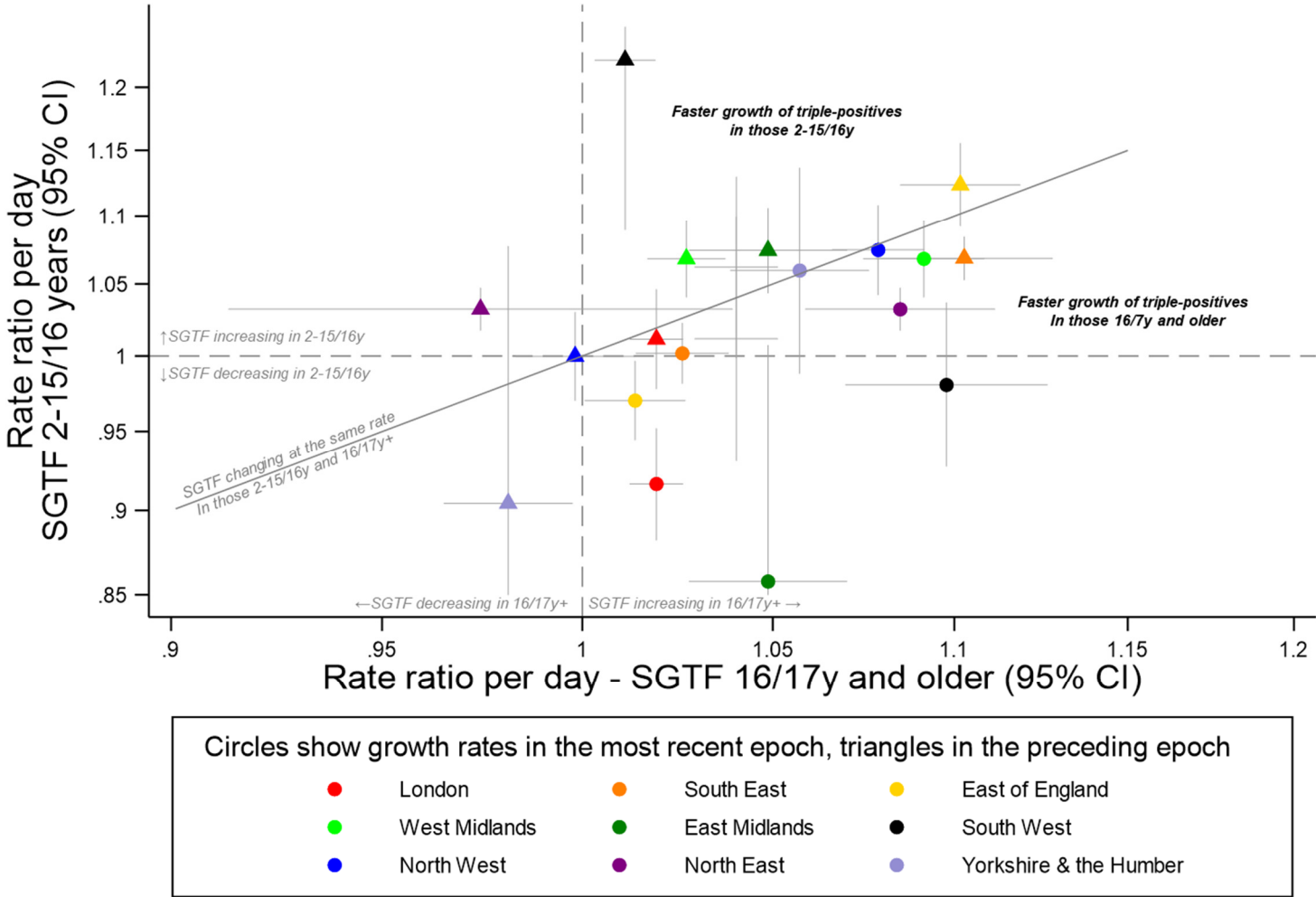
Fig.S6 Percentage of the population positive with SGTF (ORF1ab+N positive, compatible with B.1.1.7) according to self-reported symptoms at the test



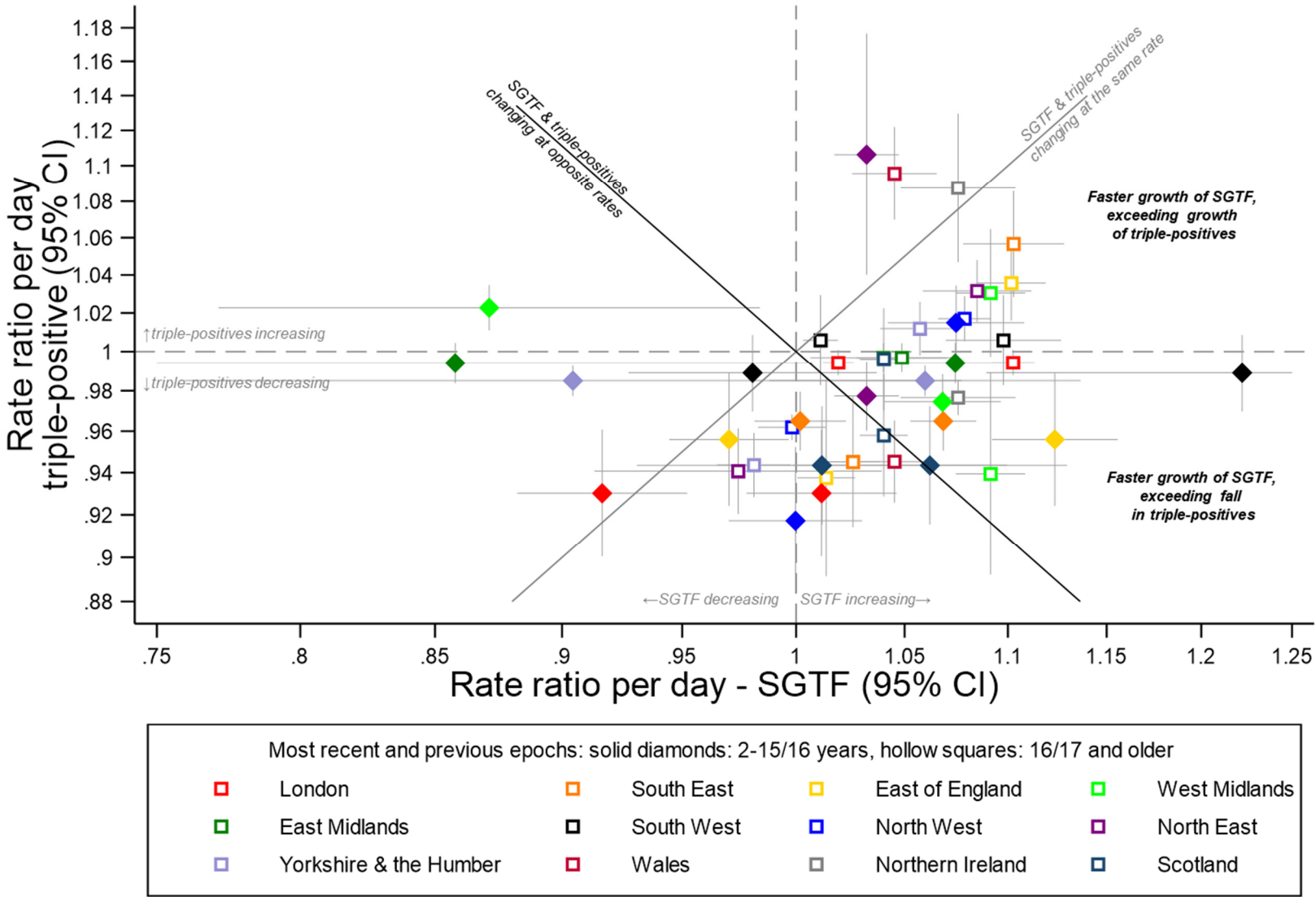
Note: gray shading shows national restrictions/stay at home for the majority of the region.

Fig.S7 Impact of age on SGTF growth rates (A), comparison between SGTF and with triple-positive growth rates by age (B) and differences in growth rates in those aged up to high school (C) and older (D)

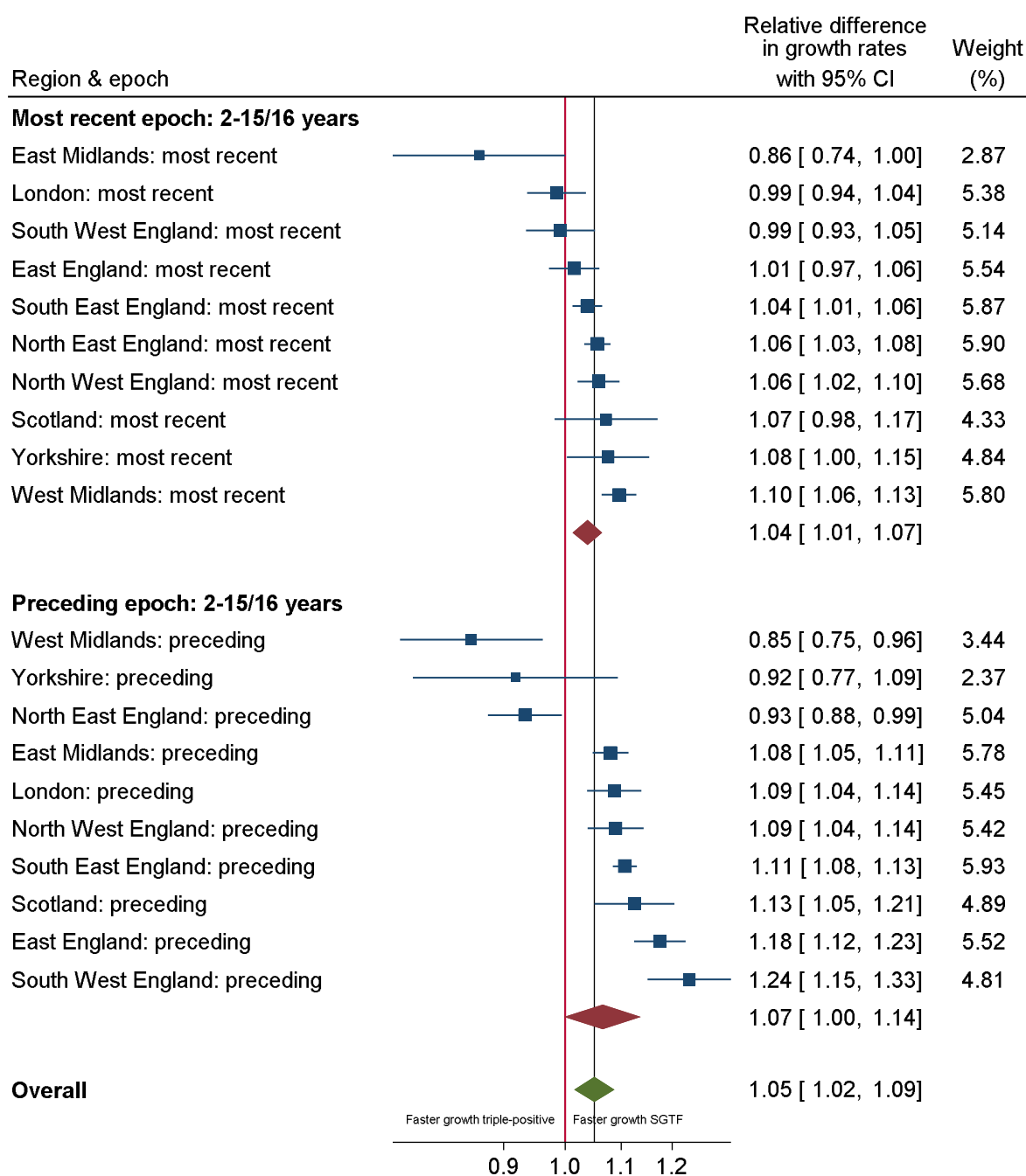
(A) SGTF growth rates in those up to high school age versus older in the two most recent epochs



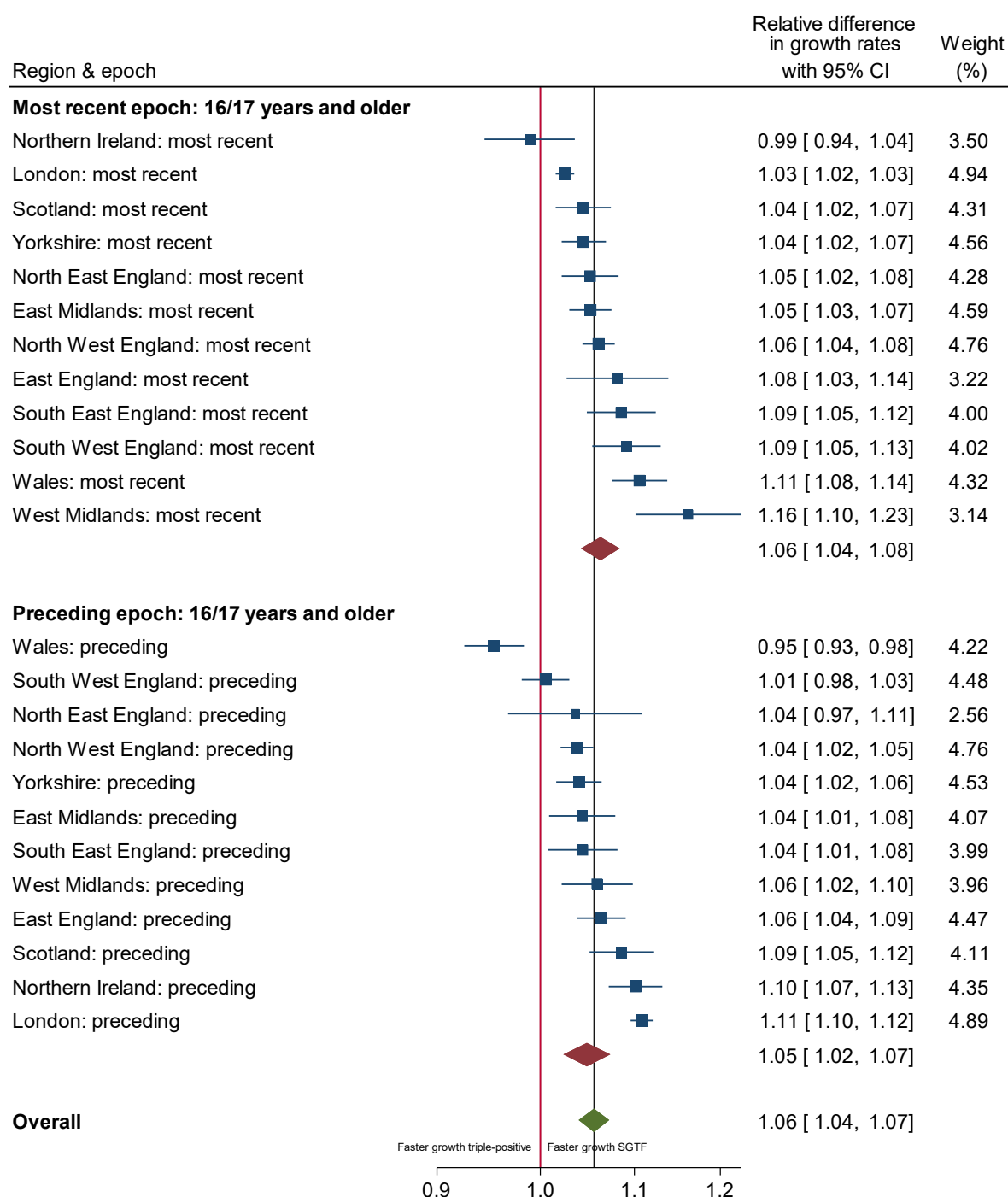
(B) Growth rate in SGTF vs triple in those aged up to high school age and older



(C) Difference in growth rates SGTF vs triple-positive in those aged up to high school age



(D) Difference in growth rates SGTF vs triple-positive in those aged over high school age



Note: panel (A) shows SGTF growth rates in younger vs older individuals. Panel (B) shows growth rates (rate ratio (RR) per day) of SGTF (x-axis) and triple (y-axis) positives within the same region in epochs defined by changepoints (change in trend) identified by ISR and shown in **Supplementary Table 4**. 95% CI are truncated at 0.75 and 1.2. $RR > 1$ mean positivity rates are increasing, < 1 that they are decreasing. Points to the right of the gray diagonal line are periods of time where, within one region, SGTF positives are increasing faster than triple positives; and points on/around the gray line where SGTF and non-positives are changing at similar rates within a region. The black diagonal line indicates opposite growth rates, that is SGTF are increasing at the same rate triple are decreasing or vice versa within a region, consistent with replacement. Points above the black line are consistent with addition. Panels C and D show difference between growth rates in SGTF and triple from panel B, combined using random effects meta-analysis.

Supplementary Table 1 Characteristics of included participants

Characteristic	Total, n (%) or median (IQR) (N=381,773 visits)
Age (years)	50 (31, 65)
Female	200,951 (53%)
Ethnicity	
White	352,757 (92%)
Asian	14,939 (4%)
Black	3,505 (1%)
Mixed	6,705 (2%)
Other	3,715 (1%)
Missing	152 (0%)
Household size	
1	62,318 (16%)
2	162,410 (43%)
3	61,182 (16%)
4	66,248 (17%)
5+	29,615 (8%)
Deprivation decile (1 = most deprived, 10 = least deprived)	5 (3, 8)
Region	
London	70,496 (18%)
North West England	46,410 (12%)
North East England	14,660 (4%)
Yorkshire	31,738 (8%)
West Midlands	28,969 (8%)
East Midlands	24,302 (6%)
South East England	49,414 (13%)
South West England	31,011 (8%)
East England	40,706 (11%)
Northern Ireland	9,263 (2%)
Scotland	21,718 (6%)
Wales	13,086 (3%)
Study visits per participant	4 (3,6)

Supplementary Table 2 Estimates of additive increase in growth rates for SGTF compared to three-gene positives in positives only

Positives	Difference in Malthusian growth rate SGTF vs. triple-positives
Any	0.041 (0.038 – 0.043)
Reporting symptoms	0.052 (0.047 – 0.057)
Not reporting symptoms	0.036 (0.033 – 0.039)
<17 years of age	0.043 (0.038 – 0.048)
17+ years of age	0.040 (0.037 – 0.042)
Any & Ct<30	0.072 (0.069 – 0.076)
Reporting symptoms & Ct<30	0.094 (0.076 – 0.112)
Not reporting symptoms & Ct<30	0.069 (0.061 – 0.077)
<17 years & Ct<30	0.076 (0.067 – 0.086)
17+ years & Ct<30	0.069 (0.064 – 0.075)

Supplementary Table 3 Changepoints, growth rates and current predicted positivity rates from ISR models for SGTF (A) and triple positives (B)

(A) SGTF positive		Most recent epoch											Previous epoch										
Region	Most recent change point	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI	Current positivity (%) [THIS MODEL]	lower SE	upper SE	Previous change point	lower 95% bound	upper 95% bound	Previous rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI		
North East England	09/12/2020	02/12/2020	13/12/2020	1.080	1.059	1.101	9	7	12	1.20	1.05	1.35	05/11/2020	05/11/2020	05/11/2020	1.007	0.982	1.032	105	22	-37		
North West England	17/12/2020	17/12/2020	17/12/2020	1.088	1.070	1.106	8	7	10	1.11	1.03	1.19	03/12/2020	11/10/2020	03/12/2020	1.025	0.995	1.056	28	13	-130		
Yorkshire and the Humber	08/12/2020	01/12/2020	08/12/2020	1.056	1.038	1.074	13	10	19	0.44	0.38	0.50	08/11/2020	11/10/2020	18/11/2020	0.978	0.960	0.996	-31	-156	-17		
East Midlands	13/12/2020	10/12/2020	13/12/2020	1.045	1.027	1.065	16	11	26	0.80	0.70	0.89	24/11/2020	17/11/2020	24/11/2020	1.049	1.018	1.081	14	9	40		
West Midlands	14/12/2020	11/12/2020	14/12/2020	1.085	1.067	1.104	8	7	11	1.34	1.23	1.46	27/11/2020	27/11/2020	08/12/2020	1.057	1.014	1.103	12	7	50		
East England	16/12/2020	11/12/2020	16/12/2020	1.015	1.005	1.025	47	28	144	1.49	1.40	1.59	27/11/2020	27/11/2020	27/11/2020	1.129	1.105	1.153	6	5	7		
London	16/12/2020	11/12/2020	16/12/2020	1.014	1.008	1.020	50	35	88	2.40	2.31	2.49	21/11/2020	15/11/2020	21/11/2020	1.104	1.095	1.114	7	6	8		
South East England	17/12/2020	17/12/2020	17/12/2020	1.022	1.011	1.032	32	22	62	1.51	1.42	1.59	03/12/2020	30/11/2020	03/12/2020	1.112	1.085	1.139	7	5	9		
South West England	21/12/2020	03/12/2020	21/12/2020	1.084	1.059	1.110	9	7	12	0.61	0.54	0.68	*	*	*	1.014	1.007	1.021	51	33	105		
Wales	30/11/2020	20/11/2020	30/11/2020	1.042	1.024	1.061	17	12	29	0.47	0.39	0.56	11/10/2020	11/10/2020	11/10/2020	0.990	0.973	1.008	-73	83	-25		
Northern Ireland	04/12/2020	22/11/2020	04/12/2020	1.066	1.041	1.092	11	8	17	0.54	0.44	0.65	16/10/2020	14/10/2020	16/10/2020	0.975	0.954	0.995	-27	-150	-15		
Scotland	*	*	*	1.041	1.030	1.051	17	14	23	0.35	0.31	0.39											

(B) Triple gene positive		Most recent epoch											Previous epoch										
Region	Most recent change point	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI	Current positivity (%) [THIS MODEL]	lower SE	upper SE	Previous change point	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI		
North East England	06/12/2020	01/12/2020	06/12/2020	1.029	1.014	1.044	25	16	51	0.88	0.76	0.99	17/11/2020	11/11/2020	17/11/2020	0.942	0.924	0.961	-12	-17	-9		
North West England	13/12/2020	05/12/2020	13/12/2020	1.017	1.007	1.028	41	25	105	0.65	0.59	0.70	08/11/2020	05/11/2020	16/11/2020	0.962	0.957	0.968	-18	-21	-16		
Yorkshire and the Humber	05/12/2020	03/12/2020	08/12/2020	1.001	0.990	1.011	1213	62	-69	0.51	0.45	0.56	19/11/2020	09/11/2020	19/11/2020	0.944	0.929	0.960	-12	-17	-9		
East Midlands	29/10/2020	11/10/2020	29/10/2020	0.993	0.989	0.997	-102	-232	-65	0.55	0.50	0.60	*	*	*	1.035	1.024	1.046	20	15	30		
West Midlands	25/12/2020	22/12/2020	25/12/2020	0.934	0.891	0.978	-10	-31	-6	0.28	0.23	0.34	08/12/2020	30/11/2020	14/12/2020	1.027	0.999	1.055	26	13	-1023		
East England	27/11/2020	11/11/2020	13/12/2020	1.003	0.994	1.012	273	61	-109	0.27	0.24	0.31	28/10/2020	12/10/2020	28/10/2020	0.987	0.977	0.998	-53	-287	-29		
London	18/12/2020	08/12/2020	23/12/2020	0.963	0.947	0.978	-18	-32	-13	0.22	0.20	0.25	24/11/2020	24/11/2020	03/12/2020	1.010	0.999	1.022	68	32	-610		
South East England	22/12/2020	18/12/2020	22/12/2020	0.942	0.913	0.972	-12	-25	-8	0.16	0.13	0.19	04/12/2020	25/11/2020	04/12/2020	1.038	1.016	1.061	19	12	44		
South West England	06/12/2020	03/12/2020	06/12/2020	1.005	0.984	1.027	132	26	-43	0.14	0.11	0.17	19/11/2020	19/11/2020	25/11/2020	0.926	0.897	0.957	-9	-16	-6		
Wales	15/12/2020	06/12/2020	15/12/2020	0.954	0.936	0.972	-15	-25	-10	0.57	0.48	0.66	19/11/2020	13/11/2020	22/11/2020	1.078	1.058	1.100	9	7	12		
Northern Ireland	23/12/2020	30/11/2020	23/12/2020	1.073	1.032	1.114	10	6	22	0.55	0.45	0.66	11/10/2020	11/10/2020	15/10/2020	0.979	0.971	0.987	-33	-51	-24		
Scotland	24/10/2020	11/10/2020	02/12/2020	0.988	0.983	0.993	-57	-95	-41	0.27	0.24	0.29	*	*	*	1.054	1.022	1.088	13	8	32		

Note: doubling time = -ln(2)/ln(RR). Doubling times under 10 days shown in yellow.
* indicate no evidence for changepoint since 1 September

Supplementary Table 4 Changepoints, growth rates and current predicted positivity rates from ISR models for SGTF (A, C) and triple positives (B, D) for those aged 2 to school year 11 (15/16 years) (A, B) and school year 12 (16/17 years) and older

[A] SGTF: 2 to 15/16 years				Most recent epoch										Previous epoch									
Region	Most recent changepoint	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI	Current positivity (%) [THIS MODEL]	lower SE	upper SE	Previous changepoint	lower 95% bound	upper 95% bound	Previous rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI		
North East England		*	*	1.032	1.017	1.047	22	15	40	1.27	0.92	1.62	*	*	*	1.000	0.970	1.030	-2417	23	-23		
North West England	09/12/2020	07/12/2020	09/12/2020	1.075	1.042	1.108	10	7	17	1.06	0.85	1.28	*	*	*	1.000	0.970	1.030	-2417	23	-23		
Yorkshire and the Humber	10/12/2020	10/12/2020	12/12/2020	1.060	0.988	1.136	12	5	-58	0.35	0.19	0.50	30/11/2020	13/11/2020	02/12/2020	0.904	0.759	1.077	-7	9	-3		
East Midlands	30/12/2020	27/12/2020	30/12/2020	0.858	0.730	1.007	-5	96	-2	0.53	0.27	0.78	*	*	*	1.074	1.044	1.106	10	7	16		
West Midlands	24/11/2020	21/11/2020	03/12/2020	1.068	1.041	1.096	11	8	17	1.50	1.17	1.83	11/11/2020	11/11/2020	11/11/2020	0.871	0.771	0.984	-5	-42	-8		
East England	19/12/2020	25/11/2020	19/12/2020	0.970	0.945	0.997	-23	-202	-12	1.56	1.29	1.82	15/11/2020	15/10/2020	06/12/2020	1.123	1.092	1.156	6	5	8		
London	28/12/2020	27/12/2020	28/12/2020	0.916	0.882	0.952	-8	-14	-6	2.17	1.92	2.42	17/12/2020	08/12/2020	17/12/2020	1.011	0.978	1.046	61	15	10		
South East England	17/12/2020	11/12/2020	21/12/2020	1.002	0.982	1.023	378	31	-37	1.83	1.58	2.09	*	*	*	1.068	1.053	1.084	10	9	13		
South West England	17/12/2020	11/12/2020	20/12/2020	0.981	0.927	1.037	-35	19	-9	0.52	0.33	0.70	01/12/2020	14/11/2020	06/12/2020	1.222	1.089	1.371	3	2	8		
Wales (not fitted due to small numbers)																							
Northern Ireland (not fitted due to small numbers)																							
Scotland	20/12/2020	22/11/2020	20/12/2020	1.012	0.931	1.099	60	7	-10	0.42	0.23	0.61	*	*	*	1.062	0.999	1.130	12	6	-468		
[B] triple gene positive: 2 to 15/16 years				Most recent epoch										Previous epoch									
Region	Most recent changepoint	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI	Current positivity (%) [THIS MODEL]	lower SE	upper SE	Previous changepoint	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI		
North East England	11/11/2020	09/11/2020	17/11/2020	0.977	0.960	0.995	-30	-128	-17	0.51	0.33	0.70	26/10/2020	12/10/2020	29/10/2020	1.106	1.040	1.174	7	4	95		
North West England	03/12/2020	03/12/2020	08/12/2020	1.015	0.996	1.034	47	21	-167	0.98	0.79	1.17	19/11/2020	13/11/2020	19/11/2020	0.917	0.884	0.952	-8	-14	-6		
Yorkshire and the Humber	29/10/2020	22/10/2020	29/10/2020	0.985	0.977	0.993	-46	-92	-30	0.67	0.54	0.80	*	*	*	1.035	1.016	1.055	20	13	44		
East Midlands	03/11/2020	11/10/2020	10/11/2020	0.994	0.984	1.004	-117	160	-43	0.82	0.64	1.01	*	*	*	1.051	1.023	1.081	14	9	31		
West Midlands	19/11/2020	15/10/2020	20/11/2020	0.974	0.961	0.988	-27	-58	-17	0.47	0.35	0.60	*	*	*	1.023	1.011	1.034	31	20	63		
East England	09/12/2020	11/10/2020	15/12/2020	0.956	0.924	0.989	-15	-60	-9	0.20	0.12	0.28	*	*	*	1.030	1.017	1.044	23	16	42		
London	15/12/2020	11/10/2020	15/12/2020	0.930	0.901	0.961	-10	-17	-7	0.20	0.14	0.27	*	*	*	1.012	1.005	1.018	60	39	129		
South East England	10/11/2020	16/10/2020	10/11/2020	0.965	0.951	0.979	-19	-33	-14	0.12	0.08	0.16	*	*	*	1.054	1.032	1.077	13	9	22		
South West England	*	*	*	0.989	0.970	1.008	-62	82	-23	0.15	0.08	0.22	*	*	*								
Wales	*	*	*	1.011	0.999	1.022	66	32	-1091	1.32	0.94	1.71	*	*	*								
Northern Ireland	*	*	*	0.990	0.977	1.002	-67	286	-30	0.35	0.21	0.50	*	*	*								
Scotland	07/11/2020	11/10/2020	14/11/2020	0.943	0.916	0.972	-12	-25	-8	0.04	0.01	0.08	*	*	*	1.045	0.999	1.093	16	8	-477		
[C] SGTF: 16/17 years and older				Most recent epoch										Previous epoch									
Region	Most recent changepoint	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI	Current positivity (%) [THIS MODEL]	lower SE	upper SE	Previous changepoint	lower 95% bound	upper 95% bound	Previous rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI		
North East England	10/12/2020	10/12/2020	13/12/2020	1.081	1.059	1.111	9	7	12	1.13	0.98	1.28	26/11/2020	05/11/2020	26/11/2020	0.974	0.913	1.039	-27	18	-8		
North West England	08/12/2020	22/11/2020	08/12/2020	1.079	1.066	1.092	9	8	11	1.09	1.01	1.17	08/11/2020	14/10/2020	10/11/2020	0.998	0.985	1.013	-376	52	-41		
Yorkshire and the Humber	08/12/2020	28/11/2020	08/12/2020	1.057	1.039	1.076	12	9	18	0.45	0.39	0.52	03/11/2020	11/10/2020	05/11/2020	0.981	0.965	0.997	-37	-274	-20		
East Midlands	13/12/2020	11/12/2020	13/12/2020	1.049	1.028	1.070	15	10	25	0.76	0.67	0.86	24/11/2020	19/11/2020	24/11/2020	1.040	1.007	1.075	18	10	107		
West Midlands	13/12/2020	07/12/2020	13/12/2020	1.091	1.075	1.108	8	7	10	1.34	1.21	1.46	*	*	*	1.027	1.017	1.037	26	19	41		
East England	19/12/2020	14/12/2020	19/12/2020	1.014	1.001	1.027	51	26	1067	1.42	1.32	1.52	23/11/2020	21/11/2020	23/11/2020	1.102	1.085	1.119	7	6	9		
London	17/12/2020	12/12/2020	17/12/2020	1.019	1.012	1.026	37	27	57	2.36	2.27	2.46	22/11/2020	16/11/2020	22/11/2020	1.103	1.092	1.113	7	6	8		
South East England	18/12/2020	18/12/2020	18/12/2020	1.026	1.014	1.038	27	18	50	1.46	1.37	1.55	04/12/2020	28/10/2020	04/12/2020	1.103	1.078	1.128	7	6	9		
South West England	21/12/2020	13/12/2020	21/12/2020	1.098	1.070	1.127	7	6	10	0.62	0.54	0.70	*	*	*	1.011	1.003	1.019	63	37	215		
Wales	30/11/2020	20/11/2020	30/11/2020	1.045	1.026	1.065	16	11	27	0.48	0.39	0.57	11/10/2020	11/10/2020	11/10/2020	0.989	0.970	1.008	-60	92	-23		
Northern Ireland	04/12/2020	12/11/2020	04/12/2020	1.076	1.048	1.104	10	7	15	0.60	0.48	0.71	16/10/2020	14/10/2020	16/10/2020	0.968	0.946	0.990	-21	-68	-12		
Scotland	*	*	*	1.040	1.029	1.051	18	14	24	0.34	0.29	0.38	*	*	*								
[D] triple gene positive 16/17 years and older				Most recent epoch										Previous epoch									
Region	Most recent changepoint	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI	Current positivity (%) [THIS MODEL]	lower SE	upper SE	Previous changepoint	lower 95% bound	upper 95% bound	Most recent rate ratio per day	lower 95% CI	upper 95% CI	Doubling /halving time	lower 95% CI	upper 95% CI		
North East England	06/12/2020	01/12/2020	06/12/2020	1.032	1.015	1.048	22	15	45	0.88	0.76	1.01	17/11/2020	07/11/2020	17/11/2020	0.941	0.920	0.961	-11	-18	-8		
North West England	13/12/2020	01/12/2020	13/12/2020	1.017	1.006	1.029	41	25	126	0.60	0.54	0.66	08/11/2020	05/11/2020	11/11/2020	0.962	0.956	0.968	-18	-21	-15		
Yorkshire and the Humber	09/12/2020	04/12/2020	09/12/2020	1.012	0.998	1.026	59	27	-389	0.52	0.46	0.59	20/11/2020	11/11/2020	20/11/2020	0.944	0.928	0.959	-12	-17	-9		
East Midlands	21/11/2020	15/11/2020	21/11/2020	0.997	0.989	1.004	-216	166	-65	0.56	0.49	0.62	29/10/2020	11/10/2020	29/10/2020	0.984	0.972	0.997	-44	-211	-24		
West Midlands	25/12/2020	23/12/2020	25/12/2020	0.939	0.892	0.989	-11	-63	-6	0.28	0.22	0.34	09/12/2020	30/11/2020	14/12/2020	1.030	0.997	1.063	23	11	-274		
East England	26/12/2020	12/12/2020	26/12/2020	0.937	0.892	0.986	-11	-48	-6	0.19	0.15	0.23	28/11/2020	28/11/2020	03/12/2020	1.036	1.016	1.056					
London	24/11/2020	24/11/2020	03/12/2020	0.994	0.988	1.001	-121	853	-56	0.28	0.25	0.31	10/11/2020	06/11/2020	10/11/2020	0.967	0.950	0.984	-21	-44	-13		
South East England	22/12/2020	20/12/2020	22/12/2020	0.945	0.914	0.977	-12	-30	-8	0.17	0.14	0.21	06/12/2020	22/11/2020	08/12/2020	1.057	1.028	1.086	13	8	25		
South West England	06/12/2020	09/12/2020	06/12/2020	1.006	0.983	1.029	120	24	-40	0.13	0.10	0.17	19/11/2020	19/11/2020	25/11/2020	0.921	0.890	0.953					
Wales	15/12/2020	11/12/2020	15/12/2020	0.945	0.926	0.965	-12	-19	-9	0.49	0.41	0.58	22/11/2020	14/11/2020	22/11/2020	1.096	1.070	1.122	8	6	10		
Northern Ireland	22/12/2020	16/11/2020	22/12/2020	1.087	1.047	1.129	8	6	15	0.62	0.50	0.75	11/10/2020	11/10/2020	15/10/2020	0.977	0.962	0.985	-2	-10	-21		
Scotland	18/12/2020	18/12/2020	18/12/2020	0.996	0.970	1.022	-172	31	-23	0.27	0.23	0.32	04/12/2020	15/10/2020	04/12/2020	0.958	0.929	0.988	-16	-58	-9		
Note: doubling time = -ln(2)/ln(RR). Doubling times 10 days and under shown in yellow.																							
* Indicate no evidence for changepoint since start of modelling																							