Indicator	Red, amber, or green status*	Confidence level	Assessment and rationale The risk assessment is presented in comparison to the recent predominant variant (BA.5). Red indicates the assessed variant is worse than BA.5 in a characteristic, amber equivalent, green improved.
Growth advantage	**Red**	**Moderate**	At the data cut-off for the growth assessment (22 November 2022), BQ.1.1 was estimated to be approximately 40% prevalent, BQ.1, 14%, and XBB, 5%. There may be a reduction in ascertainment of BQ.1.1, which is identified through a single mutation, due to characteristics of the current amplicon scheme for sequencing. This is being updated. BQ.1 and BQ.1.1 continue to show a growth advantage over BA.5 in 2 different models in the UK. The advantage is greater for BQ.1.1 than BQ.1. BQ.1 is already predominant in France and is increasing in some other European countries. XBB also shows a similar growth advantage, though currently at low prevalence in the UK.
Immune escape	**Red**	**Moderate**	BQ.1 contains mutations at known antigenic sites and BQ.1.1 contains the additional mutation R346T, also predicted to be antigenically important. Neutralisation data from 3 UK labs and published studies all show a pronounced loss of neutralising activity by sera from a range of patients who have been vaccinated or had vaccine-breakthrough infections. This includes live virus and pseudovirus data. For those studies which have also assessed XBB, the loss of neutralising activity is at least as great as for BQ.1.1. Across these assessments, a small number of sera are noted which appear to have lost all neutralising activity against BQ.1.1. Further characterisation of these is required. Based on data from animal sera, the antigenic distance between BQ.1.1 and BA.5 is as far as between BA.5 and BA.1. XBB is equivalently distant from BA.5 but is also antigenically distinct from BQ.1.1.
Infection severity	**Amber**	**Low**	A single preliminary analysis of patients admitted to hospital from emergency departments is consistent with the risk of admission being either the same or slightly increased for BQ.1 (and sub-lineages) compared to BA.5. The sample size is currently limited and there is substantial uncertainty. More data is required to allow estimates that fully control for potential confounding variables such as detailed vaccination history and demography. There is insufficient laboratory data to comment on any change in viral phenotype. Admission to hospital is not necessarily a proxy for intrinsic viral severity in the current context, and may also reflect contributions from immunity and other factors such as co-circulating infections.
Assessment			BQ.1 (primarily BQ.1.1) is showing a moderate growth advantage and XBB, whilst still at low prevalence, is also showing early signs of growth advantage. These variants have antigenic distance from the vaccine and BA.5 but also each other. It is likely that they will contribute to an increase in community transmission, which may be sustained due to the mixture of variants. However, community transmission will also be influenced by season, behaviour and the vaccine booster campaign.

* Refer to scale and confidence grading slide.