Question	Prompts for facilitators
Part 1	
Discuss in your groups: What questions might genomics help you answer? (5 mins)	- Identify resistance mechanisms - Is there likely local transmission or repeated introductions from overseas? - Is there suspected intra- or inter-hospital spread? - Is there potential environmental acquisition? - Are there any particular focuses of transmission (wards etc.)?
1. What do you need to consider before starting? • Think about enablers & barriers	Consider: - Governance and data/sample sharing, especially inter-hospital - Politics -> Particularly in high-capacity settings, tensions between hospitals, public health labs - Capacity & resources (laboratory, surveillance, response) - What data might be available and in what format (patient movement data?) - Who needs to be involved? - Who would perform testing and sequencing? - Do all hospital labs have capacity to reliably identify relevant cases?
2. What data do you want to collect and why?	Consider metadata. Questions around importation, local transmission and inter-facility spread may require patient movement data, travel history. Clinical history to quantify burden. AST and phenotypic results? Are these data likely to be available? Who would collect them?
3. What samples would you sequence and why?	Consider objectives and capacity. Only hospital, or community too? Environmental sampling? More comprehensive sequencing possible in high capacity setting, but likely don't know the number of cases now, so consider having a strategy as numbers become apparent.
4. What types of analyses might you consider?	We haven't gone into detail about analysis, so only broad. Consider characterisation (reference databases) & transmission (phylo, clustering etc.) Do they have what they need to do this?
Part 2	
1. What would be the key objectives of CR-Ab surveillance?	Consider scope – is this a national system, or local/facility-based? In high-capacity, consider : - active surveillance for colonised cases, - real-time/sensitive outbreak detection, and - more research-focused questions like identifying new resistance mechanisms. In moderate-capacity, high prevalence and limited response capacity may hinder ability to do sensitive outbreak detection, may be more about: - monitoring characteristics over time, - identifying high-risk groups/settings for interventions, - monitoring effectiveness of infection control programs (e.g. changes in circulating strains).
2. How would it interact with existing	No right or wrong here, but consider: - Notifiable diseases / public health surveillance capacity - Existing AMR surveillance systems - Relationships between stakeholders

surveillance systems?	- Regulation and data-sharing mechanisms
3. Would you incorporate genomics into your system, and if so, how?	Hopefully yes for both, but please ask them to consider: - Sampling strategy - How genomics can be used to support stated aims. Settings will likely differ on sampling strategy. Suggest more comprehensive for Country A, for sensitivity to outbreak detection. Consider if targeted approaches, periodic monitoring could be appropriate.
4. What are the data and sample flows?	Please map on butcher's paper. Try to include: - How data gets back to end users / decision makers - What data are included - Who is responsible for aspects of the surveillance program (testing/analysis/response)
5. What are the key challenges you would need to address?	Setting description should provide some things to consider, such as: - Governance and collaborations - Resources - Response capacity (IPC / Public health) - Representativeness, especially in the moderate capacity setting, where micro access might be more limited - Politics, particularly in high-capacity settings, tensions between hospitals, public health labs & increasing access to genomics outside public health system risks fragmentation of data.