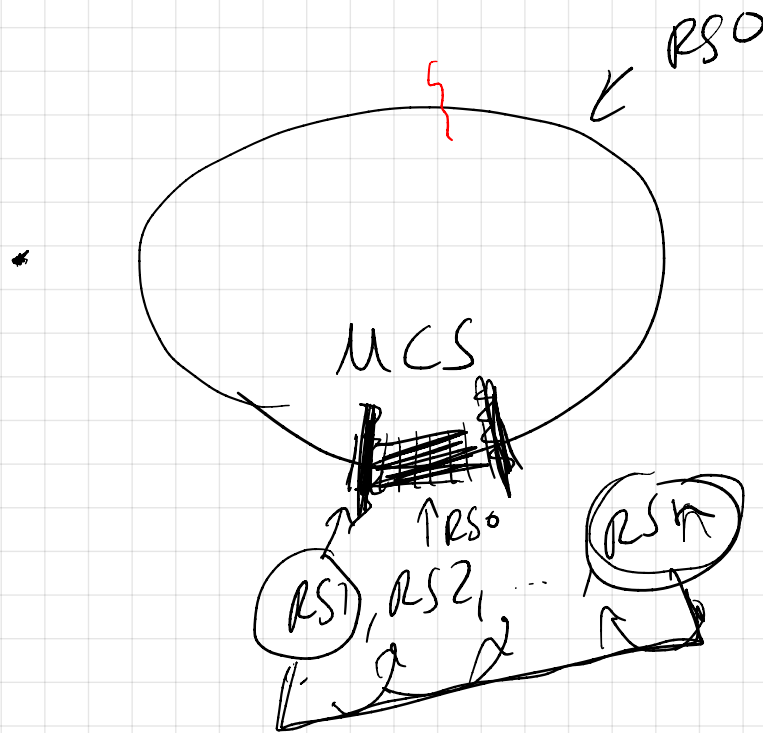


- 1) walk backward
start ≥ 100 bps from end of gene,
look for restriction site
- 2) add another 100 bps from the
left of the RS, and check whether
RS would be unique in whole
plus mid

• unique in $X + \text{linker} + \text{FPG} + \alpha X$



Outlook:

