Use independent tracers to validate chronology

Check if depth distribution of other elements is homogeneous with depth.
Analyze short-lived radionuclides at the SML.
Check for burrowing evidence → e.g. X-ray radiographs or visual description of sed. core.
CRS or CF:CS model below SML → check residence time of $^{210}$Pb in SML.
The profile is likely undatable if entirely affected by mixing.

Check if changes in grain size distribution, DBD and OM content also occur.
Normalize radionuclide concentrations to the parameter driving $^{210}$Pb distribution.
Analyze $^{226}$Ra in all sections.
CF:CS model in normalized profiles.
The profile is likely undatable if normalization fails and other chronological tools are unavailable.

Compare $^{210}$Pb$_{xs}$ inventories with those at a reference site.
Check for coarser grain size.
Presence of short-lived radionuclides at reference site to check entire core recovery.
CF:CS or CIC models to estimate mean MAR.

Only if OM is high (> 30 %) and mostly labile (0.01–0.03 d$^{-1}$)

Analyze radionuclides in the fine sediment fraction (sieve to <63 µm or <125 µm) → check new profile
$^{226}$Ra by gamma spectroscopy
Check for records of event sedimentation
If sieving increases $^{210}$Pb$_{xs}$ concentrations but its shape is similar, the profile is undatable and cannot be used for accumulation rate calculations.