

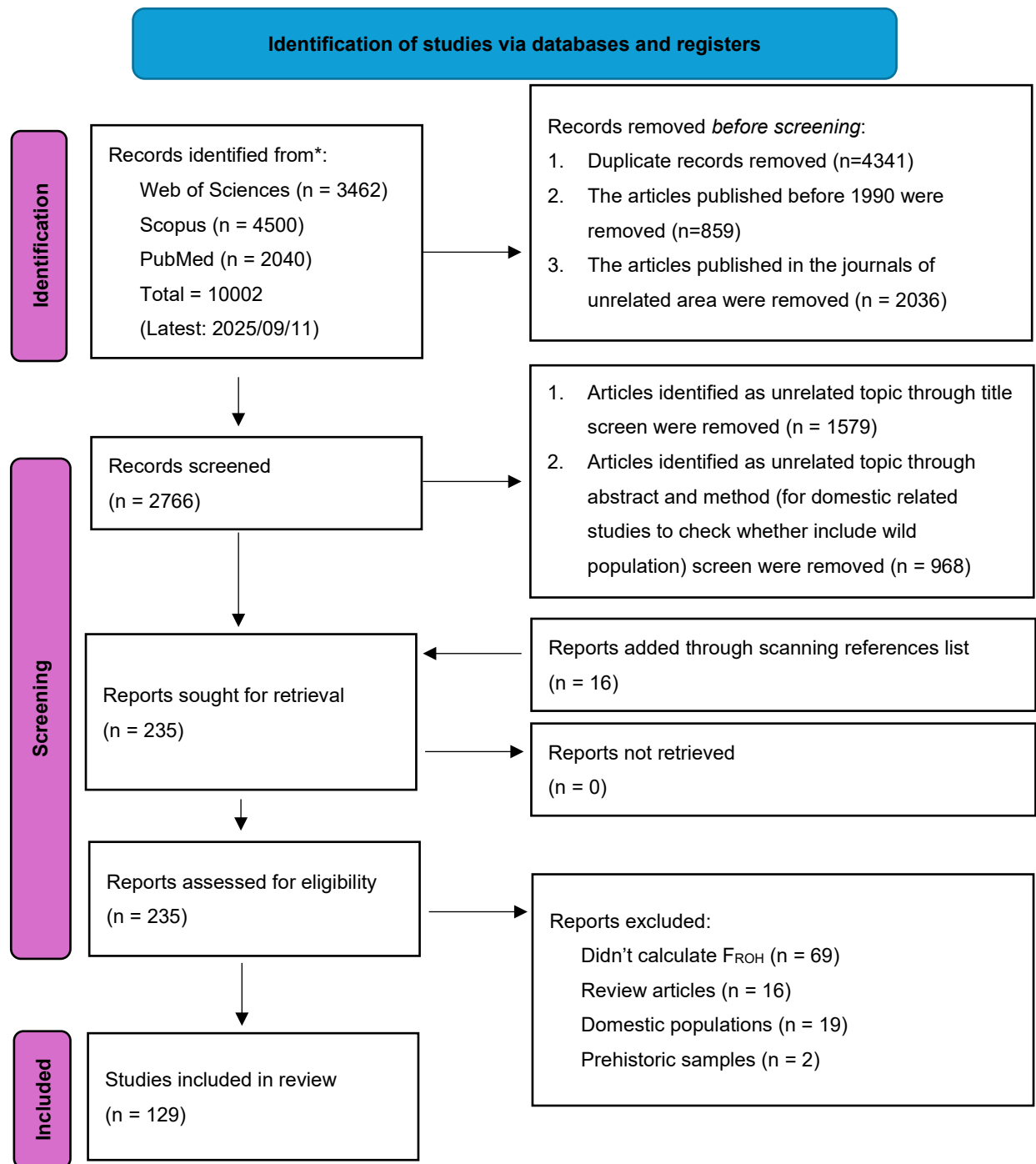


Figure S1. PRISMA diagram. The literature search and study-selection process for empirical records.

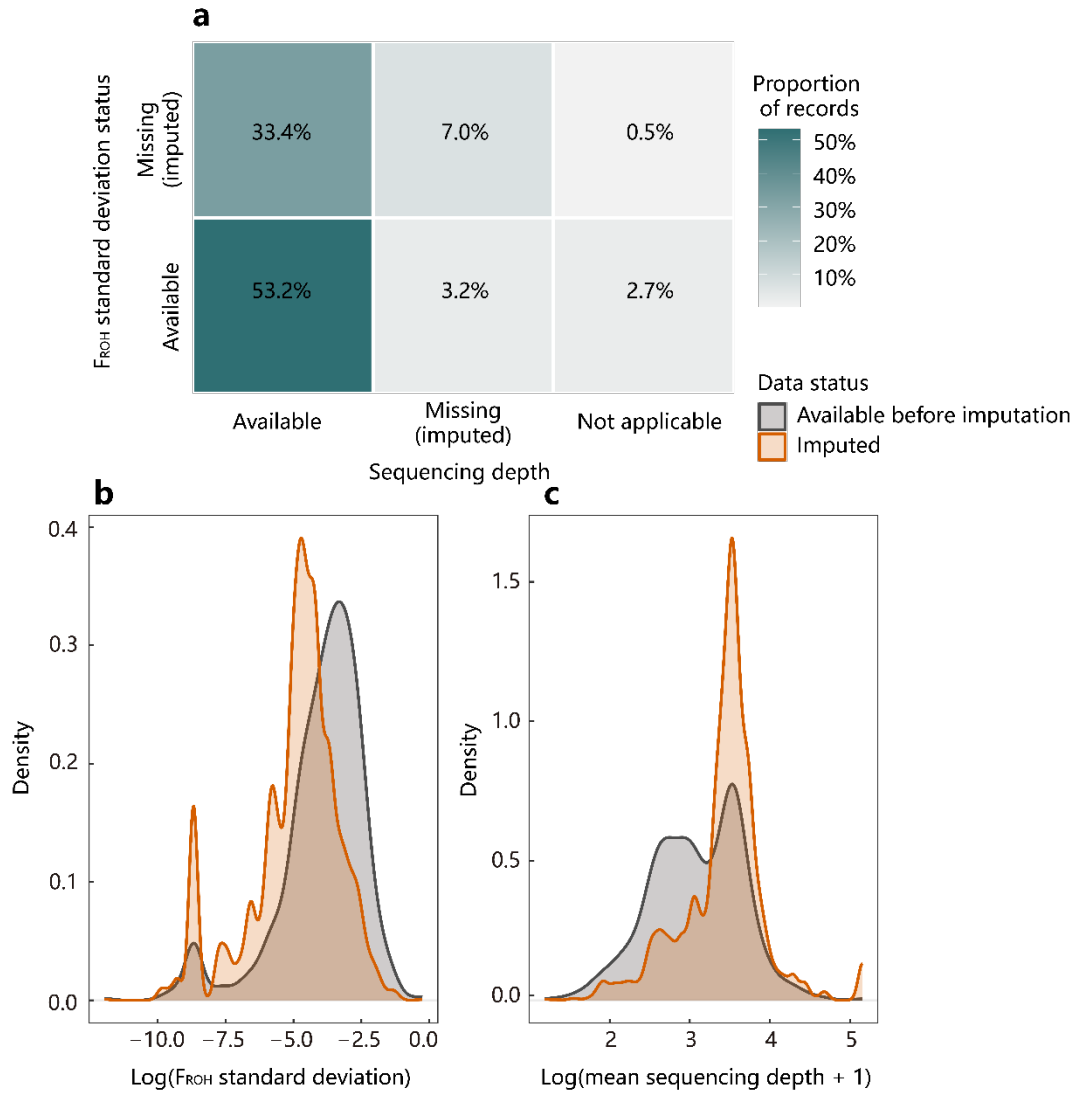


Figure S2. Missing-data details and multiple-imputation results. (a) Joint availability of F_{ROH} standard deviations (SD) and sequencing-depth data before imputation. Cell labels show the percentage of all records, with darker shading indicating a larger proportion. Sequencing depth was classified as not applicable for SNP-array and hybridization-capture data. (b) Distributions of available and imputed log-transformed SDs. (c) Distributions of available and imputed mean sequencing depths, shown as $\log(\text{depth} + 1)$. Grey and orange curves represent values available before imputation and imputed values, respectively. Imputed distributions pool values across the 50 completed datasets for visualization. Available standard deviations include reported values and values reconstructed or adjusted during data preparation