

Supplementary information

Construction and evaluation of in-house methylation-sensitive SNaPshot system and three classification prediction models for identifying the tissue origin of body fluid

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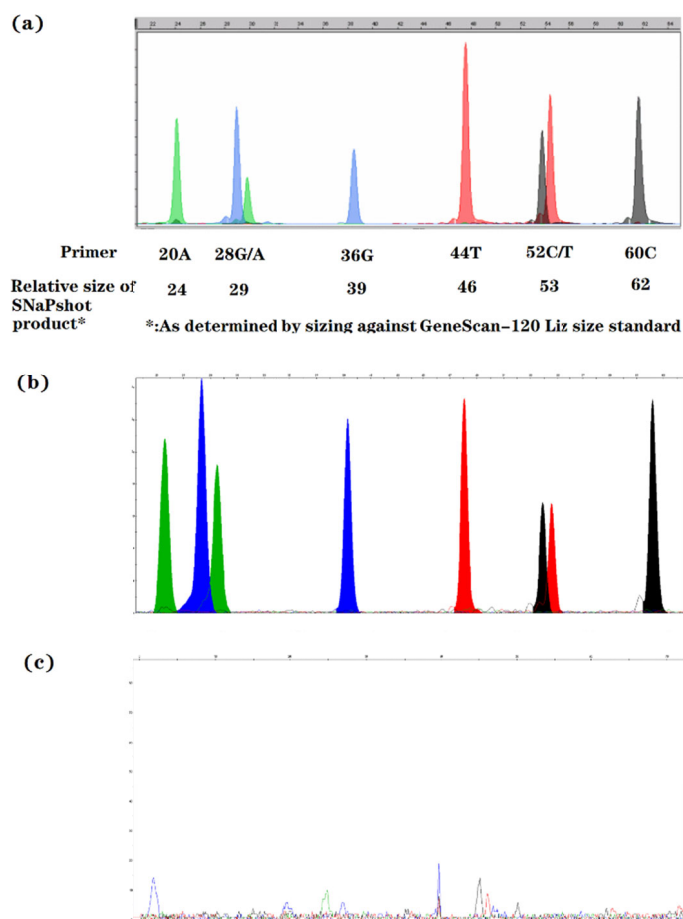


Fig. S1 Positive control electrophoresis profile of control DNA in the kit instruction (a), and positive (b) and negative (c) control electrophoresis profiles of control DNA detected by the SNaPshot platform established by our laboratory.

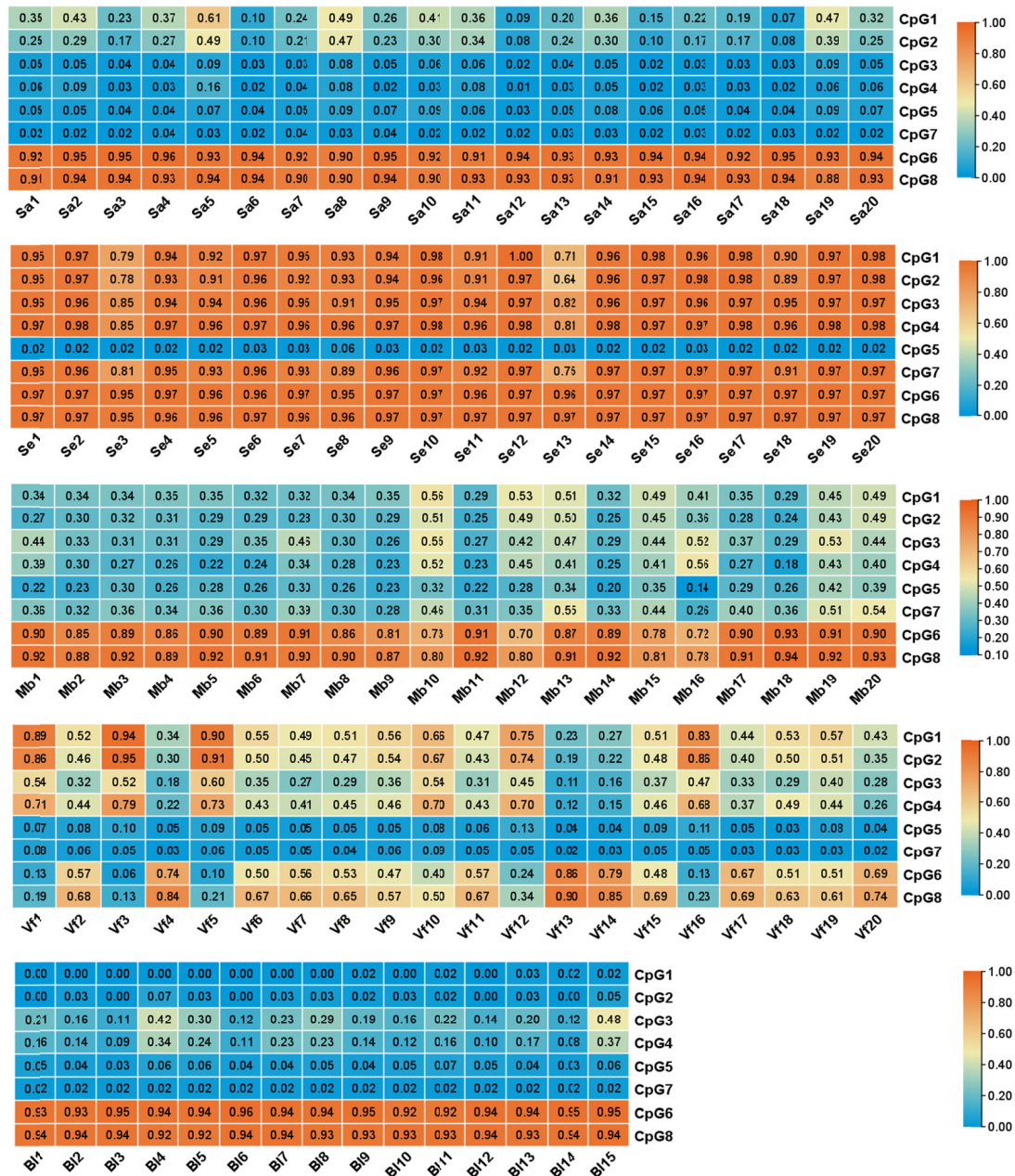


Fig. S2 Heat maps of methylation values of eight body fluid-specific differential DNA methylation sites in multiple SNaPshot test results ($n=95$). Bl, Sa, Mb, Vf, and Se represent venous blood, saliva, menstrual blood, vaginal secretions, and semen, respectively.

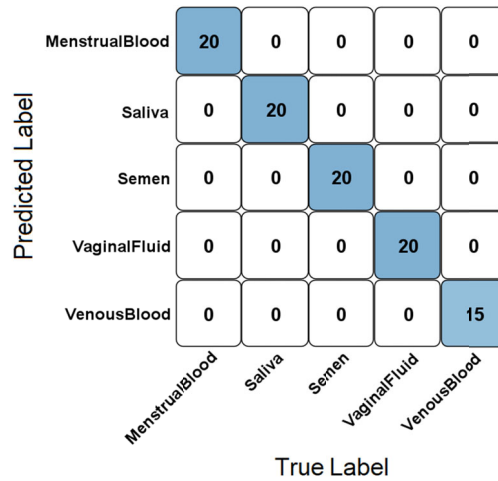


Fig. S3 A confusion matrix of the random forest prediction model based on eight body fluid-specific DNA methylation markers ($n=95$).

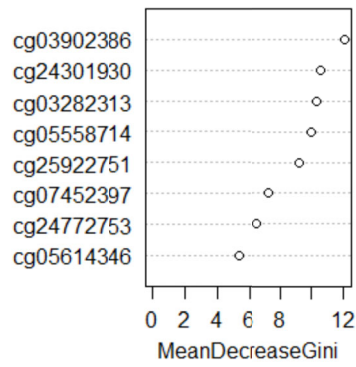


Fig. S4 Mean decrease Gini values of eight CpGs in the random forest model for five body fluid identifications.

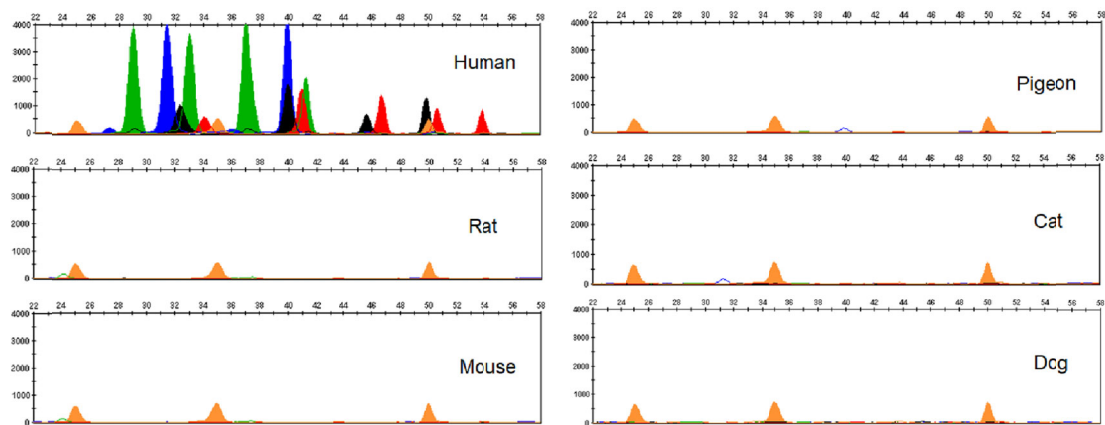


Fig. S5 Multiplex SNaPshot electropherograms for species specificity.