Naming Convention and Laboratory Methods: PROVEDIt Database – SUDA samples

Naming Convention and Laboratory Methods

Single source sample names will follow the format below and are best explained through example:

SUDA0001-01-11-0.0033-E-PP6c-QNA-04-24sec.hid

SUDA0001 is the project, 01 is the sample identifier, 11 is the contributor identifier, this is followed by the total DNA template amplified in nanograms (0.0033 ng in the example above), "E" or "S" is the cell type identified denoting if the sample is sperm (S) or buccal epithelial (E) cells and the amplification kit used (i.e., PowerPlex Fusion 6C (PP6c)) and 29 PCR cycles at half reaction volume; QNA is used to denote that the Quality index was not measured; 04 indicates the capillary number and 24sec indicates the injection time used.

All SUDA samples were detected using a Life Technologies 3500xL Genetic Analyzer.

Note, DNA quantities are based on the physical count of cells detected (0.0033 ng per haploid copy of template DNA), quantitative PCR was not used. The number of cells can be calculated by using the DNA quantity and the cell type – if the cell type is *E* (epithelial), divide the DNA quantity by 0.0066ng; if the cell type is *S* (sperm) divide the DNA quantity by 0.0033ng. All samples were recovered using the DEPArray [1].

Contributor	02	03	04	08	11
AMEL	[X_X]	[X_Y]	[X_Y]	[X_Y]	[X_Y]
D3S1358	[18_18]	[16_18]	[17_17]	[14_15]	[16_18]
D1S1656	[17.3_17.3]	[15_16]	[12_16.3]	[13_15]	[12_18.3]
D2S441	[11_11]	[10_14]	[13_14]	[10_11]	[10_11.3]
D10S1248	[15_15]	[15_16]	[13_16]	[13_14]	[13_15]
D13S317	[8_12]	[8_12]	[11_12]	[12_14]	[12_13]
Penta E	[5_7]	[5_12]	[5_12]	[5_16]	[10_11]
D16S539	[13_14]	[13_13]	[11_12]	[9_10]	[11_12]
D18S51	[12_16]	[12_12]	[14_19]	[15_18]	[14_14]
D2S1338	[17_19]	[17_24]	[17_22]	[19_20]	[17_23]
CSF1PO	[14_15]	[10_12]	[10_11]	[11_12]	[10_14]
Penta D	[10_14]	[13_13]	[10_14]	[9_10]	[11_12]
TH01	[9.3_9.3]	[6_6]	[6_7]	[9_9]	[6_7]

vWA	[16_18]	[17_19]	[17_18]	[17_17]	[17_17]
D21S11	[29_31]	[28_29]	[29_30]	[30_31]	[29_29]
D7S820	[10_12]	[10_12]	[9_11]	[8_11]	[8_8]
D5S818	[11_12]	[12_12]	[11_12]	[11_12]	[12_13]
TPOX	[8_11]	[8_8]	[8_8]	[8_8]	[8_11]
D8S1179	[13_14]	[13_14]	[13_15]	[10_14]	[10_15]
D12S391	[20_21]	[18_23]	[20_22]	[18_22]	[24_25]
D19S433	[13_15]	[14_15]	[13_15]	[13_14.2]	[14.2_15]
SE33	[19_19.2]	[17_19.2]	[19_31.2]	[14_26.2]	[14_31.2]
D22S1045	[15_16]	[11_16]	[11_15]	[12_16]	[15_16]
DYS391	[0_0]	[11_0]	[10_0]	[11_0]	[10_0]
FGA	[20_22]	[19_20]	[19_22]	[20_23]	[22_24]
DYS576	[0_0]	[17_0]	[17_0]	[16_0]	[16_0]
DYS570	[0_0]	[21_0]	[17_0]	[19_0]	[21_0]

[1] V.R. Williamson, T.M. Laris, R. Romano, M.A. Marciano, Enhanced DNA mixture deconvolution of sexual offense samples using the DEPArray™ system, Forensic Sci. Int. Genet. 34 (2018) 265–276. doi:10.1016/j.fsigen.2018.03.001.