IS IT POSSIBLE TO PREDICT THE ORIGIN OF EPITHELIAL CELLS? – A COMPARISON OF SECONDARY TRANSFER OF SKIN EPITHELIAL CELLS VERSUS VAGINAL MUCOUS MEMBRANE CELLS BY DIRECT CONTACT

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Abstract:

In alleged sexual assault and rape cases, the focus has often been to collect samples from the victim's body, for detection of body fluids or skin cells from the offender. But in many cases intimate body samples from the perpetrator(s) can also be informative. However, in cases where the female victim claims vaginal penetration, the defendant may display an alternative explanation to the DNA findings, i.e. that the victim's skin cells has been secondarily transferred to his penis. We hypothesized that female DNA will be detected in a significantly greater amount on swabs from penis after intercourse than after secondary transfer by skin contact.

Fourteen male-female couples were recruited to test the above hypothesis, by collecting penile swabs from 3 specified anatomical locations: Glans, shaft, and the coronal sulcus, after two different situations: Vaginal intercourse and secondary transfer of epithelial cells by skin contact. The results show that penile swabs following intercourse produce significantly higher DNA concentrations than after secondary transfer by skin contact. Our results, indicates which of the anatomical regions is best suited for sampling. The DNA profiling results show a preponderance of female profiles over male profiles following intercourse compared to secondary skin contact.

Based on these data, it is possible to make a statistical model to distinguish between samples taken after intercourse and samples taken after secondary transfer by skin contact based on the amount of female DNA and mixture proportion (Mx) between female and male DNA in samples collected from penis swabs.

1 Introduction

General knowledge about the persistence of different cell types on the body surfaces or in body cavities is an important aspect in a forensic perspective, since the evaluation of such information is of interest to the legal system (judges, prosecutors and defence lawyers).

Knowledge in this field is partly based on small individual studies or casework experience from investigated and analysed samples. The general experience, based on empirical data, indicates that the time aspect between deposition and sample collection is of importance, regardless of cell type [1]. Another aspect believed to be crucial, but difficult to control in casework, is the activity between deposition and sample collection [2]. Furthermore, it is postulated that the type and amount of cells deposited differs depending on biological source [3]. It is therefore desirable to obtain a greater understanding of these elements based on controlled experiments, in which various parameters are examined.

In alleged rape cases the focus has for a long time been to secure samples from the victim's body, for detection of body fluids, spermatozoa or skin cells from the offender. However, such biological material is not always possible to detect, either because the offender has not deposited cells or the amount of cells is at a minimum compared to the predominance of the victim's cells. In recent years, there has therefore been more focus on the possibility to detect mucous cells transferred from the victim on to the offender's body surface. However, there is not much published literature on this specific topic, perhaps because it can be challenging to recruit couples to such controlled studies.

Intimate body samples from the offender can also be informative. In cases where the female victim claims vaginal penetration, cellular material from the victim can be transferred to and detected on penile swabs collected from the offender. Studies, though few and small, on this topics have shown that such transfer is possible and that time and activity between the event and the forensic examination is crucial for these discoveries [4, 5].

It is also known that cell material, such as epithelial cells from the surface of the skin can be transferred between individuals or objects; skin cells from individual A can be transferred to individual/object B (primary transfer) and possibly on to a surface C (secondary transfer) [2, 6, 7]. Following allegations of penile penetration and detection of the victim's DNA on the defendant's penis, the defendant may display an alternative explanation to the DNA findings, i.e. that he touched the victim's skin with his hands and subsequently transferred the victim's cells to his penis during a bathroom visit. However, the skin is considered to be a poor source of DNA compared to the vaginal mucous. Jones et. al [8] studied secondary transfer of female DNA to a male participant's penis following non intimate social contact and a subsequent bathroom visit. They discovered only few occasions of transfer of female DNA to the male participants, and that all these results were low level. The PCR amplification analysis utilized in this study was SGM Plus (Applied Biosystems™), it is however possible that detection of this type of transfer could be more frequent when analysis is performed with the more sensitive analysis kits, utilised by many forensic laboratories, e.g. AmpFLSTR™ NGM SElect™ PCR (Applied Biosystems™). In addition, the Jones study only includes few samples following transfer during sexual intercourse (samples from one couple

at three different occasions), and does therefore not represent the variation that could exist e.g. between different couples.

Based on previous studies and casework experience, we hypothesized that vaginal mucous epithelial cells will be transferred to a greater extent by direct contact than skin epithelial cells in a secondary transfer scenario. Consequently, female DNA will be detected in a significantly greater amount on penile swabs collected after intercourse than after secondary transfer by skin contact, and with a sufficient dataset it is possible that differences can be modelled.

None of today's routine methods or presumptive tests can decipher if the female DNA profile detected originates from skin or mucous epithelial cells. A more efficient way to assign the presence of specific body fluids in a sample is by mRNA analysis [9, 10]. However, such analyses are currently not implemented by many routine analysis laboratories and have limitations, e.g. in cases of mixed samples, or where the sample is already handled/extracted and therefore not available for further mRNA analysis.

In the study presented here, 14 male-female couples were recruited to test the possibility of secondary transfer of cells from skin contact to the penis, and the difference in DNA results from penile swabs after vaginal penetration and secondary transfer of skin cells. We also investigated if swabbing different anatomical locations on the penis had an impact on the DNA results.

We used statistical models to study the effect of different experimental factors on the proportion of female DNA observed in the samples. Further, we fitted a model that with high accuracy predicts whether female DNA is more likely to result from secondary transfer of skin cells or from vaginal penetration.

2 Materials and Methods

The 14 couples constituting the participants in this study were students in the age of 20-40 years, with no known medical conditions. This study was approved by the Norwegian ethical research committee (REK).

2.1 Sampling kit

All the participating couples received a prepacked sampling kit. The kit contained general information on the project, a consent form, a user manual with instructions on how and when to collect samples, envelopes with cotton swabs for reference samples (oral mucous) for both male and female participants, and an envelope with pre-labelled sampling bags containing cotton swabs and distilled water for sample collection. The sampling bags were labelled with couple number, sampling locations (penis shaft, penis glans or the coronal sulcus), situation (vaginal intercourse or manually touching) and replication number (1, 2 or 3, respectively).

2.2 Transfer situations

The sampling, both after skin contact and vaginal penetration was repeated three times for all couples with at least 24 hours delay, and the participants were instructed to shower in between. The female participants were instructed to perform the experiments in between menstruations.

2.2.1 Secondary transfer of skin epithelial cells

The male participant was instructed to rub with medium pressure the skin surface on the upper arms of the female participant for 5-10 minutes, continuously, and then simulate a bathroom visit by touching his penis with the same hand used for touching his partner. It was stressed that he, to the greatest extent possible, should avoid contact with other surfaces (door handles, etc.) between touching his partner's skin and touching his penis. Samples a-c were collected immediately after hand-to-penis contact.

2.2.2 Transfer of vaginal mucous membrane epithelial cells after vaginal penetration

The male participants were instructed to collect samples a-c within one hour post vaginal intercourse, before performing other activities.

2.3 Sampling guidelines for penile swabs

All penile swabs were collected by the male participant himself. The participant was instructed to moisten the tip of the cotton swab with a drop of distilled water, then to rub the swab against the surface (firm contact – not too weak) for a minimum of 30 seconds. Three samples were collected in the order a-c, by the following instructions:

- a) Penis shaft: Use the swab in the lengthwise direction to secure cell material from the shaft in whole. Rub 4-5 times in the lengthwise direction, and make sure that the whole surface is covered.
- b) Glans penis (head): Use the swab to secure cell material from the glans, avoid the urethra.
- c) The coronal sulcus ("the pit" *under glans*): Use the swab to secure cell material from the sulcus

2.4 Sample processing

The tips of swabs were cut by sterile scissors and placed into extraction tubes. The samples were stored at room temperature until DNA was extracted by the 5% Chelex® procedure [11] (no prior incubation with water) where 200µL Chelex® (Bio-Rad) was added to swabs, according to current practice at the department. All samples were quantified with Quantifiler® Duo Kit (Applied Biosystems™) on the 7500 Real-Time PCR system (Applied Biosystems®) using the manufacturers' recommendations. All samples were amplified using the AmpFLSTR™ NGM SElect™ PCR Amplification Kit (Applied Biosystems™) as recommended by the manufacturer (1 ng template 25 µL reaction volume and 29 amplification cycles). Amplification was carried out using a GeneAmp® PCR System 9700 (Applied Biosystems®). Samples were injected on the Applied Biosystems 3130xl Genetic Analyzer at 3 kV for 5 s. The results were analysed using the GeneMapper® ID –X Software v 1.2 (Applied Biosystems®). The limit of detection (LOD) for alleles was set to 50 RFU and the stochastic threshold was set to 150 RFU. The total amount of human DNA and the male human DNA quantity was determined from the quantitation results of the human and male targets in the Quantifiler® Duo analyses. The proportion of female DNA was estimated as [1- amount of male human DNA (ng/ul)/ total amount of human DNA (ng/ul)]. DNA profiles were compared

to the reference samples of the participants, and both the observed number of male and female alleles were counted. The mixture proportion (Mx) of female and male DNA was estimated using EuroForMix (EFM) v2.2.1 [12] using default drop-in model, fst=0, detection threshold 50 rfu. Stutter model was turned off but we compared both with and without degradation model (very similar results were obtained).

The Mx was determined as a number between 0 and 1, where 0 indicates no female profile (no DNA in sample or single source male profile) and 1 indicates single source female profile. Samples with DNA-results in less than 8 markers, and with alleles outside of the stochastic threshold were determined to be not interpretable.

2.5 Statistical analysis

To investigate the relationship between the amount of female DNA detected in a sample, the transfer situation and the sampling location, we looked at three different statistical models. In the models we, for simplicity reasons, refer to the transfer situation as “cell type”, reflecting that the two scenarios involve different cell types. Further, secondary transfer of skin epithelial cells was referred to as “skin” and transfer of vaginal mucous membrane epithelial cells after vaginal penetration as “mucous”. Thus, we have a categorical variable named “cell type” with two levels, “skin” and “mucous”. Other considered experimental factors were sampling location (shaft/glans/sulcus) and couple (random factor).

Model 1

With the first model we wanted to investigate how different experimental factors impact the overall DNA quantity in the sample. We fitted a linear mixed model with total DNA quantification (quant) as the response and cell type, location and couple as explanatory variables. An interaction term between location and cell type was also included.

Model 2

The second model investigates which of the experimental factors are significant for explaining the proportion of female DNA in the sample. We have two measures of the proportion of female DNA: 1) estimated with EFM based on the DNA profile (Mx), and 2) estimated from the quant. We fitted two linear mixed models, one with the proportion of female DNA from the DNA profile as the response (model 2A), and one with the proportion of female DNA from the quant as the response (model 2B). For both models the response was logit-transformed, and 0.001 was added or subtracted to female DNA proportions of exactly 0 or 1.

All mixed effects models (models 1, 2A and 2B) were fitted with the R function lmer in the package lme4[13].

Model 3

Finally, we wanted to see if we could predict the transfer situation based on all information that is typically available in a case. This includes sampling location, proportion of female DNA from the quant, proportion of female DNA from the DNA profile (Mx) and total DNA quant. We used a logistic regression

with cell type (mucous/skin) as response, fitted with the glm function in R. To estimate the prediction accuracy of the model we performed a K-fold cross-validation. For each iteration, we removed all samples from a couple (a total of 11 segments), refitted the model and predicted the cell type of the samples that were left out. Samples with a probability higher than 0.5 were classified as skin and the remaining were classified as mucous.

3 Results

In total, eleven of the fourteen participating couples that started in the trial completed the study. Hence, the total number of samples included in the study was 198; 99 samples from skin contact and 99 samples from vaginal penetration.

3.1 Quantification data

The quantification results document a higher amount of total human DNA in samples collected from the penis shortly after vaginal intercourse versus after skin contact for all three penile locations (Fig. 1a). Figure 1b shows the proportion of female DNA based on the quantification results, calculated as described in Section 2.4. The proportion of female DNA is higher for samples collected after vaginal penetration compared to samples collected after skin contact.

Fig 1: Boxplots displaying the quantification results with Quantifiler Duo of a) total amount of human DNA (ng/uL) and b) the proportion of female DNA in each sample (n=33 in each column) categorized by the three different sampling locations on penis: Glans, shaft and sulcus at two different activity situations: “mucous”= samples collected from penis after contact with vaginal mucous membrane cells, and “skin”= samples collected from penis after social contact (secondary transfer). In a) the data are represented on a log10 scale, and three observations that had 0 measured quant are not shown.

Variation in DNA quantities (female and male) between couples, and all replicates for each sampling location, and in both transfer scenarios is displayed in Figure 2.

Fig. 2: Bar plot displaying the total human DNA quantity for each couple (1-11) and each replicate, categorized by the three different localizations on penis: Glans, shaft and sulcus at two different activity situations: “mucous”= samples collected from penis after contact with vaginal mucous membrane cells (direct transfer) and “skin”= samples collected from penis after social contact (secondary transfer). The colours of the bars indicate female and male contribution.

The results presented in figure 1 and 2, indicates that there is a difference in female DNA quantities related to cell types, and sampling locations only showed marginal differences in the secondary skin contact scenario. In addition some variations between the couples can be observed.

3.2 DNA profiling results

All results from allele counts and Mx calculations can be found in appendix

3.2.1 DNA profiling results after vaginal penetration

The DNA profiling results from the samples collected after vaginal penetration showed in most cases mixtures with the female DNA profiles as the main contributor (Fig 3 and 4).

Considering sampling location, samples collected from the shaft showed less male alleles and highest female DNA contributions (Fig 3 and 4).

3.2.2 DNA profiling results after secondary transfer of skin epithelial cells

The DNA profiling results from the samples collected after transfer of skin epithelial cells showed mainly male DNA profiles or mixtures with the male DNA profiles as the main contributor (Fig 3 and 4), but with some exceptions for couple 3 and 11 which also display high DNA quantities (Fig 2).

Fig 3: Bar plot displaying the number of observed female and male alleles in the DNA profiling result for each couple (1-11) and each replicate, categorized by the three different localizations on penis: Glans, shaft and sulcus at two different activity situations: “mucous”= samples collected from penis after contact with vaginal mucous membrane cells (direct transfer) and “skin”= samples collected from penis after social contact (secondary transfer).

Fig 4: Bar plot displaying the Mx proportion (defined in section 2.4) of female and male DNA, evaluated and interpreted by the DNA profiling result, for each couple (1-11) and each replicate. The results are categorized by the three different localizations on penis: Glans, shaft and sulcus at two different activity situations: “mucous”= samples collected from penis after contact with vaginal mucous membrane cells (direct transfer), and “skin”= samples collected from penis after social contact (secondary transfer).

3.3 Statistical analysis

Model 1

The first model explored how cell type, location and couple affect the total DNA quantity in the sample. Table 1 shows that cell type is highly significant in explaining differences between measured DNA quantities (p-value= 3.6e-16). Sampling location also appears to have an effect (p-value = 0.06). In addition there seems to be some interaction between cell type and sampling location (p-value = 0.06),

indicating that there is not one overall “best” sample location independent of the cell type (i.e. the transfer situation). This is also supported by the interaction plot in Fig. 5; in the secondary transfer situation (skin) the location that shows the highest DNA quantity is sulcus, while after intercourse (mucous) the highest quantity is detected in samples from the shaft.

Table 1: Results for model 1, showing p-values for the fixed effects computed with type II Wald chi square tests, and the estimated variance components for the random effect couple and the residual variance.

Fixed effects	p-value	Random effects	Variance
Cell type	3.6e-16	Couple	1.2
Location	0.06	Residual	17.8
Cell type : Location	0.06

Fig. 5: Interaction plot showing the average total DNA quantity for each location and each cell type.

Model 2

Before analysing the data with model 2 (A and B) and model 3, we removed samples with no detected DNA in the quant (in total 3 observations; 2 for couple 1 and 1 for couple 9). This left us with a total of 195 samples, of which 99 were “mucous” samples, and 96 were “skin” samples. Divided into the category of locations, there were 65 samples from the glans, 64 from the shaft, and 66 samples from the

259 sulcus. Note that for some samples the measured total DNA quantity was lower than the measured male
 260 quantity, and these samples we assigned a male proportion of 1.

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 262 **Fig. 6:** Proportion female DNA in the quant for the three different sampling locations, where “mucous”= samples collected
 263 from penis after contact with vaginal mucous membrane cells (direct transfer), and “skin”= samples collected from penis
 264 after social contact (secondary transfer). Each line represents a couple, averaged over the three replicates.

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Fig. 7: Proportion female DNA in the DNA profiling result (Mx) for the three different sampling locations, where “mucous”= samples collected from penis after contact with vaginal mucous membrane cells (direct transfer), and “skin”= samples collected from penis after social contact (secondary transfer). Each line represents a couple, averaged over the three replicates.

Fig.6 shows the proportion of female DNA, based on the quantification results, for the different couples and different combinations of the categorical variables cell type and location. Fig. 7 shows the same graph with the proportion of female DNA from the DNA profiling result (Mx) as the response on the y axis. In both graphs, each point represents the average of the three replicates for a couple. Both plots show that the mucous samples in general have a higher proportion of female DNA compared with the skin samples, and that samples collected from the shaft in general give the highest amount of female DNA. The difference between mucous and skin is more obvious for the DNA profiling result compared to the DNA quant. However there are quite large variations between couples. One couple (couple 3) on average displays a slightly higher female DNA proportion in the skin samples from shaft compared to the mucous samples from shaft, both when considering the DNA quantity and the DNA profile.

Table 2 and 3 show the results from the two mixed models that were fitted to the data: Model 2A where the proportion of female DNA in the DNA profiling result was used as the response and model 2B where the proportion of female DNA based on the quantification results was used as response. In both models, cell type is highly significant (p -value $< 2.2e-16$), indicating that the proportion of female DNA differs considerably between mucous and skin samples. There is also an effect of the location the sample was taken from, with a p -value of $1.2e-3$ for the model with the proportion of female DNA in the DNA profiling results and a p -value of $1.92e-02$ in the model with the quantification results. The variability in the proportion of female DNA that is due to couple is slightly higher for model 2A (15 %) compared to model 2B (13 %).

Table 2: Results for model 2A, showing p-values for the fixed effects computed with type II Wald chi square tests, and the estimated variance components for the random effect couple and the residual variance.

Fixed effects	p-value	Random effects	Variance
Cell type	<2.2e-16	Couple	6.1
Location	1.2e-3	Residual	33.7

Table 3: Results for model 2B, showing p-values for the fixed effects computed with type II Wald chi square tests, and the estimated variance components for the random effect couple and the residual variance.

Fixed effects	p-value	Random effects	Variance
Cell type	<2.2e-16	Couple	1.9
Location	1.92e-02	Residual	12.4

To investigate the effect of the individual sampling locations on the proportion of female DNA, independent of cell type, we performed Tukey's HSD test with confidence level 0.95 for both models 2A and 2B (Fig. 8). The shaft has the highest average proportion of female DNA, both when considering the DNA profile and the quantification results. There are significant differences between samples from the shaft and the sulcus for both models. Model 2A also showed a significant difference between shaft and glans, while for model 2B this 95 % confidence interval just covers 0. The difference between glans and sulcus was not significant with either model.

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Model 2A: Proportion of female DNA from DNA profile (Mx)

Model 2B: Proportion of female DNA from quant

Fig. 8: 95% confidence intervals from Tukey's HSD for pairwise comparison of locations. Model 2A (left) shows significant differences between shaft and both glans and sulcus, but not between glans and sulcus. Model 2B (right) shows significant differences only between shaft and sulcus.

Model 3

When fitting this logistic regression model we were concerned with finding the model that best predicts whether the sample is “skin” (female DNA stems from secondary transfer) or “mucous” (female DNA stems from direct transfer). We first fitted a model with total DNA quant, location, proportion female from quantification results and proportion female from the DNA profiling results as the explanatory variables (results not shown). However, a model with only the proportion of female DNA from the DNA profiling results as predictor gave the best prediction results estimated with cross-validation, so this was our final choice of model. The results of the cross-validation indicate a good predictive ability. The proportion of mucous samples correctly predicted as mucous (specificity) is 0.95, while the the proportion of skin samples correctly predicted as skin (sensitivity) is 0.83. Further, the proportion of samples predicted as mucous that are truly mucous (negative predictive value) is 0.85, and the proportion of samples predicted as skin that are truly skin (positive predicted value) is 0.94.

Fig. 9: Logistic regression (model 3). The fitted regression line (left) shows the probability of skin as a function of the proportion female in the DNA profile. The circles represent the observations (the samples with probability of skin equal 1 are the skin samples, and the samples with probability 0 are the mucous samples). The ROC curve (right) indicates a good predictive ability of the model (AUC=0.93).

The left plot in Fig. 9 shows the fitted regression line plotted together with the observations. The majority of the skin samples have a low female proportion, and the majority of the mucous samples have a high female proportion. However, there are some exceptions; such as in some skin samples with high proportion of female DNA. The model will assign a high probability of skin to an unknown sample that shows a low proportion of female DNA. Likewise, a sample that has a high proportion of female DNA will obtain a low probability of skin.

The ROC curve in the right plot in Fig. 9 shows how the sensitivity (true positive rate) and the specificity (false positive rate) vary for different cut-offs for classifying a sample as skin or mucous. The area under the curve (AUC) is 0.93, which indicate a good predictive ability for the model.

4 Discussion

Based on the DNA quantification and DNA profiling results in our data set, we have shown that there is a difference between the amounts of female DNA transferred after vaginal penetration, and after secondary transfer of skin cells. We have shown that a statistical model can be used to predict the transfer situation. However, we experienced some deviations in the secondary transfer of skin cells experiments, where a relatively high proportion of female DNA was detected in some of the samples, and especially for one of the female participants. This could be due to a difference in shedder status of the female participants (not tested), as we observed a difference between the participants in amount of DNA from skin cells transferred (Fig. 2, 6 and 7). It is known that some individuals are more prone to deposit cells from touch than others [14, 15]. All samplings were unsupervised and performed by the participants, to our knowledge there has been no deviations from the protocol. However, we cannot exclude the possibility of sampling errors, and this could also influence the results. In addition we do not have control over the activities performed prior to the experiments, such as personal hygiene (e.g. time since showering), that could influence the amount of cells transferred.

Model 1 indicates that cell type, sampling location and couple are all factors that may affect the measured DNA quantity in the sample. Similarly, model 2A and 2B showed that the same experimental factors all had a significant effect on the proportion of female DNA observed in the sample, both based on interpretation of the DNA profiling result (Mx) and the quantification results. However, when it came to predicting the transfer situation, our logistic regression model (model 3) only needed the proportion of female in the DNA profile as an explanatory variable to predict the cell type with a high accuracy. Although other types of information would be available for each sample in a case, such as the total amount of human DNA, the amount of male DNA and sampling location, our data indicates that the most important information comes from the calculated Mx. We do however emphasise that the model is based on a limited number of samples and donors, and a different data set may yield a different conclusion regarding which variables are the most informative. Further samples representative of real casework samples would be needed to generate a model that could be used in actual casework.

In this study we have shown that both DNA quantitation and mixture proportion can be used to evaluate transfer scenarios, further use of the data generated here could be in Bayesian networks in activity related questions.

In this study the participants were instructed to collect the samples within one hour after the activity was conducted, and no other activities (that could remove cells) were allowed before sampling. In casework it is seldom the case that samples are collected directly after the offence has occurred, and a longer time interval between activity and sampling is expected. When the time between the offence and sampling increases, the possibility of activities that can influence the amount of cells that are accessible

for collection will also increase, eg. the removal of cells due to contact, showering or bathroom visits. The information about these types of activities is not always available. Therefore it is expected that the proportion of female DNA will be reduced over time, and findings in casework will normally not be as high as shown in this study. Farmen et al. [4] studied the reduction in quality of female DNA profiles (allele counting) on samples collected from penile swabs in a time interval from 0 -24 hour post vaginal penetration. In all samples collected at time 0 single source profiles were detected. Female DNA could be detected up to 24 hours post penetration, however the number of detected alleles was reduced over time.

In this experiment we have seen that secondary transfer of epithelial cells is possible directly after contact, but that the number of samples where female DNA was detected, and the proportion, was significantly lower compared to samples collected after vaginal penetration. As postulated the results in this study differs to some extent from the results observed by Jones et al.[8], who only detected transfer of few female alleles in 4 out of 30 samples after skin contact, by only counting the number of female alleles in the DNA result. In this study female alleles were detected in 85 out of 99 samples and also to some extent as the major contributor based on further evaluations with Mx and DNA quantities. The probability of detecting secondary transferred cells will also be influenced by activity and is time dependent [2, 16]. Further, Jones et al. [8] detected no traces of female DNA in the penile swabs collected with a time delay of 6 hours or more before sampling. In our experiments secondary transfer of epithelial cells to the penis was performed directly after touching the other participants' skin. If surfaces had been touched in between touching the other participant's skin and then the penis, the amount of foreign DNA on the hands could be reduced by every contact made [2]. In addition, cells from other touched objects could be transferred to the penis. The amount of foreign DNA present on the penis will be reduced if there is a time delay between transfer and sample collection; hence a reduction in detection of secondary transfer of epithelial cells is expected over time. More recent studies have however shown that skin deposited on skin can be detected up to 24 hours after contact [17], and it's therefore possible that epithelial cells from secondary transfer can persist for some time after deposition, dependent on the initial amount deposited.

5 Conclusion

We have seen that there is a difference in DNA quantity and proportion of female DNA transferred to the penis after secondary skin contact compared to vaginal penetration. We have shown that this difference can be modelled. It is therefore possible to predict the scenario that lead to deposition of different cell types. However, there are some limitations. Firstly, it is known that shedder status influences the amount of DNA transferred from skin contact. Therefore it is possible that secondary transfer from a good shedder could be mistaken as direct transfer of mucous cells, especially if the male is a poor shedder in combination with a good female shedder. Secondly, the timeframe between deposition and collection of cells and activity is also known to influence the quality of the DNA profiling result, we have not included this factor in this study. How this influences the model should be included in a further study to improve predictions.

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Appendix

Model 3

Let p be the probability that the cell type is skin. We assume the following logistic regression model:

$$\ln\left(\frac{p}{1-p}\right) = \beta_0 + \beta_1 X$$

where X is the observed proportion of female from the DNA result. The estimated regression coefficients are given in the table below.

Coefficient	Estimate
β_0	3.542
β_1	-5.969

466 Sample results: Quantification , allele count and Mx

Sample num	Couple num	Couple #	Quant	total	Category	Category.nu	Cat	Quant	y	Tot. Human/ Y-human	Category	Category.nu	Cat	No XX alleles	No XY alleles	Mx (XX)	Mx (XY)
T0013220	1	1	13.13	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.36	9,654	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	24	0.912	0.0884		
T00135210	1	1	12.73	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.914	13,928	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	23	0.926	0.0738		
T00138010	1	1	11.62	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.269	43,197	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	22	0.954	0.0464		
T00150010	4	2	3.22	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.072	44,900	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	21	0.958	0.0424		
T0015330	4	2	0.368	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.157	2,344	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	24	0.68	0.32		
T00156010	4	2	1.53	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.576	2,656	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.646	0.354		
T00168010	5	3	4.98	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.341	14,604	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	29	0.878	0.122		
T00171010	5	3	4.64	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.29	3,597	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	29	0.792	0.208		
T0017430	5	3	1.78	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.38	1,29	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.202	0.798		
T00186010	6	4	5.11	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.33	3,840	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.802	0.198		
T00189010	6	4	4.39	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.92	2,286	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.759	0.241		
T0019220	6	4	4.42	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.428	10,327	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	27	0.898	0.102		
T00204010	7	5	4.55	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.063	72,337	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	11	1.837e-13			
T0020720	7	5	3.09	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.042	73,571	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	29	11	1.702e-11			
T0021020	7	5	3.43	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.198	17,323	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	11	1.9e-10			
T0033110	9	6	2.89	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.091	31,934	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	26	0.947	0.0525		
T0033410	9	6	2.68	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.145	18,483	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	27	0.917	0.0834		
T0033720	9	6	0.656	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.314	2,089	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	28	0.673	0.327		
T0022220	10	7	18.78	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.02	920,588	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	13	1.786e-11			
T0022520	10	7	13.61	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.055	252,107	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	13	1.127e-10			
T0022820	10	7	21.6	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.047	46,646	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	13	1.12e-09			
T00349010	11	8	3.06	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.125	24,48	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	21	0.966	0.0337		
T0035220	11	8	12.68	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.166	76,38	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	17	0.985	0.0147		
T0035510	11	8	3.82	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.349	10,946	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	27	0.904	0.0961		
T00240010	12	9	1.43	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.21	1,182	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	29	0.781	0.219		
T0024330	12	9	5.59	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.553	10,488	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	26	0.888	0.112		
T00246010	12	9	3.51	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.092	38,225	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	25	0.963	0.0368		
T00258010	14	10	3.12	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.91	3,429	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.873	0.127		
T0026110	14	10	3.05	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	1.29	2,364	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.733	0.267		
T00264010	14	10	1.12	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	2.46	0,455	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	30	0.725	0.275		
T00276010	15	11	2.13	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.324	6,574	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	28	0.883	0.117		
T00279010	15	11	6.5	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.144	46,139	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	21	0.968	0.0322		
T00282010	15	11	7.78	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	0.349	22,292	Sulcus Coronarius, mucosal epithelial cells	1	Sulcus, mucosal	30	21	0.958	0.0417		
T0013330	1	1	1.76	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.225	7,822	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	27	0.885	0.115		
T00136010	1	1	1.14	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.005	228	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	5	1.306e-11			
T00139010	1	1	3.44	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.144	23,889	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	23	0.943	0.0568		
T0015110	4	2	3.68	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.053	69,829	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	10	1.554e-10			
T00154010	4	2	1.79	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.06	29,685	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	25	0.967	0.0328		
T0015720	4	2	0.642	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.062	10,405	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	26	0.933	0.0673		
T00169010	5	3	0.581	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.016	36,313	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	14	0.987	0.0134		
T0017220	5	3	0.977	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.343	2,848	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	30	0.619	0.381		
T0017520	5	3	0.149	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.134	1,112	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	27	30	0.0832	0.917		
T00187010	6	4	3.62	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.02	36,02	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	15	1.59e-13			
T00190010	6	4	11.76	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.061	19,843	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	7	1.851e-12			
T00193010	6	4	5.93	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.182	32,582	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	24	0.945	0.0546		
T00205010	7	5	0.454	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.019	24,278	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	11	1.236e-10			
T00208010	7	5	2.83	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.021	132,243	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	11	1.322e-11			
T00211010	7	5	9.39	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.111	84,595	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	11	1.179e-11			
T0033220	9	6	1.64	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.134	12,22	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	15	1.161e-10			
T00335010	9	6	2.87	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.158	18,165	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	15	1.121e-10			
T00338010	9	6	0.33	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.268	1,231	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	28	0.63	0.37		
T00223010	10	7	13.33	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.015	876,974	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	13	1.185e-09			

Sample num	Couple num	Couple #	Quant	total	Category	Category.nu	Cat	Quant	y	Tot. Human/ Y-human	Category	Category.nu	Cat	No XX alleles	No XY alleles	Mx (XX)	Mx (XY)
T0022610	10	7	8.78	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.127	69,134	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	13	1.745e-11			
T0022910	10	7	21.67	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.037	579,412	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	13	1.256e-10			
T0035010	11	8	3.62	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.286	12,657	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	19	0.978	0.0219		
T0035310	11	8	9.96	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.186	53,548	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	17	0.985	0.0154		
T0035610	11	8	6.51	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.289	22,526	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	21	0.973	0.0267		
T0024110	12	9	24.59	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.209	117,656	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	12	0.988	0.0122		
T0024410	12	9	22.77	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.069	331,441	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	12	0.989	0.0108		
T0024710	12	9	26.49	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.025	97,825	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	12	0.989	0.0106		
T0029010	14	10	2.14	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.348	6,149	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	29	0.885	0.115		
T0026210	14	10	10.63	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.16	66,438	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	19	0.991	0.0095		
T0026510	14	10	3.45	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	1.27	2,717	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	30	0.797	0.203		
T0027710	15	11	8.31	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.082	101,218	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	12	1.135e-10			
T0028010	15	11	5.22	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.035	147,875	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	12	1.111e-10			
T0028310	15	11	9.96	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	0.017	600	Penile shaft, mucosal epithelial cells	2	Shaft, mucosal	30	12	1.701e-11			
T0013410	1	1	4.07	Gians, mucosal epithelial cells	3	Gians, mucosal	0.998	4,078	Gians, mucosal epithelial cells	3	Gians, mucosal	30	26	0.855	0.145		
T0013710	1	1	5.01	Gians, mucosal epithelial cells	3	Gians, mucosal	0.55	9,109	Gians, mucosal epithelial cells	3	Gians, mucosal	30	27	0.898	0.102		
T0014010	1	1	6.31	Gians, mucosal epithelial cells	3	Gians, mucosal	1.82	3,467	Gians, mucosal epithelial cells	3	Gians, mucosal	28	19	0.903	0.0968		
T0015210	4	2	19.75	Gians, mucosal epithelial cells	3	Gians, mucosal	0.13	151,923	Gians, mucosal epithelial cells	3	Gians, mucosal	30	19	0.977	0.0233		
T0015510	4	2	0.415	Gians, mucosal epithelial cells	3	Gians, mucosal	0.102	4,089	Gians, mucosal epithelial cells	3	Gians, mucosal	30	26	0.775	0.225		
T0015810	4	2	1.3	Gians, mucosal epithelial cells	3	Gians, mucosal	1.08	1,204	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.471	0.529		
T0017010	5	3	4.57	Gians, mucosal epithelial cells	3	Gians, mucosal	0.384	11,901	Gians, mucosal epithelial cells	3	Gians, mucosal	30	27	0.918	0.0819		
T0017310	5	3	3.25	Gians, mucosal epithelial cells	3	Gians, mucosal	0.766	4,243	Gians, mucosal epithelial cells	3	Gians, mucosal	30	29	0.838	0.162		
T0017610	5	3	2.63	Gians, mucosal epithelial cells	3	Gians, mucosal	2.4	1,096	Gians, mucosal epithelial cells	3	Gians, mucosal	27	30	0.126	0.874		
T0018810	6	4	2.29	Gians, mucosal epithelial cells	3	Gians, mucosal	0.449	5.1	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.849	0.151		
T0019110	6	4	2.27	Gians, mucosal epithelial cells	3	Gians, mucosal	0.252	3,008	Gians, mucosal epithelial cells	3	Gians, mucosal	30	27	0.922	0.078		
T0019410	6	4	0.538	Gians, mucosal epithelial cells	3	Gians, mucosal	0.051	10,487	Gians, mucosal epithelial cells	3	Gians, mucosal	30	27	0.908	0.0925		
T0020610	7	5	2.78	Gians, mucosal epithelial cells	3	Gians, mucosal	0.005	579,167	Gians, mucosal epithelial cells	3	Gians, mucosal	30	11	1.234e-10			
T0020910	7	5	2.73	Gians, mucosal epithelial cells	3	Gians, mucosal	0.005	494	Gians, mucosal epithelial cells	3	Gians, mucosal	30	11	1.166e-12			
T002210	7	5	8.49	Gians, mucosal epithelial cells	3	Gians, mucosal	0.155	54,774	Gians, mucosal epithelial cells	3	Gians, mucosal	30	11	1.316e-11			
T0033310	9	6	1.51	Gians, mucosal epithelial cells	3	Gians, mucosal	0.151	10	Gians, mucosal epithelial cells	3	Gians, mucosal	30	29	0.848	0.152		
T0033610	9	6	1.73	Gians, mucosal epithelial cells	3	Gians, mucosal	0.418	4,139	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.791	0.209		
T0033910	9	6	0.327	Gians, mucosal epithelial cells	3	Gians, mucosal	0.212	1,542	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.519	0.481		
T0022410	10	7	0.968	Gians, mucosal epithelial cells	3	Gians, mucosal	0.003	345,714	Gians, mucosal epithelial cells	3	Gians, mucosal	30	13	1.29e-11			
T00222710	10	7	8.22	Gians, mucosal epithelial cells	3	Gians, mucosal	0.037	22,162	Gians, mucosal epithelial cells	3	Gians, mucosal	30	13	1.456e-10			
T0022010	10	7	17.71	Gians, mucosal epithelial cells	3	Gians, mucosal	0.032	50,443	Gians, mucosal epithelial cells	3	Gians, mucosal	30	13	1.29e-10			
T0035110	11	8	1.74	Gians, mucosal epithelial cells	3	Gians, mucosal	0.175	9,943	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.871	0.129		
T0035410	11	8	3.04	Gians, mucosal epithelial cells	3	Gians, mucosal	0.182	16,703	Gians, mucosal epithelial cells	3	Gians, mucosal	30	25	0.946	0.0541		
T0035710	11	8	0.467	Gians, mucosal epithelial cells	3	Gians, mucosal	0.132	3,538	Gians, mucosal epithelial cells	3	Gians, mucosal	30	28	0.867	0.133		
T0024210	12	9	2.38	Gians, mucosal epithelial cells	3	Gians, mucosal	0.353	6,742	Gians, mucosal epithelial cells	3	Gians, mucosal	30	29	0.796	0.204		
T0024510	12	9	2.39	Gians, mucosal epithelial cells	3	Gians, mucosal	0.034	70,294	Gians, mucosal epithelial cells	3	Gians, mucosal	30	12	0.989	0.012		
T0024810	12	9	0.469	Gians, mucosal epithelial cells	3	Gians, mucosal	0.113	70,546	Gians, mucosal epithelial cells	3	Gians, mucosal	30	21	0.984	0.0563		
T0026010	14	10	1.9	Gians, mucosal epithelial cells	3	Gians, mucosal	0.333	5,706	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.871	0.129		
T0026310	14	10	2.27	Gians, mucosal epithelial cells	3	Gians, mucosal	0.972	2,335	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.72	0.28		
T0026610	14	10	2.42	Gians, mucosal epithelial cells	3	Gians, mucosal	1.2	2,017	Gians, mucosal epithelial cells	3	Gians, mucosal	30	30	0.745	0.255		
T0027810	15	11	0.918	Gians, mucosal epithelial cells	3	Gians, mucosal	0.121	7,582	Gians, mucosal epithelial cells	3	Gians, mucosal	30	29	0.862	0.138		
T0028110	15	11	5.29	Gians, mucosal epithelial cells	3	Gians, mucosal	0.112	42,717	Gians, mucosal epithelial cells	3	Gians, mucosal	30	23	0.965	0.0394		
T0028410	15	11	4.57	Gians, mucosal epithelial cells	3	Gians, mucosal	0.046	2,046	Gians, mucosal epithelial cells	3	Gians, mucosal	30	29	0.971	0.029		
T0014110	1	1	0.003	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.004	0.658	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0	0	0	0	0	0
T0044410	1	1	0.008	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.008	1	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0	2	0	0	0	0
T0014710	1	1	0.001	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.001	1	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	6	0	0	0	0	0
T0015910	4	2	0.013	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.022	0.596	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	2	6	0	0	0	0
T0016210	2	1	0.05	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.028	1.75	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	17	30	0.948	0.096		
T0016510	2	1	0.06	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.118	0.899	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	1	30	0.44e-12			
T0017710	5	3	4.74	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	0.098	3.926	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	30	29	0.883	0.117		
T0018010	5	3	6.94	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	3.22	2,155	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	30	30	0.745	0.255		
T0018310	5	3	2.7	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	2.61	1,034	Sulcus Coronavirus, skin epithelial cells	4	Sulcus, skin	30	30	0.32	0.68		

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Sample num	Couple num	Copuple #	Quant total	Category	Category.nu/Cat	Quant y	Tot. Human/ Y-human	Category	Category.nu/Cat	No XX alleles	No XY alleles	Mx (XX)	Mx (XY)
T0019510	6	4	0,001	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,001		1 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	3	7	0	0
T0019810	6	4	0,009	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,009		0,968 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	8	30	2.37e-10	1
T0020110	6	4	0,009	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,007		1,329 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0	0	0	0
T0021310	7	5	0,009	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,01		0,969 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	19	20	0.486	0.514
T0021610	7	5	0,089	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,005		17,82 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	16	6	1.7.39e-11	
T0021910	7	5	0,062	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,007		9,224 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	16	8	0.91	0.0896
T0034010	9	6	10,07	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	21.76		0,463 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	6	12	2.93e-09	1
T0034310	9	6	1.35	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	2.43		0,556 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	11	21	0.0159	0.984
T0034610	9	6	7.72	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	9.69		0,797 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	16	30	7.74e-13	1
T0023110	10	7	0	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,003		0 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	1	4	0	0
T0023410	10	7	0,021	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,012		1,786 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	14	30	2.08e-10	1
T0023710	10	7	0,065	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,1		0,651 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	16	30	0.0177	0.982
T0035810	11	8	0,001	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,004		0,333 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	3	8	0	0
T0036110	11	8	0,038	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,028		1,327 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	16	30	0.0789	0.921
T0036410	11	8	0,001	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,001		1 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	1	1	0	0
T0024910	12	9	0,002	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,002		0,833 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0	0	0	0
T0025210	12	9	0,008	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,007		1,135 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0	0	0	0
T0025510	12	9	0,023	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,014		1,626 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	7	14	0.12	0.88
T0026710	14	10	0,004	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,004		1 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0	0	0	0
T0027010	14	10	0,018	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,03		0,594 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	5	14	0.102	0.898
T0027310	14	10	0,001	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,001		1 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0	0	0	0
T0028510	15	11	0,169	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,151		1,119 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	21	30	0.126	0.874
T0028810	15	11	0,008	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,008		0,976 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0	1	0	0
T0029110	15	11	0,057	Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	0,018		3,269 Sulcus Coronarius, skin epithelial cells	4 Sulcus, skin	30	30	0.734	0.266
T0044210	1	1	0	Penile shaft, skin epithelial cells	5 Shaft, skin	0		1 Penile shaft, skin epithelial cells	5 Shaft, skin	0	4	0	0
T0044510	1	1	0,001	Penile shaft, skin epithelial cells	5 Shaft, skin	0,002		0,417 Penile shaft, skin epithelial cells	5 Shaft, skin	2	7	0	0
T0044810	1	1	0	Penile shaft, skin epithelial cells	5 Shaft, skin	0		1 Penile shaft, skin epithelial cells	5 Shaft, skin	0	7	0	0
T0046010	4	2	0,008	Penile shaft, skin epithelial cells	5 Shaft, skin	0,004		1,951 Penile shaft, skin epithelial cells	5 Shaft, skin	13	16	0.368	0.632
T0046310	4	2	0,154	Penile shaft, skin epithelial cells	5 Shaft, skin	0,171		0,901 Penile shaft, skin epithelial cells	5 Shaft, skin	8	28	6.06e-11	1
T0046610	4	2	0,023	Penile shaft, skin epithelial cells	5 Shaft, skin	0,013		1,779 Penile shaft, skin epithelial cells	5 Shaft, skin	17	30	0.124	0.876
T0017810	3	5	0.89	Penile shaft, skin epithelial cells	5 Shaft, skin	0,031		28.435 Penile shaft, skin epithelial cells	5 Shaft, skin	30	18	0.964	0.0361
T0038110	5	3	0,629	Penile shaft, skin epithelial cells	5 Shaft, skin	0,057		11,113 Penile shaft, skin epithelial cells	5 Shaft, skin	30	29	0.893	0.107
T0018410	5	3	0,137	Penile shaft, skin epithelial cells	5 Shaft, skin	0,107		1,28 Penile shaft, skin epithelial cells	5 Shaft, skin	23	30	0.0649	0.935
T0019610	6	4	0,018	Penile shaft, skin epithelial cells	5 Shaft, skin	0,015		0,578 Penile shaft, skin epithelial cells	5 Shaft, skin	21	30	0.222	0.778
T0019910	6	4	0	Penile shaft, skin epithelial cells	5 Shaft, skin	0,008		0 Penile shaft, skin epithelial cells	5 Shaft, skin	23	22	0.529	0.471
T0020210	6	4	0,013	Penile shaft, skin epithelial cells	5 Shaft, skin	0,011		1,276 Penile shaft, skin epithelial cells	5 Shaft, skin	8	30	0.0129	0.999
T0021419	7	5	0,067	Penile shaft, skin epithelial cells	5 Shaft, skin	0,081		0,824 Penile shaft, skin epithelial cells	5 Shaft, skin	11	30	3.34e-11	1
T0021710	7	5	0,037	Penile shaft, skin epithelial cells	5 Shaft, skin	0,028		1,341 Penile shaft, skin epithelial cells	5 Shaft, skin	23	30	0.133	0.867
T0022010	7	5	0,005	Penile shaft, skin epithelial cells	5 Shaft, skin	0,003		1,96 Penile shaft, skin epithelial cells	5 Shaft, skin	8	17	0.0946	0.905
T0034110	9	6	0,014	Penile shaft, skin epithelial cells	5 Shaft, skin	0,009		1,473 Penile shaft, skin epithelial cells	5 Shaft, skin	18	30	0.0549	0.945
T0034410	9	6	0,019	Penile shaft, skin epithelial cells	5 Shaft, skin	0,016		1,195 Penile shaft, skin epithelial cells	5 Shaft, skin	30	30	0.348	0.652
T0034710	9	6	0,035	Penile shaft, skin epithelial cells	5 Shaft, skin	0,023		1,276 Penile shaft, skin epithelial cells	5 Shaft, skin	29	30	0.163	0.837
T0021210	10	7	0,002	Penile shaft, skin epithelial cells	5 Shaft, skin	0,005		0,46 Penile shaft, skin epithelial cells	5 Shaft, skin	12	19	0.286	0.714
T0023510	10	7	0,013	Penile shaft, skin epithelial cells	5 Shaft, skin	0,017		0,736 Penile shaft, skin epithelial cells	5 Shaft, skin	14	26	0.0562	0.944
T0023810	10	7	0,272	Penile shaft, skin epithelial cells	5 Shaft, skin	0,285		0,954 Penile shaft, skin epithelial cells	5 Shaft, skin	14	30	8.53e-13	1
T0035910	11	8	0,045	Penile shaft, skin epithelial cells	5 Shaft, skin	0,056		0.8 Penile shaft, skin epithelial cells	5 Shaft, skin	10	30	0.00652	0.993
T0036210	11	8	0,048	Penile shaft, skin epithelial cells	5 Shaft, skin	0,022		2,176 Penile shaft, skin epithelial cells	5 Shaft, skin	30	30	0.486	0.514
T0036510	11	8	0,226	Penile shaft, skin epithelial cells	5 Shaft, skin	0,343		0,659 Penile shaft, skin epithelial cells	5 Shaft, skin	15	30	0.0103	0.99
T0025010	12	9	0,01	Penile shaft, skin epithelial cells	5 Shaft, skin	0,009		1,074 Penile shaft, skin epithelial cells	5 Shaft, skin	16	29	0.0629	0.937
T0025310	12	9	0,026	Penile shaft, skin epithelial cells	5 Shaft, skin	0,019		1,359 Penile shaft, skin epithelial cells	5 Shaft, skin	18	30	0.0769	0.923
T0025610	12	9	0,02	Penile shaft, skin epithelial cells	5 Shaft, skin	0,019		1,053 Penile shaft, skin epithelial cells	5 Shaft, skin	16	30	0.067	0.933

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Sample num	Couple num	Copuple #	Quant total	Category	Category.nu/Cat	Quant y	Tot. Human/ Y-human	Category	Category.nu/Cat	No XX alleles	No XY alleles	Mx (XX)	Mx (XY)
T0025810	14	10	0,047	Penile shaft, skin epithelial cells	5 Shaft, skin	0,064		0,745 Penile shaft, skin epithelial cells	5 Shaft, skin	15	30	0.0753	0.925
T0027110	14	10	0,391	Penile shaft, skin epithelial cells	5 Shaft, skin	0,148		3,995 Penile shaft, skin epithelial cells	5 Shaft, skin	30	30	0.786	0.214
T0027410	14	10	0,213	Penile shaft, skin epithelial cells	5 Shaft, skin	0,224		0,951 Penile shaft, skin epithelial cells	5 Shaft, skin	12	30	0.0239	0.976
T0028610	15	11	1.69	Penile shaft, skin epithelial cells	5 Shaft, skin	0,054		31,296 Penile shaft, skin epithelial cells	5 Shaft, skin	30	24	0.973	0.0272
T0028910	15	11	0,049	Penile shaft, skin epithelial cells	5 Shaft, skin	0,052		0,944 Penile shaft, skin epithelial cells	5 Shaft, skin	11	30	0.02	0.98
T0029210	15	11	0,529	Penile shaft, skin epithelial cells	5 Shaft, skin	0,05		10,517 Penile shaft, skin epithelial cells	5 Shaft, skin	30	26	0.946	0.0536
T0014310	1	1	0,004	Glands, skin epithelial cells	6 Glands, skin	0,002		1,542 Glands, skin epithelial cells	6 Glands, skin	0	5	0	0
T0044610	1	1	0,001	Glands, skin epithelial cells	6 Glands, skin	0,003		0.4 Glands, skin epithelial cells	6 Glands, skin	1	7	0	0
T0014910	1	1	0,006	Glands, skin epithelial cells	6 Glands, skin	0,016		0,391 Glands, skin epithelial cells	6 Glands, skin	9	23	0.0815	0.918
T0016110	4	2	0	Glands, skin epithelial cells	6 Glands, skin	0,002		0 Glands, skin epithelial cells	6 Glands, skin	0	0	0	0
T0016410	4	2	0,028	Glands, skin epithelial cells	6 Glands, skin	0,024		1,196 Glands, skin epithelial cells	6 Glands, skin	8	29	3.58e-09	1
T0016710	4	2	0,012	Glands, skin epithelial cells	6 Glands, skin	0,017		0,699 Glands, skin epithelial cells	6 Glands, skin	8	30	6.14e-11	1
T0017910	5	3	4.63	Glands, skin epithelial cells	6 Glands, skin	0,147		31,497 Glands, skin epithelial cells	6 Glands, skin	30	18	0.978	0.0222
T0018210	5	3	3.85	Glands, skin epithelial cells	6 Glands, skin	1.08		3,565 Glands, skin epithelial cells	6 Glands, skin	30	30	0.76	0.24
T0018510	5	3	0,893	Glands, skin epithelial cells	6 Glands, skin	0,941		0,949 Glands, skin epithelial cells	6 Glands, skin	22	30	0.0556	0.944
T0019710	6	4	0,001	Glands, skin epithelial cells	6 Glands, skin	0,0201		0,035 Glands, skin epithelial cells	6 Glands, skin	2	5	0	0
T0020010	6	4	0	Glands, skin epithelial cells	6 Glands, skin	0,008		0 Glands, skin epithelial cells	6 Glands, skin	4	17	1.06e-08	1
T0020310	6	4	0,006	Glands, skin epithelial cells	6 Glands, skin	0,004		1,703 Glands, skin epithelial cells	6 Glands, skin	6	16	1.28e-10	1
T0021510	7	5	0,013	Glands, skin epithelial cells	6 Glands, skin	0,008		1,536 Glands, skin epithelial cells	6 Glands, skin	14	8	0.745	0.255
T0021810	7	5	0,026	Glands, skin epithelial cells	6 Glands, skin	0,002		10,792 Glands, skin epithelial cells	6 Glands, skin	30	11	1.448e-10	
T0022110	7	5	0,012	Glands, skin epithelial cells	6 Glands, skin	0,001		11.5 Glands, skin epithelial cells	6 Glands, skin	27	18	0.795	0.205
T0034210	9	6	1.74	Glands, skin epithelial cells	6 Glands, skin	2.39		0,728 Glands, skin epithelial cells	6 Glands, skin	10	21	3.18e-12	1
T0034510	9	6	0,255	Glands, skin epithelial cells	6 Glands, skin	0,286		0,892 Glands, skin epithelial cells	6 Glands, skin	13	26	1.32e-09	1
T0034810	9	6	0.7	Glands, skin epithelial cells	6 Glands, skin	0,762		0,919 Glands, skin epithelial cells	6 Glands, skin	17	30	0.00735	0.993
T0023310	10	7	0,002	Glands, skin epithelial cells	6 Glands, skin	0,001		1.6 Glands, skin epithelial cells	6 Glands, skin	0	0	0	0
T0023610	10	7	0,004	Glands, skin epithelial cells	6 Glands, skin	0,009		0,389 Glands, skin epithelial cells	6 Glands, skin	1	5	0	0
T0023910	10	7	0,182	Glands, skin epithelial cells	6 Glands, skin	0,189		0,963 Glands, skin epithelial cells	6 Glands, skin	5	10	0	0
T0036010	11	8	0,012	Glands, skin epithelial cells	6 Glands, skin	0,015		0,792 Glands, skin epithelial cells	6 Glands, skin	9	30	1.28e-09	1
T0036310	11	8	1.17	Glands, skin epithelial cells	6 Glands, skin	0,03		39,661 Glands, skin epithelial cells	6 Glands, skin	8	22	0.0553	0.945
T0036610	11	8	0,02	Glands, skin epithelial cells	6 Glands, skin	0,021		0,976 Glands, skin epithelial cells	6 Glands, skin	9	30	1.81e-10	1
T0025110	12	9	0	Glands, skin epithelial cells	6 Glands, skin	0		0 Glands, skin epithelial cells	6 Glands, skin	0	0	0	0
T0025410	12	9	0,001	Glands, skin epithelial cells	6 Glands, skin	0,001		0.9 Glands, skin epithelial cells	6 Glands, skin	2	4	0	0
T0025710	12	9	0,003	Glands, skin epithelial cells	6 Glands, skin	0,003		1,067 Glands, skin epithelial cells	6 Glands, skin	2	9	0	0
T0026910	14	10	0,004	Glands, skin epithelial cells	6 Glands, skin	0,004		0,925 Glands, skin epithelial cells	6 Glands, skin	1	5	0	0
T0027210	14	10	0,076	Glands, skin epithelial cells	6 Glands, skin	0,079		0,958 Glands, skin epithelial cells	6 Glands, skin	5	11	0.0803	0.92
T0027510	14	10	0,006	Glands, skin epithelial cells	6 Glands, skin	0,009		0,685 Glands, skin epithelial cells	6 Glands, skin	4	6	0	0
T0028710	15	11	0,024	Glands, skin epithelial cells	6 Glands, skin	0,022		1.1 Glands, skin epithelial cells	6 Glands, skin	26	30	0.243	0.757
T0029010	15	11	0,018	Glands, skin epithelial cells	6 Glands, skin	0,02		0,899 Glands, skin epithelial cells	6 Glands, skin	10	30	0.0323	0.968
T0029310	15	11	0,057	Glands, skin epithelial cells	6 Glands, skin	0,023		2,535 Glands, skin epithelial cells	6 Glands, skin	30	29	0.832	0.168

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