

The following profile comes from case [REDACTED] P2: (Sexual Offences): 6.11 (starting at page 41)

I refer to this profile in section 5.10 of my report dated 21/11/2022

It is sample [REDACTED] an endocervical swab from an alleged rape victim

The next four slides show the 4 different dye lanes of the DNA profile at full scale (upper half) and zoomed in on the baseline (lower half)

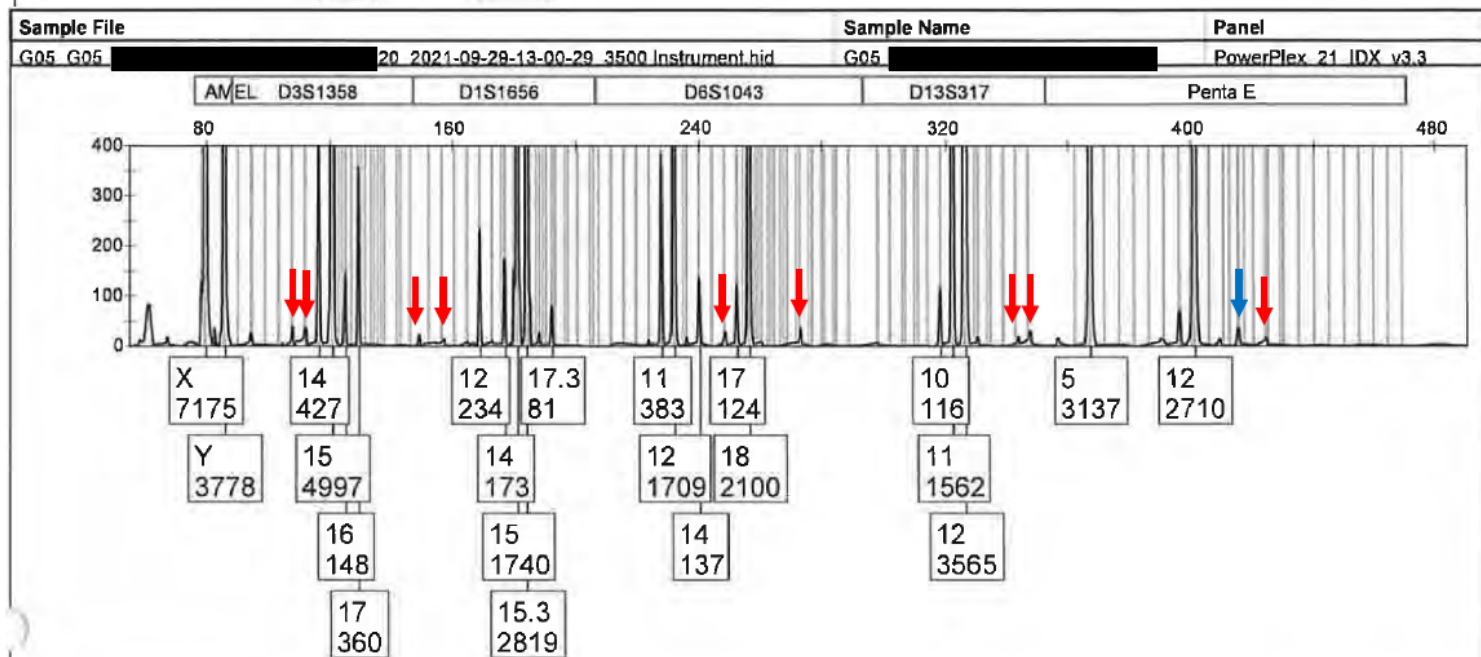
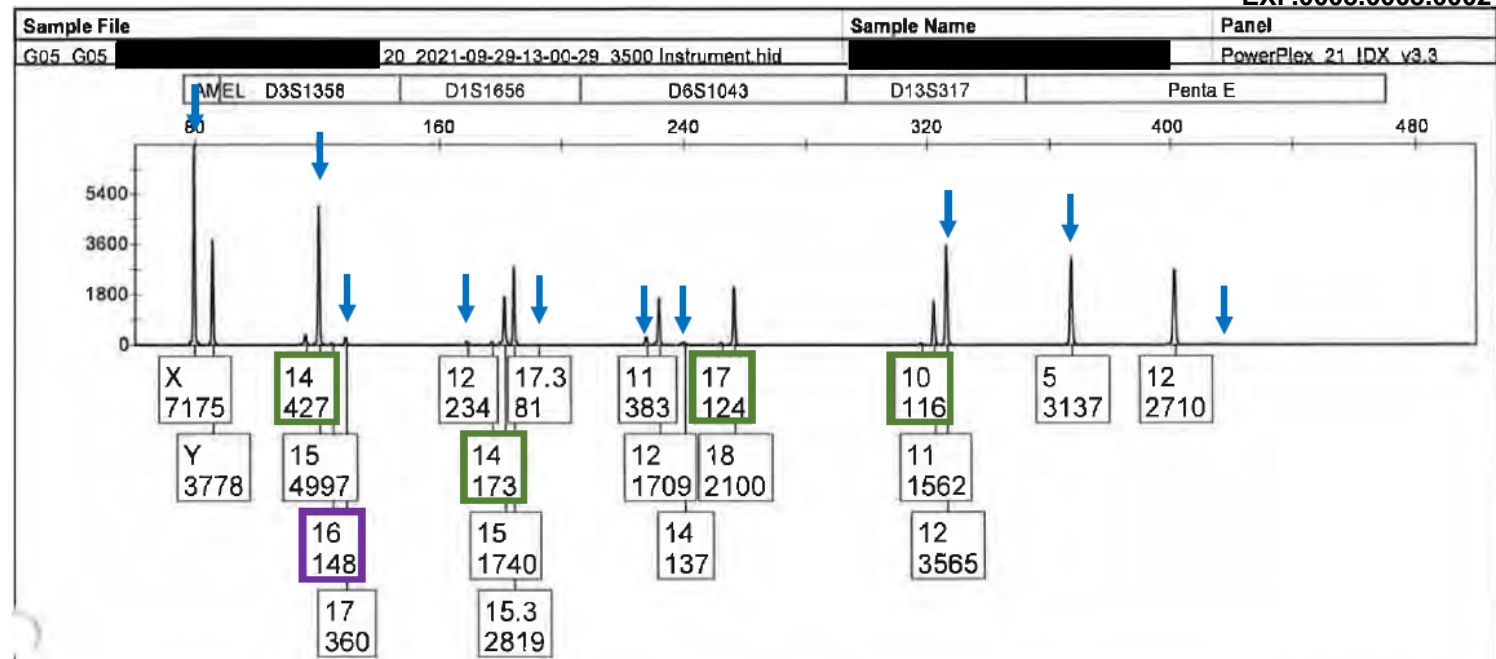
I have annotated the profiles to assist with interpretation based on the information that should be used during interpretation (i.e. the evidence profile and the victim's reference profile)

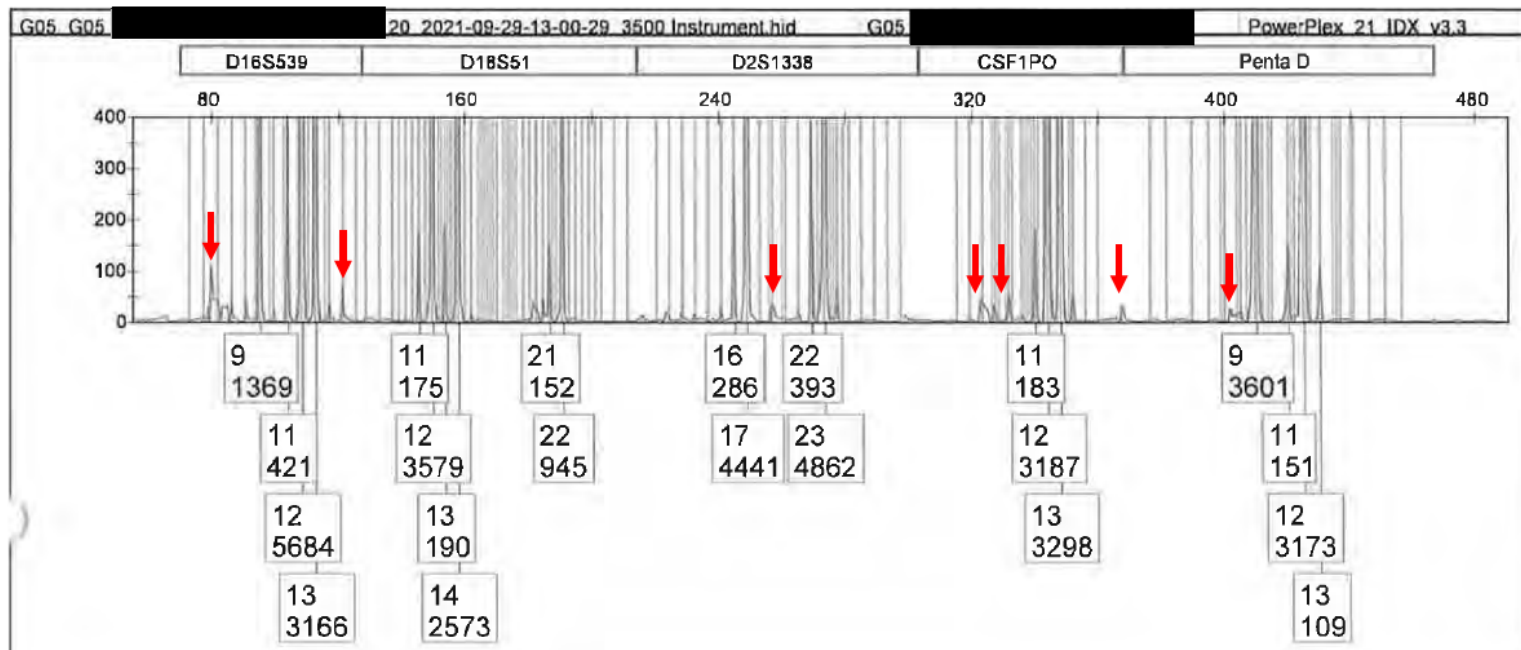
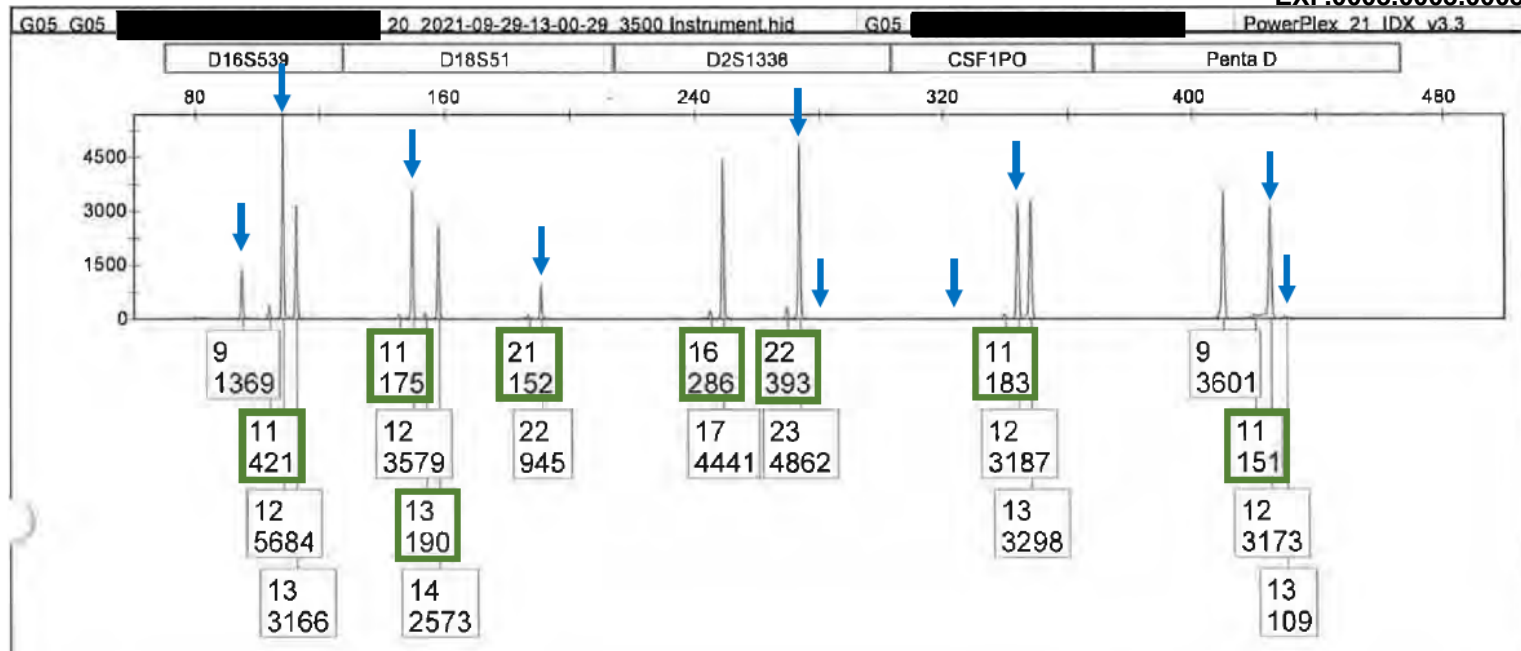
↓ Alleles corresponding to the victim  
(assumed to be a contributor of  
DNA to the sample)

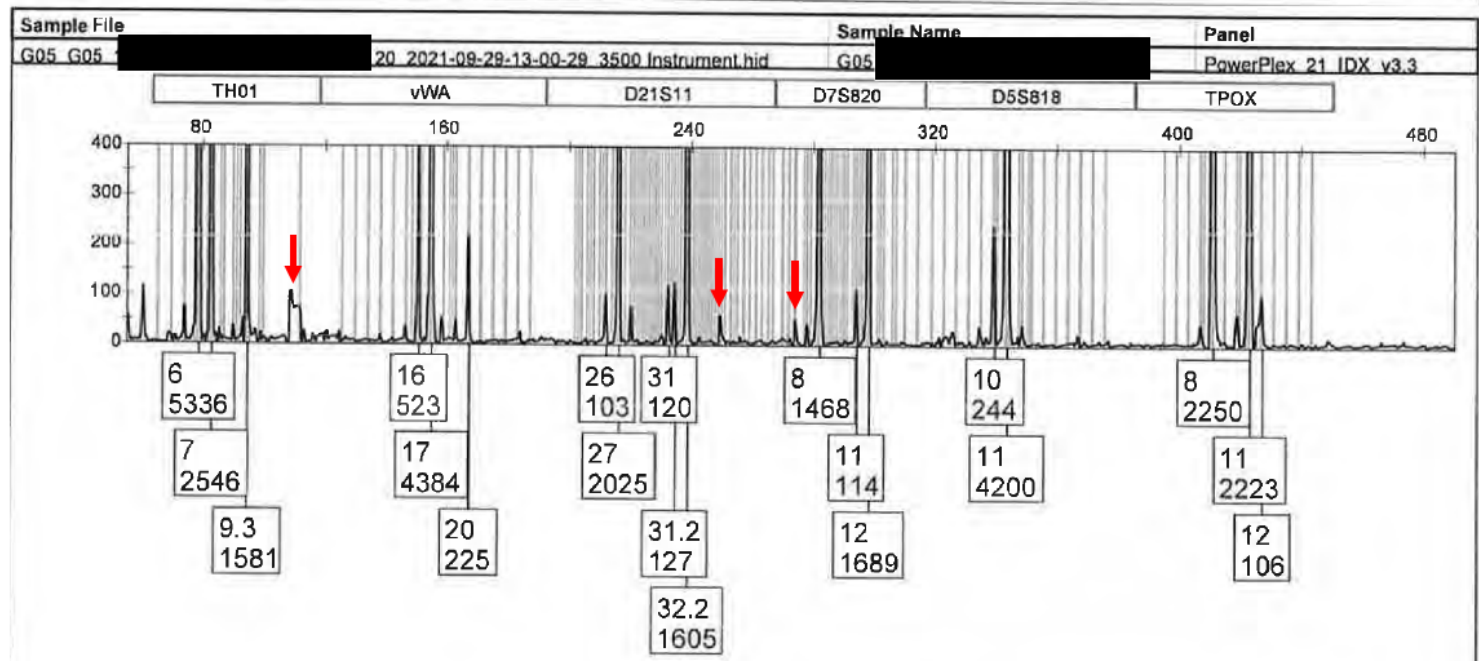
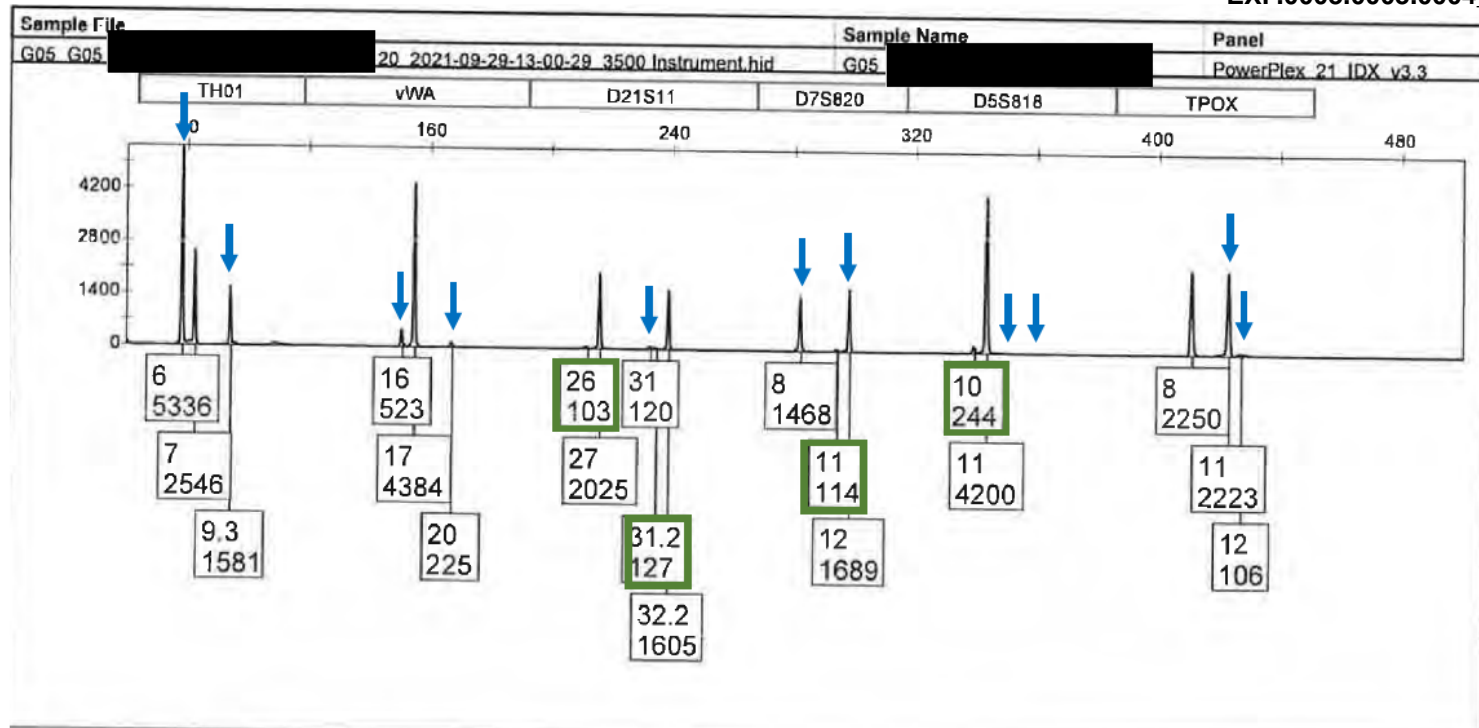
↓ Pull-up artefact peaks (not counted  
towards assigning a number of  
contributors)

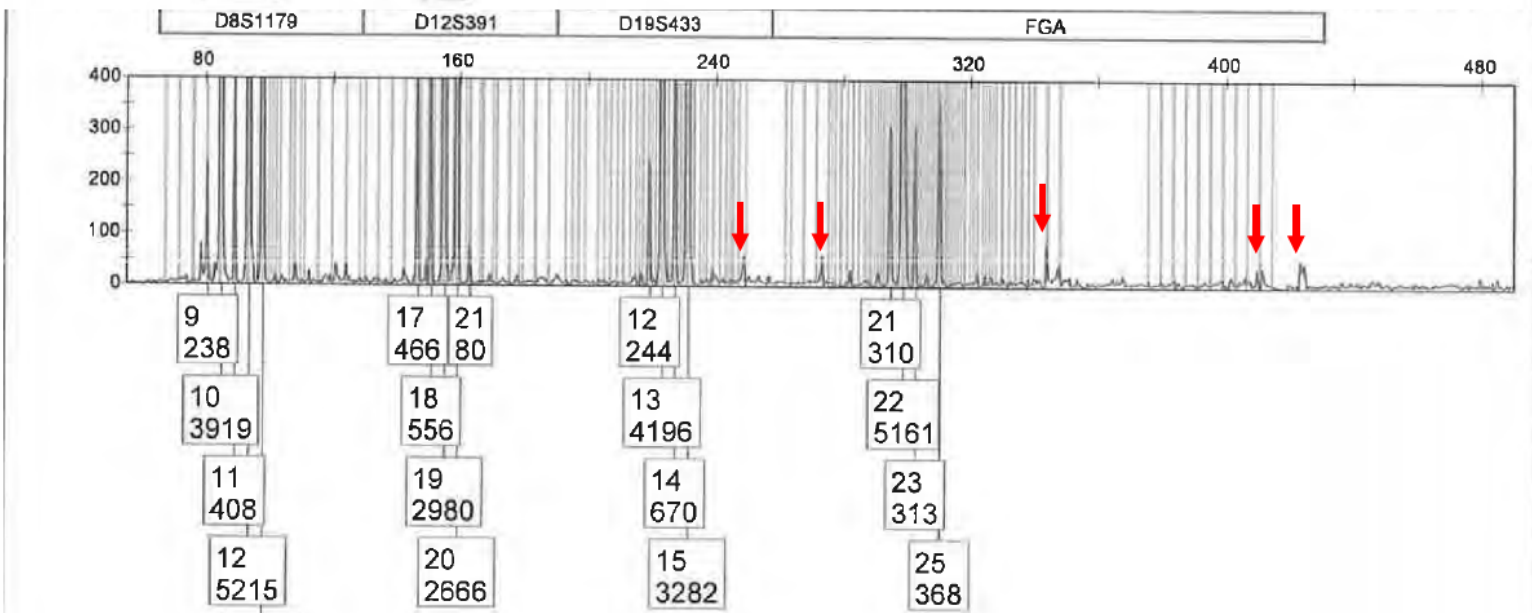
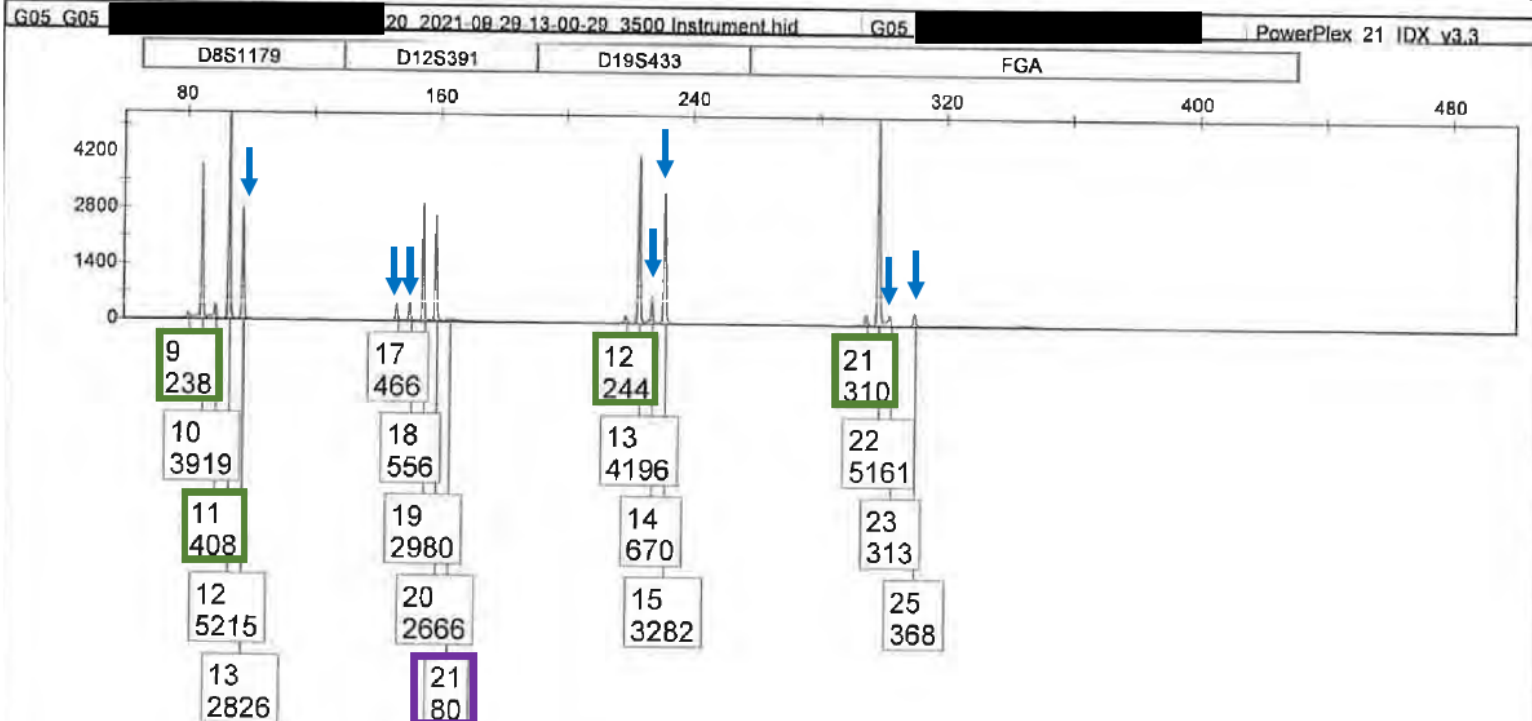
□ Peaks in stutter positions that fall  
below the QH threshold

□ Peaks in stutter positions that fall  
above the QH threshold (which I  
assume is being used to drive the  
assignment of three contributors)









D3S1358

D12S391

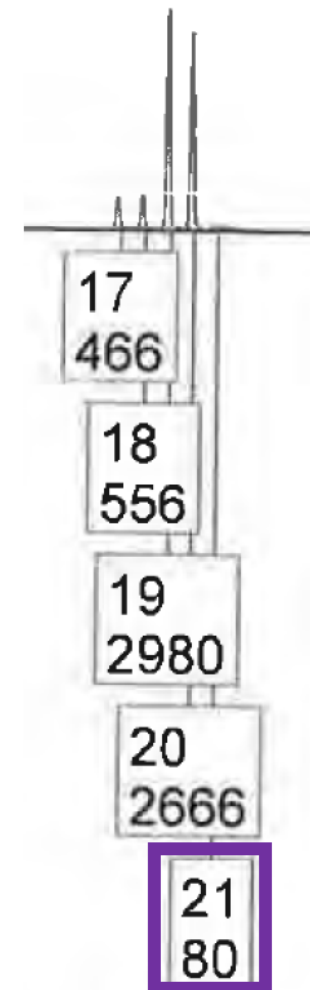
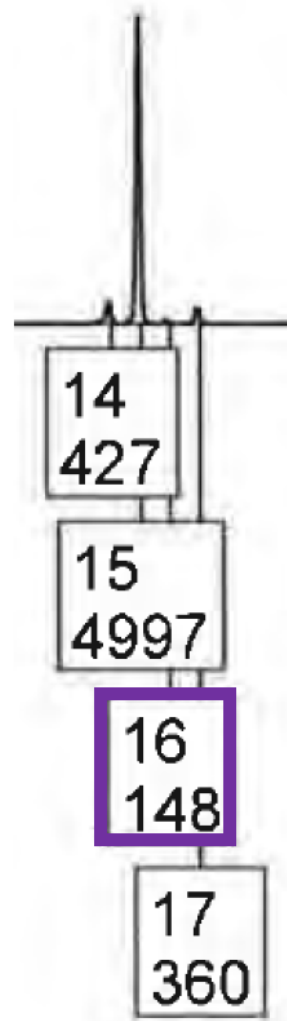
Looking at these two peaks

These are very minor indications that an additional contributor might be present

Using the QH stutter threshold we might expect to see the 16 peak at D2S1358 up to 123rfu and it is observed here at 148rfu

Similarly we might expect to see the 21 peak at D12S391 at 68rfu and it is observed here at 80rfu

Looking at the STRmix analysis to see how often it required these peaks to be allelic in the minor component can also give an indication of how much 'need' there is for these peaks to be allelic



This table shows which peaks were considered as allelic > 99% of the time for each contributor during the STRmix analysis

Notice that at D3S1358 the 16 peak is not present and at D12S391 the 21 peak is not present, meaning that the analysis did not 'need' them to be allelic to explain the profile

I would have personally considered those peaks as high stutters and analysed the profile as a 2-person mixture

As a minimum I would have requested a rework (second PCR amplification) to investigate the nature of these peaks before assigning the profile as coming from three people

LOCUS	CONTRIBUTORS		
	1 (23.45%)	2 (75.67%)	3 (0.88%)
D3S1358	15, 17	15, 15	0, 0
D1S1656	12, 17.3	15, 15.3	0, 0
D6S1043	11, 14	12, 18	0, 0
D13S317	12, 12	11, 12	0, 0
Penta E	5, 15	5, 12	0, 0
D16S539	9, 12	12, 13	0, 0
D18S51	12, 22	12, 14	0, 0
D2S1338	23, 24	17, 23	0, 0
CSF1PO	9, 12	12, 13	0, 0
Penta D	11, 13	9, 12	0, 0
TH01	6, 9.3	6, 7	0, 0
vWA	16, 20	17, 17	0, 0
D21S11	31, 31	27, 32.2	0, 0
D7S820	8, 12	8, 12	0, 0
D5S818	12, 13	11, 11	0, 0
TPOX	11, 12	8, 11	0, 0
D8S1179	13, 13	10, 12	0, 0
D12S391	17, 18	19, 20	0, 0
D19S433	13, 14	13, 15	0, 0
FGA	23, 25	22, 22	0, 0