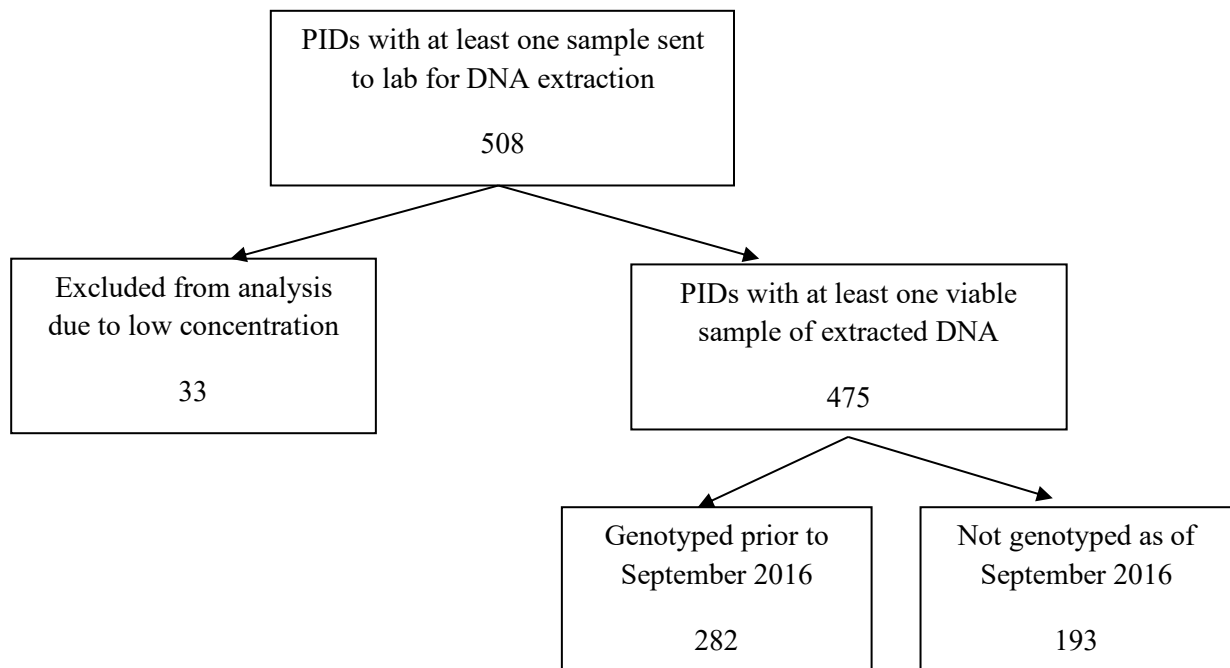


EPOCH I & II: Child DNA Sample Inventory

Participation	Sent to lab for extraction
E1 & E2	240
E1 only	112
E2 only	123
TOTAL	508



Total PIDs with extracted DNA eligible for genotyping = 193 (40%)

PID genotyped?	N (%)
No	193 (40.6)
Yes	282 (59.4)
Total	475 (100.0)

Participation summary of remaining PIDs eligible for genotyping

Characteristics of remaining Child PIDs eligible for genotyping
Source: FreezerPro

Sex	Frequency	Cumulative Frequency
Female	90	90
Male	88	178

Frequency Missing = 15

Exposure_Status	Frequency	Cumulative Frequency
Exposed	14	14
Not Exposed	164	178

Frequency Missing = 15

Table of Exposure_Status by Sex				
Frequency				
Row Pct	Exposure_Status	Sex		
Col Pct		Fema	Male	Total
	Exposed	6	8	14
	Not Exposed	84	80	164

Total	90	88	178
--------------	----	----	-----

Frequency Missing = 15

Summary:

We have maternal samples from EPOCH I, but they have not yet undergone DNA extraction. This means we'd have to plan for the additional cost of DNA extraction and assume that our sample size would be smaller after extraction. The sample size of maternal DNA I provided you last night represents how many DNA samples were obtained and stored, but we would expect that some samples wouldn't pass quality control.

After extraction of EPOCH I child DNA, 26/362 (7.2%) of the samples were excluded due to low concentration. The proportion of exclusions was much higher in the EPOCH II child DNA extractions, but I've been told that was likely due to an error in how the samples were stored before extraction. So if for any reason you need to forecast the final sample size of maternal DNA, 7.2% could serve as an estimate of how much our sample size would decrease after extraction.

EPOCH Mother-Child Pairs

The FREQ Procedure

Exposure_Status	Frequency	Cumulative Frequency
Exposed	109	109
Not Exposed	437	546

The FREQ Procedure

Sex	Frequency	Cumulative Frequency
Fema	277	277
Male	269	546

Y:\EPOCH EPIGENETIC\EPOCH_I_II_DNASampleList_Nov2015