

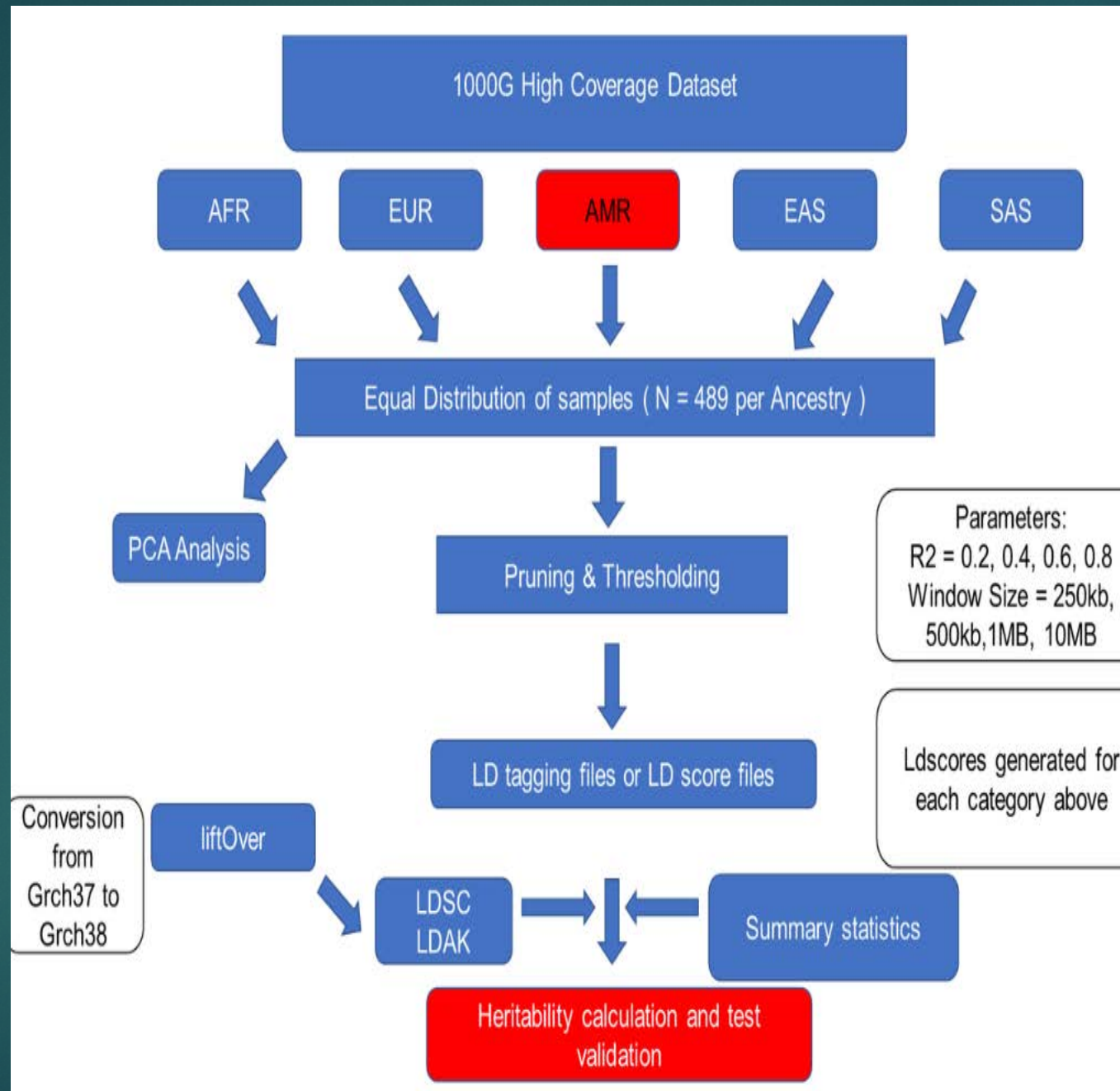


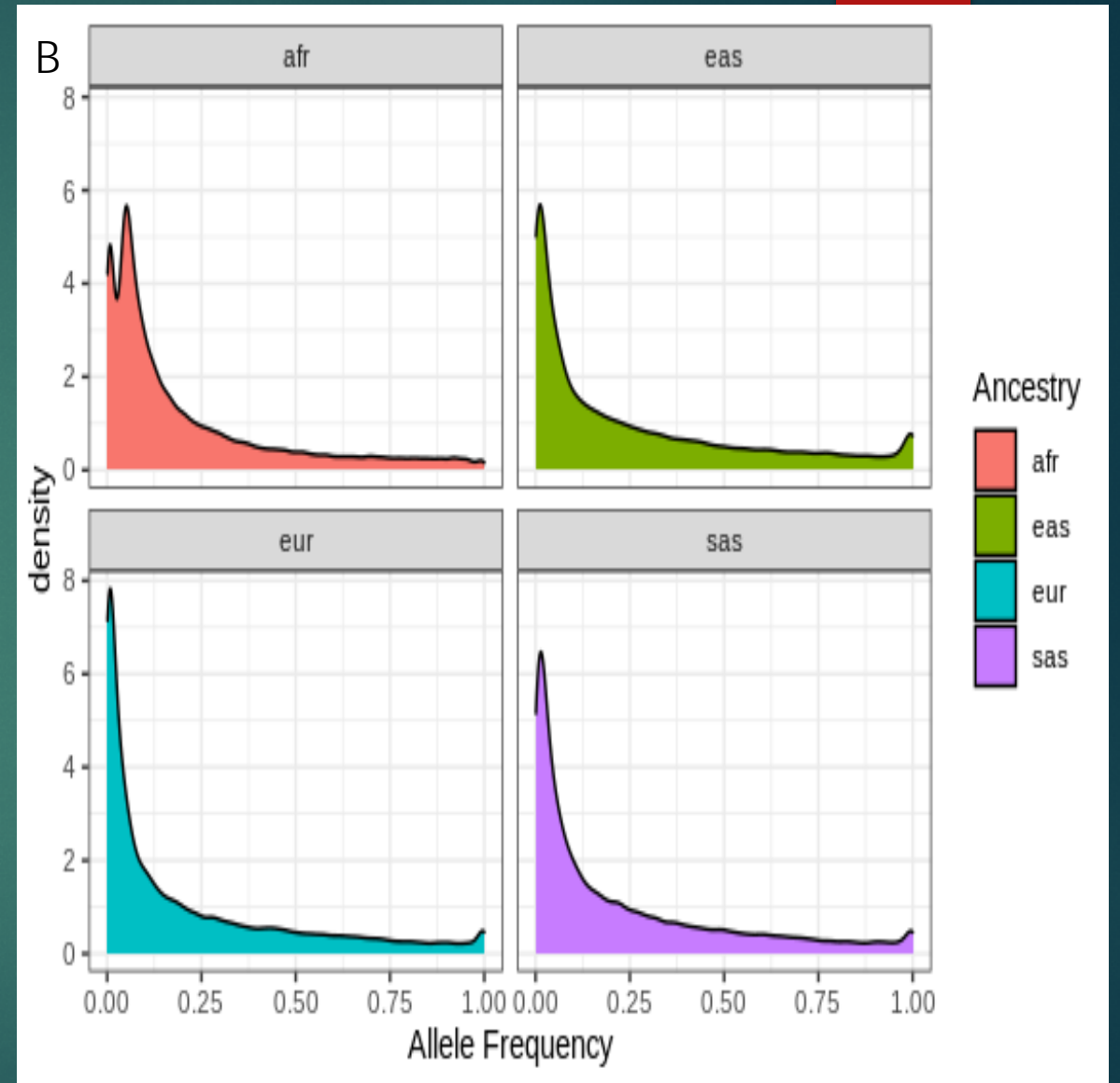
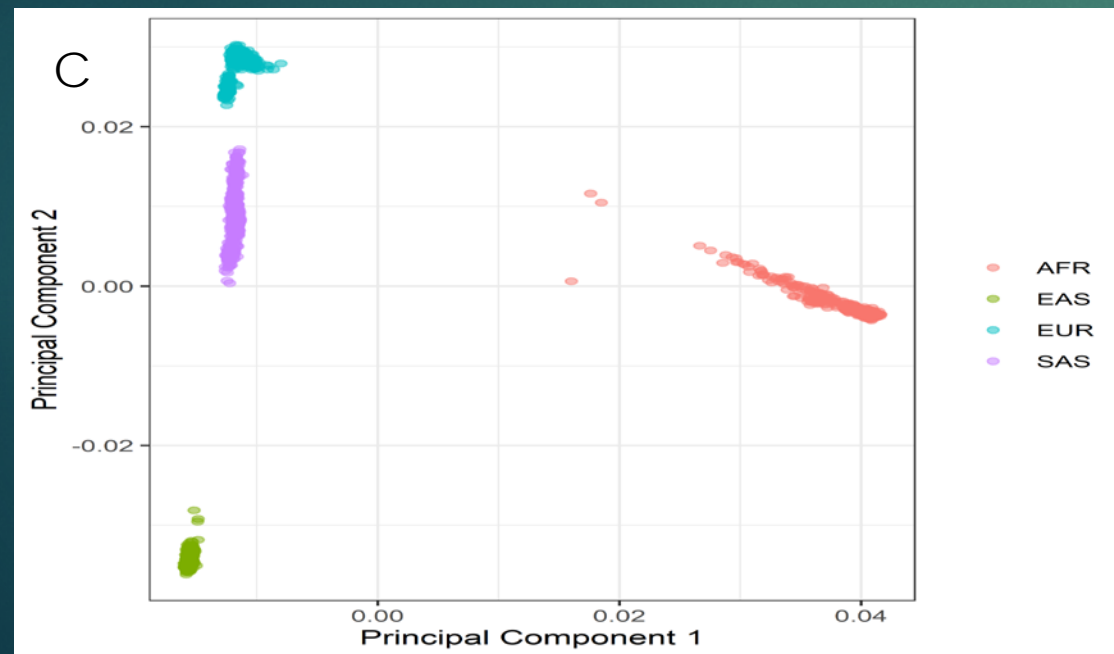
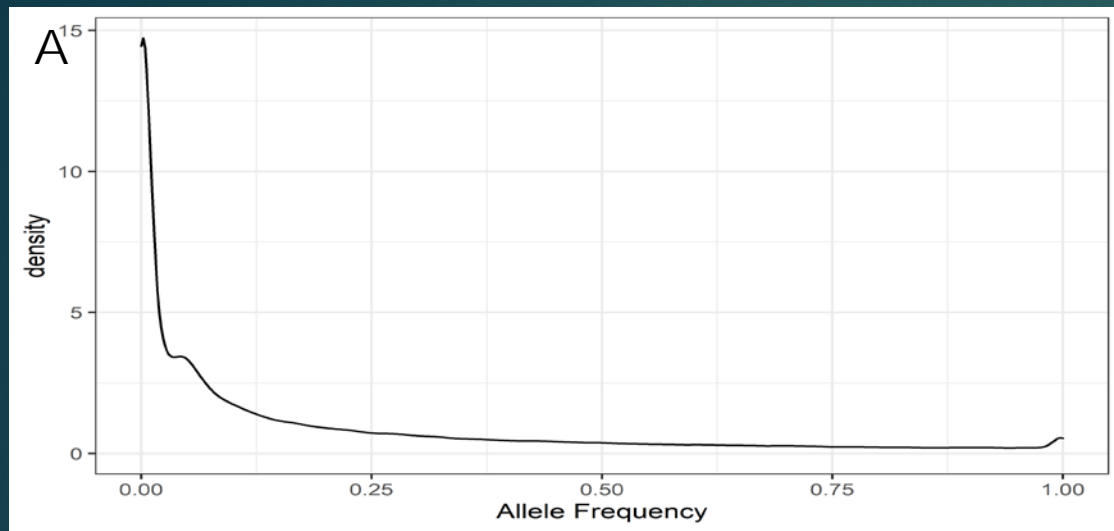
Quantifying Combined Heritability of a Trait Based on a Multi-Ethnic LD Panel with Equal Distribution of Individuals among Ancestry Groups

By
Team HeriVar

Hypothesis

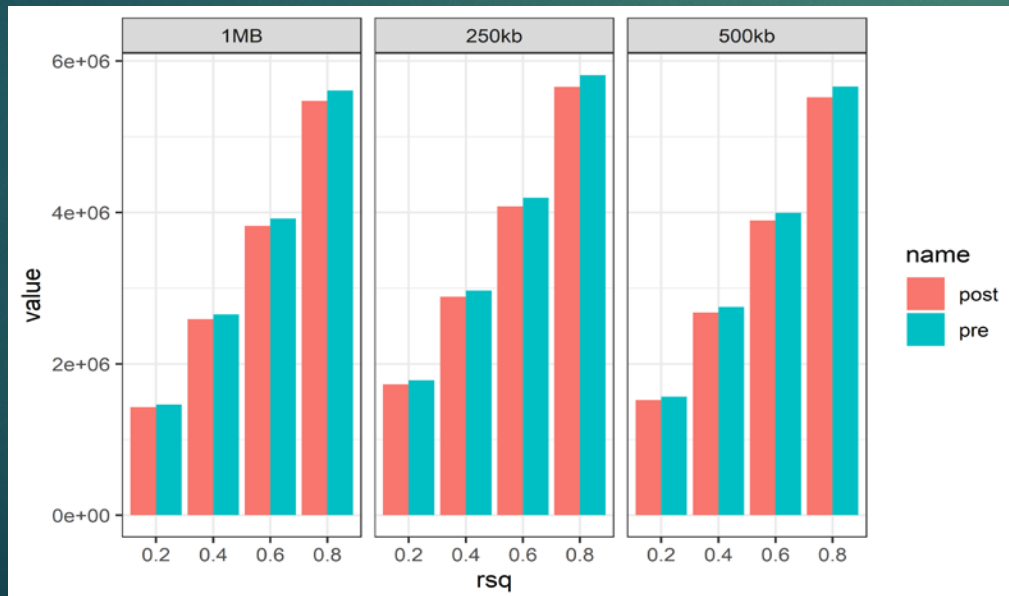
- Number of variants among each ancestry accounts for LD structure for that group.
- When there is an equal distribution of individuals per ancestry group, chances of identifying the combined heritability of a trait will be maximized





Pruning & Thresholding

- ▶ We did pruning and thresholding based on coefficient of determination (R^2) and window size parameters as below
 - ▶ R^2 cutoff: 0.2, 0.4, 0.6, and 0.8.
 - ▶ Window size: 250kb, 500kb, 1Mb & 10Mb.



Variants After Pruning & Thresholding			
R2	Window Size	Variants Pre High LD regions removed	Variants Post High LD regions removed
0.2	1MB	1464882	1428081
	10MB	1419960	Couldn't complete
	250kb	1781998	1729865
	500kb	1564861	1522257
0.4	1MB	2654295	2589766
	10MB	2614719	Couldn't complete
	250kb	2969688	2887059
	500kb	2749811	2678502
0.6	1MB	3917502	3822824
	10MB	3886309	Couldn't complete
	250kb	4192945	4079616
	500kb	3996646	3895068
0.8	1MB	5608699	5471764
	10MB	5588520	Couldn't complete
	250kb	5814383	5660504
	500kb	5662838	5519777

Reference Panel Generation

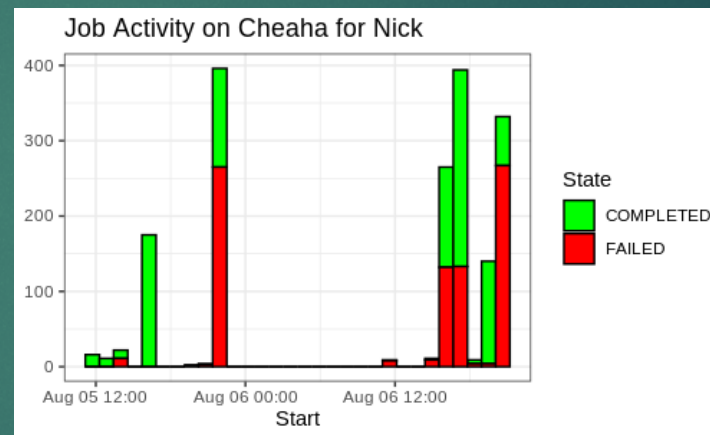
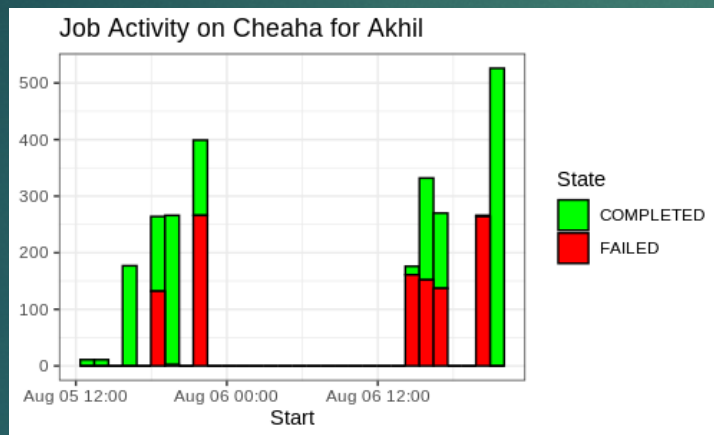
- ▶ We generated LD scores for pre/post pruned datasets using LDSC and worked on tagging files using LDAK.

Heritability Calculations

- ▶ Data needed for heritability calculation were generated.
- ▶ We could not able to complete the project because of time constraints.

Technical Milestones

- ▶ We ran 4469 task array jobs over the span of two days.
 - ▶ 93 jobs per hour → 1.5 jobs per minute



- ▶ 90 % of the project was completed in the span of two days.
- ▶ We managed to replicate each step in JetStream2 and credit goes to Frank.