Sample Reuse

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Recovery Rate

Table 1: Number of genome-wide significant SNPs recovered by standard and SynSurr GWAS across increasing ablation of the target phenotype. The oracle method establishes the number of genome-wide significant (GWS) variants ($p < 5 \times 10^{-8}$) that would be identified in the absence of missingness. Missingness was introduced by ablating 25%, 50%, 75%, and 90% of the target phenotypes. Standard and SynSurr GWAS were performed on each of the ablated data sets.

	Height				FEV1			
Missing Rate (%)	n_{obs}	Oracle	Standard	SynSurr	n_{obs}	Oracle	Standard	SynSurr
25	262,105	7,177	4,896(68.22%)	5,169(72.02%)	231,388	974	546(56.06%)	673(69.09%)
50	174,737	7,177	2,742(38.21%)	3,319(46.24%)	$154,\!259$	974	278(28.54%)	476(48.87%)
75	87,368	7,177	834(11.62%)	1,325(18.46%)	77,129	974	60(6.16%)	238(24.43%)
90	34,947	$7,\!177$	192 (2.68%)	320(4.46%)	30,852	974	0(0%)	60(6.16%)

False Discovery Rate

Table 2: False positive discoveries of the standard GWAS and the SynSurr GWAS across various missing rates. The false positive discovery was rate defined as the number of SNPs that are significant in the standard or SynSurr GWAS, but not in the oracle GWAS.

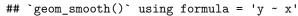
	Hei	ght	FEV1			
$Missing \ Rate(\%)$	Standard	SynSurr	Standard	SynSurr		
25	75(0.017%)	82(0.018%)	19(0.004%)	80(0.018%)		
50	18(0.004%)	27(0.006%)	6(0.001%)	101(0.023%)		
75	1(0%)	4(0%)	0(0%)	80(0.018%)		
90	0(0%)	1(0%)	0(0%)	14(0.003%)		

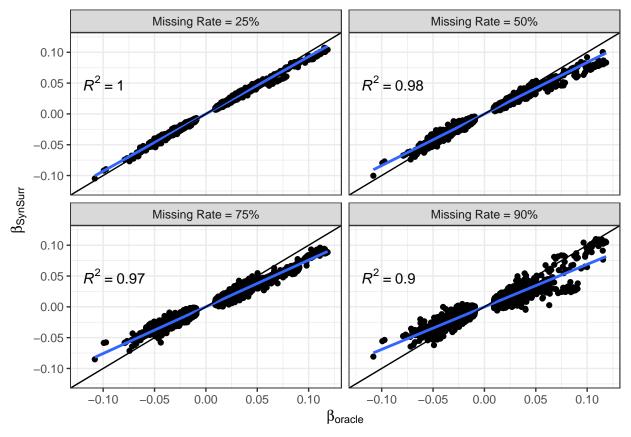
Effect Size Estimate

Height

```
##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
## filter, lag
```

```
## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union
## Warning: The dot-dot notation (`..rr.label..`) was deprecated in ggplot2 3.4.0.
## i Please use `after_stat(rr.label)` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```





FEV1

`geom_smooth()` using formula = 'y ~ x'

