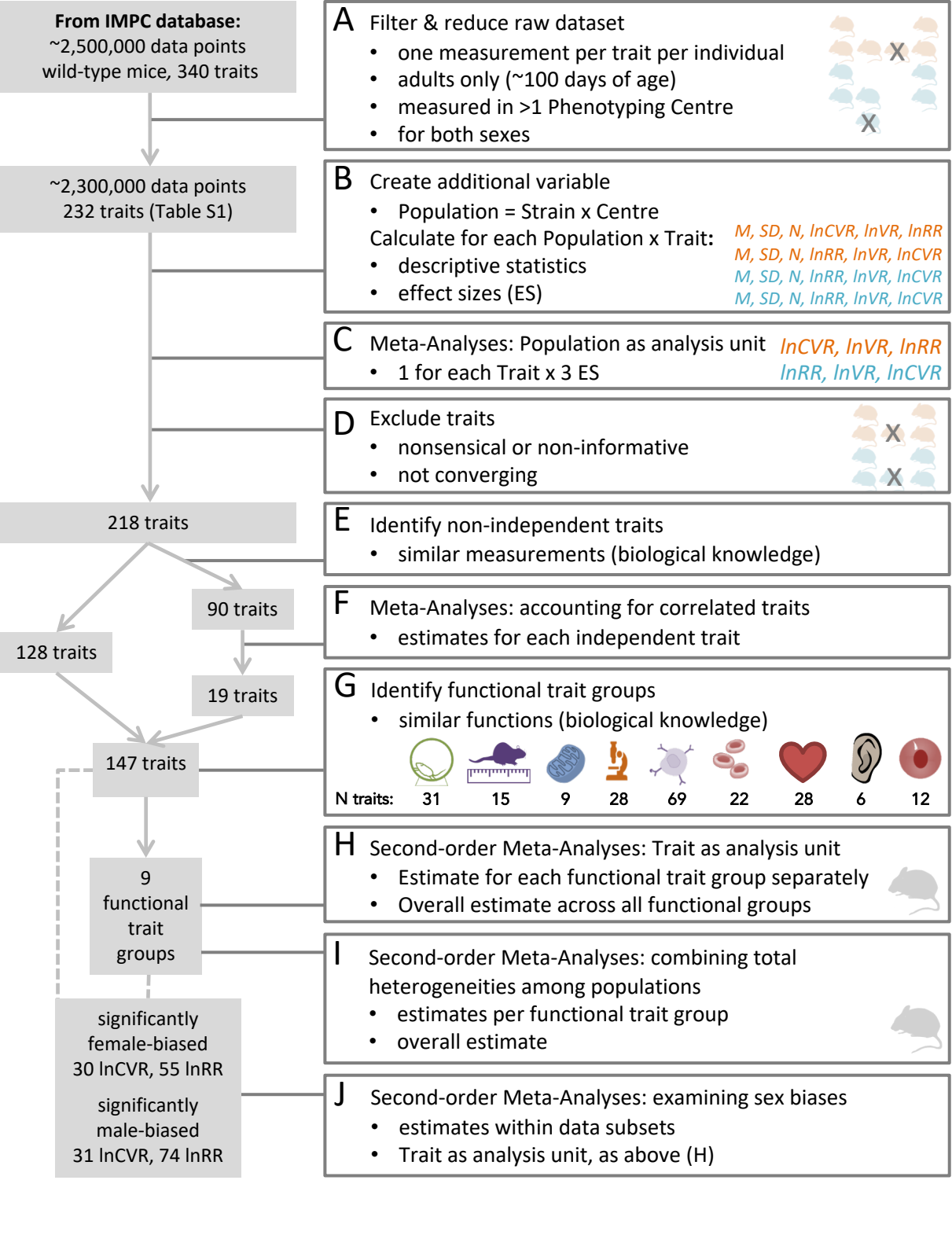
From IMPC database:
~2,500,000 data points
wild-type mice, 340 traits
A Filter & reduce raw dataset
• one measurement per trait per individual
• adults only (~100 days of age)
• measured in >1 Phenotyping Centre
• for both sexes
X
X
~2,300,000 data points
232 traits (Table S1)
B Create additional variable
• Population = Strain x Centre
Calculate for each Population x Trait:
• descriptive statistics
• effect sizes (ES)
M, SD, N, lnCVR, lnVR, lnRR
M, SD, N, lnRR, lnVR, lnCVR
M, SD, N, lnRR, lnVR, lnCVR
M, SD, N, lnRR, lnVR, lnCVR
C Meta-Analyses: Population as analysis unit
• 1 for each Trait x 3 ES
lnCVR, lnVR, lnRR
lnRR, lnVR, lnCVR
D Exclude traits
• nonsensical or non-informative
• not converging
X
X
218 traits
E Identify non-independent traits
• similar measurements (biological knowledge)
90 traits
128 traits
19 traits
F Meta-Analyses: accounting for correlated traits
• estimates for each independent trait
147 traits
G Identify functional trait groups
• similar functions (biological knowledge)
N traits: 31 15 9 28 69 22 28 6 12
9 functional trait groups
H Second-order Meta-Analyses: Trait as analysis unit
• Estimate for each functional trait group separately
• Overall estimate across all functional groups
I Second-order Meta-Analyses: combining total heterogeneities among populations
• estimates per functional trait group
• overall estimate
significantly female-biased
30 lnCVR, 55 lnRR
significantly male-biased
31 lnCVR, 74 lnRR
J Second-order Meta-Analyses: examining sex biases
• estimates within data subsets
• Trait as analysis unit, as above (H)