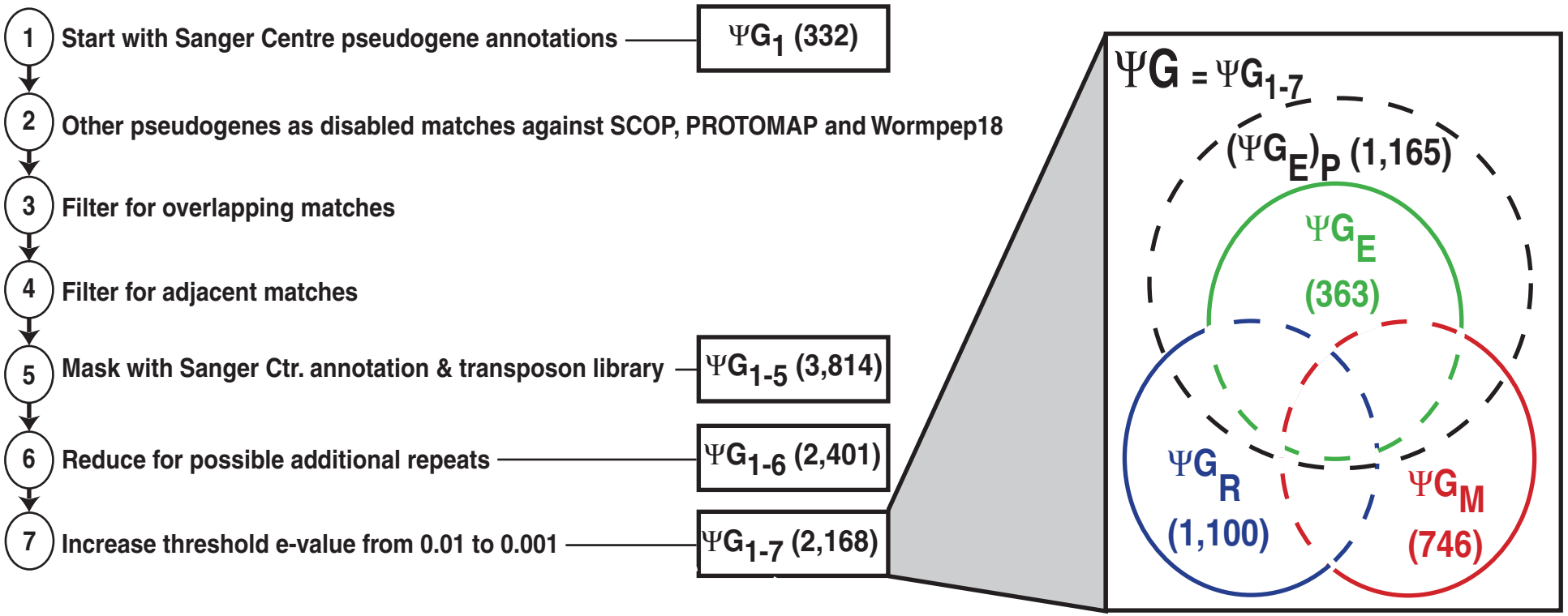
1
Start with Sanger Centre pseudogene annotations
ΨG1 (332)
2
Other pseudogenes as disabled matches against SCOP, PROTOMAP and Wormpep18
3
Filter for overlapping matches
4
Filter for adjacent matches
5
Mask with Sanger Ctr. annotation & transposon library
ΨG1-5 (3,814)
6
Reduce for possible additional repeats
ΨG1-6 (2,401)
7
Increase threshold e-value from 0.01 to 0.001
ΨG1-7 (2,168)
ΨG = ΨG1-7
(ΨGE)P (1,165)
ΨGE
(363)
ΨGR
(1,100)
ΨGM
(746)