

Inheritance dynamics of the two transgenes

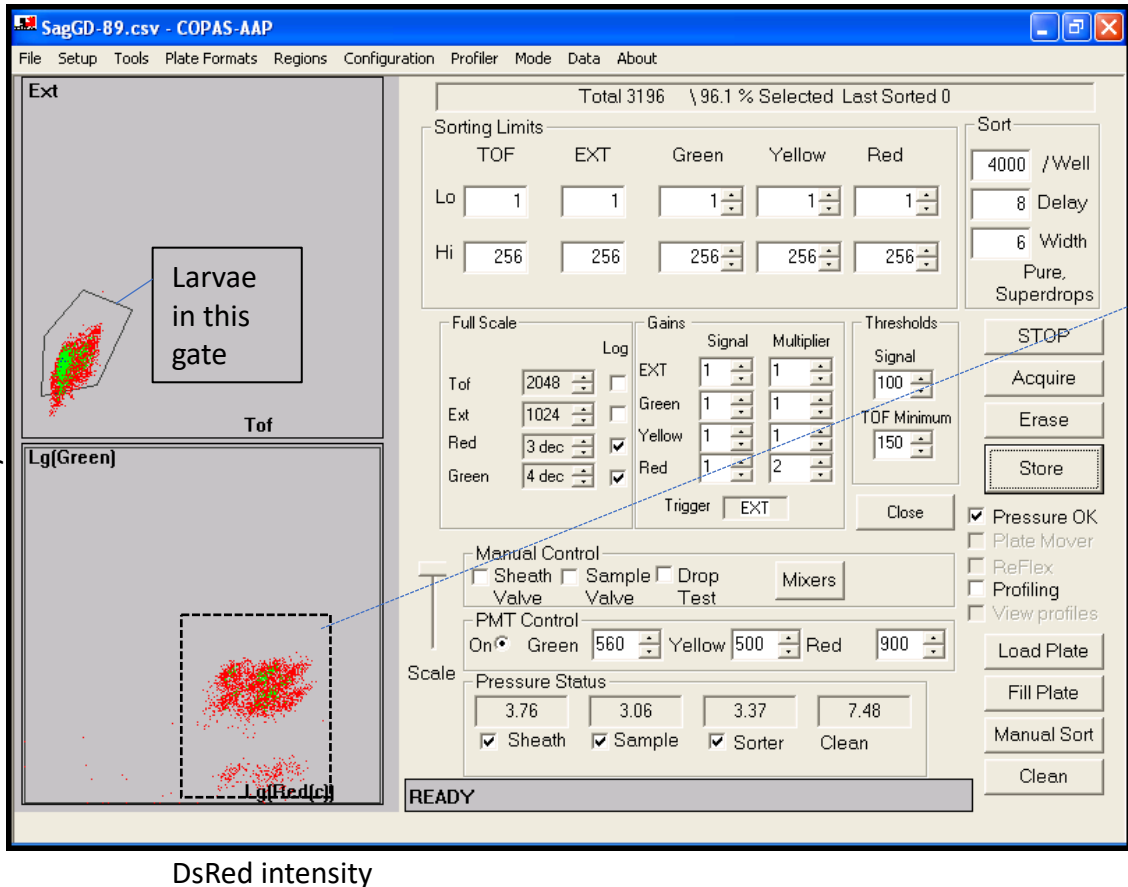
SagGDvasa (DsRed) and *Lp::Sc2A10* (GFP)

in 8 mosquito populations, tracked by COPAS flow cytometry

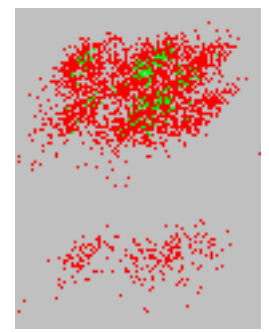
Typical COPAS analysis :

Objects separated according to size and opacity

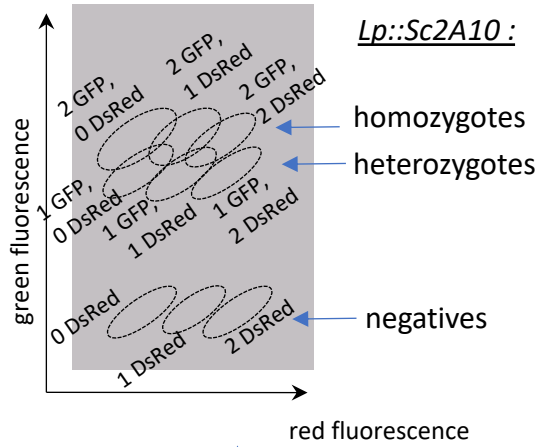
Objects from first gate separated according to fluorescence



Extract screenshots of region with larvae



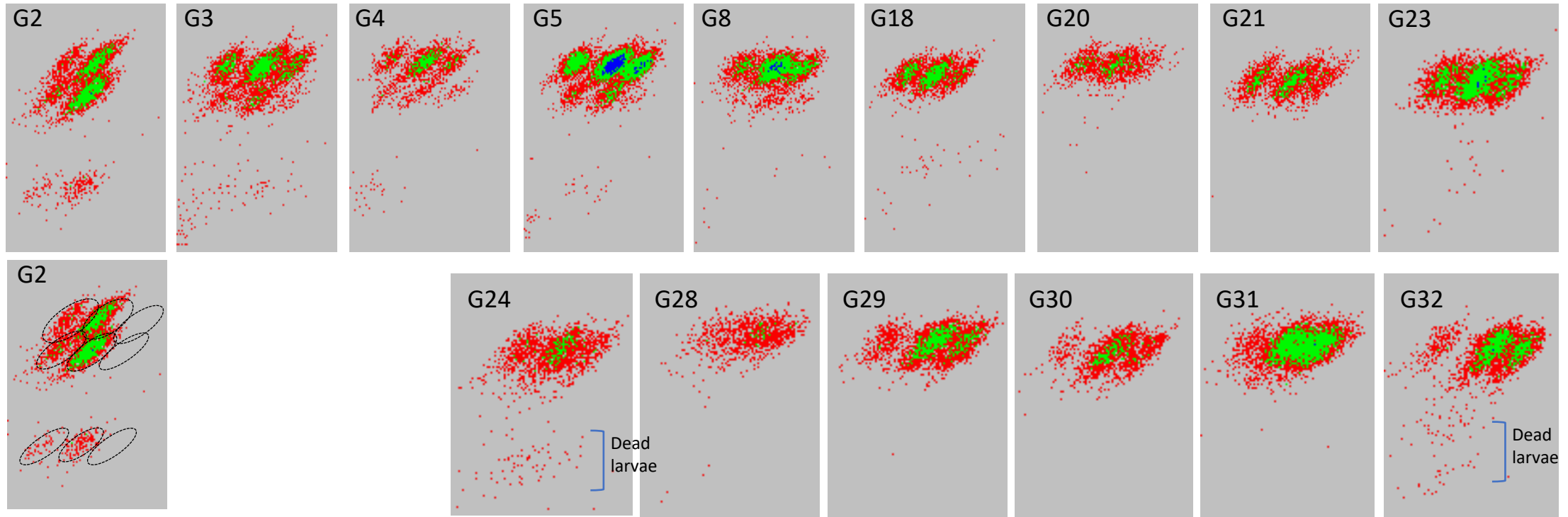
Interpretation of fluorescence :



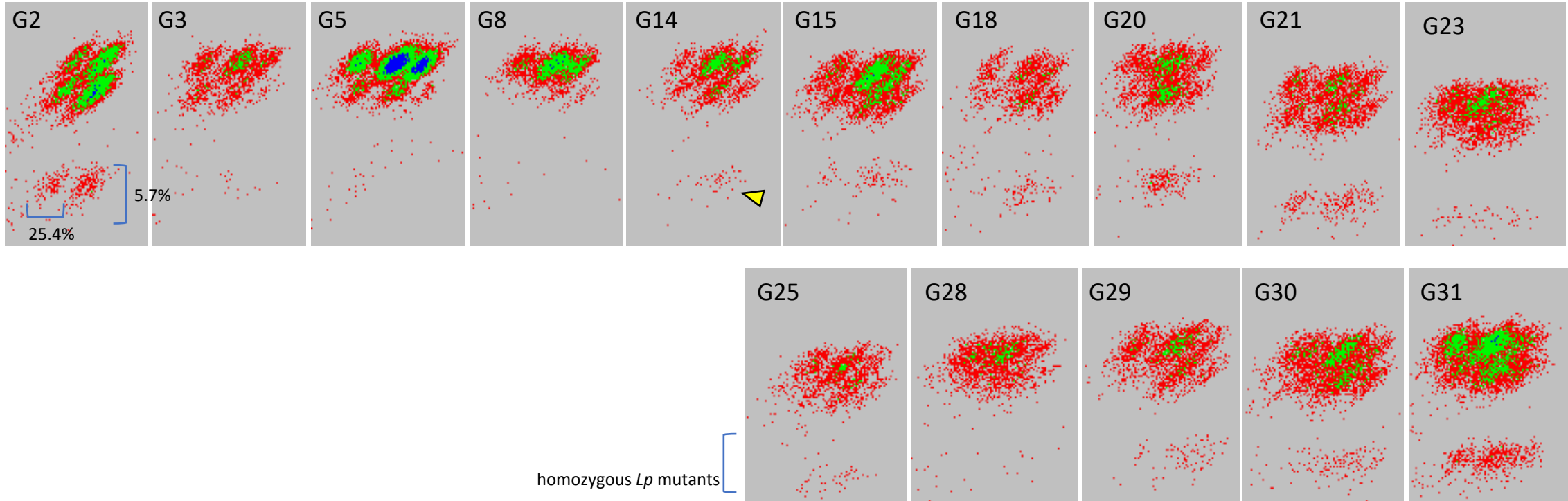
SagGDvasa :

negatives
heterozygotes
homozygotes

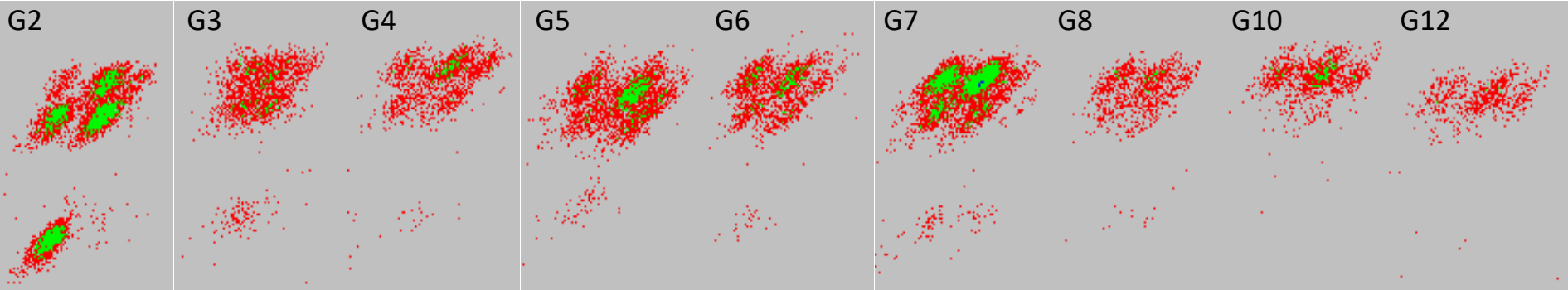
Population 1 : G0 = ♂ $\frac{SagGD^{vasa}}{Y}$; $\frac{Lp::Sc2A10}{+}$ x ♀ WT



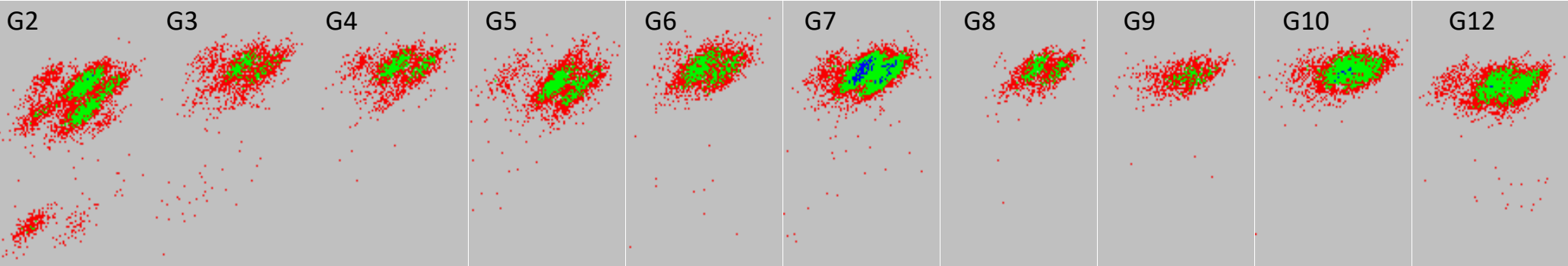
Population 2 : G0 = ♂ $\frac{SagGD^{vasa}}{Y}$; $\frac{Lp::Sc2A10}{+}$ x ♀ WT



Population 3 : G0 = ~ 1:3 mix of G10 individuals from Population 1 : WT

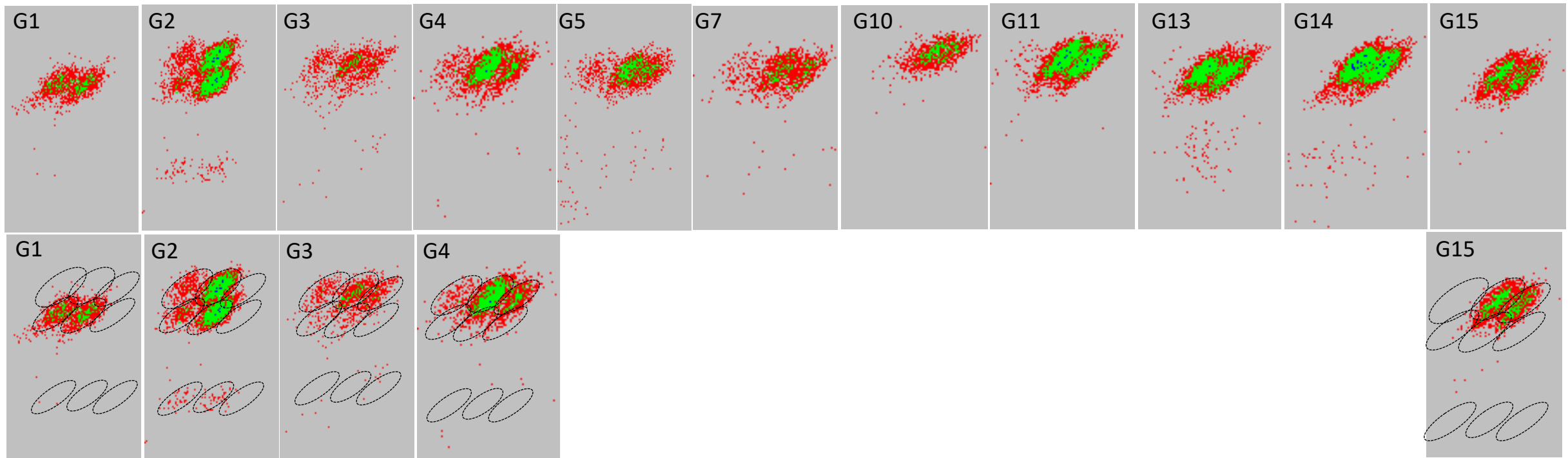


Population 4 : G0 = ~ 1:2 mix G10 individuals from Population 1 : WT



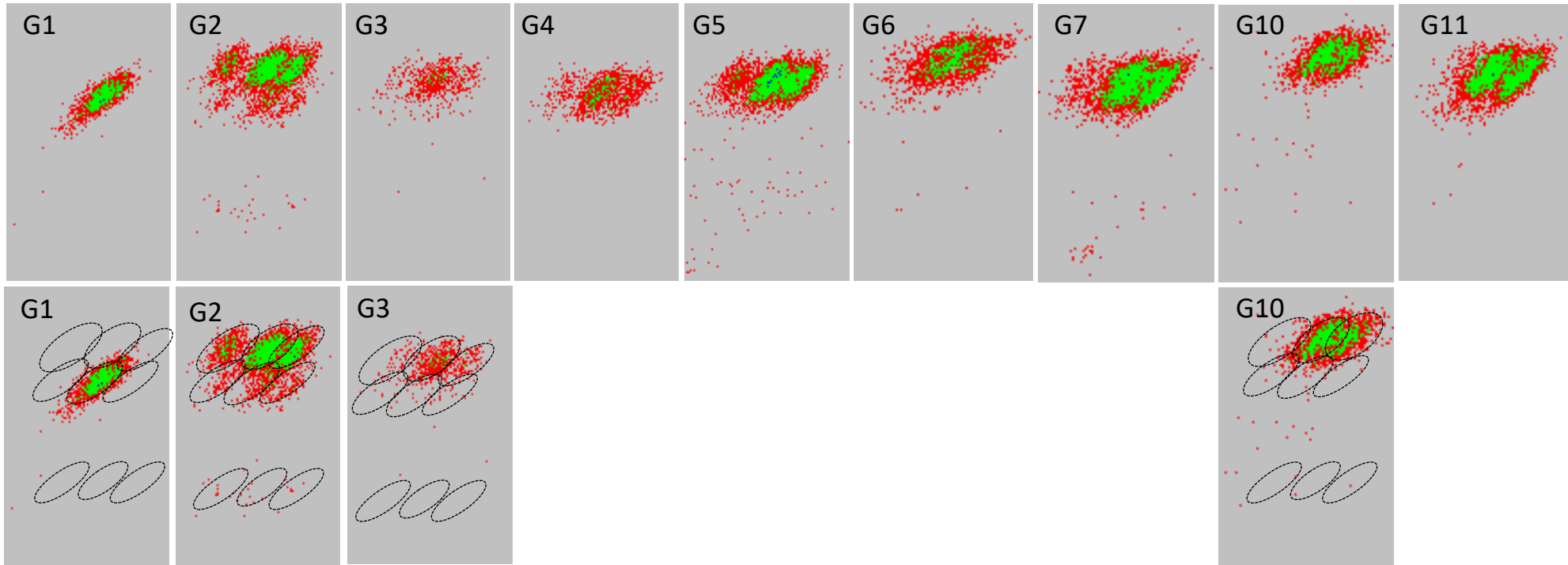
Population 5 : G0 = ♂ $\frac{SagGD^{vasa}}{Y}$; $\frac{Lp::Sc2A10}{Lp::Sc2A10}$ × ♀ WT

(from G16 of Population 1)



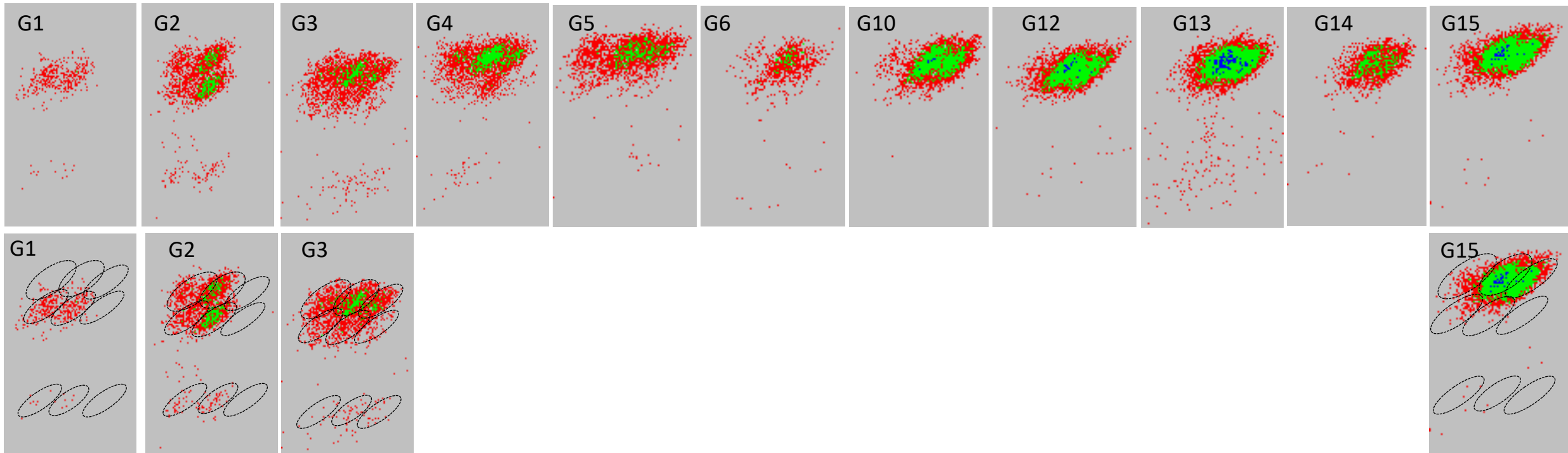
Population 6 : G0 = ♀ $\frac{SagGD^{vasa}}{SagGD^{vasa}}$; $\frac{Lp::Sc2A10}{Lp::Sc2A10}$ x ♂ WT

(from G16 of Population 1)



Population 7 : G0 = ♂ $\frac{SagGD^{vasa}}{Y}$; $\frac{Lp::Sc2A10}{+}$ × ♀ WT

(from G1 of Population 5)



Population 8 : G0 = ♀ $\frac{SagGD^{vasa}}{+}$; $\frac{Lp::Sc2A10}{+}$ x ♂ WT

(from G1 of Population 5)

