Fig. S1: Relationship between the number of VGCs and families for *Duplodnaviria,* when the PC- and PSC-based genomic trees of the Fam_DB dataset were cut with different intergenomic distances.
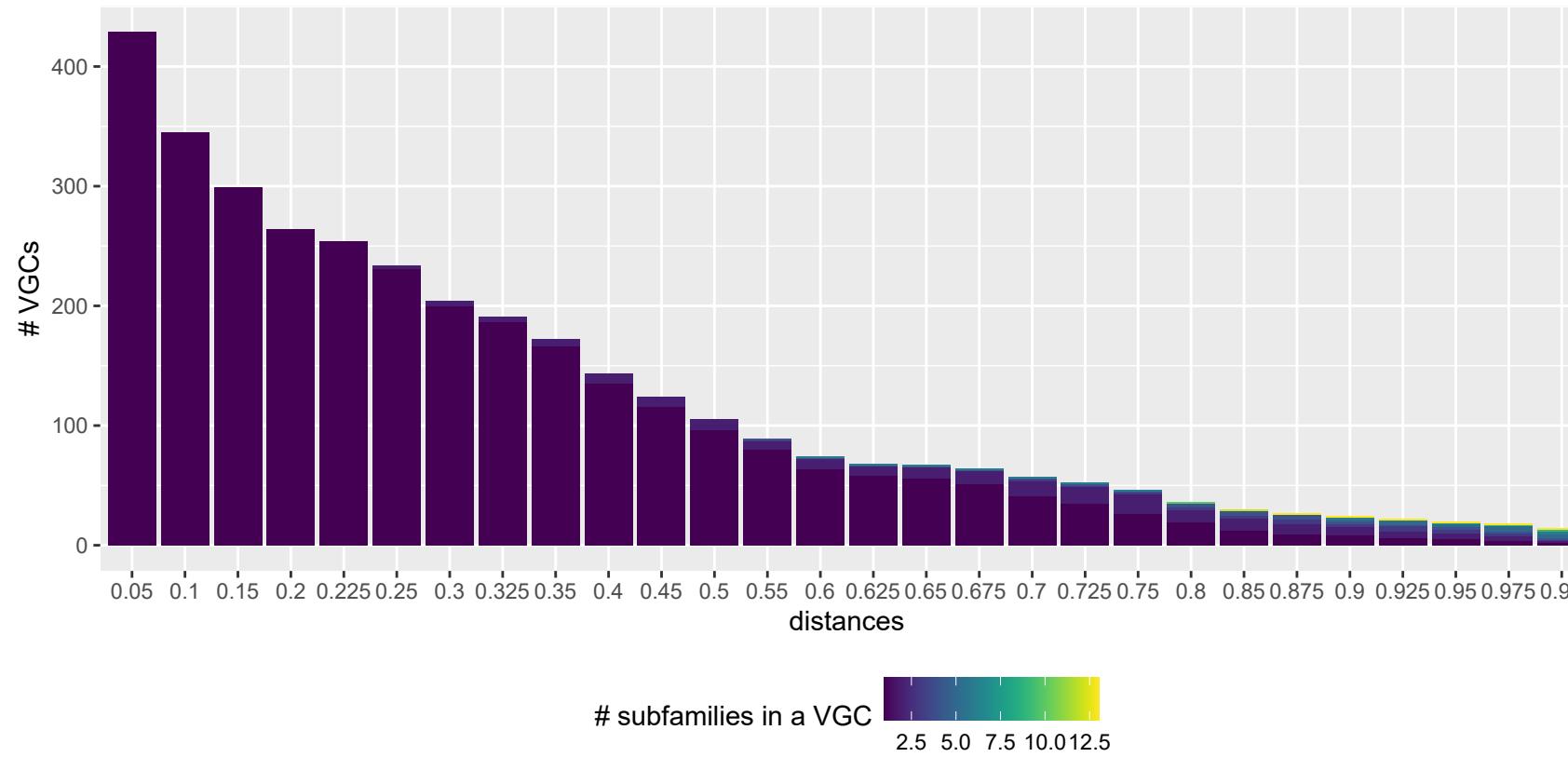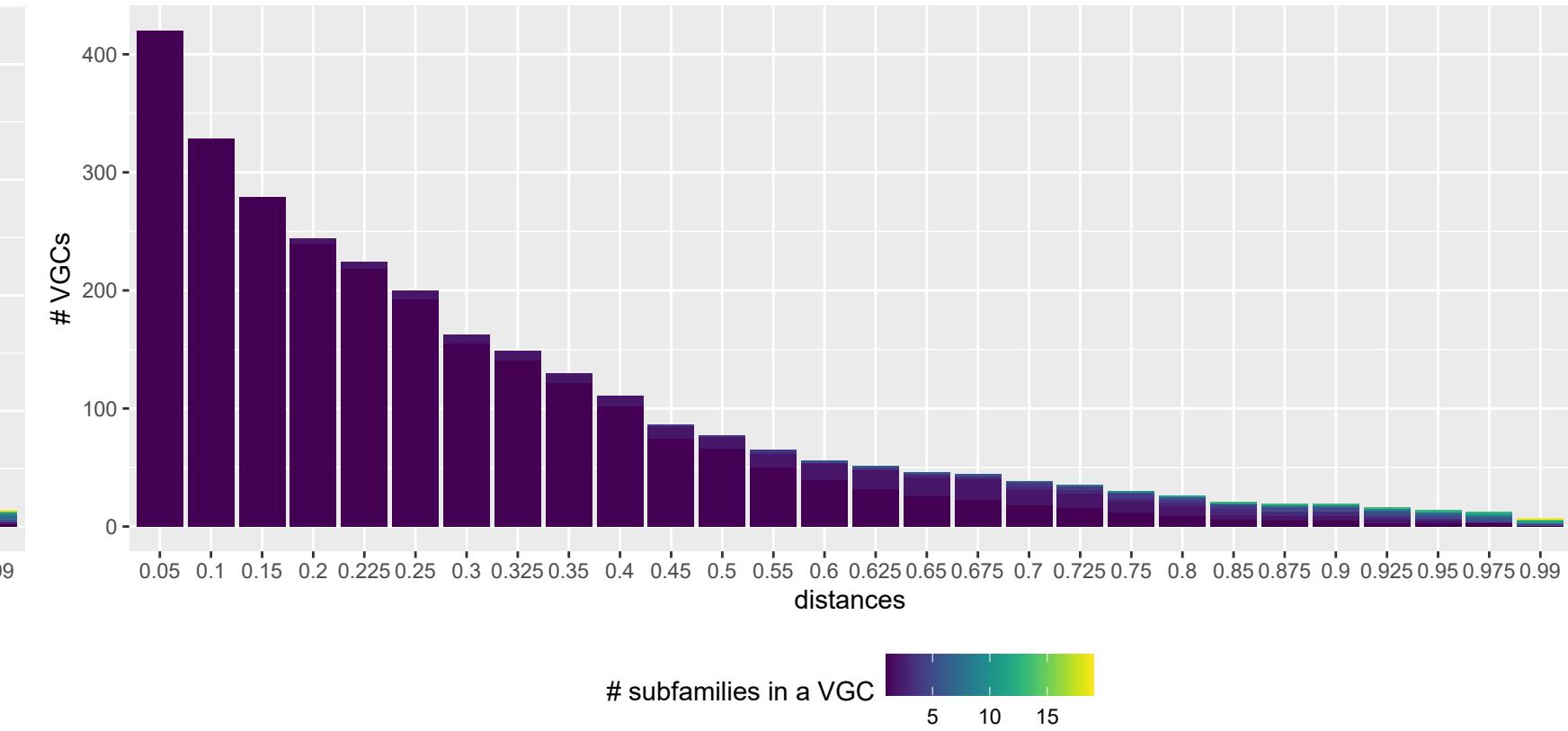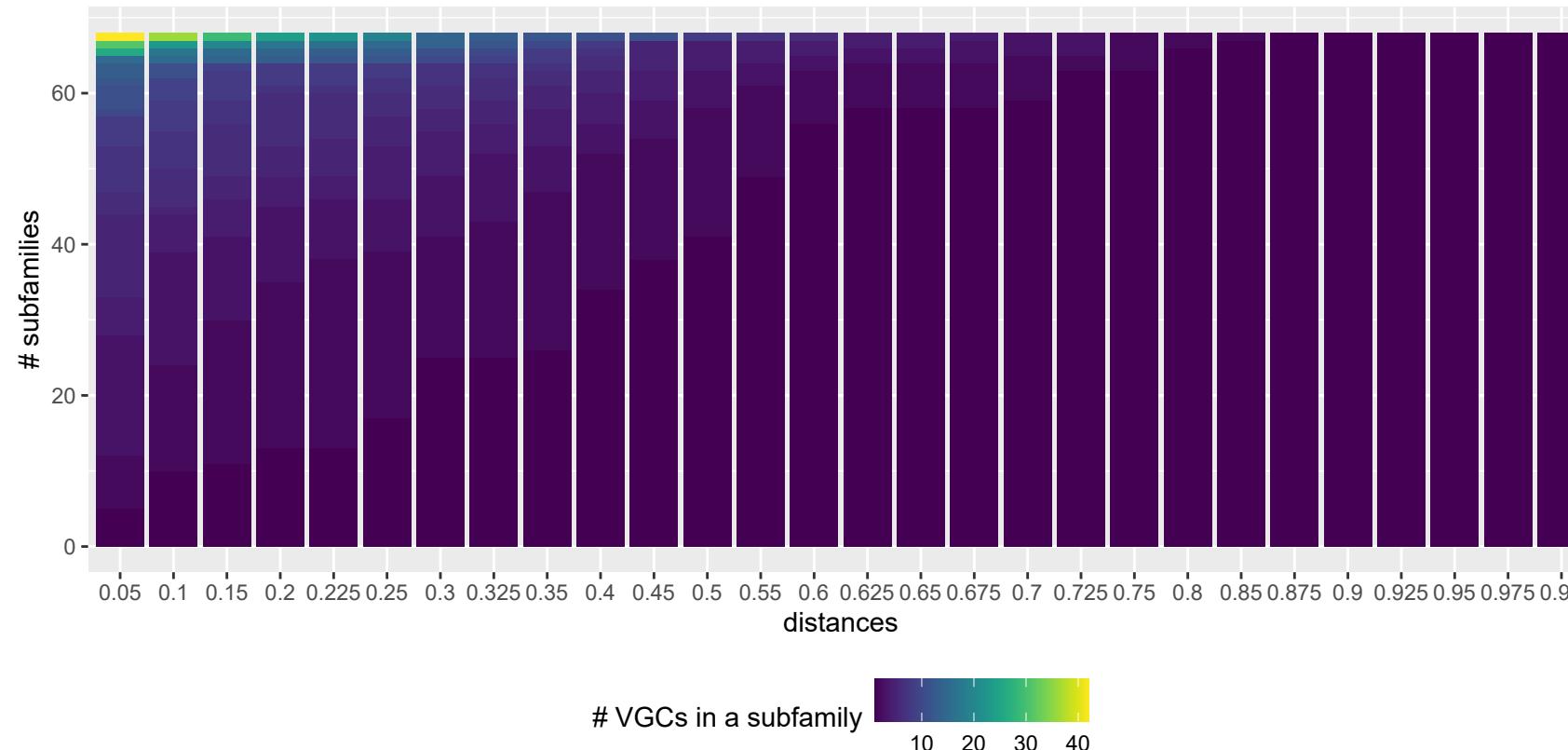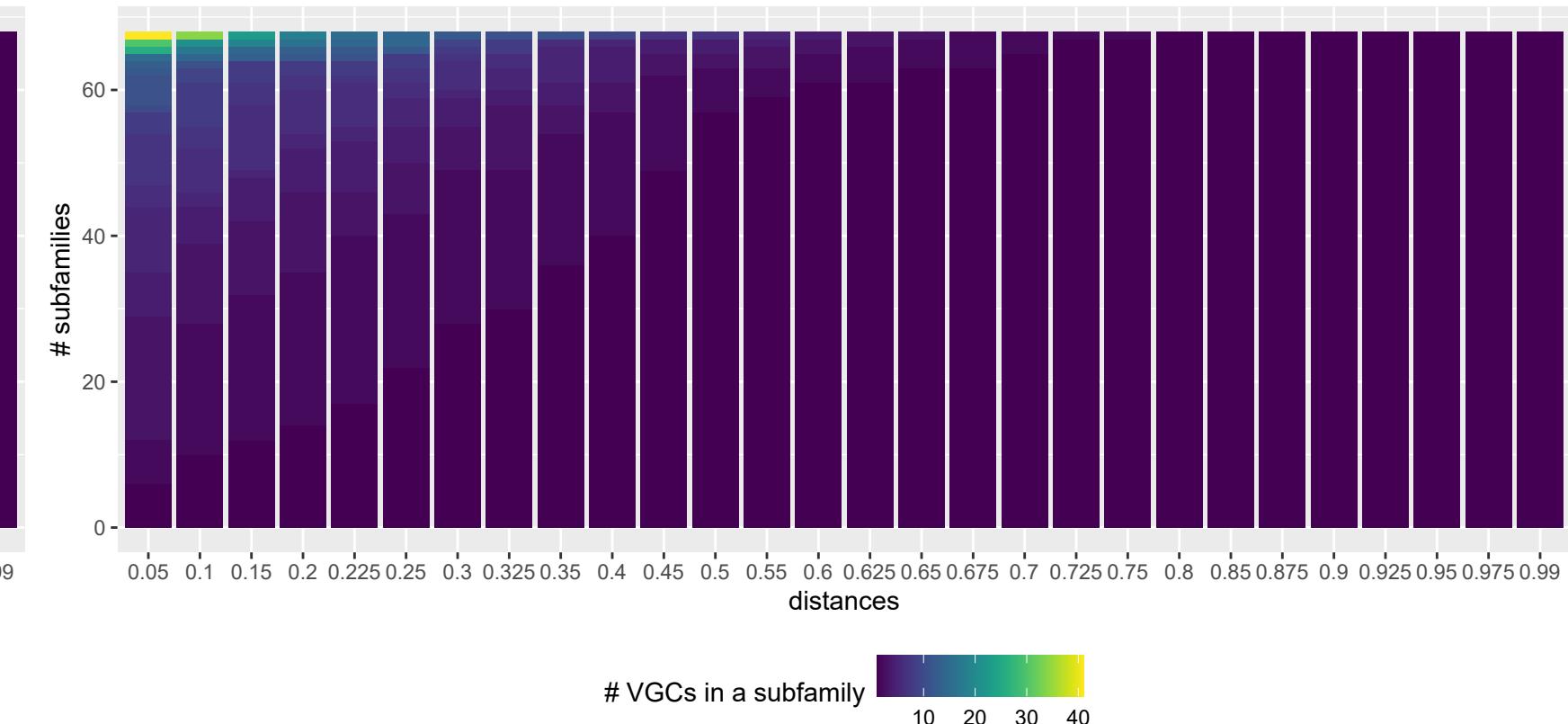
Fig. S2: Relationship between the number of VGCs and subfamilies for *Duplodnaviria,* when the PC- and PSC-based genomic trees of the Fam_DB dataset were cut with different intergenomic distances.
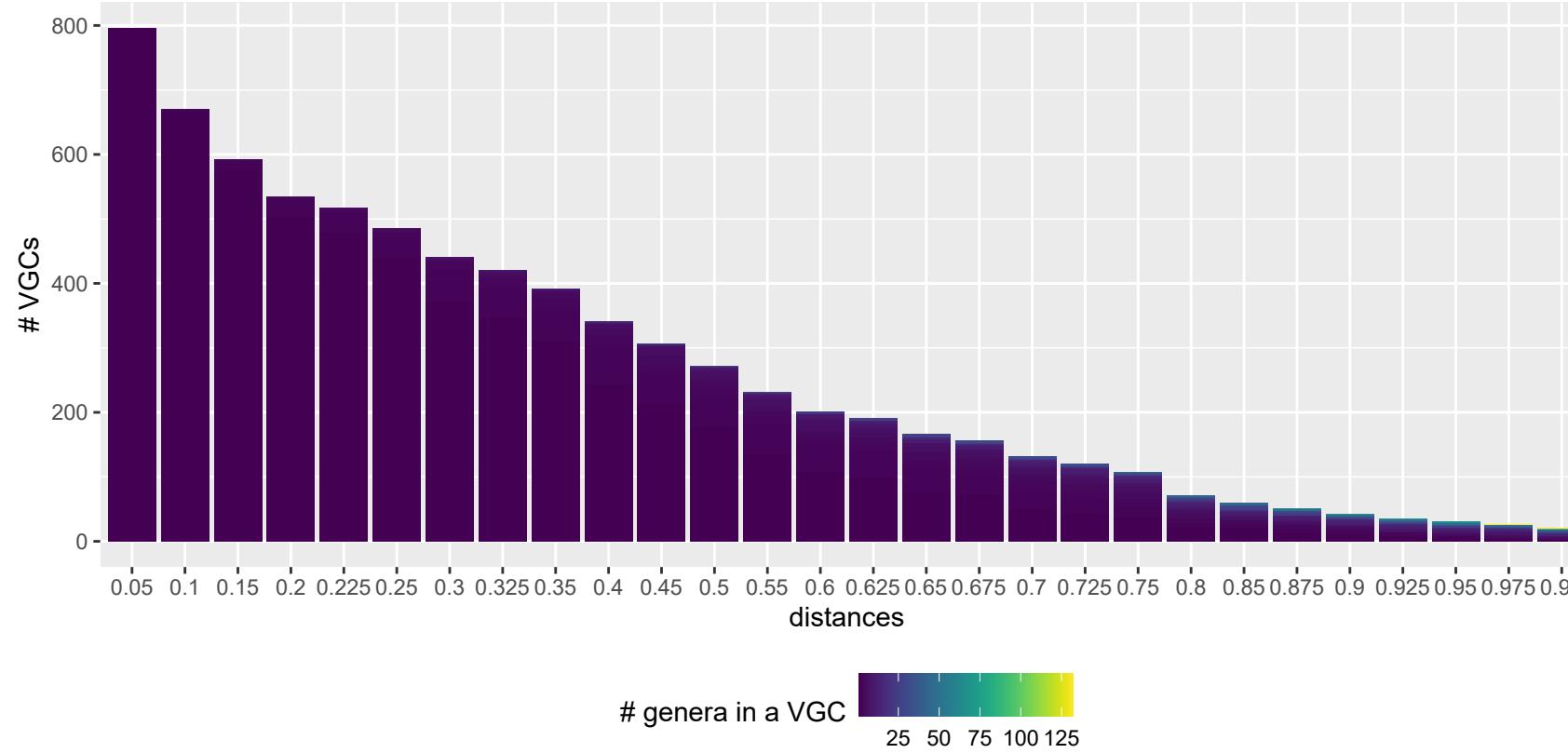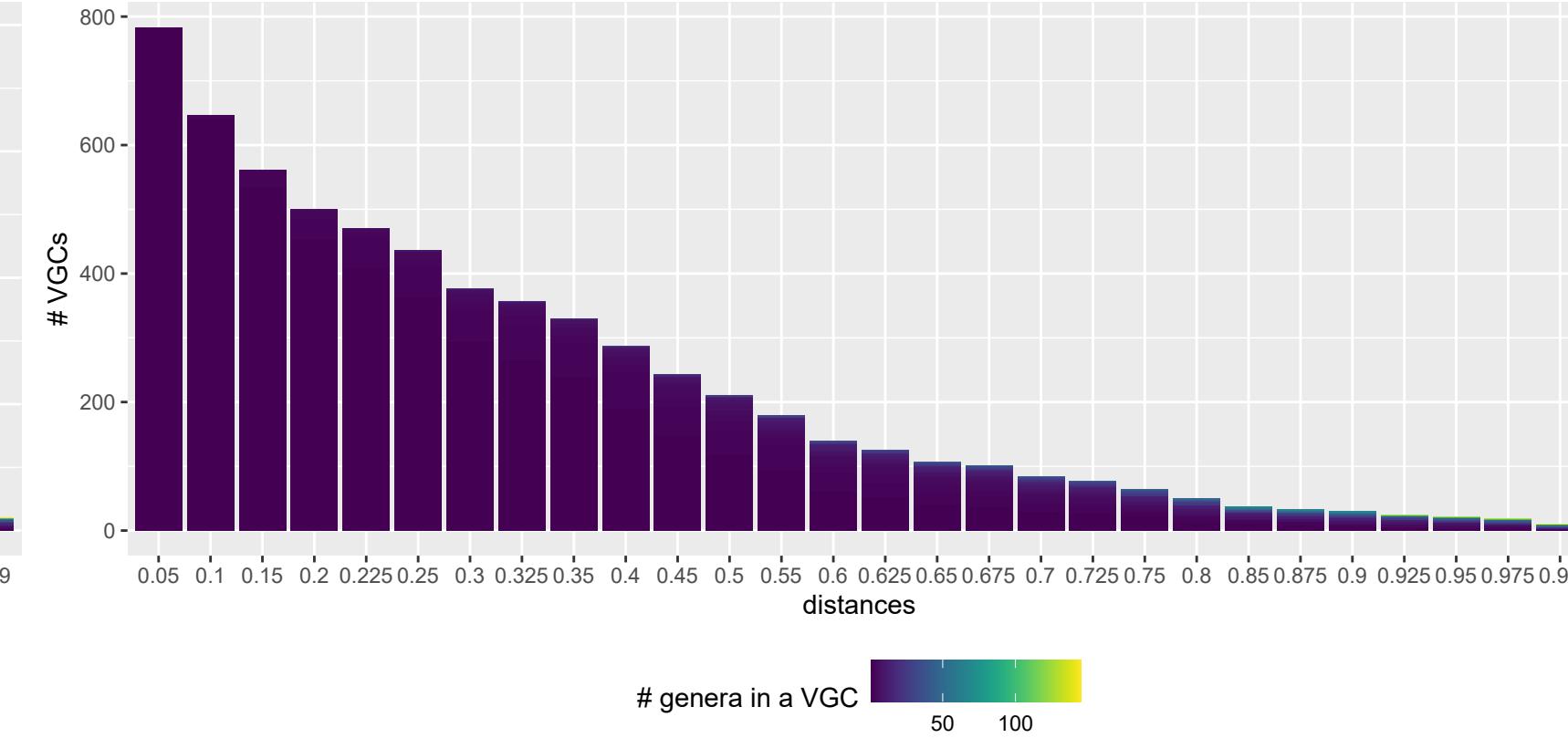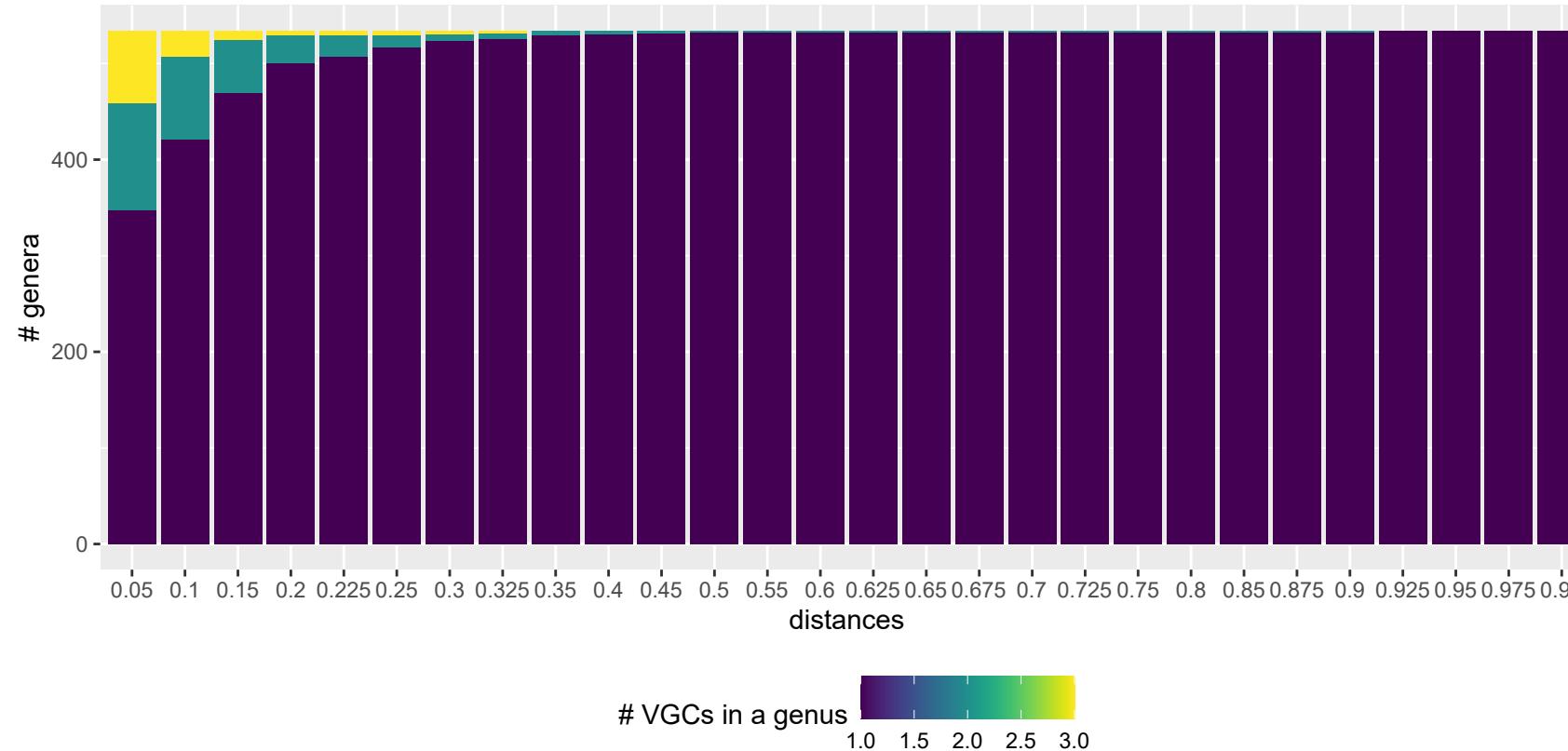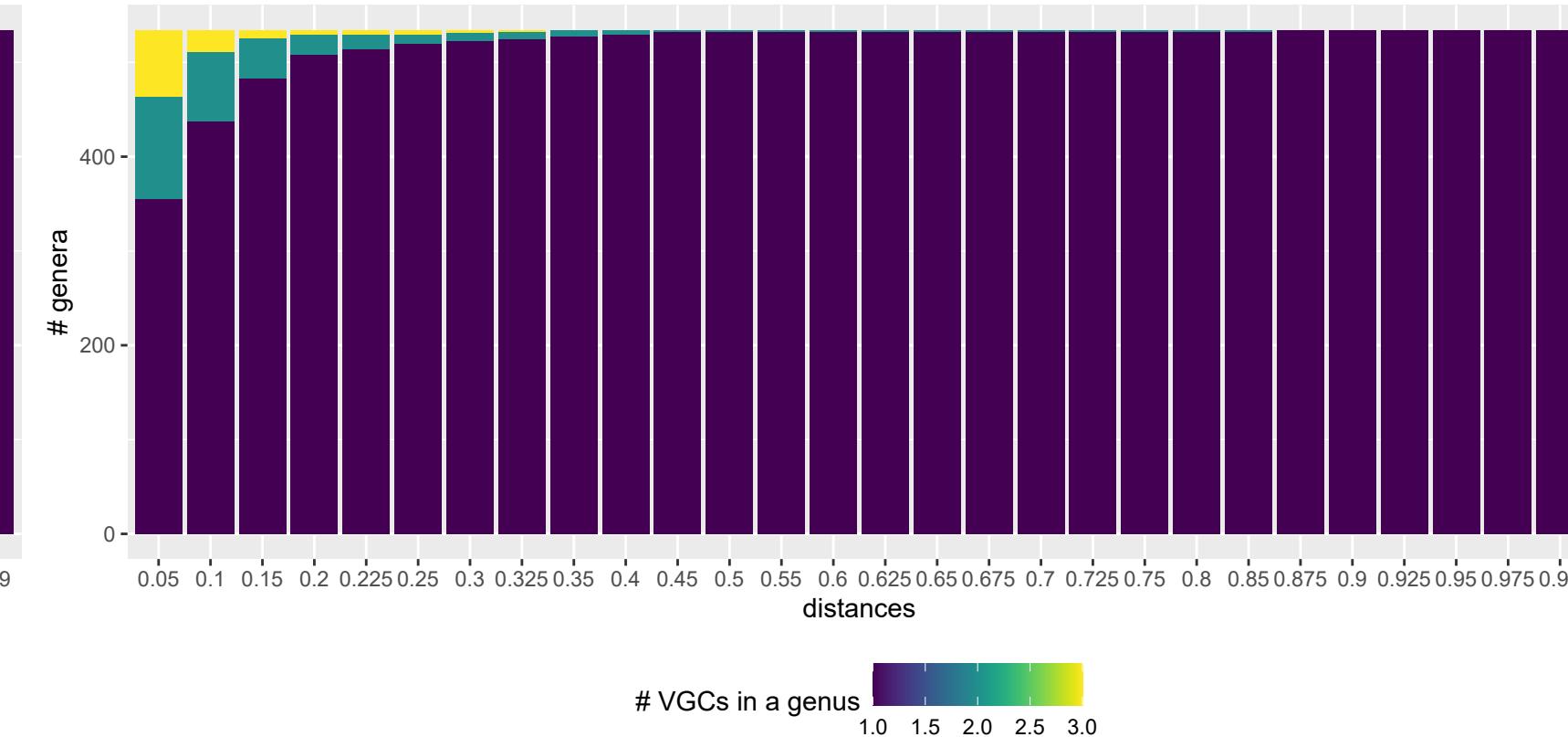
Fig. S3: Relationship between the number of VGCs and genera for *Duplodnaviria,* when the PC- and PSC-based genomic trees of the Fam_DB dataset were cut with different intergenomic distances.
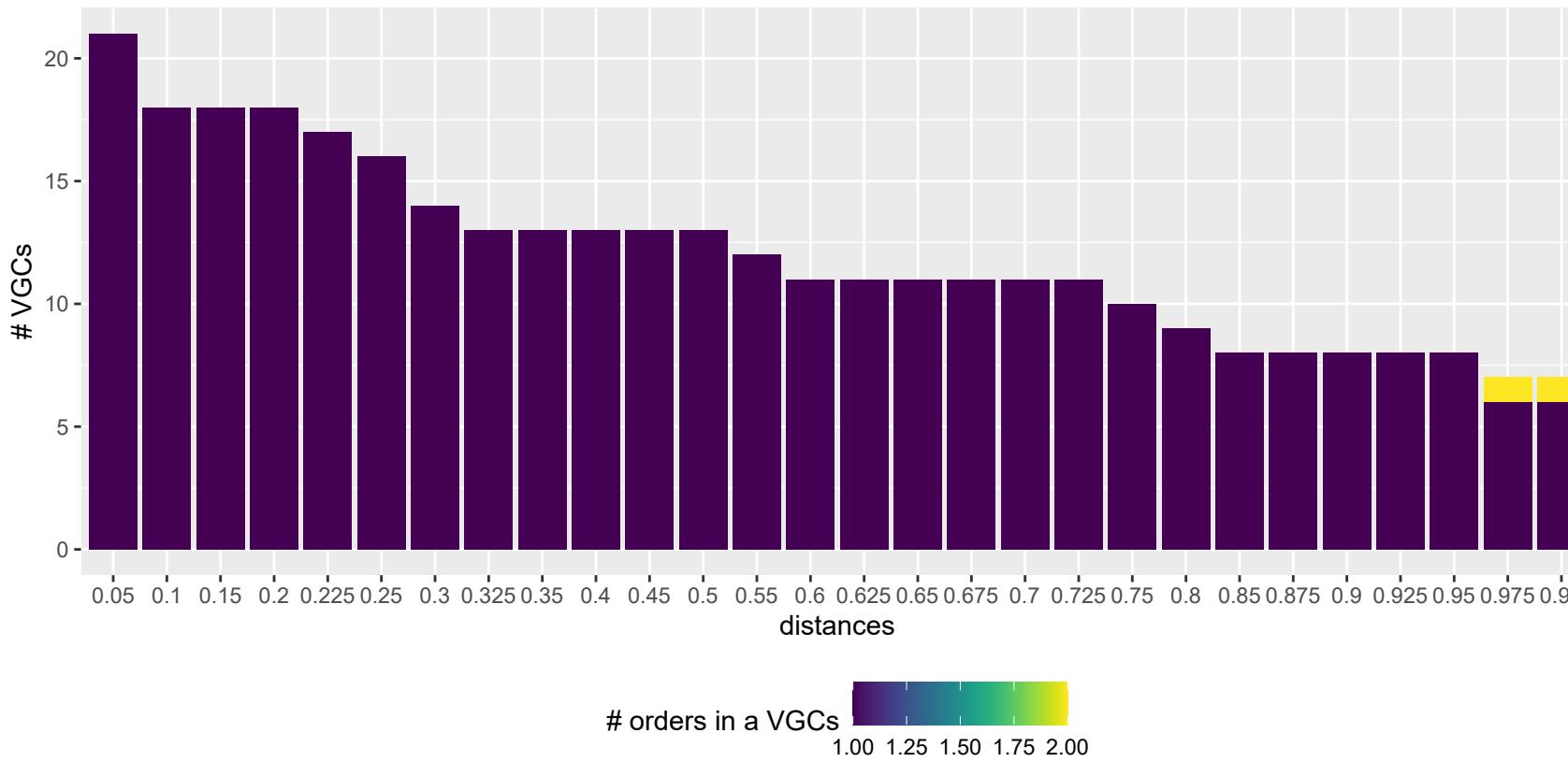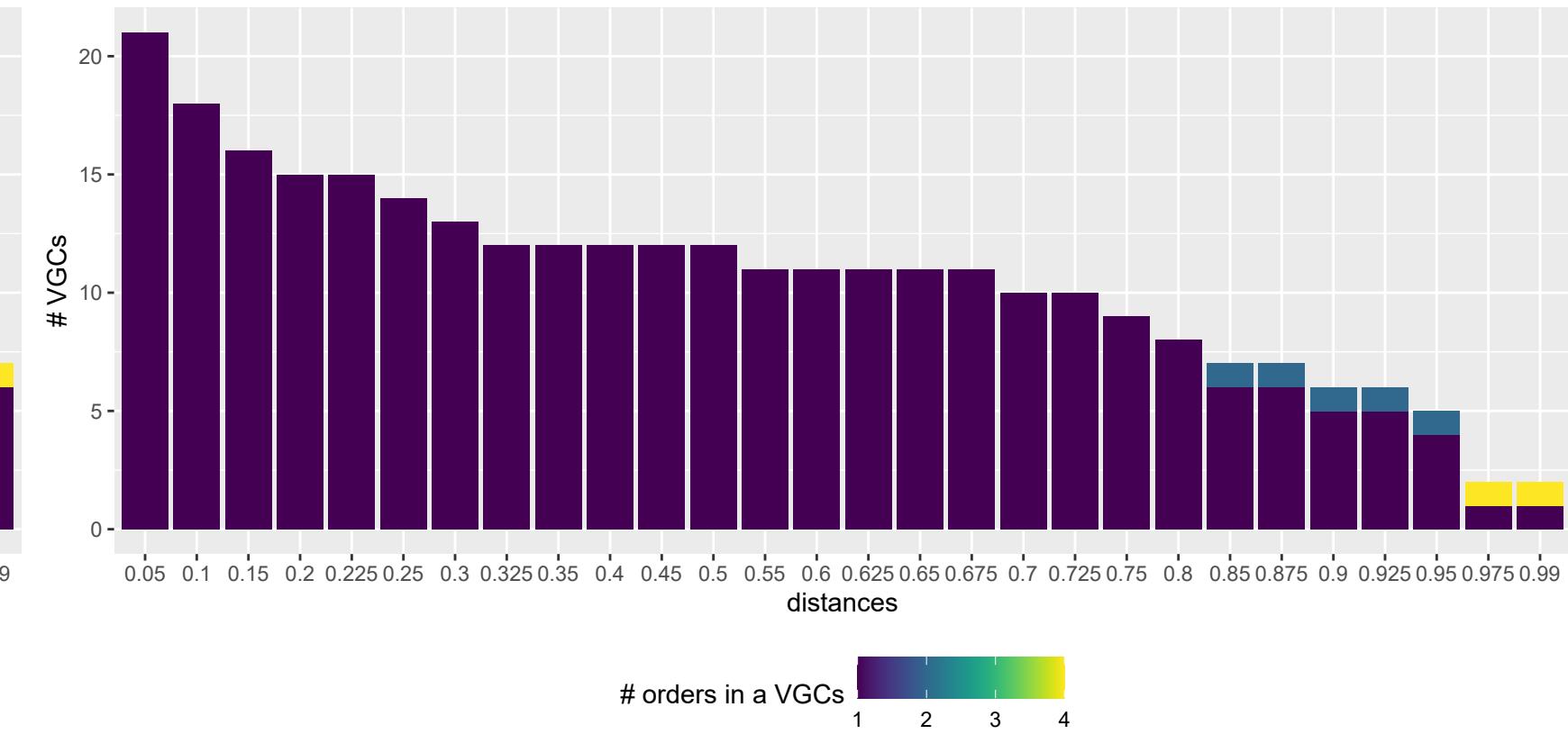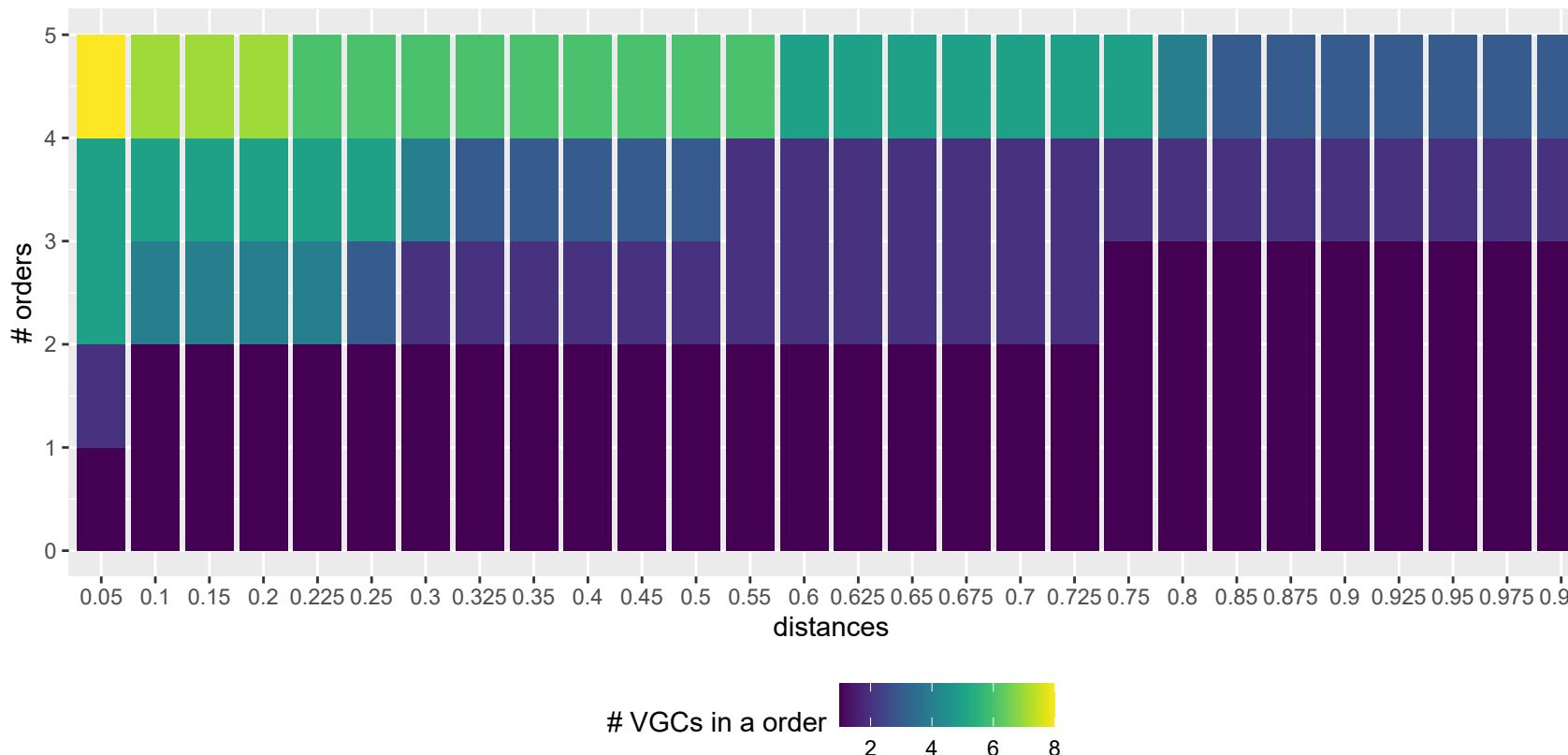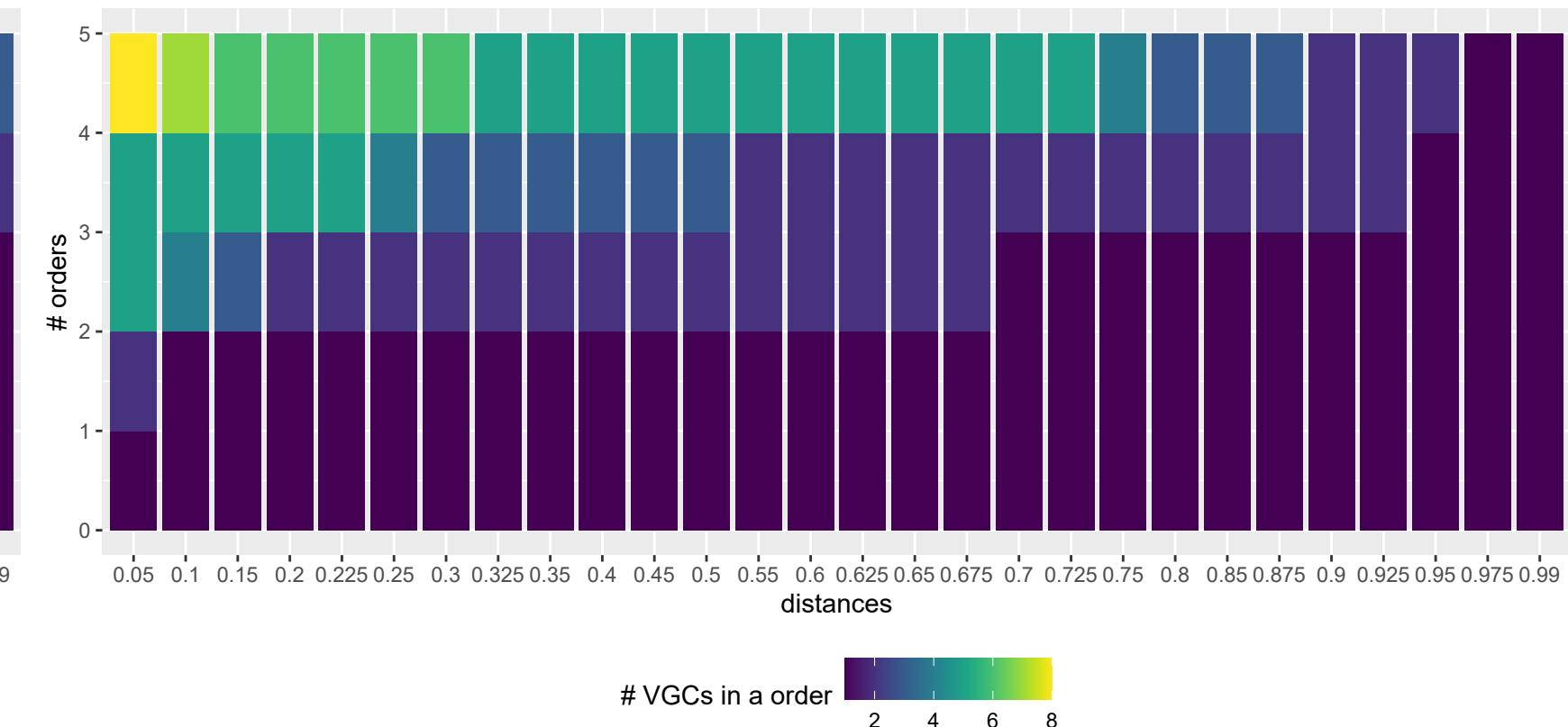
Fig. S4: Relationship between the number of VGCs and orders for *Varidnaviria,* when the PC- and PSC-based genomic trees of the Fam_DB dataset were cut with different intergenomic distances.
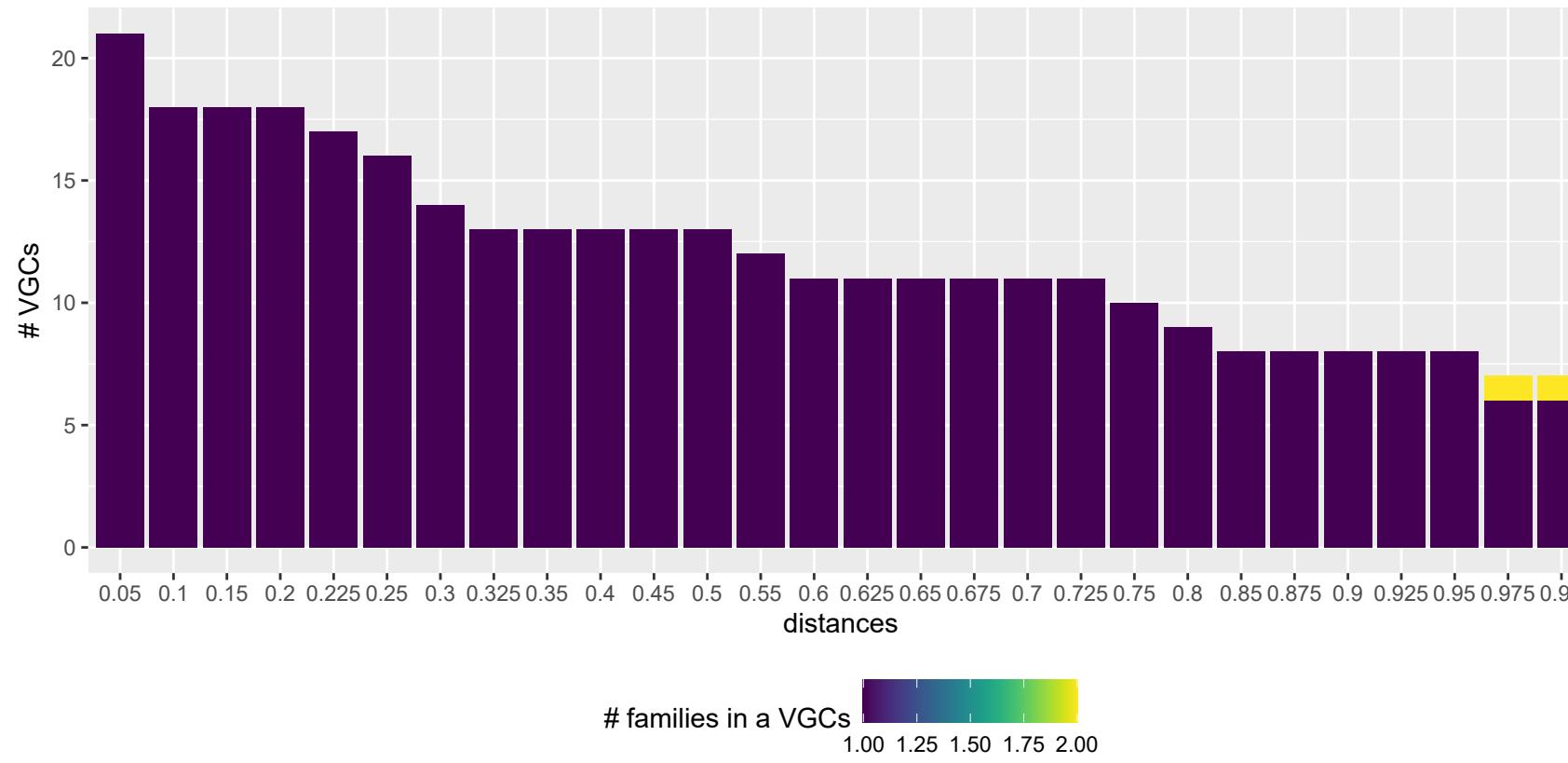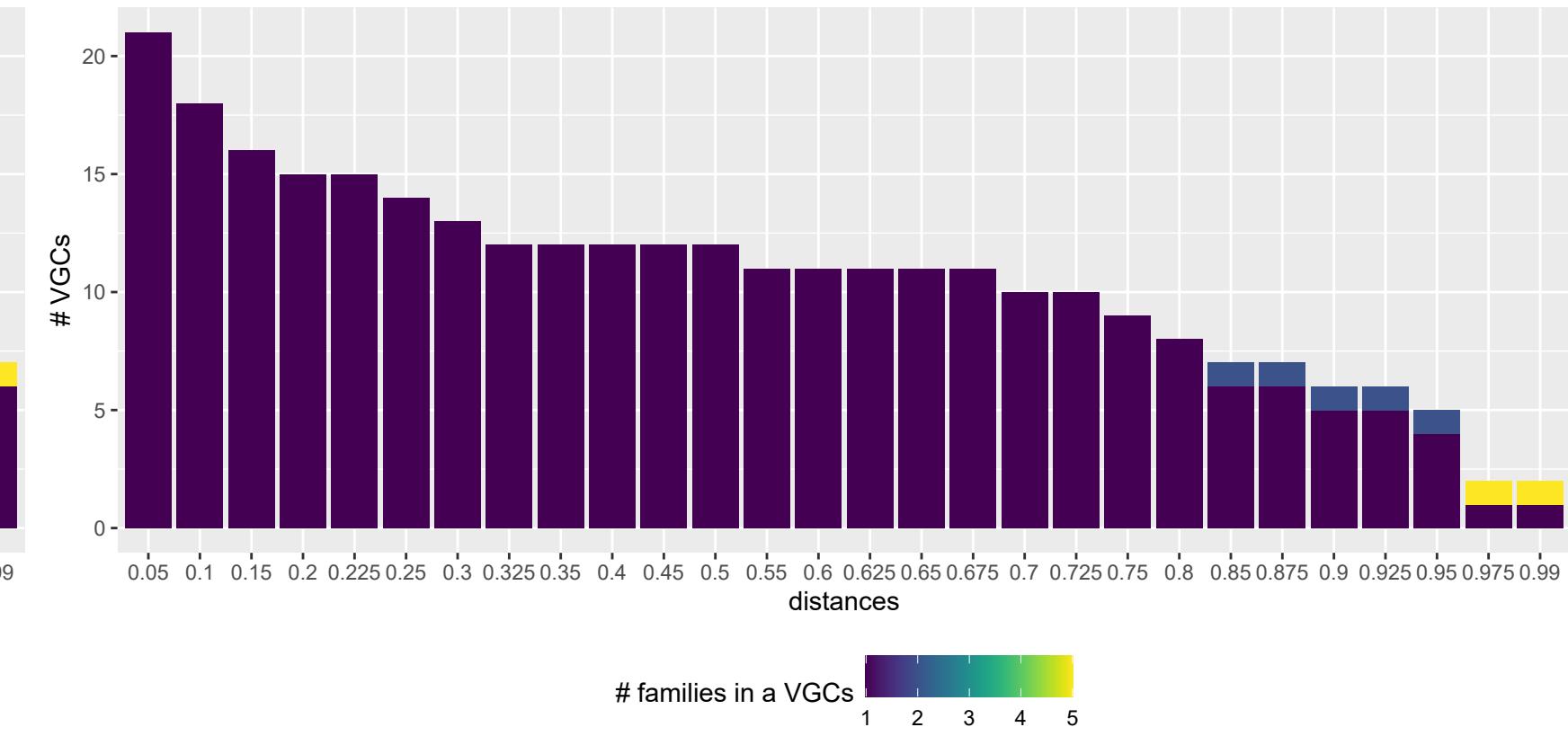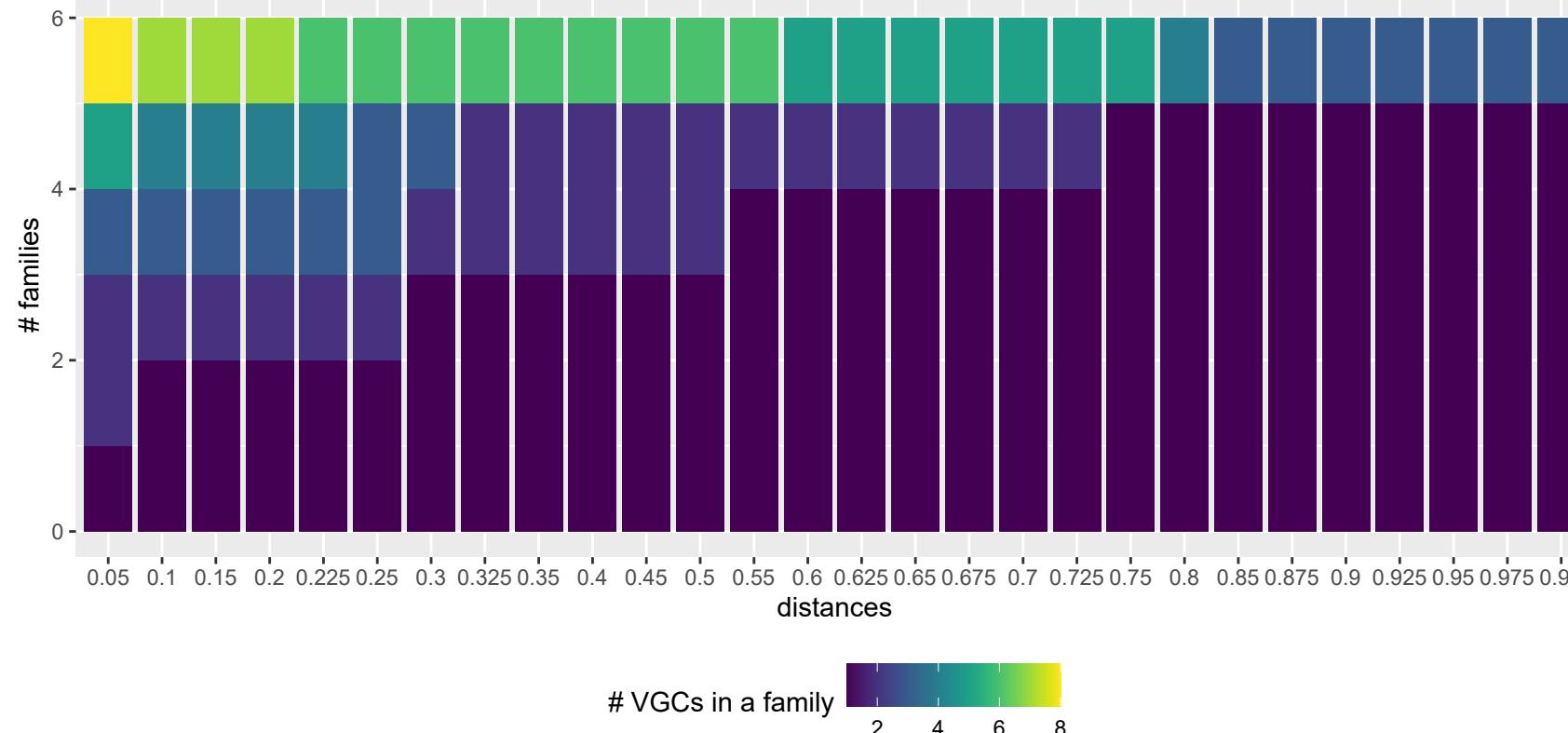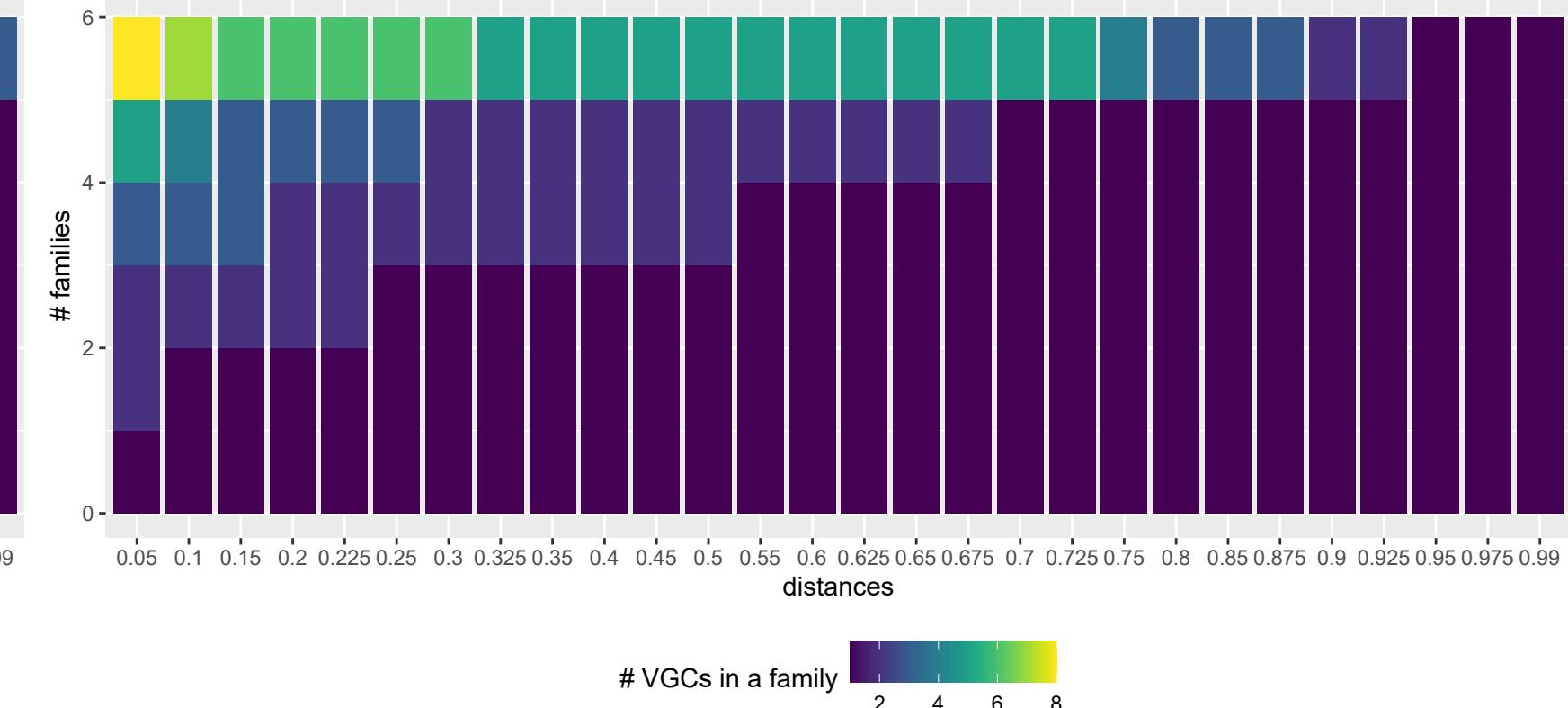
Fig. S5: Relationship between the number of VGCs and families for *Varidnaviria,* when the PC- and PSC-based genomic trees of the Fam_DB dataset were cut with different intergenomic distances.
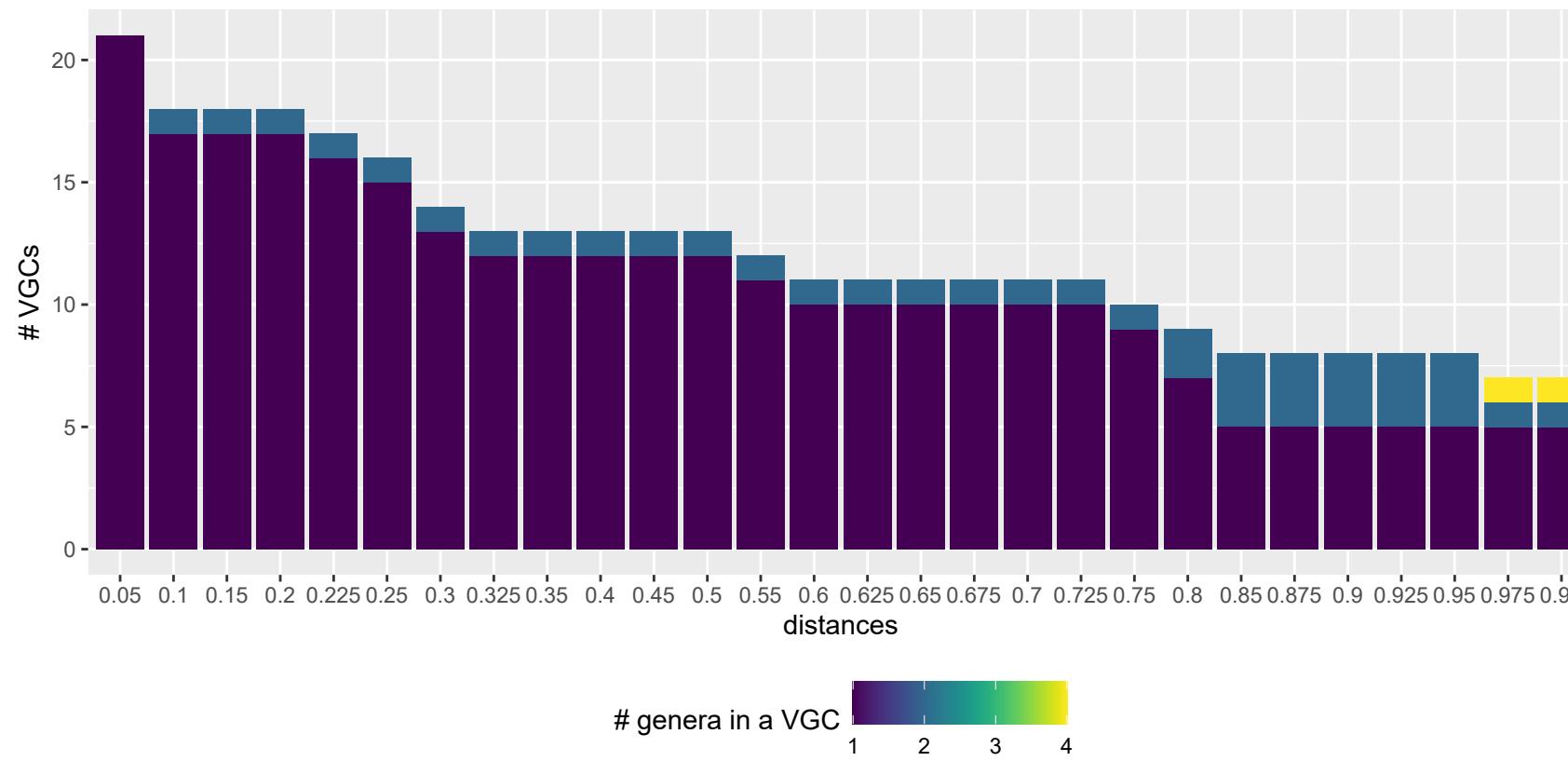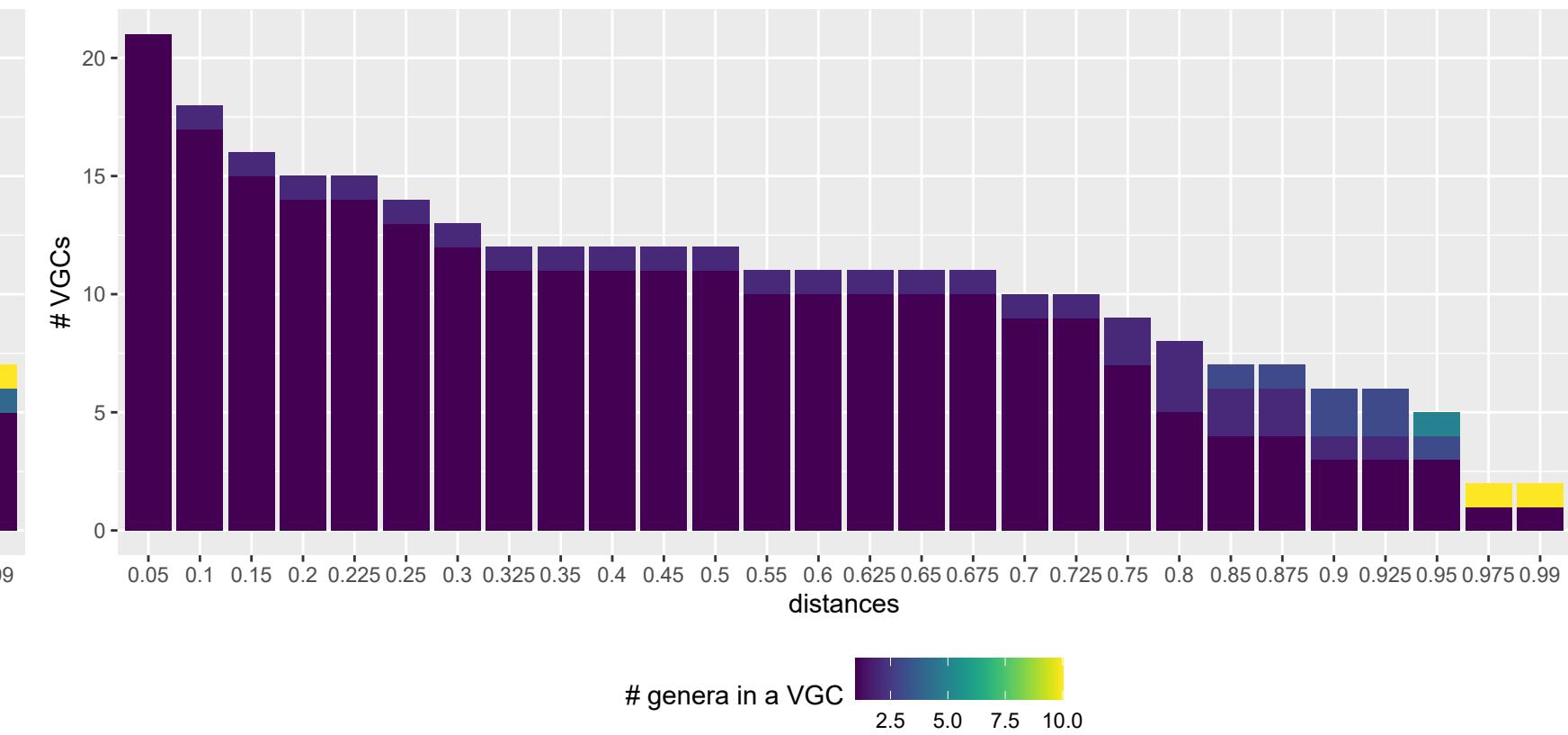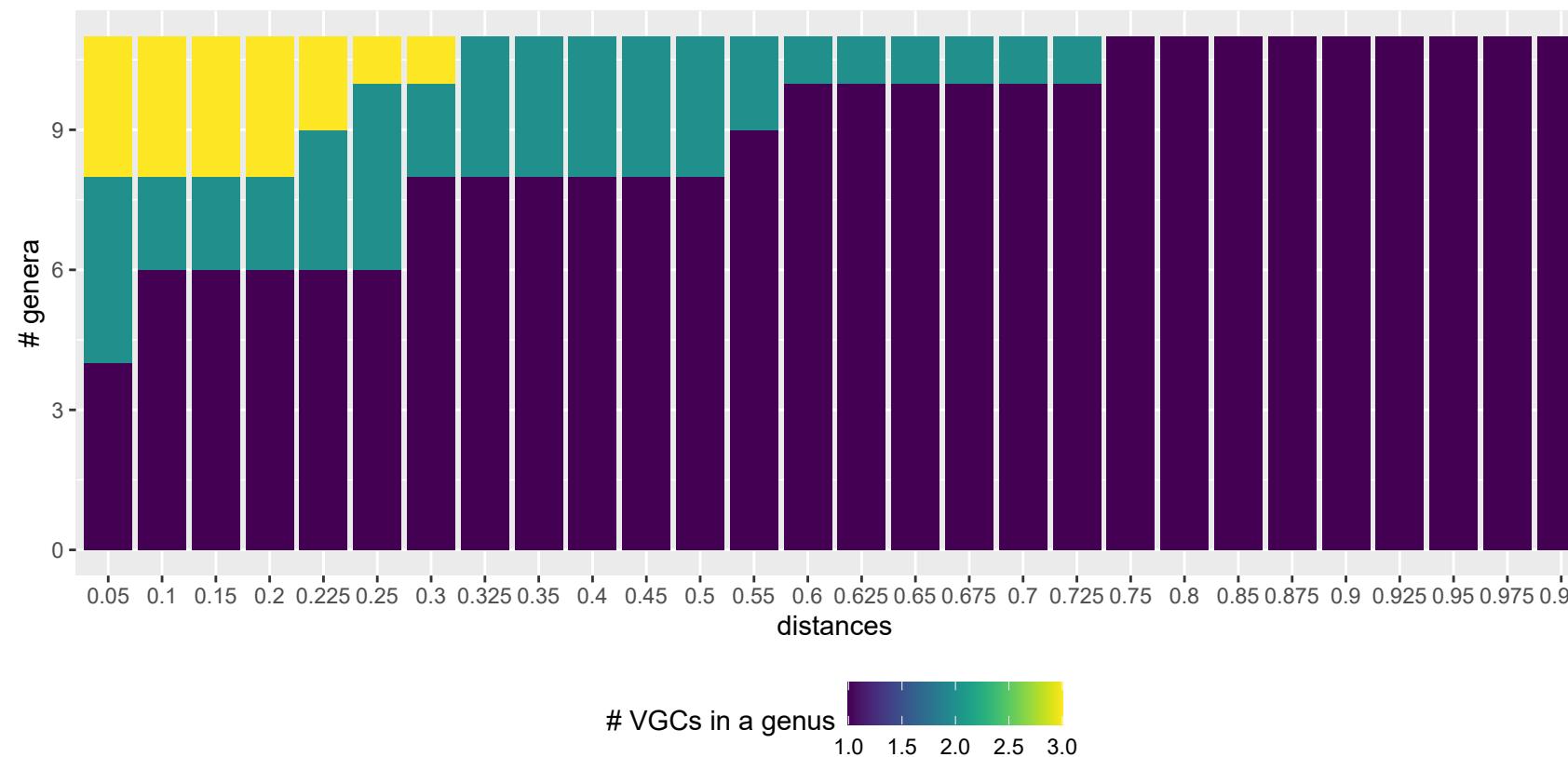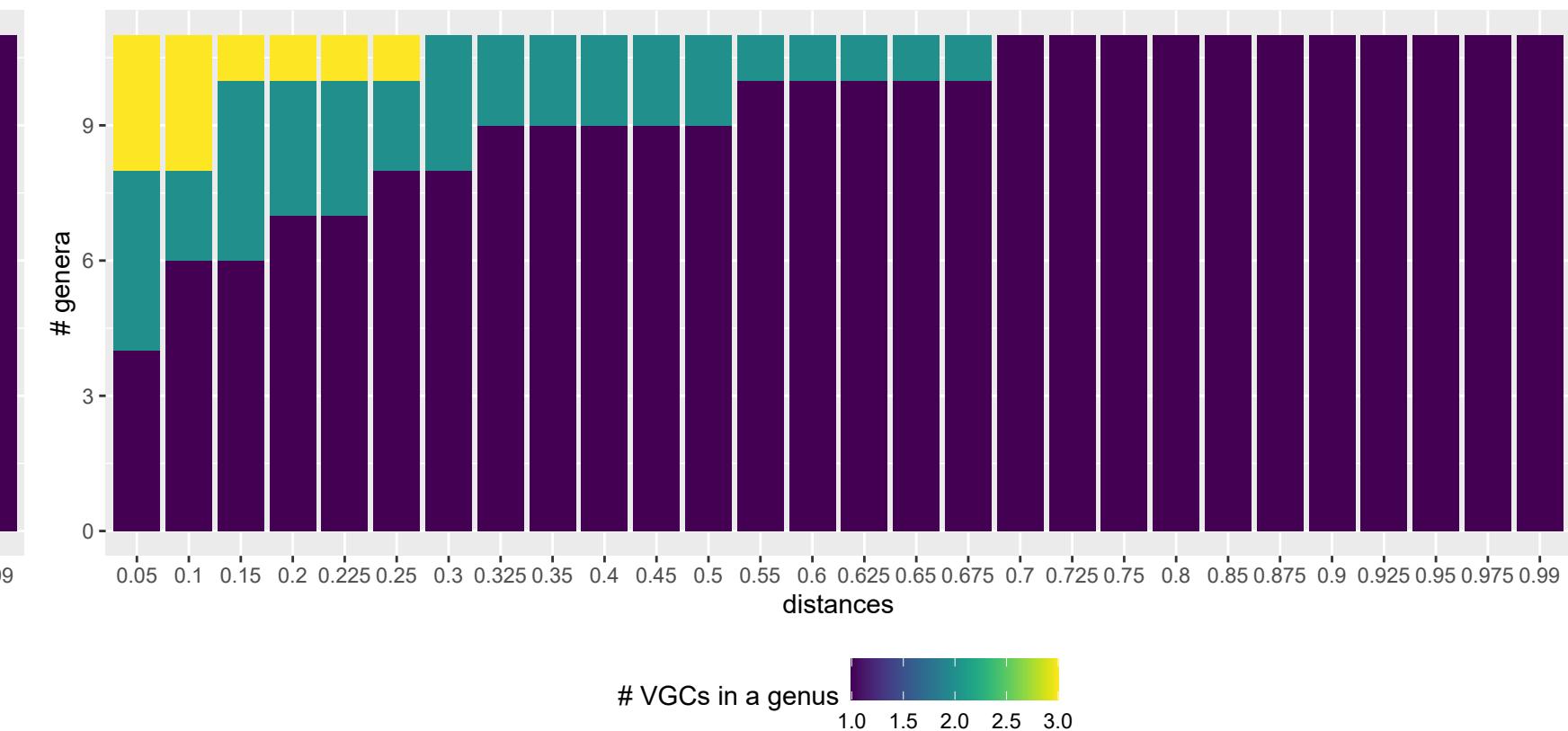
Fig. S6: Relationship between the number of VGCs and genera for *Varidnaviria*, when the PC- and PSC-based genomic trees of the Fam_DB dataset were cut with different intergenomic distances.