

FIGURES S1-S8

Figure S1: Neighbor joining tree of visual opsin genes of the *LWS*, *SWS1*, *SWS2*, *RH1* and *RH2* clades. The tree is supported by a non-parametric bootstrap analysis with 100 replicates. Bootstrap values shown at the nodes. The tree was rooted with the human *OPN3* sequence. For the sequence names, species abbreviations are applied as described in *Methods*, followed by the number of the chromosome or linkage group where the gene is located (if known) and the gene/subtype name (see Table 1). Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.705157>.

Figure S2: Phylogenetic Maximum Likelihood tree of visual opsin genes of the *LWS*, *SWS1*, *SWS2*, *RH1* and *RH2* clades. The tree is supported by a non-parametric bootstrap analysis with 100 replicates. Bootstrap values shown at the nodes. The tree was rooted with the human *OPN3* sequence. For the sequence names, species abbreviations are applied as described in *Methods*, followed by the number of the chromosome or linkage group where the gene is located (if known) and the gene/subtype name (see Table 1). Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.705157>.

Figure S3: Neighbor joining tree of visual opsin genes of the *LWS*, *SWS1*, *SWS2*, *RH1* and *RH2* clades as well as vertebrate ancient (V/A) opsins, pinopsins and *Ciona intestinalis* opsins (Ci-opsins). The tree is supported by a non-parametric bootstrap analysis with 1000 replicates. Bootstrap values shown at the nodes. The tree was rooted with the human *OPN3* sequence. Sequence names as in Figures S1 and S2. See Supplemental data 1 for a full list of sequence names and locations, including V/A opsins, pinopsins and Ci-opsins. The V/A opsins form a basal clade that clusters with the Ci-opsins. The pinopsins form a well-supported clade that clusters with the *LWS* opsins, although with weak support. Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.705157>.

Figure S4: Phylogenetic Maximum Likelihood tree of visual opsin genes of the *LWS*, *SWS1*, *SWS2*, *RH1* and *RH2* clades as well as vertebrate ancient (V/A) opsins, pinopsins and *Ciona intestinalis* opsins (Ci-opsins). The tree is supported by a non-parametric bootstrap analysis with 100 replicates. Bootstrap values shown at the nodes. The tree was rooted with the human *OPN3* sequence. Sequence names as in Figures S1 and S2. See Supplemental data 1 for a full list of sequence names and locations, including V/A opsins, pinopsins and Ci-opsins. The V/A opsins, pinopsins and Ci-opsins form well-supported clades that cluster with the *LWS* opsins. As in the NJ analysis (Fig. S3) the Ci-opsins cluster basal to the V/A opsin clade. Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.705157>.

Figure S5: Neighbor joining tree of oxytocin and vasopressin receptor (OT/VP-R) subtype genes. The tree is supported by a non-parametric bootstrap analysis with 1000 replicates. Bootstrap values shown at the nodes. Red values indicate nodes with bootstrap values lower than 50% that were not considered informative. The tree was rooted with the octopus *OTR*, *CPR1* and *CPR2* sequences. The V2C sequences do not form a well-supported clade; this is indicated by blue branches. Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.707336>.

Figure S6: Phylogenetic Maximum Likelihood tree of oxytocin and vasopressin receptor (OT/VP-R) subtype genes. The tree is supported by a non-parametric bootstrap analysis with 100 replicates. Bootstrap values shown at the nodes. Red values indicate nodes with bootstrap values lower than 50% that were not considered informative. The tree was rooted with the octopus *OTR*, *CPR1* and *CPR2* sequences. The V2C sequences do not form a well-supported clade; this is indicated by blue branches. Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.707336>.

Figure S7. Neighbor joining tree of voltage-gated calcium channel L-type alpha 1 subunit (CACNA1-L) genes. The tree is supported by a non-parametric bootstrap analysis with 1000 replicates. Bootstrap values shown at the nodes. All nodes are supported by over 50% of bootstrap iterations. The tree was rooted with the fruit fly *Ca- α 1D* sequence. Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.710637>.

Figure S8. Phylogenetic Maximum Likelihood tree of voltage-gated calcium channel L-type alpha 1 subunit (CACNA1-L) genes. The tree is supported by a non-parametric bootstrap analysis with 100 replicates. Bootstrap values shown at the nodes. All nodes are supported by over 50% of bootstrap iterations. The tree was rooted with the fruit fly *Ca- α 1D* sequence. In this tree the CACNA1D sequences do not form one well-supported clade; this is indicated by blue branches. Scale bar indicate phylogenetic distance as number of substitutions per site. The phylogenetic tree file and the alignment it was made from are available from: <http://dx.doi.org/10.6084/m9.figshare.710637>.

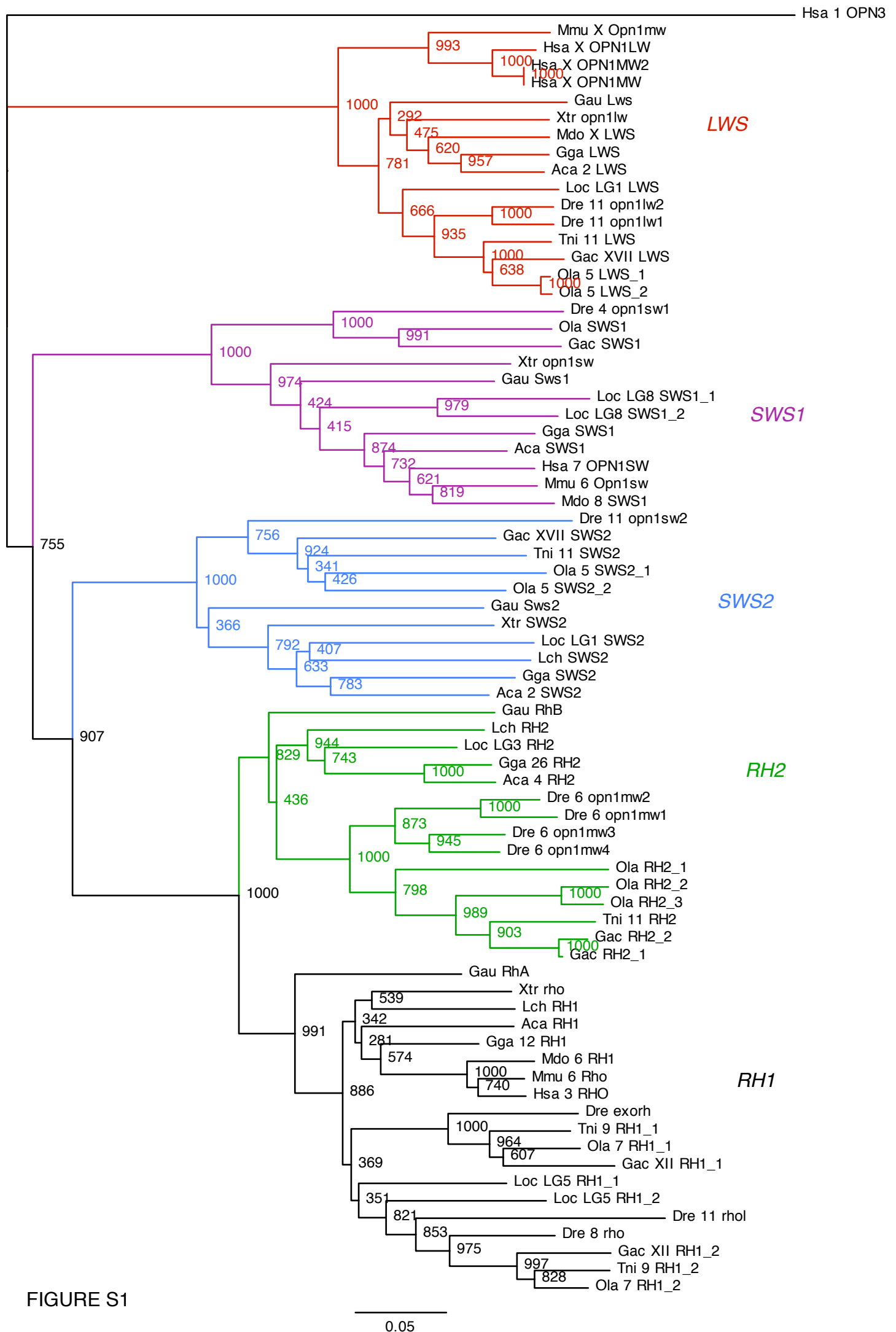


FIGURE S1

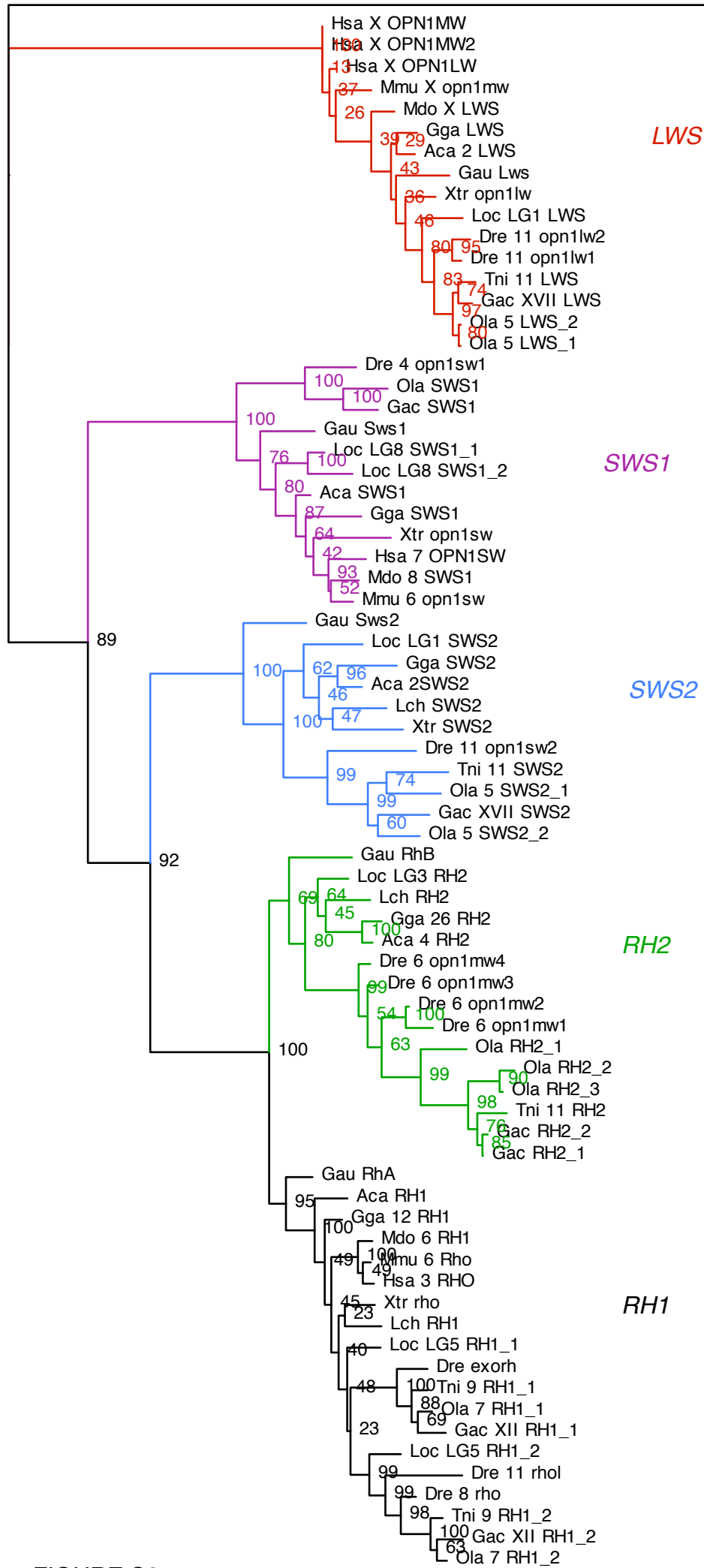


FIGURE S2

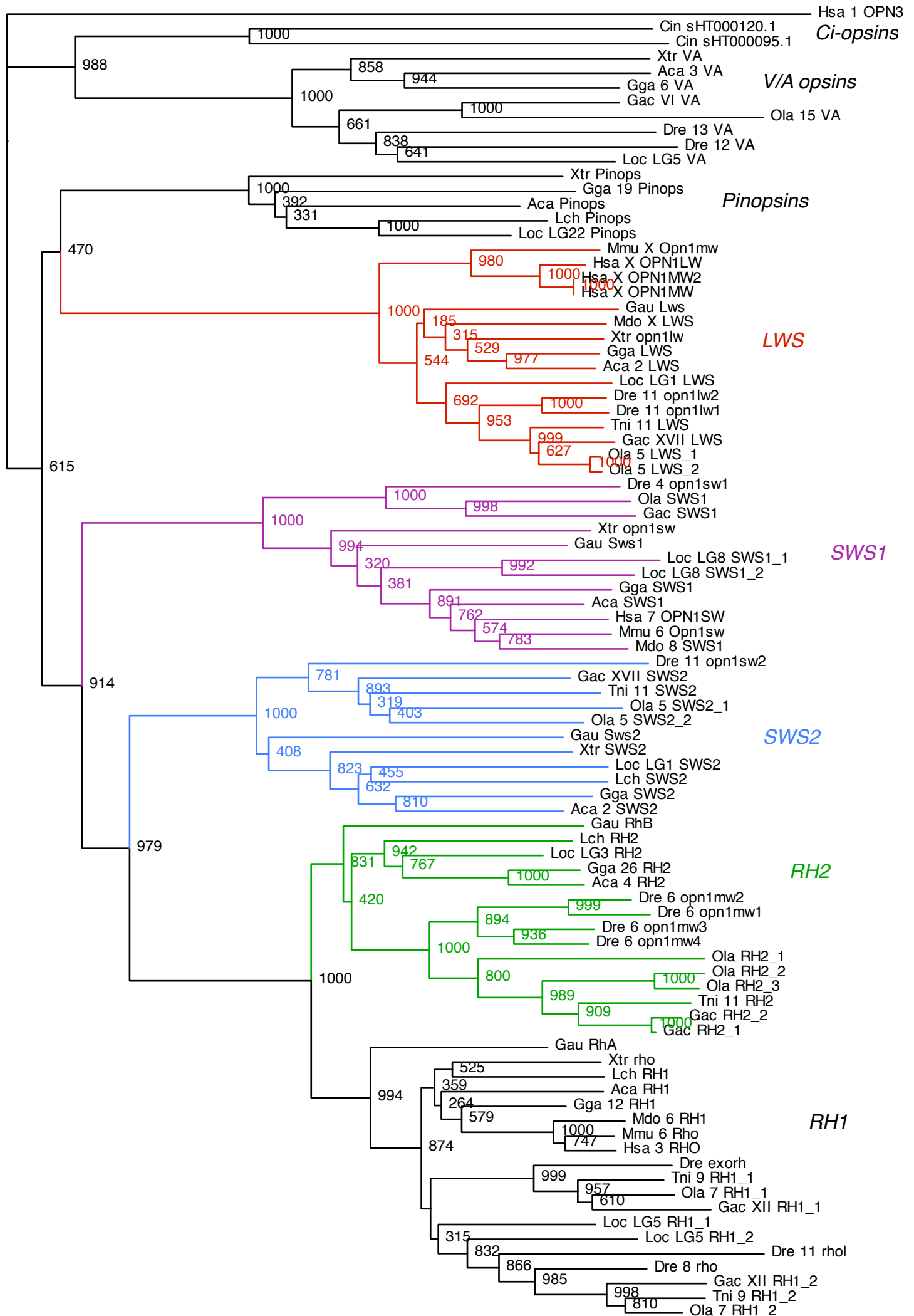


FIGURE S3

0.05

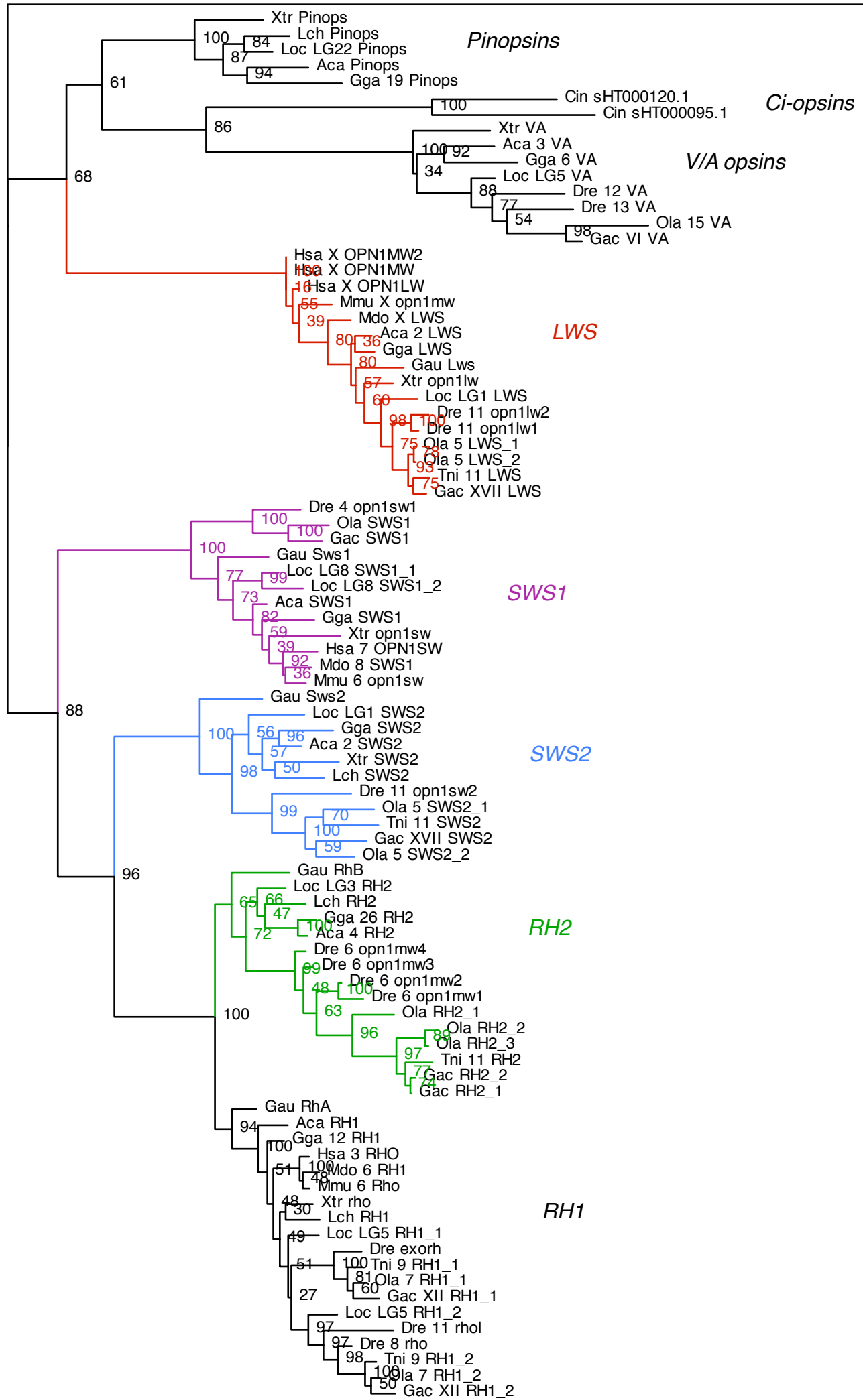


FIGURE S4

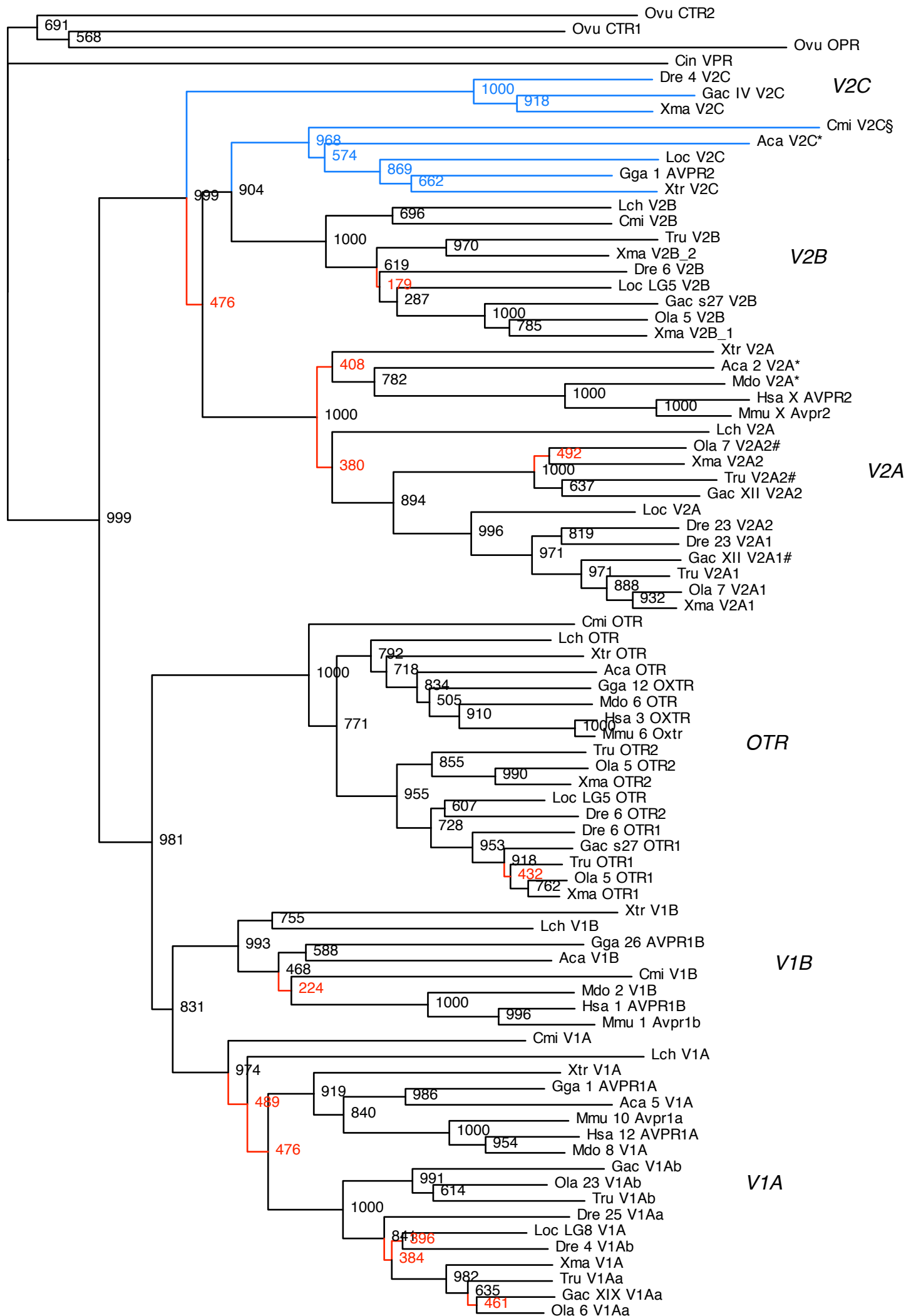


FIGURE S5

0.04

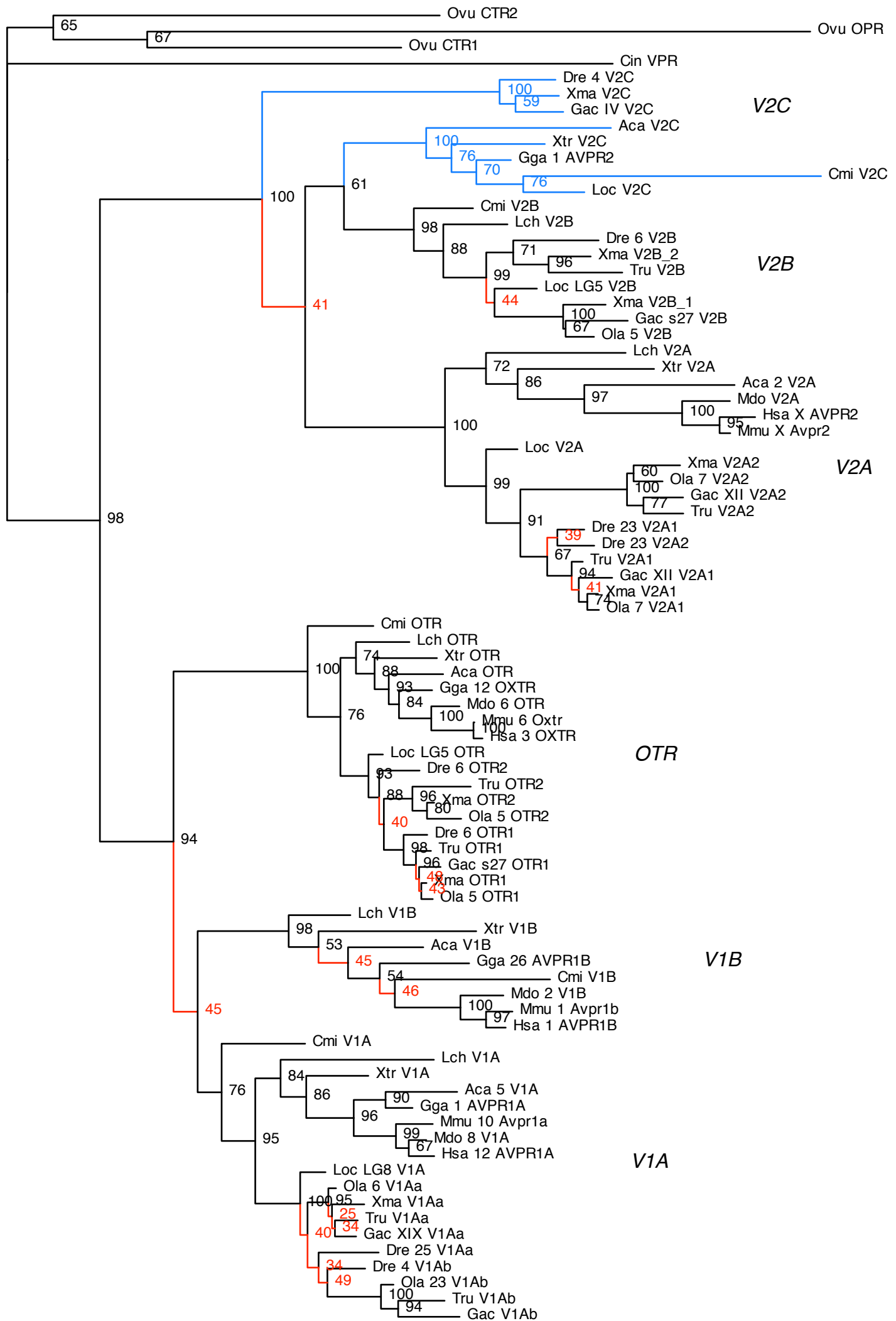


FIGURE S6

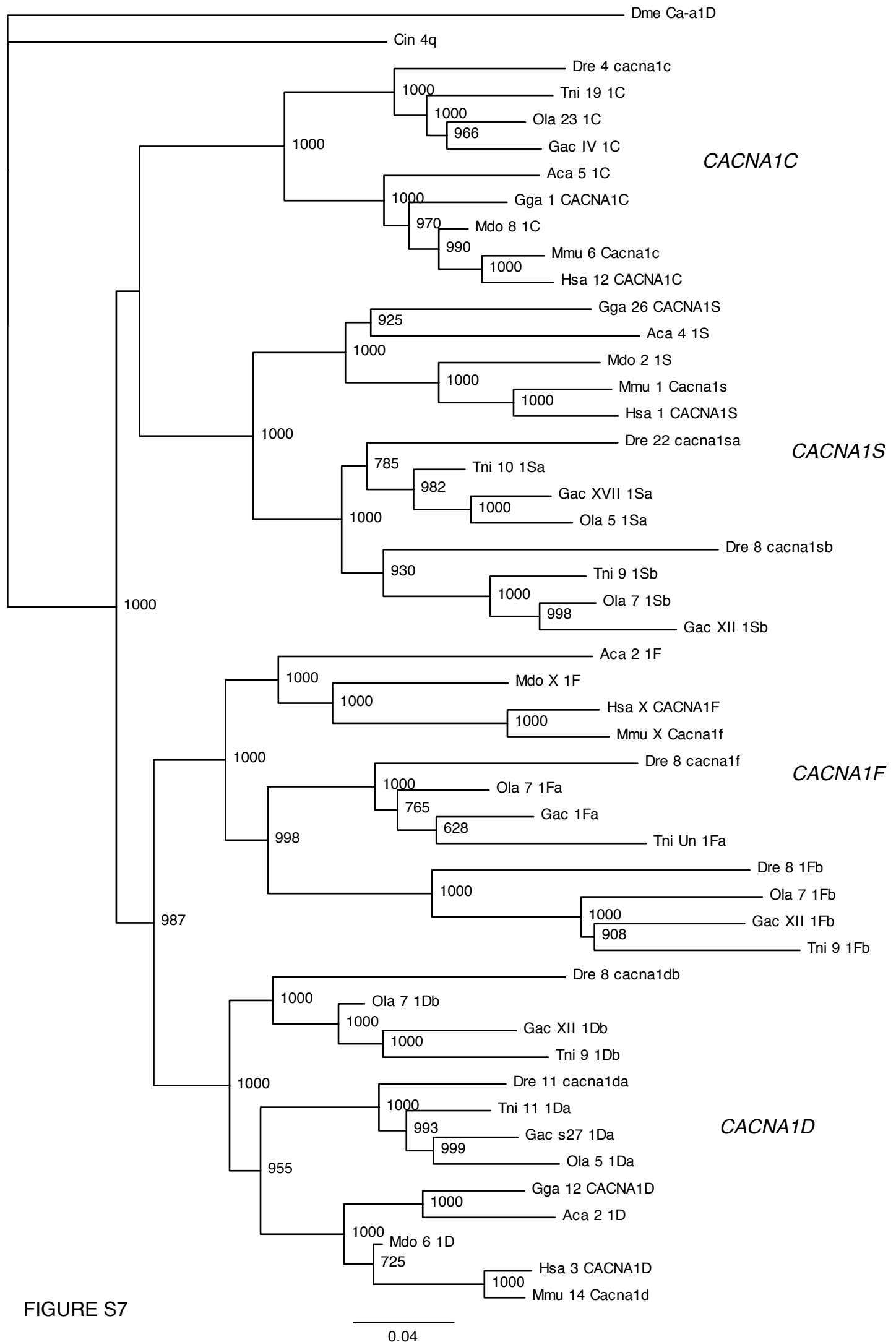


FIGURE S7

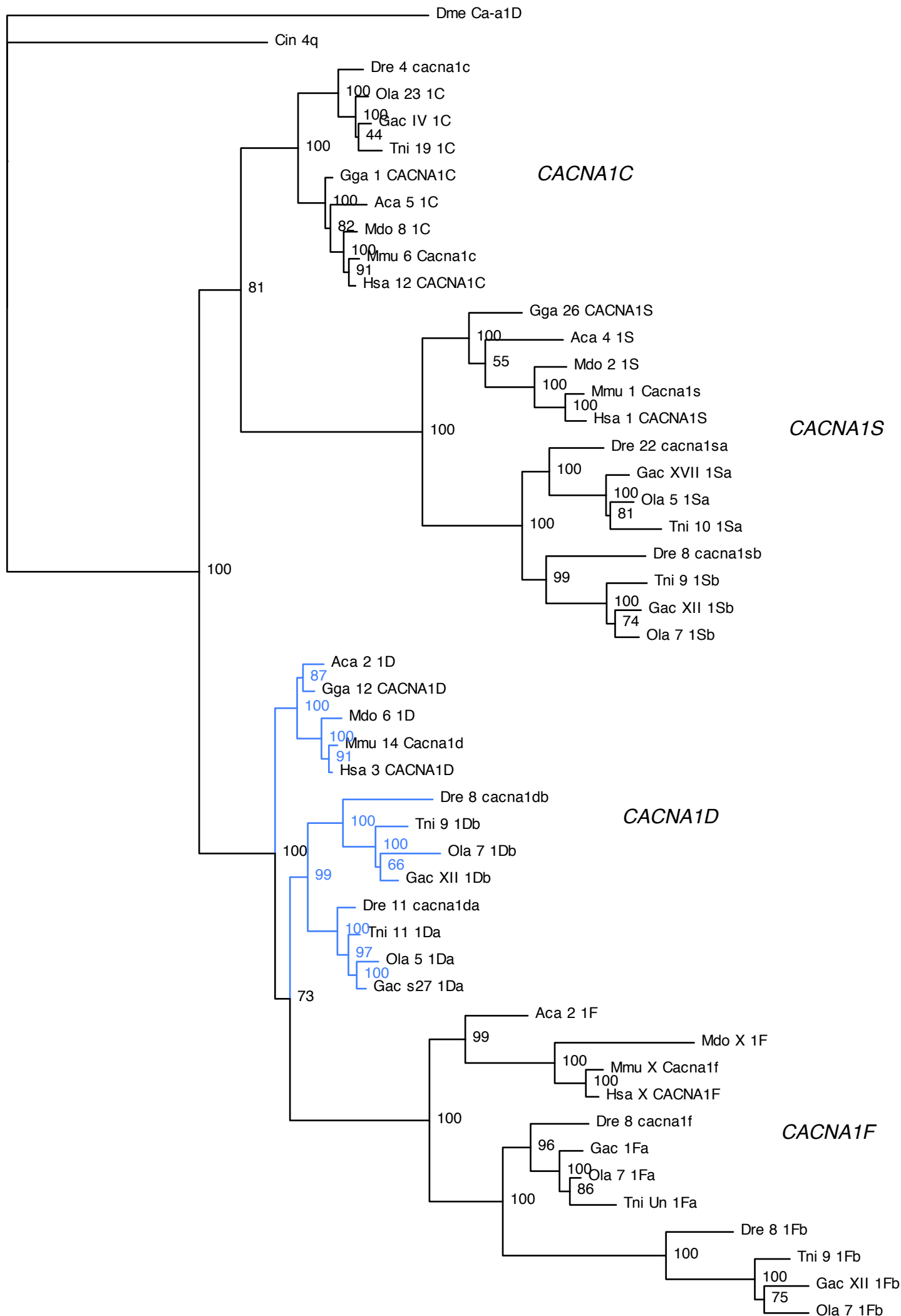


FIGURE S8