

# The genetic tale of hog species (*Suidae*), exposing deleterious mutations, inbreeding and their demographic history.

## Bachelor Thesis Supplementary Material

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### Bachelor Thesis Supplementary Material:

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Animal Breeding and Genomics

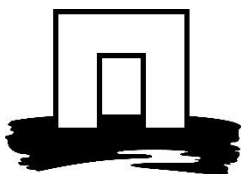
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# 1 DATA OVERVIEW

Table 1: Table with full overview of the contents of the multi-sample VCF. The data is categorized by the available annotations and the amount of individuals present in the data is displayed. Furthermore, the identifiers of the selected samples are shown.

Species	Continent	Breed	Population	Number of individual s	Individuals selected for analysis
<i>Sus scrofa</i>	Asia	Wild	Japan	11	WB20F06 WB20M01 WB20M02 WB20M03 WB20M07
			China, North	3	SSWB30U08 WB30U01 WB30U09
			China, South	5	SSWB29U12 WB29U04 WB29U13 WB29U14 WB29U16
			Thailand	2	-
		Jiangquhai	-	3	-
		Jinhua		2	-
		Leping spotted		2	-
		Meishan		10	MS20M03 MS20M05 MS21M01 MS21M05 MS21M08
		Thai pig		2	-
		Wannan spotted		2	-
		Xiang pig		2	-
		Zang pig		1	-
	Europe	Wild	Netherlands , Veluwe	5	-
			Netherlands , Mijneweg	7	WB22F03 WB22F04 WB22M02 WB22M03
			France	1	-
			Switzerland	9	WB26F06 WB26M03 WB26M04 WB26M11 WB26M12
			Italy, Cilento	2	-
			Greece, Central	2	-

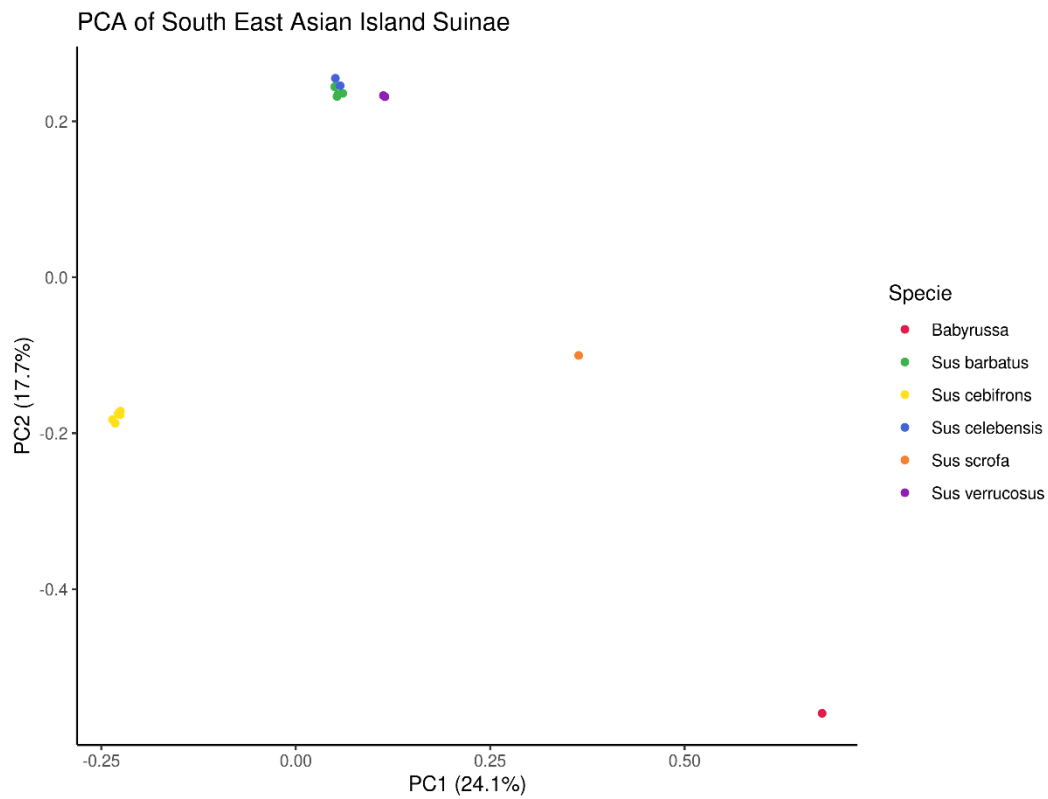
			Greece, North	2	-
			Greece, Samos	2	-
			Austria	1	-
			Poland, North-East	2	-
			Hungary	2	-
		Angler Sattelschwein	Germany	2	-
		Bunte Bentheimer		2	-
		Leicoma		1	-
		Mangalica	Hungary	7	CT01F01 CT01F06 CT01F13 CT01M33 CT01M34
		Calabrese	Italy	1	-
		Cassertana		7	-
		Cinta Senese		2	-
		Nera Siciliana		1	-
		Chato Murciano	Spain	2	-
		Negro Iberico		3	-
		Retinto		3	-
		Linderodsvinn	Sweden	2	-
		Berkshire	United Kingdom	2	-
		British Saddleback		2	-
		Gloucester Old Spot		2	-
		Large Black		2	-
		Middle White		2	-
		Tamworth		2	-
	Modern commercial	Duroc	-	53	214569 215427 216352 216797 217000
		Hampshire		10	-
		Landrace		43	215827 216779 216787 216879 217196
		Large White		97	PigWUR192 PigWUR193 PigWUR194

					PigWUR195 PigWUR196
		Pietrain		13	-
		Synthetic		37	-
	Islands of South East Asia	Wild		1	
<i>Sus barbatus</i>				4	SBSB01M01 SBSB02F03 SBSB02M02 SBSB02M03
<i>Sus cebifrons</i>				7	SCEB01F01 SCEB02M02 SCEB_Kb14130 SCEB_Kb16508 SCEB_Kb16637
<i>Sus celenensis</i>				2	-
<i>Sus verrucosus</i>				2	-
<i>Porcula salvania</i>	Asia			6	LIB5203_1Blood_3_ 7 LIB5204_2Blood_3_ 7 LIB5205_3Blood_3_ 7 LIB5206_59F4201 LIB5207_60F4192 LIB5208_61M4183
<i>Phacochoerus africanus</i>	Africa			1	
<i>Potamochoerus larvatus</i>				1	
<i>Potamochoerus porcus</i>				1	
<i>Babyrussa</i>	Islands of South East Asia			1	
<i>Pecari tajacu</i>	America			1	

## 2 RESULTS

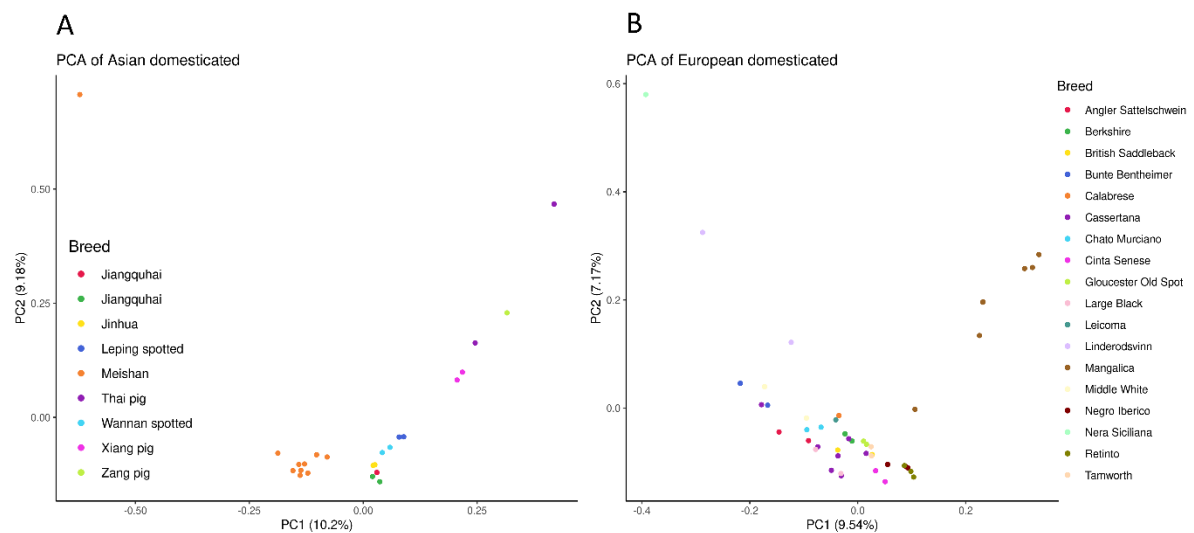
### 2.1 PCA

#### 2.1.1 South East Asian Island Suids



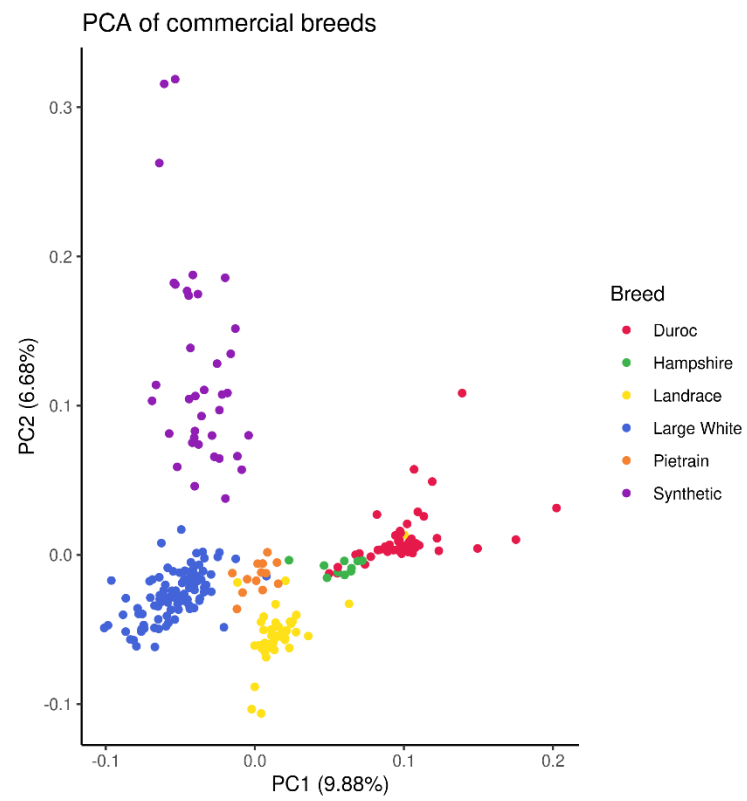
**Figure 1:** This figure displays a PCA of the Suids inhabiting the South East Asian Islands. A clear distinct separation can be witnessed between the clusters.

#### 2.1.2 Eurasian domesticated



**Figure 2:** This figure displays two PCAs. Figure A contains Asian domesticated breeds and figure B contains European domesticated breeds.

### 2.1.3 Commercial breeds



**Figure 3: PCA of commercial breeds. Colors are assigned based on breed.**

## 2.2 Effective population size analyses

### 2.2.1 South East Asian Islands *Sus*

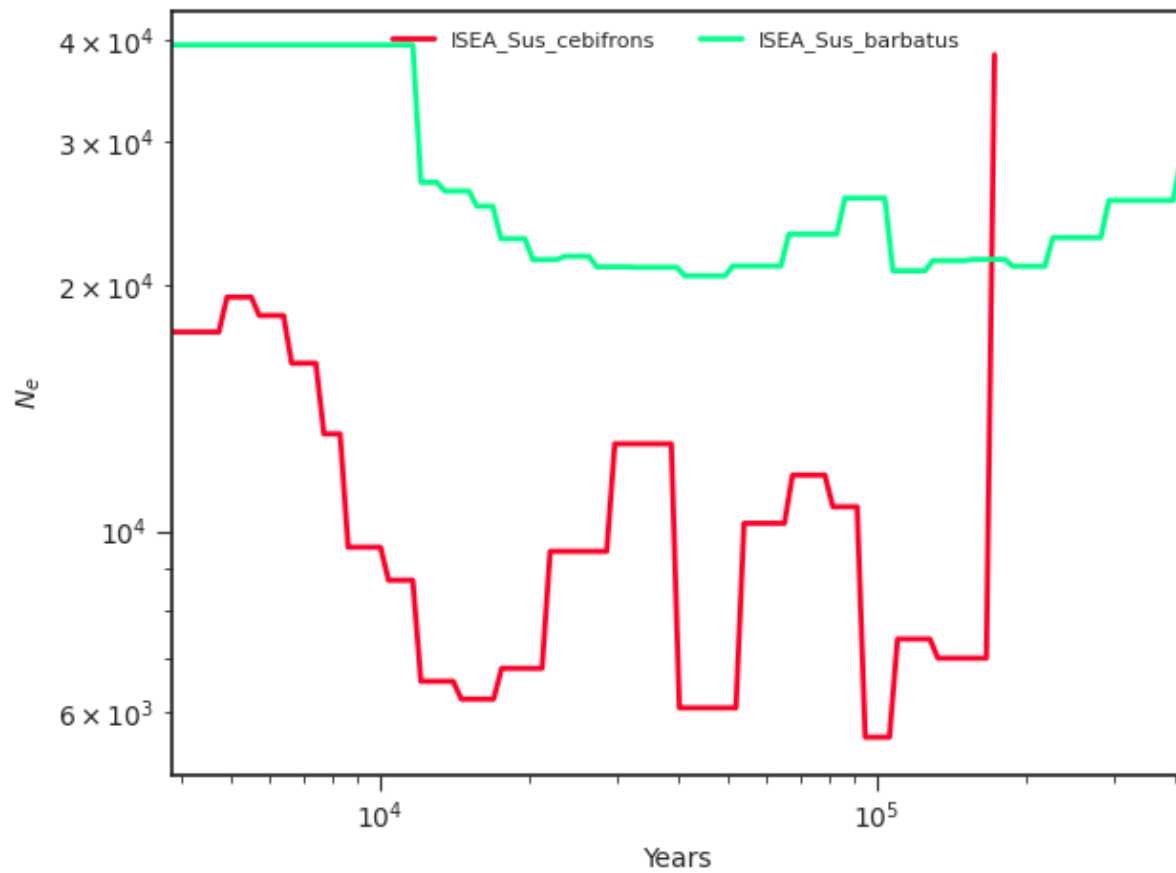


Figure 4: This figure contains a historic effective population size analysis of *Sus cebifrons* and *Sus barbatus*.



### 2.2.2 Asian wild and domesticated *Sus scrofa*

#### Effective population size of Asian *Sus scrofa*

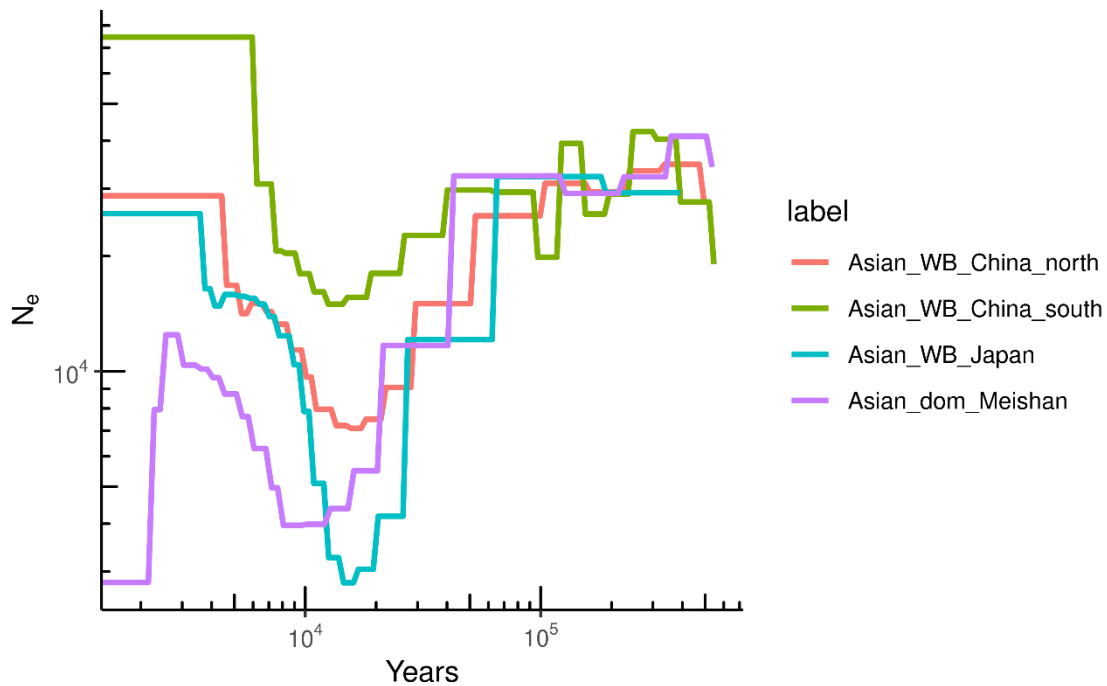


Figure 5: Effective population size of Asian wild boar and domestic pig.

### 2.2.3 European wild and domesticated *Sus scrofa*

#### Effective population size of European *Sus scrofa*

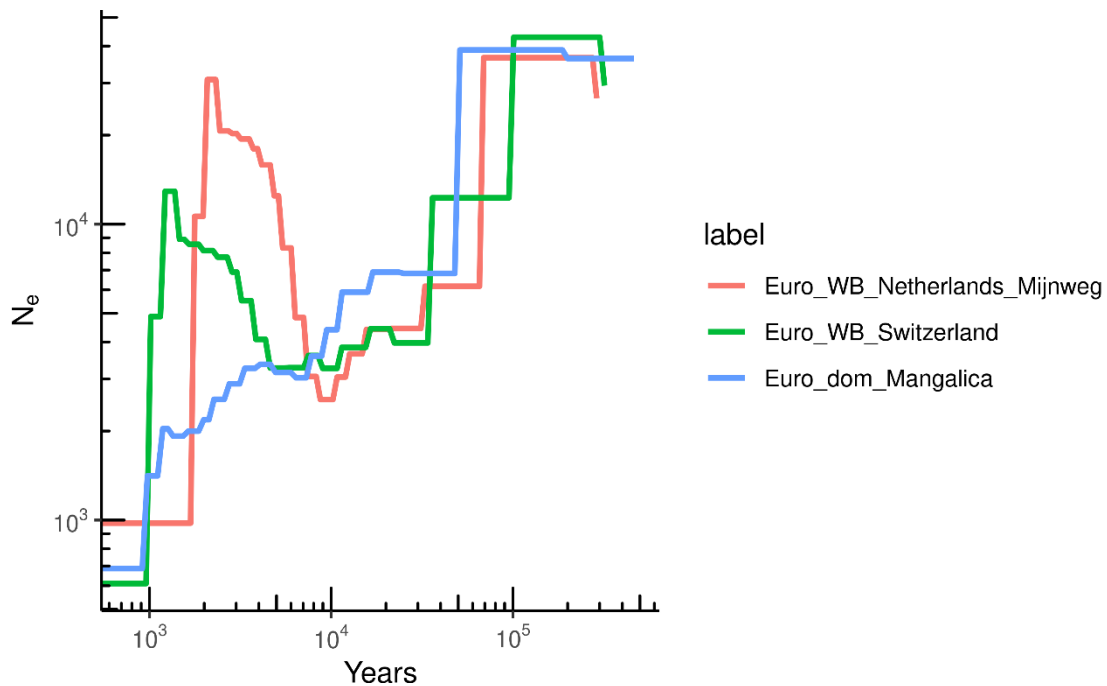


Figure 6: Effective population size analysis of European wild boar and domestic pig.

## 2.2.4 Commercial breeds

### Effective population size of Commercial

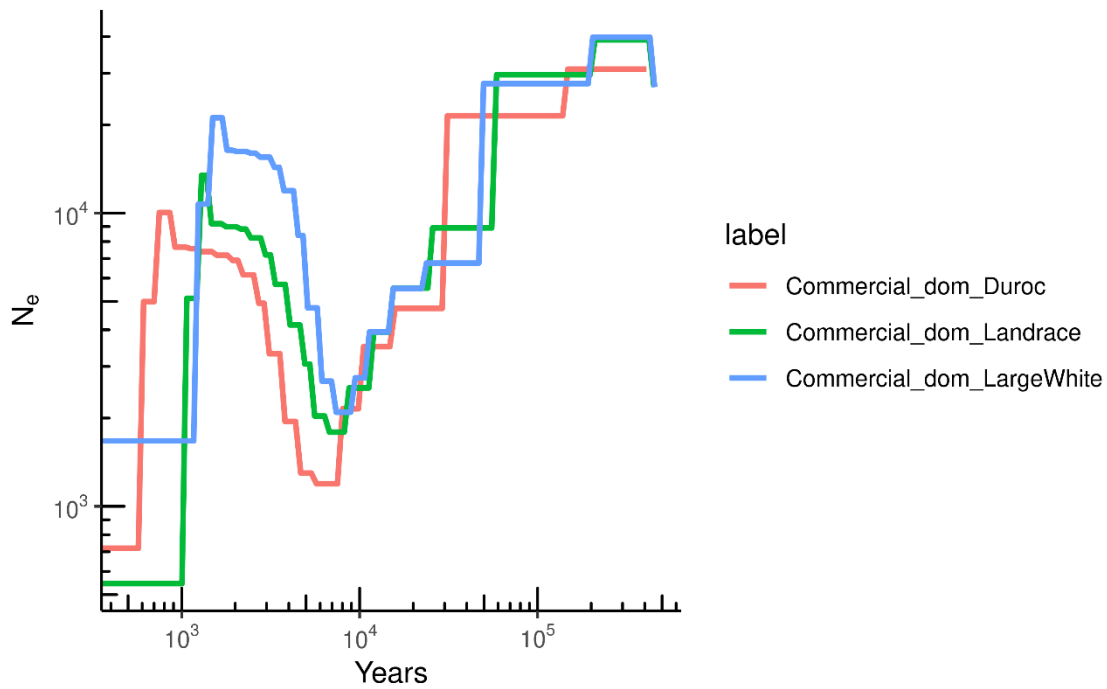


Figure 7: Effective population size analysis of commercial breeds.

## 2.3 ROH analysis

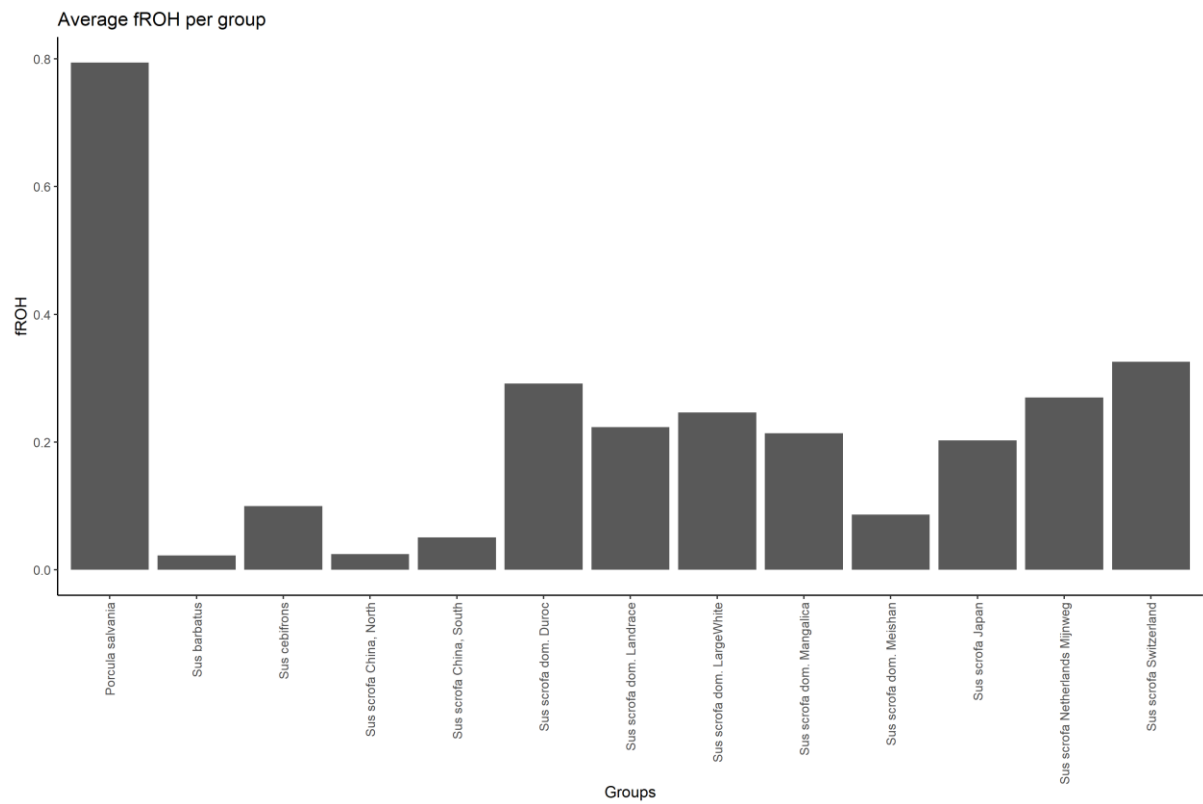
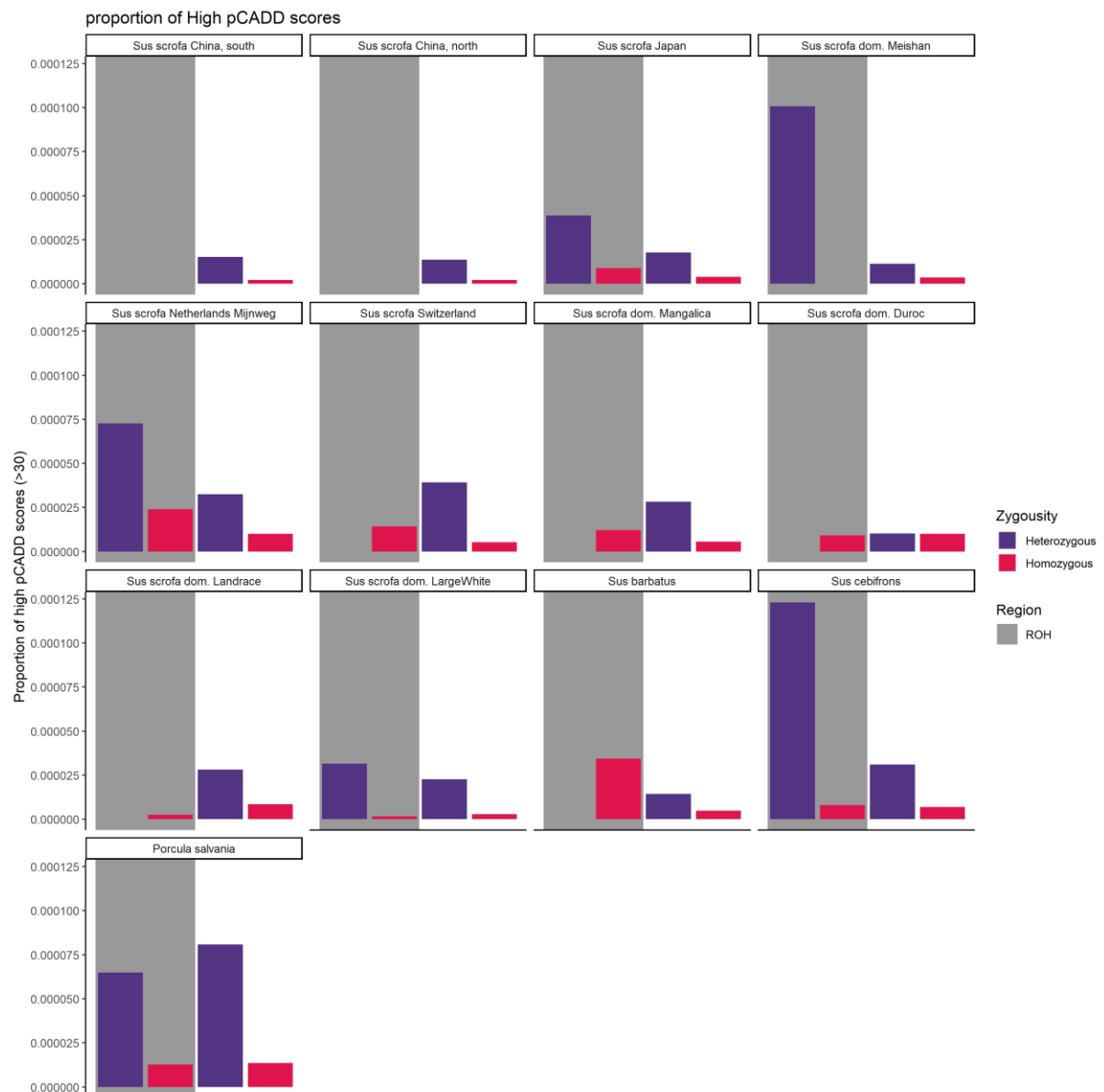


Figure 8: fROH analysis

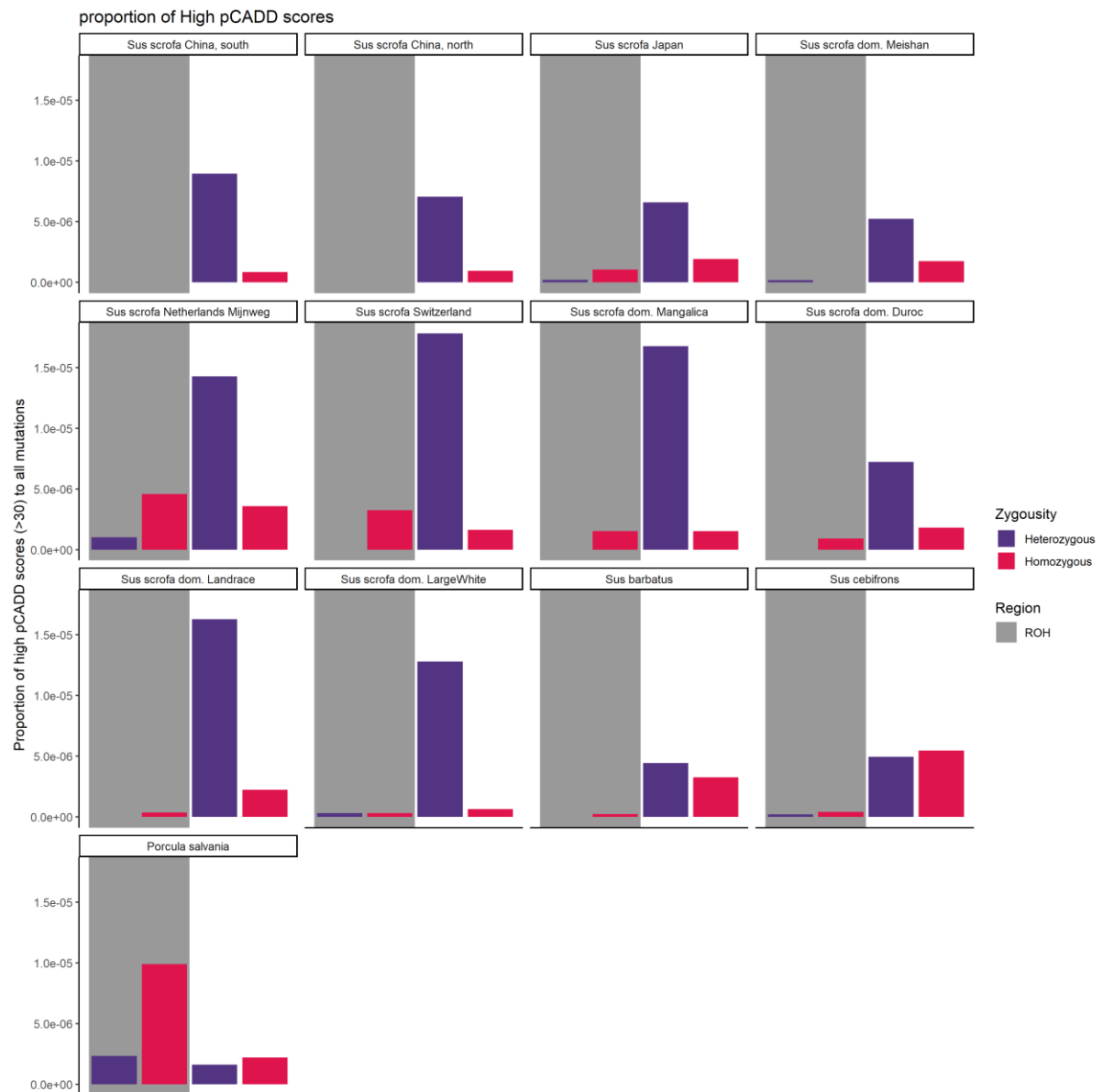
## 2.4 Deleterious mutations analysis

### 2.4.1 pCADD scores proportional to all mutations



**Figure 9: GROUPED BAR PLOT VISUALIZATION OF HIGHLY DELETERIOUS MUTATIONS. FOR THIS VISUALIZATION, ALL MUTATIONS HAVE BEEN CATEGORIZED AS EITHER HETEROZYGOUS OR HOMOZYGOUS AND AS WITHIN AN ROH AND OUTSIDE AN ROH. WITHIN EACH OF THESE CATEGORIES, THE PROPORTION OF HIGHLY DELETERIOUS MUTATIONS TO ALL MUTATIONS WITHIN THE OVERARCHING GROUP WAS CALCULATED AND VISUALIZED IN THIS FIGURE. MUTATIONS WERE CONSIDERED HIGHLY DELETERIOUS IF THEY HAD A PCADD SCORE HIGHER THAN 30.**

## 2.4.2 pCADD scores proportional to all categorized mutations



**Figure 10: Grouped bar plot visualization of highly deleterious mutations in.** For this visualization, all mutations have been categorized as either heterozygous or homozygous and as within an ROH or outside an ROH. Within each of these categories, the proportion of high mutation to all mutations within the category was calculated and visualized in this figure. Mutations were considered high if they had a pCADD score higher than 30.