**Supp\_Figure 5.3: (A)** UPGMA tree based on nucleotide diversities between 14 AA and 34 OO animals in windows of increasing size (0.5 to 40-Kb) centered on the 2.3 Kb deletion in the porcine N-acetyl-galactosaminyl transferase gene (porcine O allele). PA: *Phacochaerus Africanus*, SC: *Sus cebifrons*, SV: *Sus verrucosus*, SU: *Sus scrofa vittatus*, CB: Chinese wild boar, RB: Russian wild boar, EB: European wild boar, ERH: Erhualian, BX: Bamaxiang, T: Tibetan, LA: Laiwu, LR: Landrace, LW: Large White, PI: Piétrain, WD: White Duroc.

I received genotype data from 14 AA and 34 OO animals SNPs flanking the deletion (Datafile.txt). I wrote a Pertl script to compute pair-wise distances for a window size of defined size (line 1 in perl script) as described in Online Methods. One of the output files (dist.txt) is used directly by the R script (Phyl\_O.R) that will generate a UPGMA dendrogram using hclust.