

## Supplementary Figures:

### Meiotic gene evolution: can you teach a new dog new tricks?

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**Figure S1. Maximum likelihood tree of the *Mei2*-like family.**

Prefixes of gene models correspond to the following species: AT; *Arabidopsis thaliana*; AL; *Arabidopsis lyrata*; BD; *Brachypodium distachyon*; Bra; *Brassica rapa*; CP; *Carica Papaya*; CR; *Chlamydomonas reinhartii*; FV; *Fragaria vesca*; GM; *Glycine max*; Gorai; *Gossypium raimondii*; GSMUA; *Musa acuminata*; Lirio; *Liriodendron tulipifera*; LJ; *Lotus japonicus*; MD; *Malus domestica*; ME; *Manihot esculenta*; MT; *Medicago truncatula*; Nuphar; *Nuphar advena*; OS; *Oryza sativa japonica*; OSI; *Oryza sativa indica*; PP; *Physcomitrella patens*; PT; *Populus trichocarpa*; RC; *Ricinus communis*; SB; *Sorghum bicolor*; SM; *Selaginella moellendorffii*; Solyc; *Solanum lycopersicon*; Sotub; *Solanum tuberosum*; TC; *Theobroma cacao*; VC; *Volvox carteri*; VV; *Vitis vinifera*; ZM; *Zea mays*. Numbers at the nodes are SH-based aLRT values.

**Figure S2. Maximum likelihood tree of the RPA gene family.**

Prefixes of gene models correspond to the following species: Ambor; *Amborella trichopoda*; AT; *Arabidopsis thaliana*; AL; *Arabidopsis lyrata*; BD; *Brachypodium distachyon*; Bra; *Brassica rapa*; CP; *Carica Papaya*; CR; *Chlamydomonas reinhartii*; FV; *Fragaria vesca*; GM; *Glycine max*; Gorai; *Gossypium raimondii*; GSMUA; *Musa acuminata*; Lirio; *Liriodendron tulipifera*; LJ; *Lotus japonicus*; MD; *Malus domestica*; ME; *Manihot esculenta*; MRCC; *Micromonas*; MT; *Medicago truncatula*; Nuphar; *Nuphar advena*; OL; *Ostreococcus lucimarinus*; OT; *Ostreococcus tauri*; OS; *Oryza sativa japonica*; OSI; *Oryza sativa indica*; Persea; *Persea americana*; PP; *Physcomitrella patens*; PT; *Populus trichocarpa*; RC; *Ricinus communis*; SB; *Sorghum bicolor*; SM; *Selaginella moellendorffii*; Solyc; *Solanum lycopersicon*; Sotub; *Solanum tuberosum*; TC; *Theobroma cacao*; VC; *Volvox carteri*; VV; *Vitis vinifera*; ZM; *Zea mays*. Numbers at the nodes are SH-based aLRT values.

**Figure S3. Conservation of *DMC1* exon structure between *B. rapa* and the A genome of *B. napus*.**

*DMC1* has a single copy in *Arabidopsis*. There are three copies in *B. rapa*, one of which is full length, the other two are highly fractionated and therefore unlikely to be functional. In addition to the full length copy, the A genome of *B. napus* retains the two fractionated copies with an exon structure unchanged from that observed in *B. rapa*.

**Figure S4. Wheat meiotic gene expression.**

RNAseq expression data for a subset of 12 gene families for which copy number has been confirmed by screening BAC libraries. Columns show the relative contribution of each gene to the total expression of that homeogroup. In no case have genes triplicated in the wheat hexaploidy event returned to a single expressed copy. Several genes have only one (\*\*) or two (\*) copies on a homeologue group. These genes result from non-WGD duplications (i.e. tandem or segmental duplication) that occurred after divergence of the diploid wheat progenitors.

**Figure S5. *Brassica napus* meiotic gene expression.**

Pyrosequencing data for 7 gene families in *B. napus*, showing relative percentage of total expression contributed by the A and C genomes. In no case have genes returned to a single expressed copy. Error bars = 1 SD from 3 biological replicates.

**Figure S6. Ka/Ks of all retained duplicates.**

All retained duplicates show evidence of purifying selection.

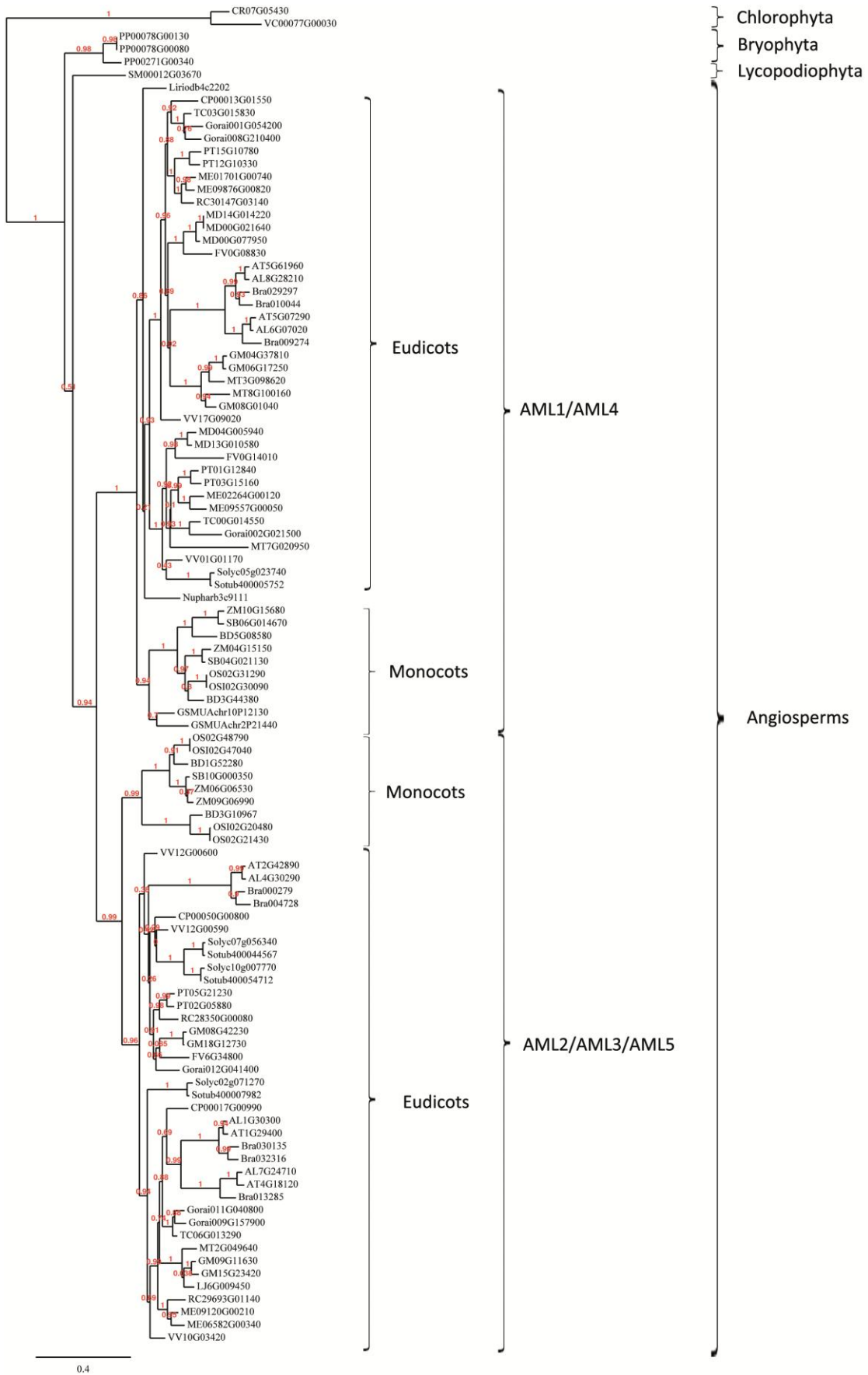


Figure S1.

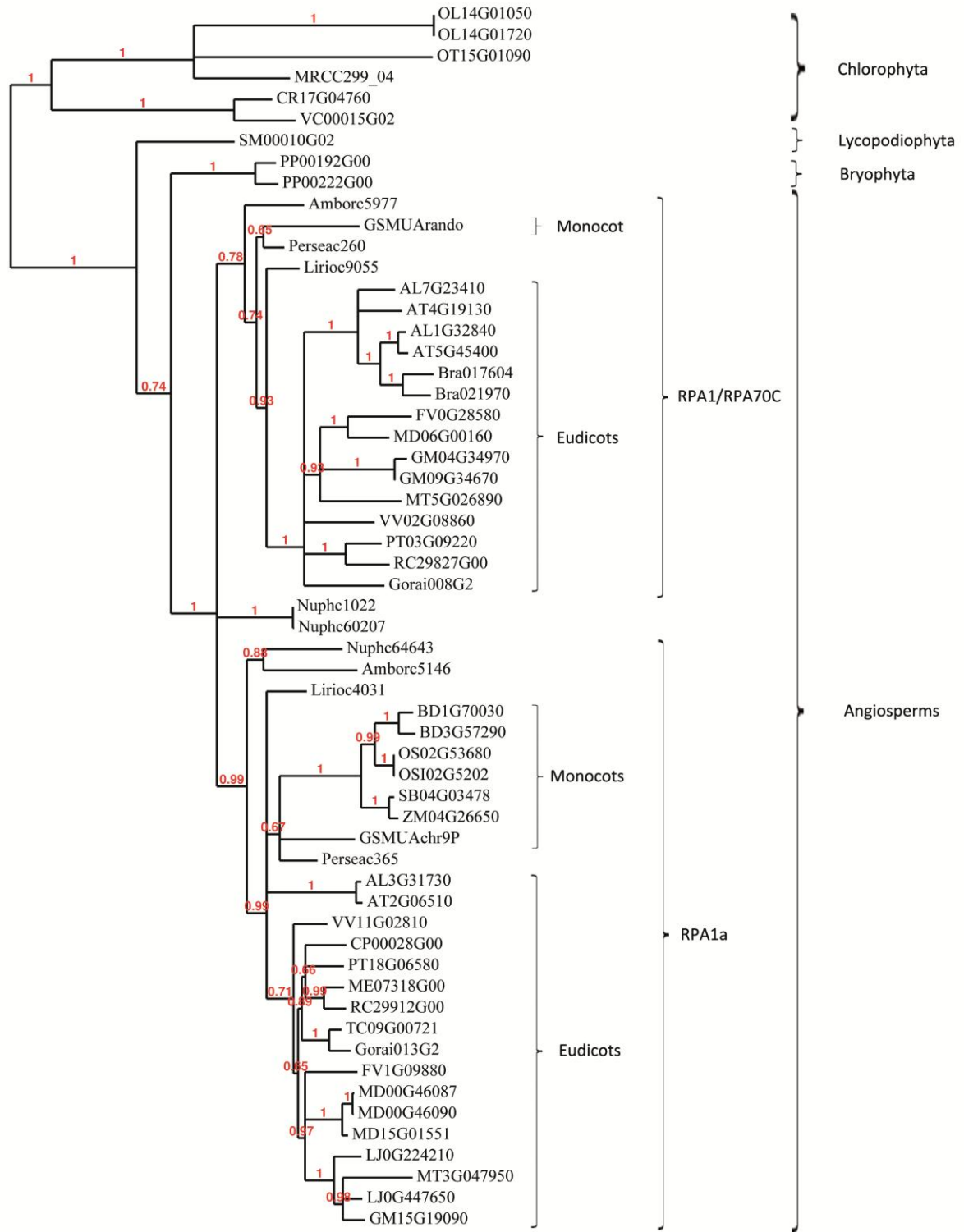


Figure S2.

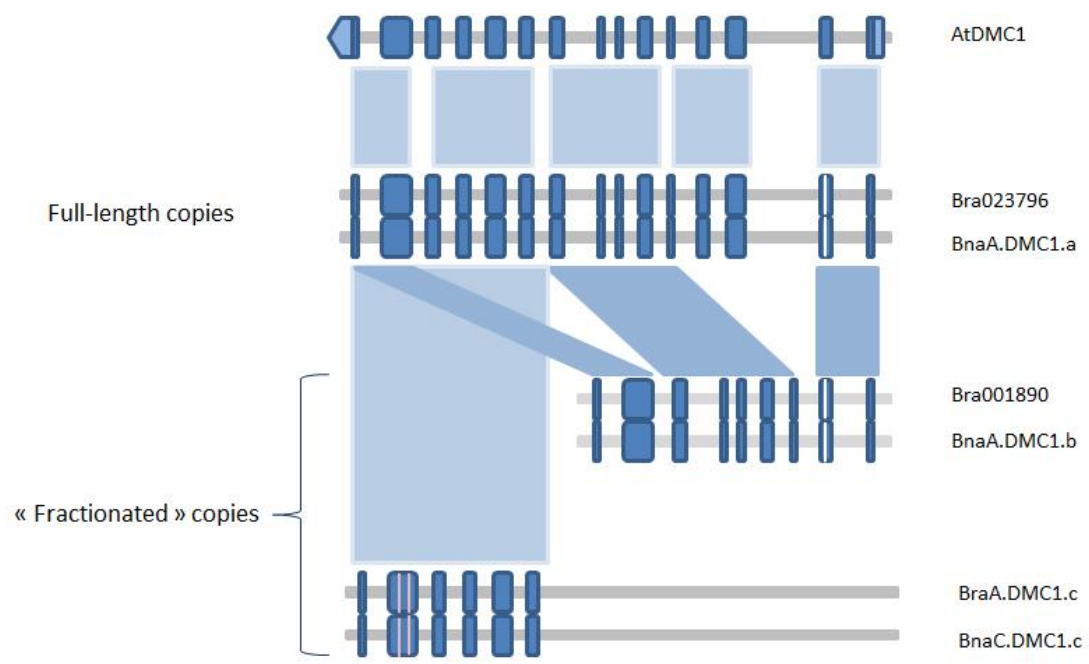


Figure S3.

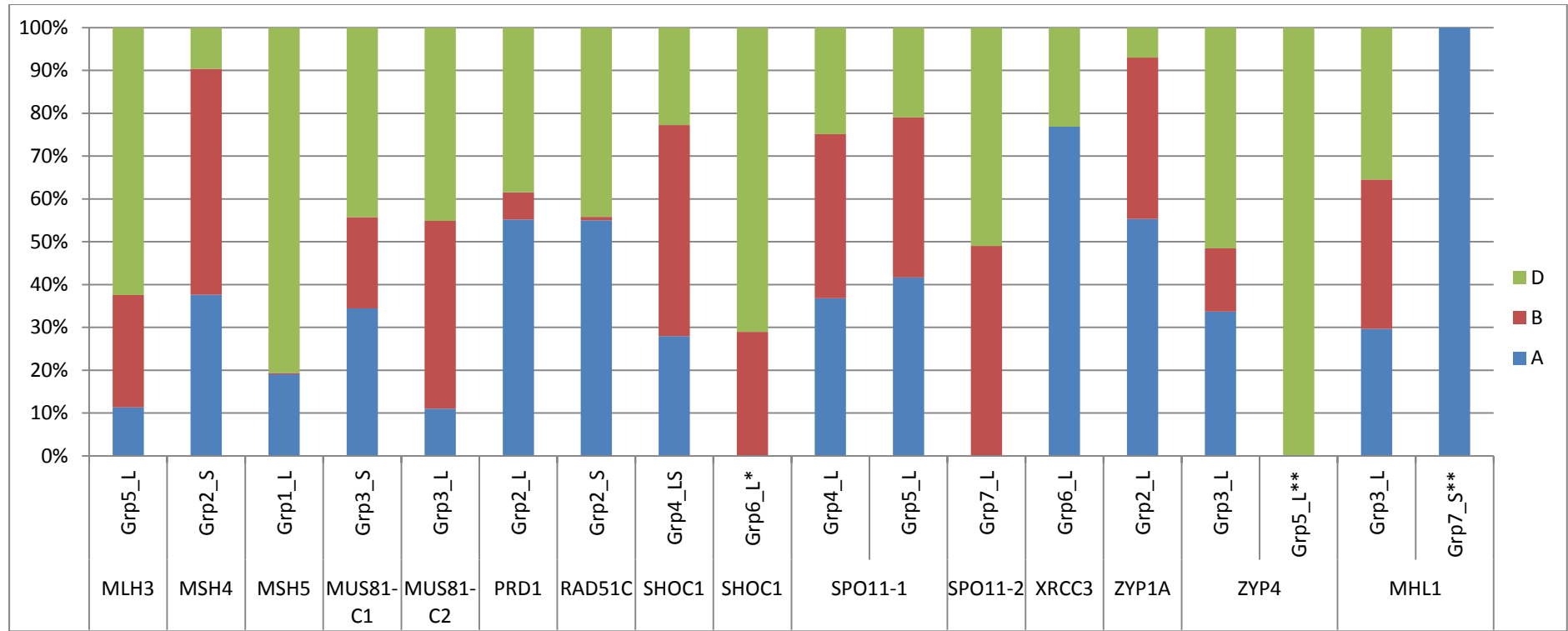


Figure S4.

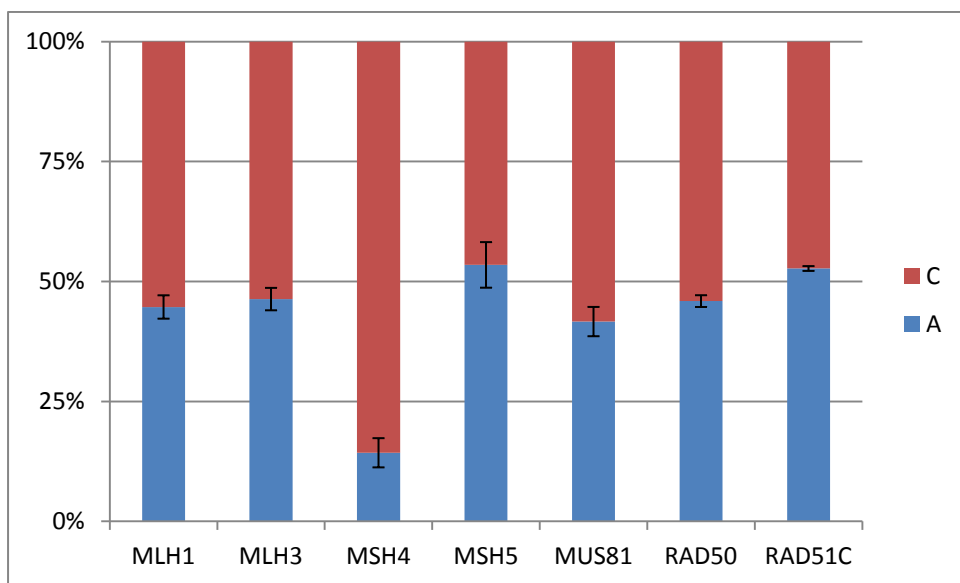


Figure S5.

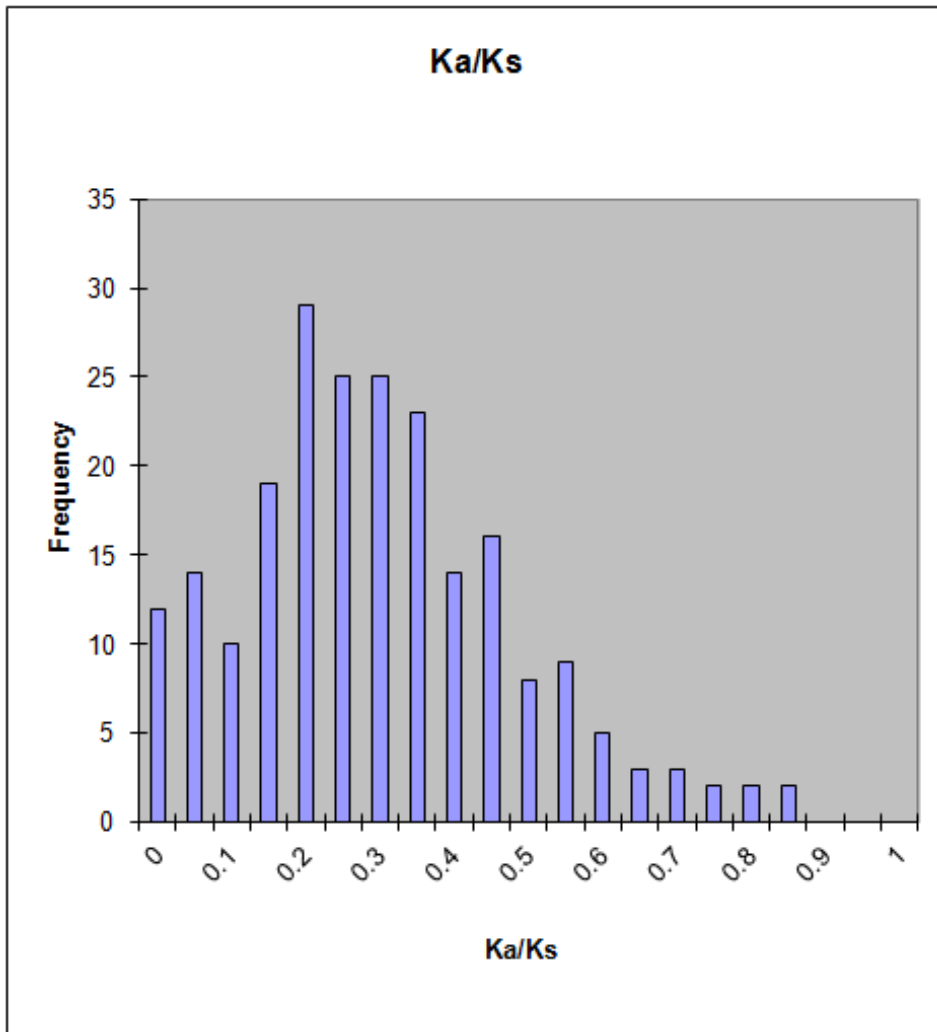


Figure S6.