

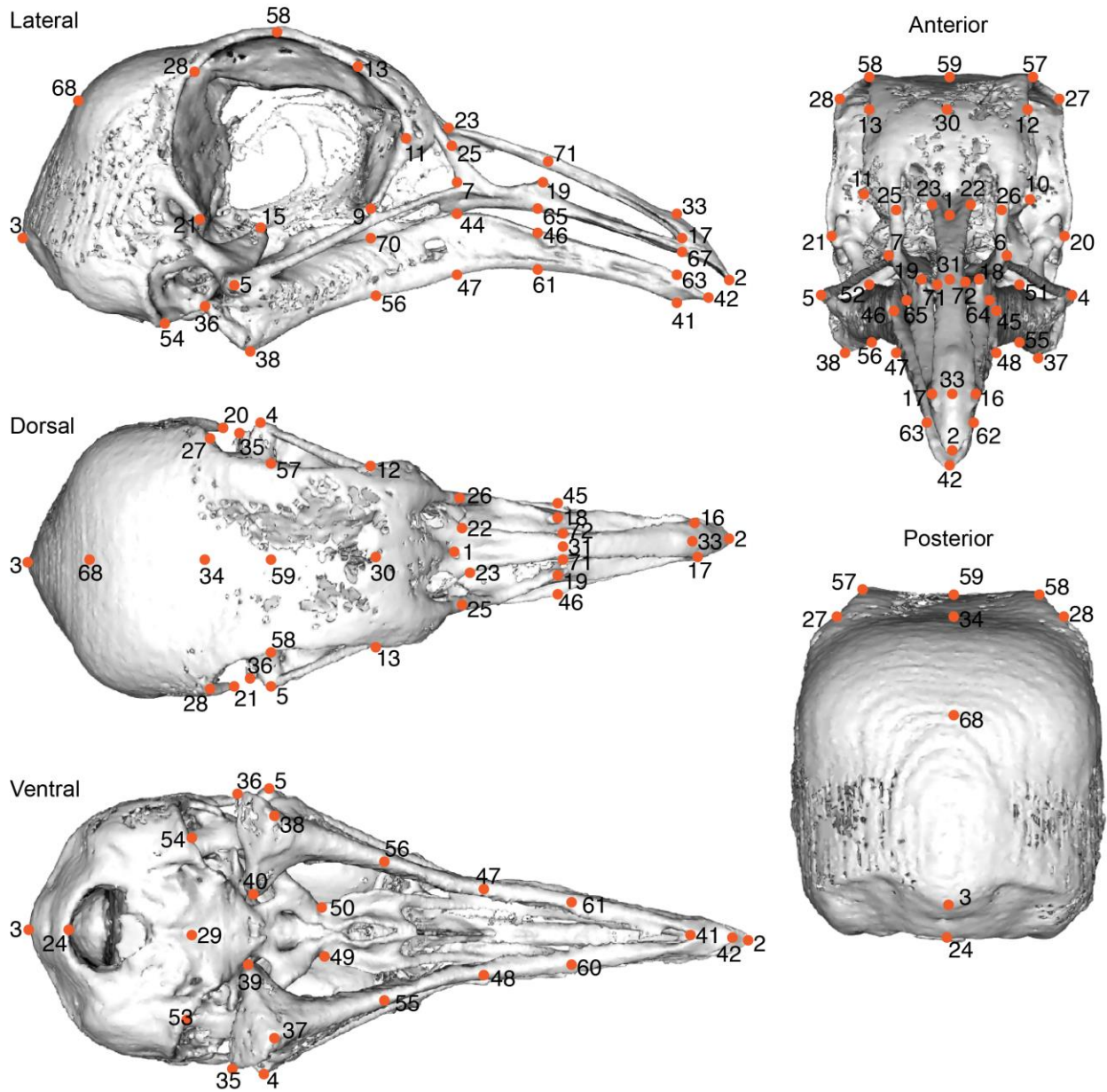
946

947

948

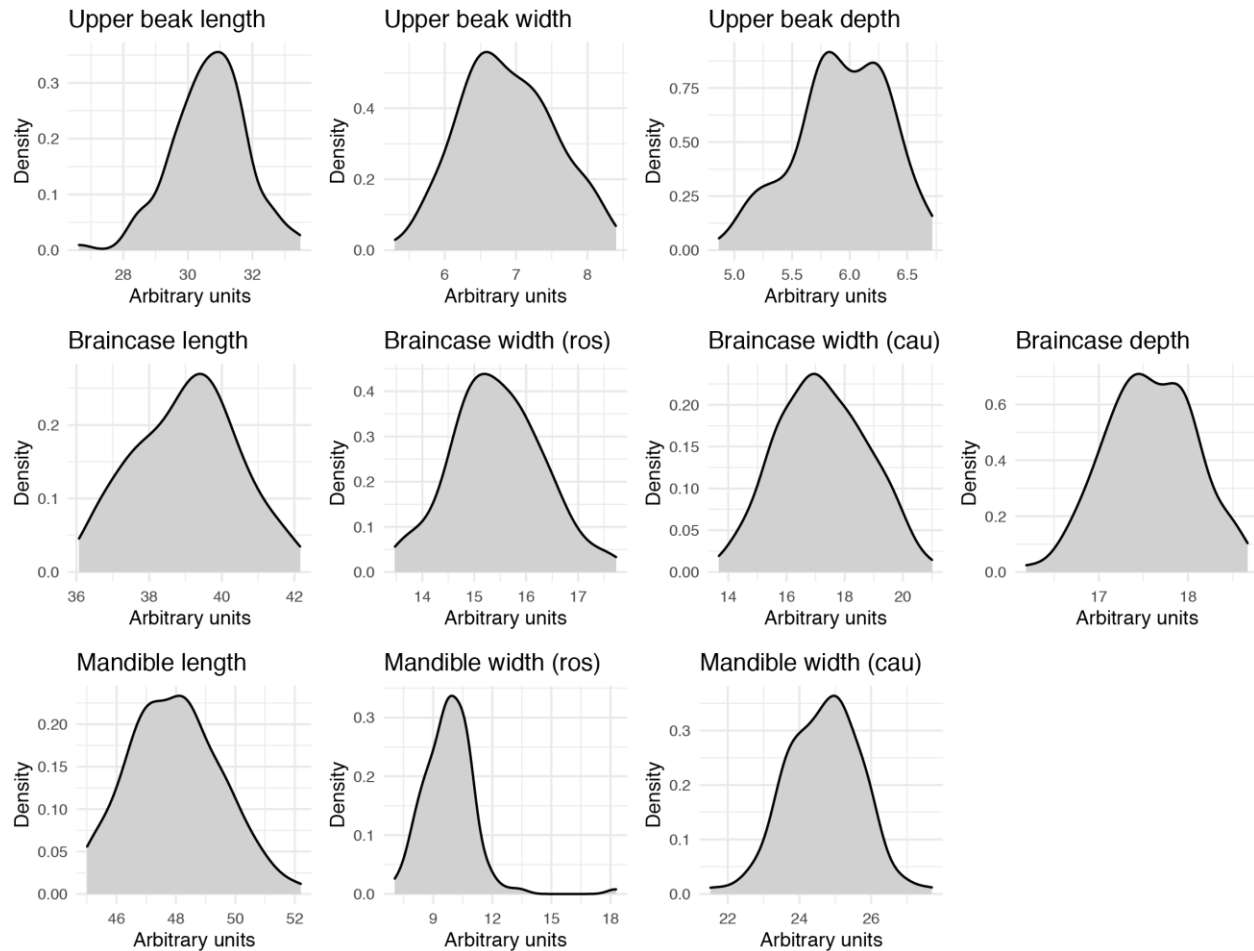
949

**Supplemental Figure 1. Surface models of the Pom x Scan founders.** Lateral (left) and dorsal (right) views of the craniofacial skeleton of the male Pom and female Scan founders used to generate the F<sub>2</sub> intercross.

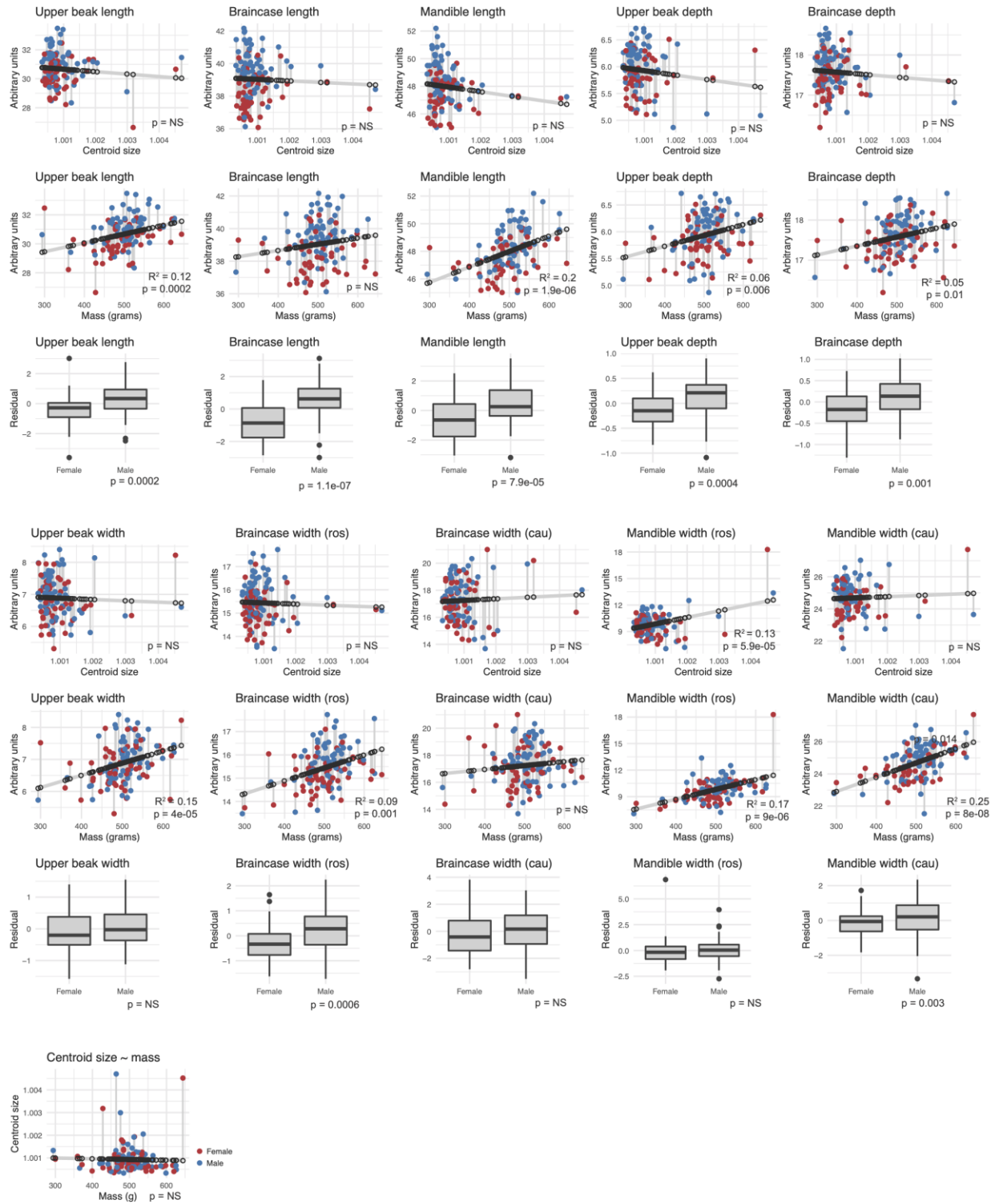


950  
951  
952

**Supplemental Figure 2. Pigeon craniofacial reference landmarks.** Landmark positions are indicated by red circles; numbers correspond to descriptions in Supplemental Table 1.

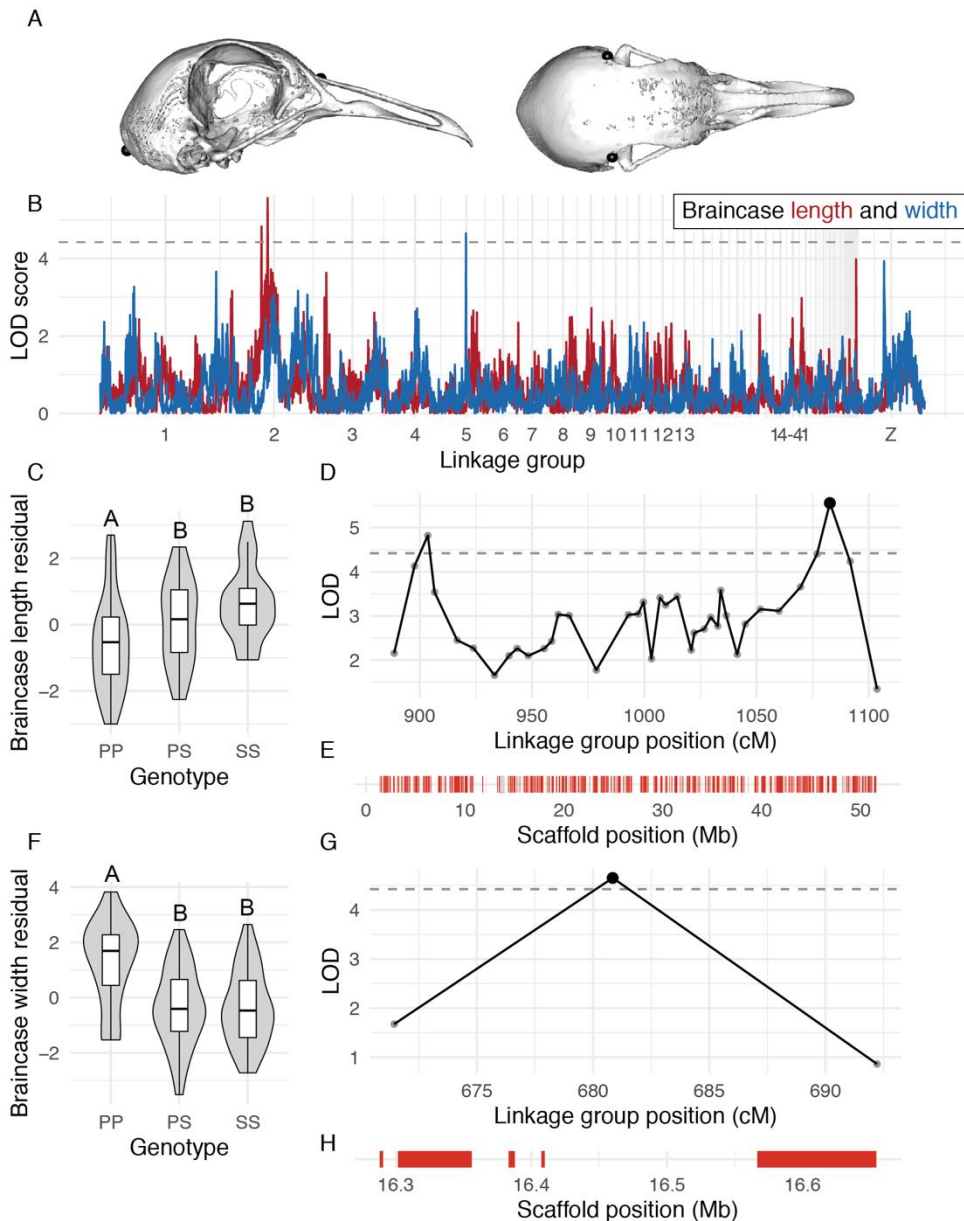


953  
 954 **Supplemental Figure 3. Distribution of 11 linear measurements in the Pom x Scan F<sub>2</sub>**  
 955 **population.** With the exception of rostral mandible width, all linear measurements are normally  
 956 distributed in the population (Shapiro-Wilk's test,  $p > 0.05$ ). For rostral mandible width, a single  
 957 F<sub>2</sub> individual is an outlier (MDS079, see Supplemental Figure 10) and causes a deviation from  
 958 normality (Shapiro-Wilk's  $p = 5.2e-09$ ). Braincase width is linear distance between landmarks 12  
 959 and 13 (rostral) or landmarks 27 and 28 (caudal). Mandible width is linear distance between  
 960 landmarks 60 and 61 (rostral) or landmarks 55 and 56 (caudal).

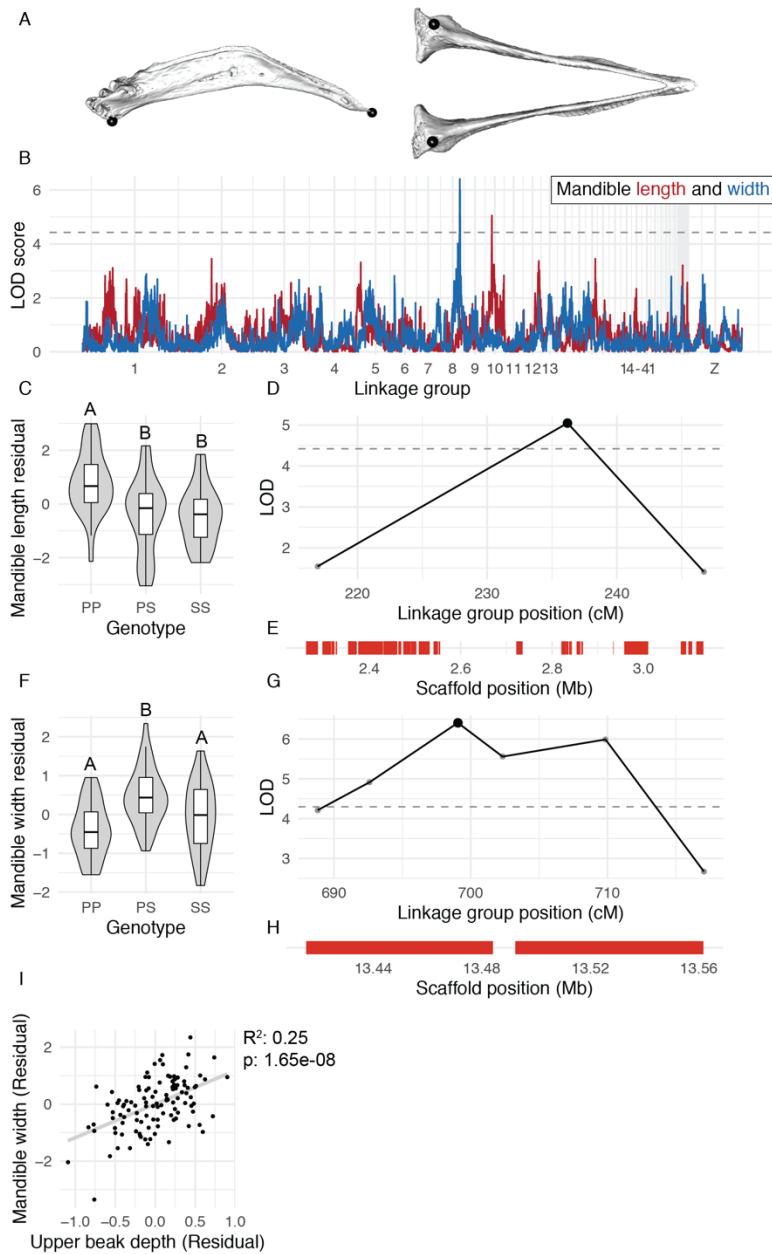


961  
 962 **Supplemental Figure 4. Linear regression of 11 craniofacial measurements on cranium**  
 963 **centroid size and body mass.** For each phenotype, linear measurement ~ cranium centroid  
 964 size regression is displayed on the top and linear measurement ~ body mass regression is  
 965 displayed in the middle with associated  $R^2$  and p-value indicated in the bottom right corner of  
 966 each plot. Each dot represents raw measurement of an  $F_2$  individual, color-coded by sex (male

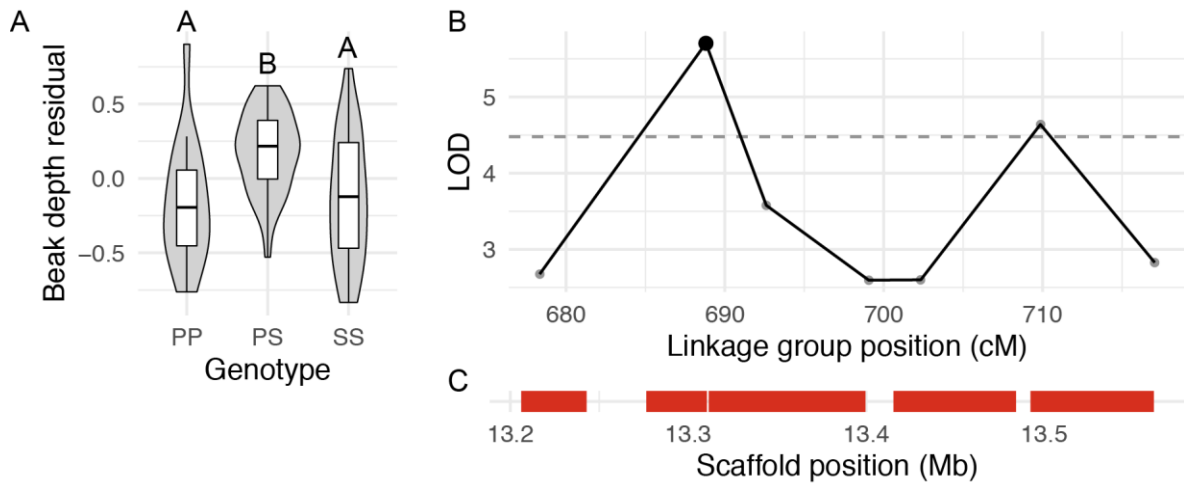
967 = blue, female = red). Each raw measurement is connected to an open circle that indicates its  
968 predicted value; grey connecting lines correspond to residual value used for QTL mapping. For  
969 each phenotype, the boxplot on the bottom displays residual values of linear measurement ~  
970 body mass regression by sex; outliers are indicated by black dots. Associated p-values are  
971 indicated in bottom right corner of each plot (two-sided Wilcoxon test). Cranium centroid size ~  
972 body mass regression is displayed in the bottom left corner of the figure. Braincase width is  
973 linear distance between landmarks 12 and 13 (rostral) or landmarks 27 and 28 (caudal).  
974 Mandible width is linear distance between landmarks 47 and 48 (rostral) or landmarks 37 and  
975 38 (caudal).



976  
 977 **Supplemental Figure 5. QTL associated with braincase length and width.** (A) Landmark  
 978 pairs used to measure braincase length (left) and width (right). (B) QTL scans for braincase  
 979 length (red) and width (blue). Dashed horizontal lines denotes 5% genome-wide significance  
 980 threshold. (C) Effect plot for braincase length QTL on LG2. Letters denote significance groups,  
 981 p-values determined via Tukey test: PP vs. PS =  $8.7e-03$ , PP vs. SS =  $2.2e-04$ . (D) LOD  
 982 support interval for braincase length on LG2. Dots indicate linkage map markers; the black dot  
 983 highlights the peak marker that was used to estimate QTL effects. (E) Genes located within  
 984 braincase length QTL LOD support interval, color coded based on if gene is expressed in HH29  
 985 facial primordia (red) or not expressed (gray). (F) Effect plot for braincase width QTL on LG5.  
 986 Letters denote significance groups, p-values: PP vs. PS =  $5.8e-05$ , PP vs. SS =  $7.5e-05$ . (G)  
 987 LOD support interval for braincase width QTL on LG5. (H) Genes located within braincase width  
 988 QTL on LG5. P = allele from Pom founder, S = allele from Scan founder.

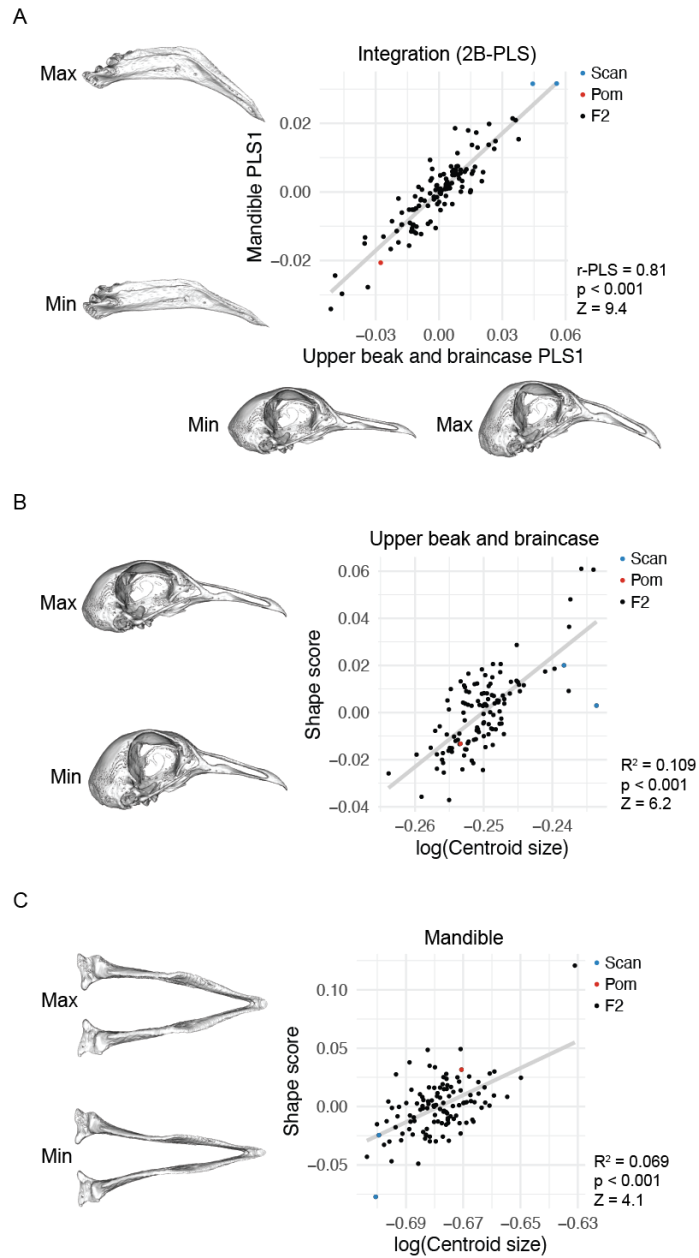


989  
 990 **Supplemental Figure 6. QTL associated with mandible length and width.** (A) Landmark  
 991 pairs used to measure mandible length (left) and width (right). (B) QTL scans for mandible  
 992 length (red) and width (blue). Dashed horizontal lines denotes 5% genome-wide significance  
 993 threshold. (C) Effect plot for mandible length QTL on LG8. Letters denote significance groups,  
 994 p-values determined via Tukey test: PP vs. PS = 5.9e-04, PP vs. SS = 1.1e-03. (D) LOD  
 995 support interval for mandible length QTL. (E) Genes located within mandible length QTL LOD  
 996 support interval. (F) Effect plot for mandible width QTL on LG10. Letters denote significance  
 997 groups, p-values determined via Tukey test: PP vs. PS = 2.7e-05, PS vs. SS = 1.7e-02. (G)  
 998 LOD support interval for mandible width QTL. (H) Genes located within mandible width QTL. (I)  
 999 Scatterplot of upper beak depth and mandible width residuals for all F<sub>2</sub> individuals. P = allele  
 1000 from Pom founder, S = allele from Scan founder.



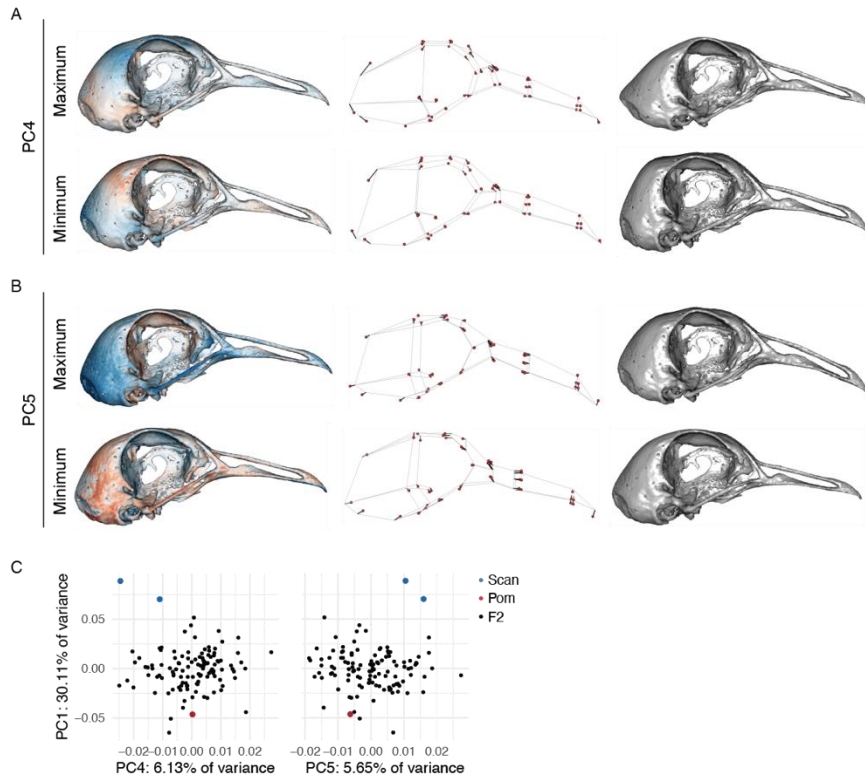
1001  
 1002 **Supplemental Figure 7. QTL on LG8 associated with upper beak width.** (A) Effect plot for  
 1003 upper beak depth QTL. Letters denote significance groups, p-values determined via Tukey test:  
 1004 PP vs. PS = 3.9e-04, PS vs. SS = 1.7e-02. (B) LOD support interval. (C) Genes in interval. P =  
 1005 allele from Pom founder, S = allele from Scan founder.





1006  
1007  
1008  
1009  
1010  
1011  
1012  
1013

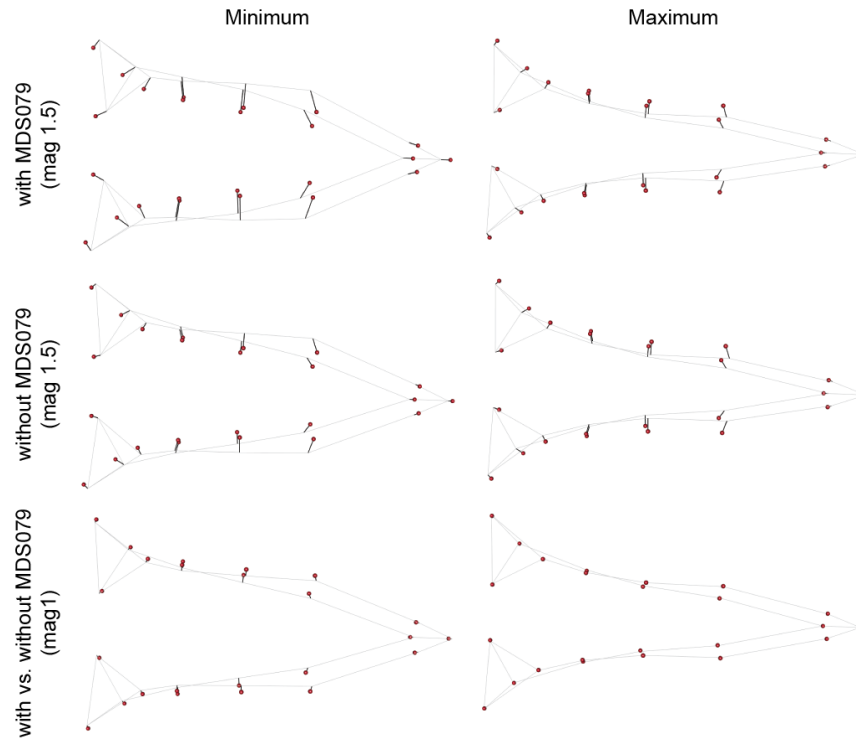
**Supplemental Figure 8. UBB and MAN integration and allometry.** (A) UBB PLS1 vs. MAN PLS1 shape. (B) UBB shape ~ centroid size linear regression. (C) MAN shape ~ centroid size linear regression. For all panels, minimum and maximum shapes are depicted by warped meshes along corresponding axis. Shape changes were magnified 2x to aid visualization.



1014  
 1015  
 1016  
 1017  
 1018  
 1019

**Supplemental Figure 9. UBB PC4 and PC5 shape variation.** (A-B) Minimum and maximum UBB PC4 (A) and PC5 (B) shapes, visualized as heatmaps (left), wireframes (center), and warped meshes (right). For wireframes and meshes, UBB PC4 and PC5 shape is magnified 3x to aid visualization. (C) PCA plots of UBB PC1 vs. PC4 (left) and PC5 (right).

1020



1021

1022

1023

1024

1025

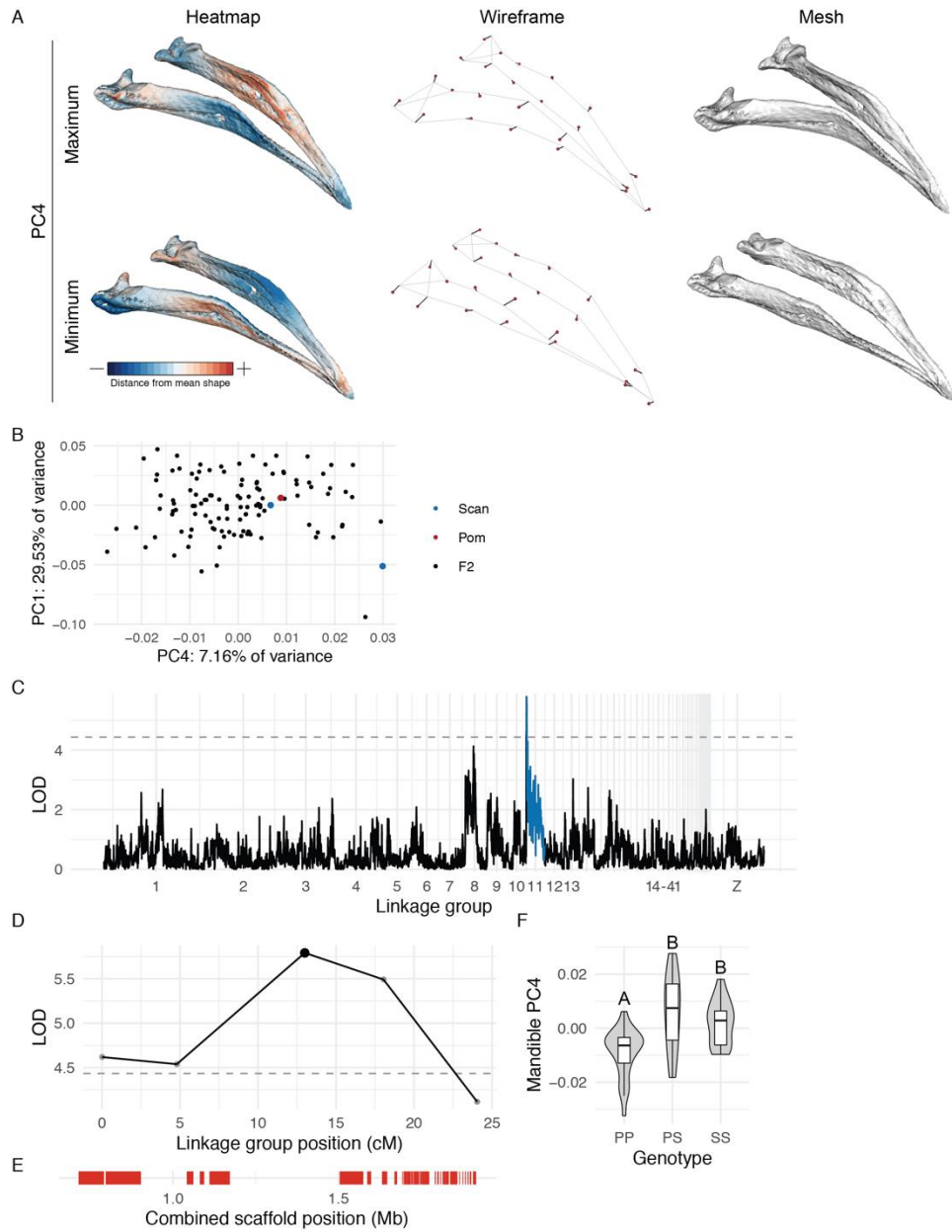
1026

1027

1028

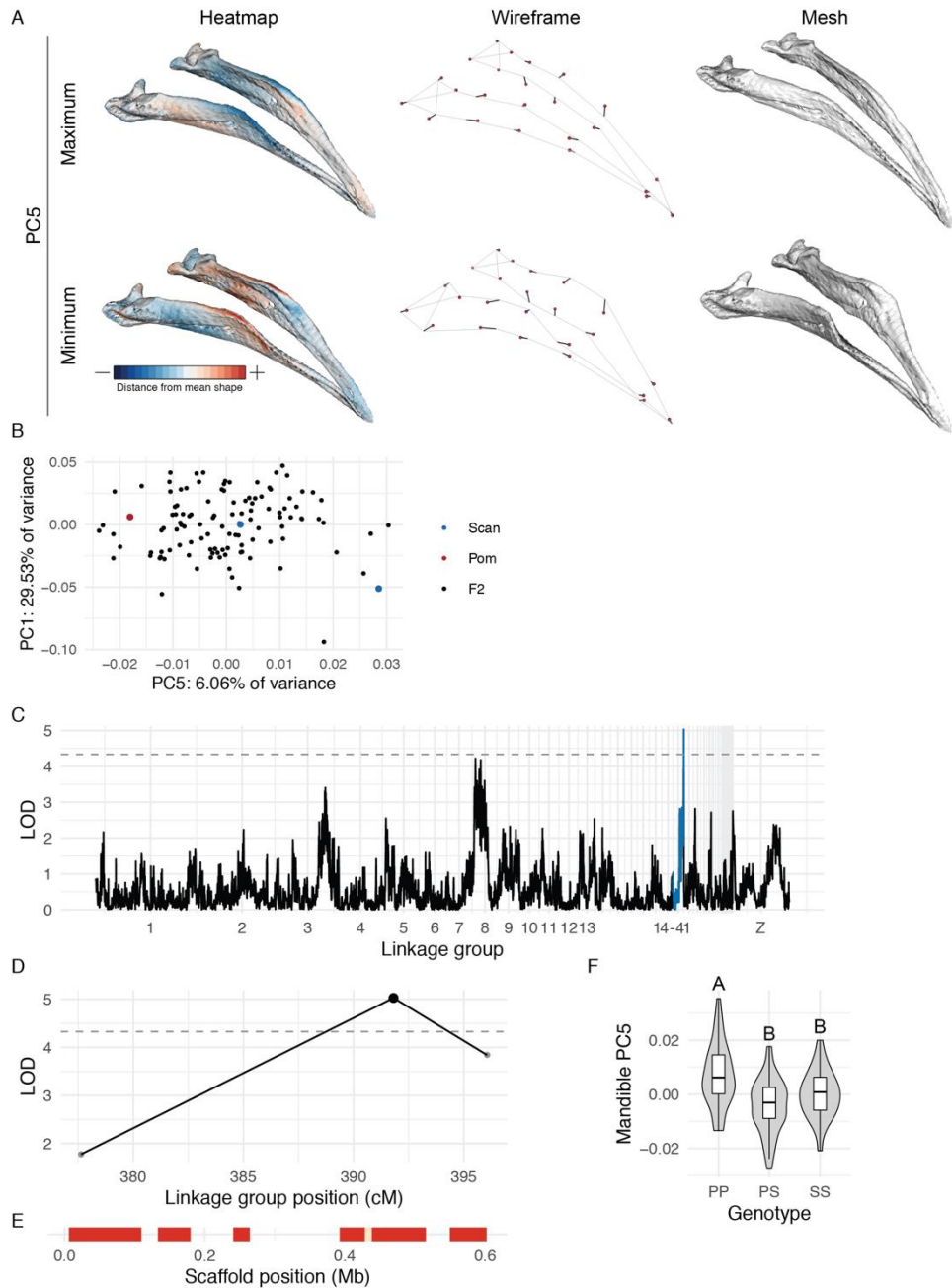
1029

**Supplemental Figure 10. MAN PC1 shape with and without MDS079.** Dorsal views of MAN wireframes showing minimum (left) and maximum (right) PC1 shapes if MDS079 is included (top panel) or excluded (center panel) from the geometric morphometric analysis. MDS079 had an exceptionally wide mandible and was an outlier from the rest of the F2 population along the MAN PC1 axis (see PCA plot in Figure 4B). Although inclusion of MDS079 changed the magnitude of the PC1 axis, it had virtually no effect on the shape described by MAN PC1, thus it was kept in all downstream analyses.



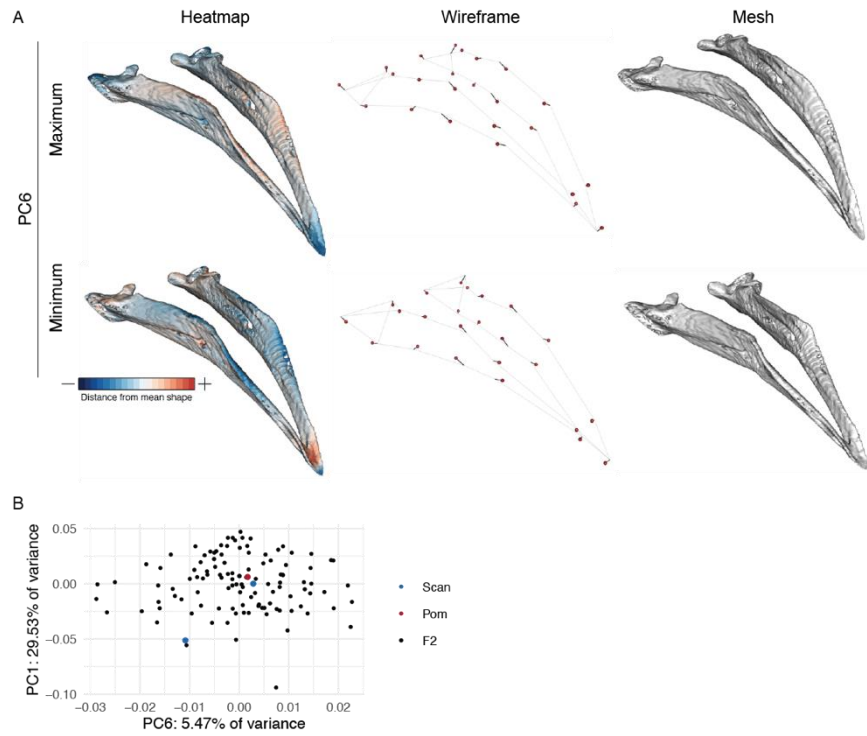
1030  
1031  
1032  
1033  
1034  
1035  
1036  
1037

**Supplemental Figure 11. MAN PC4 shape variation and associated QTL.** (A) Minimum and maximum MAN PC4 shapes, visualized as heatmaps (left), wireframes (center), and warped meshes (right). For wireframes and meshes, shape is magnified 3x to aid visualization. (B) PCA plots of MAN PC1 vs. PC4. (C) Genome-wide QTL scan for MAN PC4. (D) MAN PC4 LOD support interval for QTL on LG11. (E) Genes in LG11 QTL interval. (F) LG11 QTL effect plot. Letters denote significance groups, p-values determined via Tukey test: PP vs. PS = 2.2e-06, PP vs. SS = 2.2e-03. P = allele from Pom founder, S = allele from Scan founder.



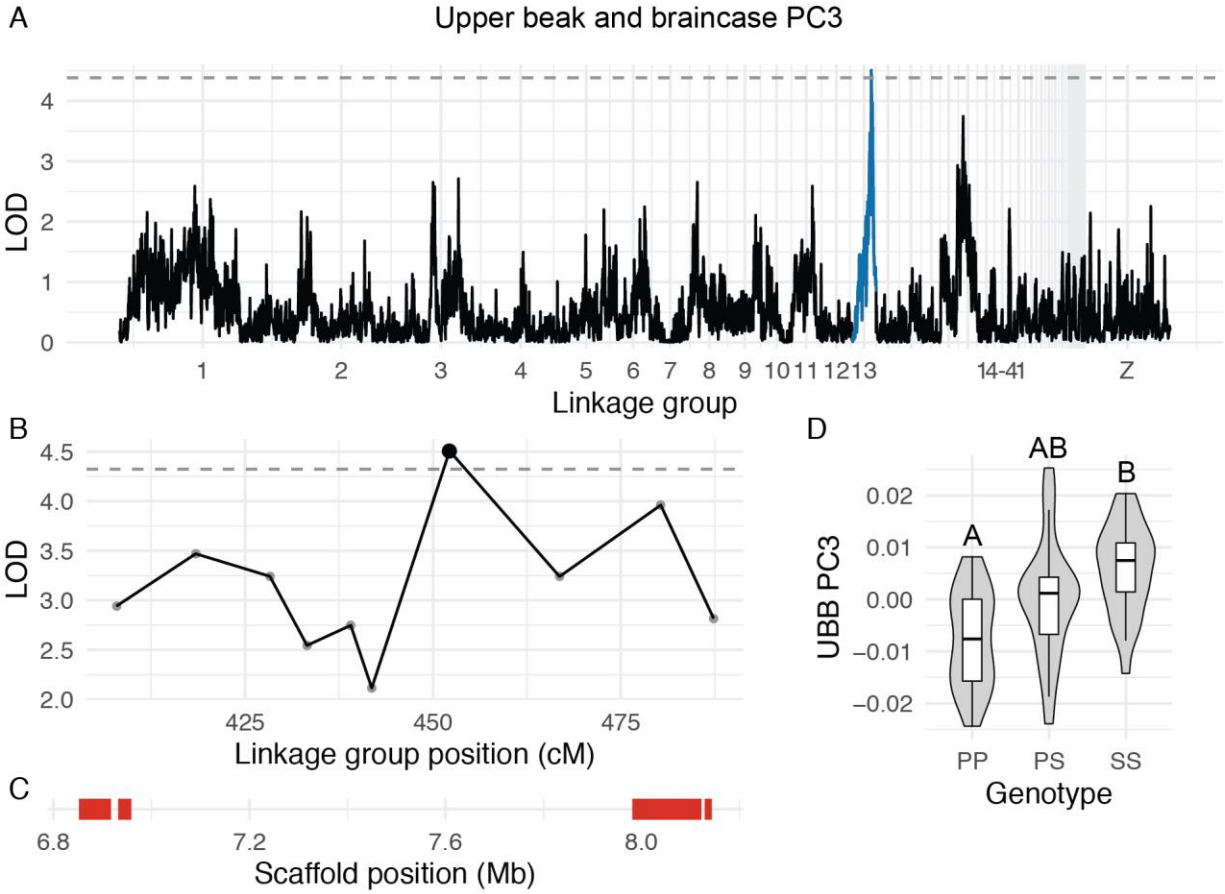
1038  
1039  
1040  
1041  
1042  
1043  
1044  
1045  
1046

**Supplemental Figure 12. MAN PC5 shape variation and associated QTL.** (A) Minimum and maximum MAN PC5 shapes, visualized as heatmaps (left), wireframes (center), and warped meshes (right). For wireframes and meshes, shape is magnified 3x to aid visualization. (B) PCA plots of MAN PC1 vs. PC5. (C) Genome-wide QTL scan for MAN PC5. (D) MAN PC5 LOD support interval for QTL on LG20. (E) Genes in LG20 QTL interval. (F) LG20 QTL effect plot. Letters denote significance groups, p-values determined via Tukey test: PP vs. PS = 1.3e-05, PP vs. SS = 1.9e-02. P = allele from Pom founder, S = allele from Scan founder.



1047  
 1048  
 1049  
 1050  
 1051

**Supplemental Figure 13. MAN PC6 shape variation.** (A) Minimum and maximum MAN PC6 shapes, visualized as heatmaps (left), wireframes (center), and warped meshes (right). For wireframes and meshes, shape is magnified 3x to aid visualization. (B) PCA plots of MAN PC1 vs. PC6.



1052

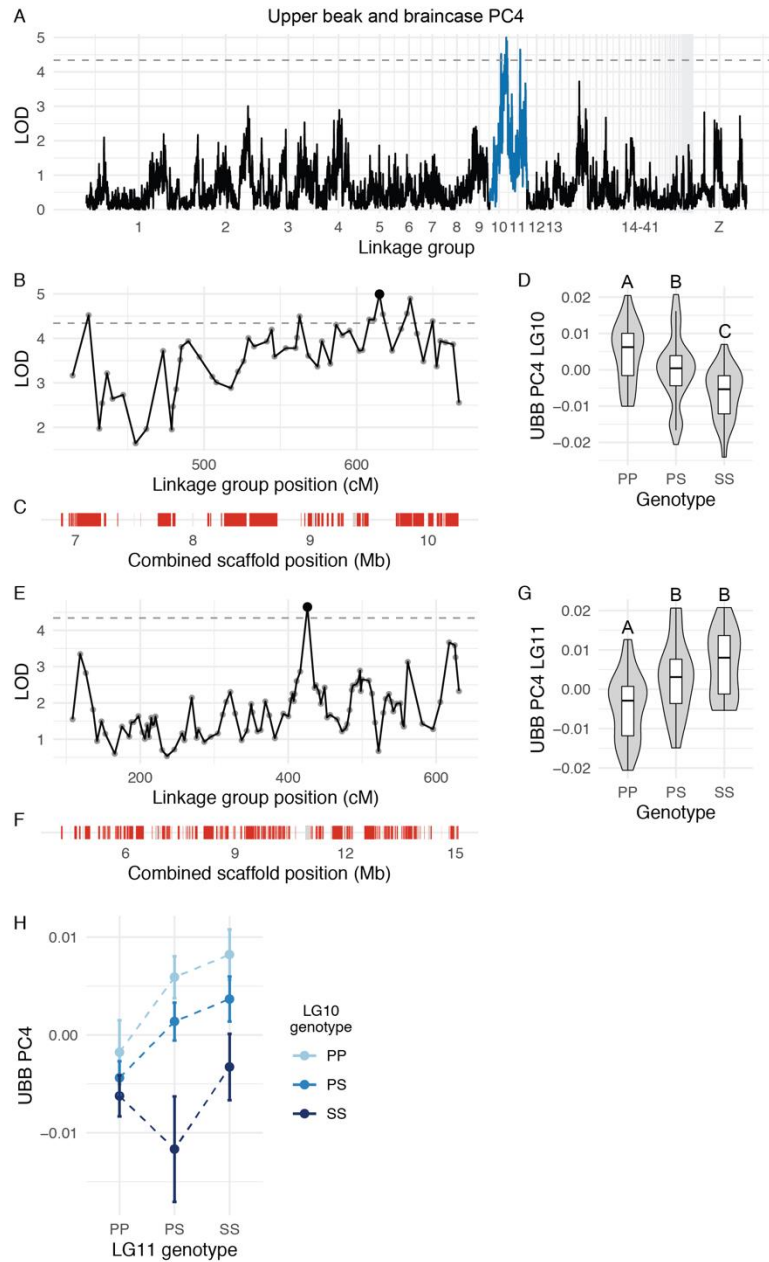
1053

1054

1055

1056

**Supplemental Figure 14. QTL associated with UBB PC3.** (A) Genome-wide QTL scan for UBB PC3. (B) UBB PC3 LOD support interval for QTL on LG13. (C) Genes in LG13 QTL interval. (D) LG13 QTL effect plot. Letters denote significance groups, p-values determined via Tukey test: PP vs. SS = 5.3e-04. P = allele from Pom founder, S = allele from Scan founder.



1057  
 1058  
 1059  
 1060  
 1061  
 1062  
 1063  
 1064  
 1065  
 1066

**Supplemental Figure 15. QTL association with UBB PC4.** (A) Genome-wide QTL scan for UBB PC4. (B) UBB PC3 LOD support interval for QTL on LG10. (C) Genes in LG10 QTL interval. (D) LG10 QTL effect plot. Letters denote significance groups, p-values determined via Tukey test: PP vs. PS =  $1.6 \times 10^{-2}$ , PP vs. SS =  $2.4 \times 10^{-5}$ , PS vs. SS =  $2.5 \times 10^{-2}$ . (E) LOD support interval for LG11 QTL. (F) Genes in LG11 QTL support interval. (G) LG11 QTL effect plot. Letters denote significance groups, p-values determined via Tukey test: PP vs. PS =  $2.4 \times 10^{-3}$ , PP vs. SS =  $7.5 \times 10^{-5}$ . (H) Interaction between LG10 and LG11 QTL. P = allele from Pom founder, S = allele from Scan founder.