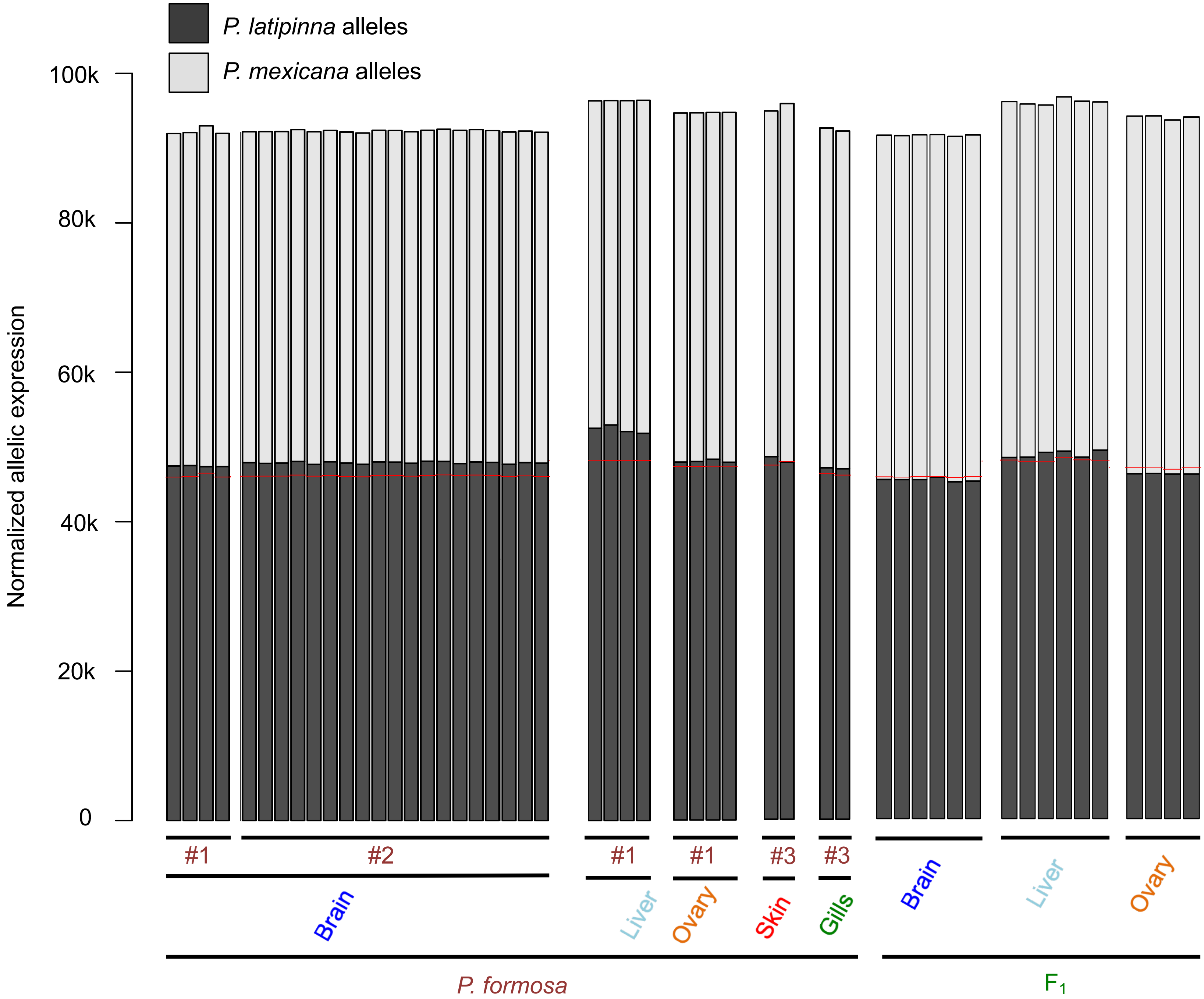
P. latipinna alleles
P. mexicana alleles
Normalized allelic expression
100k
80k
60k
40k
20k
0
#1
#2
#1
#1
#3
#3
Brain
Liver
Ovary
Skin
Gills
Brain
Liver
Ovary
P. formosa
F1

Supplemental Figure S9. Allelic expression distribution of different clones of *P. formosa* and $\mathbf{F_1}$ hybrid fish Stacked bar graph showing normalized sequencing reads that mapped to *P. latipinna* and *P. mexicana* alleles. For each individual sample, the total normalized allelic expression is plotted for both parental alleles. The red lines represent 50% of the total gene expression. Sequencing reads that mapped to polymorphic sites between *P. latipinna* and *P. mexicana* alleles were used to calculate allelic contribution of gene expression after normalization to library size and allelic length. These reads were subsequently used to calculated for allelic expression ratio, and further used to calculate allelic expression by adjusting gene expression to allelic expression ratios. Organs from 3 independent clones of *P. formosa* were assessed for allelic expression distribution analyses. These include: brains of clone #1 and #2; livers of clone #1; ovary of clone #1; skin and gills of clone #3.