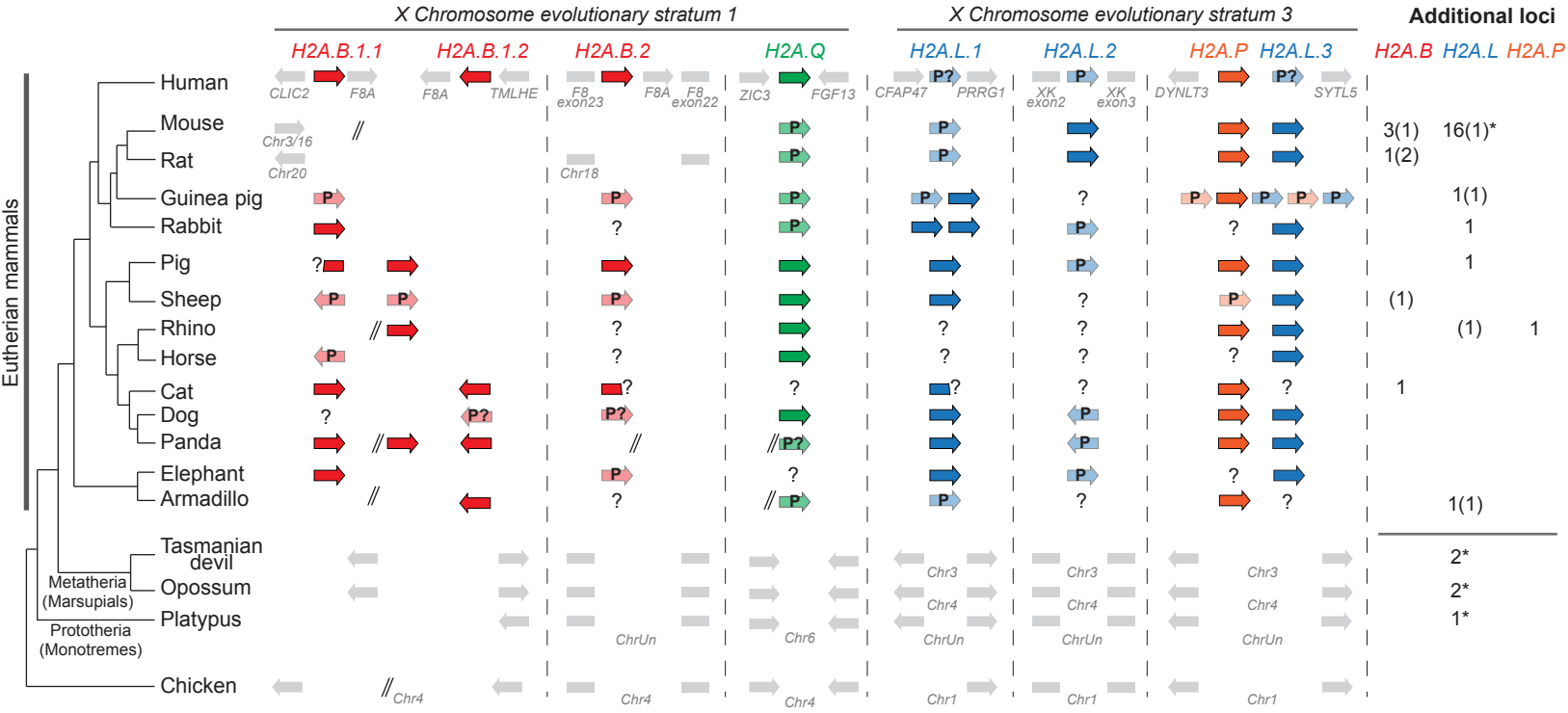

Supplemental Fig S2: Synteny and conservation of short H2A histone variants in mammalian genomes.
We present details of the synteny analysis shown in Figure 1B. We show the six short H2A loci (containing seven to eight genes) that existed in the common eutherian ancestor with colored arrows and additional lineage-restricted loci are enumerated on the right (with pseudogenes in parentheses). "*" denotes histone gene loci that are not sex chromosome-linked – that is one copy of *H2A.L* on mouse Chr2 and all of the *H2A.R*s. In those genome assemblies where sequences have been mapped to chromosomes, the eight loci containing short H2A variant genes are all on the X Chromosome, unless indicated. A species tree of representative mammals is rooted using chicken as an outgroup. Flanking genes (grey arrows) define the syntenic locations of three ancestral *H2A.B* genes (*H2A.B.1.1, H2A.B.1.2* and *H2A.B.2*, red arrows), three ancestral *H2A.L* genes (*H2A.L.1, H2A.L.2* and *H2A.L.3*, blue arrows), *H2A.Q* (green arrow) and *H2A.P* (orange arrow). In most cases, these syntenic loci are on the X Chromosome (X Chromosome evolutionary strata of these regions are also shown at the top); exceptions are indicated with chromosome number (chrUn refers to unassigned contigs). "P" denotes confirmed pseudogenes (with frameshifts or stop codons), "P?" denotes genes without frameshifts or stop codons but inferred to be pseudogenes upon further analysis (e.g., dog *H2A.B* genes and human *H2A.L* genes); double backslashes indicate assembly gaps that interrupt synteny, and "?" indicates that a gene is not found - in most of these cases, we have not attempted to distinguish true gene loss from absence due to assembly gaps.

Supplemental Fig S2
Molaro et al.