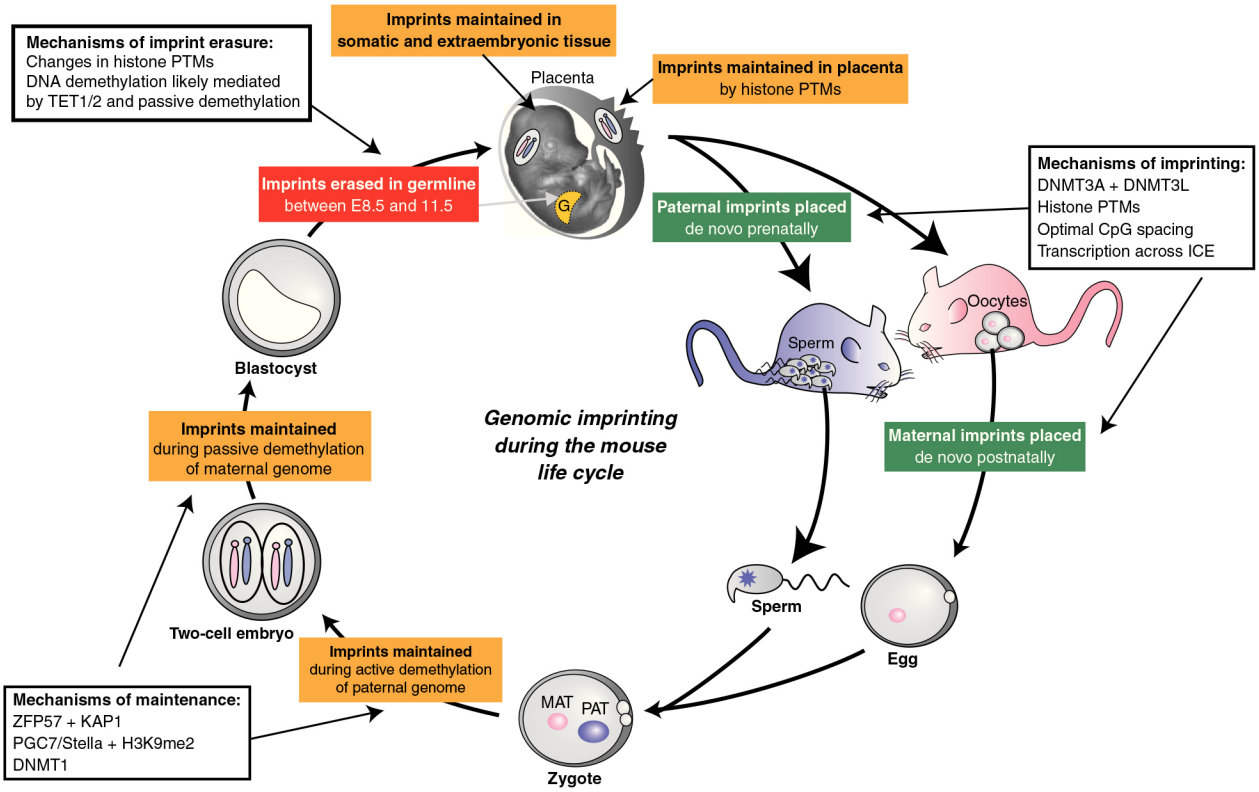

Figure 7. Establishment, maintenance, and erasure of genomic imprints in mouse development. In the germline, primordial germ cells (PGCs) undergo multiple changes in chromatin structure and DNA demethylation during migration into the genital ridge (gonad). Imprints are then acquired in a sex-specific manner in the germline (green shading). DNA methylation is targeted specifically to paternally and maternally DNA-methylated ICEs—prenatally in prospermatogonia and postnatally during oocyte maturation. These imprints are maintained despite global changes in DNA methylation after fertilization (orange shading): active demethylation of the paternal genome in the zygote and passive maternal demethylation in the preimplantation embryo. Candidates for protection of methylation regions include ZFP57 and PGC7/STELLA. De novo DNA methylation of the genome begins at the morula stage, during which time unmethylated alleles of imprinted genes must be protected. These imprints are maintained in somatic cells throughout the lifetime of the organism, whereas imprinting in extraembryonic tissues is thought to be less dependent on maintenance of DNA methylation. In the germline, imprints are erased and reset for the next generation (red shading). PTM, posttranslational modification; MAT, maternal genome; PAT, paternal genome.