Mechanisms by which epiphenotypes are transmitted between generations through the paternal germline remain poorly understood. The nuclei of mammalian sperm are highly condensed, the DNA is mostly covered by protamines with only a few retained nucleosomes, and epigenetic information stored in the form of DNA methylation is quickly erased from paternal chromosomes shortly after fertilization. Experiments carried out in our lab suggest a more complex picture of the mouse sperm epigenome, suggesting the presence of multiple histone modifications, nucleosomes positioned around transcription start sites and transcription factor binding sites, and the presence of multiple transcription factors. Most promoters in mouse sperm contain the elongating form of RNA polymerase II, and are flanked by several positioned nucleosomes marked by a variety of active histone modifications. The sperm genome is bound by several transcription factors, including Mediator, the pioneer factor FoxA1, and estrogen receptor alpha. These proteins are found at promoters, enhancers, and super-enhancers, many of which are active in mESCs or adult tissues. CTCF and cohesin are also present in sperm DNA, where they mediate interactions that organize the sperm genome into domains and compartments that overlap extensively with those found in mESCs. This information suggests that mammalian sperm contain a rich and complex palette of epigenetic information that could be altered by environmental factors to paint novel phenotypic outcomes in the next generation. This is supported by experiments in which pregnant females exposed to endocrine disruptor chemicals give rise to progeny showing a variety of phenotypes, including obesity. The obese phenotype is transmitted between generations in the absence of further exposure. Experiments indicate that approximately 200 new protein binding sites are present in the sperm and fat tissue of obese mice from the F1 through the F4 generations. These new binding sites correspond to CTCF and ERα, suggesting that effects of these proteins on 3D chromatin organization and transcription of specific genes are responsible for the establishment and transmission of epiphenotypes.