Abstract: The relevance of spatial organization of chromatin in ESCs for the maintenance of pluripotency has been extensively studied. In the sequence of events leading to pluripotency during reprogramming of a somatic cell, the genome is reorganized by a number of epigenetic modifiers. Thus, the proteins that regulate different layers of chromatin organization such as histone modifications, histone variants and chromatin remodeling are increasingly identified. In a significant contribution towards defining the role of lysine histone methyltransferase (KMT) EZH2 in reprogramming, work from my laboratory demonstrated that EZH2 drives mesenchymal to epithelial transition during human iPSC generation. Although the requirement of KMTs in cellular reprogramming has been extensively reported, most of these relied on depleting or overexpression of KMTs. In addition, there is a notable lack of understanding of how non-histone protein interactions of KMTs can influence genome reorganization during reprogramming. In my talk I will provide new insights into non-canonical functions of KMTs during human cellular reprogramming.