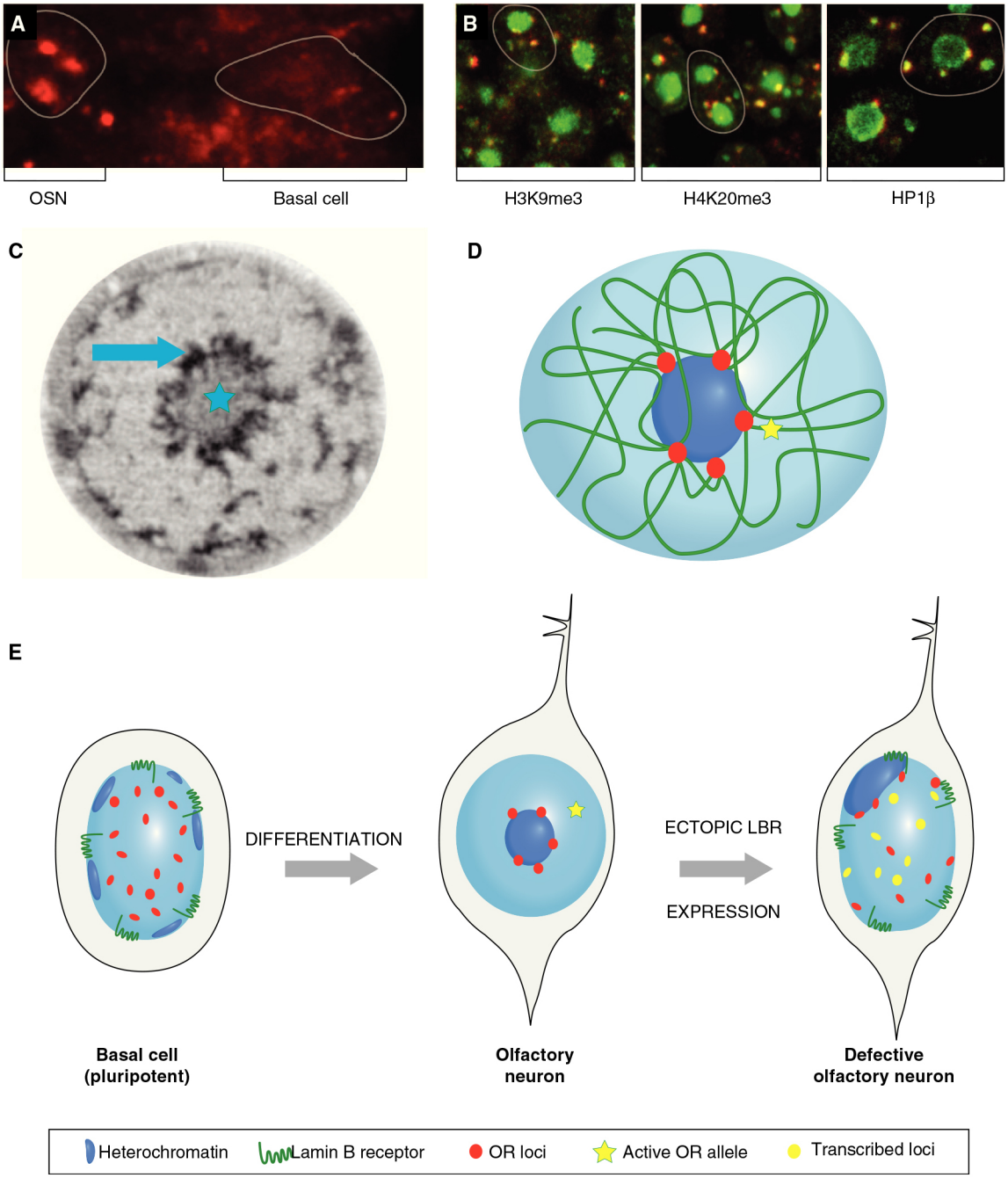

Figure 9. The spatial organization of OR gene clusters during OSN differentiation. (*A*) DNA FISH showing OR gene cluster distribution using a panOR probe (red) on MOE sections. The signal is diffuse at the basal pluripotent cells, but aggregated in neuronal nuclei (the nuclear borders are highlighted). (*B*) PanOR foci (red) are enriched at regions marked with H3K9me3, H4K20me3, and HP1β (green), suggesting that they are heterochromatic aggregates of the silent OR alleles. (*C*) Soft X-ray tomography (SXT) of an olfactory nucleus shows that compacted chromatin (highlighted by a blue star) is aggregated at the center of the nucleus. At the periphery of this heterochromatic core, SXT reveals even more compacted structures (pointed by blue arrow) that are OSN specific. (*D*) A schematic 3D nuclear landscape shows all the heterochromatic OR clusters converging, in *cis* and *trans*, to form silent foci incompatible with transcription. The active OR allele is physically separated from the inactive OR aggregates. This is based on epigenetic data obtained from ChIP-on-chip experiments depicted as heatmaps. (*E*) Prior to OSN differentiation, the precursor basal stem cell has a typical nuclear configuation with regard to heterochromatin with peripheral foci. The OR clusters are randomly distributed in nuclear space. Following differentiation, aggregation of all but one OR allele to heterochromatic foci surrounding the pericentromeric chromocenter of an OSN nucleus occurs. This serves the monogenic and monoallelic expression of these genes and depends on the down-regulation of lamin B receptor (LBR). Ectopic LBR expression in OSNs dissolves the OR foci, reverses the nuclear morphology, and causes the simultaneous expression of hundreds of ORs in a striking violation of the one receptor per neuron rule.