

Description of Additional Supplementary Files

Supplementary Data 1: Sample information

The type of experiment performed on the different cell types, the protocols used for the libraries and the sample names are indicated. For previously published datasets, the GEO accession numbers are indicated as well.

Supplementary Data 2: Quality control of Hi-C and promoter-capture Hi-C experiments

Supplementary Data 3: Transcriptional and chromatin states at promoters of all genes across cranial neural crest cell subpopulations

The table contains gene names and database identifiers; RNA levels in E8.5 WT pre-migratory progenitors and E10.5/E11.5 WT and *Ezh2cKO* frontonasal (FNP), maxillary (Mx), mandibular (Md) and second pharyngeal arch (PA2) cranial neural crest cells (CNCCs); as well as ChIP-seq profiles for H3K27me3, H3K4me2 and H3K27me3 in E8.5 WT pre-migratory progenitors and E11.5 WT FNP, Mx, Md and PA2 CNCCs. The TRUE/FALSE values indicate whether a gene has been identified as a transcription factor-encoding gene (column H; TFs) or whether its promoter has been identified as PcAct (i.e. Pc-marked in E8.5 WT pre-migratory progenitors and active in at least one post-migratory CNCC subpopulation(s) (FNP, Mx, Md and PA2) at E10.5 and/or E11.5 (column G; PcAct_genes).

Supplementary Data 4: Promoter-promoter chromatin interaction networks of PcActTF promoters, in E10.5 cranial neural crest cell subpopulations

This table lists the genomic coordinates (mm10) of PcActTF promoters, their interacting other end-promoters and ChIP-seq signal intensities for H3K27me3, H3K4me3, and H3K27ac at these promoters. Distance distribution of the interactions is also indicated.

Supplementary Data 5: Promoter-Distal Accessible Elements (P-DAEs) chromatin interaction networks of PcActTF promoters, in E10.5 cranial neural crest cell subpopulations

This table lists the genomic coordinates (mm10) of PcActTF promoters, their interacting DAEs and ChIP-seq signal intensities for H3K27me3, H3K4me3, and H3K27ac at these promoters and DAEs. Distance distribution of the interactions is also indicated.

Supplementary Data 6: E11.5 Q4 active DAEs

The table lists the genomic coordinates (mm10) of E11.5 Q4 active DAEs in each CNCC subpopulation, the corresponding target promoters at E11.5, with their PcAct or PcActTF classification, the distance to the target promoter, and the interaction type.

Supplementary Data 7: Genomic coordinates of PTEs

The table contains the genomic coordinates (mm10) of identified putative PTEs, their interacting H3K27me3-positive promoters at E8.5, and distances to the nearest E11.5 Q4 active DAE.

Supplementary Data 8: Genomic coordinates of the deleted regions and gRNAs used for the deletions

The table contains the genomic coordinates (mm10) of all regions deleted by CRISPR/Cas9 and the corresponding size of the deletions. The guide RNAs used for deletion (upstream and downstream of each region of interest) are listed with their specific protospacer sequences.

Supplementary Data 9: Genotyping information for the deleted mouse lines

The table contains PCR primer sequences and sizes of the corresponding PCR products obtained for the genotyping of mutant (KO) and wild type (WT) mice for each deleted line.