Until recently, conserved gene synteny was considered a consequence of insufficient time of separation between the observed genomes, preventing gene order shuffling by chromosomal rearrangements. New evidence shows that vertebrate chromosomes contain large territories of long-range regulation, termed Genomic Regulatory Blocks (GRBs). GRBs contain **target genes** that respond to long-range enhancers and functionally unrelated **bystander genes**, which are kept in synteny with the target gene by the regulatory elements contained in their introns or beyond.

Whole genome duplication triggers large scale erosion and relocation of bystander genes. When a ‘bystander’ gene is lost from one copy of the duplicated GRB by neutral evolution, the interlocked regulatory elements often remain in *cis* to their target genes. We investigated whether some long-range regulatory elements overlap coding exons of bystander genes, in which case they would remain under noncoding selection pressure and be conserved in a way similar to the surrounding noncoding regulatory elements.

We applied a comparative genomics approach to detect noncoding selection pressure on parts of former coding regions of lost bystander genes in GRBs around 48 developmental transcription factors that were retained in two copies after the whole-genome duplication of teleost fish. We identified candidate regulatory regions as remnants of a single exon that remained conserved and in synteny with the target gene, long after the gene to which they belonged disappeared from the GRB. We examined multiple alignments of these regions across different vertebrates and found evidence for non-coding selection pressure.