Detection of enhancer hijacking of oncogenes in multiple myeloma

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Genome rearrangements often result in copy number alterations of cancer-related genes and cause the formation of cancer-related fusion genes. A previous report found that more than half of multiple myeloma (MM) cases showed that translocations that hijacked the *IGH* super-enhancer to be near the oncogene locus. Although the enhancer hijacking of oncogenes may direct the dramatic reduction of immunoglobulin (IG) genes in malignant tumor cells in the MM cases, the relationship between the genomic rearrangments and the transcriptomic complexity still remained unexplored. Here, we observed a frequent hijacking of the *IGH* super-enhancers, Eμ and the 3' RR enhancers, to the 4p16, 6p21, 11q13, and 22q11 loci in 14 out of our 26 MM cases. Consequently, the target genes−*FGFR3*, *NSD2*, *CCND1*, *CCND3*, *MYEOV*, and *SUSD2*−near the translocations accompanying enhancer hijacking were highly upregulated relative to those in cases with no translocations. The enhancer hijacking events during the *IGH* rearrangements well reflected the upregulation of target genes according to the translocation position but the significant downregulation of IG genes, which led to the increases of transcriptomic complexity.