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Correction: RAG1/2 induces genomic insertions by mobilizing DNA into RAG1/2-independent breaks

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The authors regret that in the original version of their paper, the following funding information was not included. This text has been added to the second paragraph of their Acknowledgments section:

The cancer datasets used in this study (dbGaP: phs000341.v2.p1 and phs000340.v3.p1; EBI: EGAS00001000399) were generated with the financial support of the National Cancer Institute, the St. Baldrick's Foundation, Partners for Cures, the American Lebanese Syrian Associated Charities of St. Jude Children's Research Hospital as part of the St. Jude/Washington University Pediatric Cancer Genome Project, Cancer Research UK, Bloodwise (now Leukemia and Lymphoma Research), and the Hungarian Scientific Research Fund (OTKA).

In addition, a reference was not included in the reference list. This correction affects Materials and methods section Analysis of insertions in human tumors and Table S4. The corrected section and full reference appear below. Table S4, an online Excel file, has been replaced.

Analysis of insertions in human tumors

We designed a novel pipeline to search whole-genome sequences for insertions derived from *IG/TCR* loci. First, *IG/TCR* baits were generated that correspond to regions spanning 150 bp upstream and downstream from each physiological RSS cleavage site of human V and J segments (Ensembl, release 84). D segments were excluded, and repeat regions were masked. Second, whole-genome sequences from published human cancer datasets (Table S4; Wang et al., 2011; Holmfeldt et al., 2013; Okosun et al., 2014) were mapped with bwa mem (v0.7.12-r1039; default parameters) using the *IG/TCR* baits as references. Third, paired reads aligning to the baits were mapped against the human genome (hg38) using bwa mem (v0.7.12-r1039; default parameters). Only alignments with a Phred score of at least 20 were accepted. Finally, reads containing junctions (chimeric alignments) were filtered to yield insertions that were then manually verified using Geneious (Kearse et al., 2012). The analysis of publicly available human cancer datasets was classified as exempt activity by the Rockefeller University Institutional Review Board.

Wang, J., C.G. Mullighan, J. Easton, S. Roberts, S.L. Heatley, J. Ma, M.C. Rusch, K. Chen, C.C. Harris, L. Ding, et al. 2011. CREST maps somatic structural variation in cancer genomes with base-pair resolution. *Nat. Methods.* 8:652–654. http://dx.doi.org/10.1038/nmeth.1628

These errors have been corrected in the online HTML and PDF versions. The errors remain only in the print version.