Clinical Epigenetics

PUBLISHER CORRECTION

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Publisher Correction: Epigenome-wide analysis of T-cell large granular lymphocytic leukemia identifies BCL11B as a potential biomarker

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Following publication of the original article [1], the author noticed an error in the figure. In the published version, the image of Fig. 5 has been repeated twice. The author has informed to remove the duplicated image during correction process. The typesetter has inadvertently missed to correct the figure. However, the text citation and caption of the figure seem to be correct. The corrected Fig. 5 has been published with this erratum.

The original has been corrected.

The original article can be found online at https://doi.org/10.1186/s13148-022-01362-z.

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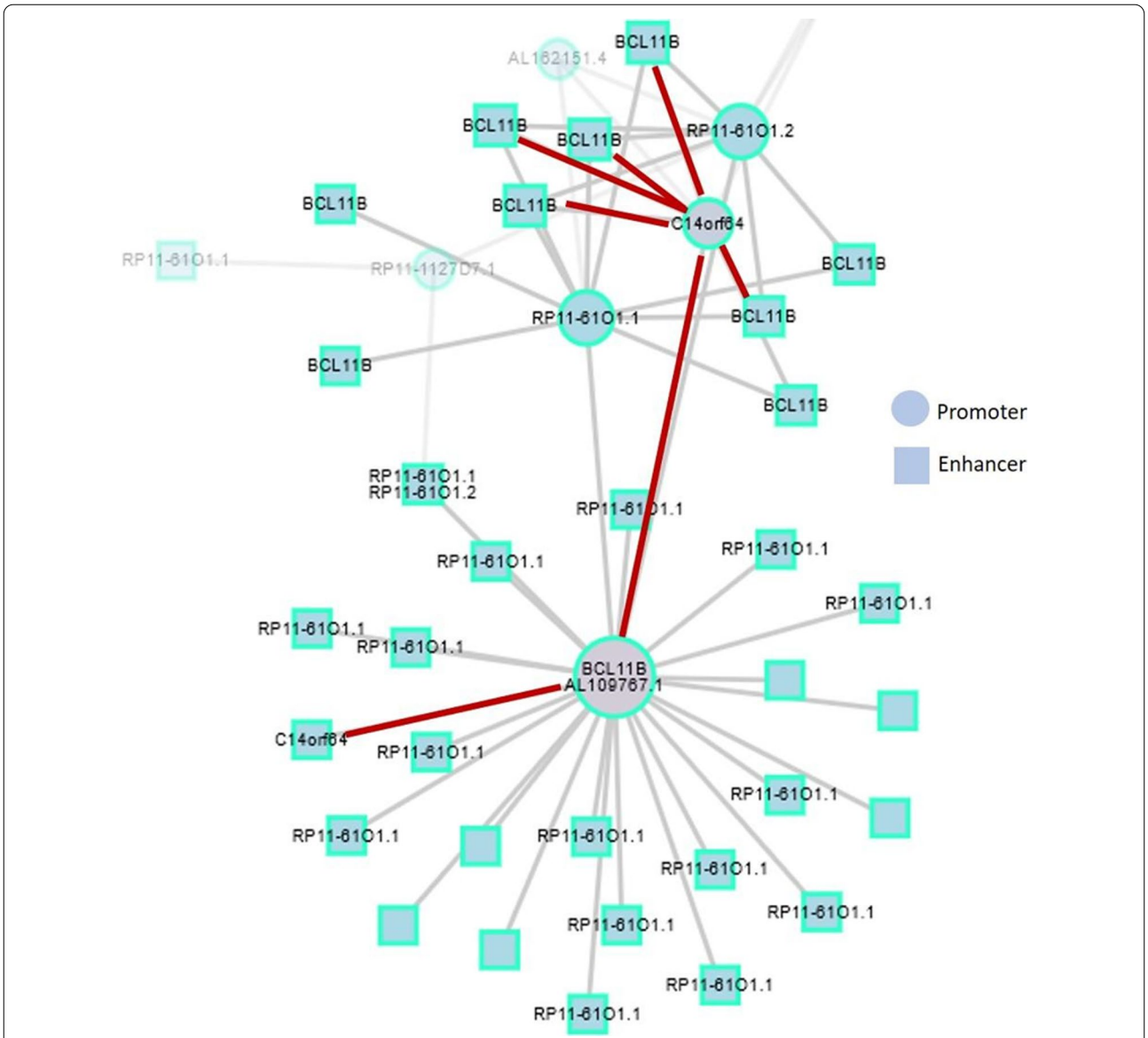

Fig. 5 Interaction of the gene BCL11B with other genes in $CD8^+$ cells. BCL11B long-range interactions from Promoter Capture Hi-C for total CD8-positive T cells (red: BCL11B–C14orf64 (LINC01550) interactions). Genomic regions are depicted in blue circles (promoter region) or blue square (enhancer region)

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Publisher's Note