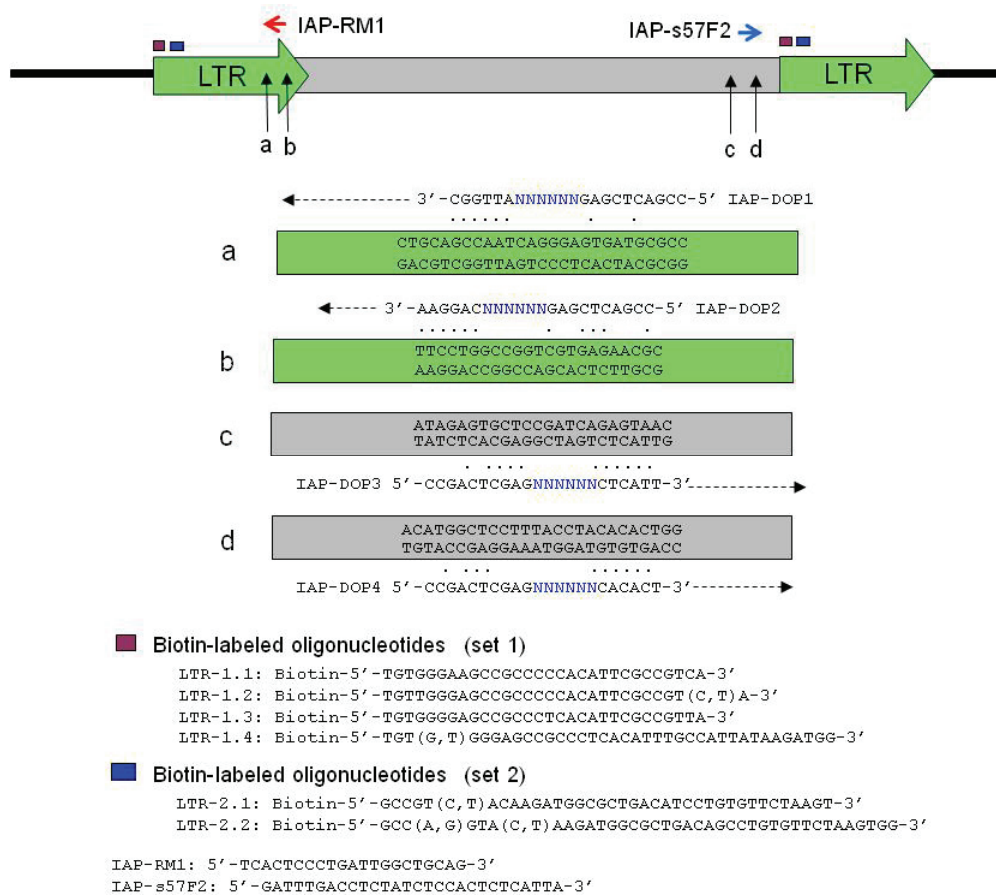


## Supplementary data for

### Microarray-based global mapping of integration sites for the retrotransposon, intracisternal A-particle, in the mouse genome

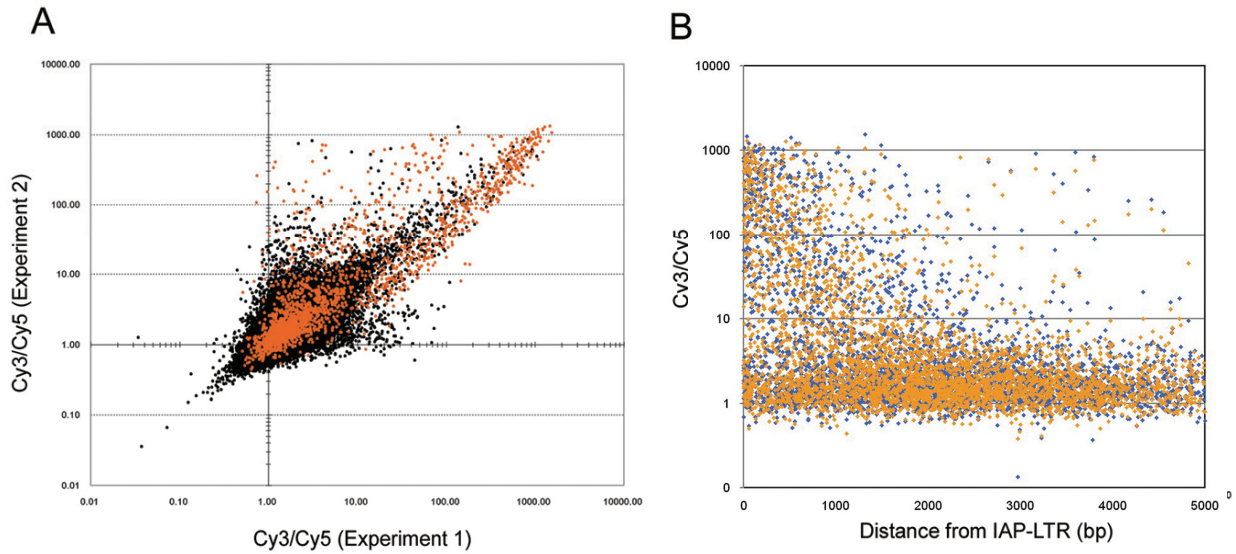
Takashi Takabatake,<sup>1</sup> Hiroshi Ishihara, Yasushi Ohmachi, Izumi Tanaka, Masako M. Nakamura, Katsuyoshi Fujikawa, Tokuhisa Hirouchi, Shizuko Kakinuma, Yoshiya Shimada, Yoichi Oghiso, and Kimio Tanaka

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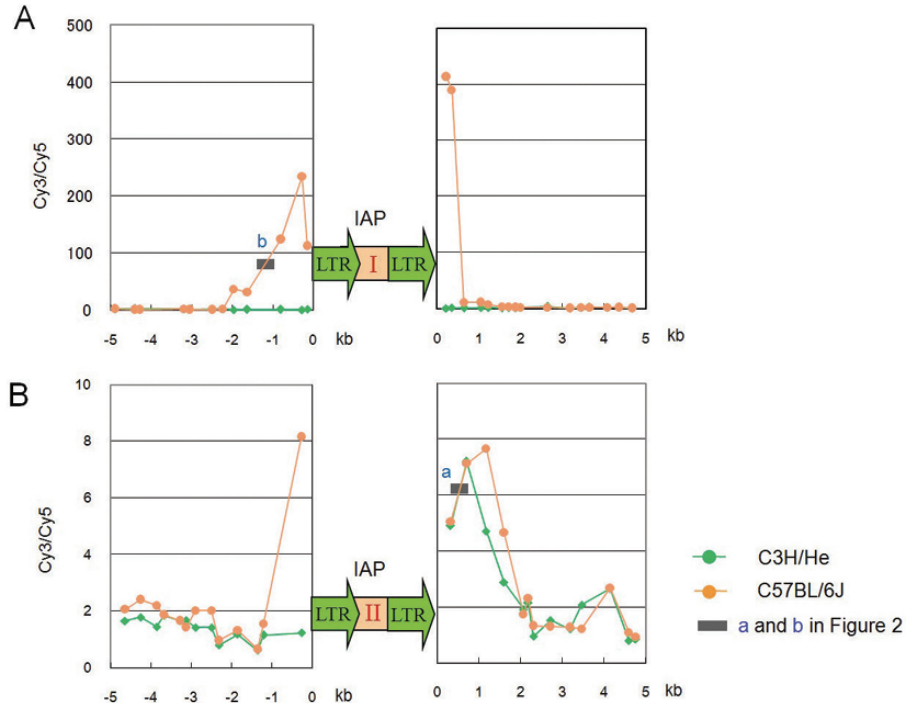
### Supplementary Figure S1

Schematic illustration showing the sequences of DOP-PCR primers and biotin-labeled oligonucleotides, and the positions of IAP elements that were used to design these oligonucleotides.



### Supplementary Figure S2

Microarray-based mapping of integration sites for IAP elements. (A) A plot of each Cy3/Cy5 ratio for all probes on the array-CGH microarray in Experiment 1 (*x* axis) and Experiment 2 (*y* axis). Orange dots indicate the ratios at probes located close (~2kb) to IAP-LTR. (B) Cy3/Cy5 ratios at neighboring 10 probes at both sides of each IAP elements in Experiment 1 (blue dots) and Experiment 2 (brown dots) are plotted to maintain the spatial relationships between the position of each probe and the IAP element in the genome database.



### Supplementary Figure S3

Cy3/Cy5 ratios for C3H/He (light green dots) and C57BL/6J (orange dots) genomes are plotted separately to maintain the spatial relationships between the position of each probe and the IAP element in the genome database. IAP elements I and II and PCR target sites a and b are described in Figure 2A.