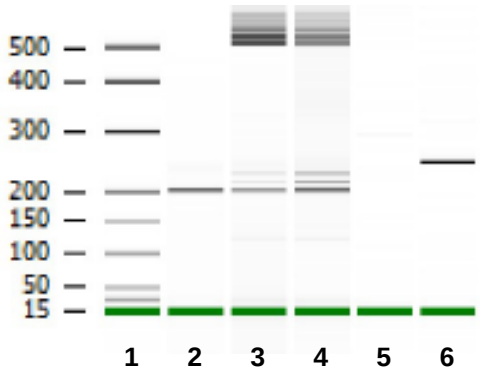
A

B



Lane1: Marker

Lane2: S002_Tumor (Control)

Lane3: S005_Normal

Lane4: S005_Tumor

Lane5: S011_Normal

Lane6: S011_Tumor

Figure S1. Representative results of PCR validation. **(A)** Two PCR strategies. MEI PCR is designed to amplify full length MEI. Both of PCR primers (F and R) are mapped outsides of the insertion point (left). MEI-junction PCR is designed to amplify a reference-MEI junction. One PCR primer (F) is mapped to an outside of the insertion point and the other primer (R) is mapped to ME. (right) **(B)** MEI PCR for germline heterozygous MEIs on a exon of *XKR9*. Wild type allele were observed at size of 200 bases (lane 2-4). *Alu* inserted allele was observed at positions of +300 bases in both of tumor and normal samples (lane 3 and 4) but not in a control (lane 2). MEI-junction PCR for a somatic MEI on a exon of *PDLIM7*. An expected size of reference-MEI junction fragment (254 base) was observed in tumor sample (lane 6) but not in normal sample (lane 5).