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CORRECTION

Correction: Importance of gastric cancer for the diagnosis and surveillance of Japanese Lynch syndrome patients

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Since the publication of the above article, the authors of the above paper have noticed errors in the description of variants, and misclassifications of the pathogenicity of two variants in the text and Supplementary Table 2 after its publication. The errors were corrected according to the recommendations of sequence variant nomenclature of Human Genome Variation Society (HGVS) in the text as described below. The misclassifications of two variants, c.2250C>G (p.Tyr750Ter) and c.279_281del (p.Leu94del), have been deleted, because they are categorized as "uncertain significance" and "likely benign," respectively, according to the recent version of ClinVar database. These changes are included in the new version of Supplementary Table 2.

In the "Result" section: Identification of pathogenic variants, we would change the descriptions and the number of pathogenic variants written in italic.

In this study, we investigated variants in the three major genes associated with LS, namely *MLH1*, *MSH2*, and *MSH6*, by PCR-direct sequencing using the Sanger's method. To investigate large deletions and duplications, MLPA was performed for subjects without pathogenic variants. As a result, 64 (57.7%) of the 111 subjects carried 55 types of pathogenic variants (Supplementary Table 2). Twenty one of the 55 have not reported in LOVD, HGMD, or ClinVar databases, and were novel variants. The 21 variants included *c.213_215delAGA*, *c.320_321delTA*, *c.469dupT*, *c.473delA*, *c.526delA*, *c.545+4_545+5delCA*, *c.1673_1676dupAACT*, *c.2200_2201dupTT*, *c.1-94948_453+716del*, *c.381-415_453+733del*, *c.1038+960_1410-429delins(101)* in *MLH1*, *c.2300_2303delinsATATATAT*, *c.2310delT*, c.2455A>T, *c.1-7545_211+2024del*, *c.1-19631_1077-3200del*, *c.793-453_1076+5896dup*, *c.943-584_1277-3562del*, *c.1077-10584_1276+207dup* in *MSH2*, and *c.3404dupC* in *MSH6*. In addition, a subject (JLS054) carried a variant, *MSH6* c.3656C>T (p.Thr1219Ile), which was judged as a variant of uncertain significance (VUS) because it was categorized as a VUS in the LOVD, and as uncertain significance or likely pathogenic variant in ClinVar. Moreover, another two subjects (JSL066 and JSL128), the former carried a variant, *MLH1 c.2250C>G* (*p.Tyr550Ter*), and the latter carried a variant, *MSH2 c.279_281del* (*p.Leu94del*), were judged as uncertain significance and likely benign, respectively, in ClinVar database. Among the 64 variant carriers, 34 had a variant in *MLH1*, 28 in *MSH2*, and 2 in *MSH6*. Regarding the method of detection, 46 of the 55 types of variants were identified by PCR-direct sequence in 47 subjects, and 11 were identified by MLPA in 17 subjects, suggesting that 17 out of 64 (26.6%) variant carriers with large structural alterations would have been overlooked if additional analysis of MLPA were not performed.

It is of note that three types of recurrent variants were identified in this study; *MLH1*, c.199G>A observed in two patients (JLS051 and JLS109), *MLH1*, *c.381-415_453+733del* encompassing exon 5 in six patients (JLS039, JLS055, JLS058, JLS070, JLS095, and JLS101), and *MSH2*, *c.1-7545_211+2024del* encompassing exon 1 in two patients (JLS023 and JLS114). It remains to be established whether the three changes are founder variants in Japanese LS.

These corrections do not alter the conclusion and discussions of the paper. The authors would like to apologize for the errors and misclassifications.