Author Correction: LKB1 loss links serine metabolism to DNA methylation and tumorigenesis

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In this Article, there were several errors, as follows. The 'Gene Expression Profiling' section of the Supplementary Methods should have included additional information about differential expression analysis, gene set enrichment analysis (GSEA) analysis and the identification of untranslated regions (UTRs). The corrected paragraph is as follows: 'RNA-sequencing was performed using total RNA isolated from two independent cell lines from the K (three replicates total) or KL (four replicates total) genotypes or from the two independent KL lines transduced with full-length *LKB1* cDNA (rescue, two replicates). RNAseq library-preparation and sequencing were performed by the Tufts University Genomics Core Facility. Data were processed using a standard RNA-seq pipeline that used Tophat2[9] to align the reads to mm9, and the Cufflinks suite[10] to calculate expression values and differential expression. Gene Set Enrichment Analysis (GSEA) (http://www.broadinstitute.org/gsea/index.jsp) of the expression data was used to assess enrichment of the KEGG as well as the SGOC geneset[11–13]. There were 2,520 differentially regulated autosomal genes between K and KL samples based on *q*-value as reported by the cufflinks suite (see Supplementary Table 1 of this Amendment). This list was uploaded to the UCSC Genome Browser to extract promoter, intron, exon and UTR sequences. 2,443 of the total 2,520 genes were identified by the algorithm and were associated with 4,706 UTRs. In all cases, pairwise GSEA was performed by creating lists of genes using the FPKM value reported by cufflinks of K to KL or KL to rescue and *P* values were obtained by permuting the gene set (1,000 permutations). To calculate the statistical significance of SGOC pathway enrichment, the SGOC genelist[13] was added to the KEGG signature list and GSEA was performed using this modified KEGG signature list. Raw sequencing files can be found under the Superseries record GSE86145 (http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE86145).' The Supplementary Information to this Amendment contains the Supplementary Table 1 cited above.

In addition, the following sentence should have been included at the end of the 'Liquid Chromatography Mass Spectrometry' section of the Supplementary Methods: 'Proteomics data were uploaded to https://massive.ucsd.edu/ and can be found under the accession number MSV000082186.'

In the 'Materials' section of the Supplementary Methods, the text 'PSAT1 (sc-133929) from Santa Cruz' should have been added after the information on the 5-hydroxymethycytosine antibody.

The following information should have been provided at the end of the 'SDS-PAGE Analysis' section of the Supplementary Methods: 'For Extended Data Fig. 1k (GLUT1, actin), Extended Data Fig. 2e (LKB1, GLDC, PSAT1, actin), Extended Data Fig. 5c (DNMT1, DNMT3A, actin), Extended Data Fig. 5h (H3K36me3, H3K27me3, H3K4me3, H3), Extended Data Fig. 7f (LKB1, total AMPK, pAMPK (T172), actin), Extended Data Fig. 7g (pACC (S79), total ACC, actin) and Extended Data Fig. 7w (p-p70S6K (T389), p70S6K, actin), samples were derived from each corresponding experiment and blots were processed in parallel. For Extended Data Fig. 7f, the actin membrane was stripped and reprobed for total ACC and the pAMPK membrane was stripped and reprobed for pACC (S79).'

Knockdown efficiencies for shRNAs against AMPKa1 and AMPKa2, and against DNMT1 and DNMT3A (as used in experiments in Extended Data Figs. 7 and 9, respectively) were not provided in the original Article, and are now included as Supplementary Fig. 1 in the Supplementary Information to this Amendment.

In Extended Data Fig. 7f, the blot for AMPKα was inadvertently vertically flipped. See Fig. 1 of this Amendment for a corrected version of the panel. In the top middle (total AMPK) and bottom left (pAMPK (T172)) blots of the panel for Extended Data Fig. 7f in Supplementary Data Fig. 1 of the original Article, the molecular mass markers for total AMPK and pAMPK were mislabelled, and the bottom three markers should have been '25', '37' and '50' kDa instead of '37', '50' and '75' kDa.

In the SGOC network diagram in Extended Data Fig. 4a, the AHCY enzyme should have been shown catalysing the reaction from SAH to HCY instead of the reaction from HCY to Met.

In the legend to Extended Data Figs. 4g and 5a, the sentence: 'The data plotted are expressed as mean-centred values' should have stated: 'The data plotted are expressed using a min-to-max relative colour scheme'.

In the legends to Extended Data Figs. 1k, 2e and 5c, the text: 'Actin was used as the loading control' should have stated: 'For western blot analyses, samples were derived from the same experiment and blots were processed in parallel. Actin was used as the sample processing control.'. Similarly, the legend to Extended Data Fig. 7f, g and w should have included the text: 'Samples were derived from the same experiment and blots were processed in parallel. Actin was used as the sample processing control.'

The legend to Extended Data Fig. 5h should have included the text: 'Samples for H3K36me3, H3K27me3 and H3 were derived from the same experiment. Samples for H3K4me3 and H3 were derived from the same experiment. Blots were processed in parallel and H3 was used as the sample processing control.'.

The Supplementary Information of this Amendment contains Supplementary Table 1 and Supplementary Fig. 1, as described above. The original Article has not been corrected online.

Supplementary information is available in the online version of this Amendment.

Fig. 1 | This is the original, incorrect published Extended Data Fig. 7f, and the corrected Extended Data Fig. 7f. The blot for AMPKα was inadvertently flipped vertically in the published figure.