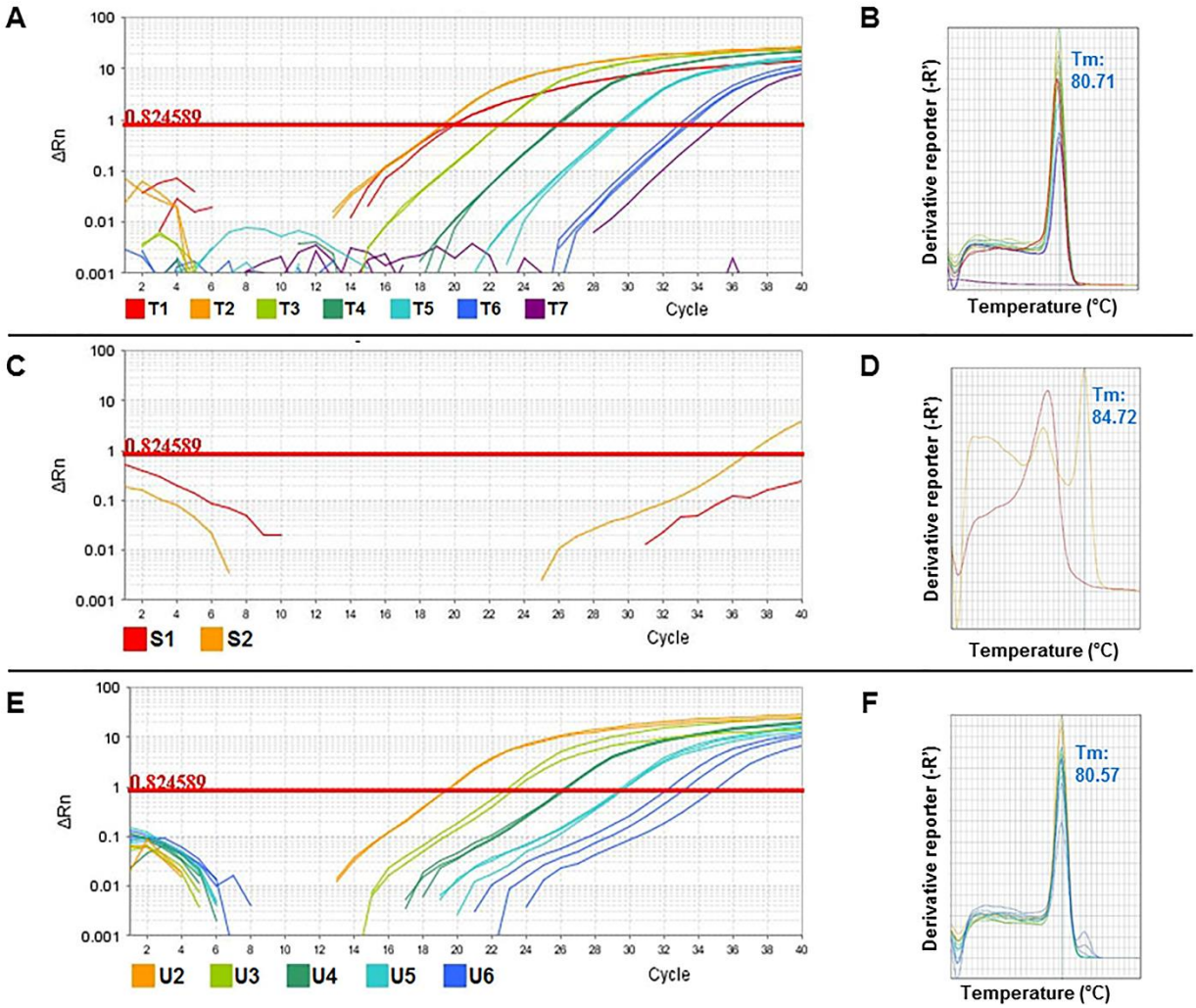
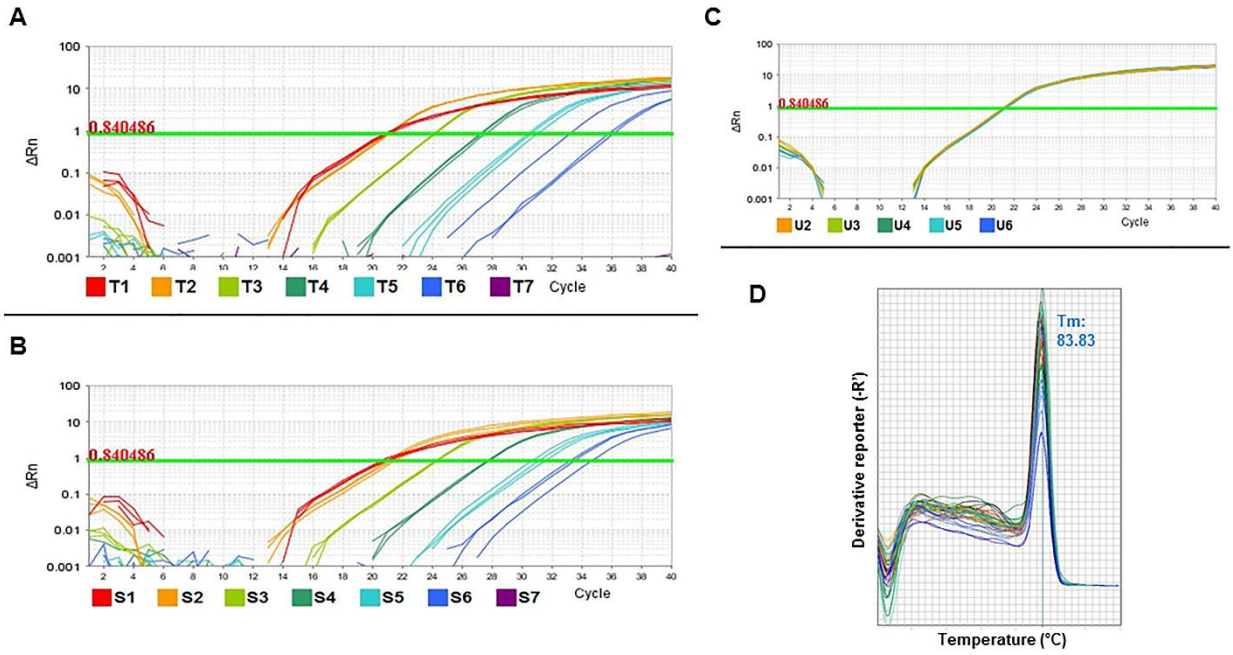
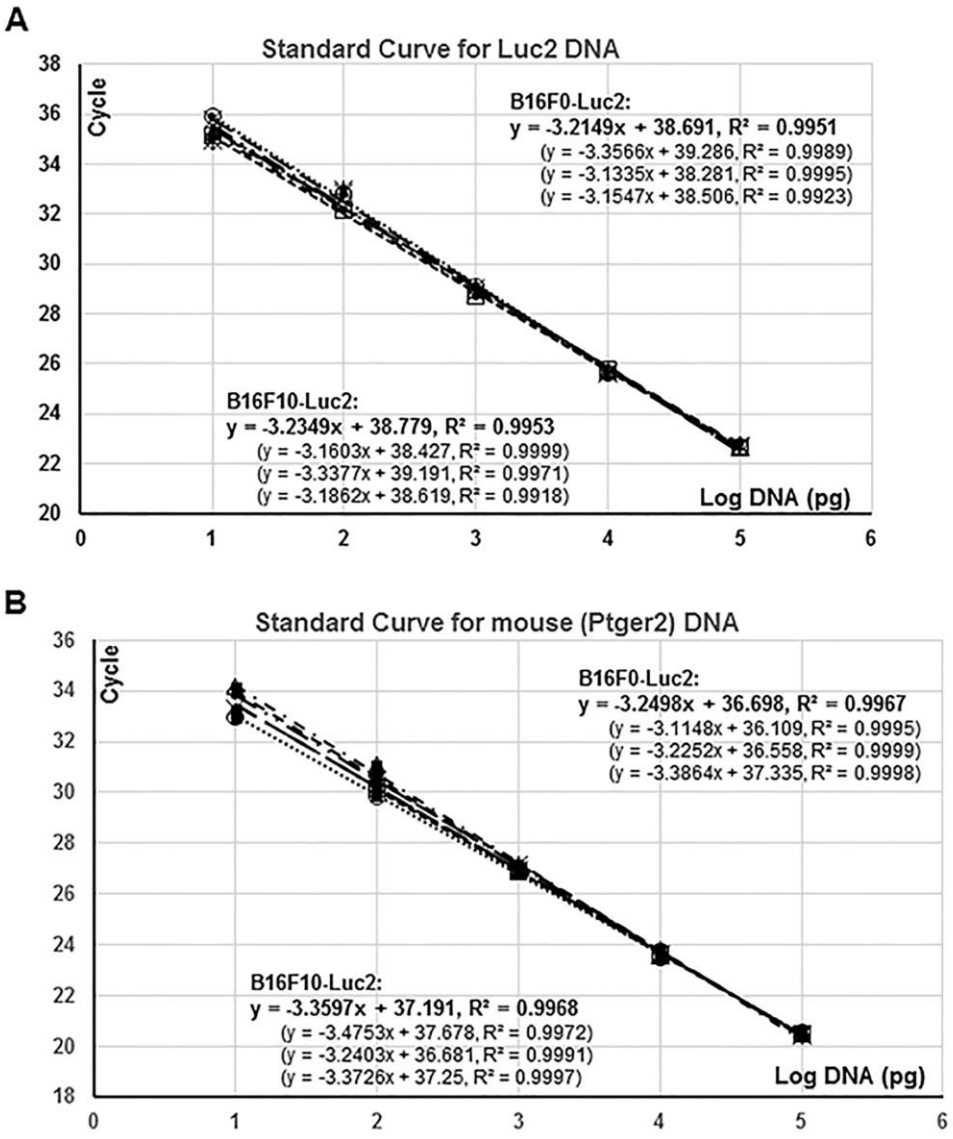
Electronic Supplementary Material (ESI) for Analyst.



Supplementary Fig. S1 Real-time PCR plots and melting curves for *Luc2* gene show specific and quantitative amplification. Fluorescent signal of amplification (ΔRn vs cycles) for each sample of group T, S, or U from Table 1 was shown as individual colored curve, with red line (0.824589) across the plot indicating the threshold. The melt curve for each sample of a group was presented as derivative reporter vs temperature. (A and B) *Luc2* amplification plots and melting curves for group T samples ($Luc2^+$ genomic DNA with a serial of 10 fold dilutions). (C and D) *Luc2* amplification plots and melting curves for two of group S samples ($Luc2^-$ genomic DNA with a serial of 10 fold dilutions). (E and F) *Luc2* amplification plots and melting curves for group U samples (mixture of $Luc2^-$ and $Luc2^+$ genomic DNA, with a serial of 10 fold dilutions on $Luc2^+$ genomic DNA).



Supplementary Fig. S2 Real-time PCR plots and melting curves for *Ptger2* gene show specific and quantitative amplification. Fluorescent signal of amplification (ΔRn vs cycles) for each sample of group T, S, or U from Table 1 was shown as individual colored curve, with red line (0.840486) across the plot indicating the threshold. The melt curve for each sample was presented as derivative reporter vs temperature. (A) *Ptger2* amplification plots for group T samples ($Luc2^+$ genomic DNA with a serial of 10 fold dilutions). (B) *Ptger2* amplification plots for group S samples ($Luc2^-$ genomic DNA with a serial of 10 fold dilutions). (C) *Ptger2* amplification plots for group U samples (mixture of $Luc2^-$ and $Luc2^+$ genomic DNA, with same amount of total genomic DNA). (D) Melting curves for each sample of group T, S, and U.



Supplementary Fig. S3 Comparison of standard curves from B16F0-Luc2 cells and B16F10-Luc2 cells for Luc2+ DNA and total mouse (Ptger2) DNA. A serial genomic DNA dilutions were made as described in Table 1 and Fig. 2 using biological triplicates of genomic DNA from B16F0-Luc2 cells and B16F10-Luc2 cells, respectively. Each sample was then amplified in technical triplicates for either Luc2 or Ptger2 gene as described in Experimental section. (A) The mean Ct's of the technical replicates from each of the three biological replicates of B16F0-Luc2 cells and B16F10-Luc2 cells, respectively, were combined and plotted against log values of DNA input to create two Luc2 DNA standard curves (formulas shown in bold). Individual Luc2 DNA standard curve from each of the biological replicate of B16F0-Luc2 cells and B16F10-Luc2 cells was also plotted on the graph (formulas in parentheses). (B) The mean Ct's of the technical replicates from each of the three biological replicates of B16F0-Luc2 cells and B16F10-Luc2 cells, respectively, were combined and plotted against log values of DNA input to create two Ptger2 DNA standard curves (formulas shown in bold). Individual Ptger2 DNA standard curve from each of the biological replicate of B16F0-Luc2 cells and B16F10-Luc2 cells was also plotted on the graph (formulas in parentheses).