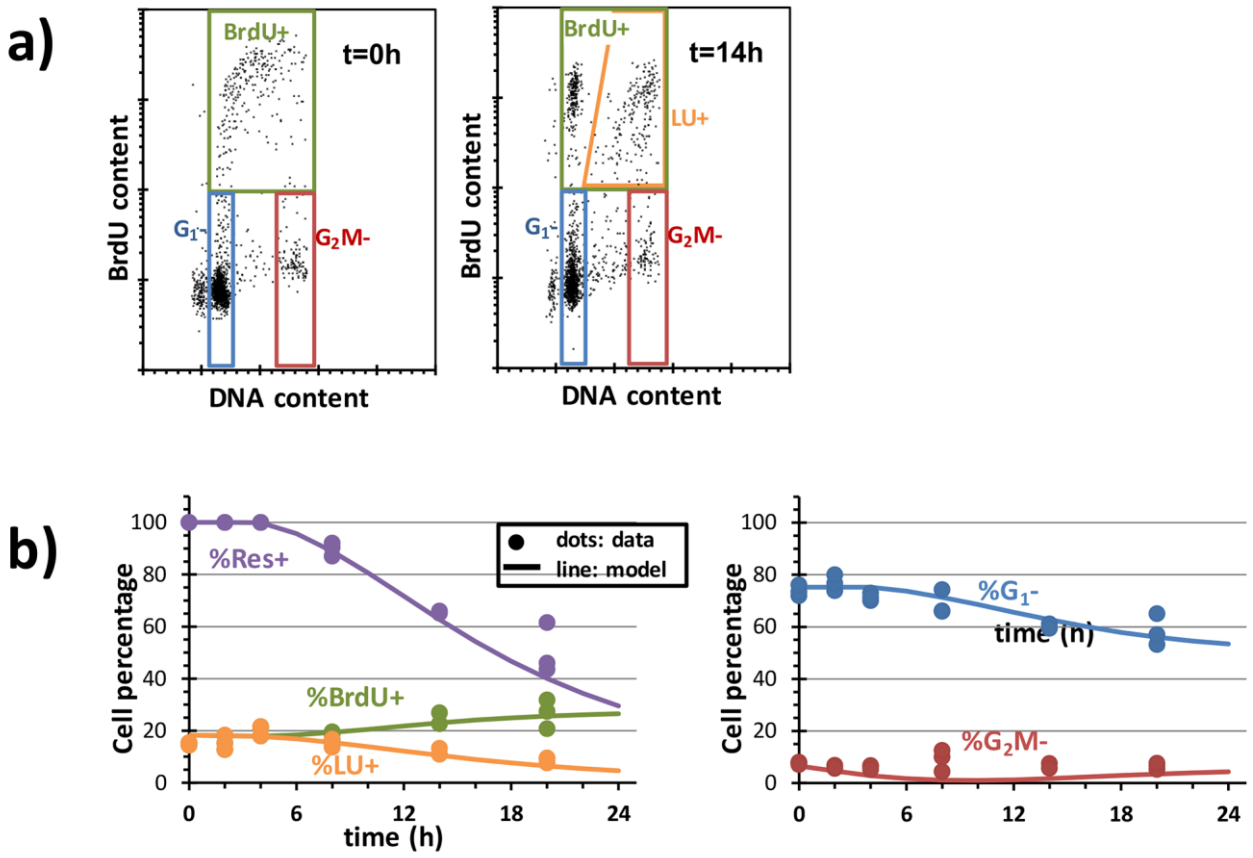
Supplementary Figure S1.

Consistency of the MNHOC18 basal proliferation model with the measures of a BrdU pulse chase experiment



Supplementary Figure S1. Consistency of the MNHOC18 basal proliferation model with the measures of a previously reported BrdU pulse chase experiment (18).

BrdU was injected into the peritoneal cavity of the mice. The cells in S phase at the time of BrdU exposure therefore became BrdU-labeled ($BrdU^+$). At the subsequent times, these cells or their descendants remained $BrdU^+$ and were definitely distinguishable from cells in G_2M and G_1 phases at the initial time (BrdU-unlabeled cell, $BrdU^-$). Three mice were killed at 0.5, 2, 4, 8, 14, 20 h after BrdU injection, tumors were collected and minced, and the cells were suspended and fixed in 70% ethanol. Fixed cells were prepared for DNA-BrdU flow cytometric analysis as previously described (10). The results of a flow cytometric DNA–BrdU measure is a cytogram similar to those shown in panels a. The biparametric DNA– BrdU histograms were analyzed using dedicated software (Cell Quest, Becton Dickinson) providing the percentages - within the tumor cell population - of cells in user-selected regions of interest: $BrdU^+$ (BrdU-labeled cells, green bordered area), labeled undivided, G_1^- (BrdU-unlabeled in G_1 phase, blue), G_2M^- (BrdU-unlabeled in G_2M phase), LU^+ (undivided BrdU-labeled, orange). Residual undivided BrdU-labeled cells (Res^+) were calculated with the formula:

$\%Res^+ = 100 \times \%LU^+ / (\%LU^+ + (\%BrdU^+ - \%LU^+) / 2)$

Panels b report the time courses of $\%BrdU^+$, $\%LU^+$, $\%Res^+$, $\%G_1^-$ and $\%G_2M^-$ (dots) with the predictions of the basic MNHOC18 model (continuous line).