Erratum to: Stochastic phenotypic interconversion in tumors can generate heterogeneity

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The original article was published with the following errors:

In the “Result” section, the second sentence in the second paragraph was incorrect. The correct sentence should read as:

“The cells included two main subpopulations: cytokeratin positive (CK20⁺ and CD45⁺), defined as epithelial cancer cells, and cytokeratin negative (CK20[−] and CD45⁺), defined as residual hematological contaminant cells (Malara et al. 2014)”.

The caption of the X-axis in Fig. 2d–g were incorrect. Figure 2 with correct caption is given below:

The online version of the original article can be found under doi:[10.1007/s00249-016-1190-6](https://doi.org/10.1007/s00249-016-1190-6).

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Fig. 2 **a** Transition matrix for the Markov model. *RHC* and *CTC* represent the two states of the system; cells in state *CTC* can replicate with rate coefficient r_{CTC} , are cleared with rate coefficient m_{CTC} , and convert to *RHC* phenotype with rate coefficient c_{CTC} . Analogous rate coefficients describe the dynamics of the *RHC* subpopulation. **b** Biochemical model for describing the transition. **c** Matrix of probabili-

ties related to the model and the experimental results. **d** N -loop of the stochastic model. Profile of a number of *RHC* and *CTC*. **e** Variation of the mean based on curves in (d). **f** Variation of standard deviation based on curves (d). **g** Variation of the mean and standard deviation for *CTC*