Supplementary information for

Computational quantification of global effects induced

by mutations and drugs in signaling networks

of colorectal cancer cells.

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Supplementary information includes 5 tables described below.

Supplementary Table S1. Table of the proteins A_i, $i = 1, \ldots, 419$, involved in the CRC-CRN related to Fig. 2. In the third column we reported the values of the initial concentrations used for computing the equilibrium state of the healthy network.

Supplementary Table S2. Table of the proteins significantly affected (i.e. $|\delta_i| > 0.03$) by the mutations related to Fig. 2.

Supplementary Table S3. Table of the chemical reactions and of the values of the rate constants involved in the CRC-CRN related to the Methods section, paragraph 'A mathematical model for CRNs'.

Supplementary Table S4. Table of the chemical reactions removed when implemented each of the GoF mutations related to Methods section, paragraph GoF mutations.

Supplementary Table S5. Table related to Fig. 4, and listing (i) the relative difference between the concentrations at the equilibrium of the network affected by a GoF of k-Ras and the concentrations at the physiological equilibrium and (ii) the relative difference between the equilibrium concentrations obtained after that about 37 nM of drug has been incorporated in the mutated network and the concentrations in the physiological equilibrium.

Supplementary Data S6. Whole chemical reaction network for colorectal cancer (CRC-CRN) in Systems Biology Markup Language (SBML) format.