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Supplementary Information

Agent-based modelling reveals the role of the tumour microenvironment on the short-term success of combination temozolomide/immune checkpoint blockade to treat glioblastoma

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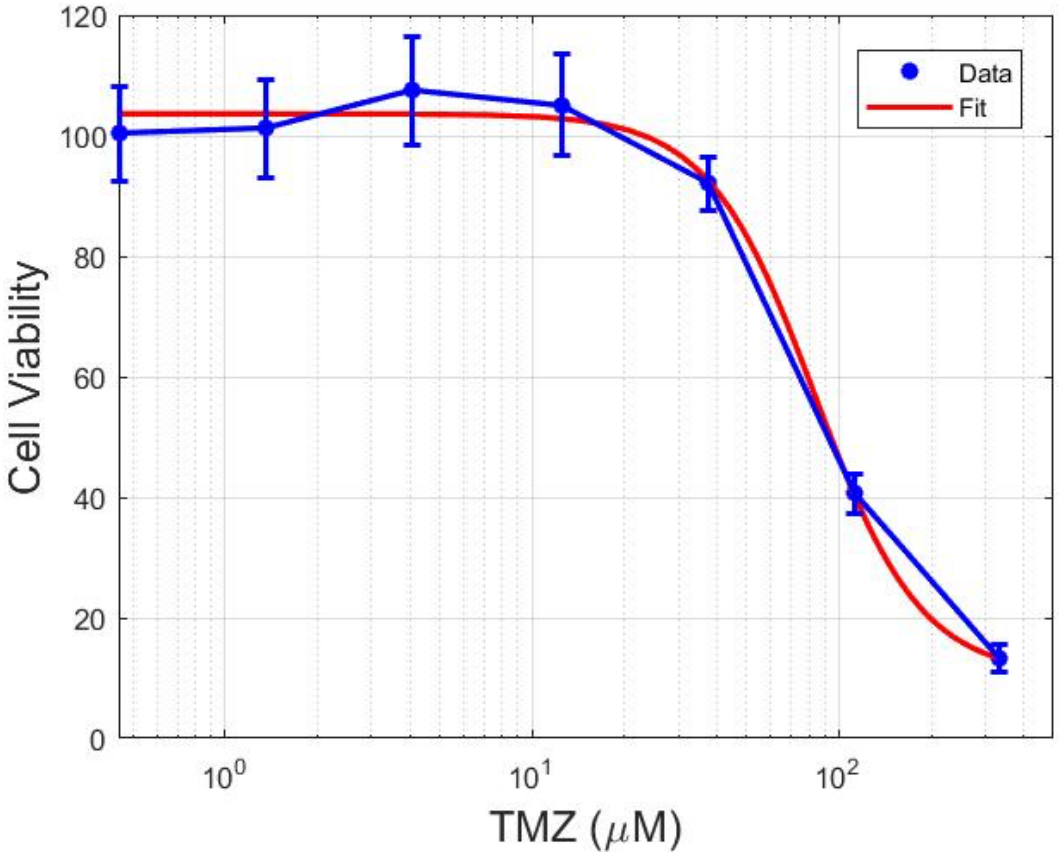
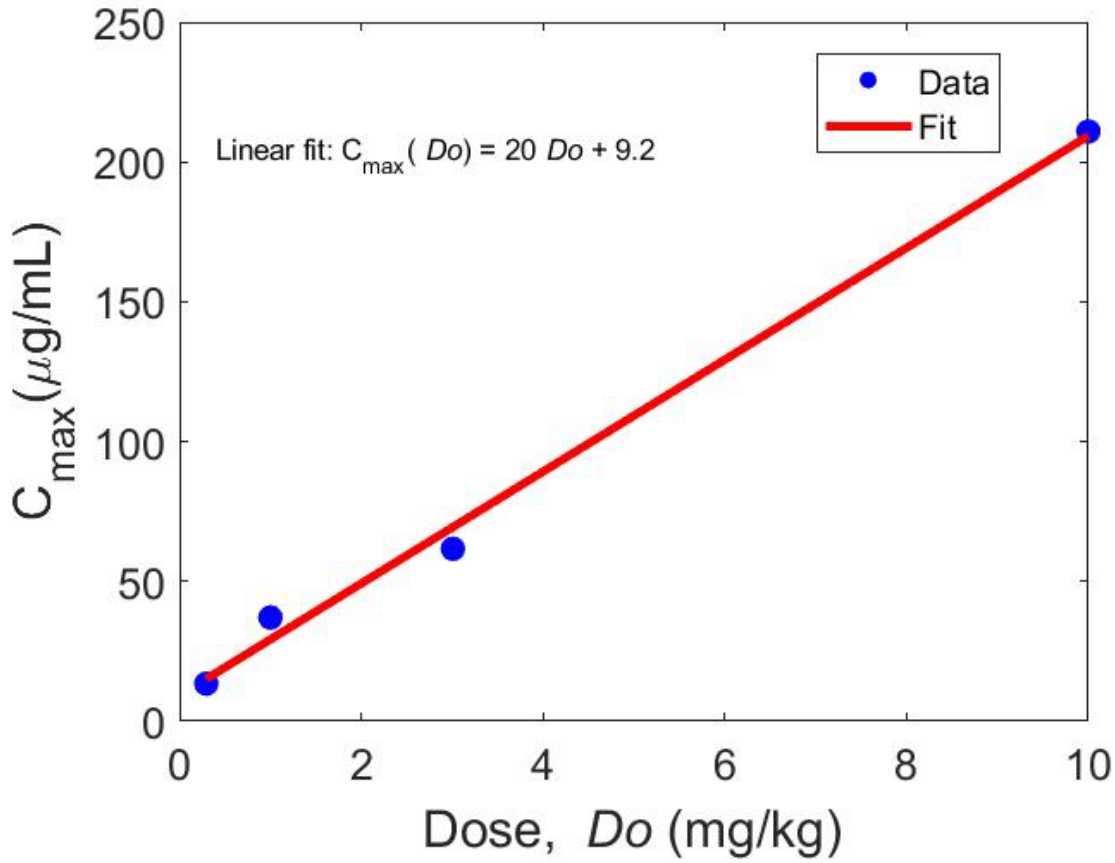
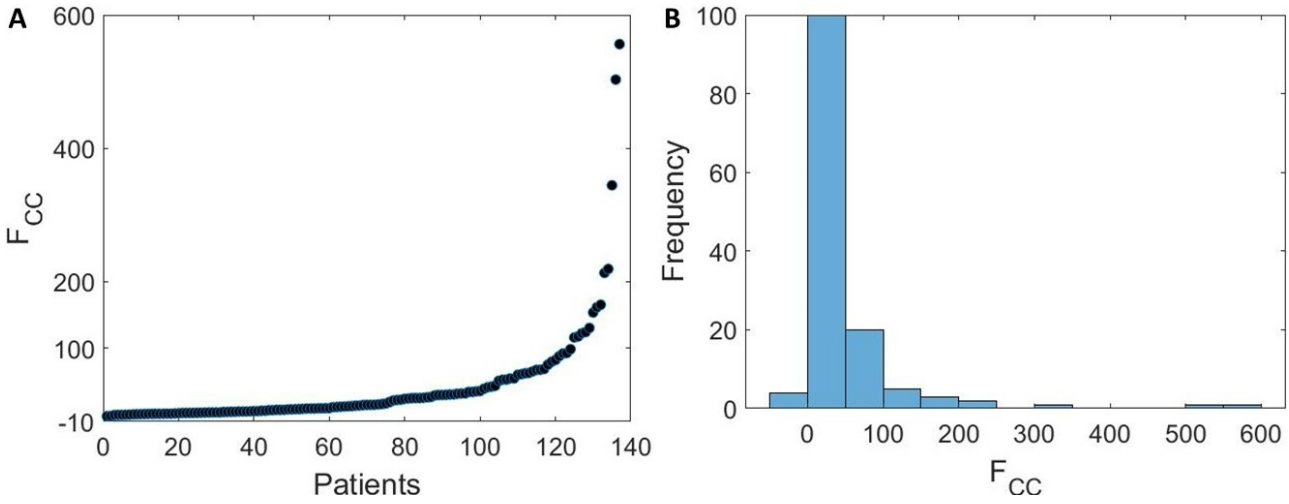


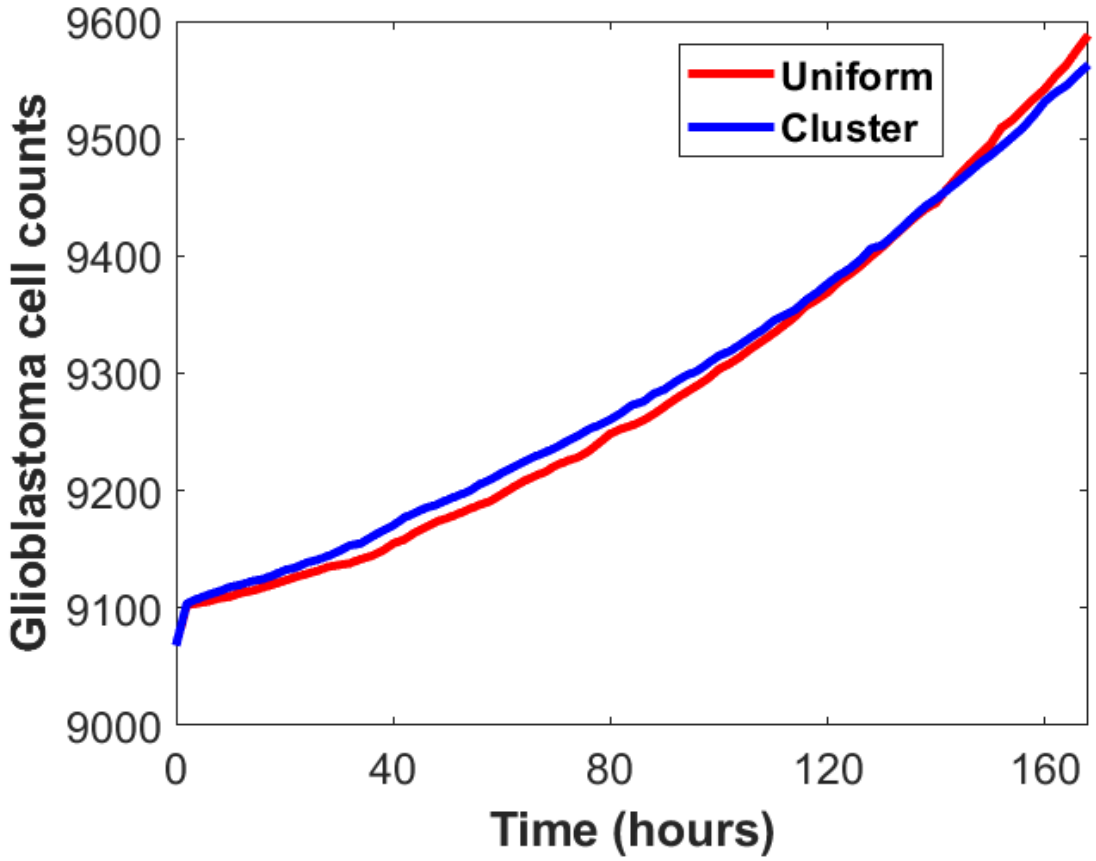
Supplementary Figure 1. *Standard Emax effects curve fitting associated with section* ***Pharmacokinetic/pharmacodynamic models of temozolomide.*** *The standard Emax effects curve,* $E(TMZ) = E_0\left(1 - \frac{I_{max}\,TMZ^h}{TMZ^h + IC_{50}{}^h}\right)$ *was fit to the dose response data of glioblastoma stem cells treated with TMZ from Saha et al., 2020. Fitting provided an estimate of* $IC_{50} = 83.4\ \mu M\ or\ IC_{50} = 0.0162\ \mu g/\mu L$. *Blue dots show the dose response measurement along with error bar and red curve show the fit obtained using lsqcurvefit function in MATLAB.*



Supplementary Figure 2. *Figure showing the linear relationship between the dose of anti-PD-1 drug (Do, in mg/kg) and plasma concentration $C_{max}(Do)$ ($\mu g/mL$), related to section* ***Treating glioblastoma using immune checkpoint blockade.*** *Linear fit is obtained using polyfit function in MATLAB and the pharmacokinetic data from Brahmer et al., 2010.*



Supplementary Figure 3. *Distributions of F_{cc} (the metric measuring the correlation between glioblastoma cells) for patient tumour samples in the glioblastoma cohort. A) Patient samples arranged in the order of increasing clustering (increasing F_{cc} values) and corresponding F_{cc} values. B) Histogram of the metric F_{cc}.*



Supplementary Figure 4. *Increases in glioblastoma cell counts in the absence of treatment for both uniform (red) and clustered (blue) tumours shown in Figure 6 in the Main Text.*