**Code for Reproducing Figures and Tables in *Ryser et al., 2022***

All code written and compiled with R version 4.2.0 (R Foundation for Statistical Computing, Vienna, Austria).

**Data Folder**

|  |  |  |  |
| --- | --- | --- | --- |
| **Main Figures** | | | |
| /Data | Annotations\_SNV/ | Driver\_mutations\_All.csv | List of detected driver mutations |
|  |  | SNV\_annotations\_complete.csv | Complete SNV annotation |
|  | Cleaned\_Mutation\_calls/ | CleanedBayesian\_Tumor\_XYZ.csv | Bayesian mutation calls (posterior probabilities) for all tumors XYZ |
|  | Cleaned\_VAF/ | CleanedMAF\_Tumor\_XYZ.csv | Variant allele frequencies for all tumors XYZ |

**Figures and Tables**

|  |  |  |  |
| --- | --- | --- | --- |
| **Main Figures** | | | |
| Figure 1 |  | No code |  |
| Figure 2 | Panel A | No code |  |
|  | Panel B | Fig\_2B.R |  |
|  | Panel C | No code |  |
| Figure 3 | Panel A | Fig\_3A.R |  |
|  | Panel B | Fig\_3B.R | *Set modeling.version=FALSE for this figure* |
|  | Panel C | Fig\_3C.R |  |
|  | Panel D | Fig\_3C.R |  |
|  | Panel E | Fig\_3E.R |  |
| Figure 4 | Panel A | Fig\_4A.R |  |
|  | Panel B | Fig\_4B.R |  |
|  | Panel C | Fig\_4C.R |  |
|  | Panel D | Fig\_4D.R |  |
| Figure 5 | Panel A | No code |  |
|  | Panel B | No code |  |
|  | Panel C | No code |  |
|  | Panel D | /Modeling/DCIS\_growth\_single.Rmd | *set: type="TEB.BT.mix"* |
|  | Panel E | /Modeling/DCIS\_growth\_single.Rmd | *set: type="Branch.surface"* |
|  | Panel D | /Modeling/ABC\_rejection\_sampling\_model\_fit.R | *Need to first sample from the posterior, see READ\_ME file in /Modeling for details* |
| Figure 6 | Panel A | Fig\_6A.R | *Select tumor first* |
|  | Panel B | Fig\_6B.R |  |
|  | Panel C | Fig\_6C.Rmd |  |
|  | Panel D | Fig\_6A.R |  |
|  | Panel E | Fig\_6B.R |  |
|  | Panel F | Fig\_6C.Rmd |  |
|  | Panel G | No code |  |
|  | Panel H |  |  |
| **Supplementary Tables** | | | |
| Table S1 | Spots | Table\_S1.R |  |
|  | Mutations | Table\_S2.R |  |
|  | Reads | Table\_S1.R |  |
| Table S2 |  | Table\_S2.R | *Select type=”DCIS” or type=”All” to specify which spots to analyze* |
| Table S3 |  | /Modeling/ ABC\_rejection\_sampling\_model\_selection.R | *Need to first sample from the posterior, see READ\_ME file in /Modeling for details* |
| Table S4 |  | No code |  |
| Table S5 |  | No code |  |
| **Supplementary Figures** | | | |
| Figure S1 |  | /Fig\_S1/Spatial\_map\_X.R | *One script per tumor* |
| Figure S2 |  | Table\_S1.R |  |
| Figure S3 |  | Fig\_S3.Rmd |  |
| Figure S4 |  | Fig\_S4.R |  |
| Figure S5 |  | Fig\_S5.Rmd |  |
| Figure S6 |  | Fig\_4A.R |  |
| Figure S7 | Panel A | Table\_S2.R | *Select type=”DCIS”* |
|  | Panel B | Table\_S2.R | *Need to first sample from the posterior, see READ\_ME file in /Modeling for details* |
| Figure S8 |  | /Modeling/ABC\_rejection\_sampling\_analysis.R |  |
| Figure S9 | Mutation networks | Fig\_6A.R | *Select tumor first* |
|  | Venn diagrams | Fig\_6B.R |  |
|  | tSNE | Fig\_6C.Rmd |  |
| Figure S10 |  | No code |  |
| Figure S11 |  | Fig\_S11.R |  |
| Figure S12 |  | No code |  |