# Description of Additional Supplementary Files

File Name: Supplementary Data 1
Description: QC summary of scLR-seq for each sample

File Name: Supplementary Data 2
Description: Differential transcript usage between tumor and non-tumor cells

File Name: Supplementary Data 3
Description: Differentially expressed genes between tumor and non-tumor cells

File Name: Supplementary Data 4
Description: Differential transcript usage and 3’ UTR length changes between tumor and non-tumor identified by scSR-seq

File Name: Supplementary Data 5
Description: Marker genes for each malignant cell type

File Name: Supplementary Data 6
Description: Differential transcript usage across malignant cell types

File Name: Supplementary Data 7
Description: Differentially expressed genes across malignant cell types

File Name: Supplementary Data 8
Description: Differentially expressed genes across malignant cell types within a single patient

File Name: Supplementary Data 9
Description: Differential transcript usage across malignant cell types identified using the MAST model

File Name: Supplementary Data 10
Description: Differentially expressed transcripts across malignant cell types

File Name: Supplementary Data 11
Description: Top extracellular–intracellular target pairs in GBM patients

File Name: Supplementary Data 12
Description: Non-FSM isoform markers detected in each malignant cell type

File Name: Supplementary Data 13
Description: Tumor-specific non-FSM isoforms in GBM

File Name: Supplementary Data 14
Description: Structural annotation and predicted coding sequences of non-FSM isoforms

File Name: Supplementary Data 15
Description: Predicted binding affinities of neoepitopes to common HLA alleles using MHCflurry and HLAthena

File Name: Supplementary Data 16
Description: HLA class I genotypes of in-house GBM patients

File Name: Supplementary Data 17
Description: Predicted binding affinities of candidate neoepitopes to patient-specific HLA alleles using NetMHCpan

File Name: Supplementary Data 18
Description: Summary of gene functions for patient-specific target pairs

File Name: Supplementary Data 19
Description: Primers used for Sanger sequencing validation

Supplementary Methods:
Differential gene and transcript expression were performed using two-sided t-tests (Supplementary Data 2, 3, 5, 6, 7, 8, 10, 12, 13) or the two-sided MAST model (Supplementary Data 9). Differential transcript usage and 3’UTR length changes were analysed using the Dirichlet–multinomial model implemented in DRIMSeq (Supplementary Data 4). In all analyses, p values were adjusted for multiple comparisons using the Benjamini–Hochberg false discovery rate (FDR) method.