

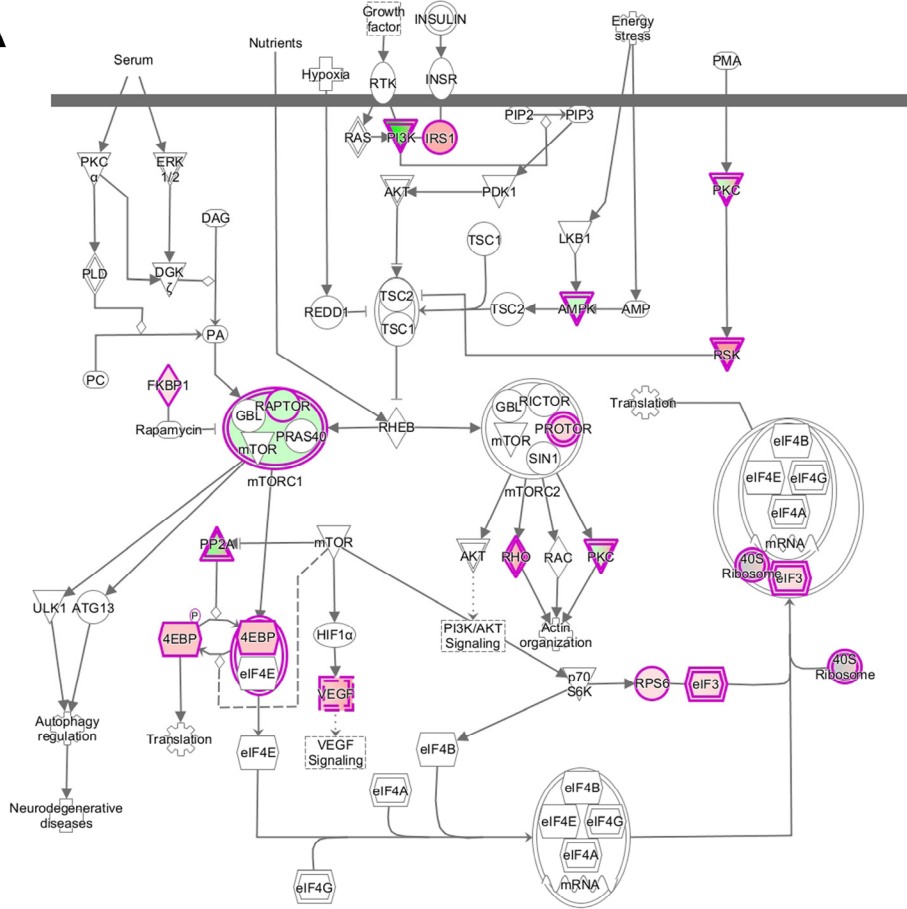
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Appendix Figure S1

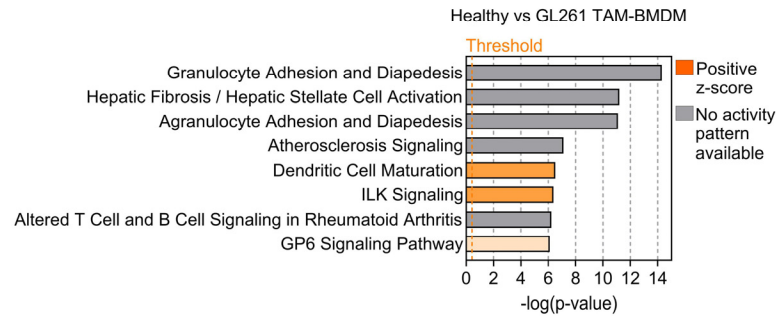
Appendix Figure S2

Appendix Figure S3

A



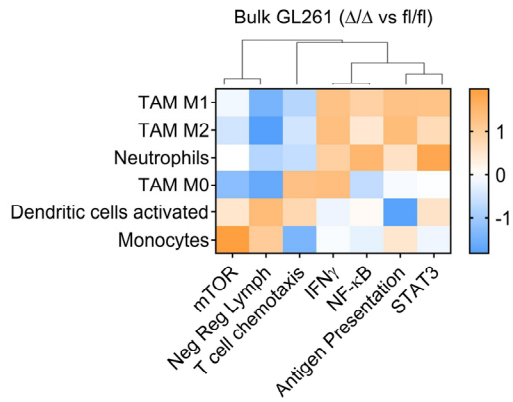
B



Appendix Figure S1

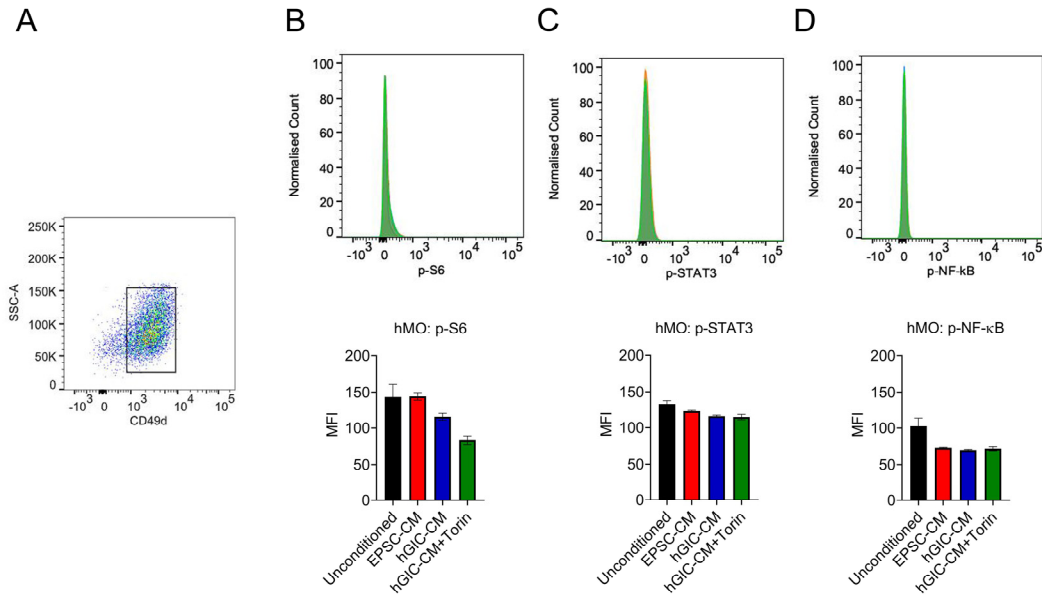
(A) Schematic representation of the mTOR pathway with genes deregulated in GL261 TAM-MG versus healthy microglia. Pink circles indicate deregulated expression of the gene, which when coloured green is downregulated and in pink upregulated. (B) Top-most deregulated canonical pathways in GL261 TAM-BMDM versus healthy blood monocytes, as identified by the IPA software. Threshold indicates $p \leq 0.05$. Z-score indicating the orientation of the deregulation.

A



Appendix Figure S2

(A) Heatmap of differential correlation analysis between CIBERSORT cell fractions and signatures enrichment scores (ssGSEA) for myeloid cells in *Cx3cr1-Rheb1*^{Δ/Δ} (n=3) versus *Rheb1*^{fl/fl} (n=3) GL261 tumours.



Appendix Figure S3

(A) Representative flow cytometry plot of CD49d expression in the healthy blood-derived monocytes/macrophages (on the right). (B) Representative histogram and quantification of the MFI levels of p-S6, (C) p-STAT3 and (D) p-NF-κB (p-P65) in conditioned human monocytes/macrophages (hMO; n=3, mean \pm SEM, One-Way ANOVA Tukey tests – on the right).