

Figure S1: Gli2-mediated transcription modulates T-cell gene expression

6 CD4⁺ splenocytes were obtained directly *ex vivo* (unstimulated) or from cultures activated with 0.01 µg/ml anti-CD3/CD28 for 6h (stimulated). Whole-genome microarray analysis was performed using Affymetrix MOE430 chips and data were analysed to compare fold change in gene expression. Transcripts in grey are significantly differentially expressed between the comparison within each scatter plot, selected genes only are labelled for clarity. Scale is FC [log₂], equivalent to a 1.5-fold change.

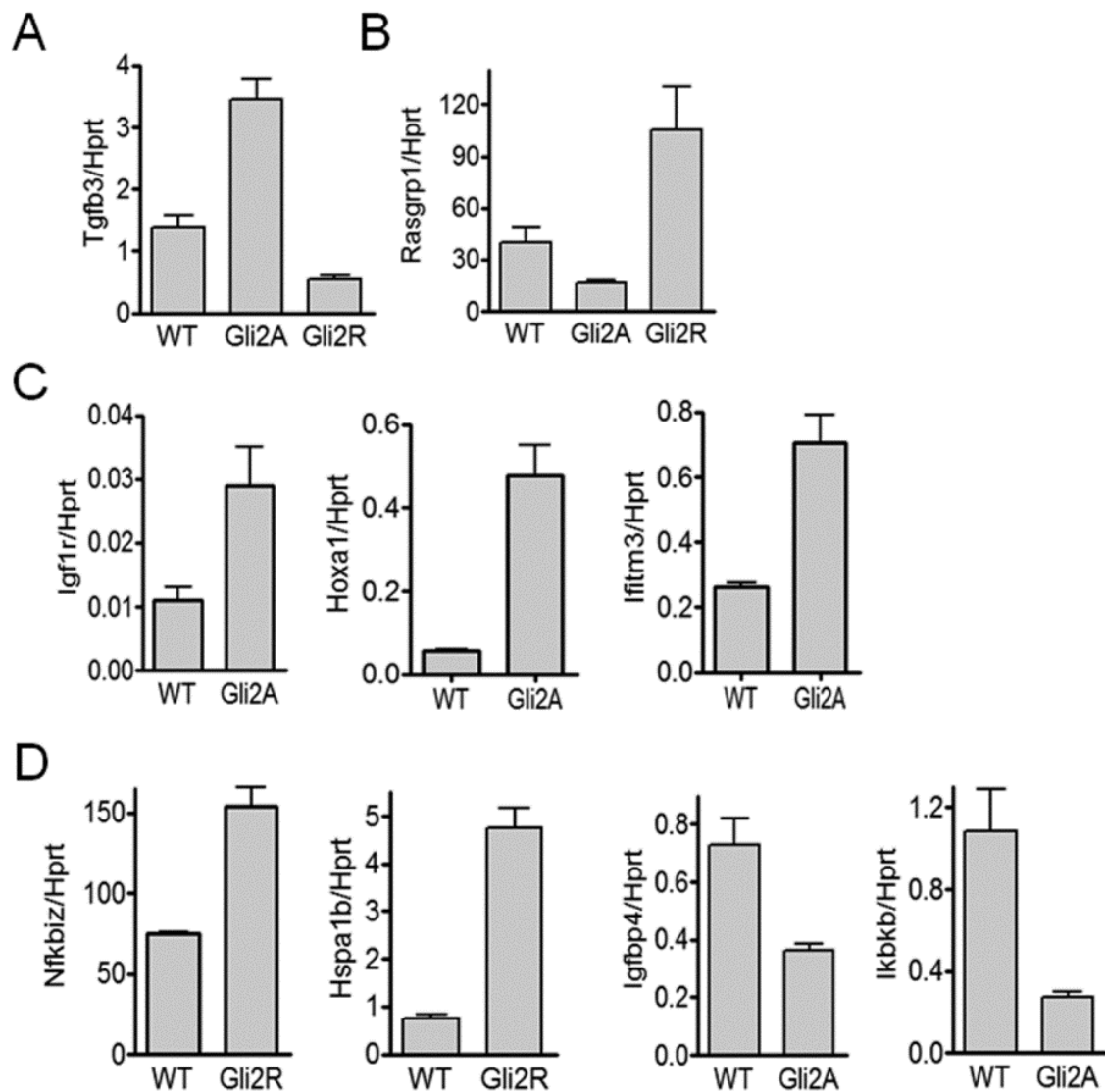


Figure S2: qPCR confirmation of Gli-target genes in T-cells

Gene expression levels in CD4⁺ T-cells were quantified in triplicate by qPCR relative to expression of *Hprt* (*Gene/Hprt*, arbitrary units), charts show a representative example of two or three independent experiments. Expression of (A) *Tgfb3*, (B) *Rasgrp1*, (C) *Igf1r*, *Hoxa1*, *Ifitm3*, (D) *Nfkbiz*, *Hspa1b*, *Igfbp4* and *Ikbkb*.

Table S1: Potential target genes of Gli2 in T-cells. Genes differentially expressed in unstimulated CD4+ T-cell populations of Gli2A vs. WT vs. Gli2R (n=3 per group). Gene lists were obtained by filtering genes that were expressed 1.5x that of WT and that had an expression profile similar ($r > 0.95$) to significant DEG or known Gli target genes (eg Ptch1) in reciprocal transgenic cells compared to WT. FC: fold change in expression relative to WT group.

Gene symbol	Gene name	FC in Gli2A	FC in Gli2R
Genes upregulated in Gli2A and downregulated in Gli2R vs. WT			
<i>Rsad2</i>	radical S-adenosyl methionine domain containing 2	4.0	-2.9
<i>Bpgm</i>	2,3-bisphosphoglycerate mutase	3.6	-1.8
<i>Mmp13</i>	Matrix metalloproteinase 13	2.9	-1.8
<i>Fam213a</i>	family with sequence similarity 213, member A (PAMM)	2.7	-1.5
<i>Sulf2</i>	sulfatase 2	2.7	-1.6
<i>Pltp</i>	Phospholipid transfer protein	2.5	-2.3
<i>Ube2l6</i>	ubiquitin-conjugating enzyme E2L 6	2.4	-2.8
<i>Slc1a3</i>	solute carrier family 1, member 3 (GLAST)	2.1	-1.8
<i>D030029J20Rik</i>	RIKEN cDNA	2.0	-3.8
<i>C6</i>	complement component 6	2.0	-2.7
<i>Hfe</i>	hemochromatosis	1.9	-1.5
<i>Kcnc1</i>	potassium voltage gated channel, Shaw-related subfamily, member 1	1.9	-1.8
<i>Ifitm3</i>	interferon induced transmembrane protein 3	1.8	-1.7
<i>Chchd7</i>	coiled-coil-helix-coiled-coil-helix domain containing 7	1.8	-3.4
<i>Mrc1</i>	mannose receptor, C type 1	1.8	-1.6
<i>Acer1</i>	alkaline ceramidase 1	1.7	-1.7
<i>Ube2e3</i>	ubiquitin-conjugating enzyme E2E 3	1.7	-1.7
<i>Usp15</i>	ubiquitin specific peptidase 15	1.7	-3.7
<i>Rab3il1</i>	RAB3A interacting protein (rabin3)-like 1	1.7	-1.7
<i>Abcg3</i>	ATP-binding cassette, sub-family G (WHITE), member 3	1.7	-1.9
<i>Timd4</i>	T cell immunoglobulin and mucin domain containing 4	1.7	-1.7
<i>Themis2</i>	thymocyte selection associated family member 2	1.7	-1.6
<i>Csf2rb1 (Il5rb)</i>	colony stimulating factor 2 receptor, beta, low-affinity	1.7	-1.7
<i>Igf1r</i>	Insulin-like growth factor I receptor	1.7	-1.5
<i>Tnfsf12</i>	tumor necrosis factor (ligand) superfamily, member 12 (TWEAK)	1.6	-1.6
<i>Slc25a39</i>	solute carrier family 25, member 39	1.6	-1.5
<i>Emr1</i>	EGF-like module containing, mucin-like, hormone receptor-like sequence 1	1.6	-1.6
<i>Slc16a9</i>	solute carrier family 16, member 9	1.6	-1.5
<i>Mbtd1</i>	mbt domain containing 1	1.6	-2.5
<i>Frmd4a</i>	FERM domain containing 4A	1.6	-1.9
<i>Qk</i>	quaking	1.6	-1.8

<i>Gas2l3</i>	growth arrest-specific 2 like 3	1.5	-1.7
<i>C2</i>	complement component 2 (within H-2S)	1.5	-1.6
<i>Genes downregulated in Gli2A and upregulated in Gli2R vs. WT</i>			
<i>Hspa1b</i>	Heat shock protein 1B	-22.9	1.9
<i>Hspa1a</i>	Heat shock protein 1A	-7.3	1.9
<i>Sostdc1</i>	Sclerostin domain containing 1	-6.8	3.8
<i>Igfbp4</i>	insulin-like growth factor binding protein 4	-3.4	1.6
<i>Tmem181</i>	Transmembrane protein 181	-2.6	1.5
<i>Serpini1</i>	serine peptidase inhibitor, clade I, member 1	-1.6	1.8