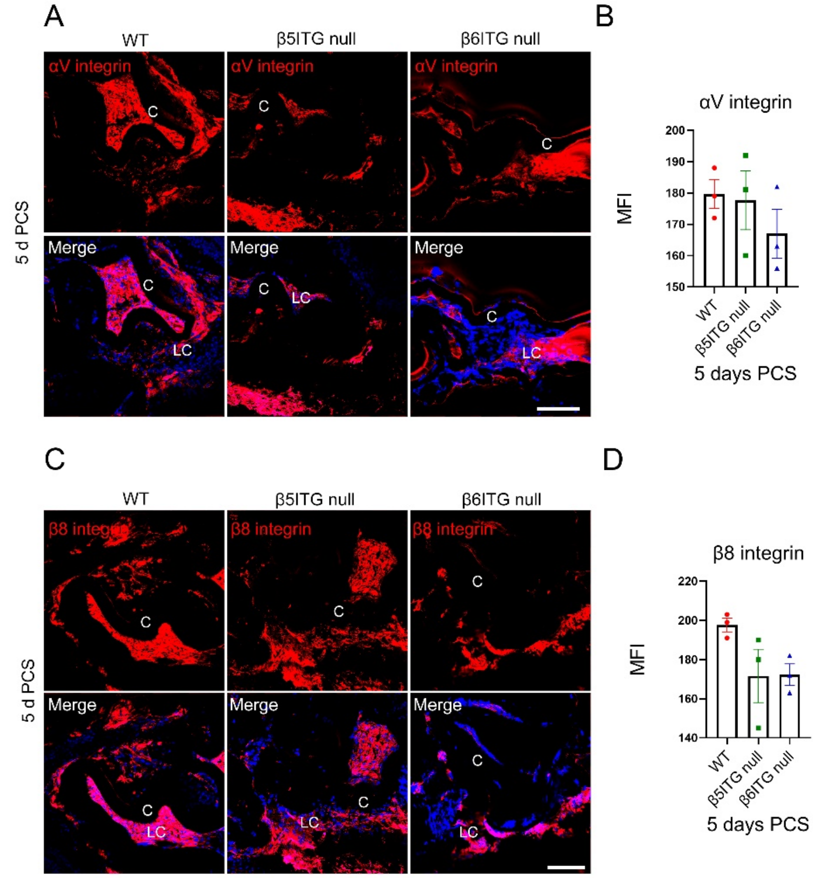
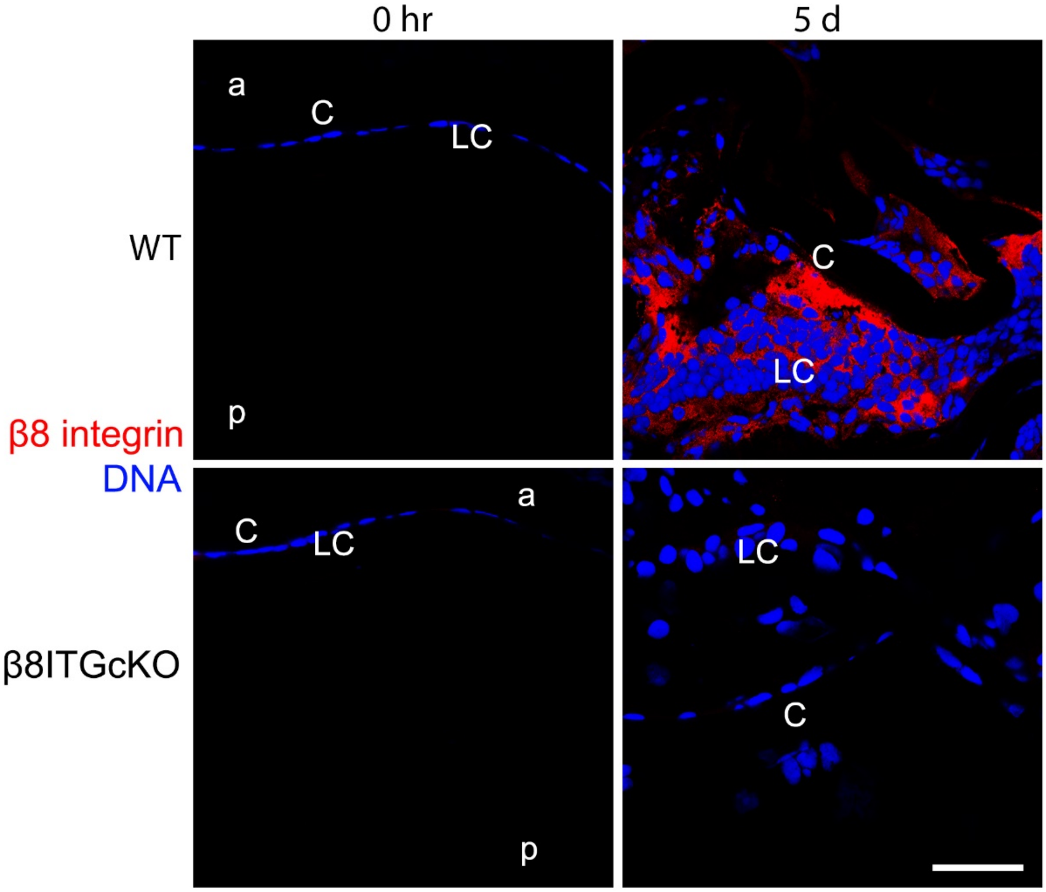
## Supplemental Figure 1



**(A-D)** Deletion of neither β5- nor β6 integrin affect the amount of αV- or β8- integrin protein produced by LCs PCS. All three mice strains (WT, β5ITG null, and β6ITG null) express comparable levels of αV integrin (A, B) and β8 integrin (C, D) protein at 5 d PCS (panels A & B; αV integrin, ( WT vs β5ITG null, $P = 0.981$), (WT vs β6ITG null, $P = 0.5$)); ( panels C & D; β8 integrin, ( WT vs β5ITG null, $P = 0.169$), (WT vs β6ITG null, $P = 0.181$)). C- lens capsule, LC- lens cells, d- day, WT- wildtype, β5ITG- β5 integrin, β6ITG- β6 integrin, blue represents DNA detected by Draq5, red represents αV integrin/ β8 integrin, scale bar- 72 μm. All experiments had N = 3. Values are expressed as mean ± SEM. Asterisks (*) indicate statistically significant MFI between two groups at 5 days PCS ($^{*}P \leq 0.05$; $^{**}P \leq 0.01$; $^{***}P \leq 0.001$); One-way ANOVA with Tukey's post hoc test. Graph legends; red (WT), green (β5ITG null), blue (β6ITG null).

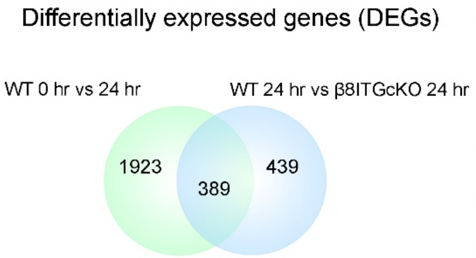
**Supplemental Figure 2**



Immunofluorescence data reveals that the expression of β8 integrin protein (red) is absent both at 0 hour and 5 days post cataract surgery (PCS) in β8ITGcKO lens cells (LCs) while wildtype LCs upregulate robust levels of β8 integrin protein (Red) at 5 days PCS suggesting the successful deletion of β8 integrin gene from the lens in β8ITGcKO. C- lens capsule, LC- lens cells, a- anterior, p- posterior, d- day, hr- hour, WT- wildtype, β8ITGcKO- β8 integrin conditional knockout, blue represents DNA detected by Draq5, scale bar- 36 μm.

## Supplemental Figure 3

A



B

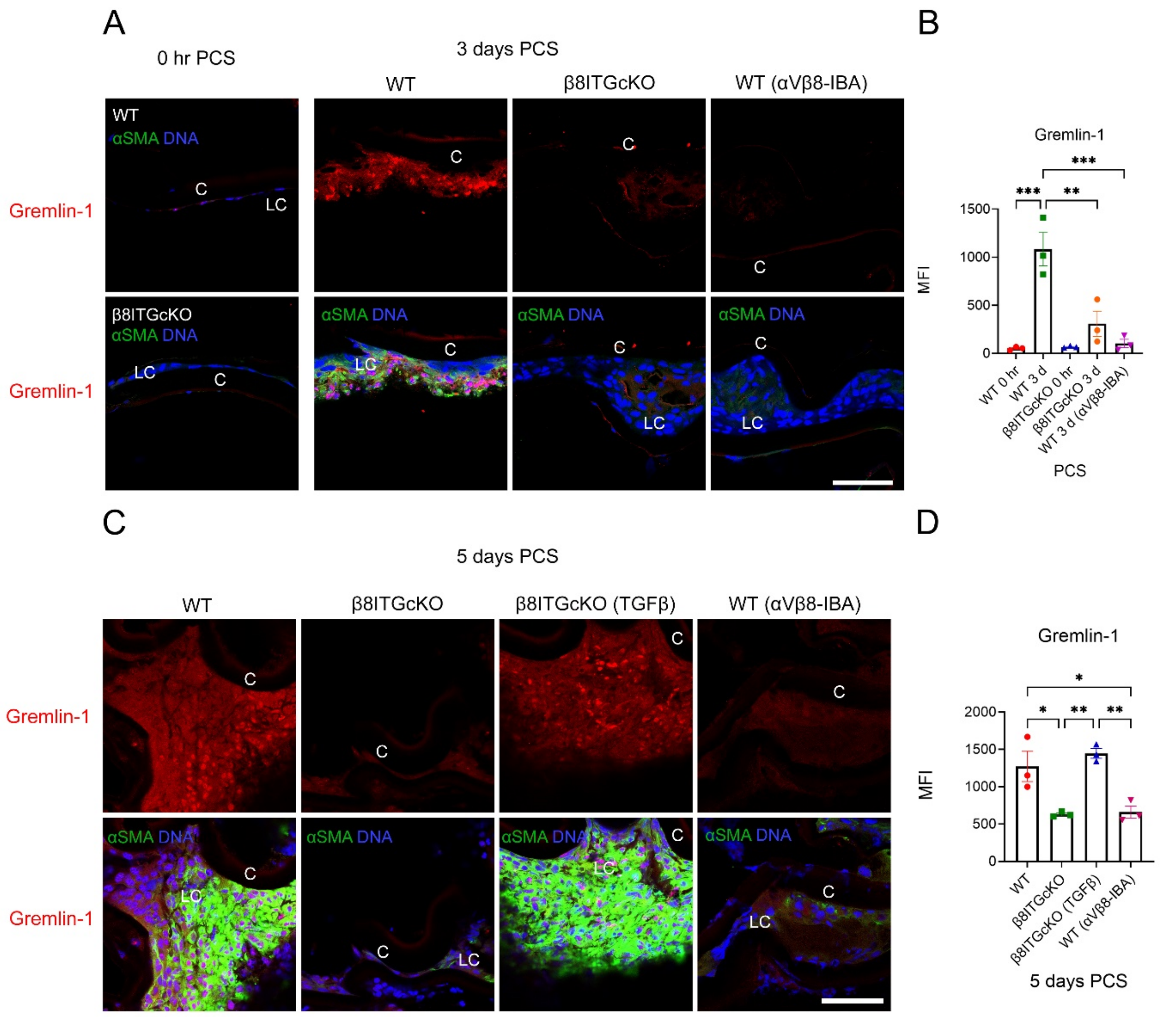
| Differentially expressed genes between Wildtype 0 hour vs 24 hours post cataract surgery (PCS) | Total | Upregulation | Downregulation |
|---|---|---|---|
| | 2312<br>(1923 + 389) | 1273 | 1039 |

| Differentially expressed genes between Wildtype 24 hours vs β8ITGcKO 24 hours post cataract surgery (PCS) | Total | Upregulation | Downregulation |
|---|---|---|---|
| | 828<br>(439 + 389) | 678 | 150 |

| Biologically significant interaction ( 389) | Wildtype 0 hour vs 24 hours PCS (upregulation) | Wildtype 0 hour vs 24 hours PCS ( downregulation) |
|---|---|---|
| Wildtype vs β8ITGcKO- 24 hours PCS ( upregulation) | 17 | 263 |
| Wildtype vs β8ITGcKO- 24 hours PCS ( downregulation) | 102 | 7 |

**(A)** A Venn diagram showing that a total of 2312 genes are differentially expressed (DEGs) in wildtype (WT) remnant lens cells (LCs) at 24-hours post cataract surgery (PCS) compared to 0 hour PCS. The expression levels of 828 genes were significantly different between WT and β8ITGcKO (β8 null) LCs at 24 hours PCS. Of these, 389 DEGs which exhibit altered expression levels (either upregulated or downregulated at 24 hours PCS from 0 hour PCS) in WT LCs in response to lens fiber cell removal, show significantly altered expression (either upregulated or downregulated) in β8ITGcKO LCs at 24 hours PCS. **(B)** A breakdown of the differentially expressed genes between wildtype 0 hour and 24 hours PCS and between wildtype and β8ITGcKO LCs at 24 hours PCS is depicted in a table.

## Supplemental Figure 4

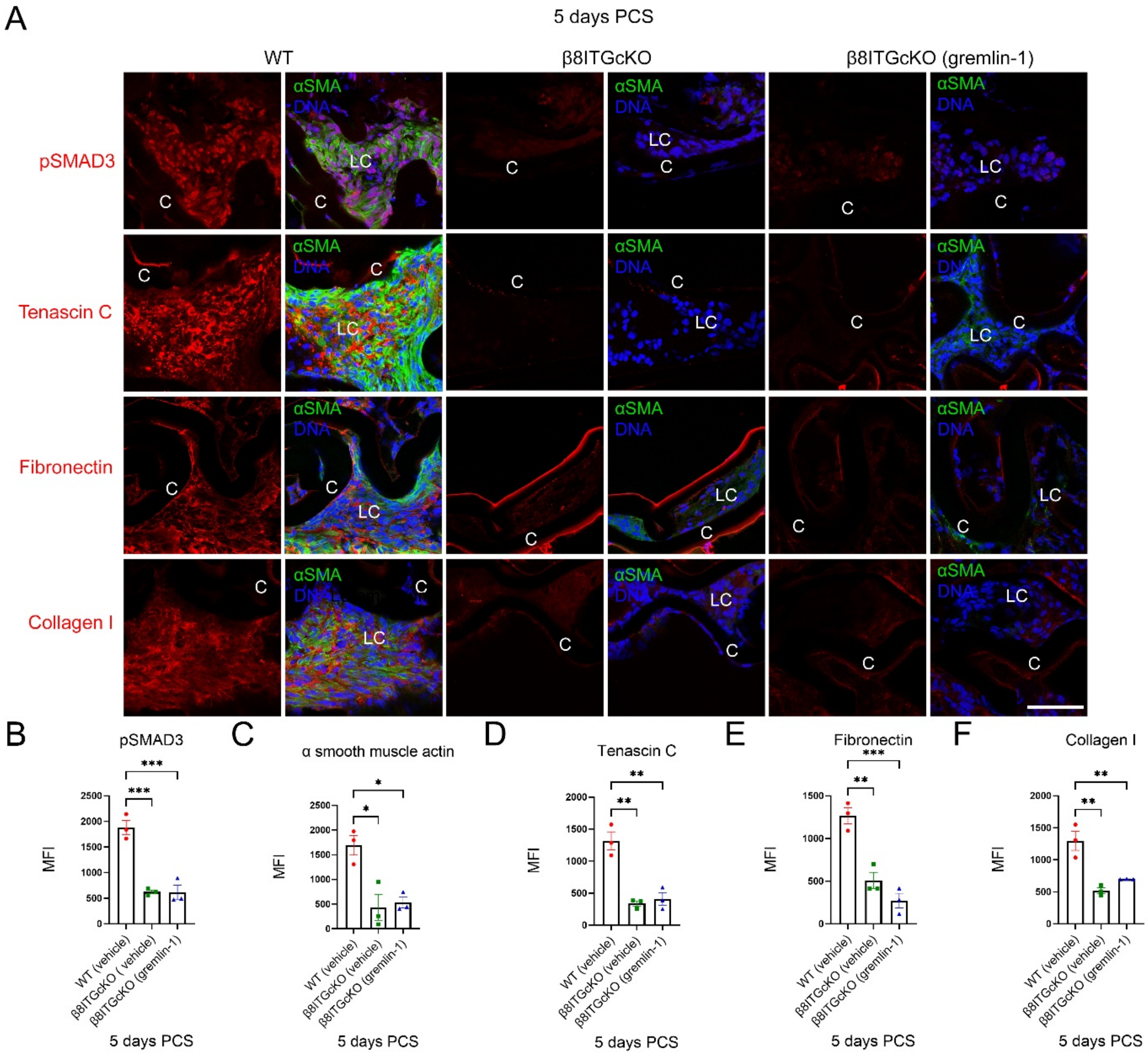


**(A & B)** WT LCs significantly upregulate gremlin-1 protein levels at 3 d PCS (****P* < 0.001) while β8ITGcKO LCs fails to do so compared to WT (***P* = 0.002). The addition of an αVβ8 integrin blocking antibody (αVβ8-IBA) to WT also inhibits the upregulation of gremlin-1 expression compared to WT (****P* < 0.001). **(C, D)** β8ITGcKO LCs exhibited lower gremlin-1 protein levels compared to WT at 5 days PCS (**P* = 0.017) while this phenomenon is rescued by treatment with active TGFβ1 in β8ITGcKO (TGFβ) (***P* = 0.004) LCs at 5 d PCS. Treatment of WT LCs with αVβ8- IBA resulted in a similar inhibition of gremlin-1 levels compared to WT LCs (**P* = 0.022) and β8ITGcKO LCs (*P* = 0.997).

Abbreviations; Scale bar- 35 µm, C- lens capsule, LC- remnant lens cells, MFI- mean fluorescence intensity, PCS- post cataract surgery, αVβ8-IBA- αVβ8 integrin blocking antibody, Control mice were treated with an isotype-matched antibody (anti-human αVβ3 integrin that does not cross-react with the mouse αVβ3 integrin protein); gremlin-1 (red), αSMA (green), DNA detected by Draq5 (blue). All experiments had N = 3. Values are expressed as mean ± SEM. Asterisks (*) indicate statistically significant MFI between WT and/or β8ITGcKO and/or β8ITGcKO (TGFβ) and/or WT (αVβ8-IBA) at a PCS or between two PCS time points (**P* ≤ 0.05; ***P* ≤ 0.01; ****P* ≤ 0.001); Student's t-test (correct for multiple comparisons using the Holm-Šídák method) or one-way ANOVA with Tukey's post hoc test.

Graph legends; (B) red (WT 0 hour), green (WT 3 days), blue (β8ITGcKO 0 hour), orange (β8ITGcKO 3 days), purple (WT 3 days (αVβ8-IBA)); (D)- red (WT), green (β8ITGcKO), blue (β8ITGcKO (TGFβ)), purple (WT (αVβ8-IBA)).

## Supplemental Figure 5



**(A - F)** The addition of gremlin-1 to β8ITGcKO capsular bags does not rescue the defects in LC fibrotic response measured by pSMAD3 activation (panels A & B; *P* > 0.999), αSMA ( panels A & C; *P* = 0.933) , tenascin C (panels A & D; *P* = 0.874), fibronectin ( panels A & E; *P* = 0.241), and collagen I ( panels A & F; *P* = 0.385)  at 5 d PCS compared to β8ITGcKO (vehicle).

Abbreviations: Scale bar- 35 µm, C- lens capsule, LC- remnant lens cells, MFI- mean fluorescence intensity, PCS- post cataract surgery, pSMAD3, Tenascin C, Fibronectin, Collagen I (red), αSMA (green), DNA detected by Draq5 (blue). All experiments had N = 3. Values are expressed as mean ± SEM. Asterisks (*) indicate statistically significant MFI between WT and/or β8ITGcKO and/or β8ITGcKO (gremlin-1) at a PCS (*$P \leq 0.05$; **$P \leq 0.01$; ***$P \leq 0.001$); One-way ANOVA with Tukey's post hoc test.

Graph legends; red (WT), green (β8ITGcKO), blue (β8ITGcKO (gremlin-1)).

**Supplemental Table 1: Primers and PCR conditions used to perform genotyping in this study**

| **Gene** | **Forward Primer** | **Reverse Primer** | **PCR conditions (genotyping)** |
|---|---|---|---|
| β6- integrin (Tail) (64) | 5’-TAAGTGAGTGAACTCCCTGG- 3’ (WT)<br>5’-CAGTAAATCGTTGTCAACAG-3’ (β6-integrin null) | 5’-CAGCAATGAGTGAAAGCCA- 3’ | 1. Initiation/Melting- 94ºC (2 min.)<br>2, Denaturation- 94ºC (1 min.)<br>3. Annealing- 60ºC (1 min.)<br>4. Elongation- 72ºC (1 min.)<br>Steps 2-3-4 cycle in sequence-40 cycles<br>5. Amplification- 72ºC (5 min.)<br>6. Hold- 15ºC<br>band size –wildtype- 450 kb;<br>β6-integrin null- 250 kb; het- both bands. |
| β8- integrin (tail) (65) | 5’-GAGATGCAAGAGTGTTTACC-3’ | 5’-CACTTTAGTATGCTAATGATGG-3’ | 1. Initiation/Melting- 94ºC (5 min.)<br>2, Denaturation- 94ºC (15 sec.)<br>3. Annealing- 65ºC to 55 ºC (↓1ºC/cycle) (30 sec.) for first 10 cycles, next 30 cycles anneal at 55 ºC<br>4. Elongation- 72ºC (40 sec.)<br>Steps 2-3-4 cycle in sequence<br>5. Amplification- 72ºC (5 min.)<br>6. Hold- 15ºC<br>band size –wildtype- 250 kb;<br>β8-integrin floxed – 370 kb; het- both bands.<br>This PCR protocol is developed by MMRRC at the University of California, Davis, USA.<br>https://mmrrc.ucdavis.edu/protocols/014108Geno_Protocol.pdf |
| β8- integrin (lens) (65) | 5′-GTGGTTAAGAGCACCGATTG-3′ (F1)<br>5′-GAGATGCAAGAGTGTTTACC-3′ (F2) | 5′-CACTTTAGTATGCTAATGATG-3′ (R1) | |

**Supplemental Table 2: Primary antibodies used in this study**

| **Primary antibody** | **Fixation** | **Blocking buffer** | **Primary antibody conditions** |
|---|---|---|---|
| Fibronectin (ab2413, Abcam) | 4% PFA | 2% BSA in PBS | 1:200; 1 hour at RT |
| Collagen I (PA5-95137, Invitrogen) | 4% PFA | 5% goat serum and 2% BSA in PBS | 1:100; overnight at 4°C |
| Tenascin C (T3413, Sigma-Aldrich) | 4% PFA | 2% BSA in PBS | 1:200; overnight at 4°C |
| Aquaporin0 (AB3071, Millipore) | 1:1 acetone-methanol | 2% BSA in PBS | 1:200; overnight at 4°C, |
| α-SMA (1A4 F3777 & C6198, Sigma-Aldrich) | 1:1 acetone-methanol | 2% BSA in PBS | 1:250; 1 hour at RT, |
| Ki 67 (D3B5, Cell Signaling) | 4% PFA | Blocking buffer-5% NGS with 0.3 % TritonX-100 in PBS, Antibody buffer- 2% BSA with 0.3% TritonX-100 in PBS | 1:100; overnight at 4°C |
| α5-integrin (ab150361, Abcam) | 4% PFA | 2% BSA and 5% NGS in PBS | 1:200; overnight at 4°C |
| β1-integrin (MAB 1997, Millipore) | 1:1 acetone-methanol | 2% BSA in PBS | 1:100; 1 hour at RT, |
| Phospho- S423/S425 SMAD3 (ab52903, Abcam) | 4% PFA | 10 min. wash in 5% BSA followed by 5% NGS, 10% horse serum and 0.3% Triton X-100 in PBS | 1:100; overnight at 4°C |
| Gremlin-1 (PA5-13123, Invitrogen) | 4% PFA | 5% goat serum and 2% BSA in PBS | 1:200; overnight at 4°C |
| αV-integrin (AB1930, Millipore Sigma) | 4% PFA | 5% goat serum and 2% BSA in PBS | 1:200; overnight at 4°C |
| pFAK (44-624G, Thermofisher) | 4% PFA | 5% goat serum and 2% BSA in PBS | 1:100; overnight at 4°C |
| β8 integrin (ab80673, Abcam) | 4% PFA | 5% goat serum and 2% BSA in PBS | 1:100; overnight at 4°C |
| E-cadherin (24E10) Rabbit mAb #3195, Cell Signaling) | 4% PFA | 5% goat serum and 2% BSA in PBS | 1:100; overnight at 4°C |

## Supplemental Table 3: Secondary antibodies and DNA dye used in this study

| **Reagents** | **conditions** |
|---|---|
| Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 488 (Cat # A-11008, Invitrogen) | 1:200; 1 hour at RT |
| Goat anti-Rat IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 488 (Cat # A-11006, Invitrogen) | 1:200; 1 hour at RT |
| Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 568 (Cat # A-11011, Invitrogen) | 1:200; 1 hour at RT |
| Goat anti-Rat IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 568 (Cat # A-11077, Invitrogen) | 1:200; 1 hour at RT |
| Goat anti-Rabbit IgG (H+L) Cross-Adsorbed Secondary Antibody, Alexa Fluor 647 (Cat # A-21244, Invitrogen) | 1:200; 1 hour at RT |
| Draq-5 (Biostatus Limited) | 1:2000; 1 hour at RT |
| DAPI (Fluoropure D21490, Thermofisher) | 1:2000; 1 hour at RT |

**Supplemental Table 4: Genes known to be involved in inflammation are upregulated by LCs by 24 hr PCS.**

| Gene ID | Gene description | Fold_ Change | FDR | WT_0_Hour_Avg_ FPKM | WT_24_Hour_Avg_ FPKM |
|---|---|---|---|---|---|
| *S100a9* | S100 calcium binding protein A9 (calgranulin B) | ∞ | 3.92E-4 | 0.00 | 36.69 |
| *Cxcl3* | chemokine (C-X-C motif) ligand 3 | ∞ | 3.92E-4 | 0.00 | 33.77 |
| *S100a8* | S100 calcium binding protein A8 (calgranulin A) | ∞ | 3.92E-4 | 0.00 | 20.44 |
| *Csf3* | colony stimulating factor 3 (granulocyte) | 199.24 | 2.76E-2 | 0.24 | 47.06 |
| *Cxcl5* | chemokine (C-X-C motif) ligand 5 | 140.46 | 3.92E-4 | 0.31 | 44.06 |
| *Lcn2* | lipocalin 2 | 123.32 | 3.92E-4 | 28.66 | 3533.70 |
| *Ccl6* | chemokine (C-C motif) ligand 6 | 44.75 | 3.92E-4 | 0.57 | 25.32 |
| *Ptgs2* | prostaglandin-endoperoxide synthase 2 | 29.33 | 3.92E-4 | 0.77 | 22.58 |
| *Ptx3* | pentraxin related gene | 28.99 | 1.05E-3 | 1.95 | 56.58 |
| *Cxcl2* | chemokine (C-X-C motif) ligand 2 | 11.78 | 3.92E-4 | 4.36 | 51.38 |
| *Ier3* | immediate early response 3 | 9.42 | 3.92E-4 | 4.76 | 44.90 |
| *Ctsc* | cathepsin C | 5.02 | 3.92E-4 | 8.48 | 42.60 |
| *Csf1* | colony stimulating factor 1 (macrophage) | 4.98 | 3.92E-4 | 6.45 | 32.15 |
| *Cxcl1* | chemokine (C-X-C motif) ligand 1 | 4.96 | 3.92E-4 | 7.18 | 35.62 |
| *S100a6* | S100 calcium binding protein A6 (calcyclin) | 4.05 | 3.92E-4 | 324.59 | 1314.14 |
| *Ptges2* | prostaglandin E synthase 2 | 3.77 | 3.92E-4 | 2.51 | 9.47 |

**FDR- False Discovery Rate, Avg- Average, FPKM- Fragments Per Kilobase Million**

**∞ Fold change could not be calculated as no RNA molecules were detected in LCs at 0 hours PCS**

**Supplemental Table 5: Genes upregulated in LCs at 24 hr PCS that are known to be involved in fibrosis either in PCO or other systems.**

| Gene ID | Gene description | Fold_ Change | FDR | WT_0_Hour_Avg_ FPKM | WT_24_Hour_Avg_ FPKM |
|---|---|---|---|---|---|
| *Tnc* | tenascin C | 175.38 | 3.92E-4 | 1.01 | 176.76 |
| *Grem1* | gremlin 1, DAN family BMP antagonist | 170.52 | 3.92E-4 | 0.97 | 165.86 |
| *Ecm1* | extracellular matrix protein 1 | 79.11 | 3.92E-4 | 2.00 | 158.17 |
| *Tgfbi* | transforming growth factor, beta induced | 47.81 | 3.92E-4 | 5.80 | 277.16 |
| *Arg1* | arginase, liver | 46.89 | 1.93E-3 | 0.59 | 27.82 |
| *Fn1* | fibronectin 1 | 34.21 | 3.92E-4 | 4.71 | 161.08 |
| *Fbln2* | fibulin 2 | 28.91 | 3.92E-4 | 1.89 | 54.50 |
| *Spp1* | secreted phosphoprotein 1 | 28.19 | 3.92E-4 | 1.02 | 28.89 |
| *Itga7* | integrin alpha 7 | 23.71 | 3.92E-4 | 3.82 | 90.67 |
| *Tagln2* | transgelin 2 | 10.54 | 3.92E-4 | 13.16 | 138.74 |
| *Nes* | nestin | 9.71 | 3.92E-4 | 22.12 | 214.74 |
| *Acta2* | actin, alpha 2, smooth muscle, aorta | 9.71 | 3.92E-4 | 83.37 | 809.26 |
| *Emp1* | epithelial membrane protein 1 | 9.58 | 3.92E-4 | 4.66 | 44.63 |
| *Wisp2* | WNT1 inducible signaling pathway protein 2 | 9.33 | 3.92E-4 | 1.32 | 12.35 |
| *Lox* | lysyl oxidase | 9.31 | 3.92E-4 | 0.57 | 5.32 |
| *Itga5* | integrin alpha 5 (fibronectin receptor alpha) | 9.06 | 3.92E-4 | 7.28 | 65.93 |
| *Emp3* | epithelial membrane protein 3 | 8.01 | 3.92E-4 | 6.19 | 49.55 |
| *Thbs1* | thrombospondin 1 | 6.12 | 3.92E-4 | 7.56 | 46.22 |
| *Runx1* | runt related transcription factor 1 | 6.12 | 3.92E-4 | 4.21 | 25.72 |
| *Col1a1* | collagen, type I, alpha 1 | 5.28 | 3.92E-4 | 2.06 | 10.89 |
| *E2f1* | E2F transcription factor 1 | 3.57 | 3.92E-4 | 1.66 | 5.94 |
| *Ltbp1* | latent transforming growth factor beta binding protein 1 | 3.51 | 3.92E-4 | 31.57 | 110.70 |
| *Tgfb1* | transforming growth factor, beta 1 | 2.70 | 3.92E-4 | 21.88 | 59.05 |
| *Aebp1* | AE binding protein 1 | 3.33 | 3.92E-4 | 32.16 | 107.15 |
| *Mmp14* | matrix metallopeptidase 14 (membrane-inserted) | 2.67 | 3.92E-4 | 7.80 | 20.81 |
| *Itgb1* | integrin beta 1 (fibronectin receptor beta) | 2.58 | 3.92E-4 | 69.11 | 178.41 |
| *Junb* | jun B proto-oncogene | 2.24 | 3.92E-4 | 35.58 | 79.86 |
| *Itgav* | integrin alpha V | 1.89 | 3.92E-4 | 49.77 | 93.90 |

**FDR- False Discovery Rate, Avg- Average, FPKM- Fragments Per Kilobase Million**

**Supplemental Table 6: Genes that are preferentially expressed in the lens or important for the lens cells homeostasis downregulate in LCs by 24 hr PCS.**

| Gene ID | Gene description | Fold_ Change | FDR | WT_0_Hour_Avg_ FPKM | WT_24_Hour_Avg_ FPKM |
|---|---|---|---|---|---|
| *Crygd* | crystallin, gamma D | -352.63 | 1.15E-2 | 236.24 | 0.67 |
| *Crygb* | crystallin, gamma B | -280.30 | 3.92E-4 | 460.69 | 1.64 |
| *Crygc* | crystallin, gamma C | -75.95 | 3.92E-4 | 597.43 | 7.87 |
| *Lenep* | lens epithelial protein | -21.99 | 3.92E-4 | 125.29 | 5.70 |
| *Mip* | major intrinsic protein of lens fiber | -8.58 | 3.92E-4 | 440.29 | 51.29 |
| *Bfsp1* | beaded filament structural protein 1 | -8.55 | 3.92E-4 | 471.63 | 55.17 |
| *Lim2* | lens intrinsic membrane protein 2 | -7.69 | 3.92E-4 | 213.55 | 27.76 |
| *Fgf1* | fibroblast growth factor 1 | -6.76 | 3.92E-4 | 14.89 | 2.20 |
| *Cryba4* | crystallin, beta A4 | -6.70 | 3.92E-4 | 2153.80 | 321.65 |
| *Crybb1* | crystallin, beta B1 | -5.61 | 3.92E-4 | 1660.04 | 295.71 |
| *Crygn* | crystallin, gamma N | -5.53 | 3.92E-4 | 194.88 | 35.23 |
| *Cryba1* | crystallin, beta A1 | -5.43 | 3.92E-4 | 7251.02 | 1335.36 |
| *Lctl* | lactase-like | -4.27 | 3.92E-4 | 50.70 | 11.87 |
| *Gas6* | growth arrest specific 6 | -4.04 | 3.92E-4 | 111.42 | 27.56 |
| *Cryba2* | crystallin, beta A2 | -3.97 | 3.92E-4 | 7397.48 | 1862.57 |
| *Gja3* | gap junction protein, alpha 3 | -3.96 | 3.92E-4 | 203.81 | 51.49 |
| *Dkk3* | dickkopf WNT signaling pathway inhibitor 3 | -3.33 | 3.92E-4 | 1032.30 | 309.94 |
| *Cryab* | crystallin, alpha B | -2.92 | 7.12E-3 | 19582.00 | 6705.13 |
| *Tdrd7* | tudor domain containing 7 | -2.84 | 3.92E-4 | 96.90 | 34.07 |
| *Id3* | inhibitor of DNA binding 3 | -2.66 | 3.92E-4 | 77.94 | 29.29 |
| *Foxe3* | forkhead box E3 | -2.34 | 3.92E-4 | 126.31 | 53.87 |
| *Col4a4* | collagen, type IV, alpha 4 | -2.31 | 1.15E-2 | 194.46 | 84.08 |
| *Col4a3* | collagen, type IV, alpha 3 | -2.29 | 1.93E-3 | 211.67 | 92.42 |
| *Pitx3* | paired-like homeodomain transcription factor 3 | -2.20 | 3.92E-4 | 56.28 | 25.63 |
| *Prox1* | prospero homeobox 1 | -2.15 | 3.92E-4 | 160.02 | 74.56 |

**FDR- False Discovery Rate, Avg- Average, FPKM- Fragments Per Kilobase Million**

**Supplemental Table 7: Genes that normally upregulate in remnant LCs whose upregulation is attenuated in β8ITGcKO LCs at 24 hr PCS**

| Gene ID | WT_0 hr vs 24 hr _FC | WT_0 hr vs 24 hr_ FDR | 24 hr_ WT vs β8ITGcKO_FC | 24 hr_ WT vs β8ITGcKO_FDR | WT 24 hr_ Avg_ FPKM | β8ITGcKO 24 hr_ Avg _FPKM |
|---|---|---|---|---|---|---|
| *Acod1* | ∞ | 3.92E-4 | -2.42 | 9.36E-3 | 4.27 | 1.76 |
| *Acta2* | 9.71 | 3.92E-4 | -2.18 | 1.01E-3 | 869.12 | 399.19 |
| *Akap2* | 2.27 | 6.93E-3 | -2.41 | 1.01E-3 | 55.04 | 22.82 |
| *Ankrd1* | 14.76 | 3.92E-4 | -4.90 | 1.01E-3 | 33.03 | 6.74 |
| *Anxa8* | 58.46 | 2.01E-2 | -3.87 | 1.01E-3 | 22.77 | 5.88 |
| *Apbb1ip* | 11.03 | 3.92E-4 | -2.31 | 1.04E-2 | 4.16 | 1.80 |
| *Apol9a* | 12.57 | 1.05E-3 | -2.40 | 2.73E-2 | 4.93 | 2.06 |
| *Arc* | 2.43 | 3.92E-4 | -2.60 | 1.01E-3 | 19.05 | 7.31 |
| *Asb5* | 4.05 | 1.74E-2 | -5.12 | 2.04E-2 | 4.32 | 0.84 |
| *Blnk* | 6.42 | 3.92E-4 | -2.43 | 1.01E-3 | 9.69 | 3.99 |
| *Calml3* | 2.52 | 3.86E-2 | -15.66 | 6.59E-3 | 4.00 | 0.26 |
| *Car13* | 29.47 | 1.13E-2 | -2.23 | 3.51E-2 | 3.80 | 1.71 |
| *Cbr2* | 5.10 | 3.92E-4 | -2.48 | 4.74E-3 | 16.90 | 6.83 |
| *Cd33* | 22.05 | 3.92E-4 | -3.13 | 1.01E-3 | 4.05 | 1.29 |
| *Cdk15* | 7.65 | 3.92E-4 | -2.37 | 3.07E-2 | 4.81 | 2.03 |
| *Clmp* | 6.55 | 3.92E-4 | -2.52 | 1.01E-3 | 6.62 | 2.63 |
| *Cmss1* | 2.72 | 8.97E-3 | -2.02 | 2.62E-2 | 24.80 | 12.29 |
| *Col6a1* | 2.36 | 3.92E-4 | -2.15 | 1.01E-3 | 22.96 | 10.67 |
| *Crabp2* | 19.91 | 3.92E-4 | -3.49 | 1.01E-3 | 21.17 | 6.06 |
| *Csf3* | 199.24 | 2.76E-2 | -4.86 | 1.01E-3 | 50.87 | 10.47 |
| *Cth* | 2.43 | 5.83E-3 | -2.92 | 4.04E-3 | 6.35 | 2.17 |
| *Cxcl2* | 11.78 | 3.92E-4 | -3.09 | 1.01E-3 | 55.40 | 17.94 |
| *Cxcl5* | 140.46 | 3.92E-4 | -3.83 | 1.01E-3 | 47.41 | 12.39 |

| **Gene ID** | **WT_0 hr vs 24 hr _FC** | **WT_0 hr vs 24 hr_ FDR** | **24 hr_ WT vs β8ITGcKO_FC** | **24 hr_ WT vs β8ITGcKO_FDR** | **WT 24 hr_ Avg_ FPKM** | **β8ITGcKO 24 hr _Avg _FPKM** |
|---|---|---|---|---|---|---|
| *Defb1* | 18.52 | 2.71E-2 | -10.79 | 1.68E-2 | 7.07 | 0.66 |
| *Dsg1b* | 2.61 | 3.92E-4 | -5.32 | 1.01E-3 | 3.72 | 0.70 |
| *Dyrk3* | 3.41 | 2.47E-3 | -2.09 | 2.23E-2 | 4.56 | 2.19 |
| *Ercc1* | 4.16 | 7.36E-4 | -2.53 | 1.40E-2 | 27.49 | 10.88 |
| *Errfi1* | 2.45 | 3.92E-4 | -2.11 | 1.01E-3 | 41.04 | 19.45 |
| *F3* | 8.71 | 3.92E-4 | -2.24 | 1.01E-3 | 31.38 | 14.02 |
| *Fam25c* | 10.70 | 1.82E-2 | -6.11 | 9.36E-3 | 22.71 | 3.71 |
| *Fgl2* | 10.34 | 3.92E-4 | -3.52 | 1.01E-3 | 8.06 | 2.29 |
| *Gch1* | 2.12 | 9.94E-3 | -2.97 | 1.01E-3 | 5.39 | 1.81 |
| *Grem1* | 170.52 | 3.92E-4 | -2.94 | 1.01E-3 | 178.14 | 60.60 |
| *Gsta1* | ∞ | 3.92E-4 | -3.21 | 4.52E-2 | 6.32 | 1.97 |
| *Gsta2* | ∞ | 3.92E-4 | -3.14 | 1.50E-2 | 9.19 | 2.92 |
| *Hdc* | 14.13 | 1.64E-3 | -4.48 | 5.37E-3 | 2.66 | 0.59 |
| *Hp* | ∞ | 3.92E-4 | -3.27 | 1.01E-3 | 7.44 | 2.27 |
| *Ifit1* | 6.44 | 3.92E-4 | -2.93 | 1.01E-3 | 18.61 | 6.35 |
| *Ifit3* | 5.59 | 3.92E-4 | -3.18 | 1.01E-3 | 31.67 | 9.97 |
| *Ifit3b* | 6.57 | 3.92E-4 | -2.60 | 4.74E-3 | 14.44 | 5.54 |
| *Il6ra* | 9.89 | 3.92E-4 | -2.41 | 3.33E-3 | 4.18 | 1.73 |
| *Irak4* | 4.93 | 3.92E-4 | -2.00 | 4.84E-2 | 5.46 | 2.72 |
| *Itga5* | 9.06 | 3.92E-4 | -2.76 | 1.01E-3 | 70.95 | 25.72 |
| *Krt15* | 4.33 | 3.92E-4 | -8.20 | 1.01E-3 | 29.50 | 3.60 |
| *Krt5* | 2.26 | 1.51E-2 | -11.25 | 1.01E-3 | 5.66 | 0.50 |

| Gene ID | WT_0 hr vs 24 hr _FC | WT_0 hr vs 24 hr_ FDR | 24 hr_ WT vs β8ITGcKO_FC | 24 hr_ WT vs β8ITGcKO_FDR | WT 24 hr_ Avg _FPKM | β8ITGcKO 24 hr_ Avg _FPKM |
|---|---|---|---|---|---|---|
| *Krt6a* | 5.83 | 3.92E-4 | -10.69 | 5.37E-3 | 3.60 | 0.34 |
| *Lbp* | 4.53 | 3.92E-4 | -3.07 | 1.01E-3 | 4.58 | 1.49 |
| *Lgals3* | 3.60 | 3.92E-4 | -4.14 | 1.01E-3 | 205.36 | 49.63 |
| *Lmcd1* | 15.38 | 2.04E-2 | -4.13 | 8.35E-3 | 3.47 | 0.84 |
| *Lox* | 9.31 | 3.92E-4 | -2.54 | 1.01E-3 | 5.74 | 2.26 |
| *Ly6a* | 9.13 | 3.92E-4 | -19.01 | 2.62E-3 | 13.92 | 0.73 |
| *Map3k6* | 6.36 | 3.92E-4 | -2.12 | 1.01E-3 | 8.41 | 3.97 |
| *Mmp19* | 4.93 | 9.15E-3 | -2.32 | 4.24E-2 | 5.40 | 2.33 |
| *Mmp3* | ∞ | 3.92E-4 | -2.45 | 1.01E-3 | 15.58 | 6.35 |
| *Mt2* | 2.96 | 3.92E-4 | -2.35 | 1.01E-3 | 205.55 | 87.37 |
| *Nes* | 9.71 | 3.92E-4 | -2.86 | 1.01E-3 | 231.45 | 80.99 |
| *Noct* | 2.71 | 3.92E-4 | -2.16 | 1.01E-3 | 42.35 | 19.64 |
| *Notum* | 3.23 | 3.92E-4 | -2.15 | 1.01E-3 | 10.41 | 4.83 |
| *Nov* | 4.12 | 3.92E-4 | -3.35 | 1.01E-3 | 4.18 | 1.25 |
| *Nppb* | 30.40 | 4.46E-3 | -2.55 | 2.15E-2 | 13.67 | 5.37 |
| *Oas2* | 12.38 | 3.92E-4 | -2.78 | 5.37E-3 | 3.40 | 1.22 |
| *Ocel1* | 3.15 | 9.94E-3 | -2.21 | 4.61E-2 | 4.21 | 1.91 |
| *Pak1* | 3.72 | 3.92E-4 | -2.06 | 1.01E-3 | 10.99 | 5.34 |
| *Phf11d* | 4.79 | 3.92E-4 | -2.80 | 1.01E-3 | 5.19 | 1.85 |
| *Pla2g2e* | ∞ | 3.92E-4 | -10.44 | 4.94E-2 | 2.64 | 0.25 |
| *Prrx2* | 2.45 | 4.25E-2 | -2.76 | 2.70E-2 | 4.54 | 1.65 |
| *Ptgs2* | 29.33 | 3.92E-4 | -2.50 | 1.01E-3 | 24.39 | 9.75 |
| *Ptx3* | 28.99 | 1.05E-3 | -3.03 | 1.01E-3 | 60.89 | 20.12 |

| **Gene ID** | **WT_0 hr vs 24 hr _FC** | **WT_0 hr vs 24 hr_ FDR** | **24 hr_ WT vs β8ITGcKO_FC** | **24 hr_ WT vs β8ITGcKO_FDR** | **WT 24 hr_ Avg _FPKM** | **β8ITGcKO 24 hr_ Avg_ FPKM** |
|---|---|---|---|---|---|---|
| *Pxdc1* | 2.93 | 7.36E-4 | -2.02 | 1.96E-2 | 8.78 | 4.34 |
| *Rhox8* | 4.28 | 2.99E-3 | -3.19 | 7.15E-3 | 5.99 | 1.88 |
| *Rnf125* | 20.31 | 3.92E-4 | -2.43 | 1.01E-3 | 18.73 | 7.71 |
| *Rsad2* | 24.10 | 3.92E-4 | -4.66 | 1.01E-3 | 8.24 | 1.77 |
| *S100a8* | ∞ | 3.92E-4 | -3.34 | 1.78E-2 | 21.86 | 6.54 |
| *S100a9* | ∞ | 3.92E-4 | -2.51 | 3.33E-3 | 39.28 | 15.67 |
| *Serpina3h* | 3.35 | 2.74E-3 | -21.48 | 4.74E-3 | 4.40 | 0.20 |
| *Serpinb6b* | 3.43 | 3.92E-4 | -4.48 | 1.01E-3 | 37.74 | 8.42 |
| *Serpine1* | 36.42 | 3.92E-4 | -2.32 | 1.01E-3 | 432.22 | 186.00 |
| *Sfn* | 2.05 | 2.99E-3 | -11.68 | 1.01E-3 | 14.60 | 1.25 |
| *Slco2a1* | 7.02 | 3.92E-4 | -2.23 | 1.01E-3 | 21.12 | 9.47 |
| *Slfn1* | 79.05 | 2.64E-2 | -2.26 | 7.15E-3 | 7.49 | 3.32 |
| *Slfn4* | ∞ | 3.92E-4 | -3.52 | 1.01E-3 | 37.08 | 10.53 |
| *Slpi* | ∞ | 3.92E-4 | -3.51 | 2.81E-2 | 4.82 | 1.37 |
| *Snai1* | 5.46 | 3.72E-3 | -2.69 | 3.07E-2 | 3.46 | 1.29 |
| *Sprr1a* | 24.75 | 3.92E-4 | -4.39 | 1.01E-3 | 82.49 | 18.77 |
| *Sprr2b* | ∞ | 3.92E-4 | ∞ | 1.01E-3 | 2.67 | 0.00 |
| *Stac* | 2.74 | 3.92E-4 | -2.88 | 1.01E-3 | 9.28 | 3.22 |
| *Stat5a* | 2.80 | 3.92E-4 | -2.38 | 1.01E-3 | 8.65 | 3.64 |
| *Syt17* | 2.37 | 2.20E-3 | -3.31 | 1.01E-3 | 9.84 | 2.98 |

| Gene ID | WT_0 hr vs 24 hr _FC | WT_0 hr vs 24 hr_ FDR | 24 hr_ WT vs β8ITGcKO_FC | 24 hr_ WT vs β8ITGcKO_FDR | WT 24 hr_ Avg _FPKM | β8ITGcKO 24 hr_ Avg_ FPKM |
|---|---|---|---|---|---|---|
| *Tgm1* | 11.21 | 3.92E-4 | -4.83 | 1.01E-3 | 12.74 | 2.64 |
| *Thbs1* | 6.12 | 3.92E-4 | -2.23 | 1.01E-3 | 49.51 | 22.17 |
| *Tm4sf1* | 2.74 | 3.92E-4 | -2.31 | 1.01E-3 | 106.45 | 46.00 |
| *Tpd52l1* | 2.08 | 5.15E-3 | -2.06 | 5.99E-3 | 15.26 | 7.40 |
| *Trim30c* | ∞ | 3.92E-4 | -5.24 | 3.42E-2 | 2.89 | 0.55 |
| *Tuba1c* | 3.97 | 3.92E-4 | -2.27 | 1.01E-3 | 34.21 | 15.08 |
| *Vaultrc5* | 11.64 | 3.92E-4 | -3.05 | 1.01E-3 | 123.45 | 40.41 |
| *Xaf1* | 6.28 | 3.92E-4 | -2.23 | 5.37E-3 | 16.33 | 7.33 |

**FC- Fold Change, WT- Wild Type, β8ITGcKO - β8 integrin conditional knockout, FDR- False Discovery Rate, Avg- Average, Hr- hour, FPKM- Fragments Per Kilobase Million, ∞ indicates that fold-change did not give a numerical value as FPKM of a specific gene appears 0 at WT 0 hour PCS**

**Supplemental Table 8: Attenuated upregulation of 23 genes known to be involved in fibrosis and inflammation was observed in remnant β8ITGcKO LCs at 24 hr PCS. Wildtype LCs typically upregulate the transcription of these genes in response to injury**

| Gene ID | Gene description | Fold_ Change | FDR | WT_24_Hour_ Avg_FPKM | β8ITGcKO_ 24_Hour_Avg_ FPKM |
|---|---|---|---|---|---|
| *Csf3* | colony stimulating factor 3 (granulocyte) | -4.86 | 1.01E-3 | 50.87 | 10.47 |
| *Pttg1* | pituitary tumor-transforming gene 1 | -4.78 | 1.01E-3 | 11.91 | 2.49 |
| *Mylk2* | myosin, light polypeptide kinase 2, skeletal muscle8 | -4.15 | 1.01E-3 | 3.49 | 0.84 |
| *Anxa8* | annexin A8 | -3.87 | 1.01E-3 | 22.77 | 5.88 |
| *Cxcl5* | chemokine (C-X-C motif) ligand 5 | -3.83 | 1.01E-3 | 47.41 | 12.39 |
| *S100a8* | S100 calcium binding protein A8 (calgranulin A) | -3.34 | 1.78E-2 | 21.86 | 6.54 |
| *Ccl5* | chemokine (C-C motif) ligand 5 | -3.14 | 1.01E-3 | 85.11 | 27.08 |
| *Ptx3* | pentraxin related gene | -3.03 | 1.01E-3 | 60.89 | 20.12 |
| *Grem1* | gremlin 1, DAN family BMP antagonist | -2.94 | 1.01E-3 | 178.14 | 60.60 |
| *Nes* | nestin | -2.86 | 1.01E-3 | 231.45 | 80.99 |
| *Itga5* | integrin alpha 5 (fibronectin receptor alpha) | -2.76 | 1.01E-3 | 70.95 | 25.72 |
| *Snai1* | snail family zinc finger 1 | -2.69 | 3.07E-2 | 3.46 | 1.29 |
| *Lox* | lysyl oxidaseal | -2.54 | 1.01E-3 | 5.74 | 2.26 |
| *S100a9* | S100 calcium binding protein A9 (calgranulin B) | -2.51 | 3.33E-3 | 39.28 | 15.67 |
| *Ptgs2* | prostaglandin-endoperoxide synthase 2 | -2.50 | 1.01E-3 | 24.39 | 9.75 |
| *Mmp3* | matrix metallopeptidase 3 | -2.45 | 1.01E-3 | 15.58 | 6.35 |
| *Mmp19* | matrix metallopeptidase 19 | -2.32 | 4.24E-2 | 5.40 | 2.33 |
| *Thbs1* | thrombospondin 1 | -2.23 | 1.01E-3 | 49.51 | 22.17 |
| *Acta2* | actin, alpha 2, smooth muscle, aorta | -2.18 | 1.01E-3 | 869.12 | 399.19 |
| *Tnc* | tenascin C | -1.47 | 9.77E-2 | 189.85 | 128.98 |
| *Fn1* | fibronectin 1 | -1.44 | 1.19E-1 | 172.91 | 119.86 |
| *Itgb1* | integrin beta 1 (fibronectin receptor beta) | -1.31 | 1.76E-1 | 191.15 | 146.02 |
| *Itgav* | integrin alpha V | -1.24 | 3.30E-1 | 100.72 | 81.24 |

**FDR- False Discovery Rate, Avg- Average, FPKM- Fragments Per Kilobase Million**

**Supplemental Table 9: Table of 60 TGFβ1 responsive genes that upregulate more robustly in injured wildtype lenses than in injured β8ITGcKO lenses. Transcription of these 60 genes is consistently upregulated in cultured primary cells stimulated with TGFβ1** (32)

| Gene ID | 24H_β8ITGcKO vs WT_ Fold_ Change | 24H_β8ITGcKO vs WT_FDR | 24H_ WT _ Avg _FPKM | 24H_β8ITGcKO _Avg_ FPKM |
|---|---|---|---|---|
| *Actn1* | -1.48 | 4.05E-2 | 305.75 | 206.84 |
| *Adam12* | -1.44 | 3.47E-2 | 27.47 | 19.04 |
| *Adam19* | -2.59 | 1.84E-3 | 1.61 | 0.62 |
| *Ankrd1* | -4.90 | 1.01E-3 | 33.03 | 6.74 |
| *Ano6* | -1.65 | 1.01E-3 | 28.10 | 17.08 |
| *Arpc5* | -1.43 | 3.91E-2 | 48.02 | 33.55 |
| *Cald1* | -1.53 | 4.38E-2 | 365.52 | 238.90 |
| *Ccdc80* | -1.85 | 1.01E-3 | 39.76 | 21.46 |
| *Cilp* | -5.14 | 2.15E-2 | 2.91 | 0.57 |
| *Crlf1* | -1.83 | 2.77E-2 | 11.14 | 6.10 |
| *Ctgf* | -1.92 | 1.01E-3 | 269.86 | 140.67 |
| *Dsp* | -6.95 | 1.01E-3 | 1.93 | 0.28 |
| *Dstn* | -1.55 | 1.01E-3 | 170.58 | 110.38 |
| *Dynlt3* | -1.59 | 8.35E-3 | 33.16 | 20.83 |
| *Etv6* | -1.55 | 5.99E-3 | 23.02 | 14.88 |
| *F3* | -2.24 | 1.01E-3 | 31.38 | 14.02 |
| *Fam114a1* | -1.54 | 9.88E-3 | 30.77 | 19.97 |
| *Fam46a* | -1.76 | 1.35E-2 | 4.07 | 2.31 |
| *Fermt2* | -1.46 | 2.07E-2 | 87.91 | 60.06 |
| *Flnc* | -1.72 | 1.01E-3 | 98.61 | 57.41 |

| Gene ID | 24H_β8ITGcKO vs WT_ Fold_ Change | 24H_β8ITGcKO vs WT_FDR | 24H_ WT _ Avg _FPKM | 24H_β8ITGcKO_ Avg_ FPKM |
|---|---|---|---|---|
| *Glipr2* | -1.98 | 1.01E-3 | 16.96 | 8.58 |
| *Hras* | -1.48 | 4.61E-2 | 53.01 | 35.93 |
| *Hspb1* | -1.96 | 1.01E-3 | 63.06 | 32.12 |
| *Inhba* | -1.69 | 1.84E-3 | 97.77 | 57.88 |
| *Inppl1* | -1.46 | 2.28E-2 | 23.60 | 16.21 |
| *Itga5* | -2.76 | 1.01E-3 | 70.95 | 25.72 |
| *Itpripl2* | -1.55 | 4.04E-3 | 24.77 | 16.02 |
| *Ivns1abp* | -1.64 | 9.36E-3 | 378.68 | 230.49 |
| *Krt7* | -7.21 | 2.15E-2 | 2.18 | 0.30 |
| *Lif* | -1.94 | 1.01E-3 | 33.00 | 17.02 |
| *Lmcd1* | -4.13 | 8.35E-3 | 3.47 | 0.84 |
| *Lox* | -2.54 | 1.01E-3 | 5.74 | 2.26 |
| *Msn* | -1.51 | 3.59E-2 | 331.42 | 219.50 |
| *Myl6* | -1.47 | 1.87E-2 | 451.22 | 306.63 |
| *Myl9* | -1.77 | 1.01E-3 | 57.99 | 32.78 |
| *Noct* | -2.16 | 1.01E-3 | 42.35 | 19.64 |
| *Palld* | -1.63 | 1.01E-3 | 150.24 | 92.40 |
| *Pdlim5* | -1.60 | 4.04E-3 | 34.74 | 21.71 |
| *Plaur* | -1.47 | 3.59E-2 | 61.90 | 42.21 |
| *Pnp* | -1.66 | 1.04E-2 | 12.19 | 7.33 |

| Gene ID | 24H_β8ITGcKO vs WT_ Fold_ Change | 24H_β8ITGcKO vs WT_FDR | 24H_ WT _ Avg _FPKM | 24H_β8ITGcKO_Avg_ FPKM |
|---|---|---|---|---|
| *Polr3d* | -1.50 | 2.43E-2 | 33.30 | 22.24 |
| *Ppp1r14b* | -1.63 | 5.37E-3 | 94.53 | 58.04 |
| *Prdx1* | -1.53 | 5.37E-3 | 134.90 | 87.90 |
| *Ptgs2* | -2.50 | 1.01E-3 | 24.39 | 9.75 |
| *Pxdc1* | -2.02 | 1.96E-2 | 8.78 | 4.34 |
| *Rsu1* | -1.46 | 3.59E-2 | 42.21 | 28.85 |
| *Runx1* | -1.43 | 2.39E-2 | 27.58 | 19.29 |
| *S100a11* | -1.46 | 2.51E-2 | 360.18 | 247.22 |
| *Serpine1* | -2.32 | 1.01E-3 | 432.22 | 186.00 |
| *Smad7* | -1.41 | 4.63E-2 | 27.48 | 19.51 |
| *Smim3* | -1.55 | 2.36E-2 | 34.50 | 22.21 |
| *Snai1* | -2.69 | 3.07E-2 | 3.46 | 1.29 |
| *Specc1* | -1.54 | 6.59E-3 | 36.56 | 23.78 |
| *Sphk1* | -1.85 | 1.73E-2 | 11.17 | 6.04 |
| *Tdg* | -1.91 | 4.04E-3 | 9.19 | 4.82 |
| *Tgfb1* | -1.42 | 3.73E-2 | 63.29 | 44.71 |
| *Tpm1* | -1.76 | 1.01E-3 | 526.99 | 299.04 |
| *Tpm4* | -1.57 | 5.37E-3 | 234.08 | 148.73 |
| *Trib1* | -1.48 | 9.88E-3 | 51.10 | 34.47 |
| *Tubb6* | -1.76 | 1.01E-3 | 182.83 | 103.71 |

**H- Hour; FDR- False Discovery Rate; Avg- Average; FPKM- Fragments Per Kilobase Million.**

**Supplemental Table 10: Table of 47 TGFβ1 inhibited genes that downregulate more robustly in injured wildtype lenses than in injured β8ITGcKO lenses. Transcription of these 47 genes decreases significantly 24 hours after injury, less so in β8ITGcKO lenses than in wildtype lenses. Transcription of these 47 genes is consistently downregulated in cultured primary cells stimulated with TGFβ1**(32)

| **Gene ID** | **24H_β8ITGcKO vs WT_ Fold_ Change** | **24H_β8ITGcKO vs WT_FDR** | **24H_ WT _Avg _FPKM** | **24H_β8ITGcKO_ Avg_ FPKM** |
|---|---|---|---|---|
| *Acss2* | 2.23 | 2.28E-2 | 1.42 | 3.18 |
| *Ank1* | 3.55 | 1.01E-3 | 0.57 | 2.01 |
| *Ankrd33b* | 2.67 | 1.01E-3 | 9.96 | 26.62 |
| *Arhgef26* | 4.45 | 1.01E-3 | 1.65 | 7.33 |
| *Bbs1* | 1.95 | 2.62E-3 | 2.38 | 4.65 |
| *Bbs2* | 1.88 | 2.00E-2 | 2.90 | 5.46 |
| *Bmper* | 2.23 | 2.23E-2 | 1.10 | 2.46 |
| *Cers4* | 2.03 | 1.01E-3 | 7.82 | 15.88 |
| *Cntnap1* | 2.13 | 1.01E-3 | 2.29 | 4.89 |
| *Dennd6b* | 2.47 | 1.01E-3 | 1.19 | 2.94 |
| *Frmpd4* | 1.79 | 1.91E-2 | 1.55 | 2.78 |
| *Fyco1* | 2.08 | 1.01E-3 | 14.44 | 30.05 |
| *Fzd5* | 1.54 | 3.07E-2 | 4.05 | 6.23 |
| *Ggt7* | 4.34 | 2.62E-3 | 0.66 | 2.85 |
| *Gpx3* | 1.83 | 5.37E-3 | 99.13 | 181.73 |
| *Gucy1b3* | 13.53 | 1.01E-3 | 0.24 | 3.31 |

| **Gene ID** | **24H_β8ITGcKO vs WT_ Fold_ Change** | **24H_β8ITGcKO vs WT_FDR** | **24H_ WT _Avg _FPKM** | **24H_β8ITGcKO_ Avg_ FPKM** |
|---|---|---|---|---|
| *Hmgb2* | 1.54 | 2.96E-2 | 41.03 | 63.09 |
| *Hsbp1l1* | 11.27 | 4.88E-2 | 0.13 | 1.49 |
| *Igfbp4* | 2.07 | 1.01E-3 | 15.86 | 32.79 |
| *Kbtbd3* | 2.54 | 1.14E-2 | 1.33 | 3.38 |
| *Kcnb1* | 7.22 | 1.01E-3 | 4.09 | 29.52 |
| *Klhl36* | 3.02 | 1.01E-3 | 4.24 | 12.81 |
| *Letm2* | 2.41 | 1.68E-2 | 1.32 | 3.18 |
| *Lpin1* | 1.69 | 3.27E-2 | 3.01 | 5.09 |
| *Magi2* | 1.51 | 4.08E-2 | 5.89 | 8.90 |
| *Map3k1* | 1.72 | 1.01E-3 | 17.36 | 29.92 |
| *Mctp1* | 4.13 | 4.74E-3 | 0.26 | 1.06 |
| *Mllt6* | 1.70 | 1.01E-3 | 14.48 | 24.56 |
| *N4bp2l1* | 3.51 | 2.85E-2 | 0.57 | 2.01 |
| *Nlgn1* | 2.47 | 1.01E-3 | 1.38 | 3.39 |
| *Osbp2* | 4.04 | 1.01E-3 | 5.45 | 22.02 |
| *Plekha6* | 3.59 | 1.01E-3 | 2.51 | 8.99 |
| *Plekhm3* | 1.51 | 3.00E-2 | 3.89 | 5.89 |
| *Ptp4a3* | 4.15 | 1.01E-3 | 11.49 | 47.66 |
| *Rufy3* | 1.57 | 2.39E-2 | 20.45 | 32.18 |

| **Gene ID** | **24H_β8ITGcKO vs WT_ Fold_ Change** | **24H_β8ITGcKO vs WT_FDR** | **24H_ WT _Avg _FPKM** | **24H_β8ITGcKO_ Avg_ FPKM** |
|---|---|---|---|---|
| *Shank2* | 2.14 | 4.74E-3 | 2.05 | 4.39 |
| *Stom* | 1.78 | 2.12E-2 | 4.23 | 7.55 |
| *Stx3* | 3.10 | 1.01E-3 | 11.79 | 36.54 |
| *Syne2* | 1.46 | 1.40E-2 | 14.31 | 20.95 |
| *Tbc1d8* | 4.78 | 1.68E-2 | 1.76 | 8.43 |
| *Tcea3* | 2.65 | 1.04E-2 | 3.09 | 8.17 |
| *Thsd7a* | 1.93 | 1.01E-3 | 2.26 | 4.35 |
| *Tnfsf10* | 2.08 | 1.68E-2 | 1.27 | 2.64 |
| *Trnp1* | 2.90 | 1.01E-3 | 7.16 | 20.77 |
| *Tub* | 5.13 | 1.01E-3 | 2.65 | 13.58 |
| *Vps13c* | 1.47 | 1.91E-2 | 8.72 | 12.85 |
| *Whamm* | 1.77 | 5.99E-3 | 8.41 | 14.91 |

**H- Hour; FDR- False Discovery Rate; Avg- Average; FPKM- Fragments Per Kilobase Million**