

## Identification of novel predictive factors for post surgical corneal haze

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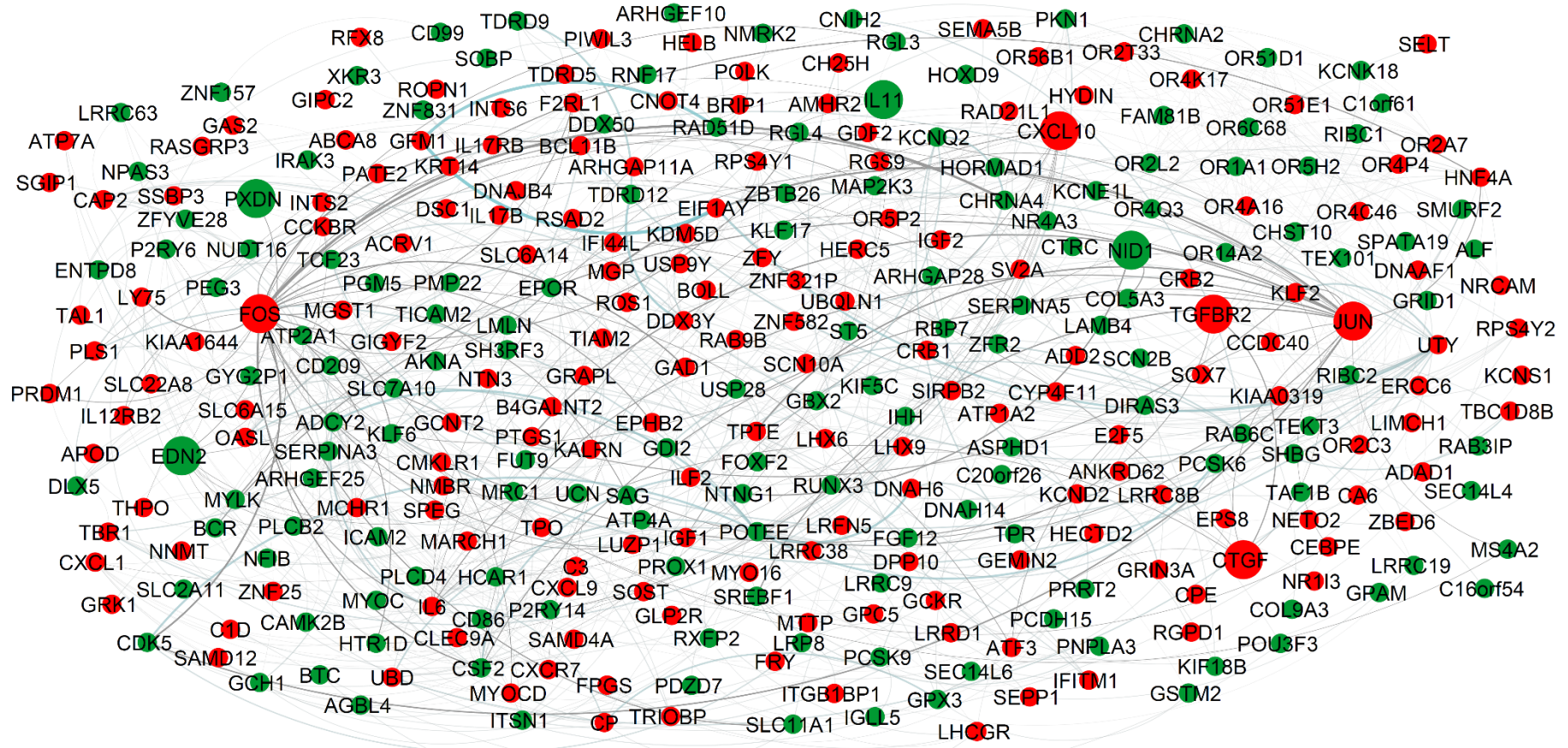
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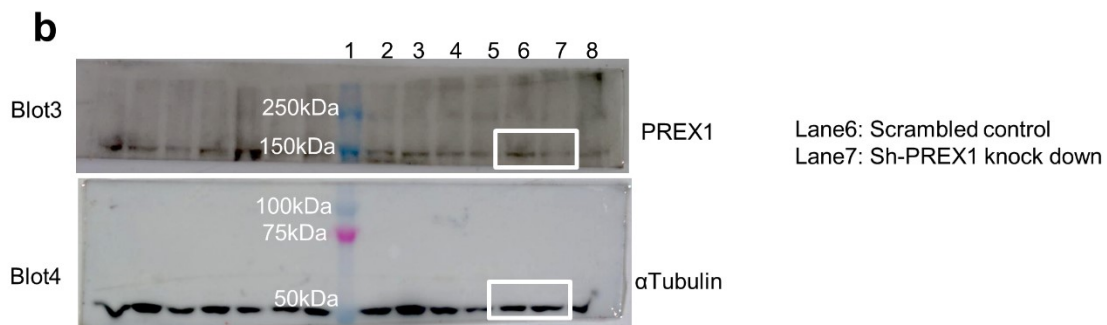
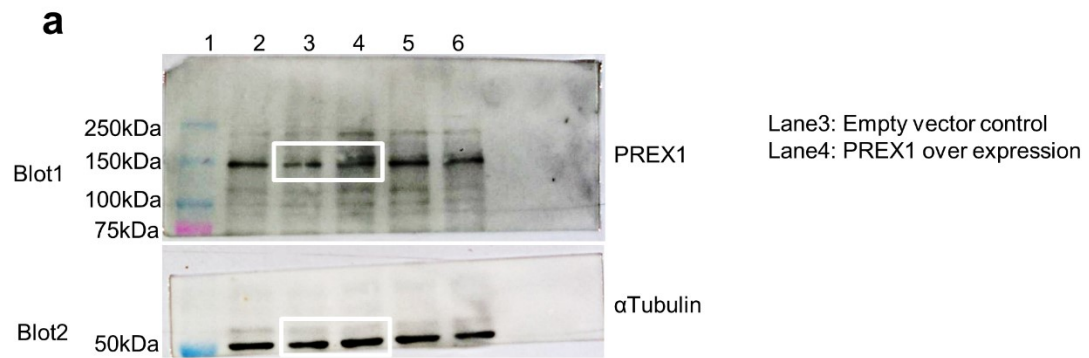
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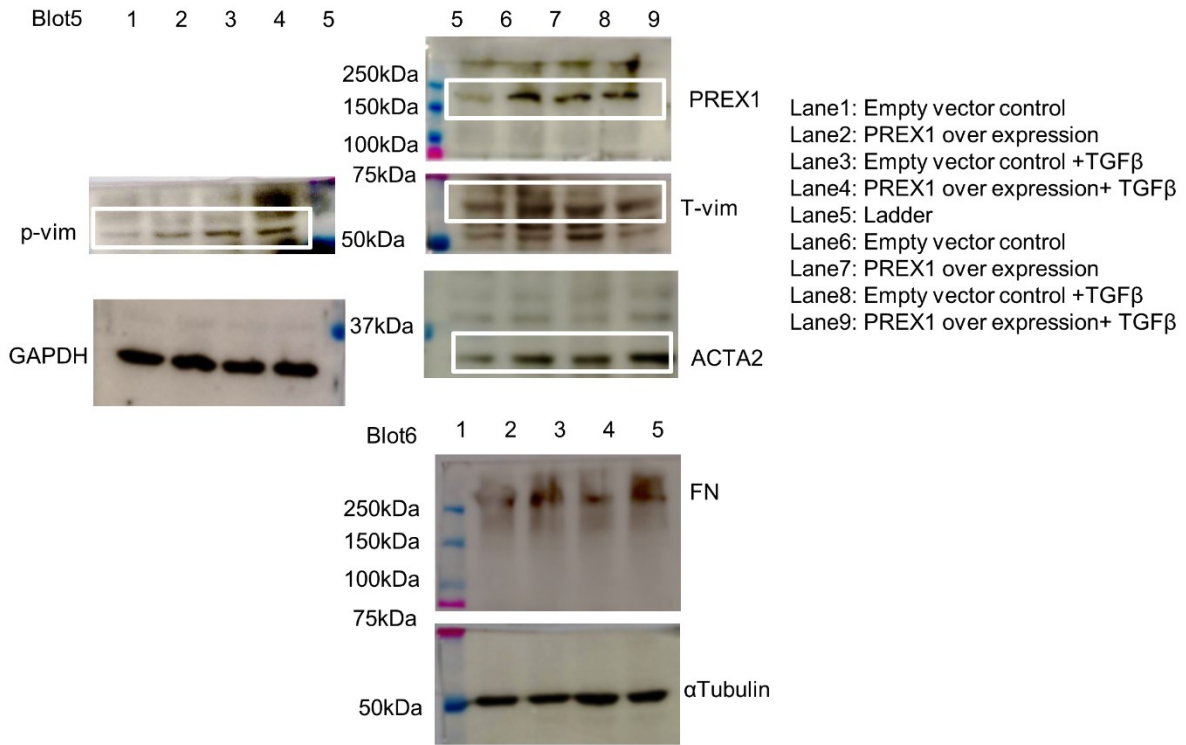


**Supplementary figure1:** Represents the network analysis showing 327 differentially expressed genes cut off  $> \pm 2$  fold change ( $p$ -value $<0.05$ ) in microarray and their protein- protein interactions. The network analysis suggested that c-FOS, IL6, c-JUN, CXCL10, EDN2, IL1 and IL11 with node degrees of 34, 26, 23, 13, 9, 8 and 5 forms the backbone of the network architecture. The size of the circle (node) represents the fold change between control and haze predisposition (red color signifies down regulation and green color signifies up regulation).

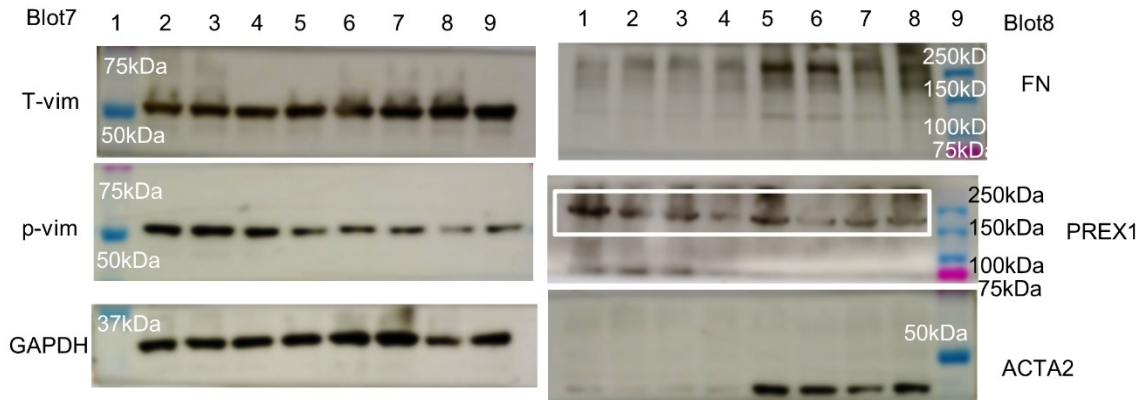


**Supplementary figure2:** Represents unedited western blot images used in the figure 4c and 5c. Panel (a) consists of blot1 representing PREX1 protein expression from empty vector transfected control (lane3) and PREX1 over expression plasmid transfected (lane4) and corresponding  $\alpha$ -tubulin in blot2 marked within white square box, shown in figure4c. Panel (b) consists of blot3 representing PREX1 protein in scrambled control (lane 6) and sh-PREX1 knock down (lane 7) with their corresponding  $\alpha$ -tubulin in blot4, delineated with white box and shown in figure5c.

**c**



**d**



Lane1: Ladder  
Lane2: Scrambled control  
Lane3: Sh-PREX1 knock down  
Lane4: : Sh-PREX1 knock down  
Lane5: : Sh-PREX1 knock down  
Lane6: Scrambled control + TGF $\beta$   
Lane7: Sh-PREX1 knock down +TGF $\beta$   
Lane8: Sh-PREX1 knock down +TGF $\beta$   
Lane9: Sh-PREX1 knock down +TGF $\beta$

Lane1: Scrambled control  
Lane2: Sh-PREX1 knock down  
Lane3: : Sh-PREX1 knock down  
Lane4: : Sh-PREX1 knock down  
Lane5: Scrambled control + TGF $\beta$   
Lane6: Sh-PREX1 knock down +TGF $\beta$   
Lane7: Sh-PREX1 knock down +TGF $\beta$   
Lane8: Sh-PREX1 knock down +TGF $\beta$   
Lane9: Ladder

**Supplementary figure2:** Represents unedited western blot images used in the figure 4h and 5h. Panel (c) consists of blot5 representing PREX1 overexpression with empty controls in human corneal epithelial cells. Lane1-9 represents the sample conditions loaded for protein analysis of p-vim, GAPDH, FN, PREX1, T-vim and ACTA2 marked within white square box, shown in figure 4h. Blot6 represents FN and its corresponding loading control tubulin. Panel (d) consists of blot 7 representing PREX1 knockdowns with scrambled control in human corneal epithelial cells. Lane1-9 represents the sample conditions loaded for protein analysis of T-vim, p-vim and GAPDH. Blot 8, lane 1-9 represents the sample conditions loaded for protein analysis of FN, PREX1 and ACTA2 marked within white square box, shown in figure 5h.