A) Module 1 (N = 293; p < 0.01):
Built around DCN, MMP2, LAMB2, LAMB3, LAMC2, and COL17A1
Involved in TGF-beta signaling, focal adhesion, and glycosaminoglycan biosynthesis

B) Module 2 (N = 242; p < 0.01):
Built around LAT, HLA-DRA, HLA-DQA2, CD74, HLA-DOA, HLA-E, HLA-G, HLA-DPA1, CTSS, HLA-DMB, HLA-F, B2M, TAP1, and TAP2
Involved in antigen processing/presentation and allograft rejection

C) Module 3 (N = 247; p < 0.01):
Built around AP2A2
Involved in antigen processing/presentation and allograft rejection
D) Module 4 (N = 221; p < 0.01):  
Built around SLC35B3  
Involved in TGF-beta signaling, focal adhesion, and glycosaminoglycan biosynthesis

E) Module 5 (N = 65; p < 0.01):  
Built around B4GALT1, LUM, ST3GAL1, ST3GAL4, MUC15, B3GNT5, and C1GALT1  
Involved in TGF-beta signaling, focal adhesion, and glycosaminoglycan biosynthesis

F) Module 6 (N = 162; p < 0.01):  
Built around ITGB3  
Involved in TGF-beta signaling, focal adhesion, and glycosaminoglycan biosynthesis

G) Module 7 (N = 157; p < 0.01):  
Built around GLCE, APOE, RBP1, ITGAM, SDC1, ITGAL, ITGAX, SDC4, and ICAM3  
Involved in TGF-beta signaling, focal adhesion, and glycosaminoglycan biosynthesis
H) Module 8 (N = 75; p < 0.01):
Built around CSF2RB and STAT5B
Involved in cytokine-cytokine receptor interaction and Jak-STAT signaling

I) Module 9 (N= 60; p < 0.01):
Built around STAT1
Involved in cytokine-cytokine receptor interaction and Jak-STAT signaling

J) Module 10 (N = 24; p = 0.03):
Built around GUCY1B3
Involved in purine metabolism

Supplementary Figure 5. Functional SMITE modules identified in cluster 3. Expression is shown on the top left edge of each gene circle (upregulated: dark pink, downregulated: light pink, grey: not significant, white: no data); scored promoter and body methylation are shown on the bottom left and top right of each circle, respectively (hypermethylated: dark blue, hypomethylated: light blue, grey: not significant, white: no data), compared to cluster 1. The symbol text sizes and center node colors are based on the total gene score (low (grey) to high (red)) and the edge colors are representative of the strength of the associations between the genes (low (grey) to high (red)). Cluster 3 module 11 is shown in Figure 3b.