Supplemental Table 1: Nanostring Analysis of Flow-Sorted tdTomato+ Cells from Bleomycin-Injured Mice

Gene	Name	Twist1 FL+Bleo	Twist1 WT+Bleo	Ratio FL/WT	P-value
Ccl5	Chemokine (C-C motif) ligand 5	327	763	0.4	0.00030
Ccl3	Chemokine (C-C motif) ligand 3	357	693	0.5	0.00296
Ccl11	Chemokine (C-C motif) ligand 11	32	15	2.1	0.00912
Ccl4	Chemokine (C-C motif) ligand 4	170	290	0.6	0.02666
Ifng	Interferon, gamma	21	40	0.5	0.02695
Il6	Interleukin 6	76	132	0.6	0.04696
Il1b	Interleukin 1, beta	1177	1887	0.6	0.23795
Ccl19	Chemokine (C-C motif) ligand 19	50	39	1.3	0.26813
Csf3	Colony Stimulating Factor 3(granulocyte)	4	3	1.4	0.27166
Ccl21b	Chemokine (C-C motif) ligand 21	560	402	1.4	0.28150
Tnf	Tumor Necrosis Factor	130	108	1.2	0.40560
Tgfb1	Transforming growth factor, beta 1	364	337	1.1	0.61105
Cxcl1	Chemokine (C-X-C motif) ligand 1	181	162	1.1	0.68362
Ccl2	Chemokine (C-C motif) ligand 5	368	333	1.1	0.74832
Il12b	Interleukin 12B (Natural Killer Cell Stimulatory Factor 2, Cytotoxic Lymphocyte Maturation Factor 2, P40	14	13	1.0	0.86060
Il13	Interleukin 13	10	9	1.0	0.92639

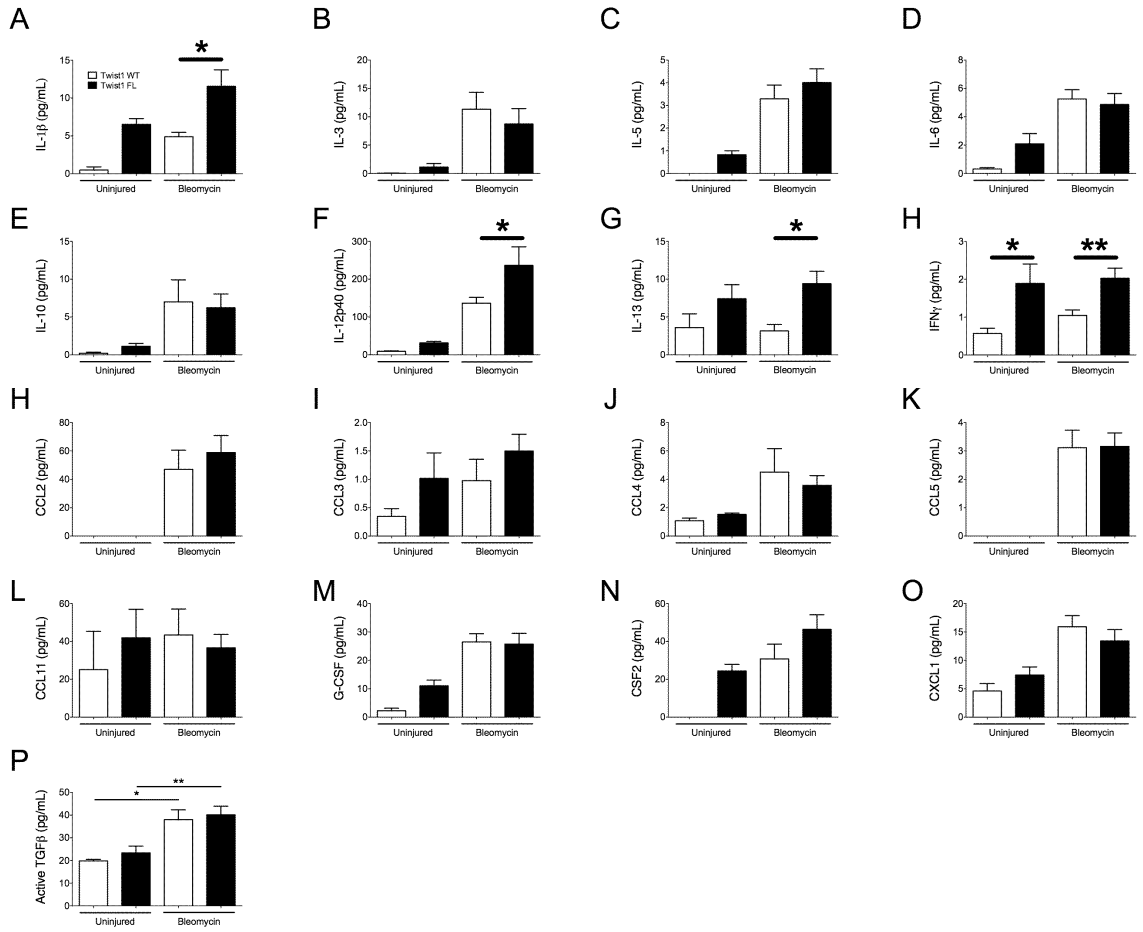

Figure S1 Luminex analysis of the bronchoalveolar lavage (BAL) shows increases in several T-cell associated cytokines BAL was obtained from uninjured and bleomycin-injured twist1 WT or twist1 FL mice. BAL was subjected to the Luminex platform as described in Materials and Methods. For all analyses, N=5 uninjured and 11-12 for bleomycin-injured). Data were analyzed by ANOVA followed by Neuman-Keuls post-hoc testing. (A) IL-1β (*P<0.025 Bleomycin + twist1 WT v Bleomycin + twist1 FL), (B) IL-3, (C) IL-5, (D) IL-6, (E) IL-10, (F) IL-12 p40 (*P<0.038 Bleomycin + twist1 WT v Bleomycin + twist1 FL), (G) IL-13, (H) IFNγ (*P<0.012 Uninjured + twist1 WT v Uninjured + twist1 FL, and **P<0.005 Bleomycin + twist1 WT v Bleomycin + twist1 FL), (H) CCL2, (I) CCL3, (J) CCL4, (K) CCL5, (L) CCL11, (M) G-CSF, (N) CSF2, (O) Active TGFβ (by ELISA), and (P) CXCL1

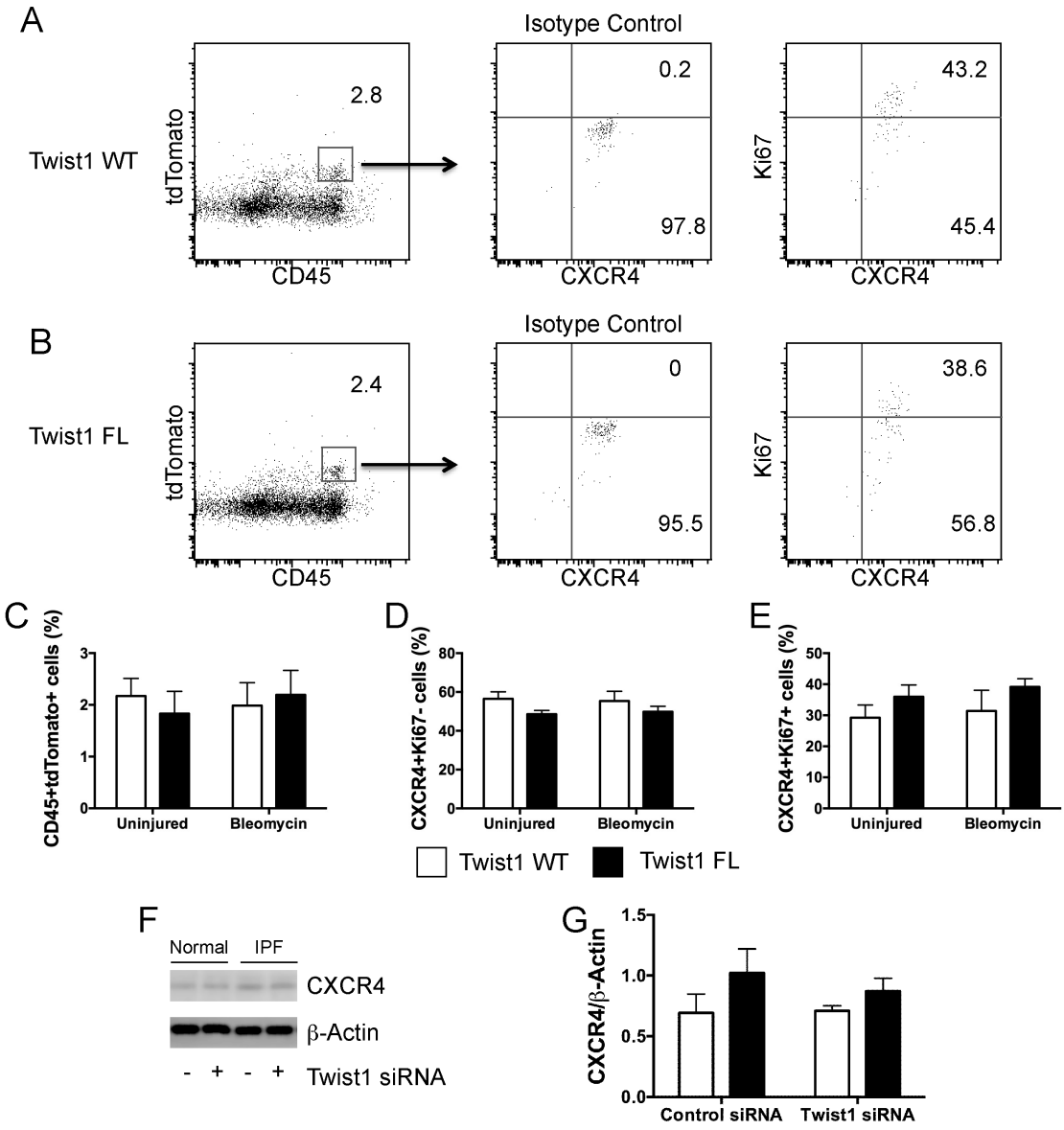

Figure S2 A subset of mouse bone marrow cells are CD45+tdTomato+ Bone marrow cells were flushed from uninjured and bleomycin-injured Twist1 WT and Twist1 FL mice. (A-B) Dot plots for detection of tdTomato, CD45, CXCR4, and Ki67+ cells. Of the tdTomato+CD45+cells, >95% are CXCR4+. (C) Quantification of CD45+tdTomato+ cells between twist1 genotype and by injury (N=5-8 per condition). (D) Quantification of CD45+tdTomato+CXCR4+Ki67- and (E) Ki67+ cells. No significant differences were observed between injury and genotype. (F) Representative immunoblotting for CXCR4 in normal and IPF lung fibroblasts with and without twist1 siRNA. (G) Densitometry of immunoblots in (F), n=3 per condition.

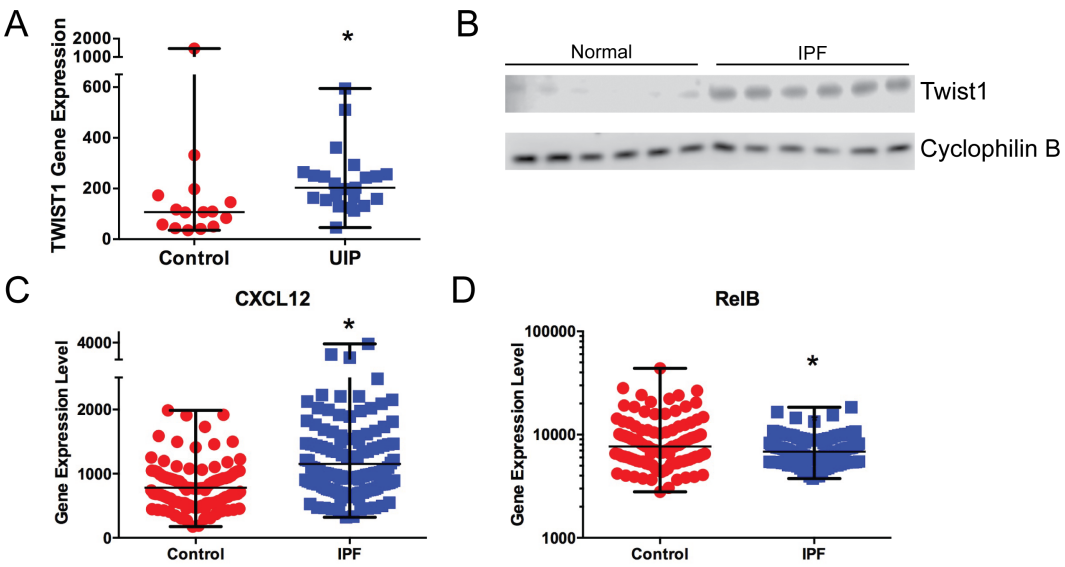

Figure S3 Twist1 gene expression is increased in UIP lungs and IPF lung fibroblasts (A) Gene expression analysis of UIP lungs (N=23) compared to normal (N=15) (Median ± range, P<0.004 by Mann-Whitney). (B) Immunoblot of unstimulated normal and IPF lung fibroblasts incubated with 10% fetal bovine serum for twist1 (molecular weight=21 kDa). The membrane was stripped and blotting was performed for cyclophilin B (MW=21 kDa) (N=6 per condition). LGRC gene expression data for (C) CXCL12 (*P<0.01 by Mann-Whitney, N=134 IPF and 107 Controls) and (D) RelB (*P<0.05).