Supporting Information

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SI Text

Administration of Tamoxifen. Littermates at 4–6 weeks of age were administered tamoxifen daily by i.p. injection (Sigma) in corn oil (12 μg/uL in corn oil) at 132 μg tamoxifen/per g of body weight per day for 5 consecutive days.

Administration of Rapamycin. For rapamycin treatment, mice at 30 DPI were administered rapamycin (LC Laboratories) by daily i.p. injection at 4 μg per g of body weight per day, or mice were administered rapamycin daily along with tamoxifen treatment from the beginning. After tamoxifen treatment was finished, mice were treated with rapamycin for another 3 days. For rapamycin treatment in competitive transplantation setting, competitive transplantation was performed as described above. Six weeks after transplantation, when these mice showed stable chimerism, *TSC1* was deleted by tamoxifen treatment for 5 days. At the time of tamoxifen treatment, rapamycin or vehicle was also administered daily to *TSC1* KO and WT mice transplants for 5 days, followed by continuous treatment every 2 days for 16 weeks. Rapamycin was first reconstituted in absolute ethanol at 25 mg/mL and then diluted in 5% Tween-80 and 5% PEG-400 before injection to make 0.5 mg/mL solution for injection.

Autopsy and Histopathology. Animals were autopsied and all tissues were examined regardless of their pathological status. Tissue samples were fixed in 10% neutral-buffered formalin (Sigma) overnight, and washed once with 1× PBS and then transferred into 70% ethanol and stored at 4 °C. Tissues were processed by ethanol dehydration and embedded in paraffin (Histoserv) according to standard protocols. Sections (5 μm) were prepared for antibody detection and H&E staining.

Competitive and Noncompetitive Repopulation Assays. In noncompetive repopulation assay, 1×10^6 bone marrow cells from both *TSC1L/L,Rosa26-CreERT2* or littermate WT mice (both CD45.2$^+$) were injected into the lateral tail veins of lethally irradiated CD45.1$^+$ recipient animals. In competitive repopulation assay, 0.5×10^6 bone marrow cells from both *TSC1L/L,Rosa26-CreERT2* or littermate WT mice (both CD45.2$^+$) were mixed with 0.5×10^6 bone marrow cells from CD45.1$^+$ WT mice, then injected into lateral tail veins of lethally irradiated CD45.1$^+$ recipient animals (950 rad in 2 dosages, 2 h apart). Six weeks after transplantation, when these mice showed stable chimerism, *TSC1* was deleted by tamoxifen treatment. Peripheral blood was collected at 1, 2, 4, 8, 12, and 16 weeks after tamoxifen treatment, and bone marrow from mice at 16 weeks was analyzed for contribution of CD45 congenic and lineage markers by flow cytometry. Tissues from the recipient mice at 16 weeks were collected for further analysis, including cell surface marker staining by flow cytometry, histology characterization, etc. Both noncompetitive and competitive transplants were carried out with 3–5 donors per genotype mice with 3 recipient mice per donor in each experiment. Generation of shRNA-expressing virus stock and virus infection of bone marrow cells were done as described (1). shRNA sequence information is available on request.

Flow Cytometric Analysis and Cell Sorting. Single-cell suspensions were prepared form spleen, thymus, and bone marrow (from femoral and tibial bones) by passing cells through a 70-μm cell strainer. Cells were lysed on ice with red blood cell lysis solution (Sigma), washed in PBS + 2% FCS, then resuspended in PBS + 2%FCS. Cells were incubated with fluorochrome-conjugated (or biotin-conjugated) antibodies for 30 min on ice, followed by washing once in PBS + 2% FCS. For lineage marker labeling, cells were stained with other fluorochrome-conjugated antibodies and biotin-conjugated lineage markers (CD3, B220, Gr-1, Mac-1, Ter119) (BD Bioscience) for 30 min on ice, followed by incubation with fluorochrome-conjugated Streptavidin (BD Bioscience) for 5 min. For the analysis of bone marrow lymphopoiesis, cells were stained with fluorochrome-conjugated anti-B220, CD19, CD43, IgM, and biotin-conjugated lineage markers (CD3, Gr-1, Mac-1, Ter119) (BD Bioscience) for 30 min on ice, followed by incubation with fluorochrome-conjugated Streptavidin for 5 min.

In Vitro Colony Assays. Myeloid and pre-B colony-plating assays were performed in methylcellulose-based medium (M3434 and M3630; Stem Cell Technologies). A total of 2×10^4 bone marrow and spleen cells were plated in duplicate and scored for colony formation at 10 and 14 days. For CFU-E assay, 100 000 bone marrow cells were plated per mL of serum-free methylcellulose (M3134; StemCell Technologies) supplemented with 10% FBS, 100 ng/ml of rmSCF (PeproTech), and 4 units/mL human erythropoietin (hEpo; Amgen). For BFU-E assay, 25,000 fresh bone marrow cells were plated in 1 mL of methylcellulose (M3134; StemCell Technologies) containing 10% FBS, 4 units/mL hEPO, 100 ng/mL rrSCF, 100 ng/mL G-CSF, and 20 ng/mL IL-3 (PeproTech). Colonies were scored on day 2 (CFU-Es) or day 10 (BFU-Es).

Quantitative Real-Time PCR analysis. RNA from various tissues was harvested by using TRIzol (Invitrogen) and the RNeasy kit (Qiagen). RNA was treated with RQ1 RNase-freeDNase (Promega), and cDNA was prepared by using SuperScript II Rnase H-Reverse transcriptase (Invitrogen). RNA from sorted cells was extracted with the PicoPure RNA Isolation Kit (Molecular Devices), and cDNA was prepared by using SuperScript II Rnase H-Reverse Transcriptase (Invitrogen). Quantitative real-time PCR was performed on cDNA samples with the Quantitative SYBR Green PCR kit (Qiagen) and was run on the Stratagene Mx3000P. Primer sequences are available on request.

Microarray Analysis. RNA from sorted LSK cells (10,000–20,000) was extracted by using the PicoPure RNA Isolation Kit (Molecular Devices), and cDNA was prepared by using SuperScript II Rnase H-Reverse transcriptase (Invitrogen). Gene expression profiling was performed with the Affymetrix 430 2.0 chips at Partners Healthcare Center for Genetics and Genomics at Harvard Medical School. dChip was used to normalize arrays and compute expression indices as described (2).

1. Thomas EK, *et al.* (2007) Rac guanosine triphosphatases represent integrating molecular therapeutic targets for BCR-ABL-induced myeloproliferative disease. *Cancer Cell* 12:467–478.
2. Paik JH, *et al.* (2007) FoxOs are lineage-restricted redundant tumor suppressors and regulate endothelial cell homeostasis. *Cell* 128:309–323.

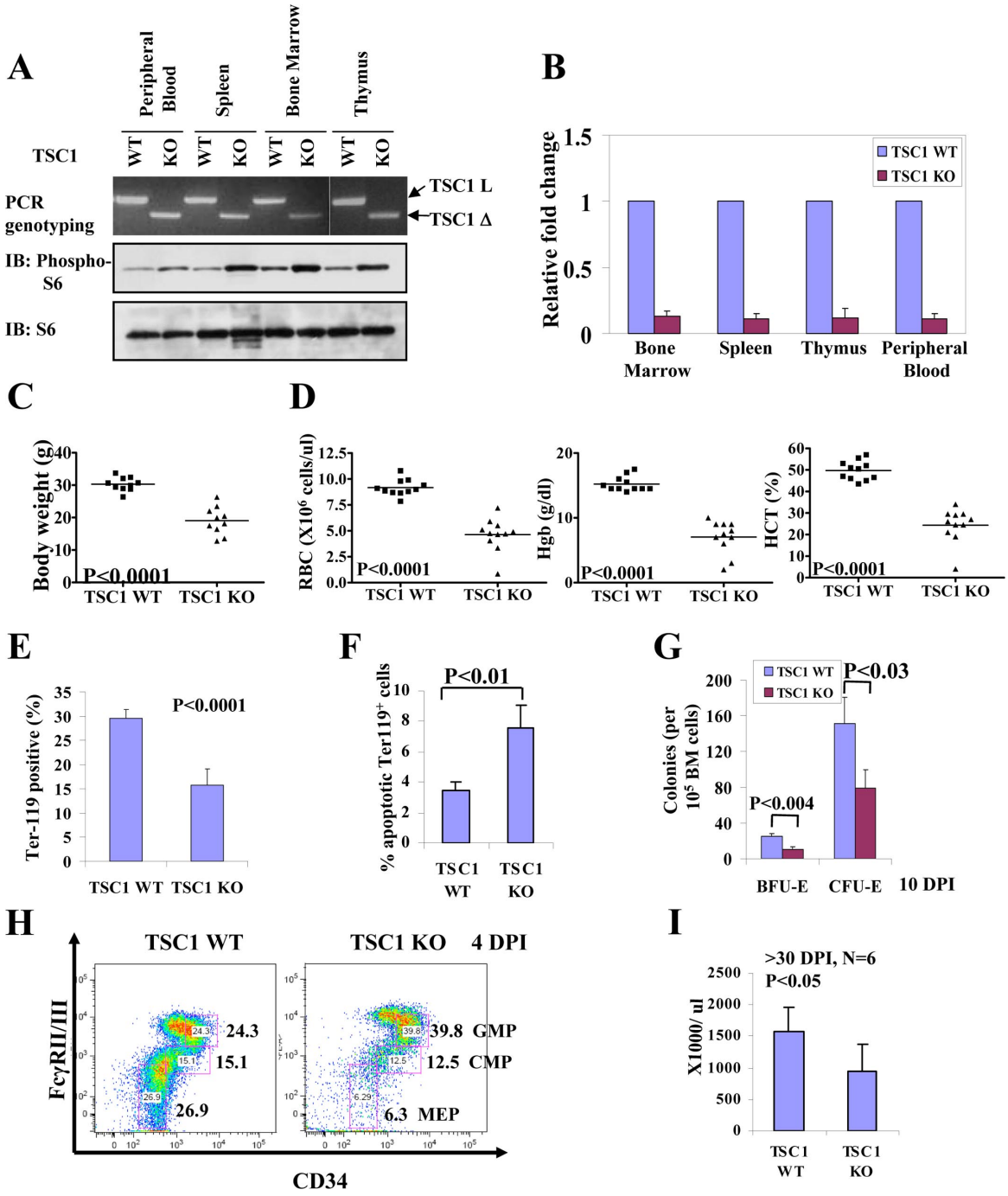

Fig. S1. Somatic deletion of *TSC1* leads to fatal bone marrow failure. (*A*) *TSC1* deletion and subsequent mTORC1 activation in various hematopoietic organs. PCR genotyping, and Western blotting by phosphor-S6, S6 were performed on bone marrow, spleen, thymus, and peripheral blood samples from *Rosa26-CreERT2*$^{+}$, *TSC1*$^{L/L}$ (*TSC1* KO), and *Rosa26-CreERT2*$^{-}$, *TSC1*$^{L/L}$ (*TSC1* WT) at 3 DPI. (*B*) Quantitative TSC1 RT-PCR of bone marrow, spleen, thymus, and peripheral blood samples from *TSC1* KO and WT mice at 3 DPI. (*C*) Body weight of female mice with indicated genotypes at 40 DPI. $n = 10$ for each genotype. Male mice show similar results. (*D*) Scatter plot showing red blood cell (RBC), hemoglobin (Hgb), and hematocrit (HCT) counts of *TSC1* WT and *TSC1* KO mice at 40–50 DPI. $n = 11$ for each genotype. (*E*) Bar graph showing the percentage of Ter119-positive cells in bone marrow of *TSC1* WT and KO mice after 30 DPI. $n = 8$ for each genotype. (*F*) Bar graph showing increased percentages of apoptotic Ter119^{+} cells in *TSC1* KO mice. $n = 3$ for each genotyping. $P < 0.01$. (*G*) Bar graph showing decreased BFU-E, CFU-E colony formation in *TSC1* KO bone marrow cells at 10 DPI. $n = 3$ for each genotype. (*H*) Flow cytometry analysis of CMP, GMP, and MEP subpopulations at 4 DPI from representative *TSC1* KO and WT mice. The percentages of CMP, GMP and MEP subpopulation from myeloid progenitor population (Lin-, Sca-1, c-Kit+) are also indicated. $n = 3$ for each genotyping. $P < 0.05$ for GMP and MEP; $P > 0.1$ for CMP. (*I*) Bar graph showing platelet counts in *TSC1* WT and KO mice after 30 DPI. $n = 6$ for each genotyping. $P < 0.05$.

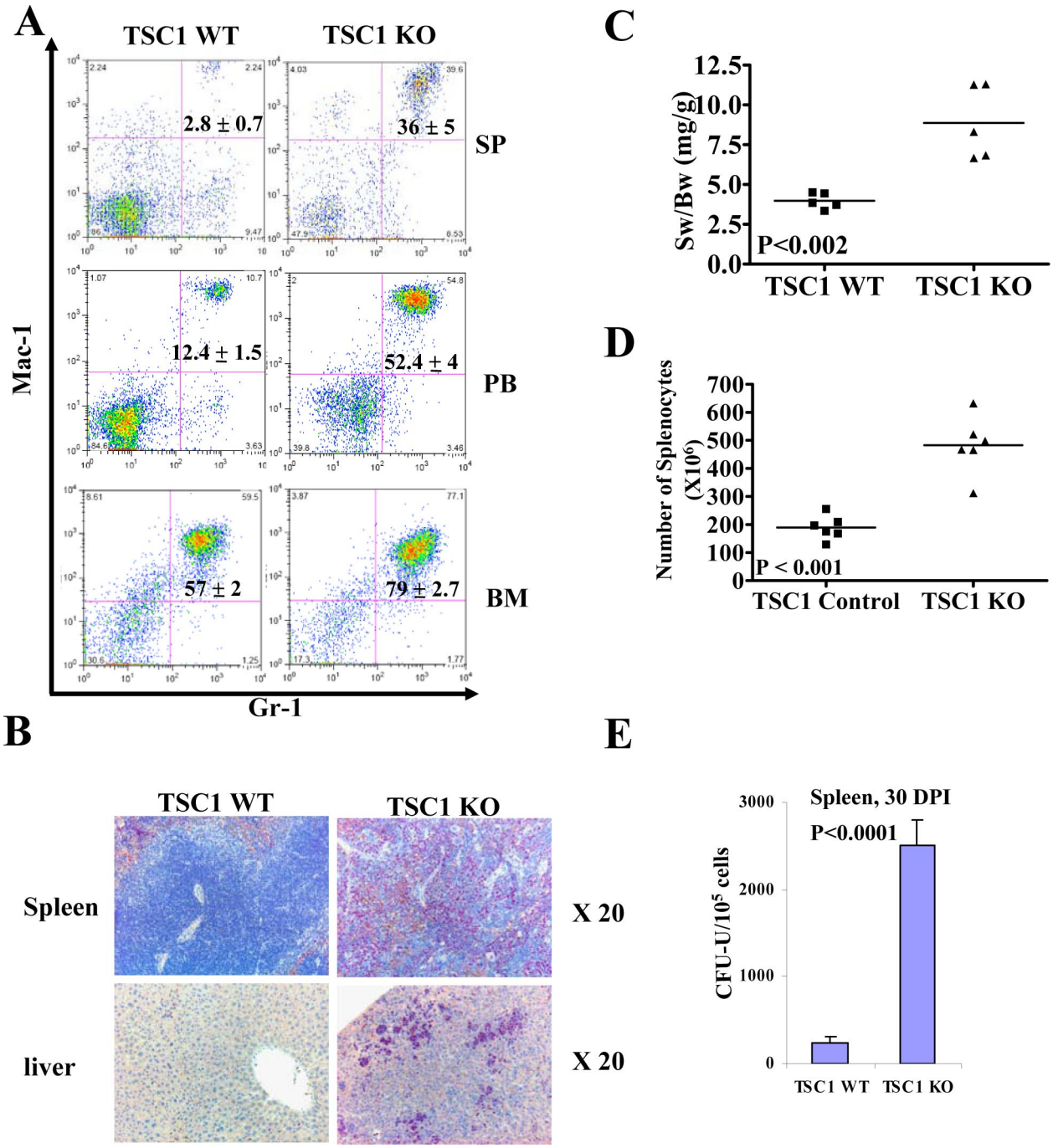

Fig. S2. *TSC1* deletion leads to myeloproliferative disease. (*A*) Flow cytometric analysis of spleen (SP), peripheral blood (PB), and bone marrow (BM) from representative *TSC1* WT and KO mice confirmed an increased population of $Gr1^+/Mac1^+$ cells in *TSC1* KO animals. The averaged percentage of $Gr1^+/Mac1^+$ cells is also indicated in each case. (*B*) Chloroacetate esterase (CAE) staining showing increased positive staining cells in *TSC1* KO spleen and liver. (*C* and *D*) Scatter plot showing spleen weight to body weight ratio (Sw/Bw) (*C*) and the total cell numbers of spleen (*D*) of *TSC1* WT and KO mice at 30 DPI. (*E*) Bar graph showing increased colony formation units from *TSC1* KO splenic cells at 30 DPI. $n = 3$ for each genotype.

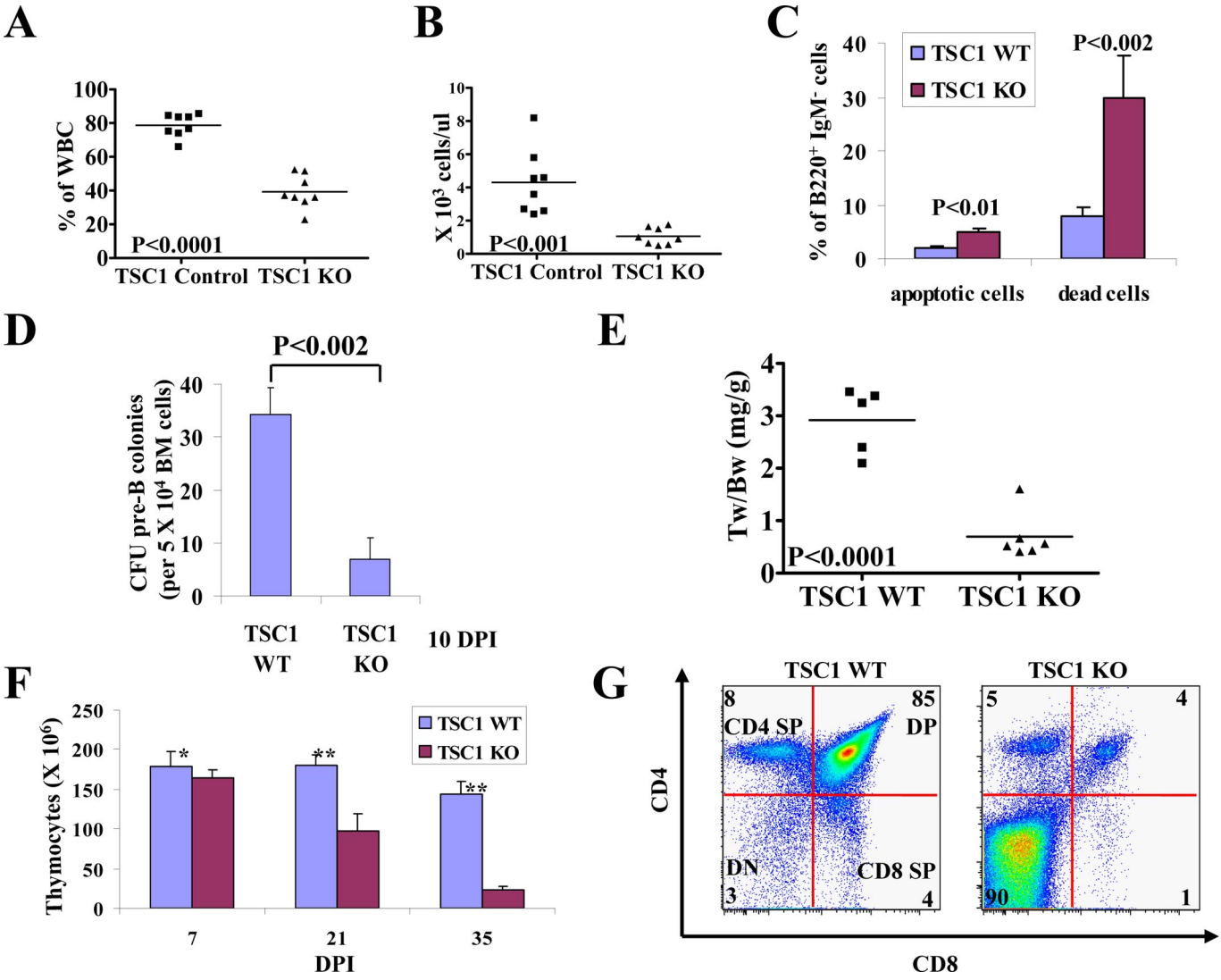

Fig. S3. *TSc1* deficiency causes impaired lymphoid lineage development. (*A* and *B*) Scatter plot showing decreased relative (*A*) and absolute (*B*) number of peripheral blood lymphocytes of *TSC1* WT and KO mice at 30 DPI. (*C*) Bar graph showing increased percentage of apoptotic and dead cells from $B220^{+}IgM^{-}$ bone marrow cells in *TSC1* KO mice. $n = 3$ for each genotype. (*D*) Bar graph showing decreased CFU pre-B colony formation in *TSC1* KO bone marrow cells at 10 DPI. $n = 3$ for each genotype. (*E*) Scatter plot showing thymus weight to body weight ratio (Tw/Bw) of *TSC1* WT and KO mice at 30 DPI. (*F*) Bar graph showing total numbers of thymocytes from *TSC1* WT and KO mice at 7, 21, and 35 DPI. $n > 3$ for each genotyping at each time point. *, $P > 0.05$; **, $P < 0.01$. (*G*) Flow cytometry analysis of thymocytes from representative *TSC1* WT and KO mice at 35 DPI by CD4, CD8. The averaged percentage of each population is also indicated. $n > 3$ for each genotype.

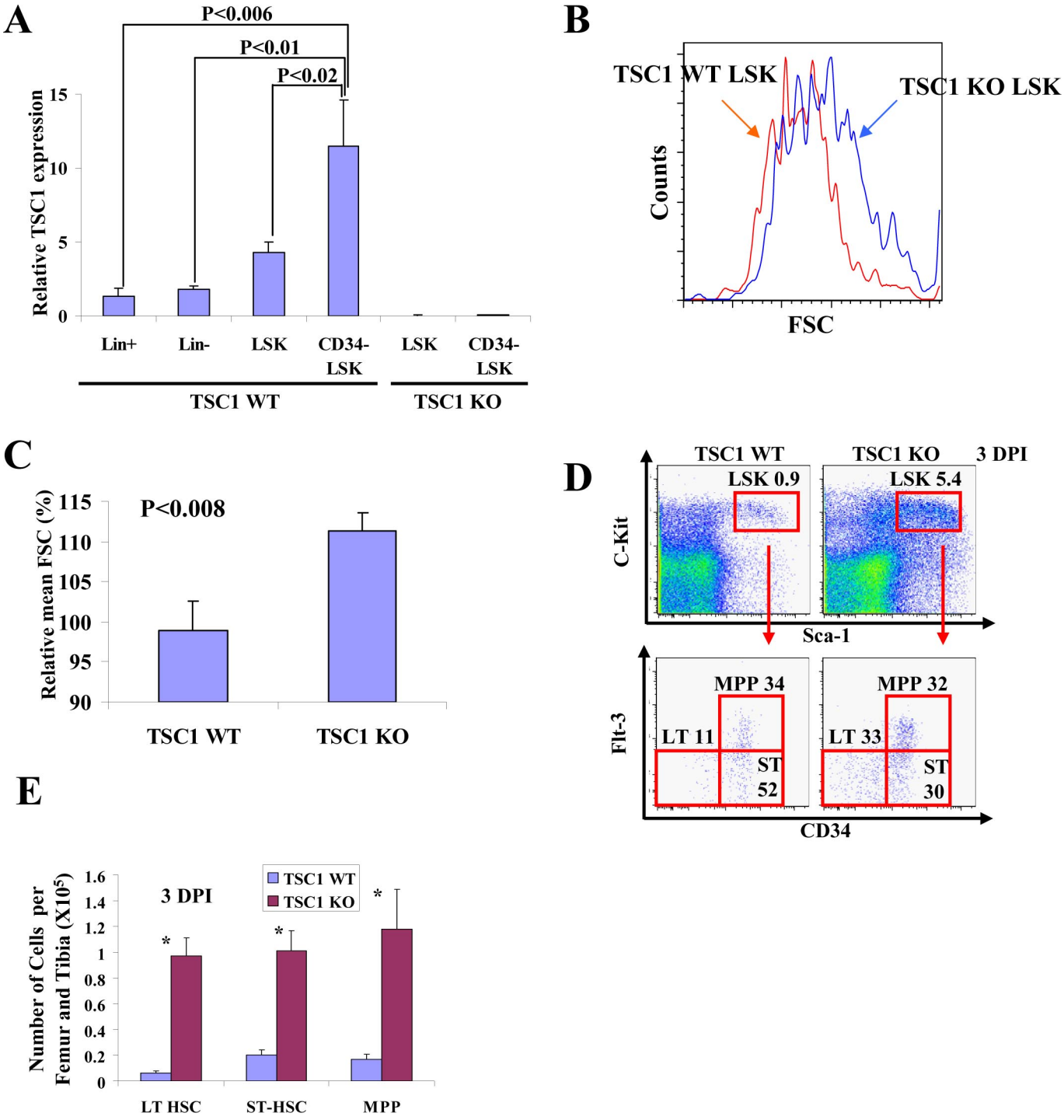

Fig. S4. Deletion of TSC1 leads to HSC short-term expansion, but long-term reduction of HSC reserves. (*A*) Quantitative RT-PCR of various sorted cells from *TSC1* KO and WT mice at 3 DPI. $n = 3$ for each genotyping. (*B*) Histogram of mean FSC-H comparing *TSC1* WT and KO LSKs at 3 DPI. (*C*) Bar graph showing increased relative mean FSC-H (corresponding to increased cell size) in *TSC1* KO LSKs. $n = 3$ for each genotyping. (*D*) Flow cytometric analysis of LSK, MPP, ST-HSC, and LT-HSC from bone marrow at 3 DPI from representative *TSC1* KO and WT mice. The averaged percentage of each population is also indicated. $n > 3$ for each genotyping. (*E*) Bar graph showing the absolute numbers of HSC, LT-HSC, and ST-HSC cells per femur and tibia at 3 DPI in *TSC1* KO and control mice. $n = 3$ for each genotype. *, $P < 0.01$.

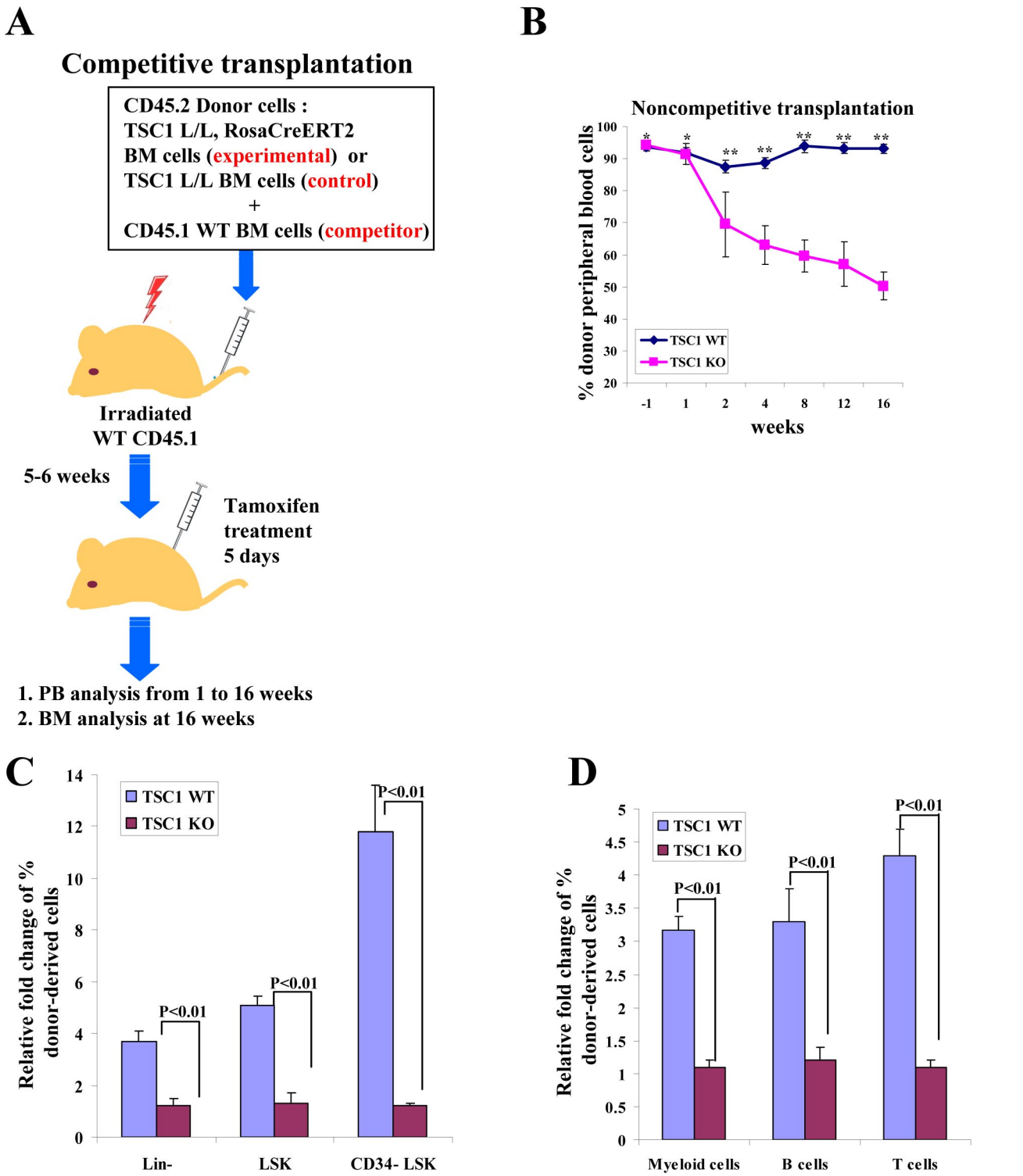

Fig. S5. Deletion of *TSC1* results in defective HSC long-term repopulating ability in vivo. (*A*) In competitive transplantation assay, bone marrow cells from both *TSC1L/L, Rosa26-CreERT2* (experimental) or littermate WT mice (control) (both CD45.2$^+$) were mixed with bone marrow cells from CD45.1$^+$ WT mice (competitor) at 1:1 ratio and transplanted into lethally irradiated CD45.1$^+$ recipient animals. Five to 6 weeks after transplantation, when these mice showed stable chimerism, *TSC1* was deleted by tamoxifen treatment. (*B*) Recipient mice from noncompetitive transplantation were analyzed by CD45 staining to examine the contribution of donor-derived cells in peripheral blood at various time points before or after tamoxifen treatment. Six recipients for each genotype were used in noncompetitive transplantation. *, $P > 0.1$; **, $P < 0.01$. (*C* and *D*) Recipient mice from competitive transplantation were analyzed for the contribution of various donor-derived hematopoietic lineages in bone marrow cells at 16 weeks after transplantation. Bar graph showing the relative fold change of percentage of various donor-derived hematopoietic lineages. $n = 6$ for each genotyping.

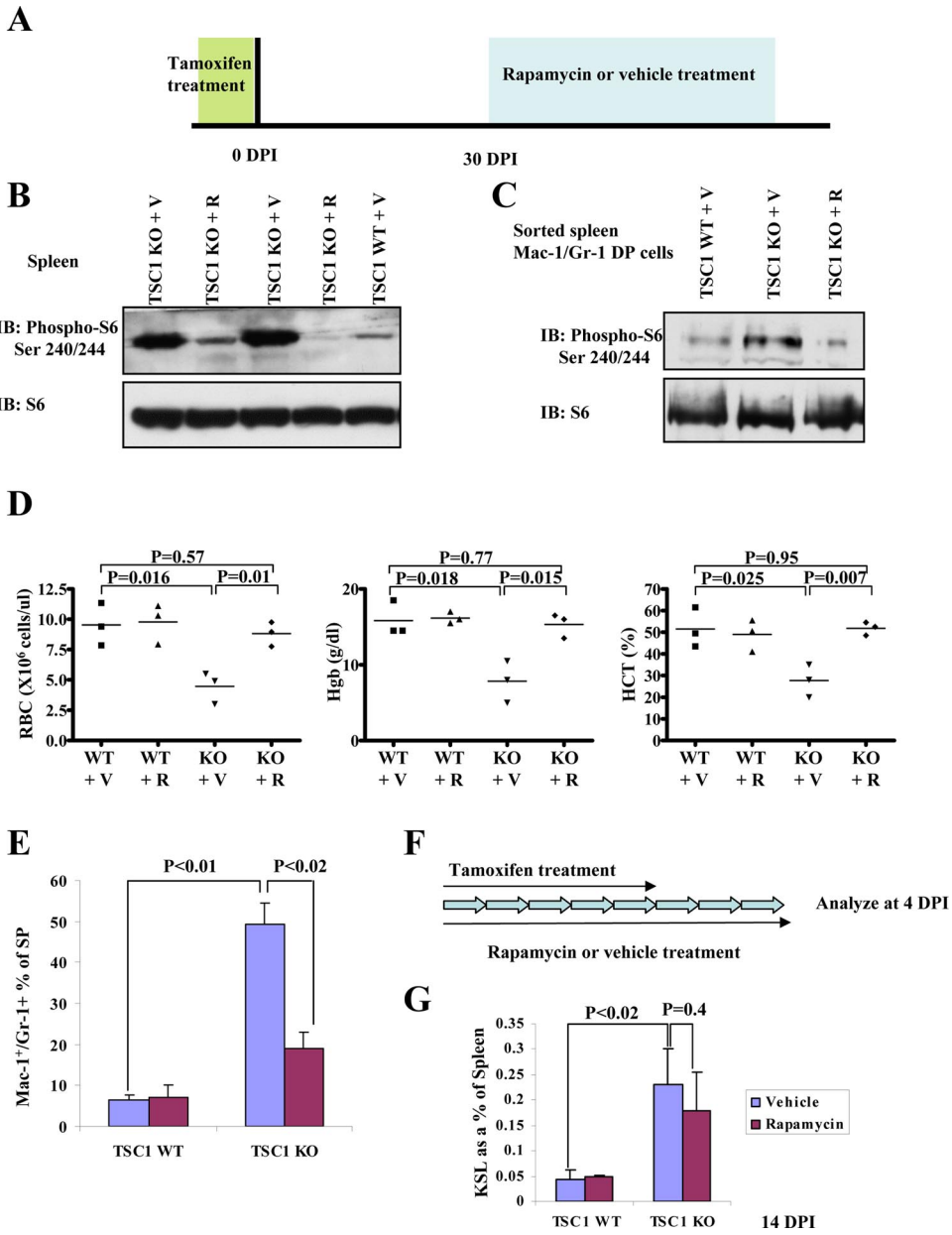

Fig. S6. TSC1 operates via both mTORC1 dependent and independent mechanisms to regulate HSC biology. (*A*) Rapamycin or vehicle was administered daily to *TSC1* KO and WT mice from 30 DPI. Mice were analyzed 7–15 days later. (*B* and *C*) Western blotting by phosphor-S6, S6 performed on splenic cells (*B*) and sorted Mac-1/Gr-1 double positive (DP) cells from spleen (*C*). (*D*) Scatter plot showing red blood cell (RBC), hemoglobin (Hgb), and hematocrit (HCT) counts of the mice in *A*. $n = 3$ for each genotype. (*E*) Bar graph showing the percentage of Mac-1^+/Gr-1^+ cells in spleen from the mice in A. (*F*) Prophylactic rapamycin administration: at the time of tamoxifen treatment, rapamycin or vehicle was administered daily to *TSC1* KO and WT mice for 5 days. The continuously treated mice were analyzed at 4 DPI. (*G*) Bar graph showing the percentage of LSK cells from spleen in *TSC1* KO and WT mice from prophylactic rapamycin administration at 14 DPI as indicated. $n = 3$ for each genotype.

Table S1. Differentially expressed genes in TSC1 KO LSKs

Rank	Gene symbol	Log fold change	Fold change
Down-regulated genes			
1	Scin	−4.02924	0.061245832
2	Ccr9	−3.47705	0.089805486
3	Ccr9	−3.43194	0.09265826
4	Hspa1b	−3.03007	0.122421274
5	Klk1b22 /// Klk1b9	−2.65294	0.158995475
6	Dsp	−2.55318	0.170379465
7	Id2	−2.46354	0.181301699
8	Hdc	−2.31921	0.200376716
9	LOC100047138 /// Tesc	−2.15314	0.224823058
10	Chdh	−2.07478	0.237371898
11	F10	−1.84654	0.278058135
12	Ccnb1	−1.81778	0.283657932
13	Pttg1	−1.81564	0.284077491
14	Olfm1	−1.73262	0.300904357
15	Atp6v0a1	−1.71691	0.304199853
16	Ifi205 /// Mnda	−1.69647	0.308540883
17	Dntt	−1.6366	0.321613696
18	Foxp1	−1.59861	0.330195181
19	Hspa1b	−1.56563	0.337829636
20	Cnn3 /// LOC100047856	−1.55333	0.340723833
21	Ifi202b	−1.50429	0.352504595
22	Cdc42	−1.5064	0.351988002
23	Cab39l	−1.49587	0.354565841
24	Lamp2	−1.49432	0.354947695
25	LOC100046998 /// Opa1	−1.46439	0.362389957
26	Evi2a	−1.39279	0.3808289
27	Hmmr	−1.34422	0.393866374
28	Stard5	−1.31926	0.400740315
29	Fcgr2b	−1.29914	0.406369179
30	Sf3a3	−1.28286	0.410979418
31	Fen1	−1.25092	0.420179185
32	Aurkb	−1.21779	0.429939394
33	Hsp90b1	−1.2122	0.431610088
34	Cnn3 /// LOC100047856	−1.20076	0.435047445
35	Polr3k	−1.19691	0.436207975
36	Fanca	−1.19022	0.438236629
37	Cnn3 /// LOC100047856	−1.18485	0.439869919
38	Mcm10	−1.13974	0.453840688
39	Aurkb	−1.12859	0.457363896
40	Mrps23	−1.0964	0.467680875
41	Ola1	−1.08985	0.46980878
42	Rangap1	−1.08905	0.47006994
43	LOC100044385 /// Ppp2cb	−1.08494	0.471410488
44	Seh1l	−1.07249	0.47549773
45	Ctr9	−1.07204	0.475646531
46	Fcgr2b	−1.06497	0.477981465
47	Bzw1	−1.0484	0.483504999
48	Cycs /// LOC672195	−1.0476	0.483771918
49	Kif20a	−1.04337	0.485192566
50	Aars	−1.0409	0.48602371
51	Cdca3	−1.00244	0.499156352
52	Ppp4r1l	−1.00089	0.499691153
53	Tacc3	−0.99681	0.501106064
54	Nuf2	−0.96225	0.513255035
55	Rbm28	−0.96159	0.513490592
56	Tmem192	−0.95624	0.515398695
57	P2rx4	−0.93547	0.522873508
58	Erp29	−0.92604	0.526301952
59	Tex9	−0.91143	0.531658901
60	Tex9	−0.90463	0.533237431
61	5430435G22Rik	−0.90352	0.534579756
62	Fuca2	−0.90145	0.53534999
63	Ms4a6d	−0.88584	0.541174149

Rank	Gene symbol	Log fold change	Fold change
64	Snf8	−0.88135	0.542860448
65	2010111I01Rik	−0.87236	0.546251318
66	Cnn3 /// LOC100047856	−0.86398	0.549434265
67	Rrbp1	−0.85415	0.553189263
68	Tmem14c	−0.85379	0.553330618
69	Psmd13	−0.84749	0.555749823
70	Aaas	−0.84725	0.55584404
71	Dpp7	−0.83886	0.559083383
72	LOC100044230 /// Srd5a3	−0.83597	0.560205736
73	Ctsz	−0.83241	0.561589466
74	Atpbd1b /// LOC636885	−0.8296	0.562686353
75	Cbx1 /// LOC100047028	−0.8172	0.56754127
76	Smpd4	−0.80884	0.570840864
77	Ggta1	−0.80573	0.572073182
78	EG433923 /// LOC631229 /// LOC667030 /// Slc25a5	−0.80032	0.574220113
79	Slc1a4	−0.79552	0.576133551
80	Dntt	−0.78893	0.578773663
81	Ctsz	−0.78706	0.579522588
82	Gpr137b /// Gpr137b-ps /// LOC100044979	−0.77639	0.583827139
83	Pgam1	−0.77071	0.586130217
84	Calr	−0.77041	0.58624958
85	Nup43	−0.76144	0.589907935
86	Farsb	−0.75974	0.590602316
87	Med1	−0.7517	0.593902685
88	Hdgf	−0.75005	0.594584834
89	Bcl2l11	−0.74722	0.595751684
90	Eif4e2	−0.74273	0.597607438
91	Psap	−0.7395	0.598945239
92	Calr	−0.73674	0.600092482
93	Cdk2ap1 /// LOC100047490	−0.72686	0.604215852
94	Fgfr1op2	−0.71701	0.608356187
95	Psmd13	−0.70789	0.612215888
96	—	−0.70567	0.61315912
97	LOC100042343 /// Tmed2	−0.68781	0.6207949
98	Anp32e	−0.68557	0.621760284
99	Racgap1	−0.68065	0.623882294
100	Hmmr	−0.67475	0.626441359
101	Psat1	−0.67304	0.627185795
102	Dlat	−0.67029	0.628380567
103	Farsa	−0.67026	0.628392362
104	Prpf40a	−0.66304	0.631547377
105	Rrbp1	−0.65726	0.634079909
106	Pcmt1	−0.65471	0.635203008
107	Calr	−0.6472	0.63851628
108	Ugt1a1 /// Ugt1a10 /// Ugt1a2 /// Ugt1a5 /// Ugt1a6a /// Ugt1a6b /// Ugt1a7c /// Ugt1a9	−0.64635	0.638892567
109	Ube2f	−0.64496	0.639509156
110	1600012H06Rik	−0.64285	0.640447217
111	Gnptab	−0.61669	0.652163665
112	Etf1	−0.61514	0.652867264
113	Tacc2	−0.60603	0.657002284
114	EG623818 /// Hmbs	−0.60132	0.659149924
115	Trim37	−0.59275	0.663076348
116	Sdhc	−0.5925	0.663191302
Up-regulated genes			
95	Dynlrb1	0.590738	1.506016431
94	Ccnd2	0.605114	1.521099376
93	Ccnl1	0.610854	1.527162508
92	Ccdc102a	0.63316	1.55095813
91	Rab2b	0.645669	1.564464584
90	Myadm	0.656723	1.576497683
89	Gltscr2	0.659698	1.579752315
88	Galm	0.660373	1.580490803
87	Tmem191c	0.673207	1.594613513

Rank	Gene symbol	Log fold change	Fold change
86	Bnip3l	0.677381	1.599233712
85	Irf2	0.692413	1.615984231
84	Ldhb	0.699237	1.623645776
83	Serpinb6a	0.701334	1.626007644
82	Yipf2	0.748223	1.679722732
81	LOC100039656 /// LOC100040416 /// LOC100040605 /// LOC100044916 /// Rpl13	0.767344	1.702133319
80	Trfr2	0.779336	1.716340306
79	Ptpn21	0.785822	1.724074934
78	Spint2	0.791111	1.73040644
77	5730427N09Rik /// EG433230 /// LOC636306	0.796522	1.736908205
76	Trfr2	0.82791	1.775111626
75	Bsdc1	0.831437	1.7794569
74	Mboat2	0.833819	1.782397618
73	Sqrdl	0.846176	1.797730113
72	Ipo4	0.856541	1.810691719
71	Pear1	0.868976	1.826365674
70	Zfp161	0.88556	1.847480978
69	Arl3	0.906315	1.87425192
68	Foxo1	0.907301	1.875533523
67	1110031B06Rik	0.913009	1.882969106
66	Erbb2ip	0.964307	1.951126585
65	Slc2a1	0.970203	1.959116567
64	Rbpms	0.97803	1.9697733
63	Cyp4v3	0.978748	1.970754474
62	9530028C05	1.003878	2.005383309
61	EG434179	1.008297	2.01153486
60	Grb10	1.010655	2.014825493
59	Capg	1.031799	2.044572881
58	Ptgs1	1.034344	2.048182259
57	Socs2	1.035782	2.050225106
56	Zfhx3	1.061033	2.086425273
55	Ogt	1.069426	2.098598036
54	Slc2a1	1.123709	2.179064121
53	Cabc1	1.148888	2.217428952
52	Ldhb	1.159533	2.233851743
51	Vldlr	1.203568	2.303085962
50	Ltbp3	1.235172	2.354093855
49	EG622782 /// EG625349 /// EG666200 /// EG666464 /// LOC100041709 /// LOC544983 /// LOC545175 /// LOC619711 /// LOC624831	1.248354	2.375702032
48	Tpm2	1.284564	2.436083965
47	H1f0	1.285014	2.436844901
46	Nelf	1.303986	2.469101852
45	Mettl7a	1.305839	2.472274934
44	Prmt2	1.317463	2.492275336
43	Slc9a3r2	1.319794	2.49630411
42	Pitpnm1	1.325574	2.506325862
41	Pdzk1ip1	1.433605	2.701209207
40	C1qdc2	1.454608	2.74081984
39	Obsl1	1.459357	2.749856835
38	Pglyrp2	1.465158	2.760936161
37	Arhgef12	1.487933	2.80486816
36	Dos	1.509929	2.847960861
35	Sgce	1.546281	2.920632608
34	S100a8	1.612564	3.057948161
33	Itsn1	1.670406	3.183042368
32	Chi3l3 /// Chi3l4	1.689186	3.224747006
31	Tjp1	1.691872	3.230756411
30	Mllt3	1.699277	3.247381159
29	C1qdc2	1.713143	3.278744472
28	Hdac11	1.745586	3.35330965
27	Tgm2	1.824354	3.541484308
26	Tgm2	1.841642	3.584177584
25	Sbf2	1.893012	3.714099229

Rank	Gene symbol	Log fold change	Fold change
24	Tgm2	1.997634	3.993444739
23	Coro2b	2.02048	4.057186608
22	Ndn	2.026023	4.072806463
21	Mapk12	2.09874	4.283352502
20	Itsn1	2.151927	4.444209047
19	Bgn	2.179817	4.530960708
18	Col1a2	2.183038	4.541087451
17	Meg3	2.214383	4.640829773
16	Vasn	2.217946	4.652305221
15	D10Ertd610e	2.220844	4.661661794
14	Ndn	2.296636	4.913107786
13	Nov	2.407725	5.306370461
12	Nope	2.449155	5.460961894
11	Elavl4	2.721321	6.594762802
10	Lcn2	2.949104	7.722692566
9	Nov	3.062546	8.354454377
8	Fscn1	3.136315	8.792754389
7	Ear1 /// Ear12 /// Ear2 /// Ear3	3.233197	9.403494326
6	Hba-a1 /// Hba-a2	3.705012	13.04126642
5	Ceacam10	4.616695	24.53373958
4	Slc4a1	4.880442	29.45502985
3	Hbb-b1 /// Hbb-b2	5.707686	52.26182283
2	Hba-a1 /// Hba-a2	7.521218	183.7013324
1	Hba-a1 /// Hba-a2	7.582344	191.6518242

Table S2. Genes involved in cell movement and amino acid metabolism in TSC1 HSC transcriptome

Gene symbol
Genes involved in cell movement
AURKB
CCNB1
KIF20A
LOC643751
PITPNM1
RacGAP1
CALR
ID2
LCN2
MAPK12
TJP1
SLC2A1
FSCN1
NOV
CCR9
CHI3L3
HMMR
Genes involved in amino acid metabolism
FARSA
FARSB
AARS
SLC1A4
SLC4A1
PCMT1
PRMT2
HDC
LDHB
DLAT
GALM
PGAM1