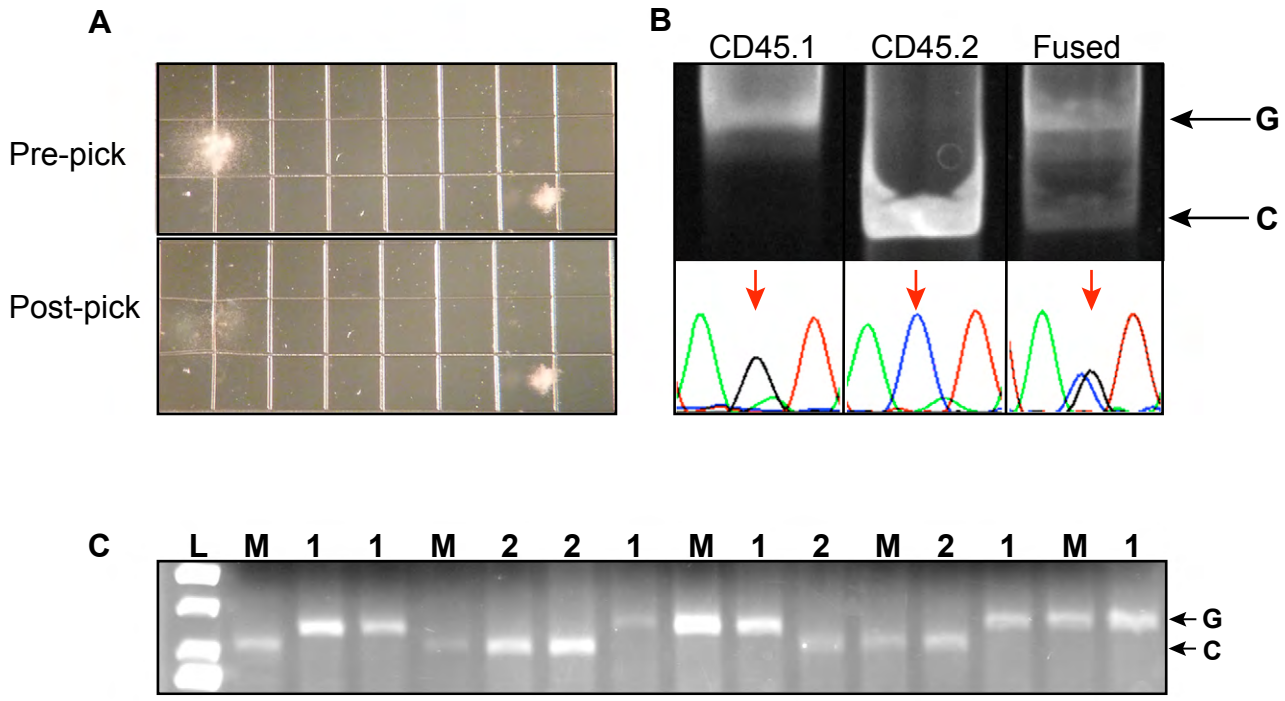

Fig. S1. SNP PCR Strategy. (A) Representative images of CFU-Cs under brightfield, magnified 1X under a dissecting microscope. CFUs were plated in 3 ml cytokine-containing methylcellulose on 60 mm plates. All CFUs characterized in our studies were picked under 4x or 10x magnification to ensure single colonies were isolated. Top panel: image of 2 colonies prior to isolation. Bottom panel: image of colony remnants (left) and untouched colony (right) following isolation. (B) SNP-PCR digest of control CD45.1 and CD45.2 CFUs (top) and sequence histograms (bottom) shown alongside a fused CFU. (C) Control experiment in which WBM was isolated and plated in cytokine-containing methylcellulose from a CD45.1 (1) animal, CD45.2 (2) animal, or WBM was mixed (M) at a ratio or 1:2 prior to plating in methylcellulose. Upon colony isolation, all samples were blinded. The genotypes of each colony were correctly determined following SNP-PCR digest. Each colony isolated from the "mixed" plate digested as a single genotype. There were no false positive fusion events.

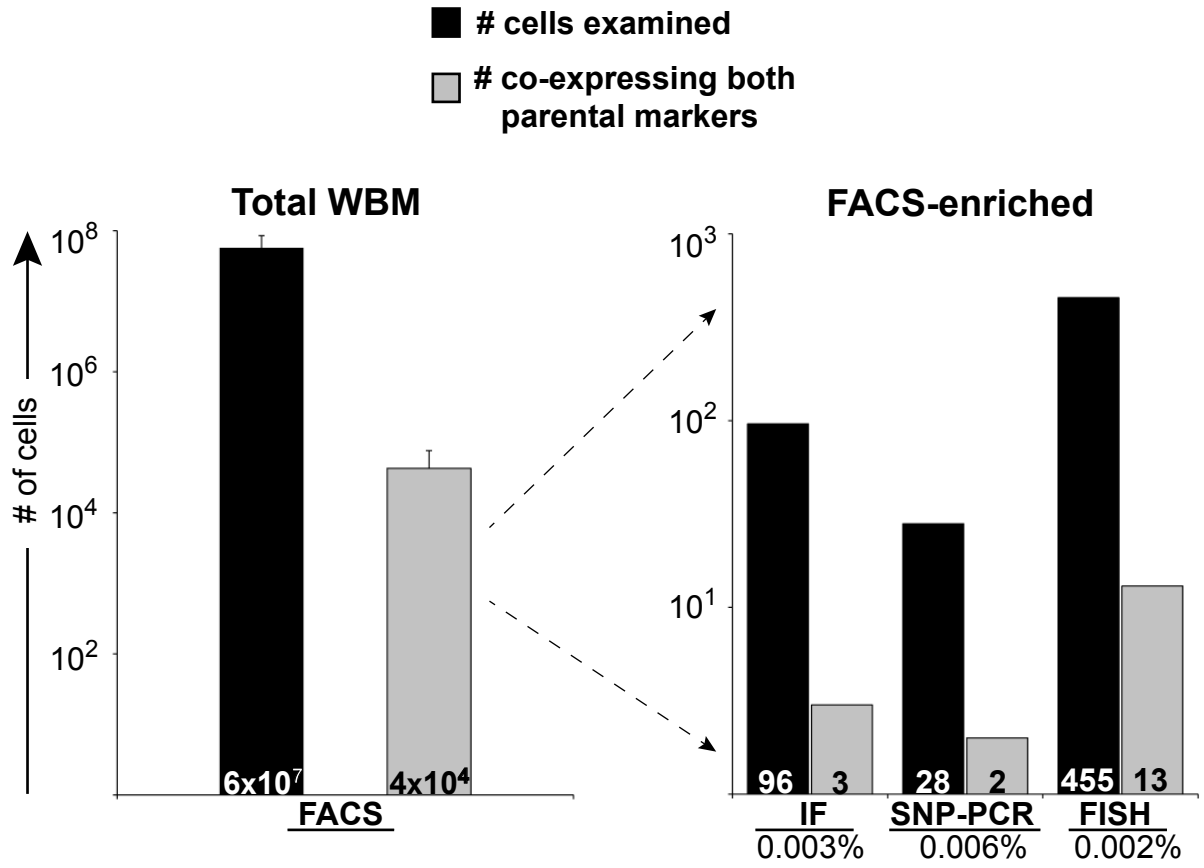

Fig. S2. Frequency of WBM cells co-expressing both parental markers determined by multiple methods. The average number of WBM cells co-expressing parental markers observed following transplantation is shown (left panel). Error bars represent standard deviation between mice. Enriched co-expressing cells were validated as fusion products using immunofluorescent microscopy with complementary antibodies (i.e. not used in FACS), as well as genetic screens: SNP-PCR or FISH. The number of cells analyzed as well as the number of observed fusion events is shown in each column (right panel). The overall frequency of intra-hematopoietic cell fusion in WBM of transplant animals was calculated by multiplying the average frequency determined by FACS by the frequency of validation by secondary assay (e.g. IF, SNP-PCR, FISH) and is shown below each method.

Supplemental Table 1

Single cell events analyzed by SNP-PCR		
Tissue	**G or C allele**	**G/C (fused) alleles**
Transplant		
WBM	28	2 (7%)
Thymus	1	1 (50%)
Total	**29**	**3 (9%)**
Parabiosis		
WBM	11	1 (8%)
Spleen	5	1 (17%)
Total	**16**	**2 (11%)**

Table S1. Single cell events analyzed by SNP-PCR.

Supplemental Table 2: Complete Blood Counts on mice examined in this study

Complete Blood Count on transplant recipients										
Mouse	**Age (Mo.)**	**Time[a] (Mo.)**	**WBC ($x10^3/\mu L$)**	**Hb (g/dL)**	**platelet ($x10^3/\mu L$)**	**Ne (%)**	**Ly (%)**	**Mo (%)**	**Eo (%)**	**Ba (%)**
1° transplant	18	17	6.0	6.6	1374	3.3	69.7	0.1	0.6	26.3
1° transplant	19	17	4.4	7.2	640	7.9	90.0	0.1	1.0	1.0
1° transplant	18	17	3.4	3.8	1200	52.3	45.0	0.0	2.7	0.0
2° transplant	9	7	7.5	18.5	1570	7.4	91.9	0.1	0.4	0.2
2° transplant	9	7	12.0	15.8	1078	11.2	87.5	0.1	1.1	0.1
2° parabiont	19	17	5.0	7.2	280	3.6	92.3	0.2	0.1	3.8
2° parabiont	19	17	4.2	5.8	564	10.3	80.9	0.2	2.1	6.5
2° parabiont	19	17	5.1	6.9	648	27.4	72.5	0.0	0.1	0.0
2° parabiont	19	17	2.4	6.6	1218	40	57.9	0.9	1.2	0.0
2° parabiont	19	17	2.7	7.2	345	53.7	37.9	0.4	8.0	0.0
ref. male*	24		13.0	14.0	3072	32.0	50.0	3.4	2.0	0.3
ref. female*	24		9.2	13.5	1562	21.8	53.7	1.5	2.5	0.5

a: Indicates the number of months elapsed between time of transplant and CBC.
***** Data from Mouse Phenome Database (http://phenome.jax.org), 24-month animals for age comparison.

Table S2. Complete Blood Counts on mice examined in this study.