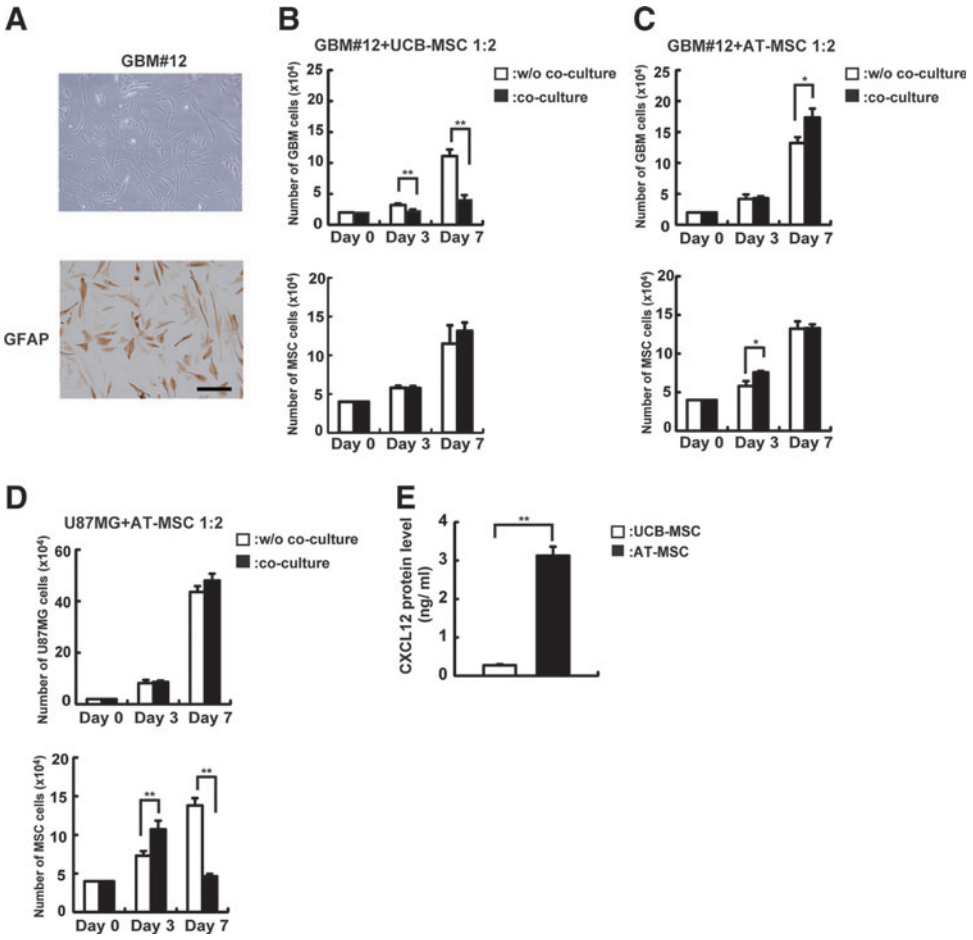
Supplementary Data



SUPPLEMENTARY FIG. S1. Analysis of glioblastoma multiforme (GBM)-derived GBM#12. **(A)** Histological analysis was performed for GBM tissues by immunostaining. Specimens were stained with glial fibrillary acidic protein (GFAP): astrocyte markers. Scale bar indicates 100 μm. **(B)** GBM#12 (2×10^4 cells/well) were cocultured with umbilical cord blood-derived MSCs (UCB-MSCs) (4×10^4 cells/well). After culture for 3 and 7 days, the number and frequency of GBM cells and GFP-labeled UCB-MSCs were measured by a hemocytometer and fluorescence activated cell sorting (FACS). GBM#12 were cocultured with UCB-MSCs at ratio of 1:2. The *top panel* represents number of GBM, and the *bottom panel* represents number of UCB-MSCs in each time point. *White bar*: w/o coculture; *black bar*: coculture with UCB-MSCs (**$P<0.01$). **(C)** GBM#12 (2×10^4 cells/well) were cocultured with adipose-tissue-derived MSCs (AT-MSCs) (4×10^4 cells/well). After culture for 3 and 7 days, the number and frequency of GBM cells and GFP-labeled AT-MSCs were measured by a hemocytometer and FACS. GBM#12 were cocultured with AT-MSCs at a ratio of 1:2. The *top panel* represents the number of GBM, and the *bottom panel* represents the number of AT-MSCs in each time point. *White bar*: w/o coculture; *black bar*: coculture with AT-MSCs (*$P<0.05$). **(D)** U87MG was cocultured with AT-MSCs at a ratio 1:2. The *top panel* represents the number of U87MG, and the *bottom panel* represents the number of AT-MSCs in each time point. *White bar*: w/o coculture; *black bar*: coculture with AT-MSCs (**$P<0.01$). **(E)** CXCL12 protein expression was analyzed in the supernatant of UCB-MSCs (*white bar*) and AT-MSCs (*black bar*) by enzyme-linked immunosorbent assay (**$P<0.01$).