**Fig. S1. Quantitative analysis of *aggrus* expression in tumorigenic and corresponding normal tissues from lung squamous cancer patients.** The first strand cDNA samples (TissueScan[TM] tissue quantitative PCR array #HLRT104, Origene, Rockville, MD) derived from tumorigenic ( ) and corresponding normal ( ) tissues of lung squamous cancer patients were used as templates for real-time quantitative PCR. We performed real-time qPCR using LightCycler 480 system (Roche Applied Science, Indianapolis, IN). The used TaqMan[TM] fluorogenic probes were #7 for *aggrus* and #64 for β-*actin*. The sequences of forward and reverse primers for *aggrus* were 5′-AAATGTCGGGAAGGTACTCG-3′ and 5′-GCCAGGCAAGTGTTCCAC-3′, respectively. The sequences of forward and reverse primers for β-*actin* were 5′-CCAACCGCGAGAAGATGA-3′ and 5′-CCAGAGGCGTACAGGGATAG-3′, respectively. The respective expression levels of *aggrus were* normalized to that of the β-*actin* transcript.

Supplementary Figure S1. Y. Nakazawa *et al.*
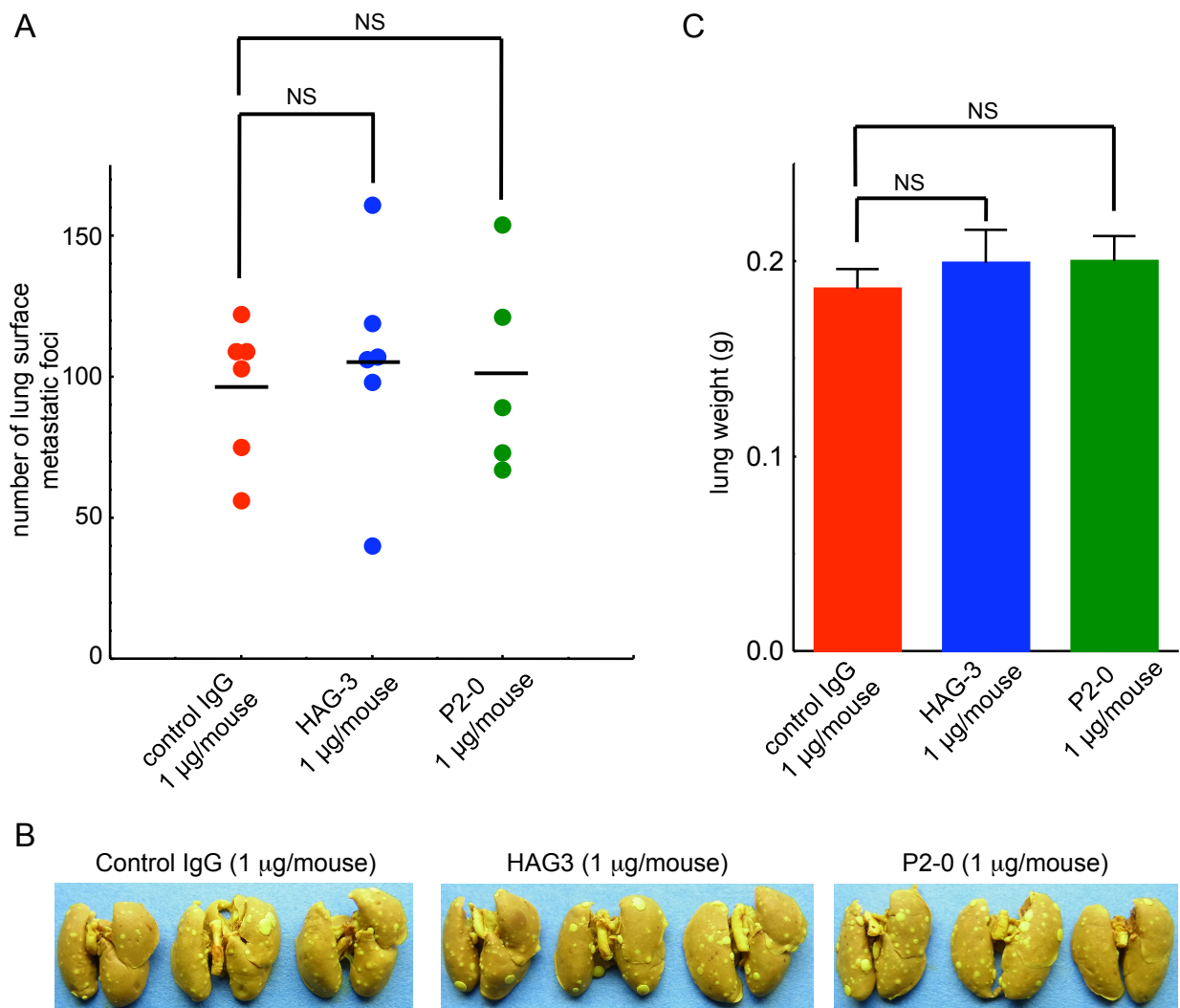
Fig. S2. Effects of P2-0 antibody on the metastasis of Aggrus-negative A375M cells. Human melanoma A375M cells were incubated with control mouse IgG1 (control IgG), P2-0, and HAG-3. The cell suspension (2.5 X 10^5 cells/mouse) was intravenously inoculated into CB-17/Icr-*scid* mice (n=6 or 5). After 30 days, lung surface metastatic foci were counted. Numbers of metastatic foci (A), representative pictures of the lungs (B), and lung weights (C) are shown. Horizontal bars in (A), average. Vertical error bars in (C), standard deviation. NS (not significant) by the Mann–Whitney *U* test.

Supplementary Figure S2. Y. Nakazawa *et al.*