

809 **Supplementary Figure 1. Flow cytometry of large T antigen expression in cervical carcinoma**
810 **cell lines.** Histograms depict flow cytometry analysis of large T antigen expression in HeLa-Sen2,
811 CaSki, and SiHa cells. Cells were either mock-treated (top panels) or treated with GM1
812 overnight (bottom panels). Cells were then mock-infected (open histograms) or infected with
813 SV40 at an MOI of 10 (shaded histograms).

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815 **Supplementary Figure 2. E2 mRNA expression in cervical carcinoma cell lines after treatment**
816 **with GM1.** Cells were left untreated or treated with GM1 and infected with Pava at an MOI of
817 20. At 48 hrs post-infection, E2 mRNA expression was measured by qRT-PCR and normalized to
818 GAPDH mRNA expression. E2 expression is reported as levels of E2 mRNA in cells infected in the
819 presence of GM1 relative to cells infected in the absence of GM1. The results of a typical
820 experiment are shown and represent the average of triplicate samples. Similar results were
821 obtained in two independent experiments.

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823 **Supplementary Figure 3. Effect of E2 expression on p53 and active p105^{Rb} levels in cervical**
824 **carcinoma cell lines.** Cells were left untreated (-) or treated (+) with GM1 and either mock-
825 infected (-) or infected (+) with Pava at an MOI of 20. Protein was harvested at 48 hrs post-
826 infection and analyzed by SDS-PAGE and immunoblotting for p105^{Rb}, p53, and actin (loading
827 control). P indicates hyperphosphorylated p105^{Rb}, and O indicates active, hypophosphorylated
828 p105^{Rb}.

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830 **Supplementary Figure 4. Comparison of E2 expression levels among primary cells.** Cells were
831 treated with GM1 overnight and infected with Pava at an MOI of 10. At 22 hrs post-infection,
832 E2 mRNA expression was measured by qRT-PCR and normalized to GAPDH mRNA levels. E2
833 expression is presented as E2 mRNA relative to infected HFKs. The passage numbers at which
834 the cells were tested are indicated in parentheses. The results of a typical experiment are
835 shown, and represent the average of triplicate samples. Similar results were obtained in two
836 independent experiments.

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838 **Supplementary Figure 5. Expression of wild-type and K339M E2 mRNA.** Cells were treated
839 with GM1 overnight and infected with Pava encoding wild-type or K339M E2 at an MOI of 10.
840 At 22 hrs post-infection E2 mRNA expression was measured by qRT-PCR and normalized to
841 GAPDH levels. E2 expression is presented as the level of K339M mRNA relative to wild-type E2
842 mRNA in these cells. The passage numbers at which the cells were tested are indicated in
843 parentheses. The results of a typical experiment are shown and represent the average of
844 triplicate samples. Similar results were obtained in two independent experiments.

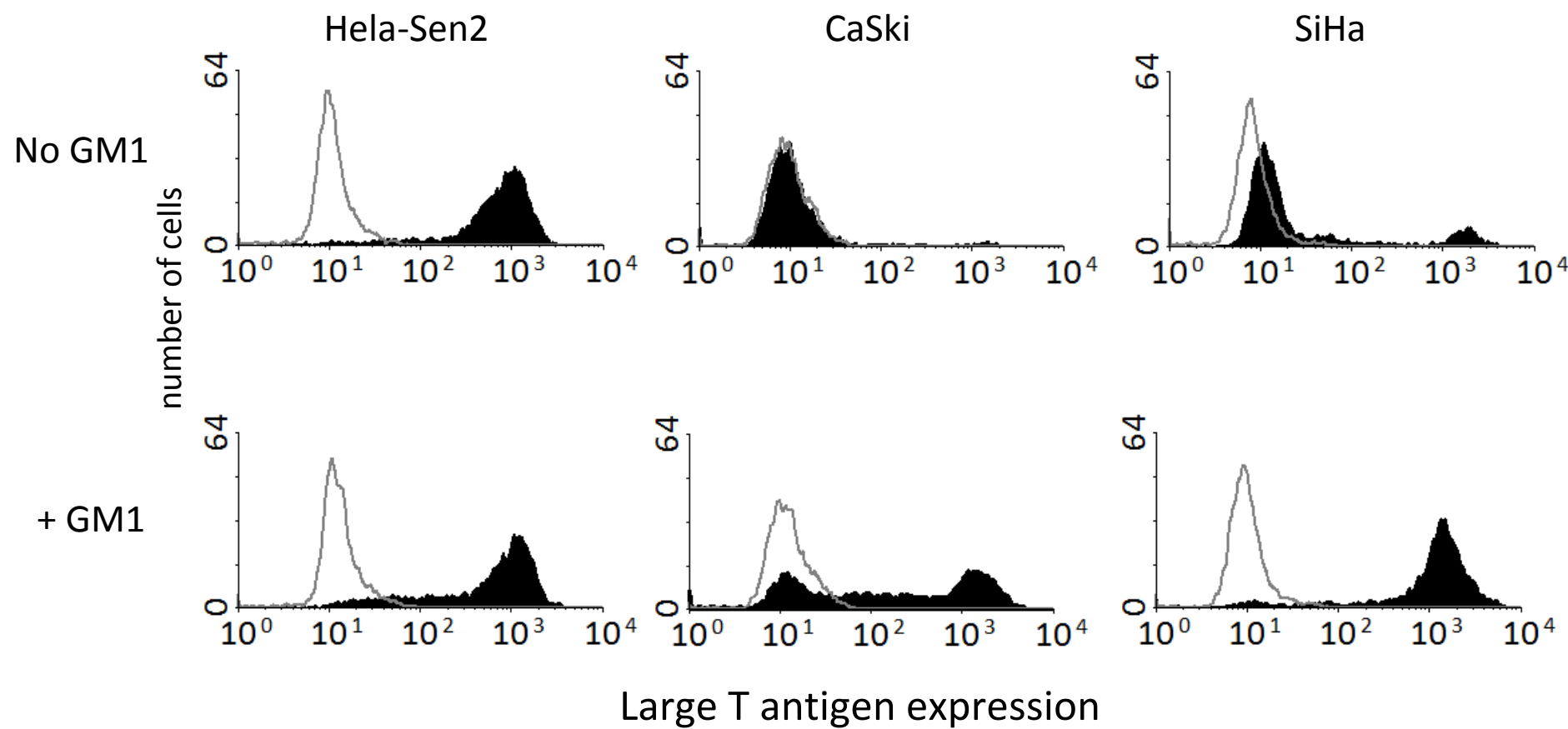
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846 **Supplementary Figure 6. Exogenous HPV 16E6 and 18E7 inhibit increased autofluorescence in**
847 **CVX-104 cells after infection with Pava.** CVX-104 cells expressing vector only (LXSN/RVY) or
848 HPV16 E6 plus HPV18 E7 (16E6/18E7) were treated with GM1 and either mock-infected or
849 infected with Pava at an MOI of 10, as indicated. Autofluorescence and cell granularity were
850 measured by flow cytometry at day four post-infection and are presented on a 2-D plot. The
851 bottom box was drawn to contain ~95% of mock-infected, control cells, and the top box was

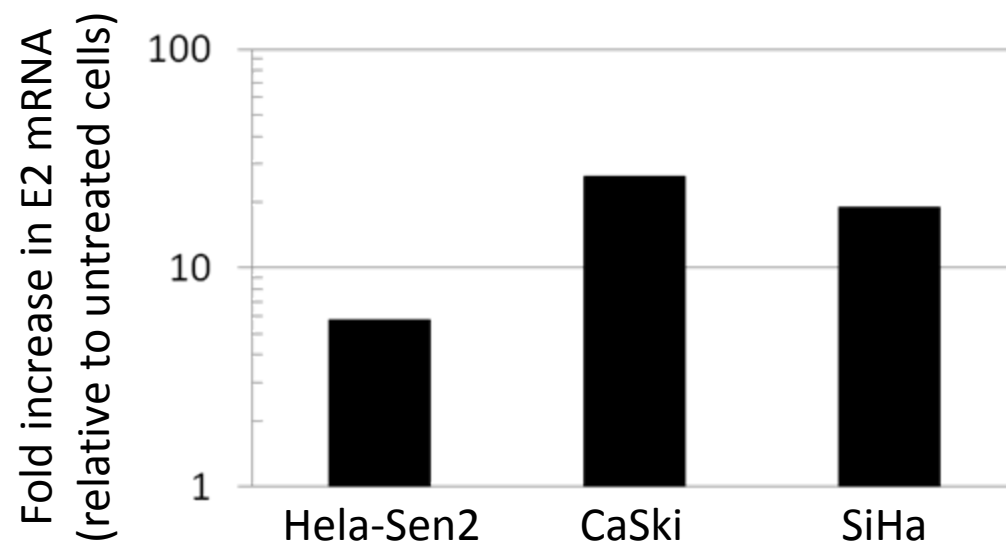
852 drawn to contain senescent cells that display an increase in both autofluorescence and
853 granularity. The numbers indicate the percent of cells in each box.

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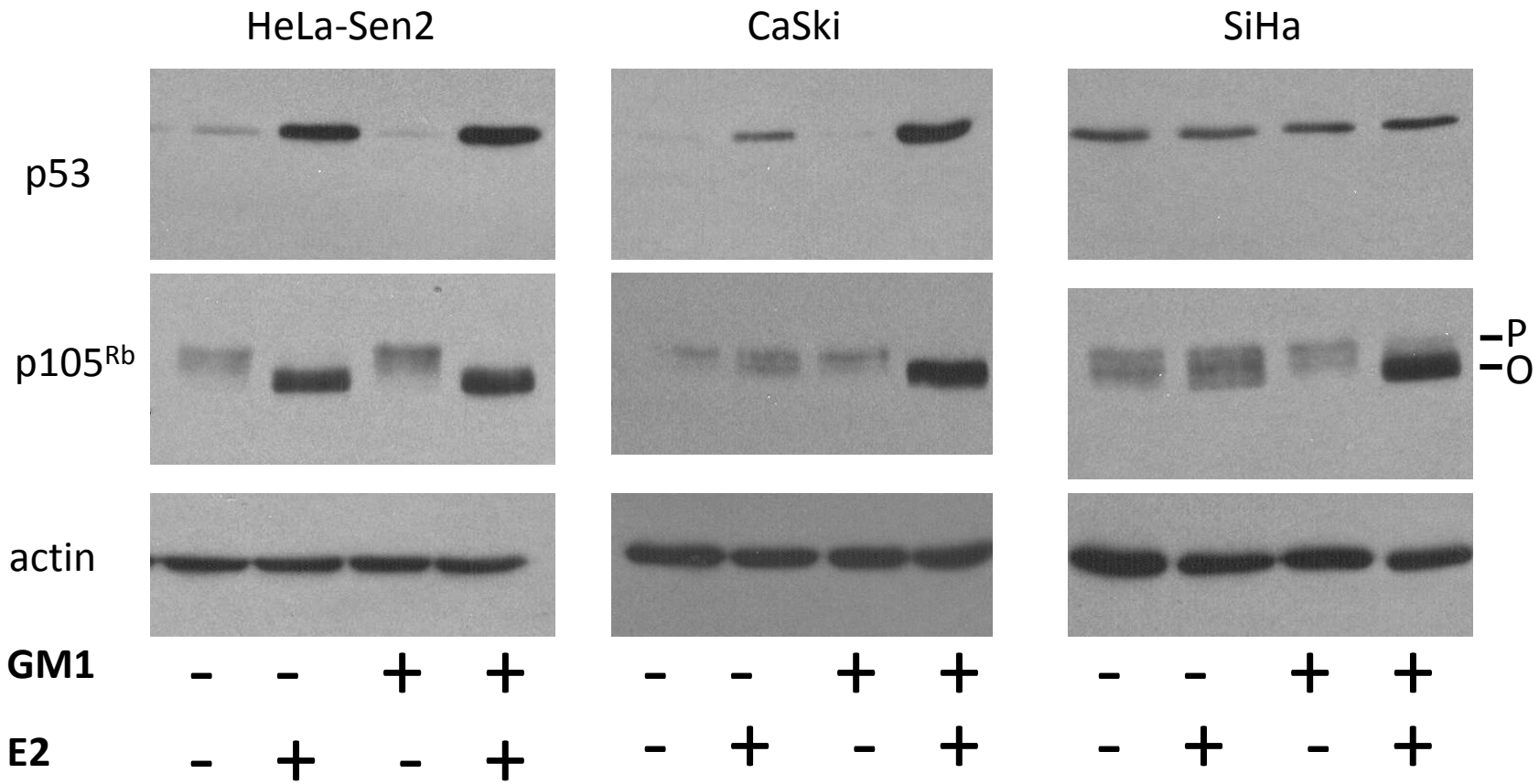
Sup. Fig. 1.



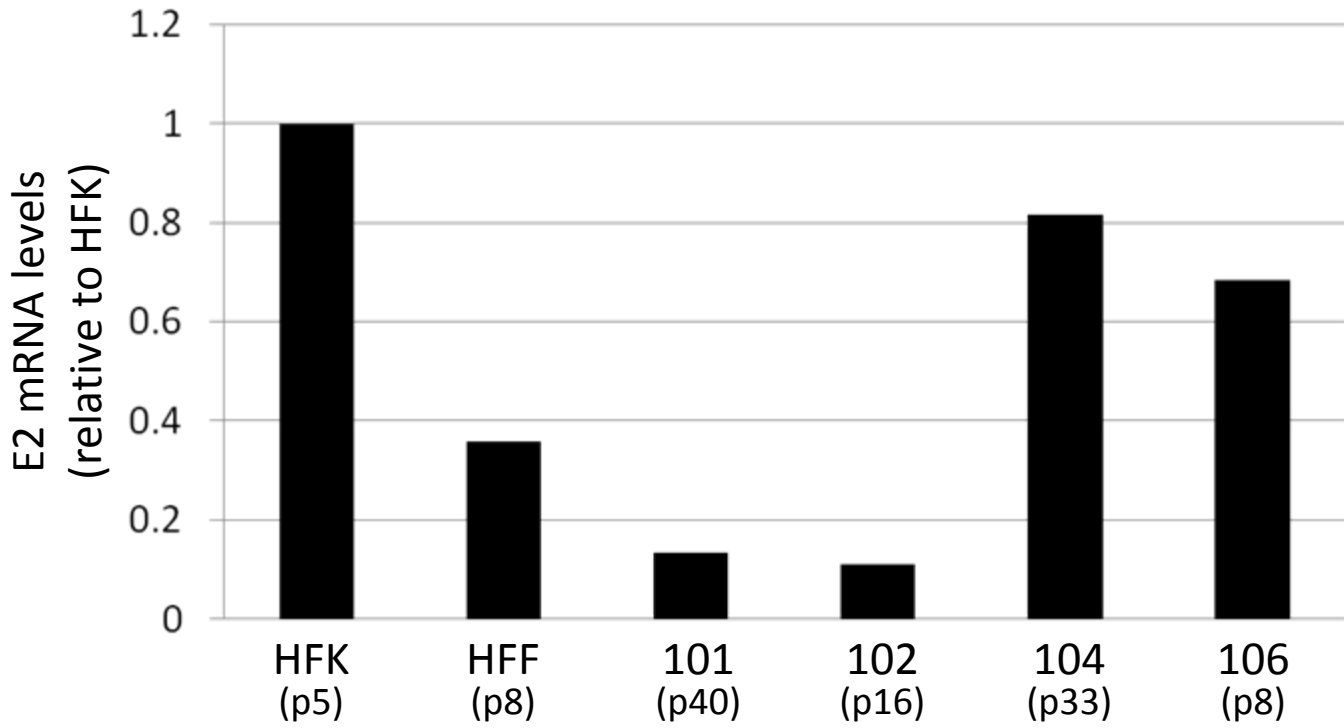
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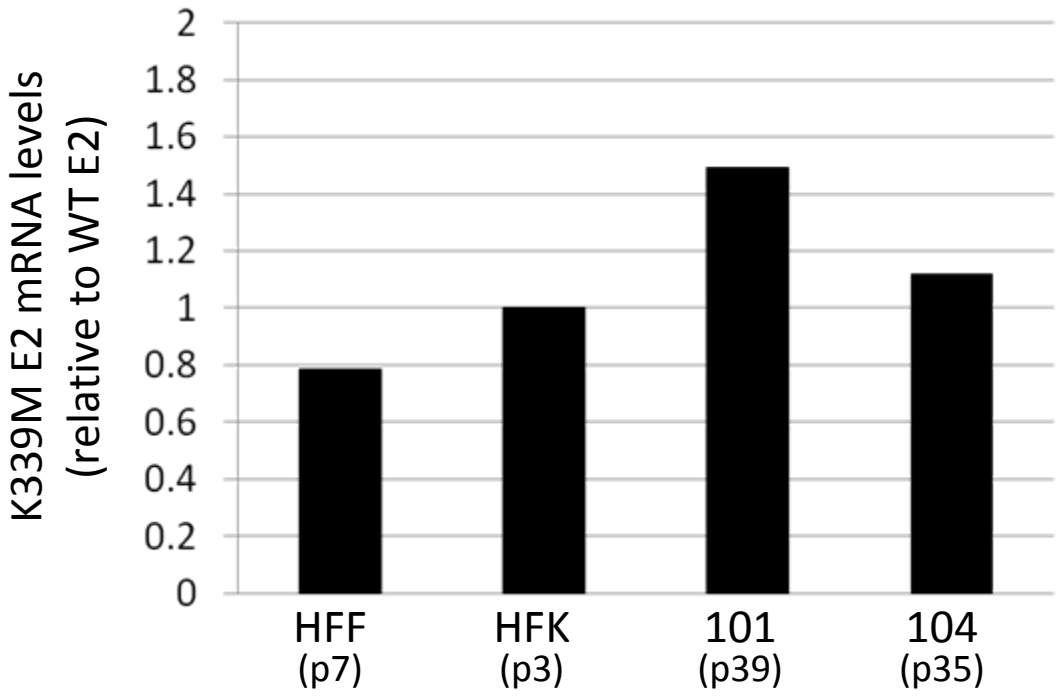
Sup. Figure 3



Sup. Figure 4



Sup. Figure 5



Sup. Figure 6

