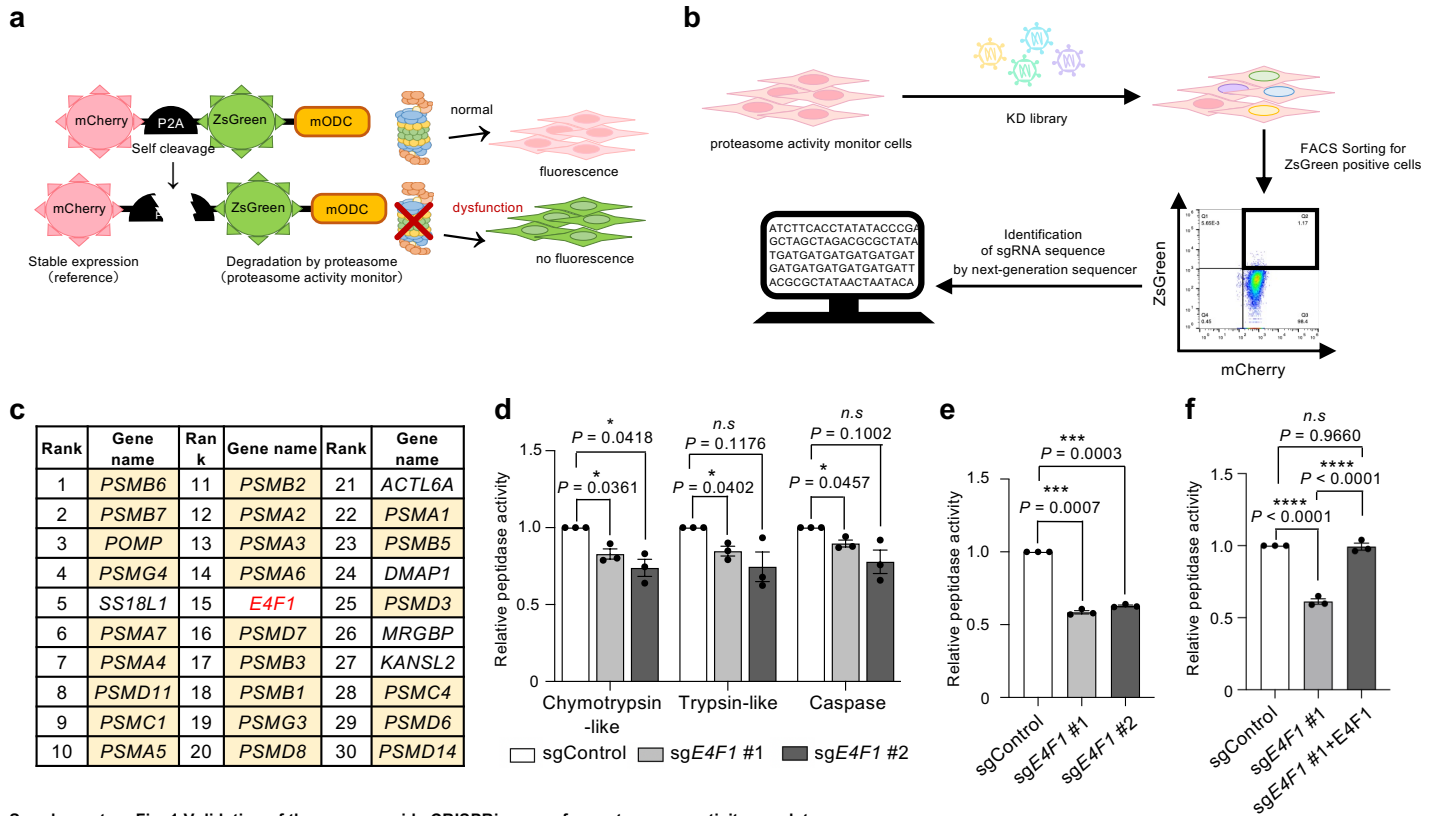




Supplementary Fig. 1 Validation of the genome-wide CRISPRi screen for proteasome activity regulators

a Schematic representation of the proteasome activity monitor. The fluorescent protein ZsGreen was fused to the mODC sequence (ZsGreen-mODC). mCherry, which serves as a reference, was linked with ZsGreen-mODC via the self-cleavage sequence P2A. **b** Schematic overview of the genome-wide CRISPRi screen. The fluorescence intensity of ZsGreen relative to that of mCherry increases when proteasome function is impaired. The cell population in the upper right-hand quadrant of the flow cytometry plot was collected and subjected to next-generation sequencing analysis. **c** List of the top 30 hit genes identified in the screen. **d** Proteasome chymotrypsin-, trypsin-, and caspase-like activities of HEK293T cells transduced with sgControl or sgE4F1. The peptidase activities were measured in the absence of SDS to assess 26S proteasome activity. **e** Proteasome caspase-like activity of HEK293T cells transfected with sgControl or sgE4F1. The peptidase activities were measured in the presence of 0.025% SDS to assess core particle activity. **f** Chymotrypsin-like proteasome activity of the E4F1-knockdown HEK293T cells following re-expression of E4F1 cDNA. The peptidase activities were measured in the absence of SDS. Data represent mean $\pm$ s.e.m. ($n = 3$ biologically independent experiments). Statistical significance was determined using an unpaired two-tailed Student's t-test with Welch's correction (**d**, **e**) or one-way ANOVA followed by Tukey's multiple-comparison test (**f**). * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$; **** $P < 0.0001$; n.s., not significant. All experiments were performed at least three biologically independent times with similar results. Source data are provided as a Source Data file.