Extended Data Figure 2 | Cyclin D/CDK4 negatively regulates PD-L1 protein stability. a, b, Immunoblot (IB) analysis of whole cell lysates (WCL) derived from wild type (WT), *cyclin A1*$^{-/-}$*A2*$^{-/-}$ or WT, *cyclin E1*$^{-/-}$*E2*$^{-/-}$ MEFs. **c,** Quantitative real-time PCR (qRT-PCR) analysis of relative mRNA levels of PD-L1 from wild type MEFs and *cyclin D1*$^{-/-}$*D2*$^{-/-}$*D3*$^{-/-}$ MEFs. Data were represented as mean ± s.d, n = 5. **d,** Cell cycle profiles for WT and *cyclin D1*$^{-/-}$*D2*$^{-/-}$*D3*$^{-/-}$ MEFs, which were labeled with BrdU and analyzed by FACS. **e,** IB analysis of WCL derived from *cyclin D1*$^{fl/fl}$*D2*$^{-/-}$*D3*$^{fl/fl}$ MEFs with or without depleting *cyclin D1* and *cyclin D3* by pLenti-Cre via viral infection (pLenti-EGFP as a negative control), selected with puromycin (1 μg/ml) for 72 hours before harvesting. **f,** IB analysis of WCL derived from *cyclin D1*$^{-/-}$*D2*$^{-/-}$*D3*$^{-/-}$ MEFs stably reintroducing *cyclin D1*, *cyclin D2*, or *cyclin D3*, respectively, with empty vector (EV) as a negative control. **g,** IB analysis of WCL derived from mouse mammary tumors induced by MMTV-*c-Myc* with/without genetic depletion of *cyclin D1*. n = 5 mice per experimental group. **h,** IB analysis of WCL derived from WCL derived from wild type and *cdk6*$^{-/-}$ MEFs. **i, j,** IB analysis of WCL derived from MDA-MB-231 cells stably expressing shCDK6 or shCDK2 as well as shScr as a negative control, respectively. **k, l,** IB analysis of WCL derived from MDA-MB-231 cells transfected with indicated constructs **(k)** and the intensity of PD-L1 band was quantified by the ImageJ software **(l)**. **m,** IB analysis of WCL derived from MDA-MB-231 cells depleted of *Rb* (with shScr as a negative control) treated with the CDK4/6 inhibitor, palbociclib, where indicated. **n, o,** IB analysis of WCL derived from mouse CT26 or 4T1 tumor cell lines treated with or without the CDK4/6 inhibitor, palbociclib or ribociclib, respectively. **p, q,** IB analysis of WCL derived from MDA-MB-231 cells pre-treated with palbociclib (1 μM) for 36 hours before treatment with cycloheximide (CHX) for the indicated time points **(p)** and PD-L1 protein abundance was quantified by the ImageJ and plotted as indicated **(q)**. **r,** IB analysis of WCL derived from 19 different cancer cell lines with indicated antibodies. **s-u,** IB analysis of WCL derived from MCF7, T47D or HLF stably expressing p16 as well as EV as a negative control. **v-x,** IB analysis of WCL derived from MDA-MB-436, BT549 or HCC1937 stably expressing three independent shRNAs against *p16* as well as shScr as a negative control.