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Supplementary Materials for

SLC36A1-mTORC1 signaling drives acquired resistance to CDK4/6 inhibitors

Akihiro Yoshida*, Yiwen Bu, Shuo Qie, John Wrangle, E. Ramsay Camp, E. Starr Hazard, Gary Hardiman, Renée de Leeuw, Karen E. Knudsen, J. Alan Diehl*

*Corresponding author. Email: jad283@case.edu (J.A.D.); axy234@case.edu (A.Y.)

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Supplemental Figure 1

С 1205Lu Control Vehicle +CDK4/6i 1205CR1 1205CR6 1205CR2 1205CR7 CDK4/6i Everolimus D 90 80 ■Vehicle SA-Bgal positive cells (%) 70 Everolimus 60 50 40 30 20 10 0 CDK4/6i + Control 1205CR1 1205CR2 1205CR6 1205CR7 Е Antigen processing and presentation Calcium signaling pathway Cell adhesion molecules (CAMs) Chemokine signaling pathway Complement and coagulation cascades Cytokine-cytokine receptor interaction DNA replication ECM-receptor interaction Hematopoietic cell lineage Herpes simplex infection Inflammatory bowel disease (IBD) Influenza A Linoleic acid metabolism Measles Osteoclast differentiation Pathways in cancer Pathways in cancer PI3K-Akt signaling pathway Regulation of actin cytoskeleton Systemic lupus erythematosus TNF signaling pathway Type I diabetes mellitus 4 5

Fig. S1. Palbociclib-resistant melanoma cells retain broad resistance to CDK4/6i or CKD4/6i's. (**A**) FACS analysis of 1205Lu, 1205CR1, 2, 6 and 7 cells treated with or without ribociclib (1 μM) for 1 day (top panel). FACS analysis of TE7 and TE7CR cells

-log10 p-value

Supplemental Figure 1 Continued

treated with or without palbociclib (1 μ M) for 1 day (bottom panel) (**B**-**C**) 1205Lu cells were treated with or without palbociclib (1 μ M) or everolimus (50 nM), 1205CR1, 2, 6 and 7 cells proliferating with palbociclib (1 μ M) with or without everolimus (50 nM) for 1 day for FACS analysis (**A**) or 8 days for SA-βgal assay (**C**). (**D**) Quantification of SAβgal positive cells from (**C**); data represent mean ± SD, * *P*<0.01 (two-tailed Student's ttest, n=3). (E) TOP biological pathways (Senescence vs Resistance) from RNA sequence.



Fig. S2. Analyses of WM3918, TE7, and TE10 cells with CDK4/6i resistance. (A)

WM3918 cells treated with or without palbociclib (1 µM) for 1 day and CDK4/6i-

resistant cells (3918CR1, 2 and 4) proliferating with palbociclib (1 μ M) were subjected to BrdU incorporation for 45 minutes. BrdU positive cells were determined by FACS analysis. (**B**) QPCR analysis of samples from (**A**) using sets of primers for SLC36A1, FXR1, CDK1, FEN1 and PCNA. Data were normalized by GAPDH and represent mean \pm SD, * *P*<0.01 (two-tailed Student's t-test, n=3). (**C**) Western blot analysis of lysates from (**A**) using antibodies to Rb, FXR1, SLC36A1, P-S6, CDK2 and βactin. (**D**) Western blot analysis of lysates from TE7, TE10, and CDK4/6i resistant cells (TE7CR and TE10 CR) using antibodies to Rb and HSP90.





Fig. S3. Different acquired resistance mechanisms between 1205CR1-2 and

1205CR6-7 cells. (**A**) Representative images of SA-βgal staining in 1205CR1-2 cells infected with vehicle (Control) or Rb1. (**B**) 1205Lu, 1205CR1, 2, 6 and 7 cells were

subjected to a 45 minutes BrdU pulse following exposure to AZD5438 (AZD) treatment (0.5 μ M). BrdU positive cells were determined by FACS analysis. (**C**) Representative images of SA-βgal staining in 1205Lu, 1205CR1, 2, 6 and 7 cells treated with AZD5438 (AZD) (0.5 μ M) or palbociclib (1 μ M) for 8 days. (**D**) 1205Lu, 1205CR1, 2, 6 and 7 cells transfected with siControl or siCDK2 were subjected to a 45 minutes BrdU pulse. BrdU positive cells were determined by FACS analysis. (**E**) Representative images of SA-βgal staining in 1205CR1, 2, 6 and 7 cells after 8 days post transfection with siControl or siCDK2. Scale bars represent 100 μ m. (**F**) Quantification of SA-βgal positive cells from (**E**); data represent mean ± SD, **P*<0.01 (two-tailed Student's t-test, n=3). (**G**) Western analysis of lysates from 1205Lu, 1205CR1, 2, 6 and 7 cells transfected with siControl or siCDK2 using antibodies against CDK2, CDK1 and βactin. (**H**) QPCR analysis of samples from (**G**) using sets of primers for CDK1, FEN1 and PCNA. Data were normalized by GAPDH and represent mean ± SD, **P*<0.01 (two-tailed Student's t-test, n=3), ***P*<0.05 (two-tailed Student's t-test, n=3).



Fig. S4. Overexpression of CDKs does not override CDK4/6i-induced senescence in melanoma. (A) Western analysis of lysates from 1205Lu cells infected with either
CDK2, CDK4 or CDK6 using antibodies to CDK2, CDK4, CDK6 and βactin. (B) FACS

analysis of cells from (**A**) treated with palbociclib (1 μ M) for 1 day (middle panel) or 8 days (bottom panel) without palbociclib (top panel). (**C**) Representative images of SA- β gal staining in cells from (**A**) treated with or without palbociclib (1 μ M). (**D**) Quantification of SA- β gal positive cells from (**C**); data represent mean \pm SD, N.S., Not Significant (two-tailed Student's t-test, n=3). (**E**) Clonogenic colony formation assay of cells from (**a**) treated with or without palbociclib (1 μ M) for 8 days. The numbers indicate quantification of colonies from three independent experiments.



Fig. S5. The impacts of adding amino acids and SLC36A1 in the context of CDK4/6i-induced senescence. (A) Western analysis of lysates from 1205Lu cells cultured in medium supplemented with (proline, alanine and glycine) for 1 day using

antibodies to phospho-S6 and total S6. (B) Clonogenic colony formation assay of 1205Lu cells treated with palboiclib (1 µM), or cultured in medium supplemented with (proline, alanine and glycine) or both for 8 days or 1205Lu cells without treatment (Control). The numbers indicate quantification of colonies from three independent experiments. (C) Clonogenic colony formation assay of 1205Lu cells treated with palbociclib (1 μ M), cultured with varying concentrations of amino acids as indicated for 8 days and 1205Lu cells without treatment (Control). The numbers indicate quantification of colonies from three independent experiments. (**D**) QPCR analysis of samples from 1205Lu cells treated with vehicle (Control), palbociclib (1 µM) for 8 days or in CDK4/6iresistant clones grown in presence of palbociclib (1 µM) (1205CR1, 2, 6 and 7) using sets of primers for indicated on the bottom of figure. Data were normalized by GAPDH (n=3). (E) Western analysis of lysates from 1205Lu cells infected with different hairpinmediated knockdown of SLC36A1 (ShSLC36A1-1, ShSLC36A1-2, ShSLC36A1-3 and ShSLC36A1-4) using antibodies to SLC36A1 and β actin. The numbers indicate quantification of SLC36A1 determined by SLC36A1/Bactin ratio. (F) Clonogenic colony formation assay of cells infected with ShControl (Control), ShSLC36A1-1 or ShSLC36A1-4 after treatment with or without palbociclib (1 μ M) for 8 days. The numbers indicate quantification of colonies from three independent experiments. (G) FACS analysis of cells expressing empty vector or SLC36A1 treated with or without palbociclib (1 μM) for 1 day. (H) Representative images of SA-βgal staining in 983B, 239A, 451Lu and WM3918 cells introduced with vector control or SLC36A1 after treatment of DMSO or palbociclib (1 µM) for 8 days. (I) 1205Lu (Control), 1205CR1, 2, 6 and 7 cells were transfected with SiControl or SiSLC36A1 and then subjected to a 45

minutes BrdU pulse. BrdU positive cells were determined by FACS analysis. (J) Representative images of SA- β gal staining in 1205Lu (Control), 1205CR1, 2, 6 and 7 cells after 8 days post transfection with siControl or siSLC36A1. Scale bars represent 100 μ m.



Fig. S6. FXR1 regulates SLC36A1 protein expression. (A) QPCR analysis of samples from 1205Lu cells treated with or without palbociclib (1 μ M) for 8 days, and 1205CR1, 2, 6 and 7 cells for FXR1. Data were normalized by GAPDH and represent mean \pm SD.

N.S., Not Significant (two-tailed Student's t-test, n=3). (**B**) Western analysis of lysates from 293T cells introduced with ShFXR1 or FXR1 using antibodies to FXR1, SLC36A1 and β actin. (**C**) QPCR analysis of samples from 1205CR6 and 1205CR7 cells with or without ShFXR1 for genes indicated on the bottom of the panels. Data were normalized by RPS18S and represent mean ± SD. N.S., Not Significant (two-tailed Student's t-test, n=3). (**D**) G-Score of SLC36A1 calculated by QGRS Mapper (http://bioinformatics.ramapo.edu/QGRS/index.php).





Fig. S7. FXR1 overrides CDK4/6i-induced senescence. (**A**) Representative images of SA-βgal staining in 1205CR6 and 1205CR7 cells introduced with vehicle (Control) or ShFXR1. (**B**) Representative images of SA-βgal staining in 1205Lu cells introduced with

vehicle (Control) or FXR1 with or without treatment of palbociclib (1 μ M) for 8 days. (C) FACS analysis of 1205Lu and 983B cells overexpressing FXR1 (FXR1-1 or FXR1-2) treated with vehicle, palbociclib (1 μ M) for 1 day (middle panel) or 8 days (bottom panel). (**D**) Western blot analysis of lysates from 1205Lu and 983B cells with vehicle (Control) or FXR1 using antibodies to FXR1 and βactin. (**E**) Representative images of SA-βgal staining in 983B cells introduced with vehicle (Control) or FXR1 with or without treatment of palbociclib (1 μ M) for 8 days. (**F**) Quantification of SA-βgal positive cells from (**E**). Data represent mean \pm SD, * *P*<0.01 (two-tailed Student's t-test, n=3). (**G**) Representative images of SA-βgal staining in 1205Lu cells introduced with vehicle (Control), ShFXR1, SLC36A1 or ShFXR1 + SLC36A1.



Fig. S8. RNA-seq analysis of additional cancers with CDK4/6i resistance. (**A**) Western blot analysis of lysates from 1205 cells overexpressed with either SLC36A1 or Raptor using antibodies to SLC36A1, Raptor, CDK2 and βactin. (**B**) QPCR analysis of

samples from (**A**) for CDK1, FEN1 and PCNA. Data were normalized by GAPDH and represent mean ± SD. (**C**) Analysis of RNA seq data in GEO database repository (V720; GSE40513, T47D; GSE117743, HEY; GSE63529, TE7; GSM3101838, LNCaP and LAPC4; GSE99675) for SLC36A1.