#### *Lukinović et al. Supplementary Information*

### **SMYD3 impedes small cell lung cancer sensitivity to alkylation damage through RNF113A methylation-phosphorylation crosstalk**

#### **Supplementary Figure Legends**

## **Supplementary Figure S1. SMYD3 is a candidate regulator of SCLC susceptibility to alkylating chemotherapy**

**A**, Synthetic lethality screening using a library comprised of 285 characterized inhibitors, testing H209 SCLC cells sensitivity to cisplatin genotoxicity. Data represent relative growth of H209 cells treated with a combination of cisplatin  $(1 \mu M)$  and different inhibitors (1  $\mu$ M each) compared to cisplatin alone. **B**, Analysis of normal human lung single-cell RNA sequencing data reveals low *SMYD3* expression in pulmonary neuroendocrine cells (PNEC); clusters of cell types are labeled; lung epithelial cell types in red (Human Lung Cell Atlas (41)). **C-H**, H209, H1092 and DMS-114 SCLC cell viability assays using different concentrations of either 4H-CP (C-E) or MMS (F-H) with or without SMYD3i (EPZ031686). Percentage of viable cells under each condition was normalized to untreated cells. *Pvalue* were calculated by two-way ANOVA with Tukey's testing for multiple comparisons. Data are represented as non-linear regression with mean ± SEM. **I**, Loewe synergy score calculated by SynergyFinder 2.0, with individual dose-response curves (left) and doseresponse matrix (right) for 4H-CP and SMYD3i. **J**, Immunoblot analyses were performed using the indicated antibodies with lysates of H1092 engineered cells used in xenograft assays presented in Figures 1F-H. Actin or Tubulin are shown as a loading control.

## **Supplementary Figure S2. Identification of RNF113A as a novel methylated substrate of SMYD3**

**A**. *In vitro* methylation assay were performed using radiolabeled S-adenosylmethionine and recombinant RNF113A and SMYD3, with increasing concentrations of SMYD3 inhibitor (EPZ031686) at the indicated concentrations. Top panel, autoradiogram of methylation assay. Bottom panel, Coomassie stain of proteins in the reaction. **B**, Specific recognition of RNF113A K20me3 peptides by the anti- RNF113A-K20me3 antibody by dot blot analysis using the indicated biotinylated peptides. Streptavidin is shown as the loading control. **C**, Non-radiolabeled *in vitro* methylation assay using recombinant SMYD3 and RNF113A biotinylated peptides with different K20 methylation states as staring material. Methylation events are detected using dot blot and immunodetection by RNF113A K20me3 antibody. Streptavidin is shown as the loading control.

In all panels, representative of at least three independent experiments is shown unless stated otherwise. The numbers below the immunoblot lines represent the relative signal quantification (see also Supplemental Table 5).

### **Supplementary Figure S3. Characterization of RNF113A methylation in SCLC cell lines**

**A**, Immunoblot analysis with the indicated antibodies of endogenous RNF113A K20me3 methylation following immunoprecipitation of total RNF113A from HeLa cells expressing doxycycline-inducible shRNA against SMYD3. Tubulin is shown as a loading control. **B**. Immunodetection of RNF113A K20me3 following immunoprecipitation of stably expressed HA-RNF113A in HeLa cells after treatment with different concentrations of SMYD3i. Tubulin is shown as a loading control. **C**, Related to Figure 3D, validation of NAPY markers expressions (NEUROD1; ASCL1; POU2F3; YAP1) in classified SCLC subtypes of human lung cancer. Boxes represent 25th to 75th percentile, whiskers: 10% to 90%, center line: median. *P-value* were calculated by Kruskal-Wallis test. Analysis was performed using FPKM data for each specified gene obtained from NIHMS782739- Suppl\_Table10 (34). NAPY SCLC subclassification was based on the original classification by Rudin et al., presented in NIHMS1023395-Supplementary\_Table\_1 (32). **D-E**, Pearson correlation analyses of SMYD3 expression and SCLC cell lines resistance to cyclophosphamide (D,  $\rho$  = 0.48) and of EZH2 and SLFN11 expressions and SCLC cell lines resistance to platinum-based therapy (E,  $p = 0.16$  and  $p = -0.26$  respectively). The area under curve (AUC) was calculated by integration under the 16-point concentrationresponse curves, using the Broad Institute and NCI's Cancer Target Discovery and Development Network: Cancer Therapy Response Portal (CTRP). Pearson correlation coefficient (ρ) was calculated between gene expression and AUC.

**F-G**, Immunoblot analysis was performed with indicated antibodies using lysates of engineered DMS-114 cells (F) which were then used in cell survival assays using different concentrations of MMS (G). Percentage of living cells under each condition was normalized to untreated cells. *P-value* were calculated by two-way ANOVA with Tukey's testing for multiple comparisons. Data are represented as non-linear regression with mean  $±$  SEM.

In all panels, representative of at least three independent experiments is shown unless stated otherwise. The numbers below the immunoblot lines represent the relative signal quantification (see also Supplemental Table 5).

### **Supplementary Figure S4. RNF113A is a phosphoprotein and its methylation repels the phosphatase PP4**

**A**, Immunoblot analysis was performed with the indicated antibodies after coimmunoprecipitation of endogenous PPP4R3a from 293T cell extracts expressing HA-RNF113A WT, K20A or K20F mutants. **B**, Immunoblot analysis of RNF113A migration using engineered HeLa extracts with stable expression of RNF113A wildtype, S6A, N4, N5 and K20F mutants. Ku80 is shown as a loading control. **C**, Model of RNF113A regulation by the crosstalk of post-translational modifications induced by PP4 and SMYD3.

In all panels, representative of at least three independent experiments is shown unless stated otherwise. The numbers below the immunoblot lines represent the relative signal quantification (see also Supplemental Table 5).

## **Supplementary Figure S5. Methylation-phosphorylation crosstalk regulation of RNF113A impacts its E3 ligase activity**

**A**, Immunoblot analysis was performed using the indicated antibodies with lysates of HeLa S3 engineered cells. Tubulin is shown as a loading control. **B**, Immunoblot analysis was performed with the indicated antibodies after *in vitro* E3 ubiquitin ligase activity assays using HA-RNF113A purified from HeLa S3 cells, with or without prior alkylating agent (MMS) treatment. ATP and E1/E2 enzymes were added as shown. **C**, Immunodetection

of auto-ubiquitinated RNF113A after TUBE (tandem ubiquitin binding element) pulldowns using H1048 SCLC cells extracts following treatment with 4H-CP. **D**, Immunoblot analysis was performed with the indicated antibodies after TUBE pulldowns from HeLa cells stably expressing RNF113A wildtype or catalytically inactive RNF113A ΔRING mutant, with or without MMS-induced alkylation damage. DNA damage marker  $\gamma$ H2A.X is shown as a control of damage induction. **E**, Immunoblot analysis was performed with the indicated antibodies demonstrating RNF113A auto-ubiquitination after Ni-NTA pulldown from 293T cells with or without His-Ub ectopic expression and MMS treatment as shown. **F**, Cell survival assays using increasing concentrations of cisplatin in control and engineered DMS-114 SCLC cells with stable expression of SMYD3 and RNF113A. Percentage of living cells under each condition was normalized to untreated cells. *P-value* were calculated by two-way ANOVA with Tukey's testing for multiple comparisons. Data are represented as non-linear regression with mean ± SEM. **G**, Immunoblot analysis was performed with the indicated antibodies after TUBE pulldowns from HeLa cells stably expressing HA-RNF113A wildtype, S6A, N4 or N5 mutants, with or without MMS treatment. **H**, Immunoblot analysis was performed with the indicated antibodies after TUBE pulldowns from HeLa cells stably expressing HA-RNF113A wildtype or K20F mutant, with or without MMS treatment. **I**, Immunoblot analysis was performed with the indicated antibodies using HeLa cells stably expressing either RNF113A wildtype or K20F mutant, with or without MMS treatment. **J**, Immunoblot analysis of auto-ubiquitinated RNF113A after Ni-NTA pulldown from 293T cells with ectopic expression of His-Ub, HA-RNF113A wildtype or K20F mutant and MMS treatment; where indicated. **K**, Immunoblot analysis was performed with the indicated antibodies after TUBE pulldowns from HeLa cells stably expressing HA-RNF113A wildtype, K20F, N5 or K20F/N5 mutants, with or without MMS treatment.

In all panels, representative of at least three independent experiments is shown unless stated otherwise. The numbers below the immunoblot lines represent the relative signal quantification (see also Supplemental Table 5).

## **Supplementary Figure S6 (related to Figure 6). RNF113A regulation impacts its function in DNA dealkylation repair**

**A**, Immunoblot analysis with indicated antibodies for comparison of SMYD3 and RNF113A expression levels in HeLa, U20S and H1048 SCLC cells. **B**, Immunoblot analysis was performed using the indicated antibodies with lysates of U2OS cells expressing the indicated vectors. **C**, Immunoblot analysis was performed as in (G) using lysates of U2OS cells expressing the indicated vectors. **D**, Immunoblot analysis of shRNA control (shControl) or shRNA RNF113A knockdown (shRNF113A) in U2OS cells. GAPDH is shown as a loading control. **E**, Representative images of MMS-induced ASCC3 foci in U2OS cells reconstituted with either RNF113A wildtype, S6A or N5 mutants after shRNA knockdown of endogenous RNF113A. Foci were monitored by immunofluorescent staining of ASCC3 (left panels) and the DNA damage marker  $\gamma$ H2A.X (right panels). **F**, Quantification of U2OS cells from (E) with five or more MMS-induced ASCC3 foci. At least 100 cells were counted for each experimental condition. *P-value* were calculated by twotailed unpaired Student's t test, error bars represent mean ± SD. **G**, Representative images of immunofluorescent staining signal intensity of MMS-induced ASCC3 foci in U2OS cells related to Figure 4D. **H**, Quantification of immunofluorescent staining signal intensity of individual ASCC3 foci from RNF113A wildtype ( $n = 26$  foci) and RNF113A K20F mutant (n = 18 foci) expressing U2OS cells as shown in (G). *P-value* were calculated by two-tailed unpaired Student's t test, error bars represent mean ± SEM. **I-J**, Cell survival assays with the indicated concentrations of MMS in HeLa cells with or without SMYD3i (I) or in engineered HeLa cells stably expressing either control vector, RNF113A WT or K20F mutant (J). Percentage of living cells under each condition was normalized to untreated cells. *P-value* were calculated by two-way ANOVA with Tukey's testing for multiple comparisons. Data are represented as non-linear regression of the mean  $\pm$  SEM. In all panels, representative of at least three independent experiments is shown unless

stated otherwise.

## **Supplementary Figure S7. SMYD3 inhibition sensitizes SCLC to alkylating agents**  *in vivo*

**A**, Schematic of the SCLC mouse model that recapitulates canonical genetic alterations that co-occur in human disease. The triple knockout (TKO) model was generated by breeding mice that carry conditional deletion of *Rb1LoxP/LoxP*, *Rbl2LoxP/LoxP* and *Tp53 LoxP/LoxP*. Tumorigenesis in mice is induced by intratracheal installation of adenovirus expressing Cre-recombinase (Ad-Cre). **B**, Representative IHC staining of normal lung tissue and TKO and RPM (*RbLoxP/LoxP;p53LoxP/LoxP;H11LSL-MycT58A*) SCLC mouse models (representative of n = 12 samples for each group). Of note all analyzed *TKO* and *RPM* samples showed nuclear and cytoplasmic SMYD3 expression with H-score >150. Tumors in *TKO;Smyd3* mutant mice were negative for SMYD3 expression which confirms correct Cre-recombination of mutant allele. Scale bars, 50 µm. **C**, *Smyd3* expression in wildtype lung and *TKO* tumor samples by RTq-PCR, n = 12 samples for each group. *P-values* were

calculated by two-tailed unpaired t-test. **D,** Schematic of the *Smyd3* conditional allele. In the presence of Cre recombinase, exon 2 is deleted to disrupt *Smyd3* expression. **E**, Immunoblot analysis with the indicated antibodies of lysates from *Smyd3<sup>LoxP/LoxP* lung</sup> fibroblasts transduced with Ad-Cre or vehicle (control). Tubulin is shown as a loading control. **F**, Immunoblot analysis with the indicated antibodies of tumor biopsy lysates from *TKO and TKO;Smyd3* mutant mice treated with cyclophosphamide (CP) or vehicle (control). Two independent and representative samples are shown for each condition. Tubulin is shown as a loading control.

## **Supplementary Figure S8. SMYD3 inhibition sensitizes SCLC PDX to alkylating agents.**

**A**, Representative H&E and IHC staining for cell proliferation marker phospho-histone 3 (pH3) and apoptosis maker cleaved Caspase 3 (cl. Caspase 3) in biopsies collected from therapy naïve SCLC patient derived xenografts (PDX-1) treated with SMYD3 inhibitor EPZ031686 (SMYD3i) and cyclophosphamide (CP). Representative of  $n = 6$  mice for each experimental group. Scale bars, 50 μm. **B-C**, Quantification of phospho-Histone 3 (pH3) (B) and cleaved Caspase 3 (cl. Caspase 3) positive cells (C) in PDX samples as in (A). Boxes represent 25th to 75th percentile, whiskers: min. to max., center line: median; *Pvalue* were calculated by two-way ANOVA with Tukey's testing for multiple comparisons. **D**, Weight analysis over time of mouse groups from the PDX-1 study. **E**, Representative H&E and IHC staining for cell proliferation marker phospho-histone 3 (pH3) and apoptosis maker cleaved Caspase 3 (cl. Caspase 3) in biopsies collected from chemotherapy (Carboplatin and Etoposide) relapsed SCLC patient-derived xenografts (PDX-2) treated with SMYD3 inhibitor EPZ031686 (SMYD3i) and cyclophosphamide (CP). Representative

of n = 6 mice for each experimental group. Scale bars, 50 μm. **F-G**, Quantification of phospho-Histone 3 (pH3) (F) and cleaved Caspase 3 (cl. Caspase 3) positive cells (G) in PDX samples as in (E). Boxes represent 25th to 75th percentile, whiskers: min. to max., center line: median; *P-value* were calculated by two-way ANOVA with Tukey's testing for multiple comparisons. **H**, Weight analysis over time of mouse groups from the PDX-2 study.

### **Supplementary Tables**

**Supplementary Table S1. List of compounds used in cell growth inhibition screen with 4 hydroperoxy-cyclophosphamide (4H-CP) and cisplatin.** Data represents ratio of 4H-CP or cisplatin to DMSO cell growth  $\pm$  SD.

















#### **Supplementary Table S2. List of potential SMYD3 substrates identified by biochemical**

**protein array screen.** Proteins in grey are predicted false positives with potential auto-methylation



activity.

**Supplementary Table S3: List of identified proteins binding to RNF113A-K20me0 and RNF113A-K20me3 peptides in the peptide-pulldown quantitative proteomics analysis.** Two independent experiments using forward (Heavy: RNF113A-K20me3, Light: RNF113A-K20me0) and reverse (Heavy: RNF113A-K20me0, Light: RNF113A-K20me3) labeling were performed.

*Table provided in a separate .xls file.* 

**Supplementary Table S4. List of RNF113A phosphorylated sites collected from PhosphoSitePlus database and in-house identification by 2 independent mass spectrometry analyses of RNF113A purified from HeLa cells.** Sites in grey are potential substrates for the Serine/Threonine PP4 phosphatase.



# **Supplementary Table S5. Graphical representations of immunoblots quantification from the study.** Calculation was performed using Image J software comparing the integrated density of immunoblot signals using at least three different exposures. Background was subtracted and when relevant, signal was normalized with proper references (total protein level, level of immunoprecipitated protein, control, untreated condition, …).









#### **Figure 4**































### **Figure 6**

Panel F





Panel B



**Figure S2**

Panel A







Panel A **Panel A** Panel B





Panel A



#### **Figure S5**

Panel B Panel C





























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