

Legends to Supplementary Figures

Supplementary Fig.1: (a-b) Data obtained from GSE24080 dataset showing prognostic relevance of LIG1 and LIG4 expression on Overall Survival (a) and Event free Survival (b) of MM patients. **(c)** Analysis of LIG1 and LIG4 mRNA levels in healthy donors and patients' multiple myeloma and plasmacell leukemia cells from GSE39683. *, $P < 0.001$; **, $P < 0.0001$. **(d)** Copy number variation analysis of LIG3 gene in MM patients from MMRF researcher gateway portal (<https://research.themmr.org>). **(e)** Analysis of LIG3 mRNA levels according to molecular risk-classification of MM, as evaluated by interrogating GSE19784 dataset. *, $P < 0.0001$. **(f)** LIG3 mRNA levels in MM patients harboring indicated cytogenetic abnormalities as compared with patients that are negative for the same lesions, as result from analysis of proprietary MM dataset. * $P < 0.05$. **(g)** Analysis of GSE9782 dataset showing LIG1 and LIG4 mRNA levels in MM patients with clinical response or progressive disease after Bortezomib treatment. * $P < 0.05$. **(h)** Data obtained from GSE9782 dataset showing prognostic relevance of LIG3 mRNA levels on therapy response and Overall Survival of MM patients enrolled to Dexamethasone therapy.

Supplementary Fig.2: (a) *Left panel:* Western blot for LIG3 performed on AMO1 cells transduced with 3 different shRNAs and scramble control. GAPDH was used as a loading control. After 4 days of infection, puromycin selected cells (48h, 1,5 $\mu\text{g/ml}$) were harvested and whole-cell lysates were subjected to immunoblot analysis. *Right panel:* Indicated cell lines were transduced with either scramble control or LIG3-shRNA clone #3: CTG Assay was performed on cell lines transduced with shRNA#3 or scrambled controls after 6 days from infection. LIG3 knockdown was confirmed by western blot analysis 4 days after infection. **(b)** LIG3 downregulation was confirmed by qRT-PCR analysis, 72h after vehicle or IPTG treatment. **(c)** Colony formation of MM cells transduced with either inducible IPTG CTRL-shRNA or LIG3-shRNA lentiviral particles. Light microscopy is shown. Numbers of colonies after 2 weeks (average of 3 independent experiments; * $P < 0.01$) **(d,e,f)** AMO1 and RPMI-8226 cells were transfected with scramble control or LIG3-siRNA clone #2. (d) γ -H2AX foci

evaluation by immunofluorescence 48h after cell transfection. DAPI (blue) was used for nuclear staining. (e) Immunoblot analysis of LIG3, p-H2AX, cleaved form of caspase-3 and PARP. GAPDH was used as a loading control. Analysis was performed 48h after transfection. (f) Annexin V-positive cells 72h after transfection. (g) *Left panel:* CTG Assay was performed on AMO-1 and ABZB treated for 24h with increasing dose of Bortezomib. Difference of basal LIG3 expression was evaluated by western blot analysis. *Right panel:* CTG Assay was performed on AMO-1 transfected with LIG3 ORF or control ORF (CNT) and then treated for 24h with increasing dose of Bortezomib. LIG3 overexpression was confirmed by western blot analysis. (h) CTG Assay was performed on ABZB transfected with scramble control or LIG3-siRNA clone #2. LIG3 knockdown was confirmed by western blot analysis.

Supplementary Fig.3: (a) Bioinformatic screening of LIG3-targeting miRNAs was performed using mirDIP prediction software. Five miRNAs, were predicted to target LIG3 with excellent score range (≥ 0.3) in 12 different data sources. (b) Graphs of correlations between endogenous mRNA expression levels of LIG3 and mirDIP-selected miRNAs in PCL patients from proprietary dataset. (c) qRT-PCR analysis of miR-22-3p expression using total RNA from 3 primary patient MM cells, 5 MM cell lines and 2 samples of bone marrow-derived plasma cells from healthy donors. miR-22-3p levels in PBMC#1 were set as an internal reference. (d) *Left panel:* miR-22 levels in MM patients stratified according TC classification; *Right panel:* miR-22 levels in AMO-1 cells transfected with scramble control or MYC-siRNA. (e) Schematic representation of LIG3 3'-UTR. The color red indicates the seed sequence of miR-22-3p. (f) miR-22 overexpression or inhibition were confirmed by qRT-PCR analysis 48h after miR-22 mimics or inhibitor transfection, respectively. miR-22 levels in miR-NC or anti-miR-NC transfected cells were set as internal reference. *, $P < 0.01$.

Supplementary Fig.4. (a) CTG assay was performed on indicated MM cell lines 6 days after transduction with either miR-NC or miR-22 expressing lentiviral particles. Results are expressed as percentage of NC-transduced cells. *, $P < 0.01$. (b) Cell viability was evaluated on AMO1 cells transduced with either inducible-CTRL or inducible-miR-22 expressing lentiviral particles and then treated with

or without doxycycline (500 ng/mL) for 6 days. *, $P < 0.01$; LIG3 knockdown was confirmed by Western blotting 4 days from doxycycline induction. miR-22 overexpression was confirmed by qRT-PCR analysis 4 day after infection. **(c)** Colony formation of inducible-CTRL or inducible-miR-22 AMO1 cells treated with or without doxycycline (500 ng/mL). Light microscopy is shown. Number of colonies after 2 weeks. **(d)** Annexin V / 7-AAD staining flow cytometry assay of inducible-CTRL or inducible-miR-22 AMO1 cells treated with or without doxycycline (500 ng/mL) for 5 days. **(e)** Annexin V / 7-AAD staining of AMO1 and R8226 cells transfected with miR-22 or miR-NC. **(f)** CTG Assay was performed 96h after transfection of indicated MM cell lines with miR-22 inhibitor or scrambled controls (anti-miR-NC). Results are expressed as percentage of NC-transfected cells. **(g)** CTG Assay was performed 96h after transfection of INA6 cells alone or co-cultured with HS5 cells, with miR-22 mimics or scrambled controls (miR-NC). **(h)** ABZB cells were co-transfected with LIG3 ORF or control ORF and miR-22 mimics or miR-NC and then treated with Bortezomib: CTG survival assay were performed 48h after transfection. *, $P < 0.01$. Data represent the average \pm SD of 3 independent experiments.

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Supplementary Fig.5 (a,b) Affymetrix CytoScan HD Array analysis, using genomic DNA from AMO1 overexpressing miR-22 or negative control (miR-NC). **(a)** Acquisition of new copy number variations (CNV) is expressed as percentage of miR-NC cells. **(b)** Representative images of new deletions acquisition on chromosome 1(1p22.2) and chromosome 14 (14q23.3-24.1). Red lines represent deletions. Blue arrows indicate deletions only existing in miR-NC AMO1 cells. **(c)** ROS-Glo H2O2 Assay performed on AMO1 48 hours after cell transfection. **(d)** Primary plasmacells (Pt #3) were transfected with miR-22 or miR-NC. *Left panel:* Immunoblot analysis was performed after 48h from transfection. *Right panel:* γ -H2AX foci evaluation by immunofluorescence 48 hours after cell transfection. **(e)** AMO1 cells were transfected with miR-22 mimics or miR-NC. 6 hours after electroporation either vehicle or Caffeine (5mM) were added to culture medium. Cell cycle analysis was performed 48h after transfection. **(f)** AMO1 cells were transfected with miR-22 mimics or miR-NC. 6 hours after

electroporation either DMSO (NT) or Z-VAD-FMK were added to culture medium, at final concentration of 25 μ M: *Left panel*: Annexin V staining 72 hours after transfection. *Right panel*: Immunoblot analysis was performed 48 hours after cell transfection. **(g)** AMO1 cells were co-transfected with LIG3 ORF or control ORF and miR-22 mimics or miR-NC Annexin V/7-AAD staining 72 hours after transfection. **(h)** Cell cycle analysis 48 hours after cell transfection. Results are representative of three independent experiments \pm SD. *, P < 0.05; **, P < 0.01.

Supplementary Fig.6: **(a)** miR-22 overexpression was confirmed by qRT-PCR from a representative AMO1 xenograft per group; miR-22 levels in miR-NC-tumor were set as internal reference. *, P < 0.01. **(b)** IVIS images and BLI-based measurement of tumor volumes (5 animals for each group) of NOD SCID mice s.c. xenografted with luciferase gene-marked AMO1, were performed before (t0) and 1 week after treatment.