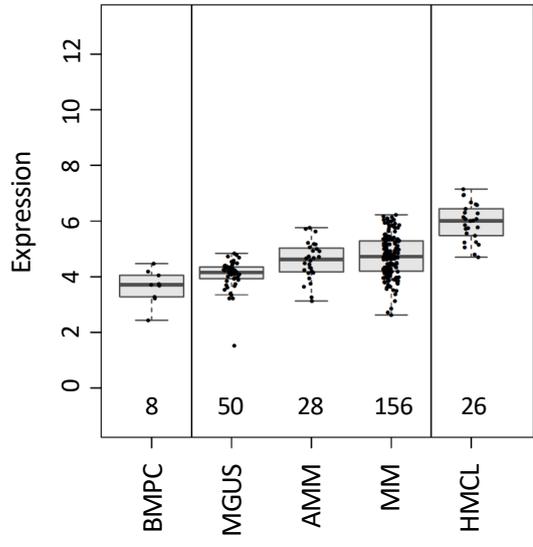
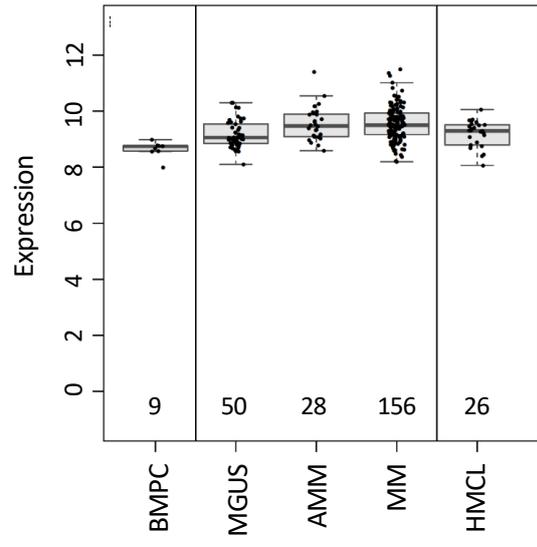
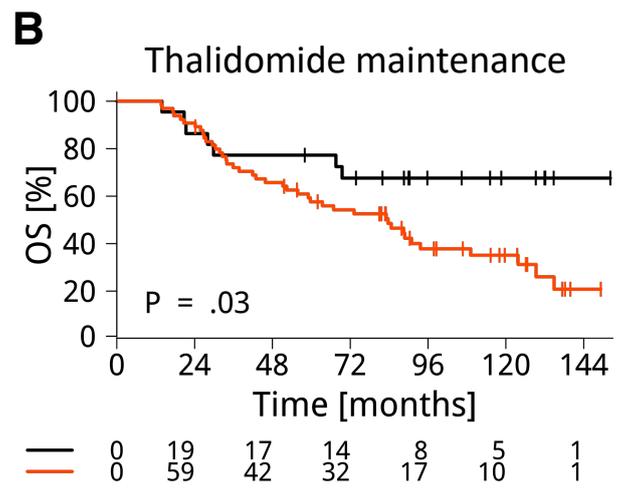
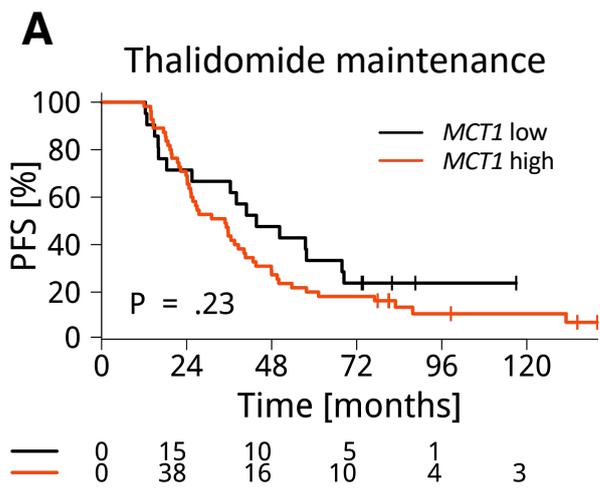


**A****B**

**Supplemental Figure 1: Expression of *MCT1* and *CD147* by RNA-sequencing.**

*MCT1* (A) and *CD147* (B) gene expression in plasma cell disorders (n=234) and normal bone marrow plasma cells (BMPC, n=9) as assessed by RNA-sequencing. Monoclonal gammopathy of unknown significance (MGUS); asymptomatic multiple myeloma (AMM); previously untreated, therapy-requiring multiple myeloma (MM); human myeloma cell line (HMCL). Numbers indicate number of patients in the respective group.



**Supplemental Figure 2: Expression of *MCT1* determines PFS and OS in patients receiving thalidomide-based maintenance therapy.**

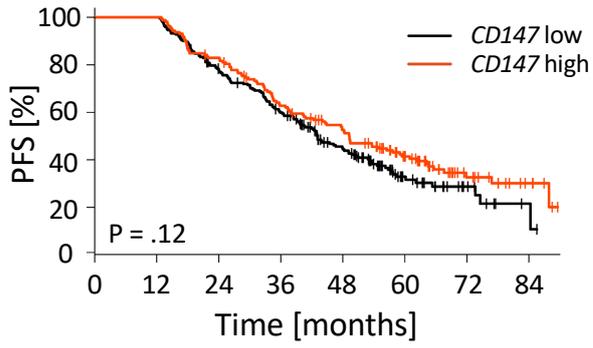
Landmark analysis of MM patients undergoing maintenance treatment after ASCT, GMMG-HD4 trial. Expression of *MCT1* was assessed by gene expression profiling and RNA-sequencing in CD138-purified myeloma cell samples and correlated with progression-free (PFS) and overall survival (OS) data. Red colored curves show high *MCT1* expression. Black colored curves show low *MCT1* expression. Log-rank *P* values are shown in the lower left corner of each panel.

(A) PFS of 98 patients undergoing thalidomide maintenance therapy, 34.8 vs. 43.7 months in *MCT1*<sup>high</sup> vs. *MCT1*<sup>low</sup>, *P*=0.23 and

(B) OS of 98 patients undergoing thalidomide maintenance therapy, 83.6 months vs. not reached in *MCT1*<sup>high</sup> vs. *MCT1*<sup>low</sup>; *P*=0.03.

**A**

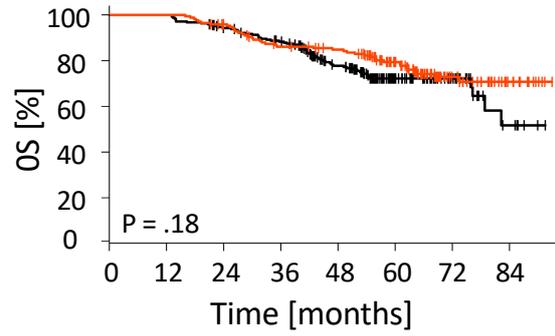
## Lenalidomide maintenance



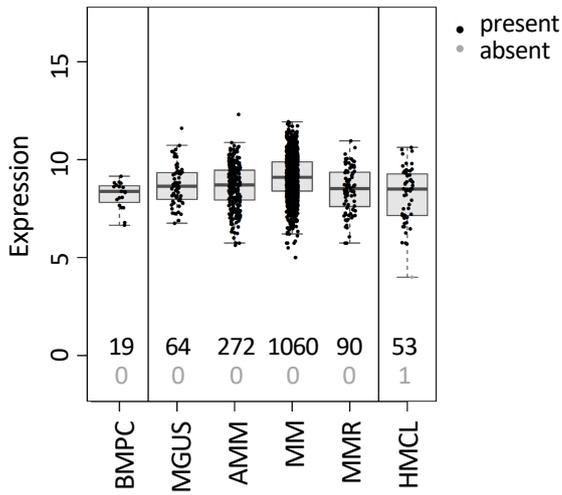
—	0	0	170	128	78	26	10	2
—	0	0	130	95	75	46	17	6

**B**

## Lenalidomide maintenance



—	0	0	224	205	146	62	28	7
—	0	0	158	139	132	100	36	13

**C**

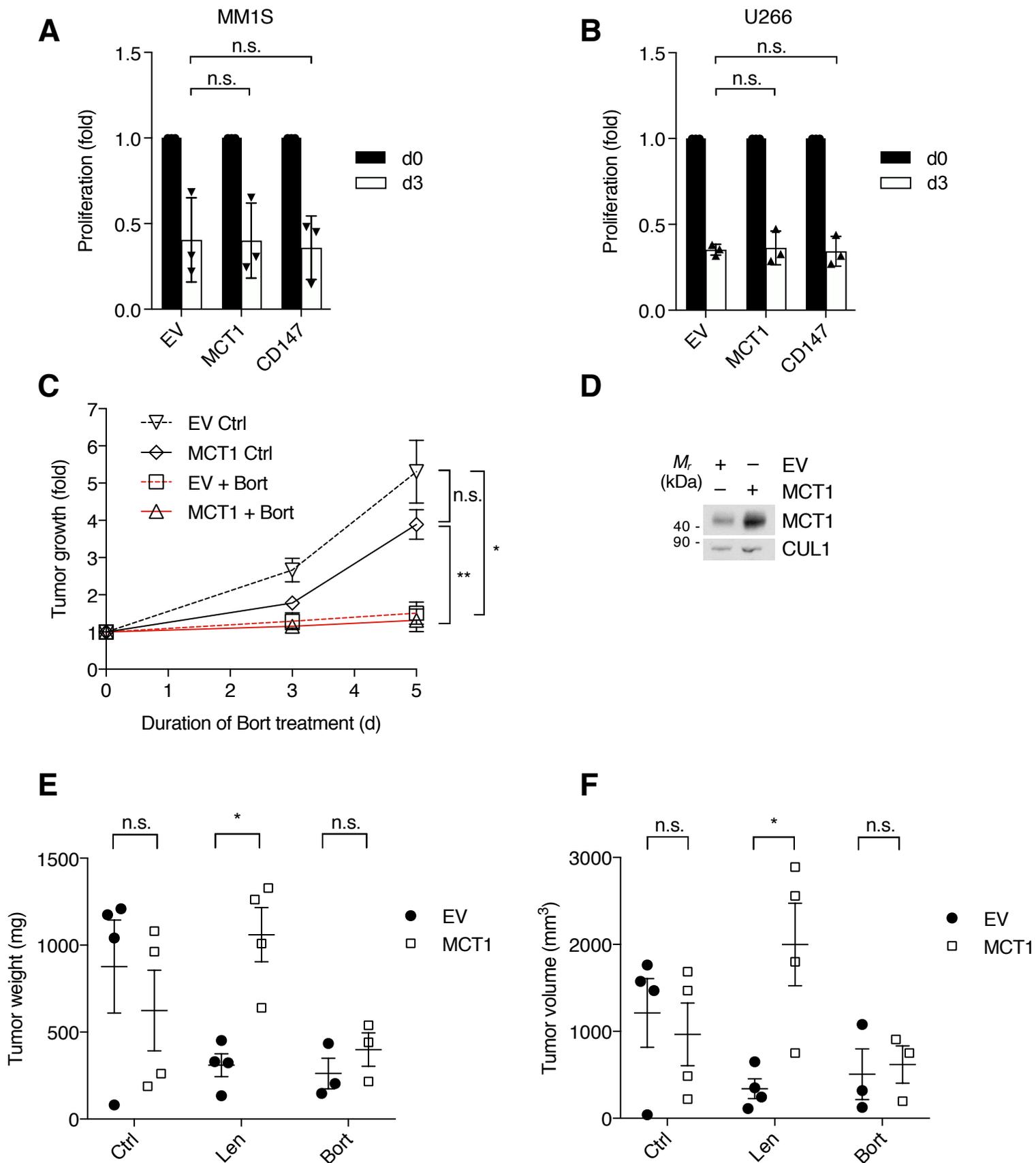
**Supplemental Figure 3: Expression of *CD147* and lack of determination of PFS and OS in patients receiving lenalidomide-based maintenance therapy.**

(A-B) Landmark analysis of MM patients undergoing lenalidomide maintenance treatment after ASCT. Expression of *CD147* was assessed by gene expression profiling in CD138-purified myeloma cell samples and correlated with PFS and OS data. Red colored curves show high *CD147* expression. Black colored curves show low *CD147* expression. Log-rank *P* values are shown in the lower left corner of each panel.

(A) PFS of 455 patients undergoing lenalidomide maintenance therapy, GMMG-MM5-trial, *P*=n.s. and

(B) OS of 455 patients undergoing lenalidomide maintenance therapy, GMMG-MM5-trial; *P*=n.s.

(C) *CD147* gene expression in plasma cell disorders (n=1486) and normal bone marrow plasma cells (BMPC, n=19). Monoclonal gammopathy of unknown significance (MGUS); asymptomatic multiple myeloma (AMM); previously untreated, therapy-requiring multiple myeloma (MM); relapsed/refractory multiple myeloma (MMR); human myeloma cell line (HMCL). Numbers in black (grey) color indicate number of patients expressing (not expressing) *CD147*.



Supplemental Fig. 4

**Supplemental Figure 4: Efficacy of Bortezomib is not affected by overexpression of MCT1 in *vitro* and *in vivo*.**

(A-B) Cell proliferation analysis of MM1S (A) and U266 (B) cells, which were lentivirally infected with empty vector constructs (EV) or constructs to induce MCT1 or CD147 expression treated with DMSO or 6nM bortezomib for 72hrs.

(C) Quantification of tumor growth during bortezomib or vehicle control treatment using caliper measurements (Ctrl: n=4 tumors, Bort: n=3 tumors).

(D) Immunoblot analyses of U266 cells prior to injection probed with the indicated antibodies.

(E-F) Tumor weight (in mg) and tumor volume (in mm<sup>3</sup>) after necropsy (n=4 tumors per condition) of mice shown in Figures 2C-D and supplemental Figures 4C-D.

Data in this figure are expressed as mean  $\pm$  s.d.; n.s., not significant; \*  $P < 0.05$ , \*\*  $P < 0.01$ , by one sample t-test or Student's t-test.