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A metabolic switch in proteasome inhibitor resistant multiple myeloma ensures higher mitochondrial metabolism, protein folding and sphingomyelin synthesis

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Contributions: AB and LB performed the experiments, analyzed the data, designed and wrote the manuscript, MML helped with functional assays, KV, MS and PV performed the TEM experiments and evaluated the ultrastructural data, MK performed viability assays, JB adapted the cells to proteasome inhibitors, BL, RF, and RC provided the TCyDTDO compound and CD designed and critically revised the manuscript.