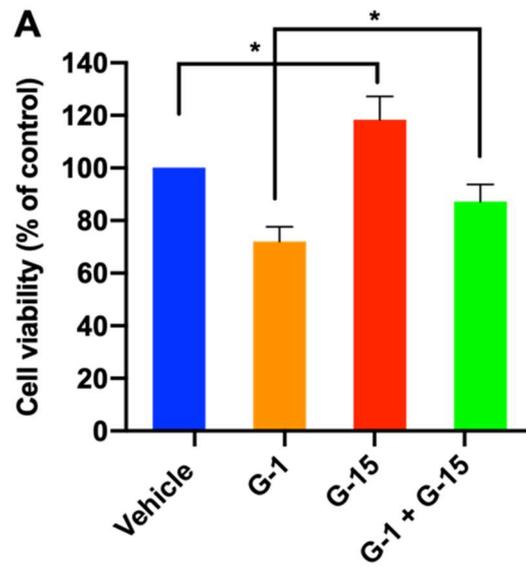


# GPER1 activation exerts anti-tumor activity in multiple myeloma

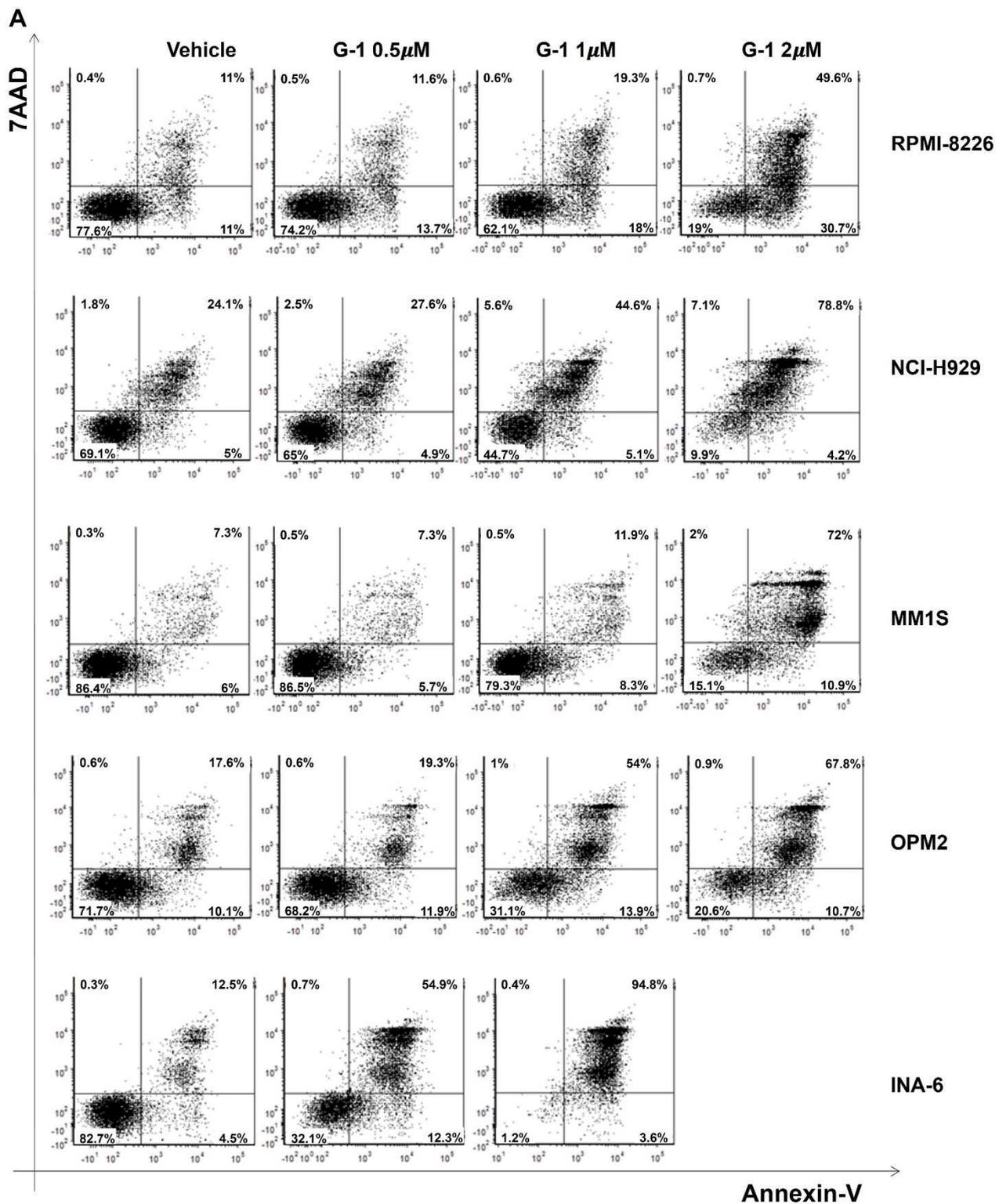
Maria Eugenia Gallo Cantafio<sup>1</sup>, Roberta Torcasio<sup>1,3</sup>, Francesca Scionti<sup>2</sup>, Maria Mesuraca<sup>1</sup>, Domenica Ronchetti<sup>4</sup>, Mariaelena Pistoni<sup>5</sup>, Dina Bellizzi<sup>6</sup>, Giuseppe Passarino<sup>6</sup>, Eugenio Morelli<sup>7</sup>, Antonino Neri<sup>8</sup>, Giuseppe Viglietto<sup>1</sup>, and Nicola Amodio<sup>1,\*</sup>

		IC <sub>50</sub> ±SD (μM)
<b>MM cell lines</b>	AMO wt	0.84±0.05
	AMO-BZB	0.863±0.06
	AMO-CFZ	0.877±0.1
	MM1S	0.367±0.05
	MM1R	1.077±0.1
	INA6	0.726±0.07
	U266	0.744±0.08
	NCI-H929	0.782±0.08
<b>MM primary cells</b>	MM pt#1	>2
	MM pt#2	>2
	MM pt#3	>2

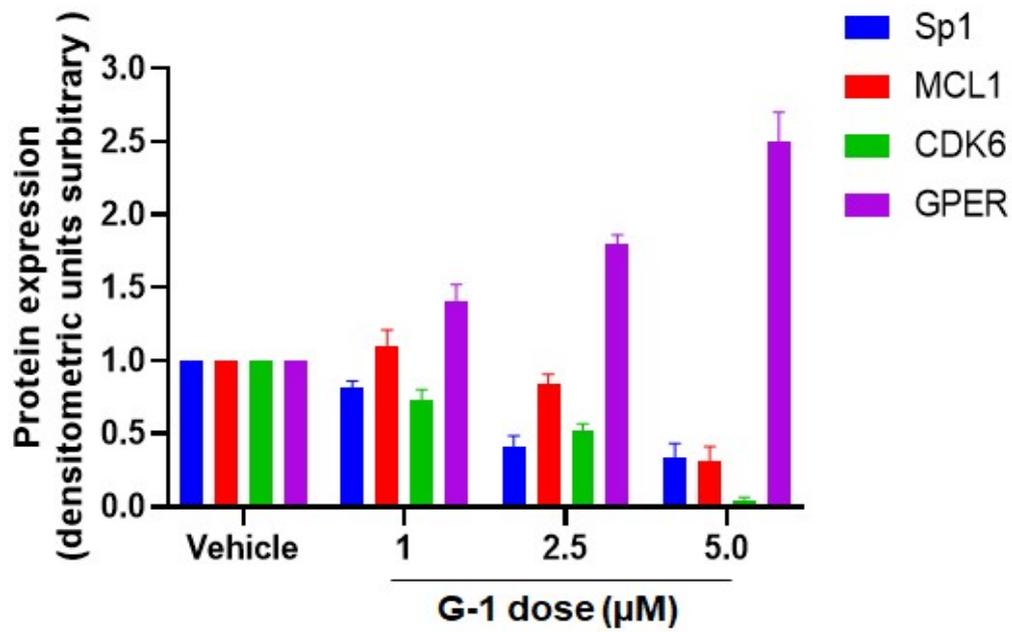
**Supplementary Table S1.** IC<sub>50</sub> values of G-1 in MM cell lines and primary cells from newly diagnosed MM patients. Cells were treated with different concentrations of G-1 for 48h, and cell viability assayed using the CTG method. IC<sub>50</sub> values were calculated using GraphPad Prism 8 software and reported as mean of three independent experiments ±SD.



**Supplementary Figure S1.** Cell viability was assessed by CTG assay in NCI-H929 cells, 48h after 2  $\mu$ M G-1 treatment, alone or in combination with 0.5  $\mu$ M G-15. Histogram bars are representative of the percentage of viable cells compared to control. \* $p < 0.05$ .



**Supplementary Figure S2.** FACS flow analysis of Annexin V/7-AAD stained RPMI-8226, NCI-H929, MM1S, OPM2 and INA-6 cells, 48h after G-1 treatment. Dot plots are representative of the percentage of apoptotic cells from an independent biological replicate (n = 3).



Supplementary Figure S3. Densitometric analysis of Sp1, MCL1, CDK6 and GPER1 protein fold change of expression in NCI-H929 cells treated for G-1 for 24h. GAPDH was used as loading control.