Supporting Information

Immunomodulatory Effects of Dendritic Poly(ethyleneimine) Glycoarchitectures on Human Multiple Myeloma Cell Lines, Mesenchymal Stromal Cells, and in Vitro Differentiated Macrophages for an Ideal Drug Delivery System in the Local Treatment of Multiple Myeloma

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Table S1. Structural parameters of dendritic glycoarchitectures

glycoarchitecture	M_n [g/mol][a]	Maltose units[a]	D_h [nm][b]
PEI-5-Mal B	14084	32	6,6
PEI-25-Mal B	35508	79	8,6
PEI-PGlu-Mal	63137	56	5,8

[a] Determined by elemental analysis. Following the approach described in *Biomacromolecules* **2009**, *10* (5), 1114.
[b] Dynamic light scattering determined by volume plot.

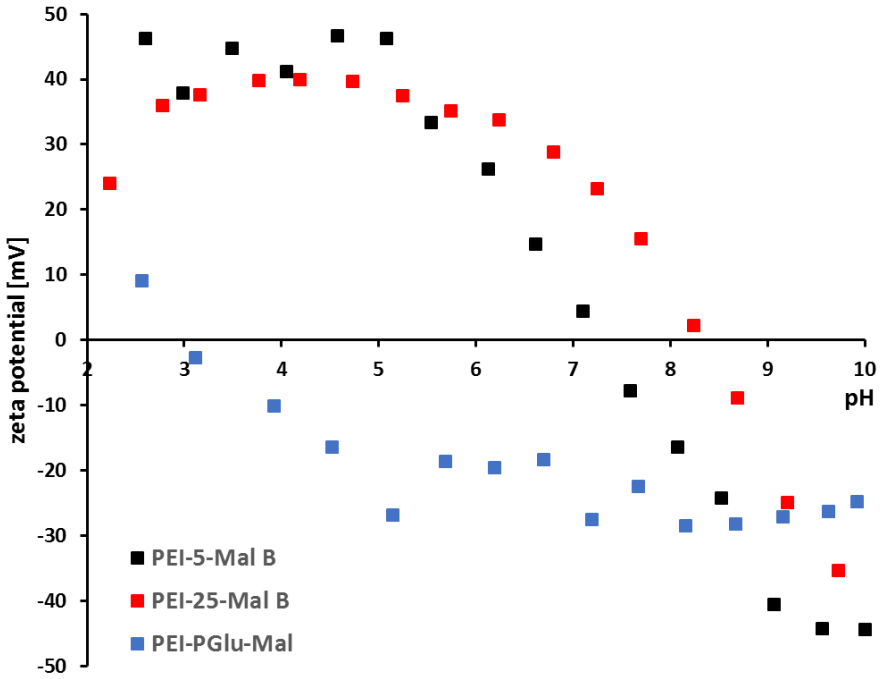

Figure S1. pH-dependent zeta potential measurements of dendritic glycoarchitectures.

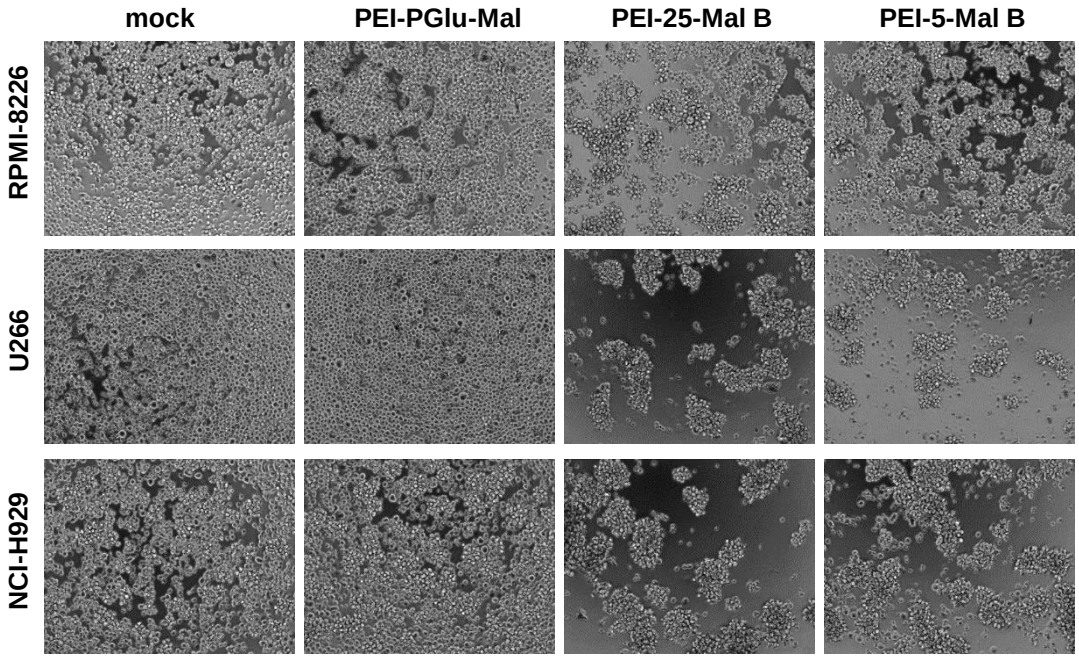

Figure S2. Visualization of multiple myeloma viability after PEI-DGAs incubation.

Multiple myeloma cell lines (RPMI-8226, U266, NCI-H929) were incubated with 1 mg/mL PEI-DGAs for 24h. Macroscopic visualization of cell viability was admitted with 10x magnification.

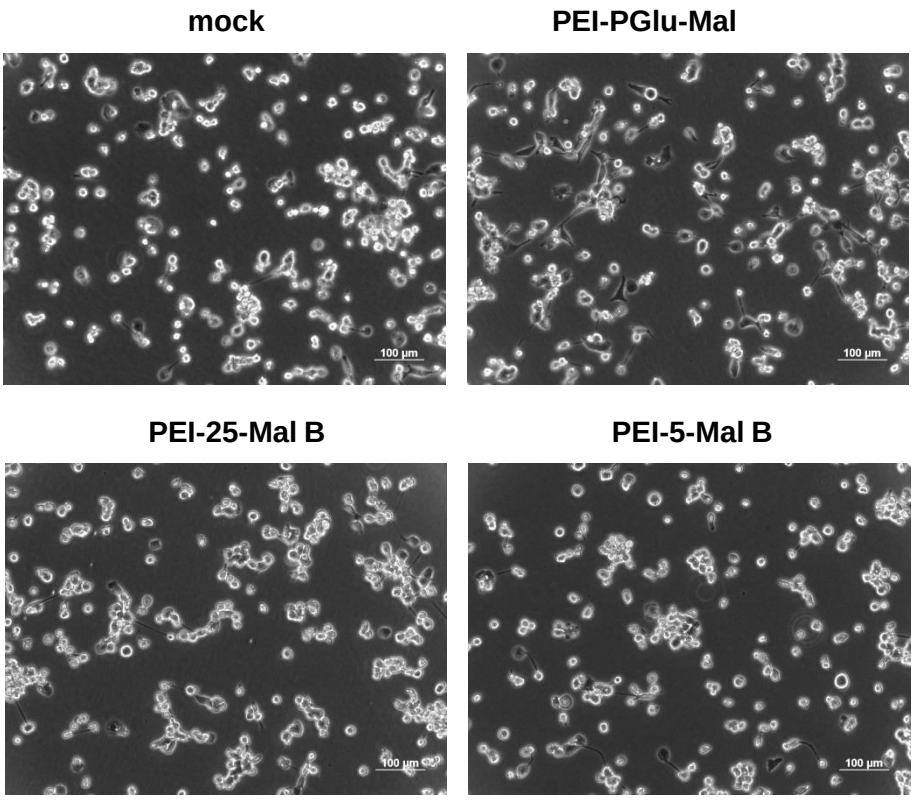

Figure S3. Visualization of macrophage viability after PEI-DGAs incubation.

Differentiated THP-1 cells were incubated with 1 mg/mL PEI-DGAs for 24h. Macroscopic visualization of cell viability was admitted with 10x magnification.

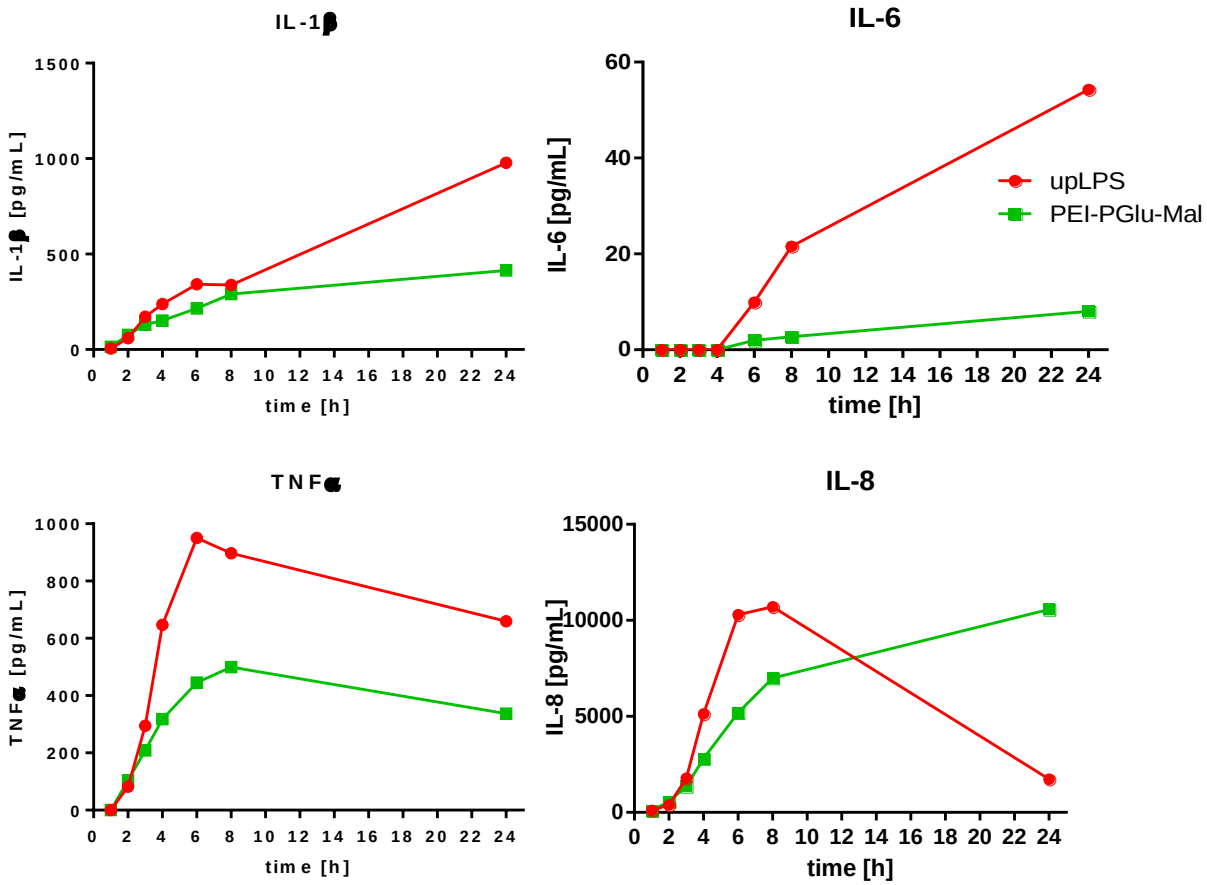

Figure S4. Time dependent cytokine release after PEI-DGA incubation.

Differentiated THP-1 cells were stimulated 50 ng/mL upLPS or with 1 mg/mL PEI-PGlu-Mal for indicated time points. Cytokine concentration was measured by CBA.

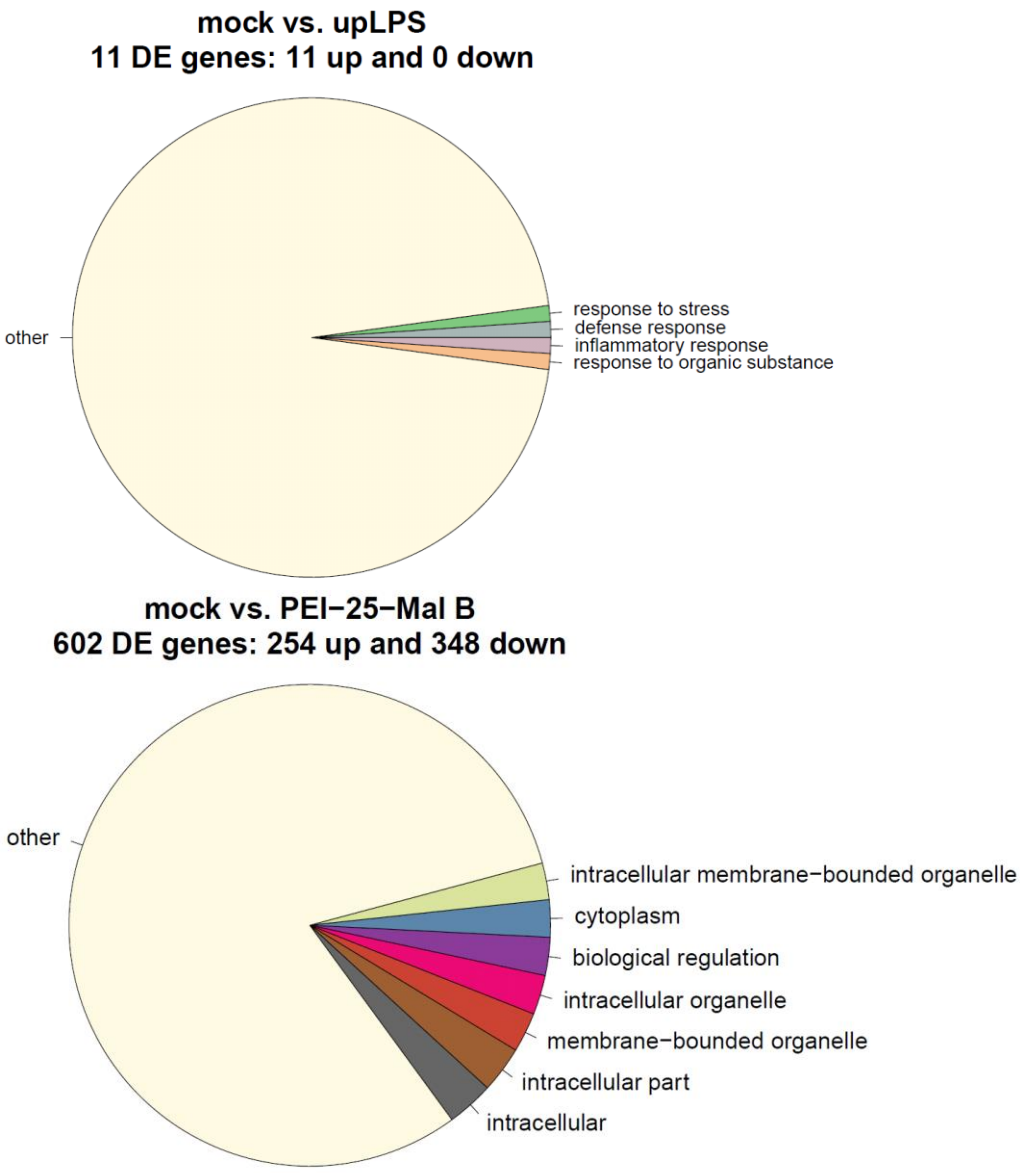

Figure S5. GO annotation of significantly regulated genes by upLPS and PEI-25-Mal B

Human MSCs were stimulated for 24h with 1mg/mL PEI-PGlu346-Mal, PEI-25-Mal B and PEI-5-Mal B or 50ng/mL upLPS. Afterwards transcriptome was analyzed through RNA sequencing. The goana function of edgeR was used to perform an over representation analysis for gene ontology (GO) terms of the differentially expressed genes. GO terms with a p-value <= 0.01 were selected. In the pie charts GO terms which match to at least 50% of the differentially expressed genes are shown.