

Title:

# **Decellularised Human Umbilical Artery as a Vascular Graft Elicits Minimal Pro-inflammatory Host Response *Ex Vivo* and *In Vivo***

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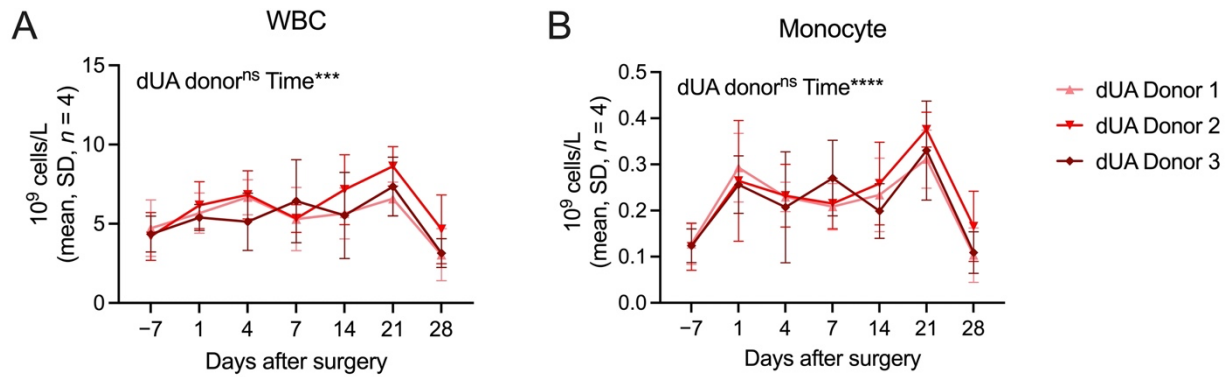
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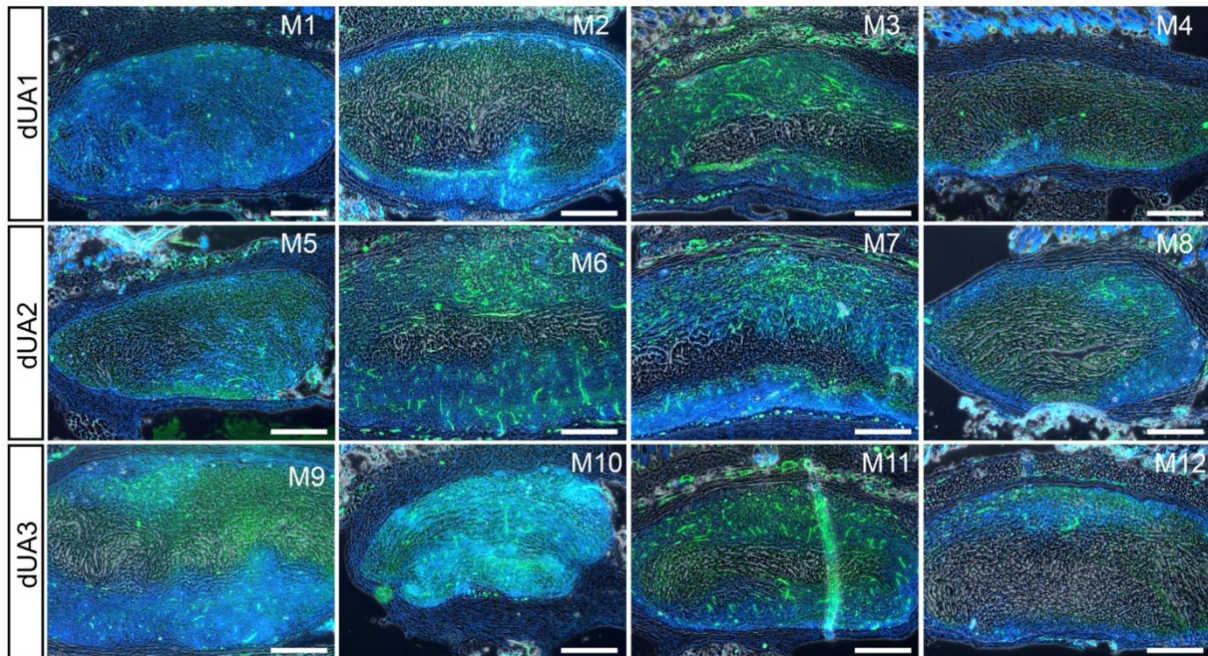
\* These authors contributed equally to this work

## Supplementary figures



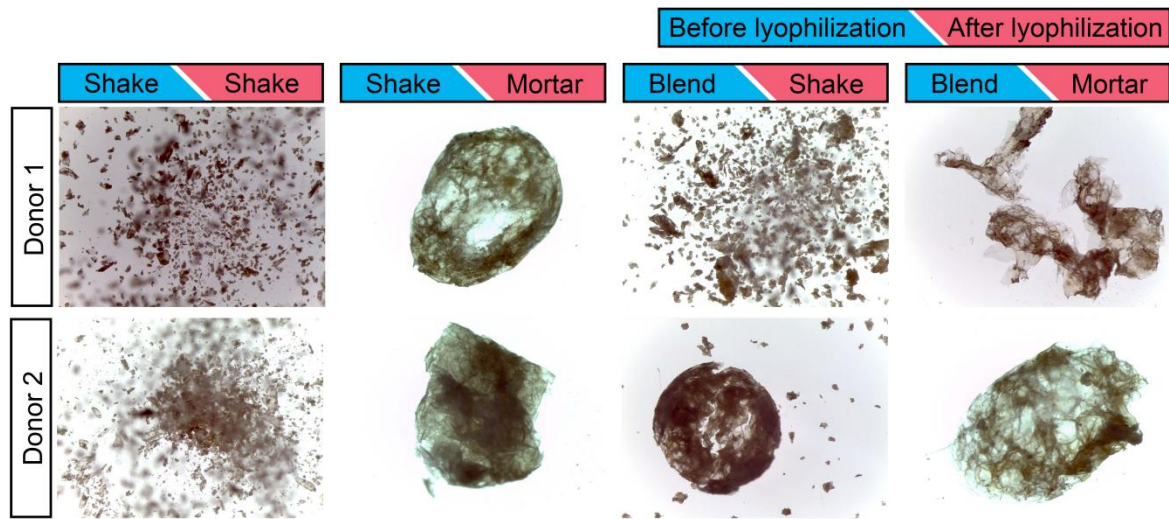
**Figure S1. Overall systemic immune response upon dUA implantation in mice.**

(A) White blood cell (WBC) count and (B) monocyte count measured for each test group (dUA donor 1, 2 and 3) 7 days before surgery and 1, 4, 7, 14, 21, and 28 days after surgery. Mixed-effects analysis (post-test: Tukey test) was performed for statistics (n=4). For both WBC and monocyte count, there are no significant differences among different dUA donor groups and data was thus pooled together as one group and used in Figure 1D in the main text.



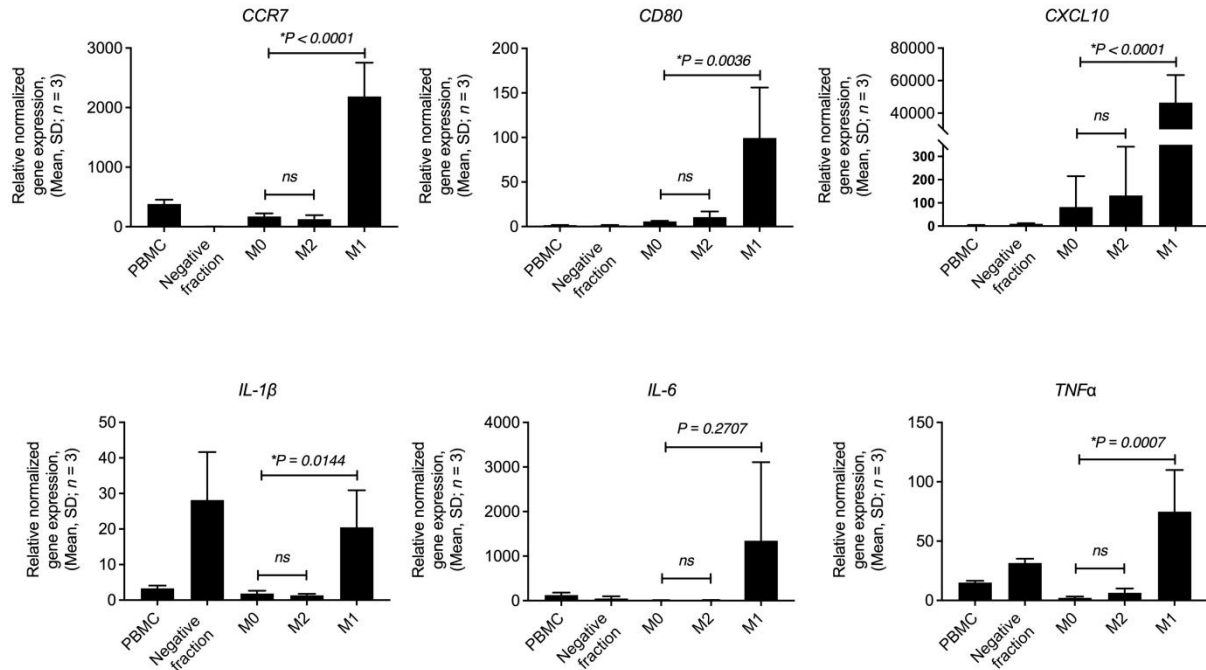
**Figure S2. Identification of endothelial remodelling inside the dUA upon *in vivo* implantation.**

Representative images from fluorescent staining of the endothelial marker CD31 in all dUA explants (mouse individuals: M1-M12). Scale bars = 500 μm.



**Figure S3. Optimisation of dUA powdering methods for *ex vivo* stimulation of human macrophages.**

(A) Microscopic analysis of pulverisation methods before and after lyophilisation. dUA was lyophilised and pulverised through a combination of three different methods: shaking the samples with steel beads, crushing the samples with mortar and pestle, and blending the samples. The most effective pulverisation was seen in the combination of shaking the samples with steel beads both before and after the lyophilisation.



**Figure S4. M1 macrophage specific gene expression.**

PBMCs and negative selected monocytes as well as differentiated macrophage descendants (M0, M1 and M2) were analysed by qRT-PCR for expression of M1 markers suggested in the literature. Three independent experiments based on three different donors were run. Ordinary one-way ANOVA (post-test: two-stage step-up method of Benjamini, Krieger and Yekutieli) was used for statistical analysis ( $n = 3$ ), and qRT-PCR raw data were normalised against multiple stably expressed endogenous controls according to the qbase+ platform (data not shown).