Fastq files were generated using bcl2fastq2 v. 2.20.0, then reads were aligned to the GRCm38 primary assembly using STAR v. 2.7.2b [1] against a reference built using the GENCODE vM25 gene model [2]. Aligned reads were counted against the same gene model using featureCounts v. 1.6.2 [3] counting only reads where both ends mapped to the same strand. Separation between tissues and homogeneity within tissues was visually inspected using MDS plots. Two samples were excluded for having almost no reads and one sample was excluded for being heavily enriched for genes related to wound healing and immune system processes. Visual inspection revealed extraction pool to separate samples. Genes with sufficient counts were selected using the filterByExpr function from the edgeR v. 3.30.2 [4] package and were transformed using the voomWithQualityWeights function [5]. Differential expression was calculated using limma v. 3.44.0 [6] using a model of the form *~ group + extraction\_pool*, where *group* encoded tissue, treatment and timepoint and *extraction\_pool* encoded the extraction pool. Animal specific effects were modelled using the duplicateCorrelation function which is part of limma. Contrasts were specified as described in the limma manual. Gene ontology and reactome enrichments were found using the camera function [7]. All plots were generated using ggplot2 [8].

1 <https://doi.org/10.1093/bioinformatics/bts635>  
2 <https://doi.org/10.1093/nar/gky955>  
3 <https://doi.org/10.1093/nar/gkt214>  
4 <https://doi.org/10.1093/bioinformatics/btp616>  
5 <https://doi.org/10.1186/gb-2014-15-2-r29>  
6 <https://doi.org/10.1093/nar/gkv007>  
7 <https://doi.org/10.1093/nar/gks461>  
8 Wickham H (2016). ggplot2: Elegant Graphics for Data Analysis. Springer-Verlag New York. ISBN 978-3-319-24277-4