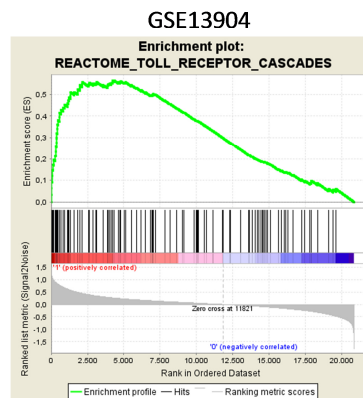
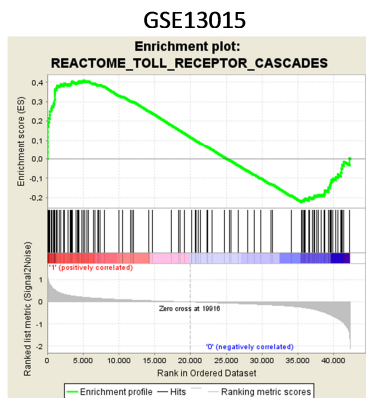
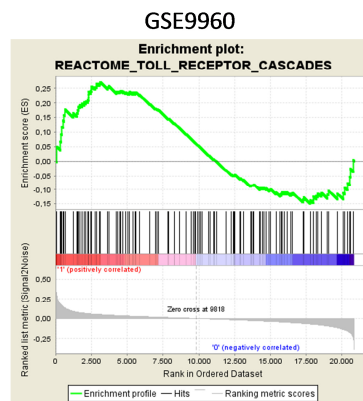
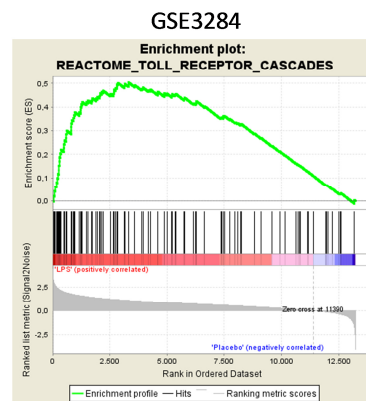
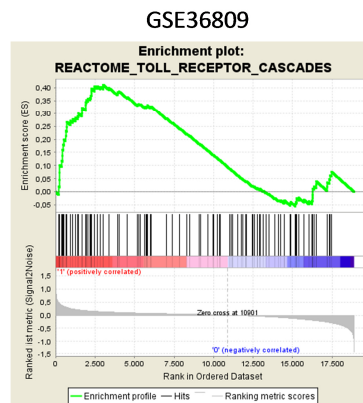
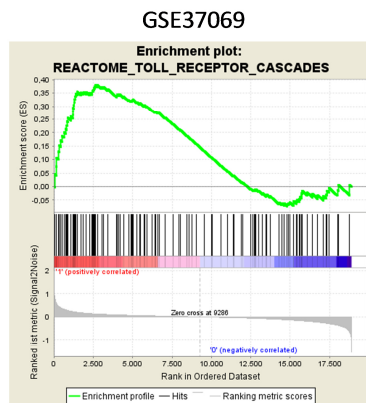


APPENDIX

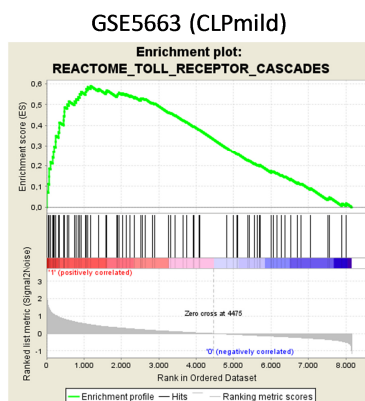
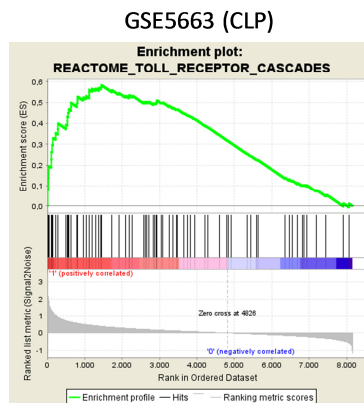
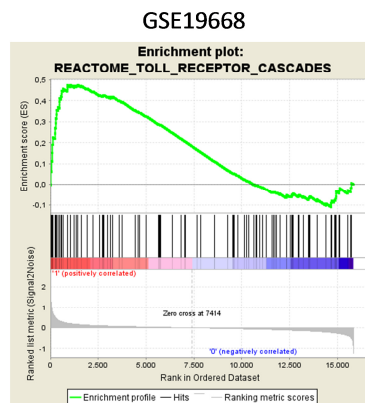
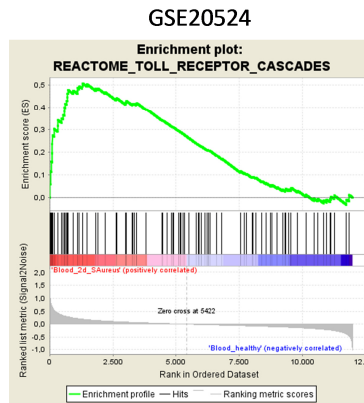
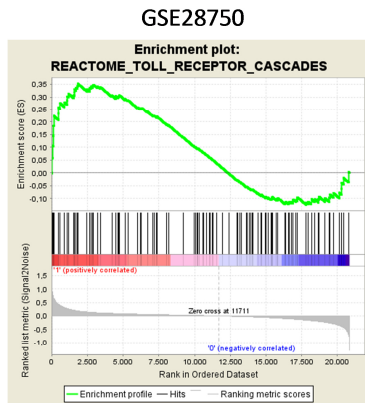
Defining the optimal animal model for translational research using gene set enrichment analysis

Christopher Weidner, Matthias Steinfath, Elisa Opitz, Michael Oelgeschläger, Gilbert Schönfelder

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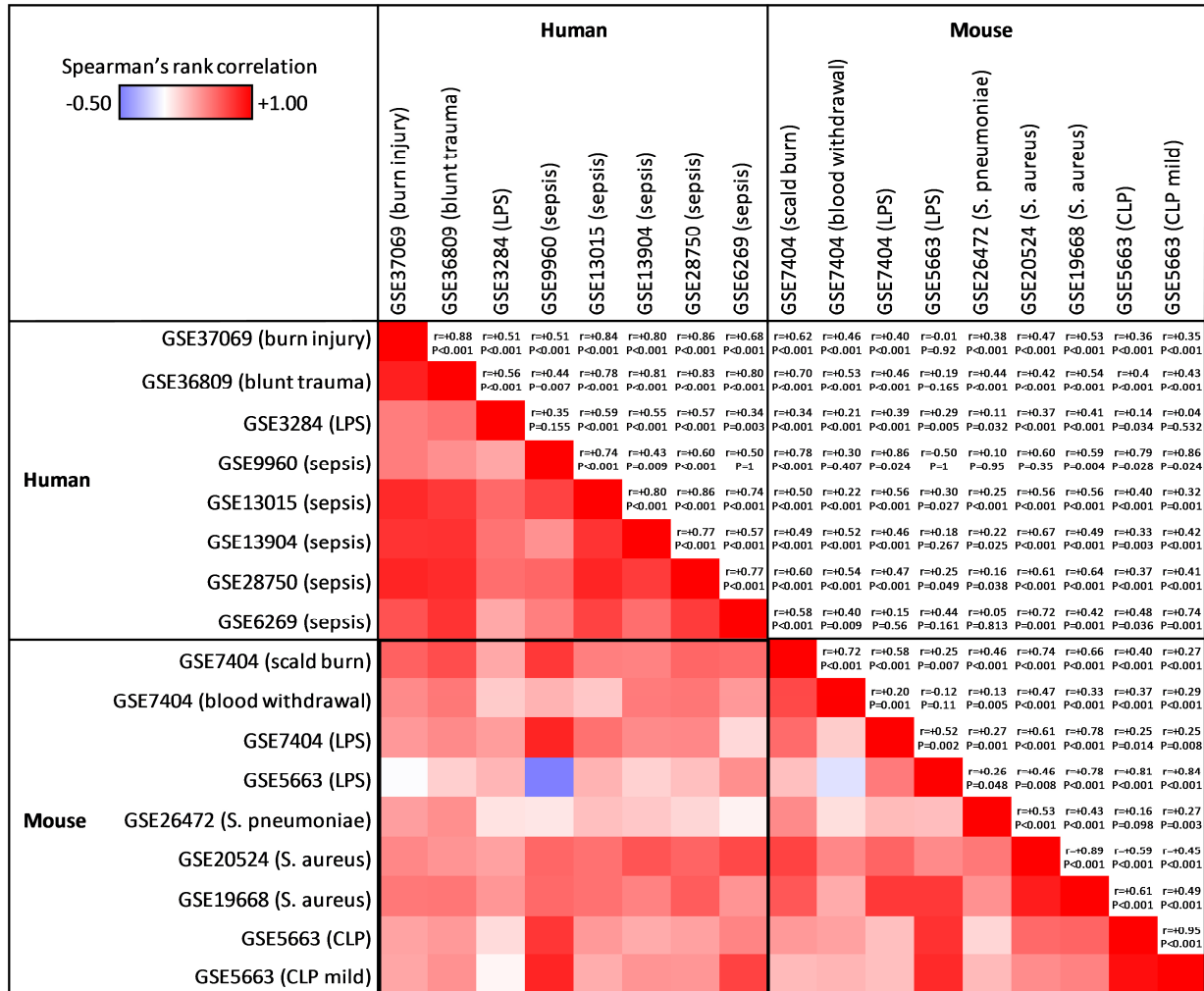


Appendix Figure S1 (continued on next page).



Appendix Figure S1. Enrichment plots of the Toll receptor cascade (Reactome) pathway for datasets with high correlation.

Enrichments plot and statistics were generated with the GSEA tool.



Appendix Figure S2. Correlations of single-gene changes among human and mouse inflammatory studies.

Spearman's rank correlation (r) was calculated based on log fold change values for differentially expressed genes according to the data selection strategy proposed by Takao et al. (Takao & Miyakawa, 2015). For correlation analyses between data sets the genes were selected as follows: fold change ratio > 2.0 or < 0.5 in human diseases, fold change ratio > 1.2 or < 0.83 in mouse models, (uncorrected) P value < 0.05 in both conditions of that comparison (note that correction of P values for multiple hypothesis testing could not be used since this would have led to some data sets with no differentially expressed genes at all). Most of the studies showed statistically significant correlations. Note that the gene selection criteria only include overlapping differentially

expressed genes and exclude genes that were differentially expressed in only one species. This single-gene approach thus tends to overestimate the correlation between human and mouse and allows no clear estimation of the best correlating mouse models.

Appendix Table S1

Transcriptomic studies used for model assessment on severe acute inflammatory diseases.

Species	GEO accession	Stimulus type	Time after sampling
Human	GSE37069	burn injury	4 days
Human	GSE36809	blunt trauma	14 days
Human	GSE3284-GPL96	LPS (2 ng/kg) i.v.	6 hours
Human	GSE9960	Septic patients	unspecified
Human	GSE13015	Septic patients	unspecified
Human	GSE13904	Septic patients	1 day
Human	GSE28750	Septic patients	unspecified
Human	GSE6269-GPL96	Septic patients	unspecified
Mouse	GSE7404	Scald burn	7 days
Mouse	GSE7404	Blood withdrawal	1 day
Mouse	GSE7404	LPS (10 ng) i.p.	2 hours
Mouse	GSE5663	LPS (20 mg/kg) i.p.	24 hours
Mouse	GSE26472	<i>S. pneumoniae</i> intratracheal	6 hours
Mouse	GSE20524	<i>S. aureus</i> i.v.	2 days
Mouse	GSE19668	<i>S. aureus</i> i.p.	4 hours
Mouse	GSE5663	CLP	24 hours
Mouse	GSE5663	CLP (mild)	24 hours

Appendix References

Takao K, Miyakawa T (2015) Genomic responses in mouse models greatly mimic human inflammatory diseases. *Proc Natl Acad Sci U S A* 112: 1167-72