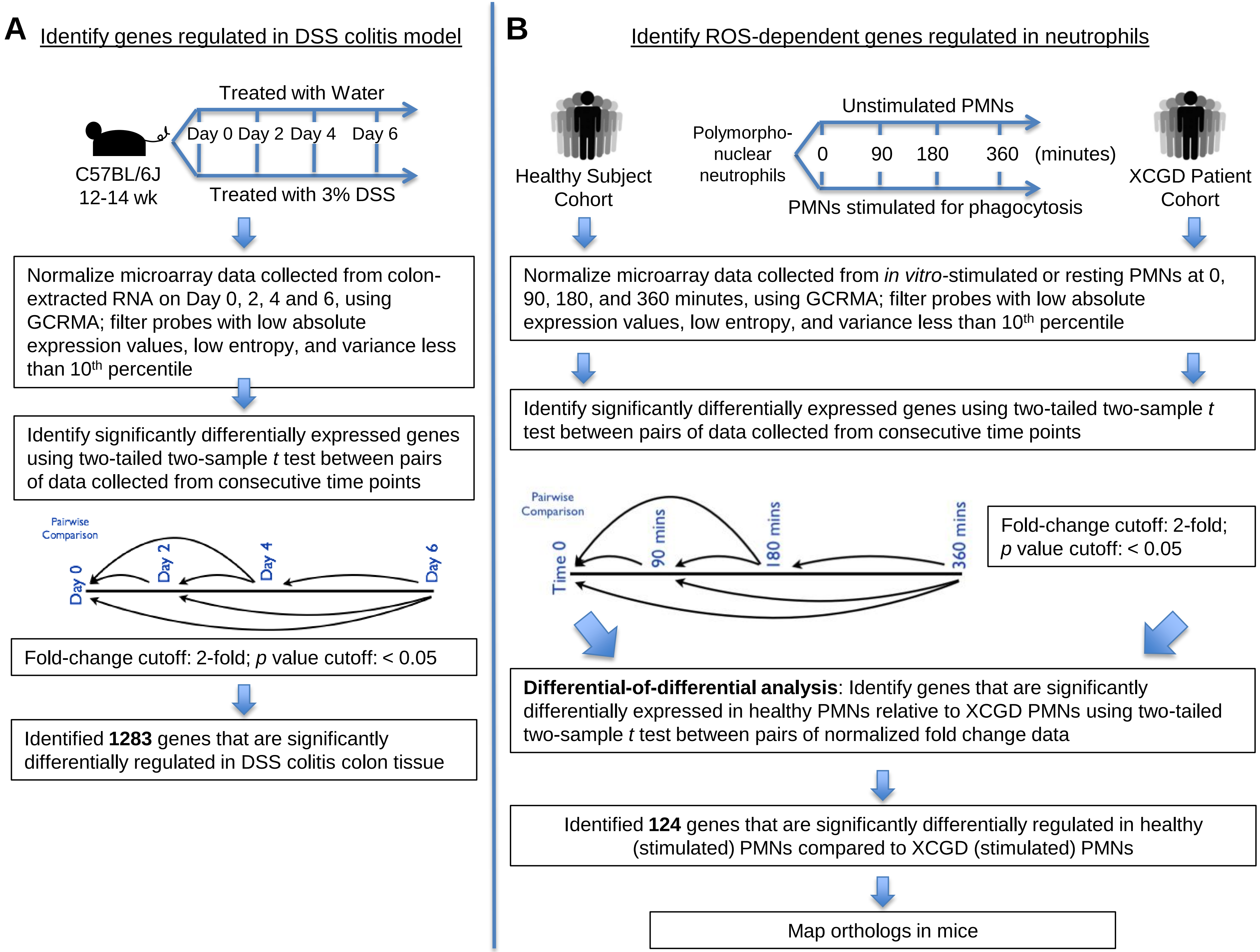

A Identify genes regulated in DSS colitis model

Normalize microarray data collected from colon-extracted RNA on Day 0, 2, 4 and 6, using GCRMA; filter probes with low absolute expression values, low entropy, and variance less than 10th percentile

Identify significantly differentially expressed genes using two-tailed two-sample *t* test between pairs of data collected from consecutive time points

Fold-change cutoff: 2-fold; *p* value cutoff: < 0.05

Identified **1283** genes that are significantly differentially regulated in DSS colitis colon tissue

B Identify ROS-dependent genes regulated in neutrophils

Normalize microarray data collected from *in vitro*-stimulated or resting PMNs at 0, 90, 180, and 360 minutes, using GCRMA; filter probes with low absolute expression values, low entropy, and variance less than 10th percentile

Identify significantly differentially expressed genes using two-tailed two-sample *t* test between pairs of data collected from consecutive time points

Fold-change cutoff: 2-fold; *p* value cutoff: < 0.05

Differential-of-differential analysis: Identify genes that are significantly differentially expressed in healthy PMNs relative to XCGD PMNs using two-tailed two-sample *t* test between pairs of normalized fold change data

Identified **124** genes that are significantly differentially regulated in healthy (stimulated) PMNs compared to XCGD (stimulated) PMNs

Map orthologs in mice