**SUPPLEMENTAL FIGURE LEGENDS**

**Figure S1. Different software packages detect different isoform usage events.** The Venn diagram depicts the number of genes with differential isoform usage detected by DEXSeq (FDR < 0.05), MISO (Bayes factor > 10), or Cuffdiff (differential splicing test, q-value < 0.05) when comparing resident AMs at Day 0 vs Day 3.

**Figure S2. LPS induces alternative splicing in macrophages both *in vitro* and *in vivo*.** The Venn diagram depicts the number of loci exhibiting altered isoform usage identified using DEXseq (FDR < 0.1). The grey circle represents the current study (Day 0 vs Day 3 resident AM). The pink circle represents our prior study in which RAW264.7 mouse macrophages were treated with 20 ng/ml LPS for four hours compared to untreated RAW264.7 cells ([O'Connor et al. 2015](#_ENREF_51)). Genes with overlapping exons are treated as a single entity for this purpose, since they could not be disambiguated

**Figure S3. LPS induces alternative splicing in resident alveolar macrophages.** **(A)** Depicted are Sashimi plots ([Katz et al. 2010](#_ENREF_34)) that demonstrate increased skipping of exon 2 in Nemo in resident AM that had been challenged with LPS for 12 days (compared to control resident AM that were unchallenged). Peaks show read coverage (RPKM) and numbers denote junction spanning reads. **(B)** RNA from resident alveolar macrophages from mice treated with I.T. LPS for 12 days or from untreated mice was purified, Nemo mRNA was reverse transcribed and amplified by PCR using primers that bracket exon 2, and the resulting product was visualized by agarose gel electrophoresis. Bands corresponding to wild type Nemo mRNA and Nemo2 mRNA are indicated. **(C)** Depicted are Sashimi plots that demonstrate increased production of Cav1 in resident AM that were treated with LPS for 3 days compared to control untreated resident AM.

**Figure S4. Altered isoform usage in the Idh complex in resident and recruited alveolar macrophages.** The figures depict DEXseq analysis of sequence reads for Idh3b **(A)** or Idh3g **(B)**. Day 3 resident AM data depicted in blue, day 3 recruited AM data depicted in red. Purple shading marks the DEXseq depicted change. Both genes run 5’🡪3’ right to left. In Idh3b, DEXseq identified an intron 4 retention event in recruited AM (purple box in bottom read schematic, just above the gene schematic). In Idh3g, DEXseq identified an alteration in the 3’ part of exon 5 (purple box). See Table S2 for fold-changes and adjusted p-values.

**Figure S5. Glycolytic pathway intermediates for resident and recruited alveolar macrophages.** U-13C-glucose (“heavy label”) was intravenously injected into mice on LPS Day 3 at 30 and 60 minutes prior to euthanasia. Resident and recruited alveolar macrophages were purified by fluorescence activated cell sorting.Glycolytic pathway intermediate metabolites were measured with ultra-high-performance liquid chromatography / mass spectrometry. **(A)** Total metabolite levels. **(B)** Lactate to pyruvate ratio determined using total metabolite levels. **(C)** Heavy labeled metabolites. Heavy-labeled lactate was below the limit of detection. **(D)** Percent of metabolites that are heavy-labeled.