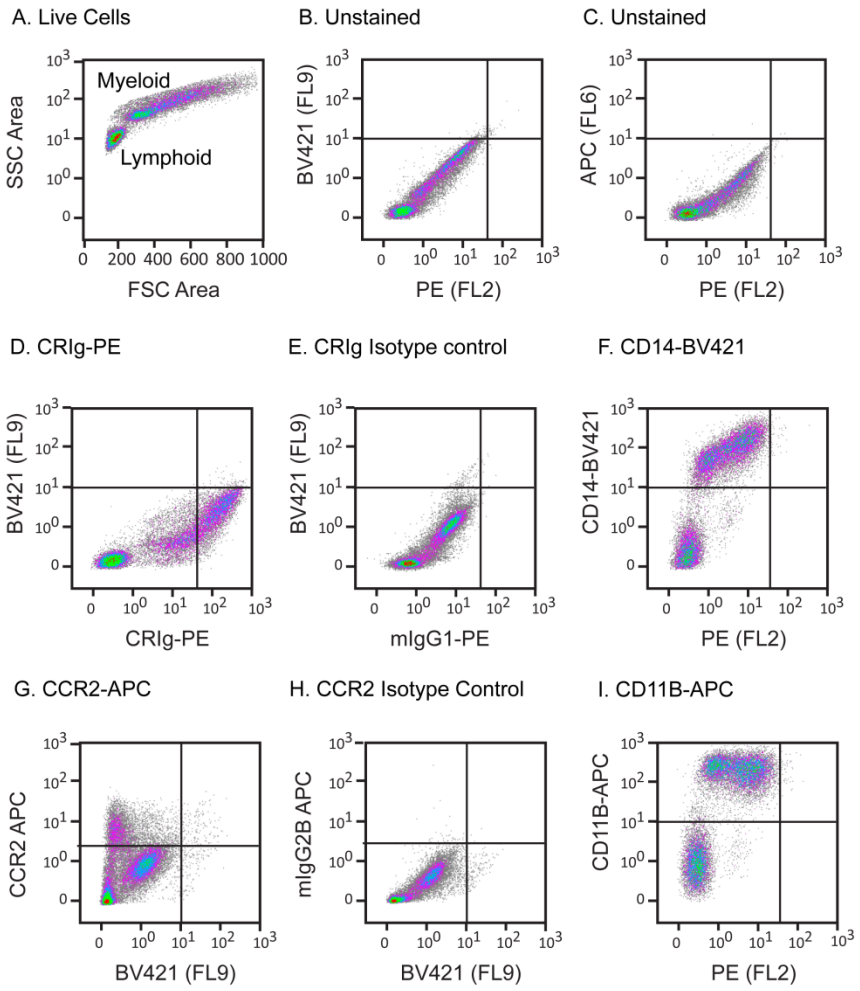
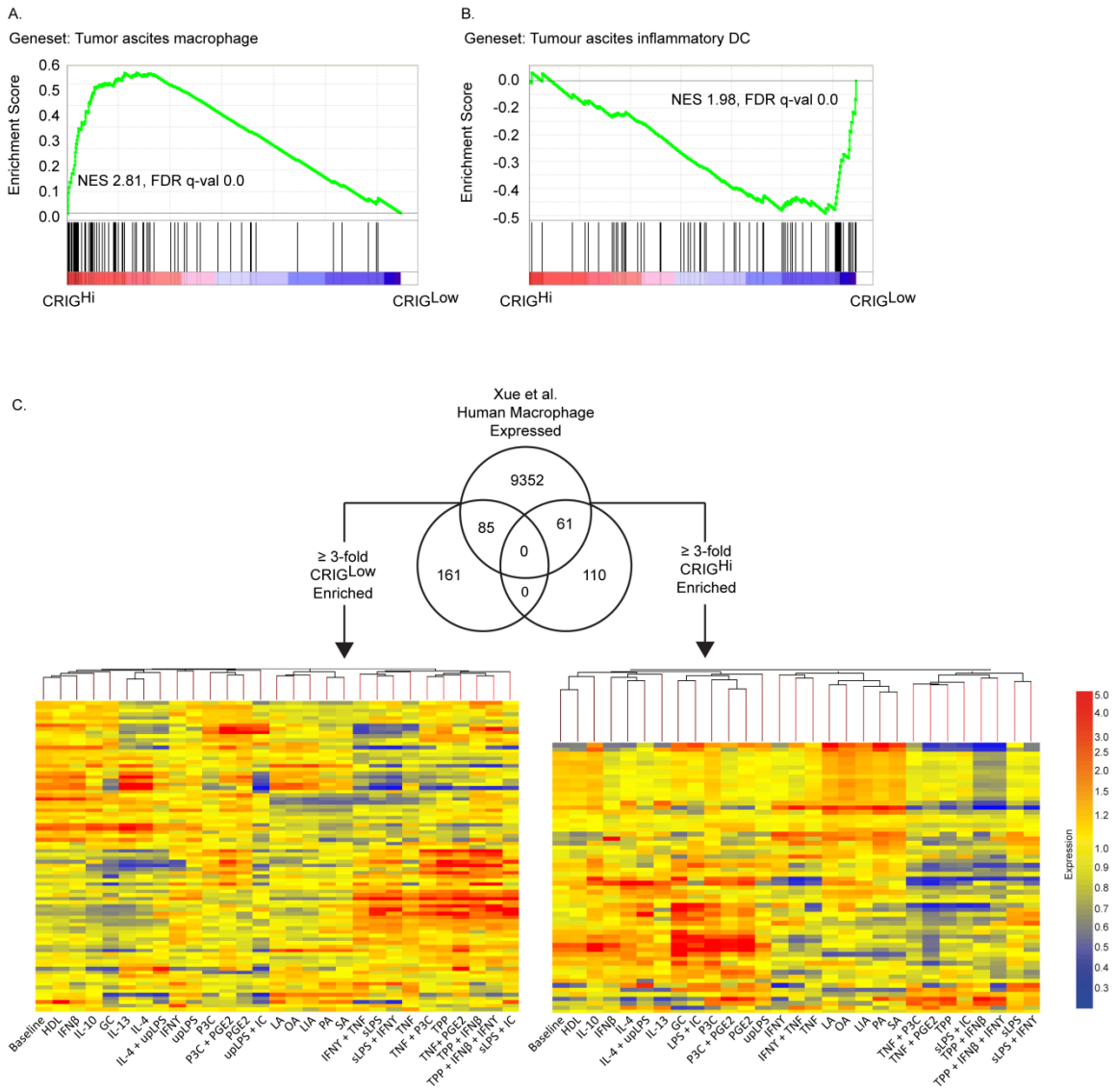
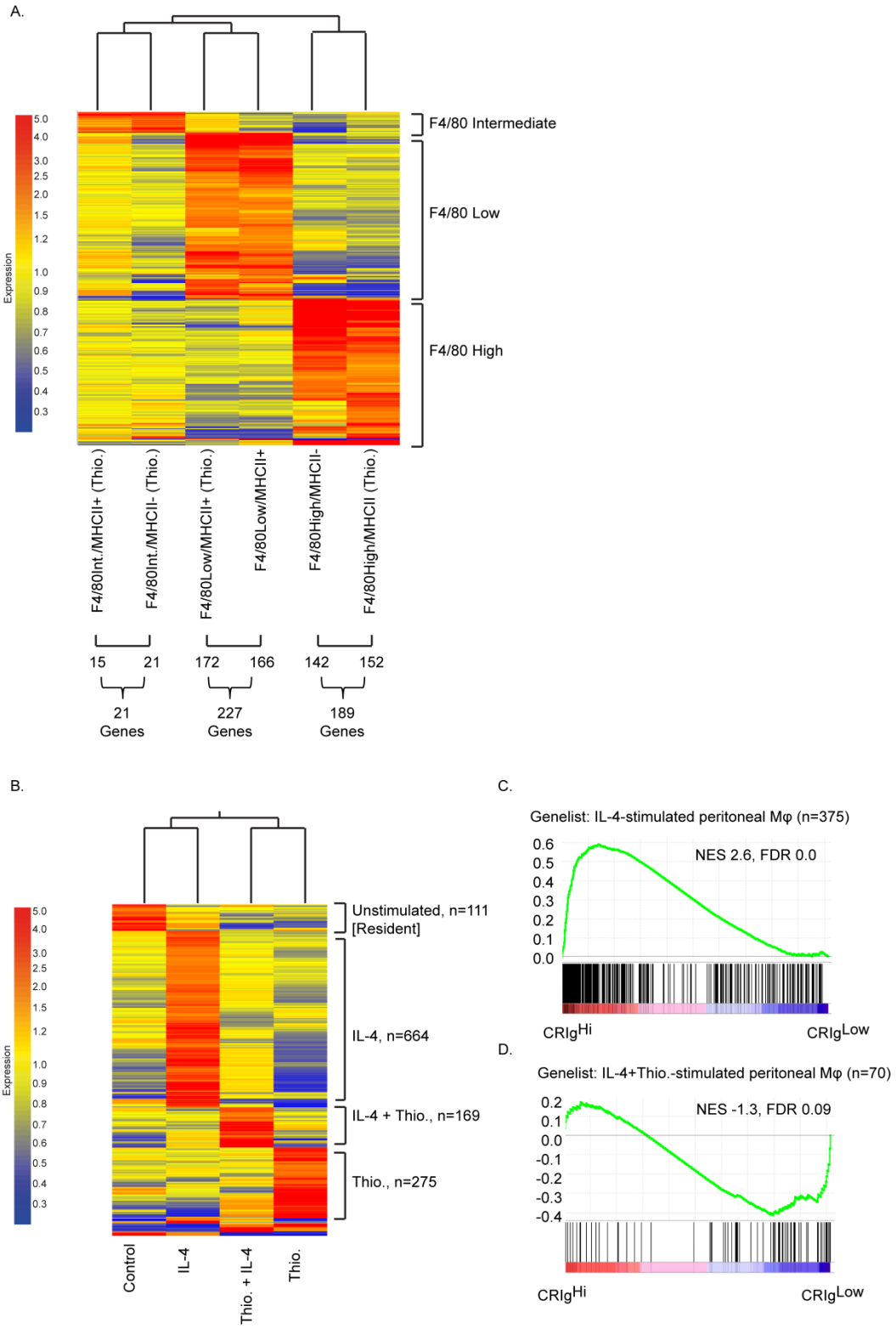


Supplementary Figure 1. Example flow cytometry controls for phenotyping human peritoneal macrophages for panel containing CRIg-PE, CD14-BV421and CCR2-APC or CD11B-APC. Forward Scatter (FSC) and side scatter (SSC) characteristics of live cells from ascites fluid (A). Unstained controls fluorescence in BV421 (CD14), PE (CRIg) and APC (CCR2) channels (B,C). CRIg-PE single colour (D) and mIgG1-PE isotype control (E). CD14-BV421 (mIgG1) single colour control (F). CCR2-APC single colour (G) and mIgG2b isotype control (H). CD11B-APC (mIgG1) single colour control (I).



Supplementary Figure 2. Tumour ascites macrophage (A) and inflammatory DC(29) (B) gene set enrichment with respect to ascites fluid macrophage profile. Ascites macrophage data is ranked according to differential expression between sub-populations (indicated by red-blue bar) and the gene set of interest is mapped onto this profile (black bars) to determine enrichment score (green line). (C) Venn diagram indicates the overlap between CRIg^{Hi} and CRIg^{Low} enriched genes (≥3-fold differentially expressed) and the macrophage-expressed gene set reported by Xue et al (30). Heatmaps illustrate the expression of CRIg^{Hi} and CRIg^{Low} enriched genes across 29 macrophage activation conditions(31) (clustering by distance correlation). GC: glucocorticoid, IC: immune complexes, P3C: Pam3CysSerLys4, TPP: TNF+PGE2+P3C, PA: palmitic acid, OA: oleic acid, LA: lauric acid, LIA: linoleic acid, SA: stearic acid, sLPS: standard LPS, upLPS: ultrapure LPS, HDL: high density lipoprotein.



Supplementary Figure 3. Mouse peritoneal macrophage gene set enrichment analysis. (A) Genes from GSE15907 were classified as subset enriched if they were ≥2-fold more highly expressed in one population (i.e. F4/80^{Hi} with or without thioglycollate (Thio.), F4/80^{Low} with or without thioglycollate, F4/80^{Intermediate} (Int.) with or without MHC-II expression) compared to both of the other macrophage

populations. (B) Genes from GSE54679 were classified as subset enriched if they were ≥2-fold more highly expressed in 1 treatment condition compared to all other treatment conditions. The total number of genes enriched in each population is shown, genes and samples were clustered using distance correlation (A and B). Alternatively activated resident (IL-4, C) and monocyte-derived (IL-4 + thioglycollate, D) murine peritoneal macrophage gene set enrichment with respect to ascites fluid macrophage profile. Ascites macrophage data is ranked according to differential expression between sub-populations (indicated by red-blue bar) and the gene set of interest is mapped onto this profile (black bars) to determine enrichment score (green line).