GENOMICS CORE FACILITY

CIBR: Center for Innovative Biomedical Resources

CORE INSTRUMENTATION

- Applied Biosystems 3730XL (Sanger sequencing)
- Affymetrix GeneChip system 3000 7G (chip-based arrays, e.g. CytoScan HD, DMET)
- Applied Biosystems 7900 RT-PCR system (genotyping by Taqman©-based methods)
- Applied Biosystems 9700 thermocycler (PCR amplification)
- Nanodrop single-channel and 8-channel spectrophotometers
- ThermoFisher QuantStudio 5
- Ion Torrent Personal Genome Machine (next generation sequencing panels, e.g. Comprehensive Cancer Panel, and Custom AmpliSeq panels)
- Ion Chef System
- Ion S5 Sequencer

MISSION

The mission of the Genomics Core Facility is to provide the technical capability with state-of-the-art instrumentation and the expertise to enable genomic research. Our services can support basic science discovery, translational studies and clinical research and with our Translational Genomics Laboratory, can provide the ability to support the bench to bedside concept. We provide training opportunities for students, fellows, staff, and faculty.

ABOUT

The Genomics Core Facility has been in operation for over 30 years. During that time, we have maintained a commitment to sustain genomic research with state-of-the-art instrumentation, methodologies, and technical capabilities. Since the 1980's, the Genomics Core has supported thousands of grants and publications, with countless numbers published in high-impact journals. Our staff are extremely knowledgeable, the majority of staff having worked in the Genomics Core for 15-20 years. In addition to standard services, we can assist in customizing services based on your needs, especially in the area of DNA sequencing.

CORE SERVICES

- Cytogenomic Arrays
- Extraction of Nucleic Acid
  - DNA
  - RNA
- Gene Expression Arrays
  - Global Expression Profiling
  - miRNA Expression Profiling
  - Transcriptome Analysis
- Genotyping
  - Taqman Assays
- Next Generation Sequencing (NGS) Gene Panels
- Sanger DNA Sequencing

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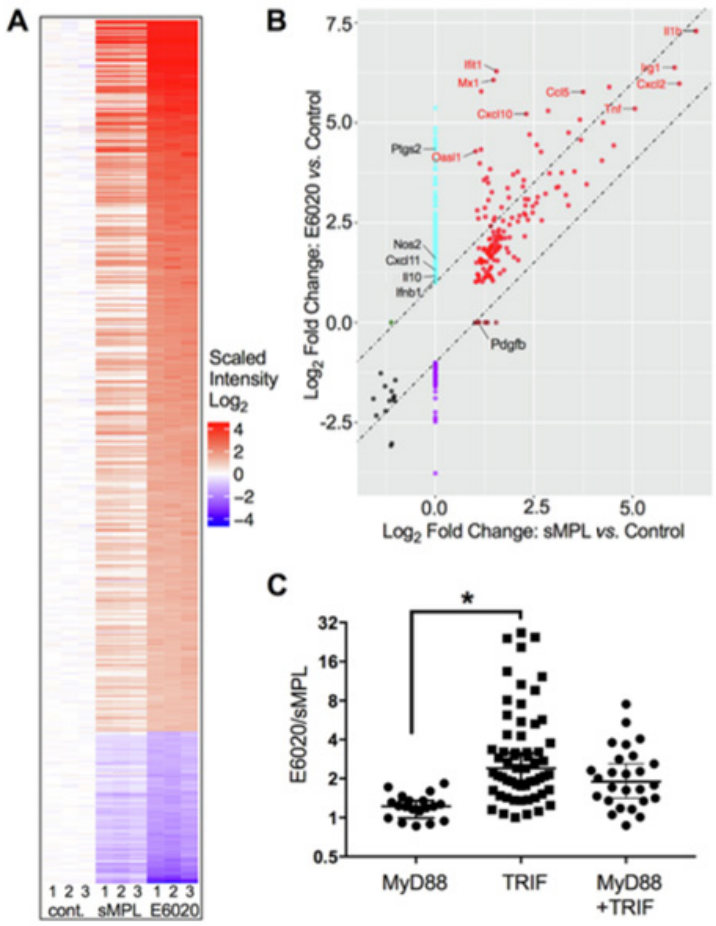

Fig. 2. E6020 induces a strong Type I IFN signature. Primary macrophages were either treated for 2 h with medium only, sMPL, or E6020 (100 ng/mL). RNA was subjected to microarray analysis. (A) Heatmap of differentially expressed (2-fold cut-off, FDR < 0.05) protein-coding and complex genes from 3 biological replicates (numbered 1–3 below), that were either left untreated (left), or treated with 100 ng/mL sMPL (middle) or E6020 (right). Each treatment per replicate was assayed on an individual chip. Intensity was plotted relative to the average of the untreated controls. (B) Quadrant plot of gene induction/suppression by sMPL versus Control (x-axis) and E6020 versus Control (y-axis). Diagonal lines are spaced 1 log2-fold difference, and genes falling within the lines are equally induced by sMPL and E6020. Genes of particular interest for TLR4-induced, MyD88-dependent and RIF-dependent activation are labeled. (C) The ratio of induction between E6020-treated cells and sMPL-treated cells was calculated for a subset of the differentially expressed genes with previously reported dependence on MyD88, TRIF, or both adapters downstream of TLR4 signaling pathways (Supplementary Table II). Richard, *et al.*, Dissociation of TRIF bias and adjuvanticity. 2020. Vaccine (38):4298-4308.

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