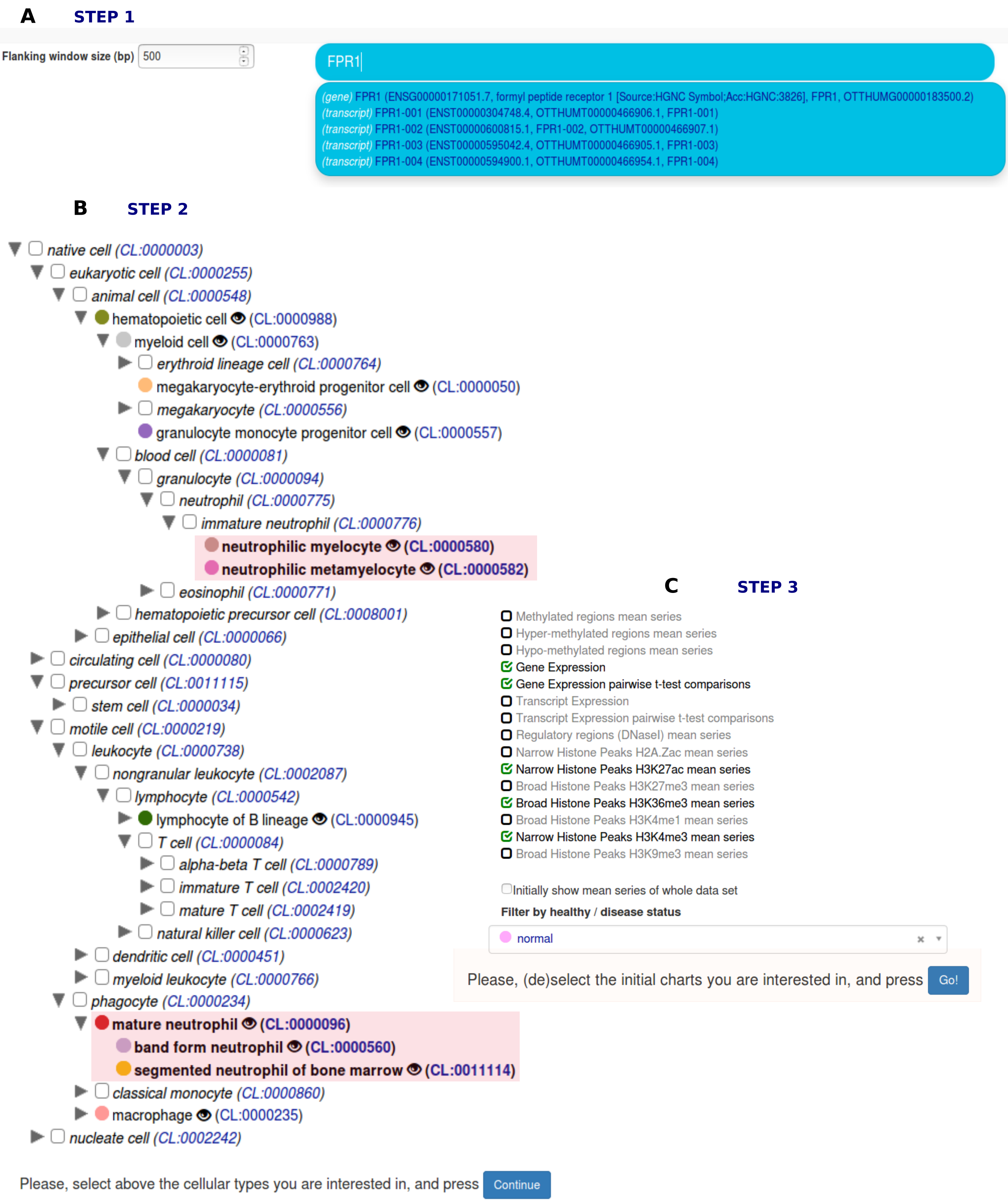
Supplemental figures

Figure S1.- A practical BLUEPRINT Data Analysis Portal usage case with FPR1 gene. Related to STAR Methods.



Flanking window size (bp) 500

FPR1

(gene) FPR1 (ENSG00000171051.7, formyl peptide receptor 1 [Source:HGNC Symbol;Acc:HGNC:3826], FPR1, OTTHUMG00000183500.2)
(transcript) FPR1-001 (ENST00000304748.4, OTTHUMT00000466906.1, FPR1-001)
(transcript) FPR1-002 (ENST00000600815.1, FPR1-002, OTTHUMT00000466907.1)
(transcript) FPR1-003 (ENST00000595042.4, OTTHUMT00000466905.1, FPR1-003)
(transcript) FPR1-004 (ENST00000594900.1, OTTHUMT00000466954.1, FPR1-004)

- ▼ ☐ *native cell (CL:0000003)*
  - ▼ ☐ *eukaryotic cell (CL:0000255)*
    - ▼ ☐ *animal cell (CL:0000548)*
      - ▼ ● hematopoietic cell (CL:0000988)
        - ▼ ● myeloid cell (CL:0000763)
          - ▶ ☐ *erythroid lineage cell (CL:0000764)*
          - ● megakaryocyte-erythroid progenitor cell (CL:0000050)
          - ▶ ☐ *megakaryocyte (CL:0000556)*
          - ● granulocyte monocyte progenitor cell (CL:0000557)
        - ▼ ☐ *blood cell (CL:0000081)*
          - ▼ ☐ *granulocyte (CL:0000094)*
            - ▼ ☐ *neutrophil (CL:0000775)*
              - ▼ ☐ *immature neutrophil (CL:0000776)*
                - ● **neutrophilic myelocyte (CL:0000580)**
                - ● **neutrophilic metamyelocyte (CL:0000582)**
            - ▶ ☐ *eosinophil (CL:0000771)*
        - ▶ ☐ *hematopoietic precursor cell (CL:0008001)*
      - ▶ ☐ *epithelial cell (CL:0000066)*
  - ▶ ☐ *circulating cell (CL:0000080)*
  - ▼ ☐ *precursor cell (CL:0011115)*
    - ▶ ☐ *stem cell (CL:0000034)*
  - ▼ ☐ *motile cell (CL:0000219)*
    - ▼ ☐ *leukocyte (CL:0000738)*
      - ▼ ☐ *nongranular leukocyte (CL:0002087)*
        - ▼ ☐ *lymphocyte (CL:0000542)*
          - ▶ ● lymphocyte of B lineage (CL:0000945)
          - ▼ ☐ *T cell (CL:0000084)*
            - ▶ ☐ *alpha-beta T cell (CL:0000789)*
            - ▶ ☐ *immature T cell (CL:0002420)*
            - ▶ ☐ *mature T cell (CL:0002419)*
          - ▶ ☐ *natural killer cell (CL:0000623)*
      - ▶ ☐ *dendritic cell (CL:0000451)*
      - ▶ ☐ *myeloid leukocyte (CL:0000766)*
    - ▼ ☐ *phagocyte (CL:0000234)*
      - ▼ ● **mature neutrophil (CL:0000096)**
        - ● **band form neutrophil (CL:0000560)**
        - ● **segmented neutrophil of bone marrow (CL:0011114)**
      - ▶ ☐ *classical monocyte (CL:0000860)*
      - ▶ ● macrophage (CL:0000235)
  - ▶ ☐ *nucleate cell (CL:0002242)*

Please, select above the cellular types you are interested in, and press Continue

- ☐ Methylated regions mean series
- ☐ Hyper-methylated regions mean series
- ☐ Hypo-methylated regions mean series
- ☑ Gene Expression
- ☑ Gene Expression pairwise t-test comparisons
- ☐ Transcript Expression
- ☐ Transcript Expression pairwise t-test comparisons
- ☐ Regulatory regions (DNaseI) mean series
- ☐ Narrow Histone Peaks H2A.Zac mean series
- ☑ Narrow Histone Peaks H3K27ac mean series
- ☐ Broad Histone Peaks H3K27me3 mean series
- ☑ Broad Histone Peaks H3K36me3 mean series
- ☐ Broad Histone Peaks H3K4me1 mean series
- ☑ Narrow Histone Peaks H3K4me3 mean series
- ☐ Broad Histone Peaks H3K9me3 mean series

☐ Initially show mean series of whole data set

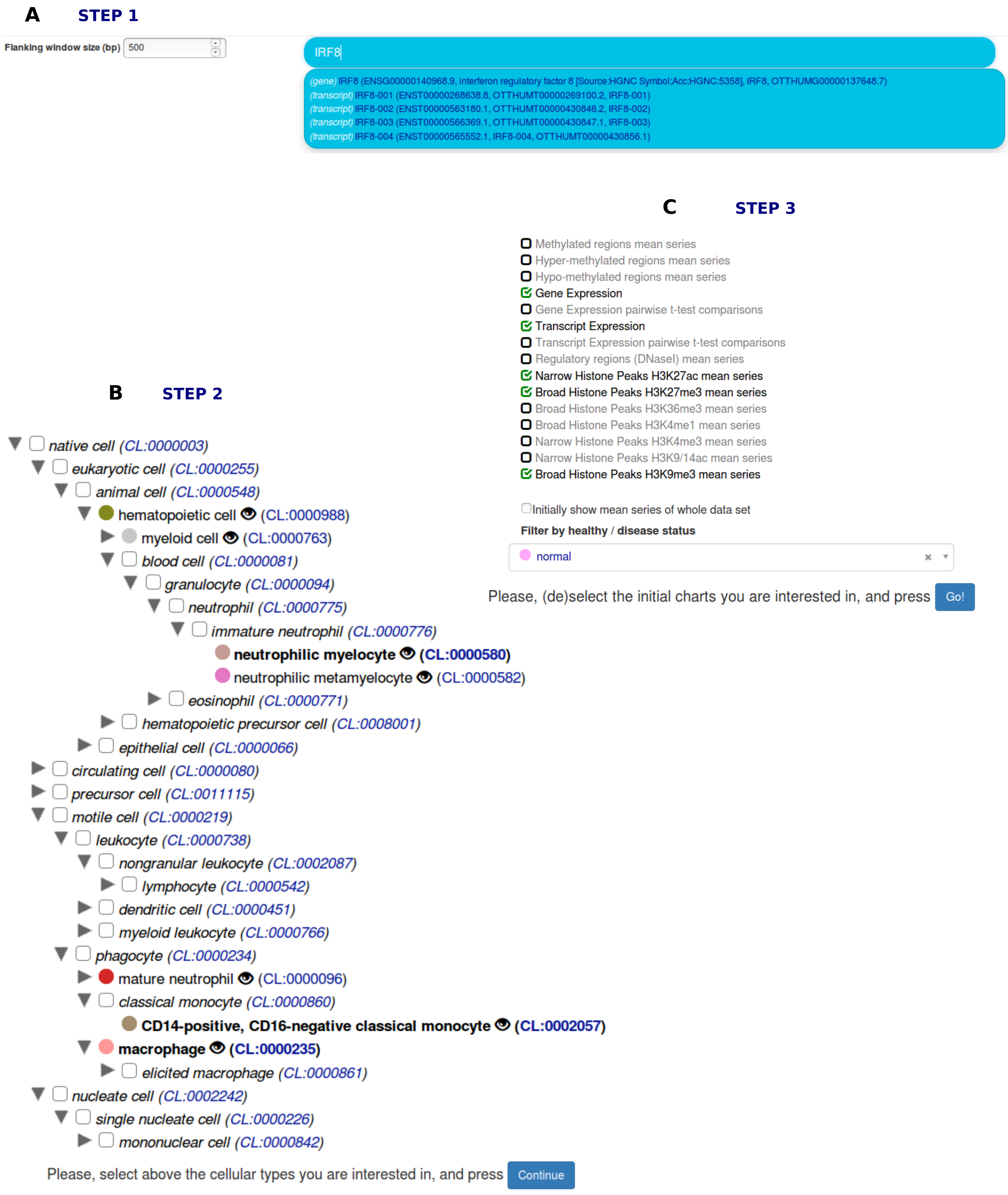
Filter by healthy / disease status

● normal

Please, (de)select the initial charts you are interested in, and press Go!

Figure S2.- A wiew of results displayed by BDAP for FPR1 gene. Related to STAR Methods.

Figure S3.- A practical BLUEPRINT Data Analysis Portal usage case with IRF8 gene. Related to STAR Methods.



A STEP 1

Flanking window size (bp) 500

IRF8

(gene) IRF8 (ENSG00000140968.9, interferon regulatory factor 8 [Source:HGNC Symbol;Acc:HGNC:5358], IRF8, OTTHUMG00000137648.7)
(transcript) IRF8-001 (ENST00000268638.8, OTTHUMT00000269100.2, IRF8-001)
(transcript) IRF8-002 (ENST00000563180.1, OTTHUMT00000430846.2, IRF8-002)
(transcript) IRF8-003 (ENST00000566369.1, OTTHUMT00000430847.1, IRF8-003)
(transcript) IRF8-004 (ENST00000565552.1, IRF8-004, OTTHUMT00000430856.1)

C STEP 3

- ☐ Methylated regions mean series
- ☐ Hyper-methylated regions mean series
- ☐ Hypo-methylated regions mean series
- ☑ Gene Expression
- ☐ Gene Expression pairwise t-test comparisons
- ☑ Transcript Expression
- ☐ Transcript Expression pairwise t-test comparisons
- ☐ Regulatory regions (DNaseI) mean series
- ☑ Narrow Histone Peaks H3K27ac mean series
- ☑ Broad Histone Peaks H3K27me3 mean series
- ☐ Broad Histone Peaks H3K36me3 mean series
- ☐ Broad Histone Peaks H3K4me1 mean series
- ☐ Narrow Histone Peaks H3K4me3 mean series
- ☐ Narrow Histone Peaks H3K9/14ac mean series
- ☑ Broad Histone Peaks H3K9me3 mean series

☐ Initially show mean series of whole data set

Filter by healthy / disease status

● normal

Please, (de)select the initial charts you are interested in, and press Go!

B STEP 2

- ▼ ☐ *native cell (CL:0000003)*
  - ▼ ☐ *eukaryotic cell (CL:0000255)*
    - ▼ ☐ *animal cell (CL:0000548)*
      - ▼ ● hematopoietic cell 👁 (CL:0000988)
        - ▶ ● myeloid cell 👁 (CL:0000763)
        - ▼ ☐ *blood cell (CL:0000081)*
          - ▼ ☐ *granulocyte (CL:0000094)*
            - ▼ ☐ *neutrophil (CL:0000775)*
              - ▼ ☐ *immature neutrophil (CL:0000776)*
                - ● **neutrophilic myelocyte 👁 (CL:0000580)**
                - ● neutrophilic metamyelocyte 👁 (CL:0000582)
            - ▶ ☐ *eosinophil (CL:0000771)*
        - ▶ ☐ *hematopoietic precursor cell (CL:0008001)*
      - ▶ ☐ *epithelial cell (CL:0000066)*
  - ▶ ☐ *circulating cell (CL:0000080)*
  - ▶ ☐ *precursor cell (CL:0011115)*
  - ▼ ☐ *motile cell (CL:0000219)*
    - ▼ ☐ *leukocyte (CL:0000738)*
      - ▼ ☐ *nongranular leukocyte (CL:0002087)*
        - ▶ ☐ *lymphocyte (CL:0000542)*
      - ▶ ☐ *dendritic cell (CL:0000451)*
      - ▶ ☐ *myeloid leukocyte (CL:0000766)*
    - ▼ ☐ *phagocyte (CL:0000234)*
      - ▶ ● mature neutrophil 👁 (CL:0000096)
      - ▼ ☐ *classical monocyte (CL:0000860)*
        - ● **CD14-positive, CD16-negative classical monocyte 👁 (CL:0002057)**
      - ▼ ● **macrophage 👁 (CL:0000235)**
        - ▶ ☐ *elicited macrophage (CL:0000861)*
  - ▼ ☐ *nucleate cell (CL:0002242)*
    - ▼ ☐ *single nucleate cell (CL:0000226)*
      - ▶ ☐ *mononuclear cell (CL:0000842)*

Please, select above the cellular types you are interested in, and press Continue

Figure S4.- A wiew of results displayed by BDAP for IRF8 gene. Related to STAR Methods.

Supplemental figure legends

Figure S1.- A practical BLUEPRINT Data Analysis Portal usage case with FPR1 gene. Related to STAR Methods.

A. Step one. Introduce the FPR1 gene symbol in the search-box and select 500 bp for flanking window.
B. Step two. Select those cell types of interest based on the cell ontology hierarchy: neutrophilic myelocyte; neutrophilic metamyelocyte; band form neutrophil;
segmented neutrophil of bone marrow; and mature neutrophil (shaded in red).
C. Step three. Select the available experiments of interests (ticked in green) and the healthy or disease filtering.

See also Figure 1.

Figure S2.- A wiew of results displayed by BDAP for FPR1 gene. Related to STAR Methods.

A. Gene expression boxplots. (Top left)
B. Heatmap with pairwise t-test comparisons for FPR1. (Top right)
C. Histone H3K27ac spline+ribbon-based scatter plots. (Middle left)
D. Histone H3K36me3 spline+ribbon-based scatter plots. (Middle right)
E. Histone H3K4me3 spline+ribbon-based scatter plots. (Bottom center)

The graphical representation of the genes in the bottom of the spline+ribbon-based scatter plots are based on the principal splicing isoform described
in APPRIS (Rodriguez et al, 2013).

See also Figure 1.

Figure S3.- A practical BLUEPRINT Data Analysis Portal usage case with IRF8 gene. Related to STAR Methods.

A. Step one. Introduce the IRF8 gene symbol in the search-box and select 500 bp for flanking window.
B. Step two. Select those cell types of interest based on the cell ontology hierarchy: neutrophilic myelocyte, the classical monocyte and the macrophages (shaded in red).
C. Step three. Select the available experiments of interests (ticked in green) and the healthy or disease filtering.

See also Figure 1.

Figure S4.- A wiew of results displayed by BDAP for IRF8 gene. Related to STAR Methods.

A. Transcripts expression boxplot. (Top left)
B. Gene Expression boxplot. (Middle left)
C. Histone H3K9me3 spline+ribbon-based scatter plots. (Middle right)
D. Histone H3K27ac spline+ribbon-based scatter plots. (Bottom left)
E. Histone H3K27me3 spline+ribbon-based scatter plots. (Bottom right)

The graphical representation of the genes in the bottom of the spline+ribbon-based scatter plots are based on the principal splicing isoform described in APPRIS (Rodriguez et al, 2013).

See also Figure 1.

Supplemental table legends

Table S1. Table with comparison between epigenomic resources for large epigenome data access (In Table_S1.xls)