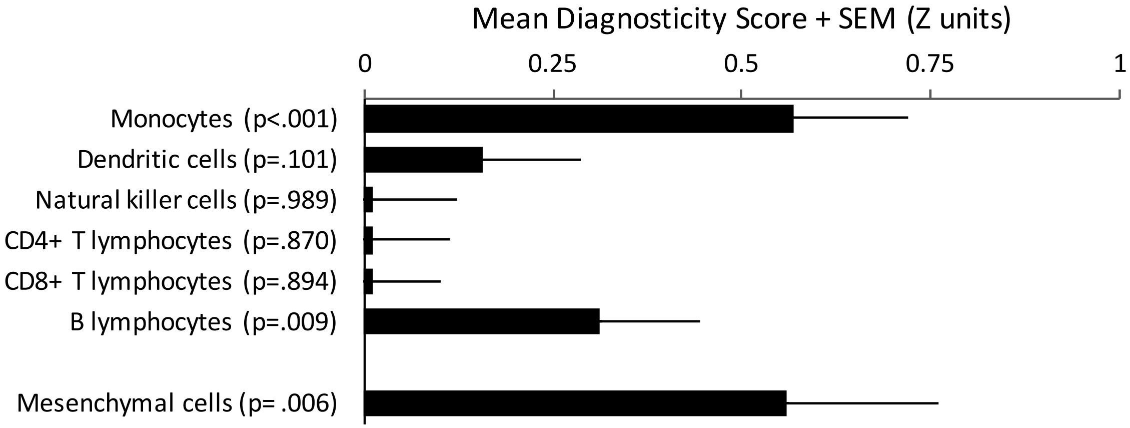
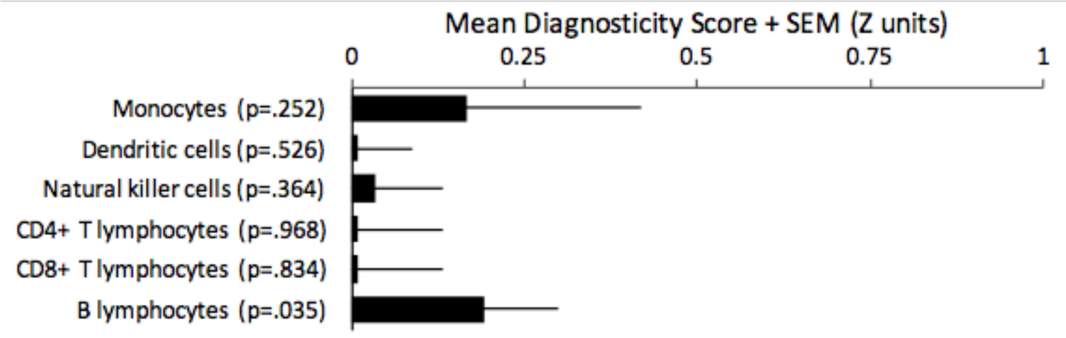
***Figure S1*. Transcript origin analysis of up-regulated placenta genes.**



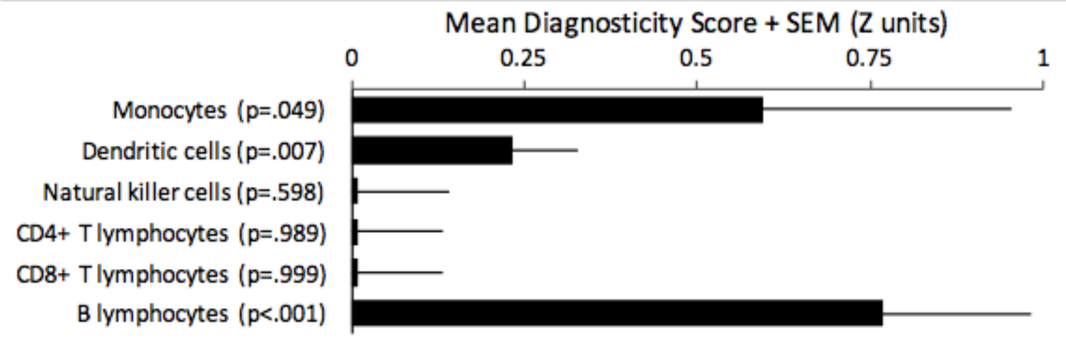
Legend: Using reference profiles from leukocyte gene expression studies, these analyses identified monocytes, B-lymphocytes, and mesenchymal cells as major sources of placental transcripts upregulated with disadvantage.

Figure S2. **Transcript origin analysis of cord blood genes.**

A. Upregulated



B. Downregulated



Legend: Using reference profiles, these analyses identified B-cells as primary source of transcripts upregulated with disadvantage (Panel A), and monocytes, dendritic cells, and B-cells as source of down-regulated transcripts (Panel B).