Supplemental Information

Stemformatics data portal enables transcriptional benchmarking of lab-derived myeloid cells

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Supplementary data: Choi et al Finding and benchmarking stem cell-derived myeloid cells using the Stemformatics platform

Fig S1. Gene to samples function finds cell types where a user specified gene is expressed highly in all datasets in Stemformatics. The result is displayed hierarchically, where multiple datasets showing high expression in the same cell type are shown together. This increases the confidence that the result is generalisable across multiple settings.

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Table S1: Example changes in sample annotation from the previous version where uniform nomenclature has been applied. Where the terminology contained cell of origin for differentiated cell, such as "hESC-derived neuron", we've added this to the "parental_cell_type" field.

Term before update	After update
CD4 T cell	CD4-positive T lymphocyte
B cell	B-lymphocyte
Blood dendritic cells	dendritic cell
human embryonic stem cell	embryonic stem cell
Embryonic stem cell	embryonic stem cell
hESC-derived neuron	neuron (+ parental_cell_type = embryonic stem cell)
primary human neural progenitor	neural progenitor cell
BMDM	macrophage (+ tissue_of_origin = bone marrow)
primary skin fibroblast	fibroblast (+ tissue_of_origin = skin)
hematopoietic multipotent progenitor	made more specific or changed to hematopoietic precursor cell (or, if FACS sorted, CD34-positive precursor cell)