

Supplement Information

1 Data Processing

The ChIP-Seq signals and RNA-Seq gene expression datasets, used in this work, have been processed and normalized by the Roadmap Epigenomics (REMC) Project [1]. The details for the same can be found at http://egg2.wustl.edu/roadmap/web_portal/processed_data.html.

2 Results

Table 1: 56 cell-types selected for this study from REMC database [1] and DeepChrome AUC scores for each of them.

Cell-type ID	Cell-type prediction	DeepChrome AUC Score
E003	H1_Cell_Line	0.77
E004	H1_BMP4_Derived_Mesendoderm_Cultured_Cells	0.81
E005	H1_BMP4_Derived_Trophoblast_Cultured_Cells	0.8
E006	H1_Derived_Mesenchymal_Stem_Cells	0.82
E007	H1_Derived_Neural_Progenitor_Cultured_Cells	0.77
E011	hESC_Derived_CD184+_Endoderm_Cultured_Cells	0.76
E012	hESC_Derived_CD56+_Ectoderm_Cultured_Cells	0.8
E013	hESC_Derived_CD56+_Mesoderm_Cultured_Cells	0.79
E016	HUES64_Cell_Line	0.79
E024	4star	0.77
E027	Breast_Myoepithelial_Cells	0.8
E028	Breast_vHMEC	0.81
E037	CD4_Memory_Primary_Cells	0.81
E038	CD4_Naive_Primary_Cells	0.83
E047	CD8_Naive_Primary_Cells	0.83
E050	Mobilized_CD34_Primary_Cells_Female	0.8
E053	Neurosphere_Cultured_Cells_Cortex_Derived	0.8
E054	Neurosphere_Cultured_Cells_Ganglionic_Eminence_Derived	0.8
E055	Penis_Foreskin_Fibroblast_Primary_Cells_skin01	0.83
E056	Penis_Foreskin_Fibroblast_Primary_Cells_skin02	0.89
E057	Penis_Foreskin_Keratinocyte_Primary_Cells_skin02	0.9
E058	Penis_Foreskin_Keratinocyte_Primary_Cells_skin03	0.84
E059	Penis_Foreskin_Melanocyte_Primary_Cells_skin01	0.9
E061	Penis_Foreskin_Melanocyte_Primary_Cells_skin03	0.84
E062	Peripheral_Blood_Mononuclear_Primary_Cells	0.8
E065	Aorta	0.76
E066	Adult_Liver	0.8
E070	Brain_Germinal_Matrix	0.76
E071	Brain_Hippocampus_Middle	0.73
E079	Esophagus	0.74
E082	Fetal_Brain_Female	0.78
E084	Fetal_Intestine_Large	0.71
E085	Fetal_Intestine_Small	0.72
E087	Pancreatic_Islets	0.74
E094	Gastric	0.73
E095	Left_Ventricle	0.82
E096	Lung	0.72
E097	Ovary	0.76
E098	Pancreas	0.74
E100	Psoas_Muscle	0.9
E104	Right_Atrium	0.79
E105	Right_Ventricle	0.78
E106	Sigmoid_Colon	0.76
E109	Small_Intestine	0.74
E112	Thymus	0.69
E113	Spleen	0.73
E114	A549	0.83

E116	GM12878	0.91
E117	HELA	0.92
E118	HEPG2	0.85
E119	HMEC	0.83
E120	HSMM	0.84
E122	HUVEC	0.83
E123	K562	0.92
E127	NHEK	0.83
E128	NHLF	0.83

[1] Kundaje, A., Meuleman, W., Ernst, J., Bilenky, M., Yen, A., Heravi-Moussavi, A., Kheradpour, P., Zhang, Z., Wang, J., Ziller, M.J. and Amin, V., 2015. Integrative analysis of 111 reference human epigenomes. *Nature*, 518(7539), pp.317-330.