Sample Summary:

Whole blood WGBS data ([1](#_ENREF_1)), WGBS data from H1 ESCs and differentiated cells ([2](#_ENREF_2)), WGBS data from human adult tissues (Salk, REF), our internal N37 WGBS data (ten tissues) and WGBS data from a cancer cell line and a colon cancer tumor tissue were used to identify the methylation blocks.

ILMN450k data from TCGA([3](#_ENREF_3)), GSE35069([4](#_ENREF_4)), GSE41169([5](#_ENREF_5)) and GSE42861([6](#_ENREF_6)) were used to infer methylation block with generalized methylation block inferring method in microarray data (average R2 replaced with average Pearson correlation coefficient). TCGA dataset were also represent solid tissues while GSE35069, GSE41169 and GSE42861 represent circulating cells.

RRBS data from Encode Project([7](#_ENREF_7)) (101 samples) were used to infer methylation block with generalized methylation block inferring method in RRBS (average R2 replaced with average Pearson correlation coefficient)

WGBS data from human adult tissues (Salk, REF), our internal N37 WGBS data (ten tissues) were used to select tissue specific methylation haplotype regions with group specific index.

RRBS data included solid cancer tissue and plasma DNA were used to evaluate the cancer diagnosis and the tissue mapping performance.

1. Heyn, H., Li, N., Ferreira, H.J., Moran, S., Pisano, D.G., Gomez, A., Diez, J., Sanchez-Mut, J.V., Setien, F., Carmona, F.J. *et al.* (2012) Distinct DNA methylomes of newborns and centenarians. *Proceedings of the National Academy of Sciences of the United States of America*, **109**, 10522-10527.

2. Xie, W., Schultz, M.D., Lister, R., Hou, Z., Rajagopal, N., Ray, P., Whitaker, J.W., Tian, S., Hawkins, R.D., Leung, D. *et al.* (2013) Epigenomic analysis of multilineage differentiation of human embryonic stem cells. *Cell*, **153**, 1134-1148.

3. Tomczak, K., Czerwinska, P. and Wiznerowicz, M. (2015) The Cancer Genome Atlas (TCGA): an immeasurable source of knowledge. *Contemp Oncol (Pozn)*, **19**, A68-77.

4. Reinius, L.E., Acevedo, N., Joerink, M., Pershagen, G., Dahlen, S.E., Greco, D., Soderhall, C., Scheynius, A. and Kere, J. (2012) Differential DNA methylation in purified human blood cells: implications for cell lineage and studies on disease susceptibility. *PloS one*, **7**, e41361.

5. Horvath, S., Zhang, Y., Langfelder, P., Kahn, R.S., Boks, M.P., van Eijk, K., van den Berg, L.H. and Ophoff, R.A. (2012) Aging effects on DNA methylation modules in human brain and blood tissue. *Genome biology*, **13**, R97.

6. Liu, Y., Aryee, M.J., Padyukov, L., Fallin, M.D., Hesselberg, E., Runarsson, A., Reinius, L., Acevedo, N., Taub, M., Ronninger, M. *et al.* (2013) Epigenome-wide association data implicate DNA methylation as an intermediary of genetic risk in rheumatoid arthritis. *Nat Biotechnol*, **31**, 142-147.

7. Wang, H., Maurano, M.T., Qu, H., Varley, K.E., Gertz, J., Pauli, F., Lee, K., Canfield, T., Weaver, M., Sandstrom, R. *et al.* (2012) Widespread plasticity in CTCF occupancy linked to DNA methylation. *Genome research*, **22**, 1680-1688.