Data Type	GEO	Description
Transcriptome	GSE16256	18 tissue type, 4 individuals = 36 mRNA-seq samples
Methylome	GSE16256	18 tissue type, 4 individuals = 36 MethylC-seq samples
Genome	GSE16256	4 whole donor genome sequences H1 genome (
ChIP-seq	GSE16256	
Dnase I data	GSE18927	

Step	Figure, Tables	Supplementary material section	Tool/Method
1. Differential Methylation - DMRs	1b	1. MethylC-seq Mapping (p. 3) 2. Methylation Calling (p.4) 3. DMR Finding (p. 4) 4. Benchmark methylpy and other DMR identification methods (p. 8)	1. Bowtie, Cutadapt 2. binomial test 3. Scripts in code_data/methylpy/ Ziller 4. Bsmooth, DSS, MOABS
1a. Hierarchical clustering on DMRs' weighted level	1c	1. Methylation Levels (p.8) 2. CG DMR Dendtrogram (p.10)	1. Ref.9 2. cmdscale command in R, heatmap2 function in R (gplots)
1b. Hierarchical clustering of deferentially expressed genes	1d	1. RNA-seq analysis (p.8) 2. RNA-seq Expression Quantification (p.9) 3. RNA-seq Differential Expression Analysis (p.9) 4. Differentially Expressed Genes Dendrogram (p.10)	1. Tophat2, GENCODE, HTseq 2. Cufflinks, normalization of FPKMs 3. edgeR R package (glmQLFtest) 4. cmdscale command in R, heatmap2 function in R (gplots)
1c. Genomic Regions Enrichment of Annotations Tool analysis	Tables 2-3	1. DMR Tissue Specificity Determination (p.10) 2. DMR GO Enrichment	2. GREAT
1d. Correlation of Methylation and Transcription	2a	1. Correlating Methylation States of DMRs with Gene Expression (p.11)	1. nearest gene model, Spearman correlation
1e. undefined intragenic DMRs (uiDMRs)	Tables 4-6	1. Annotating undefined intragenic DMRs and promoter DMRs (p.12) 2. Dnase I sensitivity analysis (p.13)	1. Homer

2. Associating variation in methylation with genetic variation 2a. Clustering the sets of tissue-specific motifs	2b	1. SNP Calling (p.3) 2. SNP-substituted Reference Genomes (p.3) 3. Measuring the genetic origins of DNA methylation (p.13)	1. GenomeAnalyzerTK 3. Chi-square test, Epigram pipeline, Transfac, Jaspar, Uniprobe, hPDI, Taipale
3. Identification of partially methylated domains (PMDs)	Tables 7-8 2c, 2d	1. PMD Identification (p.16) 2. Comparing PMDs Called in IMR90, PA-2, PA-3 and Placenta (p.17)	1. RandomForestClassifier python module sklearn.ensemble
3a. Histone Modification Profiles across PMDs	2e, f	1. Histone Modification Profiles across PMDs (p.17) 2. Testing Histone Modifications Enrichment and Depletion Inside and Outside of PMDs (p.18)	
4. non-CG methylation (mCH)	3a, 3b-d,	1. mCH Motif Calling (p.18)	1. seqLogo package in Bioconductor
4a. Functional effect of mCH in adult tissues		1. Distribution of Expression Across mCH Quantiles (p. 18)	Ref. 4
4b. Gene clustering by the patterns of CAS methylation	3e, table 9	1. mCH Pattern Clustering (p.18)	Lister 2013, DAVID
4c. CAC and CAG Correlation Analysis	3f	1. CAC and CAG Correlation Analysis (p.20)	
5. X Chromosome Inactivation	4a, 4b	1. X Chromosome Inactivation (p.20)	1. Ref. 35
6. Allele-specific methylation (ASM) and expression (ASE)	4c	1. Haplotype Reconstruction using HaploSeq (p. 22) 2. Allele-specific Mapping of methylome data (p.22) 3. Assigning methylome reads to alleles (p.23) 4. Allele-specific methylation analysis (p.23) 5. Aligning RNA-seq reads to alleles (p. 23) 6. Tissue and Individual Variability of Allele-specific Methylation and Expression (p.25) 7. Association between Allele-specific Methylation and Expression (p. 25)	1. Novoalign, GATK, HaploSeq 2. GATK 3. assign_read_to_allele_WGBS_se.pl script 5. Novoalign, Useq