Supplemental Material to:

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Table S1: Table of available Epigenetic Resources

Other Epigenetic Resources:	**Details:**	**URLs:**
NCBI Epigenomic sample browser	Current most comprehensive collection.	http://www.ncbi.nlm.nih.gov/epigenomics/browse
ChromDB	Incorporates 3 types of sequences, genome-based, transcript based and NCBI refseq.	http://www.chromdb.org/
Zhao lab (NIH) data	Genome-wide mapping of histone H3 modifications in human CD4 and T cells, High-Resolution profiling of histone methylations in the human genome and combinatorial patterns of histone acetylation and methylation in the human genome.	http://dir.nhlbi.nih.gov/papers/lmi/epigenomes/ ; http://dir.nhlbi.nih.gov/Papers/lmi/epigenomes/hgtcell.aspx ; http://dir.nhlbi.nih.gov/papers/lmi/epigenomes/hgtcellacetylation.aspx
Young Lab Data (MIT)	Genome-wide map of nucleosome acetylation and methylation in yeast.	http://web.wi.mit.edu/young/nucleosome/
REBASE (Restriction Enzyme Database)	Collection of information about restriction enzymes, methylases, the microorganisms from which they have been isolated, recognition sequences, cleavage sites, methylation specificity, the commercial availability of the enzymes, and references - both published and unpublished observations (dating back to 1952).	http://rebase.neb.com/rebase/rebase.html
Rett Syndrome DB	An interactive version of the mutation frequency and symptoms databases originally established by Dr. Brian Hendrich and Skirmantas Kriaucionis at the University of Edinburgh. Aims to collate and display mutation and symptom information from Rett Syndrome patients to allow the analysis of how symptoms correlate with MeCP2 mutation status.	http://www.mecp2.org.uk/
Web IRSF MECP2 Variation DB (RettBASE)	This is constructed by merging mutation and polymorphism data from the published literature pertaining to Rett syndrome and related clinical disorders, and by incorporating unpublished mutation and polymorphism data that have been submitted.	http://mecp2.chw.edu.au/
CREMOFAC	A web-database of chromatin remodelling factors, currently with 64 types of remodelling factors from 49 organisms	http://www.jncasr.ac.in/cremofac/

	reported in literatures.	
Antibody Validation DB	Aims to collect and share experimental results on antibodies – aiding researchers in selection and validation of antibodies. Site began with 200+ histone antibodies tested as part of the ENCODE and Roadmap Epigenomics projects. Non-histone antibodies from these projects will also be added.	http://compbio.med.harvard.edu/antibodies/

Table S2: Table of available Tools for Epigenetic Research

Tools :	Details:	URLs:
CpG Island Searcher	Screens for CpG Islands that meet the criteria listed in the website.	http://www.uscnorris.com/cpgislands2/cpg.aspx
Methylator	Predicts if CpG in a DNA sequence is likely to be methylated or not.	http://bio.dfci.harvard.edu/Methylator/
MethPrimer	Online tool for designing bisulfite-conversion-based Methylation PCR Primers. Can design primers for Methylation-Specific PCR (MSP) and Bisulfite-Sequencing PCR or Bisulfite-Restriction PCR. The input sequence is DNA sequence in any format. The program returns results in both text and graphic view.	http://www.urogene.org/methprimer/
BiSearch	Provides access to a PCR primer-test and primer-design algorithm that can be used for both bisulfite converted and not modified sequences. Search can be carried out on various genomes with the designed primers by a fast ePCR method	http://bisearch.enzim.hu/
methBLAST	Allows for checking primers for bisulfite converted DNA by blasting them against the unmethylated and methylated genomic sequences of human, mouse and rat.	http://medgen.ugent.be/methBLAST/
Snake-charmer	Tool to select restriction enzymes for COBRA	http://insilico.ehu.es/restriction/two_seq/snake_charmer.html
MethTools (ver. 1.x and 2.x)	Software tools for the analysis of bisulfite treated DNA. The software does the comparison between unconverted mother sequences and deaminated sequences, generates graphical outputs of methylation patterns and methylation density, estimates the systematic error of the experiment and searches for conserved methylated nucleotide-patterns. The software can be used to generate files suitable for the submission to MethDB.	http://genome.imb-jena.de/methtools/ ; http://194.167.139.26/methtools/MethTools2_submit.html
BiQ Analyzer	Software tool for easy visualization and quality control of DNA methylation data from bisulfite sequencing (Java tool, capable of generating archive files that can be directly uploaded to MethDB)	http://biq-analyzer.bioinf.mpi-inf.mpg.de/
CpGviewer	Simple integrated tool for handling bisulphite sequencing projects. It can process plain text sequences or a variety of electropherogram formats, and allows interactive editing of the sequences, aligned to a reference sequence.	http://dna.leeds.ac.uk/cpgviewer/
CyMATE	CyMATE (Cytosine Methylation Analysis Tool for Everyone) - a software platform to perform in silico	http://www.cymate.org/

	analyses of DNA methylation at cytosine sites. Suitable for analyses of sequence data obtained with bisulfite genomic sequencing and hairpin-bisulfite sequencing, i.e. single-strand and double-strand DNA data.	
BISMA	BISMA (Bisulfite Sequencing DNA Methylation Analysis) analyses the bisulfite sequencing data that are derived from sequencing of subcloned molecules of a PCR product.	http://biochem.jacobs-university.de/BDPC/BISMA/
EpiGRAPH	Software for advanced (epi)-genome analysis and prediction.	http://epigraph.mpi-inf.mpg.de/WebGRAPH/