Allele-specific epigenome maps reveal sequence-dependent stochastic switching at regulatory loci. [1]

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Authors	Onuchic, V [3], Lurie, E [4], Carrero, I [5], Pawliczek, P [6], Patel, RY [7], Rozowsky, J [8], Galeev, T [9], Huang, Z [10], Altshuler, RC [11], Zhang, Z [12], R Harris, A [13], Coarfa, C [14], Ashmore, L [15], Bertol, JW [16], Fakhouri, WD [17], Yu, F [18], Kellis, M [19], Gerstein, M [20], Milosavljevic, A [21]
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Abstract	To assess the impact of genetic variation in regulatory loci on human health, we constructed a high-resolution map of allelic imbalances in DNA methylation, histone marks, and gene transcription in 71 epigenomes from 36 distinct cell and tissue types from 13 donors. Deep whole-genome bisulfite sequencing of 49 methylomes revealed sequence-dependent CpG methylation imbalances at thousands of heterozygous regulatory loci. Such loci are enriched for stochastic switching, which is defined as random transitions between fully methylated and unmethylated states of DNA. The methylation imbalances at thousands of loci are explainable by different relative frequencies of the methylated and unmethylated states for the two alleles. Further analyses provided a unifying model that links sequence-dependent allelic imbalances of the epigenome, stochastic switching at gene regulatory loci, and disease-associated genetic variation.
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Links
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