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Exhaustive T-cell repertoire sequencing of human peripheral blood samples reveals signatures of antigen selection and a directly measured repertoire size of at least 1 million clonotypes
René L. Warren, J. Douglas Freeman, Thomas Zeng, Gina Choe, Sarah Munro, Richard Moore, John R. Webb, and Robert A. Holt

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Nuclear higher-order organization plays an important role in orchestrating the harmony of gene expression. Chromatin is illustrated as a musical score, with regulatory information represented as chords in the music. Accessible genomic loci (DNaseI-accessible sites) that bind multiple factors (notes highlighted in different colors) are spatially colocalized in the nucleus. These subnuclear environments allow rapid and even opposing gene expression responses to the hormone-activated glucocorticoid receptor. (Cover illustration by Ruth di Segni Hakim. [For details, see Hakim et al., pp. 697–706.])