

Abstract Submitted
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Stochastic transcriptional activity results in precise RNA distribution profiles of *Drosophila* gap genes MIKHAIL TIKHONOV¹, Joseph Henry Laboratories of Physics, Princeton University, SHAWN LITTLE², Howard Hughes Medical Institute, Department of Molecular Biology, Princeton University, THOMAS GREGOR, Joseph Henry Laboratories of Physics, Lewis-Sigler Institute for Integrative Genomics, Princeton University — How can biological systems reliably achieve a precise and reproducible response if they are constructed of noisy components? Using a novel single-molecule precision method in fixed *Drosophila* embryos we simultaneously measure the RNA distribution profiles and the transcriptional activity of individual nuclei in absolute units. We show that these RNA profiles of early patterning genes are precise at 8% in absolute units, while the instantaneous activity of any one transcription site has an intrinsic noise exceeding 45%. Thus the remarkable precision of *Drosophila* patterning system is already achieved at the RNA level and requires neither transcriptional feedback nor special mechanisms to reduce transcription noise. Instead, noise is filtered using straightforward spatiotemporal averaging. We further show that in regions where patterning genes are maximally expressed, they are all produced at the same absolute rate. This universality across gap genes suggests that the observed RNA production rate and noise are independent of promoter details and are inherent to transcription in *Drosophila*.

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