Gene syntax defines supercoiling-mediated transcriptional feedback

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Abstract

Gene syntax—the order and arrangement of genes and their regulatory elements—shapes the dynamic coordination of both natural and synthetic gene circuits. Transcription at one locus profoundly impacts the transcription of nearby adjacent genes, but the molecular basis of this effect remains poorly understood. Here, using integrated reporter circuits in human cells, we show that supercoiling-mediated feedback regulates expression of adjacent genes in a syntax-specific manner. Using Region Capture Micro-C, we measure induction-dependent formation of supercoiled plectonemes and syntax-specific chromatin structures in human induced pluripotent stem cells. Using syntax as a design parameter, we built compact gene circuits, tuning the mean, variance, and stoichiometries of expression across diverse delivery methods and cell types. Integrating supercoiling-mediated feedback into models of gene regulation will expand our understanding of native systems and enhance the design of synthetic gene circuits.

1 Main

Native gene circuits coordinate transcriptional programs to set diurnal rhythms, pattern cell fate, and orchestrate immune responses [1–3]. The non-random organization of genomes suggests that specific patterns of gene syntax—the relative order and orientation of genes and their regulatory elements—support coordinated regulation of co-localized genes [4–6]. Native gene circuits that require precise transcriptional coordination such as *Hox* genes [7, 8] and segmentation clocks [9] co-localize multiple transcriptional units within tens of kilobases. Potentially, gene syntax may constrain transcriptional noise and couple expression of adjacent genes in native and synthetic gene circuits (fig. 1a) [10]. The enrichment and depletion of syntaxes in the human genome and other genomes—which occur on the length scale of synthetic gene circuits—may suggest motifs for organizing pairs of adjacent genes for coordinated expression (figs. 1b and S1).

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Synthetic gene circuits offer programmable control of therapeutic cargoes, genome editors, and cell fate [11–19]. However, predictable forward design of gene circuits remains challenging, requiring iterative "design-build-test" loops to achieve desired functions. Harnessing syntax as an explicit design parameter may improve the predictability and performance of genome-integrated synthetic circuits [10]. While synthetic circuits are regularly integrated into the genome for cellular engineering, the reciprocal feedback between transcription and local chromatin structure remains unexplored in human cells. On the length scale of gene circuits ($\sim$ 10 kb), biophysical forces such as DNA supercoiling are predicted to rapidly couple the expression of colocalized genes [10, 20].

DNA supercoiling—the over- and under-twisting of DNA—influences a host of genomic processes [21], including transcriptional bursting [22–24], topoisomerase activity [25–30], chromatin folding [31, 32], and chromosome segregation [33]. By melting the double helical DNA polymer to read the underlying base pairs, transcribing RNA polymerases induce waves of DNA supercoiling. In yeast and human cells, supercoiling demarcates gene activity [34, 35]. Supercoiling alters RNA polymerase binding and changes the biochemical landscape of gene regulation [36, 37]. As supercoiling diffuses, transcription dynamically reshapes the structure and regulation of nearby genes, forming a feedback loop that we define as supercoiling-mediated feedback [10]. As described by the twin domain model [38, 39], transcribing polymerases generate positive supercoiling downstream and leave a wake of negative supercoiling upstream (fig. 1a). Negative supercoiling facilitates polymerase binding by reducing the binding energy, while positive supercoiling decreases binding rates by increasing this energy barrier. Thus, supercoiling-mediated feedback emerges through the directionality of transcription, which sets the energy landscape for subsequent polymerase binding events (fig. 1a)[10]. Models of supercoiling predict that transcription-induced changes in chromatin structure feed back into changes in transcriptional activity at adjacent genes [40–43], a phenomenon observed in bacteria [44], yeast [22, 45] and human cells [26, 35, 46]. However, while these forces shape gene regulation across species [22, 32, 34, 35, 45, 46], the impact of transcriptionally induced supercoiling on fine-scale chromatin structure and on the activity of gene circuits remains undefined in human cells.

DNA supercoiling is often studied through broad perturbations including loss and inhibition of toposisomerase and polymerases [22, 26, 35, 46, 47]. However, broad inhibition of transcription and topoisomerase activity can induce large changes in cellular physiology, limiting observations to acute treatments and short timescales. Alternatively, changing the transcriptional activity of a single transgene within a genetically uniform background offers the precise control required to investigate the predictions of supercoiling-mediated feedback.

Here, we use synthetic two-gene circuits as a model system to examine how transcription of a single gene couples the expression and folding of adjacent genes in human cells. By integrating inducible systems, we demonstrate that transcription-induced coupling generates syntax-specific profiles of expression across a range of human cell types and integration methods. Integrating circuits at a genomic safe harbor in human induced pluripotent stem cells (hiPSCs), we use Region Capture Micro-C [48] to characterize folding across the region surrounding the locus of circuit integration. Using the control and orthogonality of synthetic circuits, we identify transcription-induced changes in chromatin structure, demonstrating the predicted coupling of syntax-specific chromatin folding and patterns of expression. Induction of transcription perturbs chromatin structure hundreds of kilobases away, substantially altering the insulation and connectivity across the locus. Using principles of supercoiling-mediated feedback, we design compact synthetic gene circuits for efficient delivery and induction across a variety of cells. These techniques allow us to optimize production of a therapeutic antibody without substitution of genetic parts. Overall, we demonstrate how supercoiling-mediated feedback influences expression of adjacent genes, providing insights into native gene regulation and informing the design of synthetic systems.

Upstream dominance defines expression profiles of constitutive tandem transgenes

In native genes, upstream transcription can reduce expression of downstream genes [49–51]. Models of supercoiling-mediated feedback predict that positive supercoiling generated by transcription at the upstream gene reduces the rate of transcription and thus expression at the downstream locus, resulting in upstream dominance (fig. 1a) [10]. To examine upstream dominance in a synthetic system, we constructed two-gene systems in tandem. Each gene is paired with a promoter and polyadenylation signal (PAS) to form a transcriptional unit. The modularity of these synthetic systems allows us to independently switch gene positions and regulatory elements.

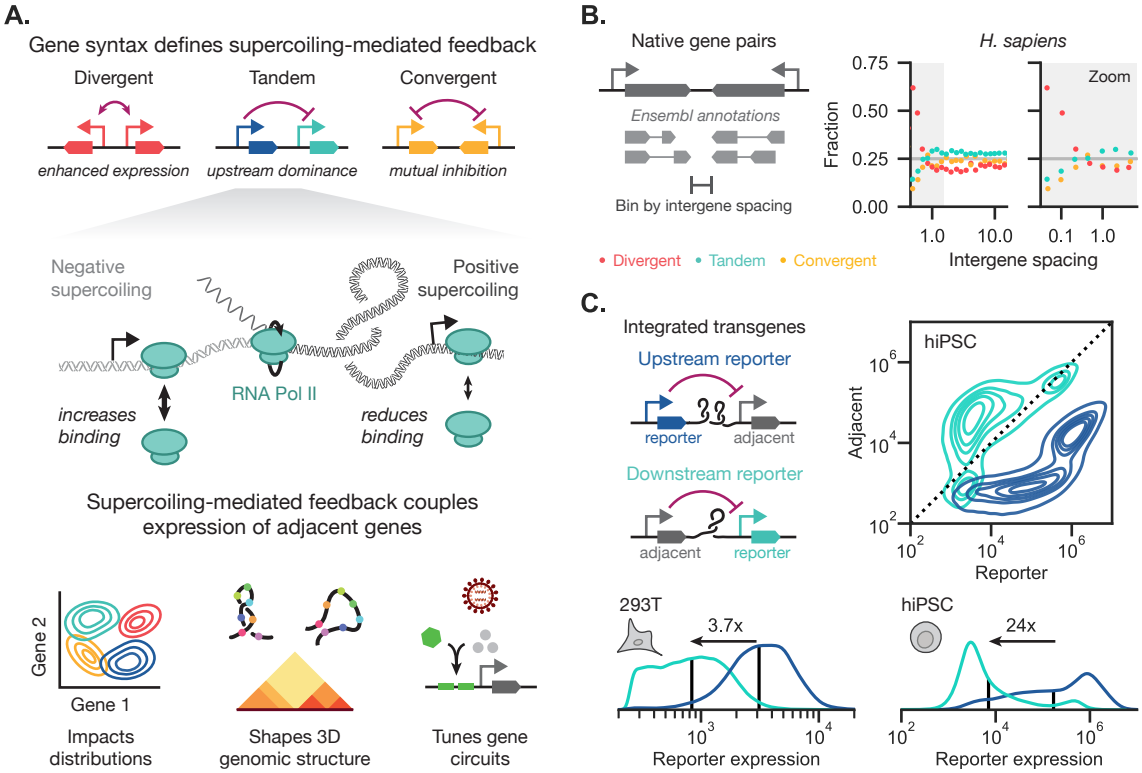

Figure 1: Supercoiling-mediated feedback couples transcription and genome folding of adjacent genes.
a) Supercoiling modifies the energy required for polymerases to bind and locally melt DNA, leading to increased or decreased polymerase initiation. This biophysical feedback loop (purple arrows) generalizes across integration method and cell type, opening new engineering capabilities.
b) Using Ensembl annotations for the human genome, gene extents were identified using the maximum extent of all annotated exons. For each pair of adjacent genes, the relative orientation and intergene spacing was computed, split into equal-sized quantile bins, and summarized by orientation.
c) Due to accumulated positive supercoiling at the downstream promoter, expression from an upstream gene is predicted to decrease expression of a downstream gene. Two-gene constructs expressing fluorescent proteins from PGK promoters were integrated using PiggyBac in HEK293T cells. For a representative biological replicate, the distribution of the reporter is shown as a function of position in the circuit. In the hiPSCs, the adjacent gene is expressed from the weak PGK promoter and the reporter gene is expressed from the strong EF1a promoter.

To measure expression, we integrated these tandem two-gene systems into two common human cell lines, HEK293Ts and hiPSCs, via PiggyBac transposase. We switch the positions of the tandem genes to isolate the effect of position on expression level. We quantified expression of the fluorescent reporter genes by flow cytometry, providing single-cell resolution needed to measure expression distributions. Using identical promoters in both positions in HEK293Ts, we found that gene position strongly influences the

expression of the reporter. The gene in the upstream position expresses at levels nearly four-times higher than when placed downstream (fig. 1c). Even when pairing a strong promoter with a weak promoter in hiPSCs, we saw clear upstream dominance with a large, 24-fold shift in expression based on position (fig. 1c). Potentially, genetically encoded sequences—such as binding sites for the CCCTC-binding factor (CTCF) [52, 53] and the cHS4 insulator [54]—that restrict chromatin-mediated interactions may reduce upstream dominance. To examine this hypothesis, we inserted tandem-oriented CTCF binding sites that were previously reported to reduce enhancer-promoter interactions [53]. Flanking the upstream gene, the downstream gene, or the entire two-gene construct with these sites does not eliminate upstream dominance (fig. S2). Instead, addition of these sites generally reduces expression of one or both genes.

The identity of regulatory elements such promoters and PAS may influence coupling between genes [55, 56]. In testing a panel of common constitutive promoters, we consistently observed upstream dominance in PiggyBac-integrated HEK293Ts (figs. S3a and S3b), lentivirally integrated HEK293Ts (fig. S3c), and PiggyBac-integrated hiPSCs (fig. S4). In exchanging the PAS, we found that the choice of PAS has a minimal effect on the shape of expression distributions, mildly tuning the levels of gene expression (fig. S5). Thus, trends in syntax-specific expression are robust across a range of genetic parts for the tandem syntax.

Transcription of an adjacent gene induces syntax-specific coupling

Expression patterns of constitutively expressed tandem gene pairs suggest that syntax influences expression. However, these constitutive systems do not support dynamic control of transcription of a single adjacent gene, making it difficult to parse the transcription-driven mechanism of supercoiling-mediated feedback. To allow controlled induction of a single adjacent gene, we generated monoclonal HEK293T cell lines containing a doxycycline (dox)-inducible two-gene system in different syntaxes (fig. 2). To build these lines, we placed a constitutive reporter gene under the control of a strong constitutive promoter and an adjacent inducible gene under the control of the dox-inducible promoter TRE (fig. 2a). Using PiggyBac, we delivered the dox-inducible two-gene systems encoded in tandem, convergent, and divergent syntaxes, which are predicted to show different transcription-induced couplings [10]. The constitutively expressed dox-responsive activator, rtTA, was integrated from a separate PiggyBac donor. We sorted single cells to establish monoclonal lines of each syntax.

Upon dox addition, all syntaxes show strong induction of the TRE-driven inducible gene (figs. S6a and S6b). To quantify changes in expression of the constitutive reporter upon induction of the adjacent gene, we normalized reporter expression to the uninduced condition for each line. In the tandem syntax, induction of the upstream gene reduces expression of the downstream reporter gene (fig. 2b, figs. S6c and S6d). Conversely, induction of the divergent syntax strongly upregulates expression from the constitutive reporter, matching predictions of amplification in divergent syntax [10]. The convergent syntax shows a near-invariant profile of reporter expression. For the tandem and divergent syntaxes, induction of the adjacent gene results in a unimodal shift in the geometric mean (fig. 2c). Unimodal shifts indicate a general mechanism of regulation, such as changes in the transcription rate, that is not restricted to a subpopulation of cells.

As a transcription-based process, supercoiling-mediated feedback should manifest in the distributions of mRNAs. To measure the mRNA distributions, we used single-cell hybridization chain reaction RNA-FISH [56, 57] to quantify the transcriptional profiles of both the constitutive reporter gene and the dox-inducible gene (fig. 2d, figs. S6e, S6f and S7). As expected, mRNA profiles generally match the syntax-specific profiles of proteins (fig. 2c). Intriguingly, the convergent syntax shows substantial bimodality in mRNA expression, matching modeling predictions of bimodality that may be obscured by stable protein reporters [10]. Overall, the mRNA profiles align with the models of supercoiling-mediated feedback that predict that syntax influences transgene expression by altering rates of transcription.

DNA supercoiling-mediated coupling is predicted to be rapid and reversible. To test the reversibility of syntax-specific coupling, we sequentially induced and removed dox for three-day periods over 13 days. We observed repeatable induction- and syntax-specific coupling of the inducible and reporter genes. Over 13 days we observed minimal hysteresis, indicating that the trends in coupling are reversible and are not due to irreversible changes in the chromatin state (fig. 2e).

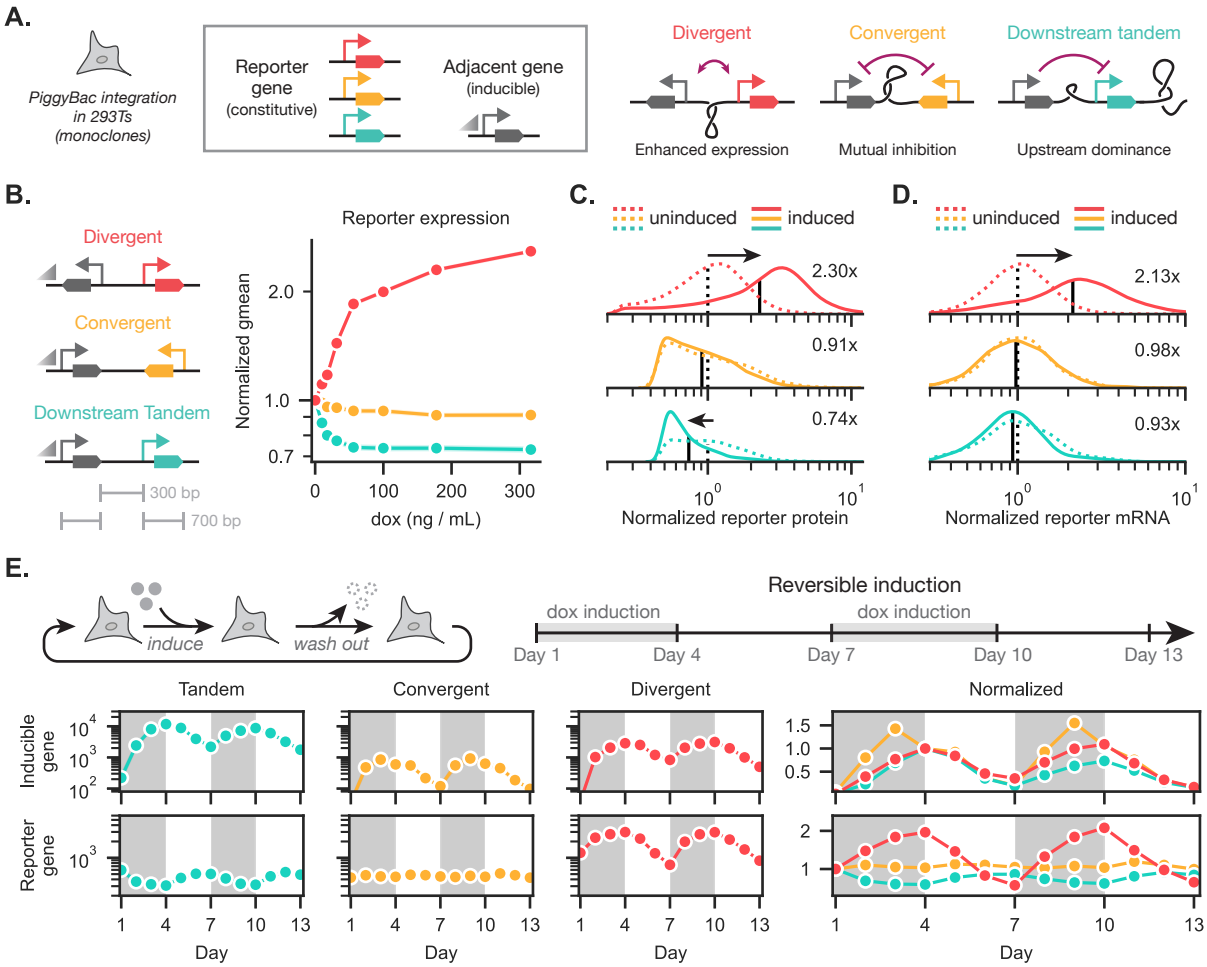

Figure 2: Transcription induces syntax-specific coupling of expression of adjacent genes.
a) We integrated two-gene systems consisting of an dox-inducible gene (TRE) and a constitutively expressed gene (EF1a). The resulting cell lines were flow sorted to single cells and expanded as monoclonal populations.
b) The geometric mean reporter expression, normalized to the uninduced condition, is shown as a function of dox concentration for the three different syntaxes. Geometric mean and associated 95% confidence interval shown over merged distributions from three wells.
c)-d) Full reporter protein and mRNA distributions are shown in the uninduced case and the second-highest dox induction state. Fold change of the geometric means are shown in black.
e) Dox was sequentially introduced and removed in order to measure the turn-on and turn-off dynamics of the integrated systems. The systems respond reversibly to the presence of dox. Geometric mean and associated 95% confidence interval shown over merged distributions from three wells.

Transcription induces syntax-specific structures across circuits and the surrounding locus

Supercoiling-mediated changes in gene expression occur alongside changes in chromatin structure. Transcription-induced supercoiling drives genome folding [58]. In bacteria and in yeast, chromatin structures correlate with supercoiling density [47, 59]. Inclusion of inducible promoters in synthetic circuits provides a facile mechanism to regulate transcriptional activity and measure transcriptionally induced chromatin structures. To understand how transcriptional activity and syntax affect the chromatin structure of our two-gene circuits, we used Region Capture Micro-C (RCMC) to measure the contact probability between genomic locations within a targeted region of interest (fig. 3) [48]. Using the STRAIGHT-IN Dual allele platform [60], we integrated dox-inducible circuits with tandem or divergent syntax into both alleles of a genomic safe harbor region located in intron 2 of the citrate lyase beta-like (*CLYBL*) gene [61] in hiPSCs, generating homozygous cell lines (fig. S8a). These circuits include the activator within the constitutively expressed gene. We confirmed that these tandem and divergent inducible circuits showed reversible, syntax-specific profiles of expression similar to those observed in the dox-inducible two-gene systems integrated into HEK293T cells (figs. 2 and S8b).

We cultured two biological replicates of each syntax with or without inducer and collected these cells for RCMC (figs. 3a and S9a). Reads from each replicate were merged and balanced (fig. S9b), resulting in matrices that quantify the probability that two chromatin regions are colocalized in 3D space. Two distal, unmodified capture regions did not show induction-dependent changes (fig. S9c). In contrast, across the locus of integration, we observed induction-specific structural changes for both the divergent syntax (fig. 3b) and downstream tandem syntax (fig. S10a).

The integration site is located at the boundary of two topologically associating domains (TADs) (fig. 3b). We quantified how induction of our small synthetic construct changes chromatin structure over the entire capture region by computing the fold-change in contact probability upon induction (fig. 3c). Induction of the divergent syntax reduces inter-TAD interactions and increases intra-TAD interactions. Using a common sliding-window insulation score [62, 63] to calculate TAD boundary strength, we observe a substantial weakening of this local boundary upon induction in the divergent syntax despite reduced inter-TAD interactions (fig. S11). Weakening of this boundary coincides with the emergence of a dual-loop domain. All conditions show a single "corner dot" that represents a loop domain between the integration site and the first intron of *CLYBL*. Induction in the divergent syntax generates a second corner dot anchored in a region 10 kb upstream of the integration locus (fig. 3d). This suggests that the weakening of the TAD boundary arises from interactions between these two loop domains.

Zooming into the 15-kB window around the circuit, we examined how induction affects local chromatin structure (figs. 3e and S10b). Plectonemes form as overwound (or underwound) DNA buckles, transferring twist into writhe. In addition to facilitating the loading of chromatin loop extruders [64], plectonemes should show higher intra-plectoneme contacts. Specifically, plectonemes should appear as small-scale off-diagonal regions of high contact probability (fig. 3f), similar in shape to the large-scale "jets" generated by cohesion loop extrusion [65]. Quantified as an off-diagonal score, we observe strong, induction-dependent plectonemic signals at the integrated locus (figs. 3f and 3g). The magnitude of these plectonemic signals is not replicated elsewhere in the capture region, strongly suggesting that induction of transcription reshapes chromatin folding around our synthetic circuit. Potentially, in addition to affecting polymerases, this local supercoiling density may affect the binding rates of other DNA-binding proteins.

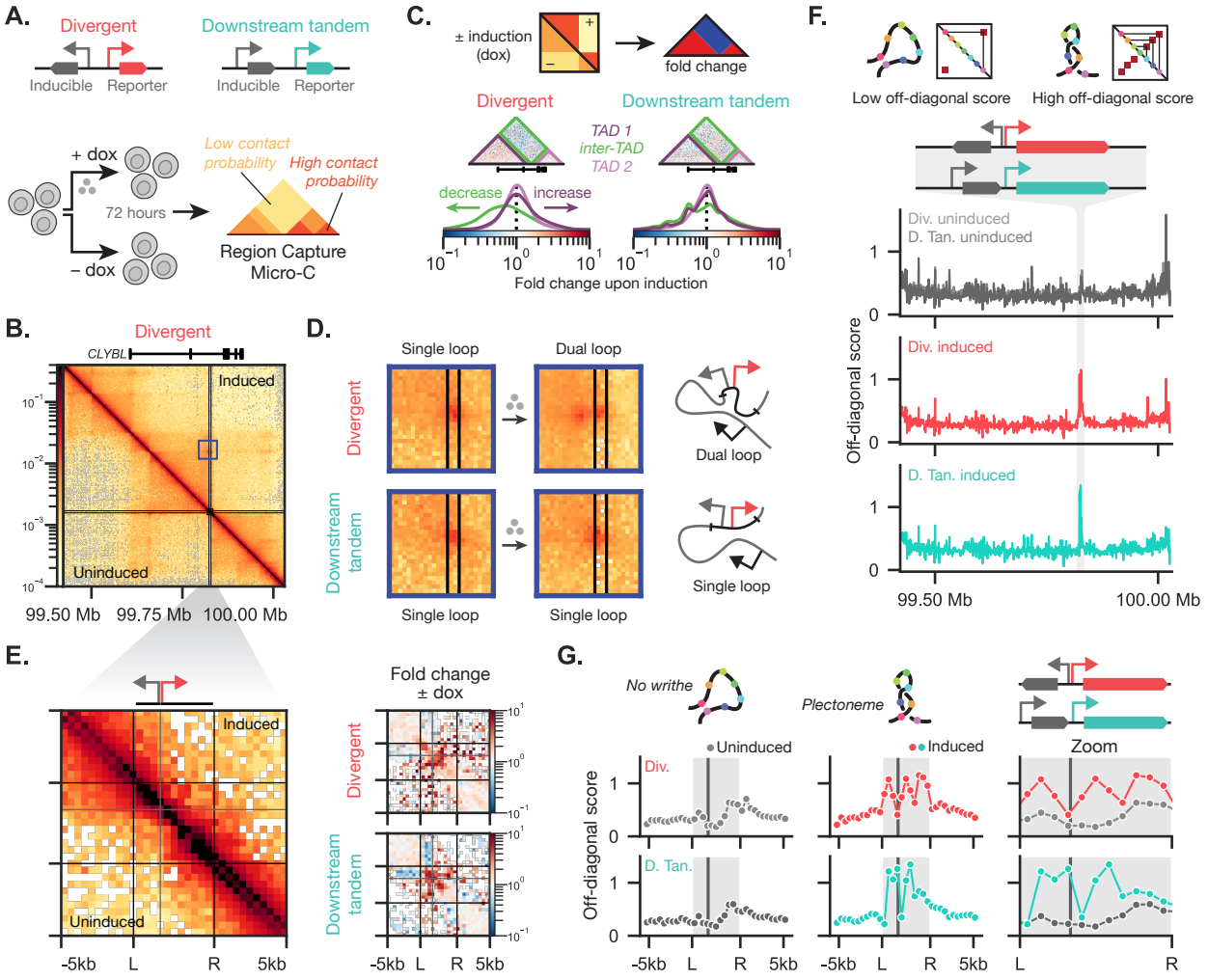

Figure 3: Transcription induces syntax-specific chromatin structures across synthetic gene circuits and the surrounding locus. a) The resulting cell lines were split into two conditions, with half induced with doxycycline (dox) for 72 hours prior to harvesting. The cells were processed following the Region Capture Micro-C protocol in order to measure population chromatin structure around the region of integration.
b) - g) Region Capture Micro-C data was binned at 500 bp and 2 kb resolution and iteratively balanced within the capture region. b) For the divergent cell line, only relatively small differences differentiate the induced and uninduced conditions across the ∼700 kb region around the integration site.
c) For each condition, the fold change in contact probability was computed. The resulting distribution was binned by region. In the divergent case, the inter-TAD region shows reduced contact probability upon induction.
d) Examining a corner dot representing a loop between the integration region and the first intron of *CLYBL*, the induced divergent condition shows two corner-dots, suggesting an induction-dependent formation of a double-loop structure. This double loop does not appear in the downstream tandem syntax. e) For the divergent cell line, the surrounding 10 kb region around the integration site is shown at 500 bp resolution. f) The off-diagonal score is shown across the entire capture region. No other region shows strong increases in off-diagonal score upon induction.
g) Local plectoneme formation can be quantified using the off-diagonal score. As opposed to a "corner dot" structure which indicates a loop domain, plectonemes should show contacts along the matrix off-diagonal. Examining the region immediately around the integration location, this off-diagonal score remains low in the uninduced case. However, upon induction, we see a strong increase in contact probability along the central off-diagonals and as measured by the off-diagonal score.

Syntax-based tuning optimizes circuit expression and biologic production without part substitution

Synthetic circuits and other transgenic systems such as biologic producer lines are often optimized through selection of transcription factors, promoters, stoichiometric ratios, copy number, and integration locus [66–68]. However, as each element may affect the dynamics of gene expression, forward design through simple exchange of parts remains iterative. Given that syntax modulates expression to a similar degree as genetic element selection [56], we propose using syntax to tune the relative levels of expression without changing the sequences of these elements or their relative copy number. To test this syntax-based tuning scheme, we explored optimization of two common biotechnological tools: a monoclonal antibody producer line and an inducible lentivirus system.

Low-cost production of antibodies, especially for those against infectious and tropical diseases [69], can improve worldwide access to these antibody drugs. Increasing antibody titers offers a simple way to reduce the cost of production and enhance affordable access. To demonstrate the promise of syntax-based optimization, we integrated two-gene constructs encoding the heavy and light chains of an anti-yellow-fever monoclonal antibody into a landing pad HEK293T cell line. Previous reports [68, 70–72] suggest that excess light chain translation can increase titers. Thus, based on the principle of upstream dominance, we would expect that by setting a high ratio of light chain to heavy chain, the downstream tandem syntax would outperform the upstream tandem syntax. In measuring total human IgG titer via both sandwich ELISA (fig. 4a) and a bead agglutination assay (fig. S12), we found a nearly four-fold difference in antibody titer as a function of syntax, with the downstream tandem and divergent syntaxes providing the highest titers as expected.

Lentiviruses offer efficient delivery of transgenes to diverse primary cells for therapeutic applications such as *ex vivo* engineering of CAR-T therapies and *ex vivo* immune cell reprogramming [73]. Gene circuits and inducible systems offer safe, clinically guided control and the ability to target specific cell states [11]. However, ensuring robust co-expression of multiple genes in these systems remains challenging. To explore syntax-based tuning of expression from an inducible lentivirus, we tested all four possible two-gene syntaxes transduced into HEK293T cells. Only the divergent and downstream tandem syntaxes display an appreciable double-positive population at maximum induction (figs. 4b, S13 and S14). Expression of the constitutive gene in the upstream tandem and convergent syntaxes strongly inhibits induction across all inducer concentrations (fig. 4c). In the two syntaxes with strong induction, syntax sets the stoichiometric ratio between the two genes (fig. 4d). Weak coupling between the two genes in the tandem syntax allows a wide range of stoichiometries upon induction, varying stoichiometry seven-fold (fig. 4d). Conversely, the strong positive coupling between genes in the divergent syntax maintains a narrower ratio of expression. Tuning the ratio of expression between elements can significantly shift the behavior of gene circuits, potentially supporting or impeding desired functions [74, 75]. Together, our results demonstrate that syntax can tune expression levels in diverse synthetic circuits without requiring part substitution.

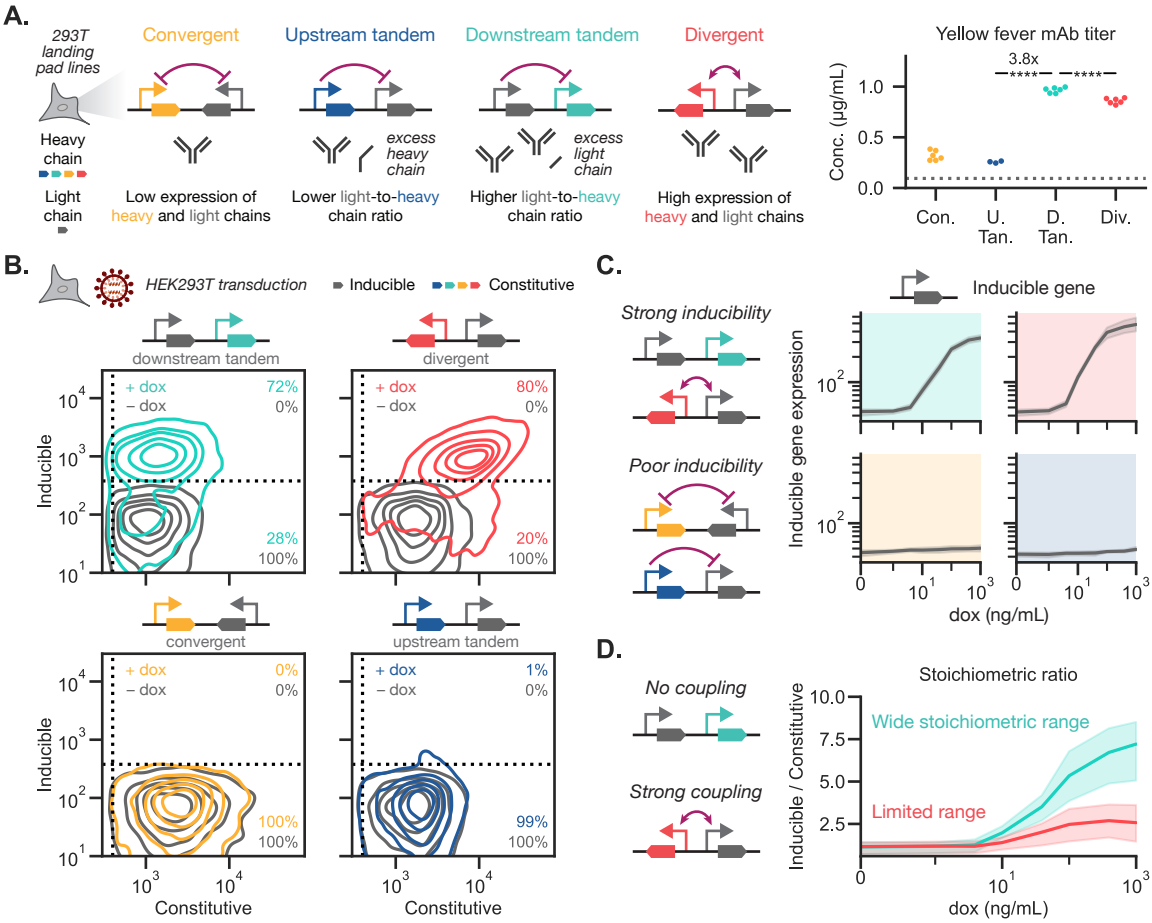

Figure 4: Syntax-based tuning optimizes circuit expression and biologic production without part substitution.
a) The light and heavy chains are expressed from two-gene constructs integrated at the *Rogi2* locus in HEK293T cells. Antibody titer, as measured via sandwich ELISA, differs across syntaxes. Points depict N=3-6 biological replicates. Statistics are two-sided student t-tests. **** : $p < 0.0001$
b) Two-gene circuits, consisting of a constitutive gene and an inducible gene, were lentivirally transduced into HEK293T cells alongside a rtTA-expression lentivirus. Joint distributions in the absence (gray) or presence (colored) of 1 μg/mL dox are shown. Percentages refer to the proportion of cells expressing (top) or not expressing (bottom) the inducible gene.
c) The geometric mean of the inducible gene (gray) is shown as a function of dox concentration. Gray shading represents the 95% confidence interval across four biological replicates.
d) The stoichiometric ratio between the inducible and constitutive genes is shown as a function of dox concentration. Strong coupling reduces the change in this ratio. Colored shading represents the 95% confidence interval across four biological replicates.

Syntax augments performance of compact gene circuits across cell types

Compact gene circuits support efficient delivery of therapeutic cargoes via size-restricted vectors such as lentiviruses and AAVs. However, the close proximity of multiple genes in these vectors introduces the potential for physical coupling between transcriptional units. To harness supercoiling-mediated feedback for improved circuit performance, we focused on optimizing a compact, lentivirally delivered "all-in-one" inducible circuit.

Unlike the inducible circuits in figs. 2 and 4, all-in-one designs include the dox-responsive activator on the same construct, resulting in both biophysical and biochemical coupling (fig. 5a). In the divergent syntax, positive supercoiling-mediated feedback should generate high, correlated expression. For both tandem syntaxes, negative feedback should reduce the degree of correlation between genes. Despite negative feedback, we expect that the downstream tandem syntax will support induction provided that activator levels remain sufficient [60].

Transducing hiPSCs, we observe robust induction from the divergent and downstream tandem syntaxes (figs. 5b and 5c). These trends are mirrored for transduction in HEK293T cells and mouse embryonic fibroblasts (fig. S15). Expression of the synthetic activator in the downstream tandem syntax is more than an order of magnitude lower than in the divergent syntax. However, for all syntaxes, expression of the activator increases relative to the uninduced case (fig. 5d). This increase may reflect a local increase in transcriptional resources that affects circuits with the activator in *cis* but not those in *trans* (i.e., with a separately integrated activator, as in figs. 2 and 4) (fig. S14) [60].

Supercoiling-mediated feedback is predicted to couple the probabilities of transcriptional bursting [10]. Even for stable protein reporters, changes in correlated bursting may be visible in the variance of co-expression. Variance between two genes across a population of cells can be decomposed into two components: intrinsic and extrinsic noise. Intrinsic noise quantifies the variability within individual single cells whereas extrinsic noise reflects differences such as cell size [76, 77]. Transcriptional co-bursting in the divergent syntax is predicted to reduce the intrinsic noise. Remarkably, across all transduced cell types, the divergent all-in-one syntax minimizes intrinsic noise (figs. 5e, 5f and S16a). Trends in intrinsic noise for these *cis* designs (i.e., all-in-one) match those for the *trans*-inducible circuits from fig. 4b (fig. 5f). However, unlike the *cis* designs, the *trans*-inducible circuit does not exhibit increased extrinsic noise in the divergent syntax relative to the tandem syntax (fig. S16b), aligning with model predictions (fig. S16c) [10]. Putatively, the lack of a biochemical positive feedback loop in the *trans* designs prevents an increase in extrinsic noise.

Insulator sequences can reduce coupling between integrated transgenes [78], potentially mitigating the effects of supercoiling-mediated feedback. To test this hypothesis, we added cHS4 insulator sequences to the intergenic region in the all-in-one circuit. For all syntaxes, addition of the cHS4 core or full insulator sequence did not substantially change expression levels or noise profiles (figs. 5g and S17). Together, these data indicate that syntax offers a powerful design parameter for coupling and tuning profiles of expression that can be harnessed to dampen or amplify noise [79, 80].

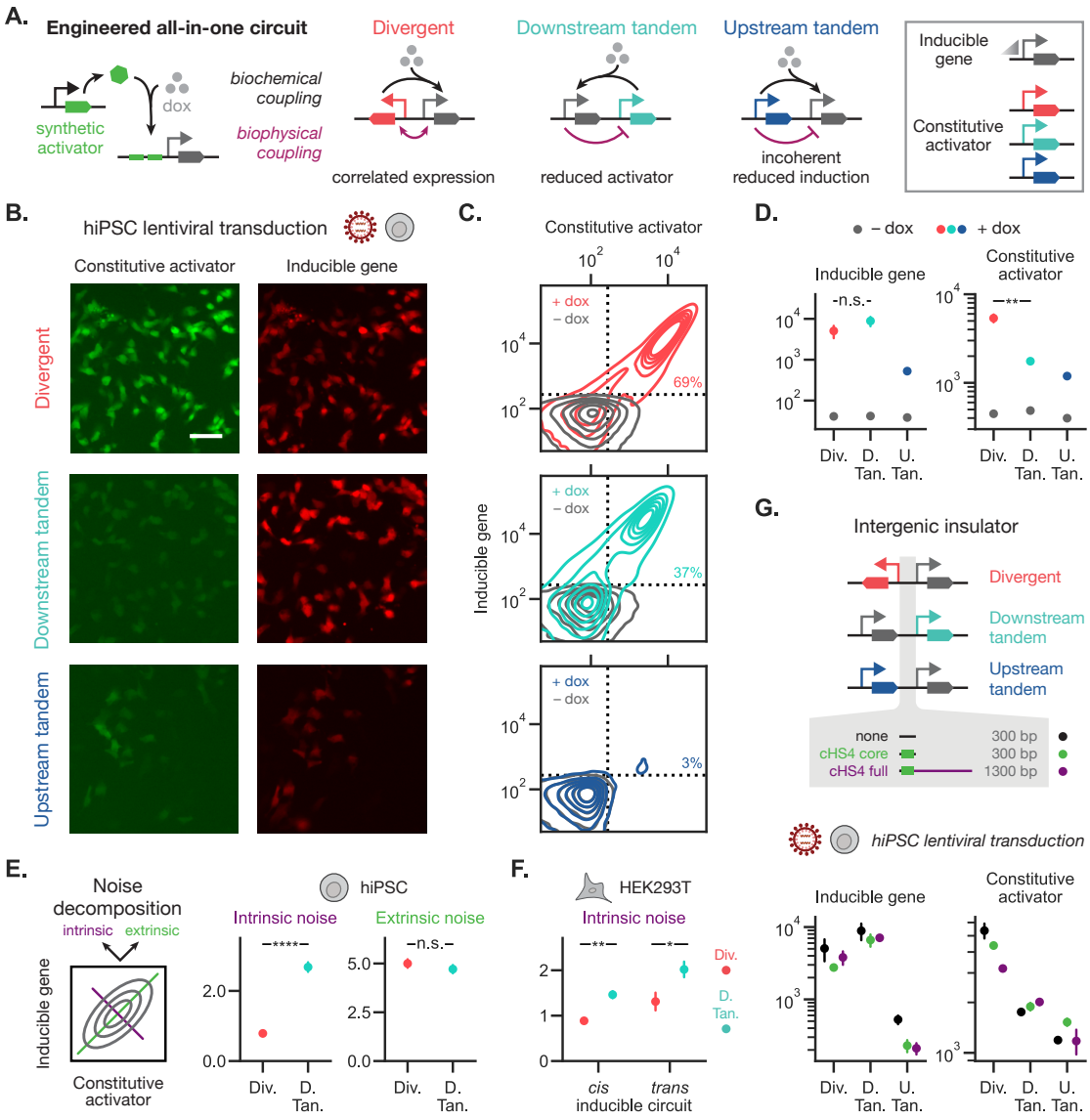

Figure 5: Syntax augments performance of compact gene circuits across cell types.
a) A dox-inducible circuit relies on expression of a synthetic activator (rtTA) to activate the TRE promoter; an "all-in-one" circuit places both the activator—co-expressed with a fluorescent protein—and the inducible gene of interest in the same cassette. The performance of the system is determined by the interplay between the biochemical coupling and the supercoiling-dependent biophysical coupling.
b) Representative microscopy images showing the expression of the constitutive activator (left) and the inducible gene (right) for the circuit in a) transduced into hiPSCs and induced with 300 ng/mL dox. Scale bar represents 50 microns.
c) Joint distributions of the activator and inducible gene expression are shown for each syntax. Dashed lines depict expression gates set by the untransduced population. Percentages refer to the proportion of double-positive cells in the induced case.
d) Geometric mean expression of the inducible gene and constitutive activator are shown for uninduced (gray) and induced (colored) populations.
e) The joint distributions of the double-positive populations for induced cells in c) can be decomposed into intrinsic (off-diagonal) and extrinsic (on-diagonal) noise.
f) The intrinsic noise is shown for HEK293T cells lentivirally transduced with the *cis*-inducible circuit in a) or the *trans*-inducible circuit from fig. 4b. Noise is calculated for double-positive populations of induced cells.
g) The cHS4 core or full insulator sequence was placed in the intergenic region of the all-in-one inducible circuit. The no insulator condition (none, black) is the same as in d). Geometric mean expression of the inducible gene and constitutive activator are shown for hiPSCs lentivirally transduced with these circuits and induced with 300 ng/mL dox.
Points represent the mean ± standard error for $n = 3$ biological replicates. Statistics are two-sided student t-tests. n.s.: $p > 0.05$, *: $p < 0.05$, **: $p < 0.01$, ***: $p < 0.001$, ****: $p < 0.0001$

Discussion

Transcription forms a dynamic feedback loop mediated by DNA supercoiling. Here we use two-gene synthetic gene circuits as model systems to probe the biophysical influence of adjacent transcription (fig. 1). Using inducible synthetic circuits, we isolate the effects of reversible biophysical coupling and examine the impact of transcriptionally induced coupling on gene expression (fig. 2) and chromatin structure. Applying fine-scale mapping of a genomic safe harbor using RCMC, we observe striking transcriptionally induced structures and perturbations of loop domains and TADs up to hundreds of kilobases away (fig. 3). Importantly, we observe formation of transcriptionally induced plectonemes for potentially the first time in living human cells. Integrating the predictions of supercoiling-mediated feedback into circuit design, we use syntax-based optimization to increase antibody production, to tune expression from lentiviruses, and to explore performance regimes of inducible circuits in diverse cell types (fig. 4). Overall, we find that syntax defines the profiles and performance of gene circuits across a range of integration methods, cargoes, and cell types, offering a design parameter for tuning the performance and predictability of circuits (fig. 5).

Syntax offers an orthogonal design variable that can be combined with library-based approaches. Growing compendiums of parts expand the potential for library-based approaches for circuit tuning [67, 81, 82], but syntax-based tuning can be used to optimize circuits even when parts are constrained [60]. When changing design features including promoters, polyadenylation sequences, cell type, and integration method, we consistently observed reproducible syntax-specific coupling of gene expression. Syntax-specific profiles persisted even in the presence of putative insulator sequences like cHS4, suggesting these features do not serve as barriers to transcriptionally induced coupling. However, exploration of additional intergene sequences, genetic elements, and locations within the genome may reveal elements that mitigate or amplify syntax-specific coupling.

In both constitutive and inducible systems, we find that upstream dominance strongly affects closely spaced tandem genes, resulting in reduced expression of the downstream gene (fig. 1). Previous work suggests that upstream dominance affects integrated transgenes [83], that choice of gene orientation and direction affects expression from adenovirus vectors [84], and that the divergent orientation offers an efficient "all-in-one" Cas9 editing circuit [85]. Increasing numbers of synthetic circuits employ divergent syntax for delivery to primary cells [11, 12, 86, 87]. As these applications require high rates of co-delivery, choice of divergent syntax may reflect the selection of functional circuits during the design process.

Supercoiling-mediated feedback provides an extremely rapid mechanism of transcriptional coupling [10]. In alignment with our predictions of supercoiling-mediated feedback, we find that transcription of an adjacent gene induces reversible, syntax-specific profiles of expression, tuning both the mean and variance (fig. 2). Parallel work in yeast showed increased burst coupling for *cis* divergent genes compared to *trans* at the *Gal1-Gal10* locus [22]. Potentially, harnessing the fast-timescale feedback of supercoiling may improve the performance of dynamic circuits such a pulse generators, toggle switches, and oscillators, which require coordinated expression of multiple genes. Supercoiling-mediated feedback may be especially useful to buffer noise in RNA-based control systems, supporting perfect adaptation and dosage control [12, 86, 88]. As noise and small changes in expression can direct cell fate [49, 79, 89, 90], syntax-based tuning offers a simple method to explore the stability of cell fate by perturbing native networks with levels of transgenes that vary in their mean and variability.

While our findings are consistent with both biophysical predictions of DNA-supercoiling-mediated feedback [10] and *in vitro* studies [91–94], we do not make direct supercoiling measurements [31, 47, 95, 96]. While the off-diagonal score in our maps of chromatin contact probability suggest the formation of plectonemes, direct measurements of supercoiling are challenging in living cells [22]. Genome-wide studies of supercoiling suggest that the twin-domain model of supercoiling describes

eukaryotic genomes [26, 47], with supercoiling affecting the performance of gene editing [97], bacterial chromosomal segregation [33], and nucleosome and structural maintenance protein placement and function [21]. Assays to measure supercoiling in living cells rely either on small molecule intercalators like psoralen that target negatively supercoiled DNA [31, 98, 99] or proteins that specifically bind to positively supercoiled DNA [26, 47]. Putatively, RCMC allows us to capture transcriptionally induced supercoils of either sign. Future work will be needed to combine region capture with assays of supercoiling to fully examine the hypothesis of DNA supercoiling-mediated feedback.

Engineered synthetic circuits are much more compact than native mammalian genomes and therefore are putatively more strongly affected by supercoiling. However, regulation of some native genes depend on adjacent gene expression. Tandem arrays of *Hox* genes show temporal activation during development that proceeds from downstream to upstream genes [100]. Potentially, supercoiling-mediated upstream dominance may reinforce other mechanisms driving the phenomenon of posterior dominance, which restricts the reactivation of downstream *Hox* genes. Transcription of non-coding RNAs tunes expression of native adjacent genes, both amplifying and attenuating expression of co-localized genes [49, 101]. Loss of transcription from an adjacent gene can induce significant developmental defects, suggesting adjacent transcription plays an essential role in tuning expression to control and coordinate cell fate [9, 49].

While supercoiling-mediated feedback offers a compelling explanation for the coupling of gene expression and syntax-specific profiles of intrinsic noise, alternative modes of regulation may influence two-gene circuits. For instance, collisions of RNA polymerases undergoing transcriptional readthrough may reduce expression in the convergent and tandem syntaxes [102]. However, rates of readthrough of single transgenes integrated into the genome are estimated to be low, representing less than one percent of polyadenylated transcripts [56], a possible underestimate if readthrough transcripts are less stable. Alternatively, methods of defining polymerase positions on single DNA fibers may resolve questions on readthrough and facilitated recruitment of RNAPII via supercoiling-mediated feedback [103]. Additionally, both transcription and supercoiling offer predictions for nucleosome positioning and histone modifications which may refine our understanding of the interlocking modes of gene regulation that control expression of synthetic and native genes.

Despite the clean, abstract way that synthetic circuits are often drawn, integration into the genome wraps synthetic circuitry in layers of native regulation. Biochemical interactions *and* biophysical forces combine to shape our genomes. By harnessing both layers of control, syntax and supercoiling-mediated feedback can enhance the predictability, performance, and functional range of engineered gene circuits.

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Author contributions

Following the contributor role taxonomy, C.P.J. contributed to project conceptualization, methodology, validation, investigation/data acquisition, statistical analysis, writing (original draft, review, editing), and visualization. K.S.L. contributed to conceptualization and methodology (all-in-one circuits), validation, investigation/data acquisition, statistical analysis, writing (review, editing), and visualization. S.R.K. contributed to investigation/data acquisition (two-gene lentiviruses) and writing (review, editing). R.J. contributed to conceptualization and methodology (constitutive hiPSC circuits), data acquisition, and visualization. A.B.A. contributed to conceptualization and methodology (STRAIGHT-IN circuits), investigation/data acquisition, and writing (review). D.S.P. contributed to conceptualization and methodology (STRAIGHT-IN circuits), investigation/data acquisition. E.L.P contributed to investigation/data acquisition (RNA-HCR-FISH) and writing (review, editing). R.L. contributed to investigation/data acquisition (constitutive PiggyBac cell lines) and writing (review). J.Y. contributed to investigation/data acquisition (constitutive hiPSC circuits). C.G.O. contributed to methodology (two-gene PiggyBac constructs) and writing (review). C.L.M. contributed to resources, writing (review), supervision, funding acquisition. R.P.D. contributed to resources, writing (review), supervision, funding acquisition. B.J.D. conceptualization and methodology (antibody experiments), resources, and writing (review). P.W.Z. contributed to writing (review), resources, supervision, project administration, and funding acquisition. K.E.G. contributed to conceptualization, methodology, validation, resources, writing (review, editing), supervision, project administration, and funding acquisition.

Declaration of interests

None

Supplementary Materials

- Materials and Methods
- Tables S1 to S5.
- Figs. S1 to S17.

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