Title

Tissue-specific transcription footprinting using RNA PoI DamID (RAPID) in *C. elegans*

Article summary

Gene expression is a major determinant of cell fate and physiology, yet it is notoriously difficult to characterize for the widely used model system *C. elegans*. By using a new method based on *in vivo* covalent modification of DNA by RNA polymerases, we determine genome-wide transcription patterns in single tissues of embryos or young adult animals. We show that the method is able to identify actively transcribed genes in tissues representing down to 0.2% of the somatic cells in adult animals. Additionally, this method can be fully performed in a single laboratory by using third generation sequencing methods (ONT).

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Abstract

Differential gene expression across cell types underlies the development and cell physiology in multicellular organisms. *C. elegans* is a powerful, extensively used model to address these biological questions. A remaining bottleneck relates, however, to the difficulty to obtain comprehensive tissue-specific gene transcription data, since available methods are still challenging to execute and require large worm populations. Here, we introduce the RNA Pol DamID (RAPID) approach, in which the Dam methyltransferase is fused to an ubiquitous RNA polymerase subunit in order to create transcriptional footprints *via* methyl marks on the DNA of transcribed genes. To validate the method, we determined the polymerase footprints in whole animals, sorted embryonic blastomeres and in different tissues from intact young adults by driving Dam fusion expression tissue-specifically. We obtained meaningful transcriptional footprints in line with RNA-seq studies in whole animals or specific tissues. To challenge the sensitivity of RAPID and demonstrate its utility to determine novel tissue-specific transcriptional profiles, we determined the transcriptional footprints of the pair of XXX neuroendocrine cells, representing 0.2% of the somatic cell content of the animals. We identified 2362 candidate genes with putatively active transcription in XXX cells, among which the few known markers for these cells. Using transcriptional reporters for a subset of new hits, we confirmed their XXX expression for a majority of them and identified novel XXX-specific markers. Taken together, our work establishes RAPID as a valid method for the determination of polymerase footprints in specific tissues of *C. elegans* without the need for cell sorting or RNA tagging.

Introduction

Differential gene expression across cell types encompasses both key determinants and markers of the cells' identity. Cataloging these differences can provide critical insights and entry points in research aiming at elucidating the mechanisms controlling fundamental biological processes, such as organismal development and cell/tissue physiology. *C. elegans* is a widely used model animal, particularly well suited for integrative studies bridging our understanding across the molecular, cellular and organismal levels. With its transparent body, *C. elegans* was the first animal used to analyze tissue-specific transcription *in vivo* with GFP reporters (Chalfie *et al.* 1994), an approach still extensively used. In contrast to the versatility of the model for individual gene expression analysis, more holistic approaches such as tissue-specific transcriptomics are much more challenging. Two main strategies have been developed to analyse specific tissues/cell types in *C. elegans*. The first one relies on the animal disruption and cell isolation, or dissociation, followed by the sorting of labelled cells, or nuclei (Haenni *et al.* 2012; Steiner *et al.* 2012) prior to transcriptomics analysis. These protocols are not straightforward to establish and work better in embryos than larvae or older animals. The tough cuticle, or eggshell, is a significant obstacle, and so far only major tissues could be analyzed in adults (Kaletsky *et al.* 2018). The second strategy involves purification of tissue-specific enriched messenger RNAs via the pull-down of poly-A binding proteins expressed in specific cell types (Roy *et al.* 2002; Pauli *et al.* 2006; Mattout *et al.* 2011; Blazie *et al.* 2015, 2017; Hrach *et al.* 2020) or the targeted expression of a modified splice leader trans-spliced to the transcripts by the cellular machinery (Ma *et al.* 2016). However, these techniques are labour intensive, require a large number of animals as starting material, or are associated with a strong unspecific background signal. Therefore, carrying cell-type specific transcriptional profiling in few differentiated cells remains challenging.

As a complementary approach that could circumvent many of these limitations, we investigated whether we could use DNA adenine methylation identification (DamID) to footprint actively transcribed genes in specific cell types. This approach has been successfully used in *Drosophila* to determine transcribed genes in rare brain cell types (Southall *et al.* 2013). DamID relies on the low-level expression of a fusion between the *E. coli* Dam methyltransferase and the protein of interest, here a subunit of the RNA polymerase. Binding of the latter to DNA leads to the methylation of GATC sites in the vicinity of the binding site (Figure 1A). After DNA extraction, methylated GATCs are specifically cleaved by the restriction enzyme *Dpn*I and amplified using adapter-mediated PCR before sequencing (Figure S1A). The adaptation of the method to *C. elegans* seemed

promising since endogenous adenine methylation/demethylation is very rare in worms and not targeted to GATC motifs (Greer *et al.* 2015). The GATC site frequency moreover allows to expect a good spatial resolution. Indeed, *C. elegans* has 269,049 GATC sequences per haploid genome , corresponding to an average of one site for every 374 bp and a median of 210 bp (Gómez-Saldivar *et al.* 2016).

Here, we describe the RAPID approach (RNA Polymerase DamID) for transcriptional footprinting in specific tissues in *C. elegans* in both embryonic blastomeres and in young adults. Using a fusion between a small subunit present in all 3 RNA polymerases, we show that the technique can be used on both fluorescently sorted blastomere cells, or DNA isolated from entire young adults using a Cre/*lox* cell-type-specific expression. To test the versatility of the method, we determined the polymerase footprints in three different tissues at each stage. In young adults, these tissues represent between 10 and 0.2% of the total cells of the animal. We show that meaningful transcriptional patterns can be recovered using this technique, in line with previously used RNA tagging methods. We have further explored how this technique can also be used to unravel tissue-specific markers and report here the identification of eight new reporters for adult XXX cells. Additionally, as a result of the phasing-out of older sequencers able to sequence amplicons from different sizes as produced by DamID-seq, we show that new long read sequencing methods can be used to sequence DamID libraries, which allows carrying out the experiments, from DNA extraction to amplicon sequencing in less than a week without any external sequencing facility.

Material and methods

Plasmids and transgenic strains

All plasmids and worm strains are listed in Supplementary Table 1 and 2. Tissue-specific DamID plasmids were generated using Gibson assembly. All DamID plasmids were integrated as single copies using MosSCI either on chromosome II or IV (see details in Supplementary Table 1; Frøkjaer-Jensen *et al.* 2008).

Worm growth

Worms were grown on solid NGM, seeded with OP50 bacteria for maintenance culture and genetic crosses. All worm cultures were grown at 20°C. For cell sorting, animals were grown on peptone plates seeded with HB101, synchronized twice by hypochlorite treatment. Young adults containing up to 10 embryos were recovered 66 hours after spreading synchronized L1 larvae. For DamID experiments in young adults, worms were grown on NGM seeded with Dam negative *E. coli* GM48 for at least two generations. Around 5,000 synchronized L1s were seeded onto 100 mm plates (1,000-1,200 per plate) and collected 53h later. Worms were washed extensively with M9 (at least 10 times) and distributed in aliquots of 30 µl removing the excess of liquid. Samples were snap-frozen and stored at −80 °C.

Sorting of embryonic blastomeres

Synchronized gravid adult hermaphrodites containing 8-10 eggs were treated with hypochlorite. Eggs were then incubated for 3 hours in M9 at 25°C until they reached the 1.5 fold stage. Eggs were then transferred to 500 µl egg buffer and pelleted 1 min at 2000 rpm. The supernatant was then aspirated, leaving 100 µl of buffer with the pellet. 500 U of chitinase (Sigma-Aldrich;C8241-25U) were added and the mixture resuspended and further incubated for one hour at room temperature. Chitinase was then neutralized with 800 µl Leibovitz medium. Digested embryos were then recovered by centrifugation at 3000 rpm for 5 minutes at 4°C. Embryos were then dissociated into isolated blastomeres by pipetting up and down with a P1000 pipette, up to 150 times until dissociation was complete. The cell population was then filtered with a Millex-SV syringe 5 µm filter (Millipore;SLSV025LS). 500 fluorescent cells were sorted using a BD FACSAria Fusion (8000 events/second; 85µm nozzle) in sterile PCR tubes containing 1ul of pick buffer (50mM Tris-HCl pH 8.3; 75mM KCl; 3mM MgCl2; 137mM NaCl). Collected samples were then frozen in liquid nitrogen before further processing. After DamID processing and PCR (see below), two technical replicates were pooled for sequencing library preparation.

DamID amplification, library preparation, and sequencing

For sorted cells, frozen samples were lysed by addition of 2 ul of lysis buffer (10mM TrisAc, 10 mM MgAc, 50 mM KA, 0.67% Tween 20, 0.67% Igepal + 1mg/ml Proteinase K) and incubated during 2 hours at 60ºC before Proteinase K inactivation at 95ºC for 15 minutes. DamID amplicons were obtained as previously described (Gomez-Saldivar *et al.* 2016) using 30 PCR cycles.

For young adults, DamID was performed on 500 ng gDNA extracted from the animals using DNeasy Blood and Tissue Kit (Qiagen #69504). Two replicates for each stage and cell type were processed. DamID amplicons were obtained as previously described (Gomez-Saldivar *et al.* 2016) with 20 PCR cycles for worm-wide DamID, 22 PCR cycles for muscle DamID, 22-24 for intestine DamID and 24-26 cycles for XXX cells DamID. New Illumina patterned flow cell technology does not allow sequencing of amplicons larger than 600 bp. Both types of DamID PCR amplicons were therefore sequenced using nanopore sequencing. After AMPure XP (Beckman-Coulter) purification with 1.8 beads volume, DamID PCR amplicons were directly used for nanopore library barcoding and preparation using NBD-104 and LSK-109 kits (Oxford Nanopore). Libraries were sequenced to obtain at least 1 million reads per library on MinION using flow cells R9.4.1. We compared the performance of both sequencing approaches by sequencing the same libraries with both old paired-end HiSeq2500 Illumina flow cells and nanopore sequencers. Coverage obtained by both approaches were similar (see snapshot of mapped reads in Figure S1E). However, nanopore sequencing allowed the direct sequencing of longer amplicons (Figure S1F), likely because cluster amplification does not work well on molecules longer than 800 bp, even on old generation (HiSeq2500) flow cells. We compared DamID samples libraries generated using previously described entire animals expressing either a free GFP-Dam fusion or a perinuclear lamin fusion (Sharma *et al.* 2014). Statistical comparison of both techniques at the single restriction fragment level led to Pearson correlation coefficient between short PE and long reads between 0.84 and 0.86 (Figure S1G).

Bioinformatic analysis

Nanopore sequences were demultiplexed using deepbinner and basecalled using guppy 3.6 with the high accuracy model before mapping to the ce11 genome using minimap2 (Li 2018). Reads were considered as DamID amplicons when both ends mapped +/- 8 bp from a genomic GATC motif. Filtered libraries were then used to call polymerase footprinting values using the damidseq_pipeline package (Marshall and Brand 2015) using bam files (parameters: --bamfiles --extend_reads=0). The damidseq pipeline normalizes for GATC

accessibility using a free Dam (in our case Dam::GFP) profile. Gene values were extracted using polii.gene.call (https://owenjm.github.io/damidseq_pipeline/) using WS270 genes definition. Correlations between libraries and methylation footprinting values were made using *ad hoc* R scripts available upon request. Normalized footprinting tracks were visualized using IGV. For the comparison with ChIP-seq tracks, fastq files were downloaded from GEO, mapped to ce11, normalized for sequencing depth with a pseudocount of 8 and log2 normalized to the input. Final figure construction was made using IGV and Adobe Illustrator.

Array construction and microscopy

Reporter plasmids were assembled using the 3-fragment MultiSite Gateway system (ThermoFisher Scientific). Promoters of candidate genes were PCR amplified from a N2 gDNA template. Primer sequences and promoter lengths are described in Supplementary Table 3. Candidate promoters were cloned into pDONR-P4-P1R vector (Invitrogen) by BP recombinations generating slot 1 Entry vectors (Supplementary Table 2). Final expression plasmids were generated by LR recombinations between promoters (slot 1), mNeonGreen fluorescent ORF (slot 2; dg353; Hostettler *et al.* 2017), unc-54 3' UTR (slot 3; pMH473, gift from Marc Hammarlund) and pDEST-R4-P3. The control localization/expression plasmid [*sdf-9p::NLS::wrmScarlet*] was generated through a LR recombination reaction between dg801 (slot 1), dg651 (slot 2; Marques *et al.* 2019), pMH473 (slot 3), and pDEST-R4-P3. Finally, *promoter::mNeonGreen* and *sdf-9p::NLS::wrmScarlet* plasmids were co-injected into N2 young adult hermaphrodites at 20 ng/ul each, with 20 ng/ul of dg9 (*unc-122p::RFP*; red coelomocyte) as a co-injection marker (Addgene #8938; Miyabayashi *et al.* 1999). Two stable lines of each candidate promoter were selected (Supplementary Table 1). For imaging, young adult animals identified based on the red coelomocyte reporter expression were transferred to a 2% agarose pad containing 0.01% sodium azide. Worms were then imaged on a Zeiss Axiovert microscope with a 20x objective driven by Visiview, using a Photometrics Coolsnap Myo CCD camera with GFP and RFP settings (60 planes spaced by 2 µm), plus a middle plane section in DIC settings. Using Fiji, the acquired optical stacks were then partially z-projected to capture the worm section containing the XXX cells, identified using the *sdf-9p::NLS::wrmScarlet* signal. Final figure construction was made using Adobe Illustrator. For each promoter except *asp-9*, two independent extrachromosomal arrays were scored with at least 5 animals.

Identification of tissue-enriched genes and validation

Gene coverage of RAPID profile is listed in Supplementary Table 4 (blastomeres) and 5 (young adults) (Sheet 1-2) Tissue-enriched genes were defined as genes that are significantly expressed (FDR < 0.05) in both replicates of one tissue (Supplementary Table 4 sheet 2 and Supplementary Table 5 sheets 3-4). Representative examples of tissue-enriched genes used in Figure 2C were selected from CeNGEN project (https://cengen.shinyapps.io/SCeNGEA/) (Hammarlund *et al.* 2018) and visualized using IGV (https://igv.org/).

Genes enriched uniquely in one tissue were defined as genes significantly and differentially expressed relative to the other two tissues (Supplementary Table 4 sheet 3 and Supplementary Table 5 sheet 5). Analysis of the uniqueness of the genes from each tissue was performed using the JavaScript library jvenn (http://bioinfo.genotoul.fr/jvenn).

For the correct comparison between the genes identified in the muscle with RAPID and the set of genes identified with SRT (trans-Splicing Rna Tagging; Ma *et al.* 2016), only SL1 trans-spliced genes were selected, based on the intersection with the 10,589 mRNAs annotated as SL1-trans-spliced by modENCODE (Allen *et al.* 2011), generating a subset of 3477 genes. For the comparison between the genes identified in the intestine with RAPID and the set of genes identified with FANS (Fluorescence Activated Nuclear Sorting; Haenni *et al.* 2012), the gene list was modified eliminating the genes downregulated and keeping only the genes found as expressed and upregulated, in total 9169 genes. For the comparison between the genes identified with RAPID and the set of genes identified with FACS (Kaletsky *et al.* 2018) in muscle and intestine, we directly used the expressed genes list from Supplementary Table 1, which contained 7690 and 9603 genes, respectively. Chi-square ($\chi 2$) statistic tests were calculated using the GraphPad QuickCalcs Web site https://www.graphpad.com/quickcalcs/contingency1/ (accessed August, 2020).

Tissue-specific prediction analysis

Tissue expression prediction test was performed using Top 500 significant unique-enriched genes of muscle and intestine (Supplementary Table 5 sheet 6), selecting a multi-gene search within the Tissue-specific Expression Predictions for *C. elegans* program, version 1.0 (http://worm-tissue.princeton.edu/search/multi). For the tissue expression prediction test using the RAPID muscle-SL1 group, the parameters published in (Ma *et al.* 2016) were used.

Gene ontology analysis

Gene Ontology terms were performed on unique tissue-enriched gene lists. GO terms and q-value were obtained using gProfiler (https://biit.cs.ut.ee/gprofiler/gost) ; (version e100_eg47_p14_7733820) with g:SCS multiple testing correction method applying significance threshold of 0.05 (Supplementary Table 5 sheet 7; Raudvere *et al.* 2019).

Candidate selection for reporter analysis

Candidate genes were selected for follow-up promoter analyses with the dual goal of demonstrating that they are indeed transcribed in XXX cells and of identifying markers with expression restrained to XXX cells. Since XXX cells represent only 0.2% of the *C. elegans* cellular content, we reasoned that XXX-specific markers should produce very little or no signal in the whole animal samples. Therefore, out of the 862 XXX-enriched genes (with a significant RAPID signal in XXX, but not in muscle or in intestine samples), we further removed genes detected in at least one worm-wide sample. We obtained a refined list of 275 XXX-marker gene candidates, which still included the known XXX cell markers *daf-9* and *eak-4* (Supplementary Table 5, sheet 8). From this candidate list, we selected *dhs-17* as an uncharacterized gene with a plausible link to XXX cell function, plus 11 random candidates. In order to limit caveats related to operons, we excluded a candidate if another transcript was located less than 200 bp upstream. The XXX-specific RAPID signals (RNA pol occupancy values) in the 12-gene subset (average=1.35, SD=0.59) were similar to those in the starting 275-gene set (average=1.47, SD=0.64; p=.16 by Student's t-test).

Data availability

Embryonic and adult DamID-seq data is available under the GEO accession codes [data submitted to GEO, waiting for accession code].

Results and discussion

RNA polymerase footprinting using RAPID

The RAPID approach relies on the expression of trace levels of the *E. coli* DNA adenine methyltransferase (Dam) fused to a subunit of the RNA polymerases, and the analysis of its occupancy to evaluate the transcriptional state of genes. We first tested whether we could use AMA-1, the largest, catalytic subunit of RNA polymerase II, as reported in Targeted DamID, TaDa, done in neuronal lineages in *Drosophila* (Southall *et al.* 2013). However, the Dam signal was too weak, possibly due to the fact that the expression level of this very large fusion protein under transcriptional control of the uninduced *hsp-16.2* promoter was too low (not shown), or that the localization of the Dam domain within the *C. elegans* polymerase complex was not favorable to access its DNA substrate. We therefore replaced AMA-1 with RPB-6, the *C. elegans* homolog of the RNA polymerase subunit F present in all 3 RNA polymerases. RPB-6 together with RPB-1 and RPB-2, form a 'clamp' that retains DNA near the active center of PolII (Cramer *et al.* 2000), stabilizing the transcription on the DNA template. In contrast to AMA-1 attempts, we obtained a strong DamID PCR signal in animals carrying a single copy transgene of the *rpb-6::Dam* fusion, which had not been subjected to heat shock and therefore expressed only low levels of the Dam fusion in the whole animal. After sequencing and signal normalization with GFP::Dam data to control for overall chromatin accessibility, we could detect general patterns of methylation that were consistent with polymerase-dependent methylation (Figure 1C) and a good correlation at the gene level (Figure 1D). We compared the RAPID profiles with recent ChIP-seq datasets for RNA polymerase II downscaled to GATC fragment resolution (Garrido-Lecca *et al.* 2016; Kalinava *et al.* 2017; Miki *et al.* 2017). Visually, the patterns appeared similar (see examples of profile in Figure 1C and D). Even if the nature of the data is not strictly identical, we performed a comparative analysis between the datasets for all genes, downscaling the resolution of the ChIP-seq data to GATC fragment (Figure 1B). RAPID and RNA polymerase ChiP-seq show a significant correlation (R=0.41-0.48). Overall, inter-replicate correlations were higher between the RAPID replicates (R=0.81) and between the RNA polymerase II ChIP experiments (R=0.63-0.97). The difference between the RAPID and RNA Pol II ChIP profiles most likely results from the different approach to recover DNA and from the fact that RAPID in adults represent a cumulative transcriptional activity picture, while the RNA pol II ChIP represents a polymerase occupancy snapshot at the young adult stage.

We also examined the profile in genes transcribed by Pol I and Pol III. As expected from the differential inclusion of AMA-1 and RPB-6 subunits in the different polymerases, RAPID with RPB-6 also labelled genes transcribed by RNA Pol I and III. RAPID showed high

enrichments on the rRNA genes at the end of chromosome I (Figure S2A), as well as a majority of previously characterized snoRNAs transcribed by RNA polymerase III (46 out of 57; Ikegami and Lieb 2013). snoRNA are sometimes located in introns of PolII-transcribed genes, making it difficult to differentiate whether the RAPID signal originates from the snoRNA transcription or from the overlapping gene. Nevertheless, 24 out of 44 RAPID-positive snoRNA genes could be unambiguously assigned to PolIII transcription as there was no overlap (Figure S2B). In contrast, the corresponding signal was markedly weaker in the young adult RNA pol II ChIP-seq datasets and very high for the RNA PolIII subunit RPC-1 (performed in embryos, Figure S2B; Ikegami and Lieb 2013). Taken together, these data show that the RAPID method is suitable to reveal RNA polymerase footprints, serving as indirect indications for transcriptional activity made by the three different RNA polymerases.

RAPID in tissue-specific sorted embryonic cells.

Since RAPID could label transcribed genes in whole animals, our next goal was to adapt the method for tissue-specific analysis. We first explored whether RAPID could be used to footprint transcription in specific cell types of the embryo purified using fluorescent sorting. Using strains constitutively expressing Dam fusions, we sorted 1000 cells for 3 different tissues of various abundance: body wall muscle, intestine and the rectal Y cell (80, 20 and 1 cell per embryo, respectively; Figure S3A, Supplementary Table 4). RAPID could produce footprints for all samples (Figure S3C), and the reproducibility of the RAPID signal at the gene level between replicas was good for the intestinal sample (*r=0.78*) yet lower for muscle and Y cell samples (*r=0.46* and *0.24*, respectively; Figure S4A). RAPID appears however suitable to identify transcription footprints of cell type specific genes, such as the intestinal *cpr-6* (cathepsin B; Pauli et al. 2006) and *elo-2* (fatty acid elongase ELOVL; Han et al. 2017), or Glutathione S-Transferase *gst-4* expressed in muscle, as well as the muscle-specific WDR1 homolog *unc-78* (Figure S3C; Mohri and Ono 2003; Hasegawa *et al.* 2007). Comparison of the footprints obtained for all three tissues allowed us to define 395 Y-specific genes (Figure S3B), and among them, shallow Y-specific RAPID signal was visible for *ceh-6* and *sox-2*, two transcription factors previously shown to be involved in Y-to-PDA transdifferentiation initiation (Figure S3C; Kagias *et al.* 2012). In contrast, we observed some unexpected RAPID footprints for genes which we expected to be expressed in a tissue-specific manner. For example, the myosin *myo-3* was observed in all 3 tissues (Figure S3D). Conversely, some genes which are known to be expressed in tissue-specific manner did not show high RAPID values, *e.g.* the intestine-specific *asp-1* and *spp-5* genes or the

muscle-specific *pat-10* one (Figure S3D). These differences might have a biological significance: most transcription patterns have been defined in older animals, yet those genes might be expressed more broadly, or not at all, in embryonic blastomeres. Alternatively, the lack of a robustly established transcription pattern might hinder faithful footprinting. Indeed, RAPID requires the enzymatic action of the methyltransferase to build up the signal, while footprints are removed at each replication round in rapidly dividing blastomeres. Together with the stochasticity of single methylation events, this might decrease the precision of the profiles. In agreement with this, intestinal cells, most of which are born and remain postmitotic early, display high reproducibility in the RAPID signal, while late-born muscle and the Y cell are less reproducible (Figure S3C,D). In conclusion, RAPID allows transcriptional footprinting of sorted cells, provided cells have been born long enough for the Dam fusions to methylate reproducibly their target genes.

Tissue-specific expression of RAPID in young adult animals.

Our next goal was to adapt the RAPID approach for the analysis of tissue-specific transcription profiles in adult worms. To circumvent the technical difficulties associated with mature animal dissociation and cell sorting, we sought to implement a transgenic approach for the cell-specific targeting of the RPB-6::Dam fusion. Several approaches have been developed to target Dam fusion expression to specific tissues, using either bicistronic constructs attenuating Dam translation (Southall *et al.* 2013), tamoxifen-induced nuclear translocation (Pindyurin *et al.* 2016; Redolfi *et al.* 2019) or tissue-specific recombination cassettes (Muñoz-Jiménez *et al.* 2017). We used the latter strategy using an insertion of a floxed mCherry ORF located between the *hsp-16.2* promoter and the Dam fusion (Figure 2A). Tissue-specific expression of the Cre recombinase leads to low-level expression of the Dam fusion (Ruijtenberg and van den Heuvel 2015). We used 3 different Cre drivers expressed in muscle, intestine and a pair of head neuroendocrine cells called XXX, using *myo-3*, *elt-2* and *sdf-9* promoters, respectively. In contrast to previous strategies used in the nematode to determine cell-type specific transcription, which require millions of worms, RAPID requires only 4’000 animals as starting material for DNA extraction. DamID signal across genes was highly correlated between replicates, and less correlated between different Cre drivers, suggesting tissue-specific DamID footprinting (Figure S4B). We called enriched expressed genes with an FDR of <0.05 for both replicates of each tissue, resulting in 2052, 2296 and 2362 genes with high RAPID footprint in intestine, muscle and XXX cells, respectively. Out of these, 1011, 747 and 862 were defined as tissue-specific in these three

cell types, while only a minority (536) harbored high RAPID footprints in all sampled tissues (Figure 2B, Supplementary Table 5).

We validated these results focusing on individual genes with well-characterized tissue-specific expression (Figure 2C). The intestine-specific prograstricsin aspartyl protease homolog *asp-1* and the saposin-like channel defense *spp-5* were exclusively footprinted in intestinal samples (Tcherepanova *et al.* 2000; Roeder *et al.* 2010). *myo-3*, the muscle myosin and *pat-10*, a troponin, both exclusively expressed in muscle tissues, harbored high RAPID footprints in muscle samples (Miller *et al.* 1986; Kagawa *et al.* 1997). Finally, the XXX-specific genes *daf-9* (encoding a P450 cytochrome homolog) and *eak-4* (encoding a membrane protein) were exclusively marked with RAPID in XXX cells (Gerisch *et al.* 2001; Hu *et al.* 2006).

To expand the validation of our RAPID footprint gene lists beyond selected tissular markers, we next engaged two more comprehensive approaches. These approaches focused on muscle and intestine, since no large-scale gene expression data are available in XXX cells. First, we compared the sets of genes with detectable RAPID footprints in body wall muscle and intestine, with sets of genes detected in these tissues using genome-wide approaches (RNA-seq of FACS-sorted cells by Kaletsky *et al.* 2018) ; of SRT messengers (Ma et al., 2016); or of FACS-sorted nuclei (Haenni et al., 2012). A majority of genes with detectable RAPID footprints were also identified with tissue-specific transcriptomics (Figure 3A,B, 77% for muscle, 72% for intestine). Second, we focused on a narrower set of genes with high RAPID footprint present exclusively in one of the tissues. These gene lists were analyzed with the tissue predictor tool with a multi-gene query (http://worm-tissue.princeton.edu/; Chikina *et al.* 2009). Muscle-only and intestine-only RAPID footprinted genes gave a high prediction score for muscle and intestine, respectively (Figure 3C,D). In contrast, their scores were much lower for non-targeted tissues (including neurons, hypodermis and germline).

Taken together, the results of our comparative analyses with previous gene expression studies suggest a valid identification of tissue-specific polymerase transcriptional activity with RAPID that largely matches the transcriptional output in these tissues. RAPID thereby allows reproducible profiling of transcription footprints in single tissues using low input material.

RAPID identifies genes expressed in XXX cells

XXX cells are neuroendocrine cells derived from hypodermal embryonic progenitors. They express enzymes required for steroid hormone synthesis such as DAF-9 and are implicated in the control of dauer formation during development (Gerisch *et al.* 2001; Ohkura *et al.* 2003). As we still have limited information on the set of genes expressed in XXX cells, as well as on the role of those cells in adults, our XXX-cell transcribed gene dataset could represent a valuable resource for future studies. We thus conducted additional experiments to confirm the validity of RAPID profiles to infer gene transcription in those cells and identify new markers.

A GO term analysis highlighted many terms related to secretory and neural functions in the gene set specific for XXX cells, while they were absent from the muscle- and intestine-enriched gene sets (Supplementary Table 5 sheet 7). These results are expected for neuroendocrine cells, with functional properties very similar to those of neurons.

To further confirm the validity of RAPID profiles to infer gene transcription, we selected 12 genes with high RAPID signal in XXX cells compared to intestine, muscle and whole animals, by comparing their profiles in the 4 tissues (Figure S5). We then created transcriptional reporters by cloning their putative promoters in front of a mNeonGreen fluorescent reporter (Hostettler *et al.* 2017). Transgenic lines bearing extrachromosomal arrays were then created by injection, together with an XXX-specific red reporter driven by the *sdf-9* promoter, which we previously used for XXX-specific RAPID. Out of the 12 promoters, eight drove expression in the XXX cells at various levels (*asic-1, dhs-17, F14H8.2, C06A1.3, asp-9, B0034.5, F52E1.5,* and *nlp-15*, Figure 4), one was impossible to score (*T22E5.6*), as it also drove high expression in the pharynx located very close to the XXX cells, and three did not show detectable expression in XXX cells (in adults; *mab-9, twk-39* and *lgc-36*). The absence of expression in the latter group could indicate that these genes represent false positives in the RAPID analysis, that the transcription was active only at earlier developmental timepoints, or that the arbitrarily defined promoters failed to reflect the endogenous transcriptional activity. Interestingly, in half of the reporters expressed in XXX cells (4/8), we observed only limited or no signal in other cell types. Reporters for *dhs-17* or *F14H8.2* were predominantly expressed in XXX cells and sequence homology suggests plausible cell-specific roles. Indeed, *dhs-17* encodes an uncharacterized member of the short-chain dehydrogenases/reductases family (SDR), which is potentially involved in steroid metabolism (Zhang *et al.* 2013) and may therefore contribute to this specific neuroendocrine function of XXX cells. Our RAPID analysis also identified *F14H8.2*, a

paralog of *eak-4* selectively expressed in XXX cells and regulating dauer formation (Hu *et al.* 2006).

Taken together, the results of our reporter gene analysis indicate that the RAPID approach applied to only two cells per animal successfully identifies actively transcribed genes in these cells, including genes with relatively low expression and potential novel cell-specific markers.

Limitations and perspectives

Determining the transcriptional profile of specific cell types has been a major hurdle for *C. elegans* researchers, as most research is carried out on intact, living animals. In addition, research on specific cell types, which can represent as little as one cell in the whole animal, is often impaired by the paucity of markers for cell identity and cell function. With RAPID, we present a simple, fast and cost-effective technique to identify transcribed genes by the footprint of DNA-engaged polymerases in individual tissues or cells, requiring only the knowledge of a tissue- or cell-specific promoter. RAPID involves the enzymatic modification of DNA, a major advantage as only cells in which the Dam fusion is expressed will produce the DamID signal. Cell-type-specific RAPID hence makes use of DNA extracted from entire animals as a template for DamID, thereby avoiding cell or RNA purification steps and reducing the size of the starting population to several thousand animals instead of millions of animals required for cell or RNA purification. However, RAPID is a stochastic average of the methylation by polymerases since the cell's last DNA replication (which erases the DamID signal). Unsurprisingly, we observed a better signal to noise ratio in older animals in which the transcriptional program has been established longer, thereby reducing the stochasticity of the methylations (Figure S4).

RAPID could be further improved by timing the expression of the Dam fusions, for instance using degron-tagged degradation (Zhang *et al.* 2015). We tested auxin-mediated Dam degradation; however, degradation is not complete and the remaining low levels of Dam fusions are sufficient to create a RAPID signal (data not shown). Alternatively, degron-tagged Cre recombinases might provide a more reliable way to time the expression of the Dam. In addition to static tissue-specific transcriptional profiles, a potential future application of RAPID would be to examine dynamic transcriptional changes occuring in response to environmental changes, as successfully achieved in *Drosophila* (Widmer *et al.* 2018). In a post-mitotic context, the approach would be limited to transcriptional up-regulation events since, in the absence of cell-replication-independent demethylation mechanisms, reduction of polymerase occupancy would not be reflected in a decreased Dam signal. Beyond transcription, cell-type-specific DamID similar to RAPID can be applied

to a variety of chromatin factors to delineate cell-type specific genome-wide binding profiles in *C. elegans*, ranging from histone marks (Marshall and Brand 2017; Villaseñor *et al.* 2020) to transcription factors (Filion *et al.* 2010; Schuster *et al.* 2010) or chromatin accessibility (Aughey *et al.* 2018).

In conclusion, our work indicates that RAPID is a valid approach to analyse transcriptional activity in specific *C. elegans* cell types. Because of its ease of implementation and relatively high sensitivity, we anticipate that it will represent a powerful complement to cell-sorting-based approaches, particularly suited for situations where the amount of starting material is limiting or the fraction of targeted cells is low.

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Figure legends

Figure 1. RAPID: RNA Pol II DamID tissue-specific scheme.

A. *Dam::rpb-6* bound to all three RNA polymerase types modifies proximal GATC motifs. DamID analysis provides RNA polymerase footprints *in vivo*.

B. Gene-level correlations in young adults whole animals of RAPID and RNA polymerase Chromatin immunoprecipitation-seq using different antibodies (a: (Garrido-Lecca *et al.* 2016); b: (Kalinava *et al.* 2017); c: (Miki *et al.* 2017)).

C, D. Profiles at large scale (C) and gene scale (housekeeping genes, D) of RAPID and the different RNA polymerase II ChIP-seq studies cited in B.

Figure 2. Tissue-specific expression profiles using RAPID by Cre/*lox* recombination in young adult animals.

A. Experimental system for tissue-specific expression of Dam fusions and RAPID analysis.

B. Venn diagram of overlap between expressed genes identified using RAPID in 3 different tissues.

C. RAPID profiles for previously characterized genes expressed in a tissue-specific manner in intestine, muscle, and the XXX neuroendocrine pair.

Figure 3. Validation of RAPID muscular and intestinal transcriptomes.

A. Overlap of genes footprinted using RAPID with muscle-expressed genes detected by FACS (left; (Kaletsky *et al.* 2018) and SRT (right; Ma et al. 2016). For the comparison to SRT data, the subset of SL1-trans spliced genes detected using RAPID was used.

B. Overlap of genes footprinted using RAPID with intestine-expressed genes detected by FACS (Kaletsky et al. 2018) and FANS (Haenni *et al.* 2012). χ^2 test for all comparisons, p-value < 0.0001.

C-D. Tissue enrichment prediction of tissue-specific RAPID transcriptomes. The top 500 hits of unique tissue-enriched genes for muscle (C) and intestine (D) were analyzed by the online program Tissue-specific Expression Predictions for *C. elegans* (http://worm-tissue.princeton.edu/search). Tissue enrichment scores (mean and SEM) showed that the top genes of each tissue identify their corresponding original tissue.

Figure 4. Promoters of genes identified as expressed in XXX cells using RAPID drive fluorescent reporter expression in XXX cells. Left panel, partial z-projections of adult heads showing expression of *sdf-9p::mScarlet* in XXX cells. Middle panel, partial z-projections of adult heads showing the expression pattern of *mNeonGreen* reporter under transcriptional

control of the promoters of indicated genes. Right panel, merge of fluorescent channels within DIC images validate the novel expression of mentioned genes in XXX cells. Bar: 10 µm.

Supplementary figures

Figure S1. DamID Sequencing using Illumina or Nanopore technologies.

A. Principle of methylated GATC identification using DamID. Methylated GATC motifs are cut using the methylation-sensitive *Dpn*I restriction enzyme, before **B.** adapter ligation and PCR amplification using a primer hybridizing in the adapter. **C.** For Illumina sequencing, classical DNA library preparation is used, involving Y adapter ligation and limited PCR amplification. DamID amplicons can only be sequenced on non-patterned Illumina flow cells as their variable length is detrimental to cluster formation and polony amplification. To solve the latter issue, amplicons from the first PCR round were directly sequenced using ligation-mediated library preparation and ONT long read sequencing. **D.** While Illumina sequencing highlights the beginning of the amplicons (and the end in case of paired end sequencing), ONT long read sequencing captures the entire length of the amplicon. **E.** Snapshot of the same library sequenced with Illumina short read sequencing (paired end, upper panel) and ONT long read sequencing (bottom panel). **F.** Comparison of amplicons length obtained from both sequencing techniques for the same library (blue, Illumina; orange, ONT). The smaller sizes of Illumina-sequenced amplicons is due to the loss of these amplicons during polony amplification in Illumina sequencing, as the average size of the amplicons determined using automated electrophoresis before loading onto the flow cell correspond to the ONT-sequenced one (data now shown). **G.** Pearson correlation at the single GATC fragment resolution for 4 different libraries of 2 different Dam fusions (with either GFP or LMN-1) sequenced with either Illumina (short PE) or ONT (Long) sequencers.

Figure S2. RAPID allows identification of PolI and PolIII transcribed genes.

A. RAPID footprinting of the rDNA locus on the right telomere of chromosome I, together with RNA polymerase II ChIP-seq (8WG16 ChIP-seq from young adult animals from Miki *et al.* 2017). **B.** RAPID signal at polIII snoRNA genes, with no PolII overlapping signal (24 out of 57 genes; 8WG16 ChIP-seq as in A). PolIII-specific genes were taken from Ikegami and Lieb 2013, ChIP-seq for RPC-1 (RNA polymerase III subunit A) performed in embryos. The 8WG16 antibody produces a low residual signal on the snoRNA genes. **C.** RAPID signal at polIII snoRNA genes with overlapping PolII ChIP-seq signal (20 out of 57 genes; data as in A

and B). **D.** snoRNA genes with no RAPID signal (13 out of 57 genes; data as in A and B). Classifications were done twice independently by visual inspection of the tracks.

Figure S3. RAPID using sorted embryonic blastomeres

A. Embryonic blastomeres from a strain expressing constitutively Dam constructs (either fused to GFP or RPB-6) are sorted based on the expression of fluorescent markers using fluorescence-activated cell sorting. For each construct and each tissue, 1'000 cells are pooled before performing DamID. **B.** Venn diagram showing overlap between RAPID footprinted genes (FDR > 0.05). **C, D.** Individual profiles for genes specific for the different tissues tested (intestine, muscle and Y cell).

Figure S4. Pearson correlation coefficient between RAPID libraries at the single gene level resolution for the different tissues tested.

A. Correlation of RAPID footprinting signal between replicates performed in different tissues in embryonic blastomeres sorted using fluorescent markers. **B.** Correlation of RAPID footprinting signal between replicates performed in different tissues using Cre-mediated recombination for tissue-specific expression of the Dam fusions.

Figure S5. RAPID profile of candidate genes with XXX-specific expression.

RAPID footprinting of candidate uncharacterized genes expressed in a tissue-specific manner in XXX cells but not in muscle, intestine and enriched worm-wide are shown. Candidate XXX neuronal genes are ordered according to the RAPID footprinting level.

Supplementary information

Supplementary Table 1

Worm strains collection

Strain name	Source	Genotype
BN195	Towbin 2012	*bqSi195[hsp-16.41p:: dam::myc::lmn-1); unc-119(+)] II*
BN196	Towbin 2012	*bqSi196[hsp-16.41p::gfp::myc::dam 3'UTR; unc-119(+)] II*
IS3675	This study	*fpSi2[hsp-16.2p::lox::degron::dam::rpb-6::unc-54 3'UTR; unc-119(+)] II*
MS438	CGC	*Irls25[elt-2p::nls::gfp::lacz; rol-6(su1006)] V*
PD4251	CGC	*ccIs4251[myo-3p::gfp::lacz::nls;myo-3p::mito gfp; dpy-20(+)] I*
IS2922	This study	*fpIs76[egl-5p(6.5kb)::Δpes-10::mcherry; Bluescript] I* *fpIs92[hlh-16p::GFP::hlh-16(exon1)::hlh-16 3'UTR;pRF4]*
IS3467	This study	*fpIs76[egl-5p(6.5kb)::Δpes-10::mcherry; Bluescript] I* *fpIs92[hlh-16p::GFP::hlh-16(exon 1))::hlh-163'UTR;pRF4]* *bqSi196[hsp-16.41p::gfp::myc::dam; unc-119(+)] II*
IS3685	This study	*fpIs76[egl-5p(6.5kb)::Δpes-10::mcherry; Bluescript] I* *fpIs92[hlh-16p::GFP::hlh-16(exon 1))::hlh-163'UTR;pRF4]* *fpSi2[hsp-16.2p::lox::degron::dam::rpb-6::unc-54 3'UTR; unc-119(+)] II*
IS3651	This study	*ccIs4251[myo-3p::gfp::lacz::nls;myo-3p::mito gfp; dpy-20(+)] I* *bqSi196[hsp-16.41p::gfp::myc::dam; unc-119(+)] II*
IS3684	This study	*ccIs4251[myo-3p::gfp::lacz::nls;myo-3p::mito gfp; dpy-20(+)] I* *fpSi2[hsp-16.2p::lox::degron::dam::rpb-6::unc-54 3'UTR; unc-119(+)] II*

IS3653	This study	*bqSi196[hsp-16.41p::gfp::myc::dam; unc-119(+)] II* *iirIs25[elt-2p::nls::GFP::lacZ + rol-6(su1006)] V*
IS3687	This study	*fpSi2[hsp-16.2::lox::degron::dam::rpb-6::unc-54 3'UTR; unc-119(+)] II* *irIs25[elt-2p::nls::gfp::lacZ + rol-6(su1006)] V*
SV1439	CGC	*heSi142[elt-2p::elg-13nls::Cre::tbb-2 3'UTR] X*
SV1461	CGC	*heSi148[myo-3p::elg-13nls::Cre::tbb-2 3'UTR] X*
DAG827	This study	*domSi827[sdf-9p::Cre::tbb-2 3'UTR; unc-119(+)] X*
PMW641	This study	*ubsSi40[hsp-16.2::lox:mcherry::lox::degron::gfp::dam::unc-54 3'UTR; unc-119(+)] IV*
DAG958	This study	*domSi958[hsp-16.2p::lox::mCherry::lox::degron::dam::rpb-6::unc54 3'UTR; unc-119(+)] II*
IS3568	This study	*heSi142[elt-2p::elg-13nls::Cre::tbb-2 3'UTR] X;* *domSi958[unc-119(+)hsp-16.2p::lox::mCherry::lox::degron::dam::rpb-6::unc54 3'UTR] II*
PMW748	This study	*heSi148[myo-3p::elg-13nls::Cre::tbb-2 3'UTR] X ;* *domSi958[hsp-16.2p::lox::mCherry::lox::degron::dam::rpb-6::unc54 3'UTR; unc-119(+)] II*
DAG879	This study	*domSi827[sdf-9p::Cre::tbb-2 3'UTR; unc-119(+)] X* *ubsSi40[hsp-16.41::lox:mcherry::lox::degron::gfp::dam::unc-54 3'UTR; unc-119(+)] IV*
DAG976	This study	*heSi148[myo-3p::elg-13nls::Cre::tbb-2 3'UTR] ttTi14042 X* *domSi958[hsp-16.2p::lox::mCherry::lox::degron::dam::rpb-6::unc54 3'UTR; unc-119(+)] II*
DAG1042	This study	*domSi827[sdf-9p::Cre::tbb-2 3'UTR; unc-119(+)] X* *domSi958[hsp-16.2p::lox::mCherry::lox::degron::dam::rpb-6::unc54 3'UTR; unc-119(+)] II*

DAG1043	This study	*heSi142[elt-2p::elg-13nls::Cre::tbb-2 3'UTR] X ubsSi40[hsp-16.41::lox:mcherry::lox::degron::gfp::dam::unc-54 3'UTR; unc-119(+)] IV*
DAG1256-1257	This study	*domEx1256-1257[asic-1p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1258-1259	This study	*domEx1258-1259[dhs-17p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1260-1261	This study	*domEx1260-1261[mab-9p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1262-1263	This study	*domEx1262-1263[twk-39p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1264-1265	This study	*domEx1264-1265[lgc-36p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1266-1267	This study	*domEx1266-1267[F14H8.2p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1268-1269	This study	*domEx1268-1269[C06A1.3p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1270	This study	*domEx1270[asp-9p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1271-1272	This study	*domEx1271-1272[B0034.5p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1273-1274	This study	*domEx1273-1274[F52E1.5::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
DAG1275-1276	This study	*domEx1275-1276[T22E.6p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*

DAG1277-1278	This study	*domEx1277-1278[nlp-15p::mNeonGreen::unc-54 3' UTR, sdf-9p::egl-13NLS::wrmScarlet::unc-54 UTR, unc-122p::RFP]*
N2	CGC	Wild type Bristol N2

Supplementary Table 2

Plasmid collection

Plasmid name	Source	Plasmid information	Backbone
#372	This study	*hsp-16.41p::degron::dam::ama-1::unc-54 3'UTR*	pCFJ151
#509	This study	*hsp-16.2p::degron::dam::rpb-6::unc54 3'UTR*	pCFJ151
#417	This study	*hsp-16.2p::lox::mCherry::lox::degron::dam::ama-1::unc-54 3' UTR*	pCFJ151
#418	This study	*hsp-16.2p::lox::mCherry::lox::degron::gfp::dam::unc-54 3' UTR*	pCFJ151
#434	This study	*hsp-16.2p::lox::mCherry::lox::degron::dam::rbp-2::unc-54*	pCFJ151
pSJ4646/ #503	This study	*hsp-16.2p::lox::mCherry::lox::degron::dam::rpb-6::unc-54 3'UTR*	pCFJ151
pSR32	Sander Van den Heuvel Lab	*pie-1p::Cre*	pCFJ355
dg9	Miyabayashi 1999	*unc-122p::rfp*	
dg353	Hostettler 2017	*mNeonGreen* Entry (slot2)	pDON221
dg651	Marques 2019	*egl-13nls::wrmScarlet* Entry (slot2)	pDON221
dg800	This study	*sdf-9p::Cre::tbb-2 3'UTR*	pCFJ355
dg801	This study	*sdf-9p* Entry (slot1)	pDONR-P4-P1R
dg802	This study	*asic-1p* Entry (slot1)	pDONR-P4-P1R

dg803	This study	*dhs-17p* Entry (slot1)	pDONR-P4-P1R
dg804	This study	*mab-9p* Entry (slot1)	pDONR-P4-P1R
dg805	This study	*twk-39p* Entry (slot1)	pDONR-P4-P1R
dg806	This study	*lgc-36p* Entry (slot1)	pDONR-P4-P1R
dg807	This study	*F14H8.2p* Entry (slot1)	pDONR-P4-P1R
dg808	This study	*C06A1.3p* Entry (slot1)	pDONR-P4-P1R
dg809	This study	*asp-9p* Entry (slot1)	pDONR-P4-P1R
dg810	This study	*B0034.5p* Entry (slot1)	pDONR-P4-P1R
dg811	This study	*F52E1.5p* Entry (slot1)	pDONR-P4-P1R
dg812	This study	*:T22E5.6p* Entry (slot1)	pDONR-P4-P1R
dg813	This study	*nlp-15p* Entry (slot1)	pDONR-P4-P1R
dg814	This study	*sdf-9p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg815	This study	*sdf-9p::egl-13NLS::wrmScarlet::unc-54 3' UTR*	pDEST-R4-P3
dg816	This study	*asic-1p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg817	This study	*dhs-17p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg818	This study	*mab-9p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3

dg819	This study	*twk-39p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg820	This study	*lgc-36p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg821	This study	*F14H8.2p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg822	This study	*C06A1.3p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg823	This study	*asp-9p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg824	This study	*B0034.5p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg825	This study	*F52E1.5p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg826	This study	*T22E5.6p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
dg827	This study	*nlp-15p::mNeonGreen::unc-54 3' UTR*	pDEST-R4-P3
pMH473	Gift from Marc Hammarlund	*unc-54 3' UTR* Entry (slot3)	pDONR- P2R-P3

Supplementary Table 3

Primers for cloning of promoters used for the transcriptional reporter analysis of XXX cell-transcribed candidate genes.

All primers start with Gateway cloning sequences, followed with the indicated sequence. (forward: `ggggacaactttgtatagaaaagtt`; reverse: `ggggactgcttttttgtacaaacttg`)

Gene name	Forward primer	Reverse primer	Size (bp)
sdf-9	*gtcgacttgtcaatgtcgc*	*ccttcattttgaaaataatatatctagtcttag*	3497
asic-1	*gacacacttgtacgggatacctt*	*tttggtggcctgaaatttgatcaa*	1992
dhs-17	*gataacacattgaccctctccac*	*ttctacaaattacagacgagacaactg*	1969
mab-9	*gccatggaacccgaatttttgcat*	*cttatggaataagaagctccggga*	2026
twk-39	*ttgtcgggtttgtcagtttcct*	*tttcagtcgtctatttgactgcca*	2006
lgc-36	*gcatcaaggaactgctttcaca*	*tggaaattcgatgaagcatttgtgtg*	560
F14H8.2	*agagttcaaaaaggtgttcccaa*	*agagttcaaaaaggtgttcccaa*	1779
C06A1.3	*ttgtctggcgtgtatttggtac*	*atgaagacgttgctaaatcctctttc*	660
asp-9	*tgacctattttgaactgctg*	*tcagctcaactatcaaaatttaatcac*	1668
B0034.5	*taatgcgtgataatgatgagac*	*taatgcgtgataatgatgagac*	1992
F52E1.5	*tccaattttatgcgttgagt*	*ggcaggttatttaaacggt*	1580
T22E5.6	*tgcaagttaatttttcgttc*	*tgtgaaaagctgaaatacag*	2037
nlp-15	*tggtcaagtacataccaggggtatg*	*cgttatgttgtgtctctttcg*	2186

Supplementary Table 4 (excel sheet)

Averaged gene-level values for RNA polymerase signal (polii), GATC number and false discovery rate (FDR) for all blastomere libraries.

Supplementary Table 5 (excel sheet)

Transcribed genes analysis determined by RAPID. Genes for each tissue are listed.

Enriched and uniques genes, and Gene ontology attributes are tabulated in different sheets.

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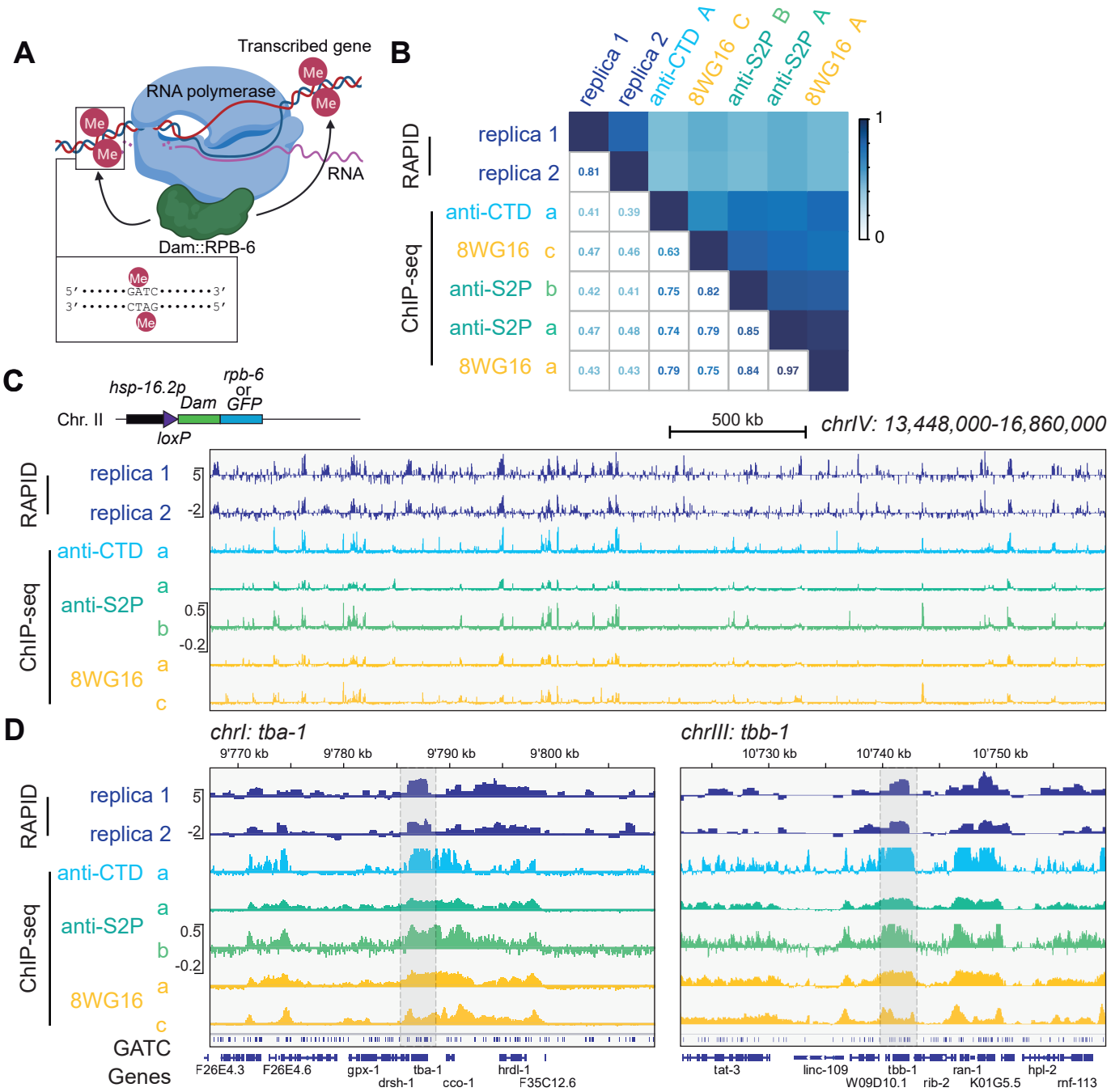
Figure 1


A
Transcribed gene
RNA polymerase
Me
RNA
Dam::RPB-6
5′ GATC 3′
3′ CTAG 5′
B
replica 1
replica 2
anti-CTD A
8WG16 C
anti-S2P B
anti-S2P A
8WG16 A
RAPID
ChIP-seq
0.81
0.41 0.39
0.47 0.46 0.63
0.42 0.41 0.75 0.82
0.47 0.48 0.74 0.79 0.85
0.43 0.43 0.79 0.75 0.84 0.97
1
0
C
hsp-16.2p
rpb-6 or GFP
Dam
Chr. II
loxP
500 kb
chrIV: 13,448,000-16,860,000
anti-S2P
8WG16
D
chrI: tba-1
chrIII: tbb-1
9'770 kb
9'780 kb
9'790 kb
9'800 kb
10'730 kb
10'740 kb
10'750 kb
GATC
Genes
F26E4.3
F26E4.6
gpx-1
tba-1
drsh-1
cco-1
hrdl-1
F35C12.6
tat-3
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tbb-1
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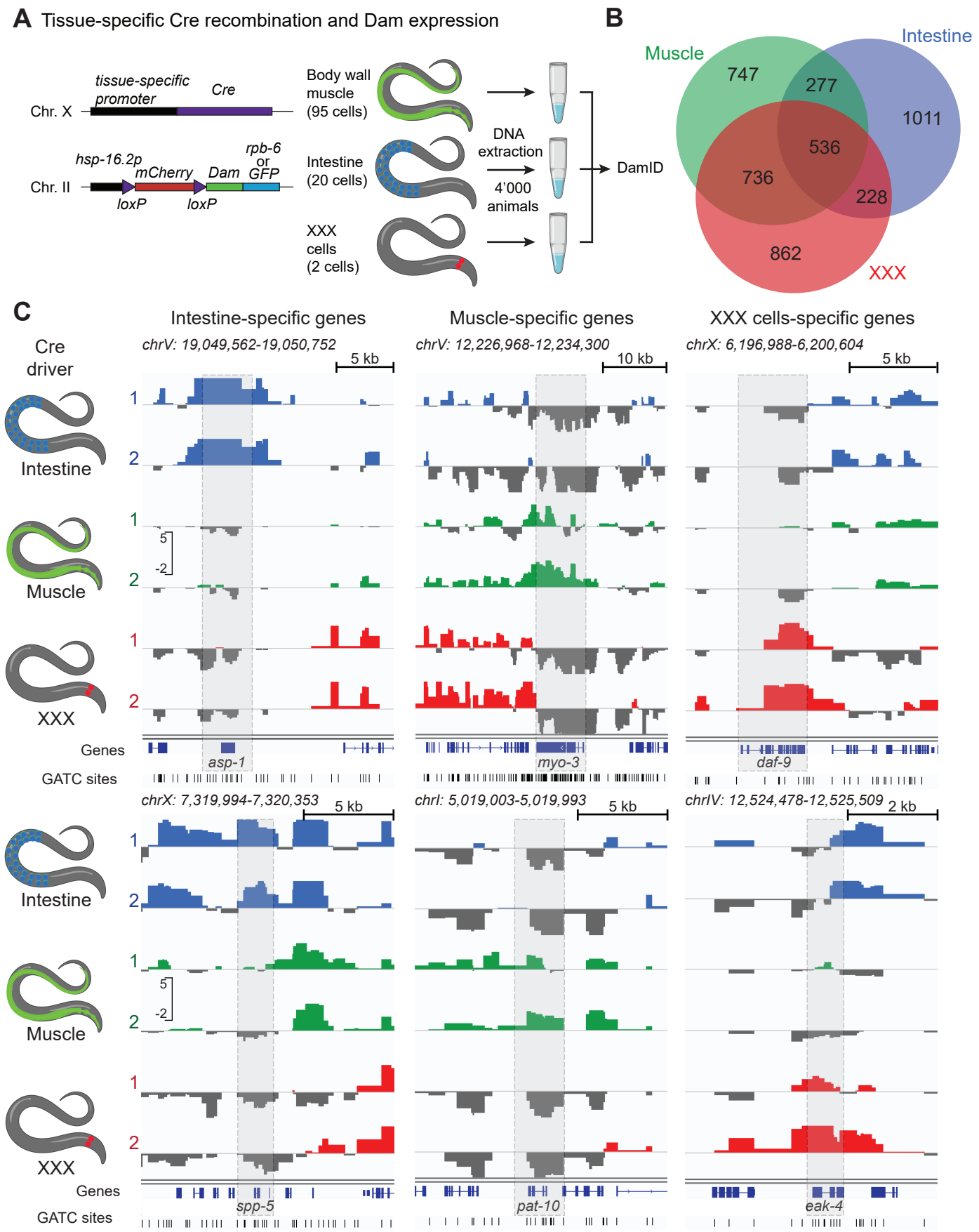
K01G5.5
hpl-2
rnf-113

Figure 2


A Tissue-specific Cre recombination and Dam expression
tissue-specific promoter
Cre
Chr. X
hsp-16.2p
mCherry
Dam
rpb-6 or GFP
Chr. II
loxP
loxP
Body wall muscle (95 cells)
Intestine (20 cells)
XXX cells (2 cells)
DNA extraction
4'000 animals
DamID
B
Muscle
Intestine
XXX
747
277
1011
536
736
228
862
C
Intestine-specific genes
Muscle-specific genes
XXX cells-specific genes
Cre driver
Intestine
Muscle
XXX
chrV: 19,049,562-19,050,752
5 kb
chrV: 12,226,968-12,234,300
10 kb
chrX: 6,196,988-6,200,604
5 kb
Genes
asp-1
myo-3
daf-9
GATC sites
chrX: 7,319,994-7,320,353
5 kb
chrI: 5,019,003-5,019,993
5 kb
chrIV: 12,524,478-12,525,509
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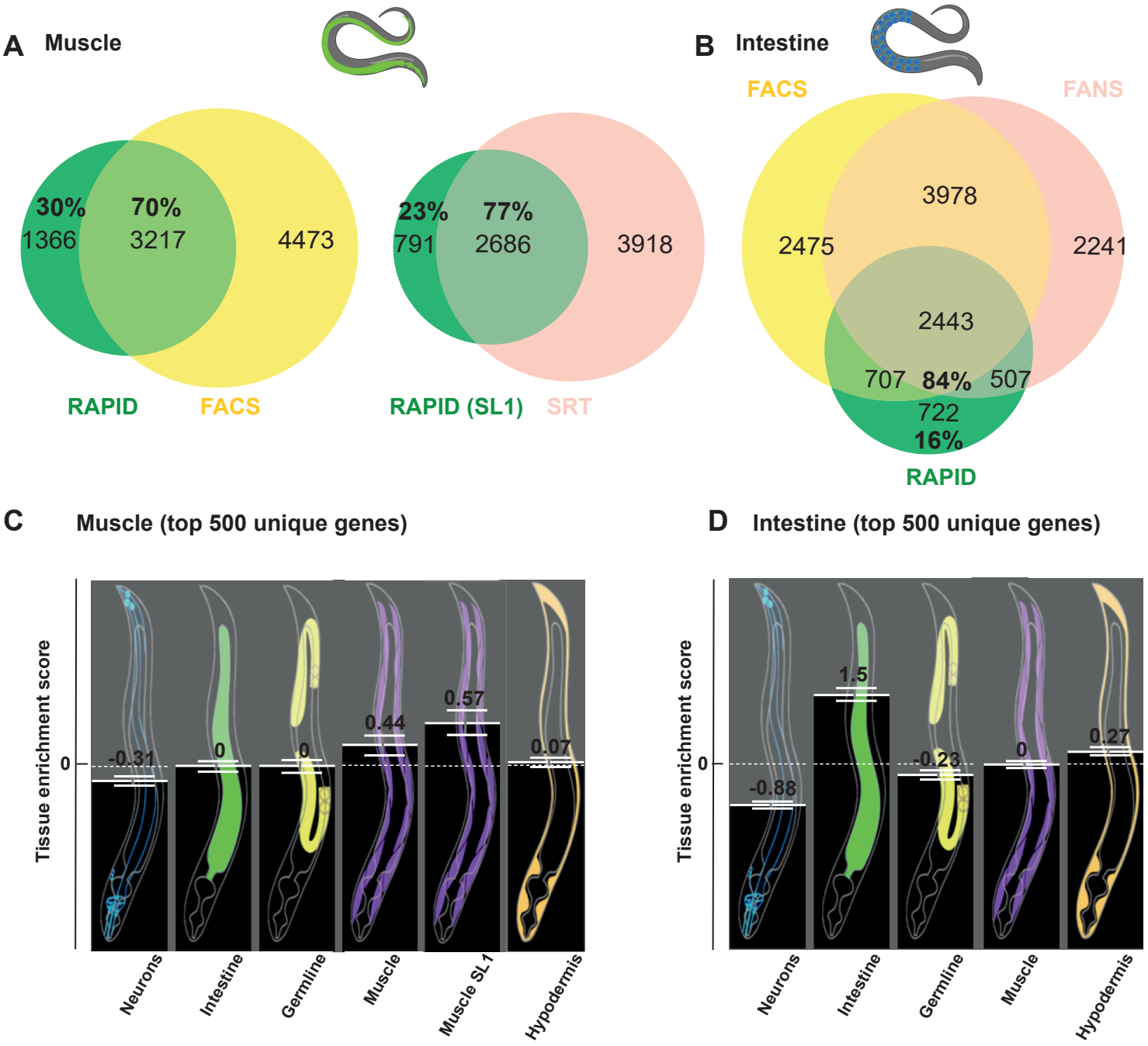
pat-10
eak-4

Figure 3


A
Muscle
30%
1366
70%
3217
4473
RAPID
FACS
23%
791
77%
2686
3918
RAPID (SL1)
SRT
B
Intestine
FACS
FANS
3978
2475
2241
2443
707
84%
507
722
16%
RAPID
C
Muscle (top 500 unique genes)
Tissue enrichment score
0
-0.31
0
0
0.44
0.57
0.07
Neurons
Intestine
Germline
Muscle
Muscle SL1
Hypodermis
D
Intestine (top 500 unique genes)
Tissue enrichment score
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1.5
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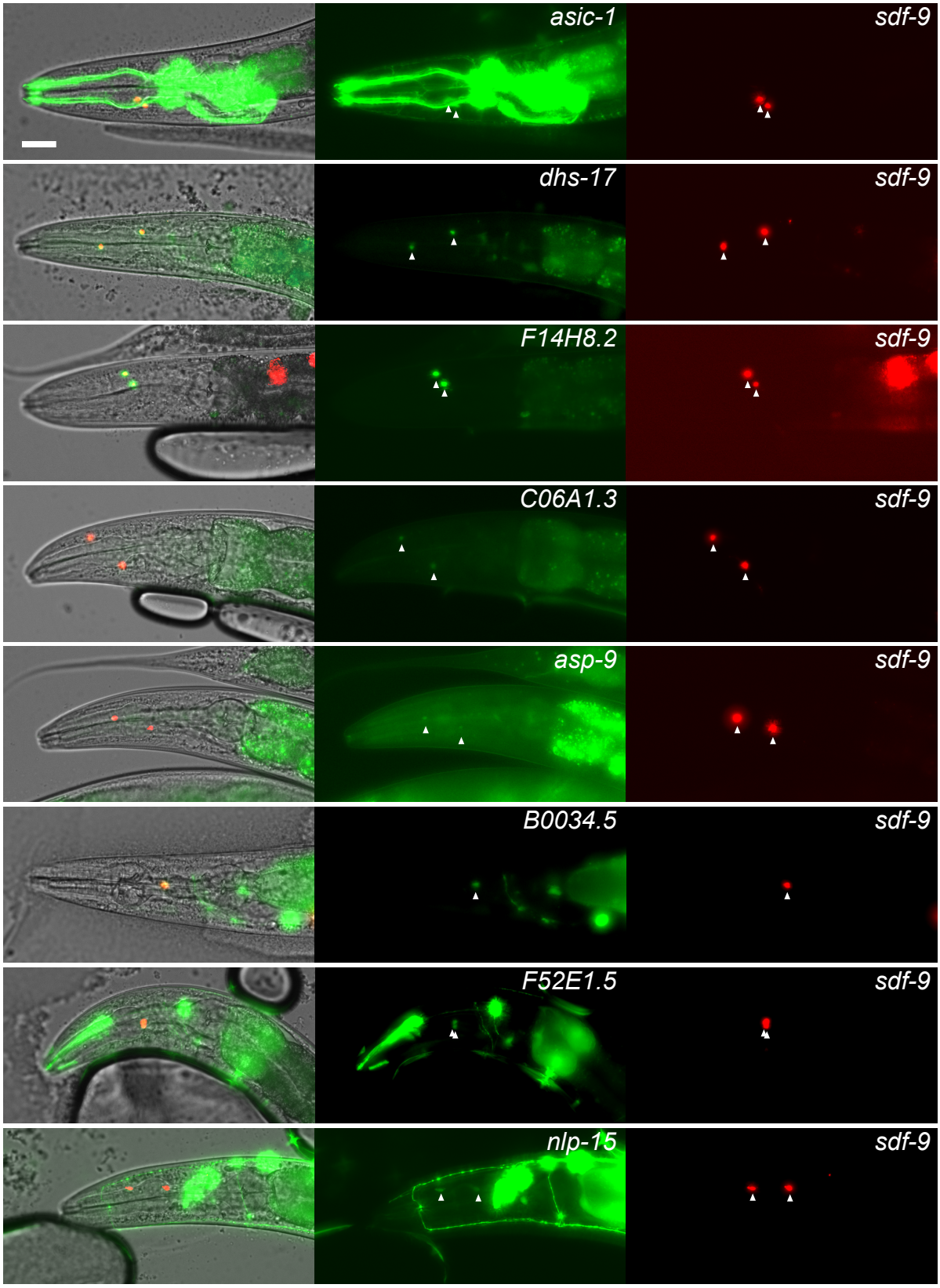
0.27
Neurons
Intestine
Germline
Muscle
Hypodermis

Figure 4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sdf-9
F14H8.2
sdf-9
C06A1.3
sdf-9
asp-9
sdf-9
B0034.5
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F52E1.5
sdf-9
nlp-15
sdf-9

Figure S1

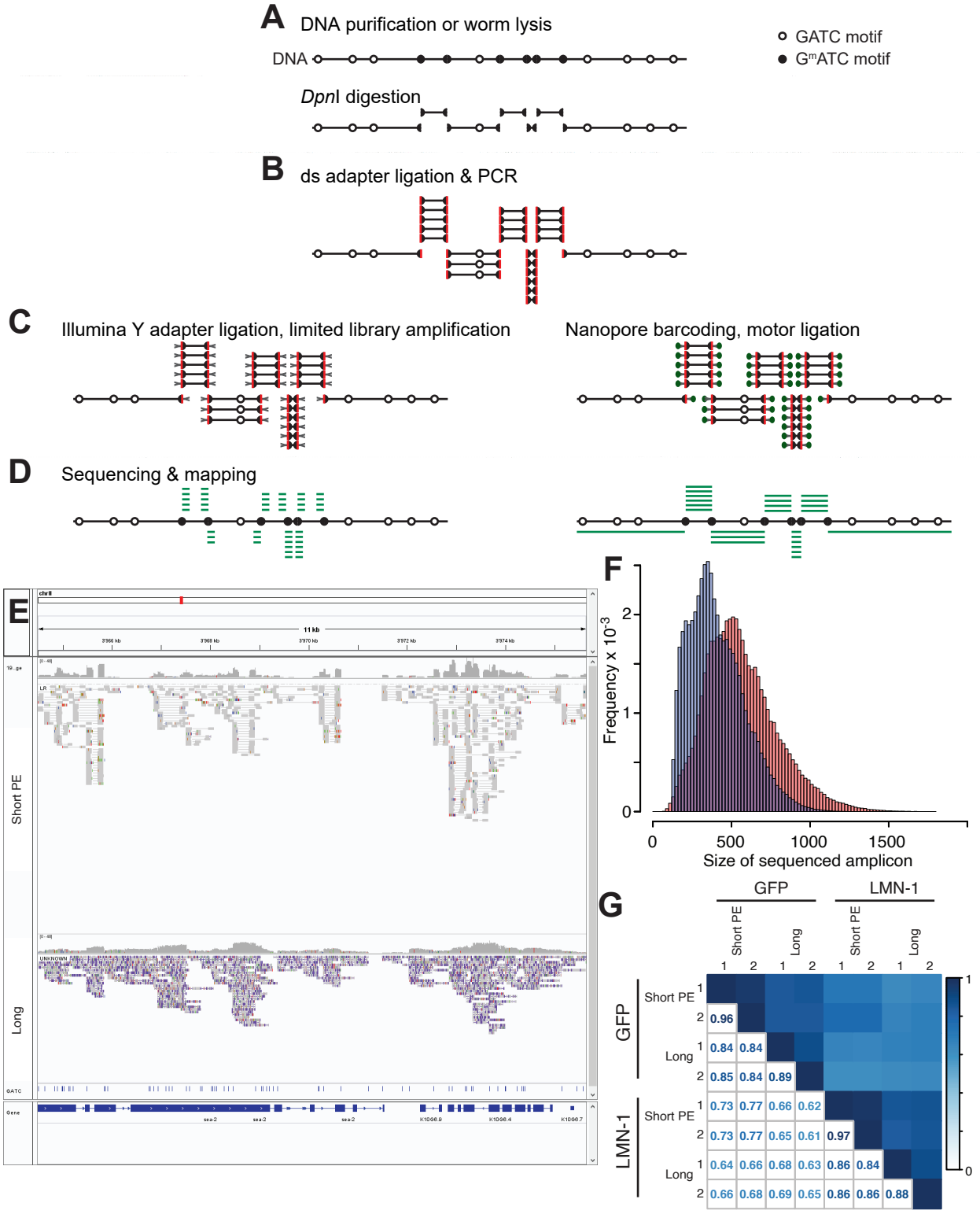
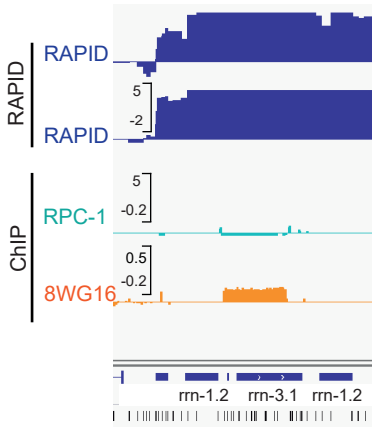
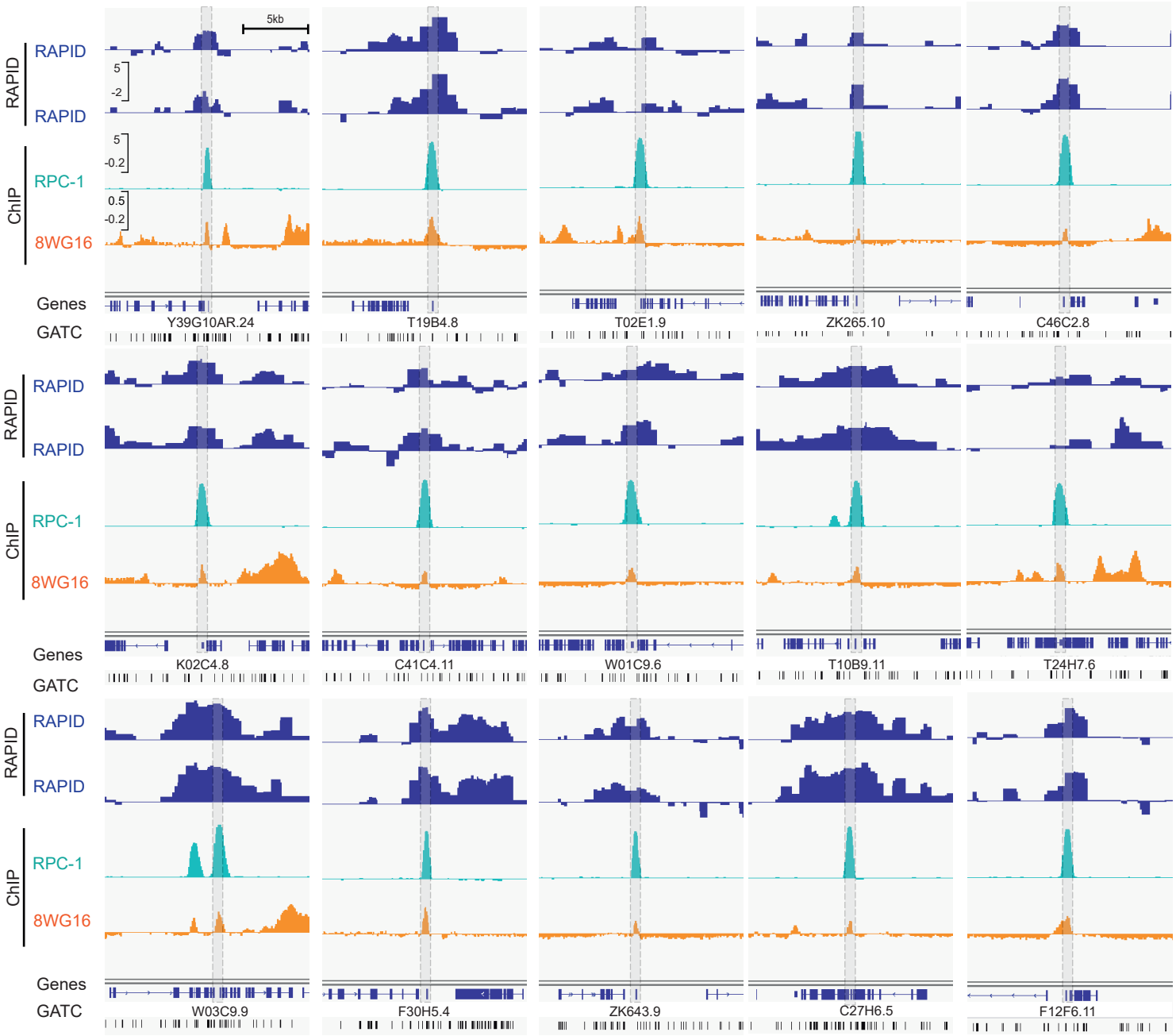

A
DNA purification or worm lysis
DNA
GATC motif
GmATC motif
DpnI digestion
B
ds adapter ligation & PCR
C
Illumina Y adapter ligation, limited library amplification
Nanopore barcoding, motor ligation
D
Sequencing & mapping
E
chrII
11 kb
Short PE
Long
GATC
Gene
F
Frequency x 10-3
Size of sequenced amplicon
G
GFP
LMN-1
Short PE
Long
0.96
0.84 0.84
0.85 0.84 0.89
0.73 0.77 0.66 0.62
0.73 0.77 0.65 0.61 0.97
0.64 0.66 0.68 0.63 0.86 0.84
0.66 0.68 0.69 0.65 0.86 0.86 0.88

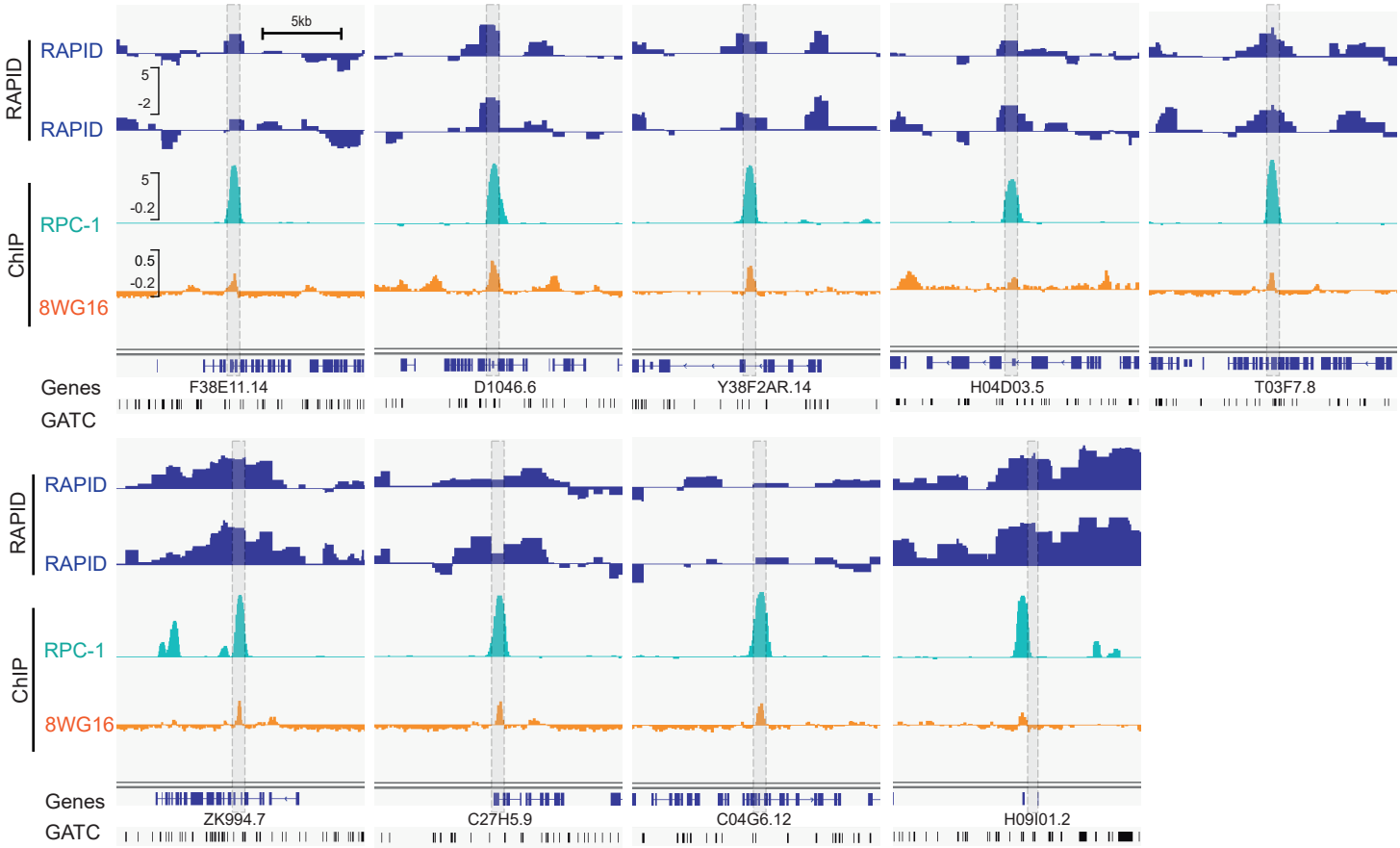
Figure S2

A RAPID signal at rDNA repeats

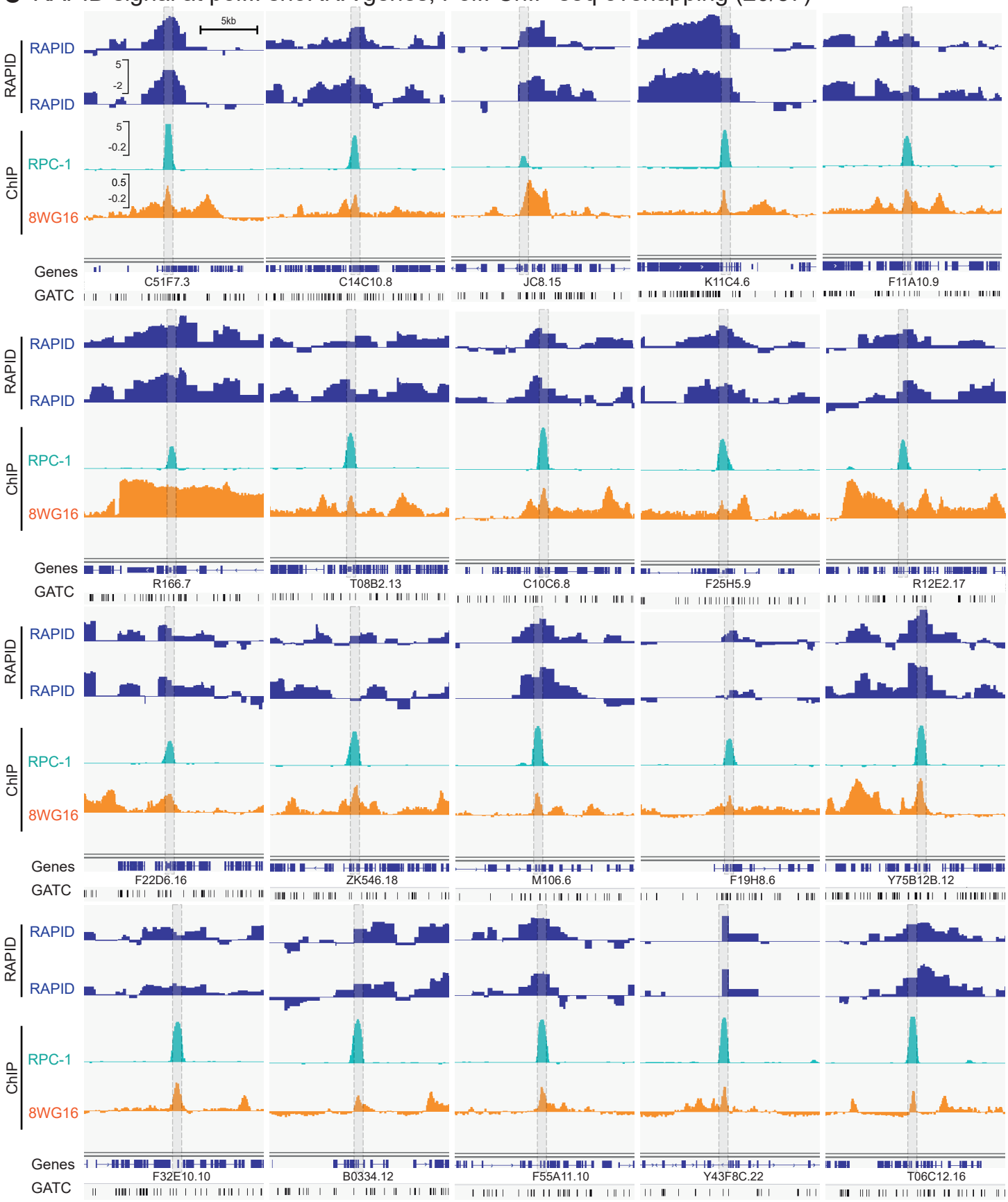


B RAPID signal at polIII snoRNA genes; no PolII overlapping (24/57)



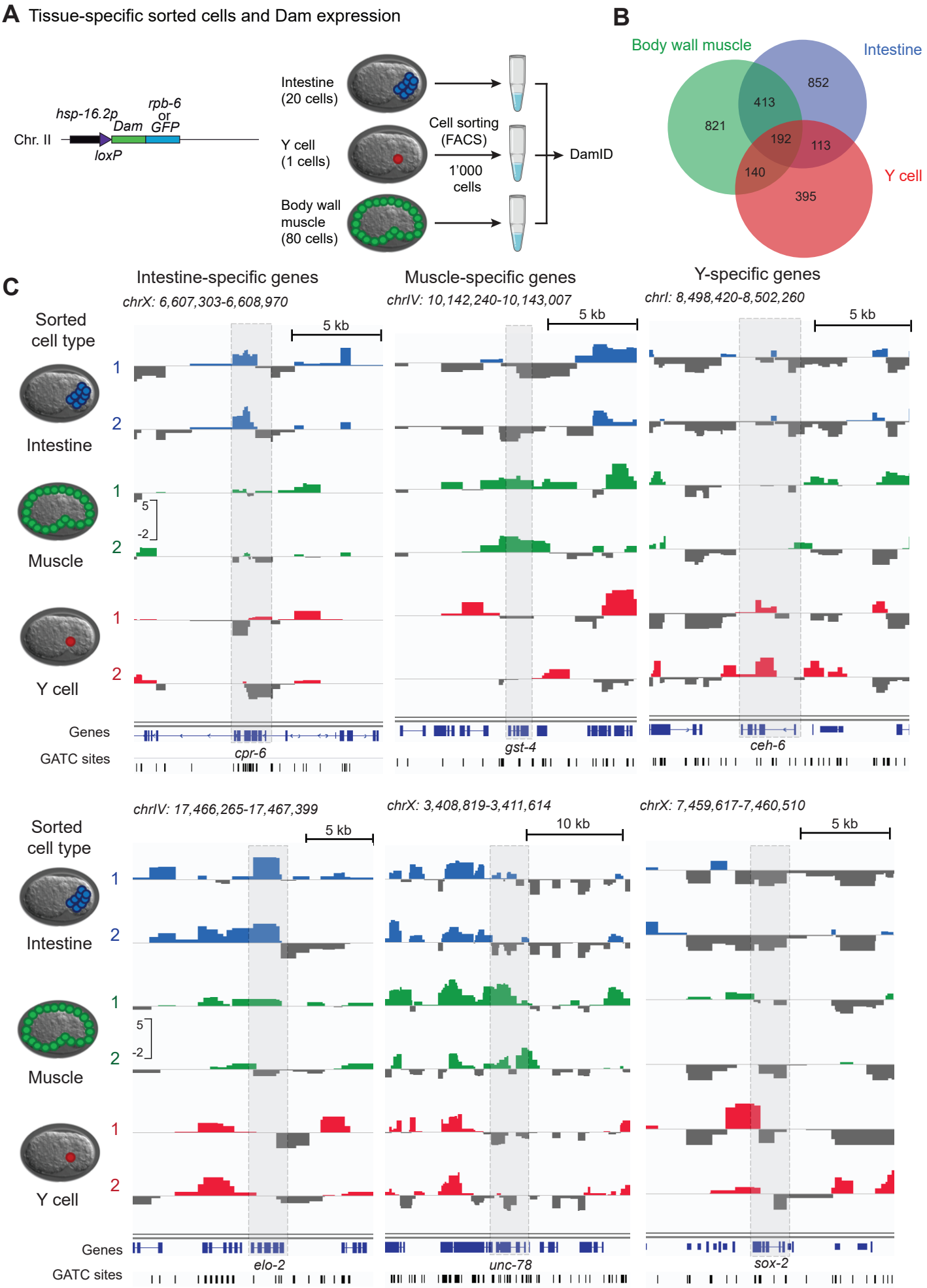

5kb
RAPID
RAPID
RAPID
5
-2
ChIP
RPC-1
5
-0.2
8WG16
0.5
-0.2
Genes
GATC
F38E11.14
D1046.6
Y38F2AR.14
H04D03.5
T03F7.8
RAPID
RAPID
RAPID
ChIP
RPC-1
8WG16
Genes
GATC
ZK994.7
C27H5.9
C04G6.12
H09I01.2

C RAPID signal at polIII snoRNA genes; PolII ChIP-seq overlapping (20/57)



D No RAPID signal (13/57)

Figure S3


A Tissue-specific sorted cells and Dam expression
Chr. II
hsp-16.2p
Dam
rpb-6
or
GFP
loxP
Intestine
(20 cells)
Y cell
(1 cells)
Body wall
muscle
(80 cells)
Cell sorting
(FACS)
1'000
cells
DamID
B
Body wall muscle
Intestine
Y cell
821
413
852
192
113
140
395
C
Intestine-specific genes
chrX: 6,607,303-6,608,970
Muscle-specific genes
chrIV: 10,142,240-10,143,007
Y-specific genes
chrI: 8,498,420-8,502,260
5 kb
Sorted
cell type
Intestine
Muscle
Y cell
Genes
GATC sites
cpr-6
gst-4
ceh-6
chrIV: 17,466,265-17,467,399
chrX: 3,408,819-3,411,614
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10 kb
elo-2
unc-78
sox-2

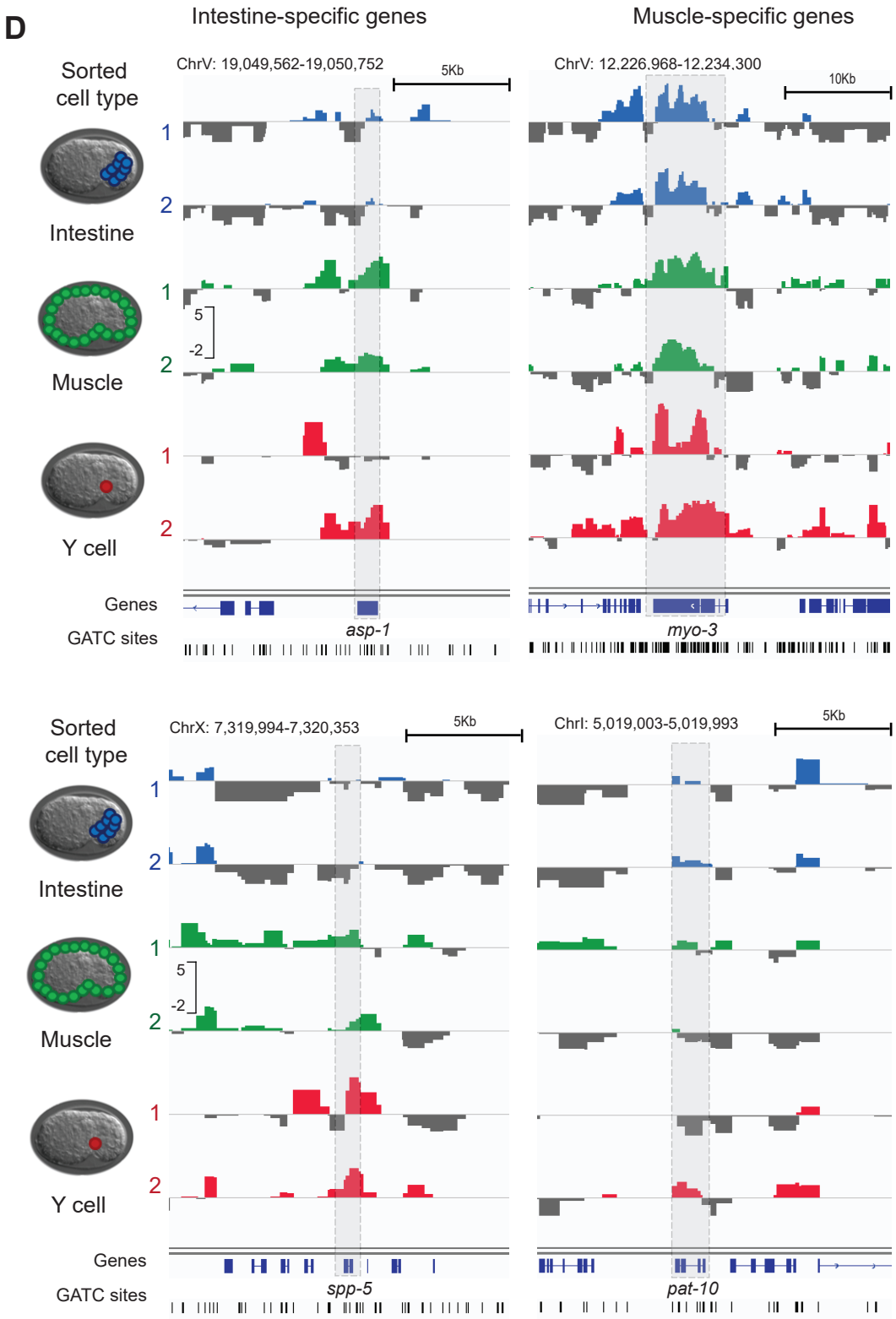

D
Intestine-specific genes
Muscle-specific genes
Sorted cell type
ChrV: 19,049,562-19,050,752
5Kb
ChrV: 12,226,968-12,234,300
10Kb
Intestine
Muscle
Y cell
1
2
5
-2
Genes
GATC sites
asp-1
myo-3
ChrX: 7,319,994-7,320,353
ChrI: 5,019,003-5,019,993
spp-5
pat-10

Figure S4

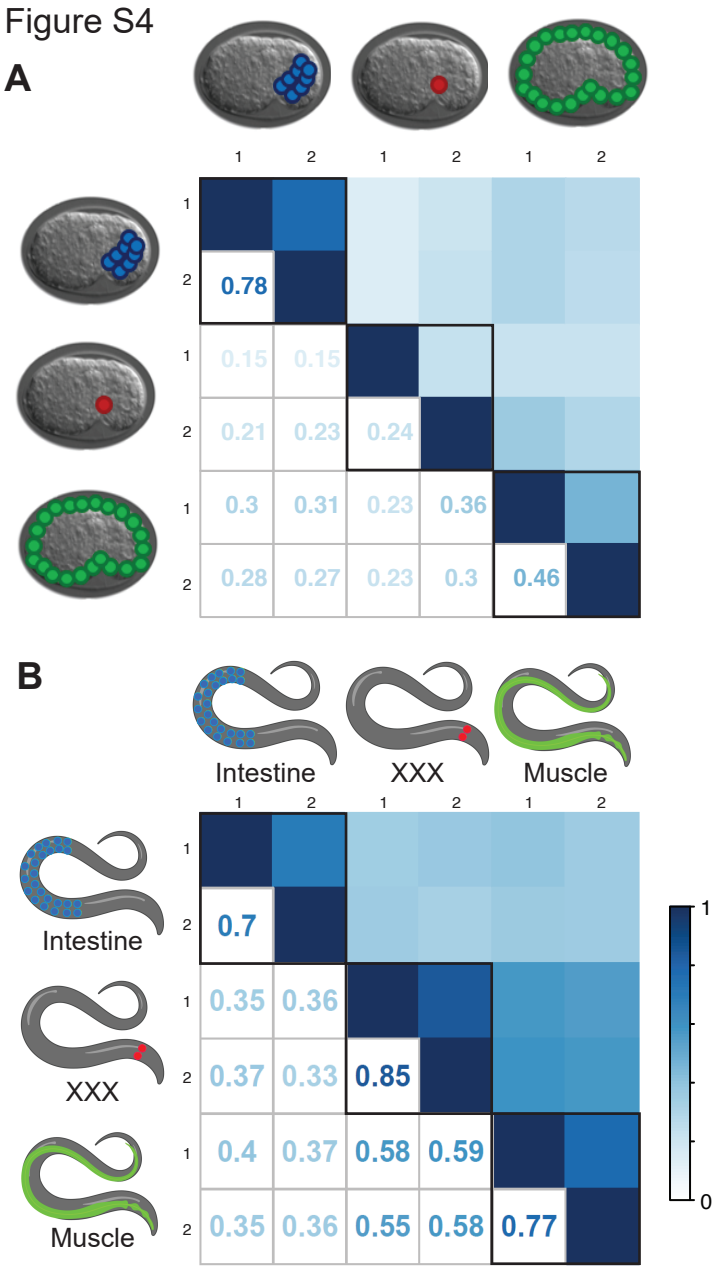
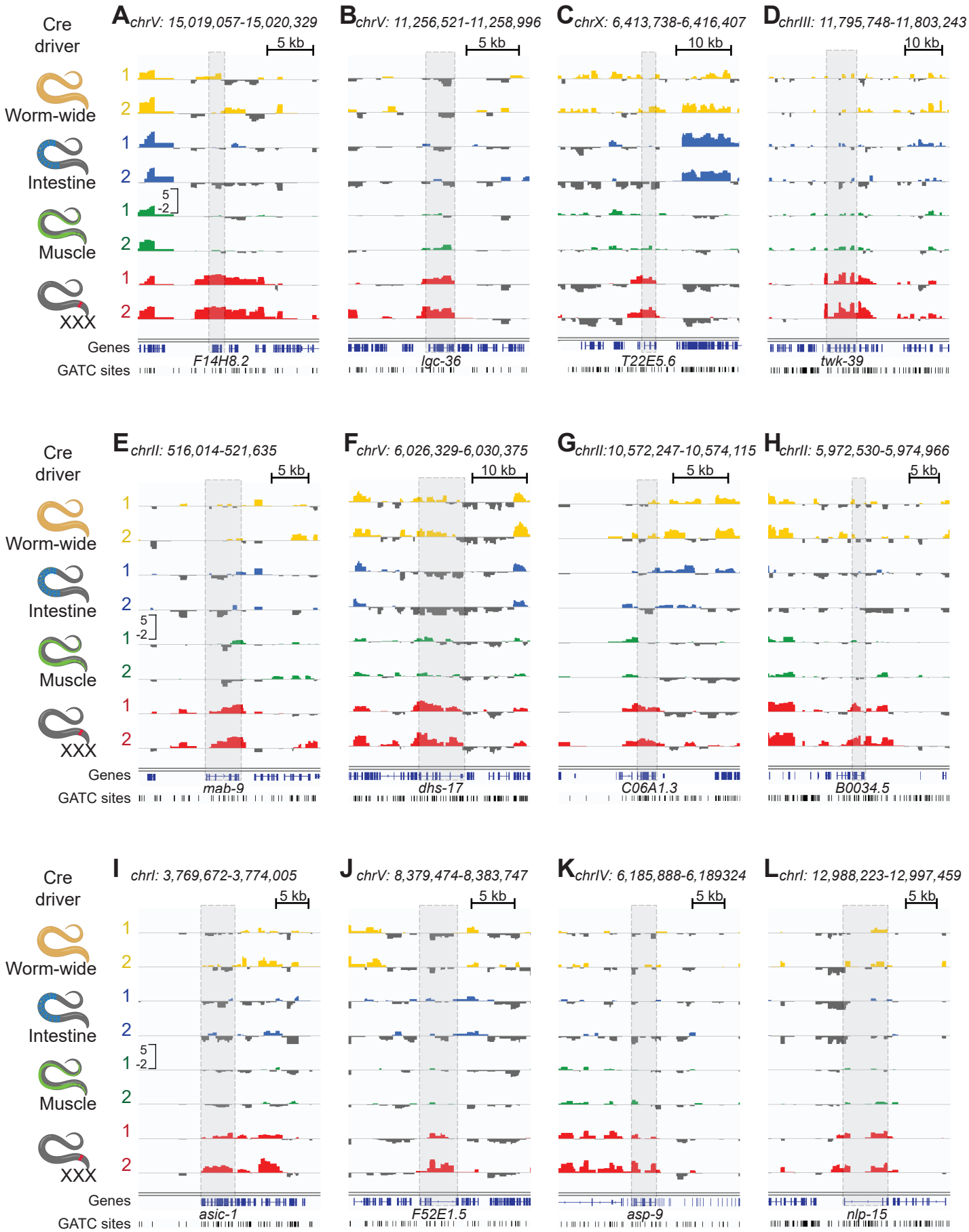

A
1 2 1 2 1 2
1 2 1 2 1 2
0.78
0.15 0.15
0.21 0.23 0.24
0.3 0.31 0.23 0.36
0.28 0.27 0.23 0.3 0.46
B
Intestine XXX Muscle
1 2 1 2 1 2
1 2 1 2 1 2
0.7
0.35 0.36
0.37 0.33 0.85
0.4 0.37 0.58 0.59
0.35 0.36 0.55 0.58 0.77
Intestine
XXX
Muscle
1
0

Figure S5


Cre driver
Worm-wide
Intestine
Muscle
XXX
Genes
GATC sites
A chrV: 15,019,057-15,020,329
5 kb
F14H8.2
B chrV: 11,256,521-11,258,996
5 kb
lqc-36
C chrX: 6,413,738-6,416,407
10 kb
T22E5.6
D chrIII: 11,795,748-11,803,243
10 kb
twk-39
E chrII: 516,014-521,635
5 kb
mab-9
F chrV: 6,026,329-6,030,375
10 kb
dhs-17
G chrII:10,572,247-10,574,115
5 kb
C06A1.3
H chrII: 5,972,530-5,974,966
5 kb
B0034.5
I chrI: 3,769,672-3,774,005
5 kb
asic-1
J chrV: 8,379,474-8,383,747
5 kb
F52E1.5
K chrIV: 6,185,888-6,189324
5 kb
asp-9
L chrI: 12,988,223-12,997,459
5 kb
nlp-15

Unique genes per tissue			Comm
Intestine	Muscle	Y cell	Intestine/Muscle
WBGene00000016	WBGene00000019	WBGene00000109	WBGene00000081
WBGene00000040	WBGene00000023	WBGene00000137	WBGene00000113
WBGene00000080	WBGene00000030	WBGene00000196	WBGene00000123
WBGene00000083	WBGene00000036	WBGene00000202	WBGene00000251
WBGene00000122	WBGene00000068	WBGene00000219	WBGene00000378
WBGene00000166	WBGene00000075	WBGene00000239	WBGene00000381
WBGene00000173	WBGene00000115	WBGene00000253	WBGene00000420
WBGene00000176	WBGene00000163	WBGene00000403	WBGene00000551
WBGene00000215	WBGene00000180	WBGene00000528	WBGene00000609
WBGene00000216	WBGene00000214	WBGene00000567	WBGene00000613
WBGene00000224	WBGene00000218	WBGene00000616	WBGene00000614
WBGene00000256	WBGene00000230	WBGene00000671	WBGene00000650
WBGene00000274	WBGene00000240	WBGene00000721	WBGene00000667
WBGene00000281	WBGene00000254	WBGene00000804	WBGene00000669
WBGene00000282	WBGene00000271	WBGene00000822	WBGene00000680
WBGene00000366	WBGene00000275	WBGene00000906	WBGene00000688
WBGene00000405	WBGene00000276	WBGene00000933	WBGene00000696
WBGene00000417	WBGene00000280	WBGene00000934	WBGene00000715
WBGene00000447	WBGene00000372	WBGene00000986	WBGene00000717
WBGene00000472	WBGene00000396	WBGene00000989	WBGene00000785
WBGene00000482	WBGene00000418	WBGene00001335	WBGene00000830
WBGene00000484	WBGene00000436	WBGene00001372	WBGene00000831
WBGene00000498	WBGene00000443	WBGene00001531	WBGene00000833
WBGene00000556	WBGene00000460	WBGene00001568	WBGene00000882
WBGene00000585	WBGene00000493	WBGene00001577	WBGene00000903
WBGene00000610	WBGene00000513	WBGene00001596	WBGene00000967
WBGene00000670	WBGene00000531	WBGene00001748	WBGene00001007
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WBGene00000691	WBGene00000618	WBGene00002070	WBGene00001102
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WBGene00000702	WBGene00000659	WBGene00003021	WBGene00001259
WBGene00000705	WBGene00000666	WBGene00003055	WBGene00001397
WBGene00000710	WBGene00000685	WBGene00003072	WBGene00001455
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WBGene00000786	WBGene00000764	WBGene00003558	WBGene00001603
WBGene00000789	WBGene00000771	WBGene00003570	WBGene00001607
WBGene00000803	WBGene00000781	WBGene00003578	WBGene00001692
WBGene00000865	WBGene00000784	WBGene00003597	WBGene00001702
WBGene00000874	WBGene00000872	WBGene00003608	WBGene00001734
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WBGene00000889	WBGene00001016	WBGene00003625	WBGene00001829
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WBGene00303011
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on genes in two tissues		Common genes in three tissues
Intestine/ Y cell	Muscle/Y cell	intestine|Muscle|Y cell
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Supplementary table 5, Sheet 8. Candidate XXX-specific markers (275 genes). Pol II occ

		Mu		
		BC_09		
Primary identifier	Symbol	polii	gatc.num	FDR
WBGene00000020	abt-2	0.08027523	50	5.54E-01
WBGene00010275	acc-1	0.19170699	11	1.18E-01
WBGene00008581	acl-13	0.6259069	10	1.11E-03
WBGene00000056	acr-17	-0.01297431	24	4.24E+00
WBGene00000042	acr-2	0.2156443	13	7.05E-02
WBGene00000071	acy-4	0.11404672	18	2.50E-01
WBGene00000166	apt-9	0.2185015	10	9.65E-02
WBGene00018060	arrd-18	-0.15079743	12	8.44E+00
WBGene00020612	arrd-22	-0.11922489	13	6.78E+00
WBGene00022815	asic-1	-0.49357752	14	1.88E+03
WBGene00015700	asp-9	-0.08538026	12	3.66E+00
WBGene00015202	B0478.3	0.03968499	4	5.32E-01
WBGene00015211	B0496.2	0.17427241	7	1.98E-01
WBGene00000248	ben-1	0.24966708	10	6.86E-02
WBGene00022251	blos-2	0.28242957	2	1.94E-01
WBGene00015298	C01F1.3	-0.02303498	13	1.83E+00
WBGene00015465	C05C8.8	-0.06813195	9	1.94E+00
WBGene00007354	C06A1.3	-0.0101258	21	3.06E+00
WBGene00015507	C06A6.2	0.17037006	19	8.36E-02
WBGene00015544	C06E8.5	-0.34582962	13	1.49E+02
WBGene00043994	C07A9.12	-0.11554913	7	2.18E+00
WBGene00007512	C10C6.3	-0.03306434	7	1.10E+00
WBGene00007548	C13C4.4	0.13326474	5	3.02E-01
WBGene00015746	C13F10.7	0.09486472	6	3.85E-01
WBGene00015865	C16E9.1	-0.25865205	12	3.33E+01
WBGene00015935	C17H12.10	0.34946823	6	5.87E-02
WBGene00007663	C18B12.1	0.35858651	1	1.85E-01
WBGene00015953	C18B2.2	-0.06800691	16	5.11E+00
WBGene00044232	C18D11.7	0.14279909	12	2.00E-01
WBGene00016109	C25G6.4	0.36063096	4	8.81E-02
WBGene00007898	C33D9.3	-0.16375388	6	2.60E+00
WBGene00007941	C34F6.7	0.15693357	16	1.30E-01
WBGene00008096	C44H4.8	0.81238112	3	1.34E-02
WBGene00050919	C45G9.15	0.27026183	12	3.94E-02
WBGene00016679	C45G9.8	-0.19513949	6	3.28E+00
WBGene00016816	C50E3.5	-0.16797144	22	1.02E+02
WBGene00008257	C52A11.3	0.2888613	6	9.18E-02
WBGene00008285	C53D6.8	0.44194066	4	5.59E-02
WBGene00016970	C56E6.2	-0.13233656	126	3.24E+10
WBGene00016979	C56G2.4	0.06646962	13	5.39E-01
WBGene00016980	C56G2.5	-0.14769401	21	5.34E+01

WBGene00009260	calm-1	0.29998095	5	1.02E-01
WBGene00000409	cdk-8	0.08468813	9	4.17E-01
WBGene00000437	ceh-13	0.5849229	6	1.03E-02
WBGene00000474	cey-3	-0.35523374	10	5.18E+01
WBGene00000525	clc-4	0.1021597	4	3.75E-01
WBGene00000715	col-142	-0.45684741	10	1.58E+02
WBGene00000716	col-143	0.0808032	7	4.29E-01
WBGene00000728	col-155	0.22066783	5	1.71E-01
WBGene00022533	cutl-19	-0.11266555	9	3.04E+00
WBGene00017042	D2007.2	-0.08741214	12	3.76E+00
WBGene00000898	daf-2	0.02733915	86	4.43E+01
WBGene00000905	daf-9	-0.36922416	9	4.02E+01
WBGene00000936	dbl-1	0.36867659	9	2.39E-02
WBGene00016104	ddr-1	0.16445974	12	1.52E-01
WBGene00000980	dhs-17	0.17786032	32	2.52E-02
WBGene00010191	dmsr-1	0.27940204	8	6.98E-02
WBGene00017038	dmsr-4	0.15368612	15	1.46E-01
WBGene00008580	dsb-1	0.83996465	11	5.43E-05
WBGene00009955	eak-4	-0.49323542	11	3.95E+02
WBGene00001159	eff-1	0.44136383	11	6.12E-03
WBGene00009701	egg-3	0.03734406	14	8.38E-01
WBGene00011806	ekl-6	0.16800187	19	8.74E-02
WBGene00001249	elt-1	-0.03751507	20	4.84E+00
WBGene00004255	epac-1	0.13988246	16	1.72E-01
WBGene00044406	F02A9.7	0.04171379	2	4.85E-01
WBGene00008554	F07C6.3	0.20191319	7	1.58E-01
WBGene00017255	F08D12.12	0.52418874	18	1.49E-04
WBGene00017246	F08D12.2	0.05738464	5	4.94E-01
WBGene00017320	F09G8.5	-0.09311006	11	3.44E+00
WBGene00008833	F14H8.2	0.1734729	6	2.15E-01
WBGene00008834	F14H8.4	0.25642647	8	8.62E-02
WBGene00008835	F14H8.5	-0.66823994	6	1.08E+02
WBGene00044774	F16B3.3	0.45532247	7	1.93E-02
WBGene00008951	F19C6.2	0.01576671	8	7.84E-01
WBGene00008952	F19C6.3	0.31409663	12	2.26E-02
WBGene00008971	F20C5.6	-0.22408398	9	9.33E+00
WBGene00017674	F21F3.4	0.24818487	8	9.30E-02
WBGene00017724	F22F7.7	-0.06246933	21	9.08E+00
WBGene00017741	F23C8.13	-8.4805E-05	15	1.56E+00
WBGene00009125	F25H5.2	-0.11480063	5	1.51E+00
WBGene00009146	F26C11.1	-0.22009093	7	5.18E+00
WBGene00017854	F27C1.4	0.3174472	6	7.44E-02
WBGene00017894	F28B12.1	0.37031722	6	5.03E-02
WBGene00017919	F29B9.1	0.00196424	9	9.59E-01
WBGene00044482	F29B9.12	0.11692734	8	3.10E-01
WBGene00018038	F35C8.8	0.27174097	12	3.87E-02
WBGene00009503	F37A8.5	0.16318834	5	2.49E-01

WBGene00018175	F38B6.6	-0.1956318	20	1.12E+02
WBGene00044556	F38G1.3	-0.02006414	8	1.09E+00
WBGene00009575	F40F8.1	0.19873372	5	1.97E-01
WBGene00009722	F45D3.2	-0.0145434	5	7.89E-01
WBGene00018462	F45E1.1	0.21017028	9	1.18E-01
WBGene00018560	F47D12.3	0.60093331	2	5.74E-02
WBGene00018569	F47F2.1	0.13664712	30	9.72E-02
WBGene00018655	F49H12.4	0.42946043	4	5.99E-02
WBGene00009916	F52A8.3	0.51023284	5	2.61E-02
WBGene00044304	F52B10.3	0.02097176	21	1.60E+00
WBGene00018694	F52E1.5	-0.03825195	12	2.01E+00
WBGene00018710	F52G3.1	0.11882718	15	2.49E-01
WBGene00010143	F56A12.2	0.18054218	9	1.59E-01
WBGene00019012	F57C9.6	-0.01373114	12	1.47E+00
WBGene00008612	fbxa-103	-0.23453185	42	1.34E+05
WBGene00009862	fbxb-67	-0.79440366	7	6.02E+02
WBGene00008611	fbxb-68	-0.50334345	4	1.11E+01
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WBGene00044686	flp-28	0.41119711	4	6.64E-02
WBGene00001494	frm-8	0.03348699	30	1.90E+00
WBGene00020023	frpr-16	-0.01917981	2	6.12E-01
WBGene00001512	gab-1	0.09348794	12	3.75E-01
WBGene00001519	gar-3	0.13925768	40	5.65E-02
WBGene00021528	gbb-1	0.06487154	19	6.20E-01
WBGene00022694	gcna-1	0.08151627	8	4.29E-01
WBGene00009387	glb-15	0.31236961	3	1.41E-01
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WBGene00020279	glb-25	0.13992512	16	1.72E-01
WBGene00001627	gly-2	0.31525149	7	6.16E-02
WBGene00018798	gnrr-1	0.21291303	7	1.44E-01
WBGene00019167	H06I04.1	0.14169135	17	1.59E-01
WBGene00019170	H06I04.6	0.02767938	9	7.41E-01
WBGene00001820	ham-1	0.17506046	12	1.33E-01
WBGene00001838	hda-10	0.03265836	22	1.32E+00
WBGene00001972	hmg-1.2	0.34116615	5	7.83E-02
WBGene00001991	hot-6	-0.28286282	8	1.21E+01
WBGene00018215	igcm-1	0.00352799	15	1.48E+00
WBGene00008977	iglr-1	0.29029632	9	5.27E-02
WBGene00007979	imp-1	0.06987904	14	5.22E-01
WBGene00002151	irk-3	0.0242982	23	1.67E+00
WBGene00002176	jip-1	0.09987906	33	2.71E-01
WBGene00002177	jkk-1	0.15504375	11	1.82E-01
WBGene00019290	K02A2.5	0.27081574	5	1.24E-01

WBGene00019346	K02G10.5	-0.04089246	8	1.32E+00
WBGene00019370	K03H6.5	0.07702661	27	5.28E-01
WBGene00019480	K07C11.8	-0.06161506	7	1.40E+00
WBGene00044361	K09F6.11	-0.16601198	4	1.68E+00
WBGene00010770	K11D2.4	0.10120976	19	3.11E-01
WBGene00002182	kap-1	0.09280582	13	3.76E-01
WBGene00002210	kin-29	0.20370965	17	5.47E-02
WBGene00002225	klp-15	-0.09458917	16	7.88E+00
WBGene00002230	klp-20	-0.01719263	33	1.08E+01
WBGene00015742	kxd-1	0.26222779	4	1.53E-01
WBGene00018523	lact-1	0.52410659	4	3.53E-02
WBGene00006505	lagr-1	0.03293154	19	1.14E+00
WBGene00002262	ldh-1	0.56355098	11	1.44E-03
WBGene00008551	lgc-36	-0.00074513	11	1.15E+00
WBGene00013914	lgc-37	0.0979621	24	3.15E-01
WBGene00017389	lgc-38	-0.00720445	22	3.13E+00
WBGene00017580	lgc-4	0.13422993	16	1.88E-01
WBGene00008022	lgc-41	0.0651728	16	5.81E-01
WBGene00003034	lin-49	-0.01933719	18	2.79E+00
WBGene00003047	lis-1	0.07657162	16	4.83E-01
WBGene00011454	lron-14	0.2180619	22	2.38E-02
WBGene00010806	M01E5.3	0.04434793	14	7.57E-01
WBGene00019754	M03E7.2	0.0284313	5	5.97E-01
WBGene00019761	M03F8.1	0.08845886	11	4.01E-01
WBGene00010849	M04B2.7	0.03819609	31	1.73E+00
WBGene00010886	M7.10	0.3065601	4	1.19E-01
WBGene00003111	mab-20	0.16860735	21	7.47E-02
WBGene00019296	mcu-1	0.03516318	9	6.87E-01
WBGene00003175	mec-12	-0.01907728	9	1.19E+00
WBGene00003166	mec-2	0.0405616	51	3.69E+00
WBGene00003237	mif-4	0.20261609	3	2.37E-01
WBGene00003245	mig-13	0.29724495	9	4.91E-02
WBGene00003397	mom-5	0.61088955	14	2.02E-04
WBGene00003509	mxl-1	-0.24316633	5	3.48E+00
WBGene00003735	nhx-8	-0.04115861	18	4.14E+00
WBGene00003753	nlp-15	0.03598875	18	1.02E+00
WBGene00006864	npr-16	-0.00548641	22	3.02E+00
WBGene00016842	npr-35	0.21478284	10	1.01E-01
WBGene00007635	npr-4	-0.01596946	36	1.37E+01
WBGene00021983	npr-5	0.22890799	10	8.61E-02
WBGene00008664	nubp-1	0.19966885	5	1.96E-01
WBGene00023520	oig-5	0.19616543	14	8.34E-02
WBGene00011482	pigk-1	0.50435695	5	2.71E-02
WBGene00018756	plpp-1.1	0.02587418	22	1.53E+00
WBGene00004197	prx-12	0.42452122	4	6.16E-02
WBGene00004205	psr-1	0.07295509	8	4.64E-01
WBGene00004121	ptrn-1	0.07403968	14	4.92E-01

WBGene00019906	R05G9R.1	-0.37089333	26	4.25E+04
WBGene00011101	R07D5.2	0.15774509	22	8.78E-02
WBGene00011217	R10E11.5	0.2152871	11	8.91E-02
WBGene00020058	R13D11.4	-0.19436042	14	2.43E+01
WBGene00003803	rae-1	0.19893293	15	7.25E-02
WBGene00004360	rib-1	0.39253318	21	7.12E-04
WBGene00004368	ric-19	-0.2518098	9	1.23E+01
WBGene00004370	rig-3	-0.16502398	17	3.11E+01
WBGene00007860	rilp-1	0.00655752	22	2.33E+00
WBGene00019712	rmh-1	-0.40122313	24	3.82E+04
WBGene00015437	scrm-3	-0.33852197	4	4.42E+00
WBGene00008819	shw-1	0.04958696	36	1.46E+00
WBGene00004831	slo-2	0.06666916	25	6.67E-01
WBGene00009654	sly-1	0.06999798	28	6.44E-01
WBGene00004880	smg-2	0.07934033	42	5.49E-01
WBGene00004893	sms-2	0.32298485	11	2.49E-02
WBGene00004913	snn-1	0.05382643	21	8.11E-01
WBGene00004928	soc-1	-0.03399123	12	1.90E+00
WBGene00013603	soem-1	0.15610196	5	2.60E-01
WBGene00007027	ssl-1	0.10693794	63	1.26E-01
WBGene00017464	sulp-2	-0.14769011	9	4.33E+00
WBGene00119203	T04A8.18	-0.43088894	17	3.02E+03
WBGene00271414	T05A7.12	-0.55931056	5	2.71E+01
WBGene00011484	T05E11.8	0.51301358	8	8.19E-03
WBGene00011512	T05H10.8	0.03209322	8	6.75E-01
WBGene00020294	T06F4.1	0.05296344	29	1.05E+00
WBGene00077607	T10C6.16	-0.67664153	17	2.07E+05
WBGene00011689	T10C6.7	0.03763274	14	8.35E-01
WBGene00011709	T11F9.1	0.161421	6	2.35E-01
WBGene00011795	T16A9.5	0.41940931	5	4.71E-02
WBGene00020565	T19C3.7	0.04420434	3	4.99E-01
WBGene00020692	T22E5.6	0.01629297	4	6.06E-01
WBGene00011958	T23G4.2	0.36054384	7	4.24E-02
WBGene00012034	T26C5.4	0.40857999	7	2.85E-02
WBGene00020854	T27C4.1	0.23498402	9	9.19E-02
WBGene00020861	T27E4.1	0.36235112	4	8.73E-02
WBGene00006384	taf-3	-0.02837307	33	1.54E+01
WBGene00013289	tag-273	0.13135478	39	7.92E-02
WBGene00006459	tag-89	0.23268031	12	6.37E-02
WBGene00018639	tbc-16	-0.2701788	11	2.81E+01
WBGene00008018	tbc-8	0.24149089	21	1.64E-02
WBGene00015704	tiam-1	0.02052962	28	2.45E+00
WBGene00006570	tig-2	0.23638257	12	6.07E-02
WBGene00020490	tmc-1	0.12977948	38	8.72E-02
WBGene00006587	tnt-2	0.59034543	11	1.05E-03
WBGene00019013	tofu-4	-0.08716171	9	2.35E+00
WBGene00008366	tpra-1	0.18101918	19	6.83E-02

WBGene00000208	trip-4	-0.0520025	35	4.14E+01
WBGene00020339	ttr-59	0.44639639	3	7.51E-02
WBGene00018187	twf-2	0.48294896	12	2.62E-03
WBGene00006681	twk-29	0.03339709	13	8.46E-01
WBGene00006690	twk-39	0.18332175	19	6.53E-02
WBGene00006475	tyra-3	0.08190801	13	4.37E-01
WBGene00006726	ubl-5	0.19143774	8	1.56E-01
WBGene00019232	ugt-13	-0.53726966	17	1.88E+04
WBGene00006757	unc-18	-0.04074429	9	1.47E+00
WBGene00006763	unc-26	-0.00353803	33	7.03E+00
WBGene00006743	unc-3	-0.01992262	23	4.54E+00
WBGene00006745	unc-5	0.0535281	61	2.68E+00
WBGene00006790	unc-55	-0.02421596	14	2.05E+00
WBGene00006791	unc-57	0.22162373	9	1.05E-01
WBGene00011553	unc-58	0.60249591	5	1.43E-02
WBGene00006875	vab-9	0.60771861	5	1.39E-02
WBGene00012243	W04D2.4	-0.13547181	20	3.39E+01
WBGene00012274	W05B5.1	0.15865692	16	1.27E-01
WBGene00012282	W05E10.5	0.00623809	8	8.55E-01
WBGene00011061	wago-1	-0.56818639	18	5.75E+04
WBGene00044441	Y119C1B.11	-0.30928479	2	1.85E+00
WBGene00022469	Y119C1B.3	0.19767351	9	1.34E-01
WBGene00012444	Y15E3A.5	0.61876768	5	1.29E-02
WBGene00012578	Y37H9A.3	0.08354356	28	4.46E-01
WBGene00012598	Y38E10A.20	-0.08991454	28	4.85E+01
WBGene00012662	Y39A1C.1	0.48028313	6	2.23E-02
WBGene00021452	Y39F10A.1	0.39447916	4	7.29E-02
WBGene00021511	Y41D4B.1	0.06496907	8	4.99E-01
WBGene00021524	Y41D4B.24	0.13206217	14	2.12E-01
WBGene00021591	Y46D2A.3	0.01949138	4	5.95E-01
WBGene00021614	Y47A7.2	-0.17104995	8	4.35E+00
WBGene00013194	Y54E2A.9	-0.21908577	6	3.91E+00
WBGene00013322	Y57G11C.32	0.02052184	19	1.44E+00
WBGene00013323	Y57G11C.33	0.66618576	5	9.49E-03
WBGene00022015	Y61A9LA.3	0.01791824	35	4.04E+00
WBGene00012387	Y6B3B.1	0.00102023	130	1.03E+04
WBGene00044581	Y81B9A.4	0.0618216	5	4.80E-01
WBGene00022530	ZC155.2	0.17449749	10	1.56E-01
WBGene00022611	ZC449.1	0.23456448	8	1.05E-01
WBGene00022614	ZC449.4	0.56325923	4	2.83E-02
WBGene00022632	ZC581.2	-0.67010861	13	1.24E+04
WBGene00022633	ZC581.3	0.07215085	15	5.12E-01
WBGene00014061	ZK673.5	0.74952523	2	3.26E-02
WBGene00022823	ZK813.4	0.30976335	7	6.45E-02
WBGene00014100	ZK849.1	0.5618728	11	1.47E-03
WBGene00013966	ztf-9	0.79229778	8	6.32E-04

upancy and FDR are listed.

scle			Intestine				
BC_12			BC_05			BC_11	
polii	gatc.num	FDR	polii	gatc.num	FDR	polii	gatc.num
0.08858172	50	9.98E-02	0.0840969	50	1.69E+00	-0.04878917	50
0.21397783	11	6.61E-02	-0.11282927	11	2.84E+00	-0.29893156	11
0.15587079	10	1.47E-01	-0.18916232	10	4.25E+00	-0.85812231	10
-0.02891716	24	3.44E+00	-0.23021295	24	8.69E+01	-0.90201895	24
0.26193171	13	2.56E-02	0.31532611	13	9.25E-02	-0.21072134	13
0.07500983	18	3.19E-01	0.53018251	18	4.91E-03	-0.26329854	18
0.41770323	10	7.69E-03	-0.57723976	10	6.39E+01	-0.5299641	10
-0.59302805	12	2.15E+03	-0.12862718	12	3.68E+00	-0.23974508	12
-0.43291585	13	4.14E+02	-0.53561909	13	1.41E+02	-0.96370666	13
-0.33184551	14	1.43E+02	-0.72910852	14	1.19E+03	-0.66851929	14
0.07642124	12	3.46E-01	-0.12635231	12	3.62E+00	-0.5685899	12
0.95309019	4	2.31E-03	0.04984203	4	6.17E-01	-0.42417135	4
0.43880159	7	1.69E-02	0.57456519	7	4.22E-02	-0.75429159	7
0.23206118	10	6.21E-02	-0.20314507	10	4.68E+00	-0.0625758	10
0.84124491	2	1.82E-02	-0.44746393	2	2.11E+00	0.04672055	2
0.47129413	13	1.38E-03	-0.14031791	13	4.68E+00	-0.63387917	13
0.2921649	9	3.90E-02	0.4653547	9	5.26E-02	-0.74994101	9
0.01931255	21	9.86E-01	0.09497822	21	7.17E-01	-0.68086502	21
0.19426422	19	3.13E-02	-0.25398428	19	4.34E+01	-0.46704293	19
0.04929912	13	4.96E-01	-0.30016823	13	1.86E+01	-0.79809883	13
0.5015778	7	9.90E-03	-0.29620357	7	4.49E+00	-0.60443942	7
0.48368708	7	1.15E-02	0.10465108	7	5.24E-01	-1.202593	7
0.18619334	5	1.86E-01	0.70731343	5	3.87E-02	-0.67501481	5
0.01250827	6	6.28E-01	0.67269126	6	3.35E-02	0.13069669	6
-0.20528623	12	1.37E+01	-0.15442783	12	4.53E+00	-0.89134147	12
0.8015368	6	1.48E-03	-0.45704699	6	7.73E+00	-0.25901049	6
0.66260017	1	6.50E-02	0.47004998	1	2.24E-01	0.00098852	1
0.21779511	16	3.07E-02	-0.11239108	16	5.46E+00	-0.19373862	16
0.1937802	12	7.48E-02	-0.17395756	12	5.31E+00	-1.33840287	12
0.66688417	4	1.24E-02	-0.21234563	4	1.64E+00	-0.17049393	4
0.2828149	6	7.90E-02	-0.05838416	6	1.13E+00	-0.42593244	6
0.19203538	16	4.71E-02	-0.47550063	16	2.25E+02	-0.75327611	16
0.16826488	3	2.57E-01	0.01393522	3	6.63E-01	-0.07507073	3
0.04431037	12	5.26E-01	-0.31951466	12	1.72E+01	-0.83313749	12
1.14393398	6	1.07E-04	0.22743957	6	2.86E-01	-0.83351127	6
0.04899341	22	5.30E-01	-0.49880048	22	2.20E+03	-1.18629224	22
0.7833665	6	1.70E-03	0.11818846	6	4.84E-01	-0.12056375	6
0.39435593	4	6.15E-02	0.73616234	4	4.76E-02	0.20359484	4
-0.20168155	126	3.91E+12	0.22524726	126	5.74E-04	-0.48986127	126
0.13889961	13	1.42E-01	-0.07881827	13	2.76E+00	-0.01334458	13
-0.38482091	21	5.03E+03	-0.73016039	21	3.14E+04	-1.39933662	21

0.31397781	5	7.83E-02	0.25954205	5	2.63E-01	-0.08109352	5
0.5867352	9	1.84E-03	0.24937763	9	2.12E-01	-0.82124913	9
0.20679763	6	1.41E-01	0.19755461	6	3.30E-01	-0.1137518	6
-0.13806289	10	4.01E+00	-0.18207489	10	4.04E+00	-0.77879228	10
0.88935389	4	3.36E-03	0.45145227	4	1.38E-01	-1.03750615	4
-0.26612625	10	1.69E+01	-0.39686099	10	1.81E+01	-1.11564442	10
0.37083017	7	3.03E-02	-0.84641268	7	8.57E+01	-0.29148895	7
0.09169526	5	3.53E-01	0.0178426	5	7.39E-01	-0.40151351	5
0.63109827	9	1.16E-03	0.60037592	9	2.21E-02	-0.61440475	9
0.04184484	12	5.43E-01	0.10557962	12	5.56E-01	-0.29491197	12
-0.00752	86	7.37E+01	-0.0045913	86	2.95E+02	-0.15135015	86
0.02192754	9	6.41E-01	-0.57439365	9	4.28E+01	-0.47266335	9
0.01564782	9	6.84E-01	-0.05721015	9	1.53E+00	-0.86315326	9
0.38163991	12	6.44E-03	0.32131983	12	9.75E-02	-0.14767168	12
0.08847065	32	1.67E-01	-0.9014172	32	1.35E+08	-1.77994035	32
0.48103584	8	8.07E-03	0.0680621	8	6.59E-01	-0.56205786	8
0.29301258	15	1.08E-02	0.06533718	15	8.54E-01	-0.12487088	15
0.11663275	11	2.16E-01	0.11089296	11	5.27E-01	-0.03331841	11
0.08514915	11	3.17E-01	0.22032949	11	2.31E-01	0.34397477	11
0.23353741	11	5.22E-02	0.21599868	11	2.39E-01	-0.21535856	11
-0.32476145	14	1.29E+02	-0.03286945	14	2.03E+00	-1.17830681	14
0.0148207	19	1.01E+00	0.15431883	19	3.42E-01	-0.0408325	19
-0.16275616	20	3.79E+01	-0.37883552	20	2.52E+02	-0.59141442	20
0.47148278	16	4.50E-04	-0.02033361	16	2.13E+00	-0.77018183	16
0.3527866	2	1.34E-01	0.85951199	2	6.63E-02	-0.04032058	2
0.2855108	7	6.30E-02	0.08152427	7	5.93E-01	0.15239302	7
0.09665248	18	2.14E-01	0.18865572	18	2.35E-01	-0.8753898	18
0.47412635	5	2.65E-02	-0.97112442	5	5.07E+01	-0.0955046	5
0.19107718	11	8.74E-02	-0.29989257	11	1.16E+01	-0.06532338	11
0.17079098	6	1.86E-01	-0.12525969	6	1.56E+00	-1.16867397	6
0.01772714	8	6.47E-01	-0.6210526	8	3.85E+01	-0.38116235	8
0.06618478	6	4.16E-01	0.65491514	6	3.65E-02	-0.66071005	6
0.17496972	7	1.62E-01	-0.24691962	7	3.45E+00	-0.98118678	7
-0.05252575	8	1.26E+00	-0.12107071	8	2.01E+00	-0.73910606	8
0.01148887	12	8.07E-01	0.10448973	12	5.61E-01	-1.57803026	12
0.13312238	9	2.03E-01	-0.0739973	9	1.70E+00	-0.91342004	9
1.04539949	8	3.87E-05	0.21283141	8	2.80E-01	0.2461141	8
0.10214148	21	1.71E-01	-0.0476526	21	4.55E+00	-0.24443296	21
0.15806393	15	9.07E-02	0.08485073	15	7.07E-01	-0.05353751	15
0.16563061	5	2.14E-01	-0.31415334	5	3.05E+00	-0.47261051	5
0.44538006	7	1.60E-02	0.3018083	7	1.82E-01	0.66642202	7
0.27519798	6	8.37E-02	0.1906856	6	3.41E-01	-1.34159106	6
-0.39273744	6	1.40E+01	-0.26557529	6	3.07E+00	-0.78261917	6
0.0066619	9	7.51E-01	-0.1554654	9	2.88E+00	-0.71648647	9
0.45463713	8	1.04E-02	0.41817612	8	8.34E-02	-0.24138446	8
0.17870589	12	9.10E-02	-0.25910917	12	1.06E+01	-0.60701769	12
-0.20722965	5	2.67E+00	-0.12634467	5	1.37E+00	-1.01695019	5

-0.00787827	20	1.65E+00	-0.38460017	20	2.70E+02	-1.11683086	20
-0.27339967	8	1.02E+01	-0.42712739	8	1.22E+01	-2.5387964	8
0.45109867	5	3.09E-02	-0.76304065	5	2.08E+01	-1.50406387	5
-0.06758979	5	1.04E+00	-0.0195235	5	8.67E-01	-2.18493813	5
0.34028263	9	2.37E-02	-0.58038258	9	4.45E+01	-0.74459242	9
0.75140541	2	2.63E-02	0.14857012	2	4.36E-01	-0.24217262	2
0.11240327	30	8.81E-02	-0.71984463	30	1.73E+06	-1.05390524	30
0.2183981	4	1.73E-01	-0.20626289	4	1.61E+00	-0.1599082	4
0.04003302	5	5.01E-01	-0.18430687	5	1.75E+00	-0.64839542	5
0.31389393	21	1.96E-03	0.07027305	21	9.88E-01	-0.39681756	21
0.11527139	12	2.08E-01	0.14891046	12	3.92E-01	-0.20985757	12
0.24102921	15	2.46E-02	0.1599206	15	3.41E-01	-0.39196256	15
0.04799409	9	4.90E-01	0.0584598	9	7.25E-01	0.19331104	9
0.35262736	12	9.41E-03	-0.15754534	12	4.65E+00	-0.65145279	12
-0.1581499	42	2.40E+03	-0.36231251	42	7.25E+04	-0.91142329	42
-1.23732338	7	2.91E+04	-0.99093294	7	1.86E+02	-0.85438643	7
-0.17546029	4	1.75E+00	-0.26754292	4	2.02E+00	-1.03199771	4
-0.23856626	7	5.61E+00	-0.30067925	7	4.60E+00	-0.8530852	7
-0.45585959	3	5.74E+00	-0.84510365	3	1.03E+01	-0.57263021	3
0.12730341	23	8.88E-02	-0.45311665	23	1.63E+03	-0.58891261	23
0.62264691	3	2.67E-02	0.25238573	3	3.10E-01	-0.36202348	3
-0.08070443	9	1.86E+00	-0.06681585	9	1.62E+00	-0.53153739	9
0.2565656	4	1.38E-01	0.55410139	4	9.39E-02	-0.41769767	4
0.18446332	30	1.07E-02	-0.10520039	30	3.01E+01	-0.09041073	30
0.44263757	2	9.26E-02	0.06305786	2	5.46E-01	-0.10189157	2
0.06475726	12	4.03E-01	0.15718853	12	3.67E-01	-0.01769614	12
0.17124809	40	5.66E-03	-0.38619302	40	7.41E+04	-0.71848819	40
0.09165389	19	2.28E-01	-0.01549469	19	2.56E+00	-0.33495549	19
0.30372032	8	4.32E-02	-0.0551557	8	1.36E+00	0.01015628	8
0.25213126	3	1.69E-01	-0.33015992	3	1.99E+00	-0.28583753	3
0.32746054	2	1.48E-01	0.54904332	2	1.51E-01	-0.97681313	2
0.26103748	16	1.49E-02	-0.11865691	16	5.82E+00	-0.47999206	16
0.37283869	7	2.98E-02	-0.50224674	7	1.35E+01	-0.18661282	7
0.07938712	7	3.68E-01	0.15129787	7	4.08E-01	-0.13307092	7
0.14077569	17	1.02E-01	0.0201785	17	1.49E+00	0.00641917	17
0.36071336	9	1.92E-02	0.21575143	9	2.63E-01	-0.21064141	9
0.5522599	12	6.95E-04	-0.25511042	12	1.02E+01	-0.39475159	12
-0.06780036	22	6.94E+00	-0.08545926	22	8.34E+00	-0.16939701	22
0.33030028	5	7.01E-02	0.0550944	5	6.30E-01	-1.24406934	5
0.62270396	8	2.11E-03	-0.41148097	8	1.12E+01	-0.94963454	8
0.21776587	15	3.55E-02	0.02587117	15	1.25E+00	-0.48077989	15
0.1012535	9	2.82E-01	0.54920285	9	3.07E-02	-0.73756978	9
0.15647637	14	1.02E-01	-0.44035565	14	8.46E+01	-0.26997658	14
0.11921024	23	1.07E-01	0.10599332	23	6.38E-01	-0.11608524	23
0.10976774	33	8.25E-02	0.02234172	33	3.69E+00	0.04231251	33
0.11144901	11	2.30E-01	-0.15829343	11	4.00E+00	-0.49354075	11
-0.18147393	5	2.24E+00	1.16388122	5	5.50E-03	-1.2527874	5

0.05414001	8	4.58E-01	-0.19403954	8	3.09E+00	-0.78114386	8
0.37229049	27	1.04E-04	-0.21295439	27	1.18E+02	-0.42504434	27
0.07209529	7	3.92E-01	0.44081645	7	8.64E-02	-1.38349583	7
0.48094369	4	3.70E-02	0.06280771	4	5.88E-01	-1.00300904	4
0.15364497	19	6.87E-02	-0.23357815	19	3.41E+01	-0.48389916	19
0.59925676	13	2.31E-04	-0.432044	13	5.78E+01	-0.50746478	13
0.29658144	17	6.67E-03	-0.04312	17	2.95E+00	0.1042407	17
-0.5956751	16	2.32E+04	-0.26587707	16	2.63E+01	-0.95833226	16
0.03620108	33	8.61E-01	-0.09403715	33	3.55E+01	-0.41687537	33
0.06546625	4	4.25E-01	0.62928733	4	7.09E-02	0.49920657	4
0.40987323	4	5.62E-02	0.20630198	4	3.44E-01	-0.76076959	4
-0.09558024	19	8.50E+00	-0.20856548	19	2.53E+01	-0.11858723	19
0.10158334	11	2.59E-01	-0.10907868	11	2.76E+00	-0.72117361	11
0.7389688	11	1.12E-04	-0.68267995	11	2.07E+02	-0.42011434	11
0.03988836	24	6.68E-01	-0.12230684	24	1.80E+01	-0.06499594	24
0.09236214	22	2.04E-01	-0.1733156	22	2.73E+01	-0.2119494	22
0.41256607	16	1.20E-03	0.06259434	16	9.10E-01	-0.21793842	16
0.24505722	16	1.95E-02	0.11940181	16	5.09E-01	-0.78581896	16
-0.04206907	18	2.76E+00	0.20928026	18	1.86E-01	0.52811243	18
0.40848985	16	1.28E-03	-0.16816545	16	9.66E+00	-0.25501389	16
0.08480785	22	2.41E-01	0.38321273	22	1.50E-02	-0.83431357	22
0.17930642	14	7.25E-02	0.28397071	14	1.11E-01	0.40063593	14
-0.04842093	5	9.11E-01	0.7107654	5	3.82E-02	-2.26676244	5
0.23435396	11	5.16E-02	-0.44917341	11	3.58E+01	-1.20902517	11
0.05497441	31	4.72E-01	-0.06717305	31	1.70E+01	-0.23209575	31
-0.07908623	4	9.93E-01	-1.4662983	4	1.77E+02	-0.21597448	4
-0.06302513	21	5.61E+00	-0.44462308	21	7.77E+02	-0.67291	21
0.14817075	9	1.73E-01	-0.31061368	9	7.82E+00	-0.197133	9
0.28119606	9	4.37E-02	0.08983707	9	5.92E-01	0.03821875	9
0.04850396	51	6.65E-01	-0.36124971	51	7.75E+05	-0.43190586	51
1.20339273	3	1.48E-03	0.72029896	3	6.96E-02	-1.15679441	3
-0.07009113	9	1.66E+00	-0.17793714	9	3.32E+00	-0.88254006	9
0.20141249	14	5.22E-02	0.86459379	14	5.48E-04	-0.1068595	14
-0.41102075	5	1.06E+01	0.38737105	5	1.52E-01	-1.49722108	5
0.15291155	18	7.60E-02	0.14458336	18	3.87E-01	0.18095265	18
0.23537479	18	1.66E-02	-0.03576394	18	2.98E+00	-0.33504992	18
0.13341438	22	8.27E-02	-0.41432739	22	7.05E+02	-0.93415355	22
0.29222192	10	3.16E-02	0.07544267	10	6.69E-01	-0.66935054	10
0.15388085	36	1.56E-02	-0.20652755	36	5.48E+02	-0.44612396	36
0.08548693	10	3.24E-01	0.27842742	10	1.62E-01	-0.12790074	10
0.80853764	5	2.75E-03	0.67869275	5	4.38E-02	-0.50022057	5
0.20076206	14	5.27E-02	0.29413738	14	1.02E-01	-0.65667927	14
0.31122633	5	7.98E-02	0.83163823	5	2.28E-02	-0.16893095	5
0.12350141	22	1.03E-01	0.08023274	22	8.92E-01	0.07054697	22
0.86069338	4	3.97E-03	0.50929837	4	1.11E-01	0.79585325	4
0.03749042	8	5.36E-01	-0.49706746	8	1.85E+01	-1.1374723	8
0.13673876	14	1.36E-01	0.02975565	14	1.14E+00	-0.24331068	14

-0.18812842	26	2.37E+02	-0.67028905	26	1.26E+05	-1.41837846	26
0.01710409	22	1.07E+00	0.25553318	22	8.38E-02	-0.39521672	22
0.80858088	11	4.81E-05	0.64876591	11	9.19E-03	-0.18745423	11
0.26993137	14	1.89E-02	-0.05174703	14	2.41E+00	-0.89539102	14
0.25935546	15	1.84E-02	-0.22395009	15	1.41E+01	-0.32203988	15
-0.11589412	21	1.72E+01	0.21027735	21	1.61E-01	-0.94634729	21
-0.06924541	9	1.65E+00	-0.19213757	9	3.64E+00	0.54143216	9
0.23163238	17	2.08E-02	-0.74123348	17	5.48E+03	-0.43451423	17
0.1707843	22	3.63E-02	-0.06782555	22	6.57E+00	-0.34320818	22
-0.76522165	24	1.42E+08	-0.30015769	24	2.41E+02	-1.18248051	24
0.13649711	4	2.80E-01	0.02246637	4	6.83E-01	0.25427161	4
0.12211479	36	4.67E-02	-0.16476382	36	2.27E+02	-0.61003274	36
0.12926846	25	7.45E-02	0.02163893	25	2.34E+00	-0.01267523	25
0.34156526	28	1.82E-04	-0.11775777	28	2.88E+01	-0.43359108	28
0.06522953	42	3.19E-01	0.08626538	42	1.32E+00	-0.17868899	42
0.19450348	11	8.38E-02	0.49327777	11	2.96E-02	-0.33583725	11
0.10991223	21	1.45E-01	0.07909643	21	8.81E-01	-0.09250287	21
0.0027423	12	9.05E-01	0.30429278	12	1.12E-01	0.24329527	12
0.25081308	5	1.20E-01	-0.50608455	5	6.94E+00	-1.09550407	5
0.03639292	63	1.48E+00	0.1019744	63	1.23E+00	0.02292831	63
0.41637303	9	1.08E-02	-0.27341669	9	6.15E+00	-0.52661613	9
0.12681939	17	1.31E-01	-0.39253586	17	1.28E+02	-1.14476279	17
0.03656511	5	5.13E-01	-0.42894136	5	4.99E+00	0.06352256	5
0.19978071	8	1.16E-01	-0.49138326	8	1.79E+01	-1.06186371	8
0.45311008	8	1.05E-02	0.04707855	8	7.46E-01	-0.75585947	8
0.38303372	29	4.37E-05	-0.11225336	29	3.00E+01	-0.48356055	29
-0.31935107	17	3.27E+02	-0.46677811	17	2.84E+02	-0.88994926	17
-0.09378798	14	4.18E+00	0.08633766	14	6.81E-01	-0.89363141	14
1.04849211	6	2.22E-04	-0.38879574	6	5.57E+00	0.10074212	6
-0.52839097	5	2.35E+01	-0.758429	5	2.04E+01	-1.1319063	5
0.34563105	3	1.06E-01	-0.72224251	3	6.94E+00	-0.51219619	3
0.50055832	4	3.30E-02	0.05947845	4	5.95E-01	-0.83284666	4
0.146488	7	2.07E-01	-0.27927985	7	4.10E+00	-0.69066739	7
0.17911553	7	1.57E-01	1.19492827	7	1.52E-03	-0.69396473	7
0.53348438	9	3.20E-03	-0.0228768	9	1.22E+00	-0.28286128	9
0.45565666	4	4.29E-02	-0.09496017	4	1.06E+00	0.282712	4
0.2259716	33	2.03E-03	0.03059899	33	3.15E+00	-0.50069911	33
0.30353014	39	4.53E-05	-0.16029331	39	3.31E+02	-0.32288216	39
0.2193512	12	5.36E-02	-0.20132171	12	6.62E+00	0.31625182	12
0.20997981	11	6.94E-02	0.0024055	11	1.19E+00	-0.65920921	11
0.10554287	21	1.60E-01	-0.19054166	21	2.89E+01	-0.65628342	21
0.08968915	28	1.81E-01	-0.20013085	28	1.15E+02	-0.10410638	28
0.12740571	12	1.78E-01	-0.01512638	12	1.47E+00	-0.13722258	12
0.17935281	38	5.17E-03	-0.33635619	38	1.40E+04	-0.75440183	38
0.16442185	11	1.21E-01	-1.30621447	11	2.27E+04	-1.70547128	11
0.12184324	9	2.28E-01	0.41762965	9	7.16E-02	-0.68556043	9
0.2091272	19	2.35E-02	0.12792178	19	4.67E-01	-0.11532058	19

0.08972088	35	1.47E-01	-0.12339307	35	8.28E+01	-0.27505655	35
0.22562932	3	1.93E-01	-0.02959544	3	7.61E-01	-1.20150536	3
0.15692136	12	1.21E-01	0.05036777	12	8.68E-01	-0.52773038	12
0.06967936	13	3.73E-01	-0.2184234	13	9.18E+00	-0.34155262	13
0.48871407	19	1.06E-04	0.00416227	19	2.03E+00	-0.26084069	19
0.26181749	13	2.56E-02	-0.30495768	13	1.93E+01	-0.5547299	13
0.14189965	8	2.00E-01	-0.32313747	8	6.63E+00	0.07196651	8
-0.58230519	17	3.29E+04	-0.39759262	17	1.35E+02	-0.76618514	17
0.09594654	9	2.98E-01	0.15831791	9	3.81E-01	-0.5005074	9
0.11972337	33	6.00E-02	-0.16859462	33	1.52E+02	-0.44347082	33
0.17280583	23	3.13E-02	-0.1123771	23	1.37E+01	-0.74915365	23
0.12181287	61	1.10E-02	-0.00703588	61	5.21E+01	-0.15299235	61
-0.17023326	14	1.30E+01	-0.2122909	14	1.05E+01	-0.75573154	14
0.37508899	9	1.65E-02	0.14103743	9	4.26E-01	-0.39820725	9
0.29320014	5	9.02E-02	-0.39432235	5	4.30E+00	-1.20959741	5
0.14103428	5	2.53E-01	-0.02655741	5	8.93E-01	-0.08253204	5
0.28860167	20	4.11E-03	-0.1328047	20	1.19E+01	-0.77641242	20
0.43701996	16	7.99E-04	-0.30603678	16	3.97E+01	-0.29906817	16
0.2535994	8	6.94E-02	0.06246251	8	6.81E-01	0.02050173	8
0.15840385	18	6.87E-02	-0.94704139	18	9.03E+04	-1.10848431	18
-0.67510961	2	8.86E+00	-1.19705871	2	1.54E+01	-1.86514039	2
0.10354545	9	2.75E-01	-0.13682785	9	2.55E+00	-0.20613116	9
0.08258779	5	3.75E-01	-1.34514402	5	2.51E+02	-0.25187956	5
0.01240703	28	1.51E+00	0.13405688	28	4.25E-01	-0.06325174	28
0.01153811	28	1.54E+00	-0.15014962	28	4.96E+01	-0.83012612	28
0.31015016	6	6.40E-02	-0.11601224	6	1.50E+00	-0.2152455	6
0.47182086	4	3.90E-02	-0.35468855	4	2.79E+00	0.06148209	4
0.21280488	8	1.02E-01	-0.05310435	8	1.35E+00	-0.10760356	8
0.1552916	14	1.04E-01	0.10240947	14	5.88E-01	0.01406616	14
0.13023109	4	2.90E-01	-0.10373023	4	1.09E+00	0.43649694	4
0.55433915	8	4.03E-03	-0.30438899	8	5.93E+00	-0.8585043	8
0.51574475	6	1.32E-02	0.57172275	6	5.44E-02	-1.78109789	6
0.02976711	19	7.53E-01	0.00227033	19	2.08E+00	0.06215637	19
0.061439	5	4.33E-01	0.02391399	5	7.20E-01	0.08955168	5
-0.04641432	35	1.44E+01	-0.01748087	35	9.40E+00	-0.23630363	35
-0.14957875	130	2.02E+10	0.16035794	130	5.00E-02	-0.15473897	130
-0.12983405	5	1.58E+00	-0.46531496	5	5.83E+00	-0.31703939	5
0.01852271	10	6.88E-01	0.07025059	10	6.94E-01	-1.15991648	10
0.37265829	8	2.25E-02	-0.01769469	8	1.09E+00	-0.20973916	8
-0.11099105	4	1.20E+00	-0.84973334	4	1.77E+01	-1.37466467	4
-0.39838542	13	2.56E+02	-0.06976347	13	2.55E+00	-1.05802239	13
0.51785583	15	3.15E-04	0.82377543	15	5.46E-04	-0.02596248	15
0.41197566	2	1.05E-01	1.09876237	2	3.52E-02	-0.28594101	2
0.43324934	7	1.78E-02	0.12196665	7	4.77E-01	0.24156889	7
0.12794475	11	1.88E-01	-0.16636807	11	4.25E+00	-1.39255652	11
0.27871501	8	5.47E-02	-0.96658618	8	2.96E+02	-1.11086596	8

	XXX-cells					
	BC_07			BC_10		
FDR	polii	gatc.num	FDR	polii	gatc.num	FDR
6.18E-02	0.12696354	50	2.13E-03	0.41680006	50	1.74E-03
2.46E+00	0.60238993	11	1.99E-03	1.03135745	11	2.27E-03
1.93E+02	1.37583999	10	6.38E-06	2.3200004	10	1.93E-06
4.02E+05	0.20707211	24	8.00E-03	0.61493163	24	2.43E-03
1.31E+00	0.75393112	13	1.97E-04	0.88883284	13	2.93E-03
3.69E+00	0.37894434	18	2.14E-03	1.16846579	18	4.28E-05
1.39E+01	0.83517723	10	4.70E-04	1.54533062	10	1.70E-04
1.61E+00	0.58842773	12	1.51E-03	1.31771815	12	2.28E-04
2.43E+03	1.15776494	13	3.66E-06	2.03331919	13	8.21E-07
1.84E+02	0.63380174	14	4.22E-04	1.52473891	14	1.70E-05
3.46E+01	0.38926717	12	9.48E-03	1.21808522	12	4.44E-04
1.71E+00	1.75978749	4	2.96E-04	2.40936097	4	4.84E-04
2.36E+01	1.366234	7	1.01E-04	2.37848472	7	2.70E-05
3.26E-01	0.90862451	10	2.62E-04	1.57297202	10	1.45E-04
3.05E-01	1.65720953	2	3.94E-03	2.64999796	2	2.16E-03
8.99E+01	0.79566308	13	1.31E-04	0.90666211	13	2.58E-03
5.33E+01	1.62249965	9	2.59E-06	1.96704203	9	3.33E-05
2.90E+03	1.30932668	21	8.42E-10	1.54372612	21	1.98E-07
6.97E+01	0.53489074	19	1.93E-04	1.15958266	19	2.99E-05
4.64E+02	0.62679009	13	6.93E-04	0.78622616	13	6.09E-03
9.51E+00	0.99478145	7	9.53E-04	1.48156795	7	1.44E-03
3.57E+02	1.83986256	7	5.83E-06	1.48011349	7	1.45E-03
6.94E+00	1.13308351	5	1.84E-03	1.8492626	5	1.27E-03
1.29E-01	0.94337914	6	2.43E-03	1.8164479	6	6.82E-04
7.05E+02	0.47906265	12	4.14E-03	1.14322123	12	7.33E-04
1.06E+00	1.66953157	6	4.84E-05	1.9778369	6	3.59E-04
3.72E-01	2.21789812	1	3.41E-03	3.0187428	1	3.50E-03
1.31E+00	0.46691363	16	1.28E-03	0.99834854	16	4.43E-04
4.58E+04	1.715628	12	4.55E-08	2.81629501	12	1.00E-08
6.06E-01	0.99746476	4	6.80E-03	2.10932441	4	1.22E-03
2.62E+00	0.97563168	6	2.04E-03	1.42803906	6	3.20E-03
1.05E+03	0.43065238	16	1.97E-03	0.73512162	16	4.15E-03
4.19E-01	1.31312779	3	4.40E-03	2.47998589	3	1.10E-03
4.09E+02	0.40517341	12	8.19E-03	1.54135941	12	5.10E-05
2.37E+01	2.41216851	6	8.84E-07	3.46653222	6	9.64E-07
1.30E+07	0.38566808	22	6.68E-04	0.65882423	22	2.19E-03
5.03E-01	1.35824728	6	2.60E-04	1.550717	6	1.96E-03
1.31E-01	1.51746472	4	8.02E-04	2.48994204	4	3.78E-04
4.09E+13	0.02290378	126	4.40E-03	0.33640674	126	6.38E-05
1.82E-01	0.44448701	13	4.19E-03	0.92408485	13	2.27E-03
1.65E+08	0.38482245	21	8.84E-04	1.11818869	21	1.93E-05

4.13E-01	1.09221219	5	2.24E-03	1.41863458	5	5.80E-03
9.01E+01	0.78661716	9	1.17E-03	1.02802153	9	4.99E-03
4.84E-01	1.18240077	6	6.70E-04	1.41025106	6	3.43E-03
1.02E+02	1.76666512	10	2.85E-07	1.96453498	10	1.51E-05
2.11E+01	1.15745836	4	3.52E-03	2.24867351	4	7.93E-04
1.53E+03	0.81701673	10	5.43E-04	1.85858982	10	2.78E-05
1.43E+00	0.98397566	7	1.02E-03	2.13293517	7	8.02E-05
1.89E+00	1.15198547	5	1.69E-03	2.46750328	5	1.44E-04
1.96E+01	2.00377381	9	1.59E-07	2.46620561	9	2.32E-06
2.69E+00	0.48637818	12	3.87E-03	1.13233974	12	7.89E-04
5.76E+00	0.29285041	86	4.35E-09	0.53673317	86	3.18E-07
6.90E+00	1.1121546	9	1.08E-04	1.45424154	9	5.13E-04
1.23E+02	2.31481847	9	1.64E-08	2.91914993	9	2.07E-07
6.80E-01	0.70383745	12	5.19E-04	0.90063379	12	3.72E-03
9.33E+15	1.34056068	32	3.29E-14	1.59418928	32	1.02E-10
9.91E+00	0.64559864	8	5.07E-03	1.67177995	8	3.15E-04
5.68E-01	0.35964146	15	5.85E-03	1.02074731	15	5.34E-04
2.46E-01	0.95481715	11	9.64E-05	1.11635273	11	1.34E-03
9.28E-03	0.63013487	11	1.57E-03	2.4380729	11	3.50E-07
1.19E+00	1.23050418	11	9.02E-06	2.0532313	11	3.87E-06
4.18E+04	0.48417926	14	2.03E-03	1.1909315	14	2.14E-04
1.84E-01	0.26347746	19	7.99E-03	0.69505107	19	2.92E-03
5.41E+02	1.50899985	20	1.13E-10	1.79377888	20	2.77E-08
1.29E+03	1.1441798	16	4.36E-07	1.70359738	16	1.10E-06
3.89E-01	1.66299945	2	3.87E-03	2.58147261	2	2.50E-03
9.69E-02	1.25951677	7	1.93E-04	1.54598216	7	1.08E-03
1.24E+04	2.1734578	18	1.38E-13	1.99341944	18	1.82E-08
4.43E-01	1.50905644	5	3.09E-04	2.10102391	5	5.24E-04
3.24E-01	0.6746955	11	1.07E-03	1.3551079	11	3.02E-04
1.45E+02	2.65322511	6	2.41E-07	3.04721397	6	5.11E-06
2.94E+00	1.28884373	8	6.93E-05	2.13643313	8	3.26E-05
9.31E+00	1.96765859	6	9.71E-06	2.26879633	6	1.13E-04
9.33E+01	0.75941335	7	3.94E-03	1.28984572	7	3.36E-03
3.25E+01	0.72778427	8	2.93E-03	1.33707122	8	1.62E-03
4.29E+05	1.4872075	12	3.75E-07	1.61942163	12	3.03E-05
1.78E+02	0.57446129	9	5.52E-03	1.04290344	9	4.61E-03
4.35E-02	1.00776222	8	4.52E-04	1.98475528	8	6.84E-05
3.75E+00	0.39341519	21	7.78E-04	0.64975434	21	2.99E-03
2.54E-01	0.67867579	15	1.67E-04	0.85321626	15	2.06E-03
2.65E+00	1.1032189	5	2.13E-03	2.38906359	5	1.90E-04
4.30E-03	0.97743007	7	1.06E-03	1.89182521	7	2.33E-04
3.69E+02	0.7387498	6	7.32E-03	1.19565202	6	8.05E-03
1.80E+01	0.78718317	6	5.64E-03	2.33603339	6	8.64E-05
4.16E+01	1.34819825	9	1.93E-05	1.82660121	9	7.04E-05
1.15E+00	1.89361596	8	1.23E-06	2.43128953	8	7.73E-06
4.96E+01	0.73229031	12	3.99E-04	1.32057063	12	2.24E-04
3.52E+01	0.81563606	5	8.34E-03	1.81956906	5	1.41E-03

1.15E+06	0.52945052	20	1.45E-04	0.92394708	20	2.18E-04
5.77E+06	0.8507004	8	1.29E-03	1.23965541	8	2.60E-03
3.56E+02	0.92866556	5	4.87E-03	1.49731592	5	4.40E-03
9.02E+03	1.86831921	5	5.61E-05	3.001723	5	2.19E-05
5.12E+01	0.49741256	9	9.70E-03	1.16666676	9	2.38E-03
6.82E-01	1.60150496	2	4.61E-03	2.72184257	2	1.85E-03
2.26E+08	0.16974049	30	6.88E-03	0.64160233	30	5.07E-04
5.81E-01	0.99712779	4	6.81E-03	2.36036311	4	5.63E-04
6.11E+00	1.4086554	5	4.98E-04	1.74929347	5	1.81E-03
3.83E+01	0.54414934	21	8.11E-05	0.68626626	21	2.02E-03
1.22E+00	0.44355734	12	5.74E-03	1.50126546	12	6.68E-05
1.16E+01	0.38364371	15	4.48E-03	0.9835422	15	7.21E-04
5.10E-02	1.03112216	9	1.96E-04	1.24422478	9	1.57E-03
7.51E+01	1.09599898	12	1.39E-05	1.62275889	12	2.96E-05
6.17E+09	1.13179039	42	1.88E-15	1.67701105	42	3.23E-14
4.33E+01	1.56177445	7	3.12E-05	1.40601198	7	2.01E-03
2.06E+01	1.35118345	4	1.59E-03	2.29809254	4	6.81E-04
4.29E+01	0.81685685	7	2.79E-03	1.46461207	7	1.55E-03
2.32E+00	1.1652235	3	7.35E-03	1.97029182	3	4.18E-03
1.34E+03	0.32006283	23	1.48E-03	0.63382888	23	2.37E-03
1.12E+00	1.71390902	3	1.10E-03	2.33353933	3	1.62E-03
1.07E+01	1.01573124	9	2.19E-04	1.1122874	9	3.18E-03
1.67E+00	1.25640885	4	2.35E-03	2.0334382	4	1.54E-03
3.24E-01	0.42376253	30	3.53E-05	0.75298268	30	9.71E-05
4.62E-01	1.76272035	2	2.92E-03	2.50984006	2	2.92E-03
2.02E-01	0.45868543	12	5.00E-03	0.83230868	12	5.88E-03
1.03E+07	0.61148976	40	1.15E-08	1.36840264	40	4.92E-11
1.11E+01	0.80151952	19	4.98E-06	0.84217135	19	6.84E-04
2.12E-01	0.59384493	8	7.16E-03	1.24796315	8	2.50E-03
8.65E-01	1.15013731	3	7.75E-03	1.72019325	3	8.05E-03
5.27E+00	1.60647548	2	4.55E-03	2.73799682	2	1.78E-03
4.02E+01	0.49785928	16	8.91E-04	1.06473723	16	2.52E-04
7.56E-01	0.63102186	7	8.55E-03	1.48500323	7	1.41E-03
5.47E-01	0.78082987	7	3.46E-03	1.20028751	7	4.99E-03
1.11E-01	0.60406993	17	1.69E-04	1.09607292	17	1.28E-04
1.00E+00	0.91969235	9	4.42E-04	1.40258532	9	6.76E-04
6.83E+00	1.08031106	12	1.61E-05	1.82823774	12	7.48E-06
1.25E+00	0.43925898	22	2.89E-04	0.63748109	22	2.78E-03
1.03E+02	1.28075245	5	9.15E-04	1.9536142	5	8.81E-04
1.34E+02	2.05287493	8	4.24E-07	2.31643491	8	1.36E-05
3.17E+01	0.31735293	15	9.38E-03	0.89096361	15	1.52E-03
4.86E+01	1.00249938	9	2.41E-04	1.91461135	9	4.40E-05
2.63E+00	0.62629505	14	4.56E-04	1.19344429	14	2.10E-04
5.37E-01	0.37636145	23	5.94E-04	0.53111923	23	7.85E-03
1.46E-02	0.36961078	33	5.00E-05	0.62674405	33	3.47E-04
1.33E+01	0.4715385	11	6.13E-03	0.83166981	11	7.91E-03
1.08E+02	1.91819217	5	4.42E-05	2.26492564	5	2.94E-04

4.31E+01	0.84432131	8	1.35E-03	1.29608164	8	1.97E-03
2.05E+02	1.54090252	27	6.16E-14	2.15861082	27	1.23E-12
1.07E+03	0.99317081	7	9.62E-04	1.39872281	7	2.07E-03
1.83E+01	2.16111994	4	5.69E-05	2.71372432	4	1.90E-04
8.81E+01	0.59684034	19	8.25E-05	0.94298921	19	2.53E-04
2.54E+01	0.5647798	13	1.28E-03	0.82028837	13	4.77E-03
3.23E-02	0.33971727	17	4.53E-03	1.28447631	17	2.36E-05
1.22E+04	0.63006568	16	1.87E-04	1.61843405	16	2.27E-06
5.90E+02	0.14097873	33	8.93E-03	0.62244585	33	3.72E-04
3.91E-02	1.22937792	4	2.62E-03	1.78781913	4	3.26E-03
6.80E+00	1.27622912	4	2.16E-03	1.8115138	4	3.04E-03
5.44E-01	0.28709139	19	5.78E-03	0.73518643	19	1.96E-03
9.63E+01	1.48809253	11	9.86E-07	1.65392619	11	4.67E-05
7.05E+00	1.64021071	11	2.67E-07	2.20238719	11	1.53E-06
2.24E-01	0.59180483	24	1.19E-05	1.10565136	24	6.32E-06
2.45E+00	0.34332942	22	1.29E-03	0.82441132	22	3.42E-04
1.75E+00	0.6736302	16	1.12E-04	1.24358934	16	5.50E-05
1.56E+03	0.63632595	16	1.74E-04	1.02289109	16	3.59E-04
1.01E-04	0.61592842	18	9.63E-05	0.95461289	18	3.20E-04
2.72E+00	0.37933449	16	3.61E-03	0.68077255	16	6.59E-03
4.84E+04	2.02306104	22	5.07E-15	2.53427549	22	1.59E-12
2.09E-03	0.38841512	14	5.57E-03	0.94987181	14	1.34E-03
1.33E+04	1.09809167	5	2.18E-03	1.57914052	5	3.30E-03
6.65E+03	1.47074989	11	1.14E-06	2.52426295	11	2.05E-07
7.02E+00	0.37490236	31	7.49E-05	0.65888953	31	3.17E-04
7.31E-01	1.32194906	4	1.79E-03	1.80650476	4	3.08E-03
2.57E+03	0.41349701	21	5.75E-04	0.68723999	21	2.00E-03
9.06E-01	1.33282461	9	2.15E-05	1.49702433	9	4.08E-04
1.60E-01	0.64619533	9	3.27E-03	1.48601092	9	4.33E-04
3.81E+04	0.2409959	51	3.89E-05	0.65899259	51	4.30E-06
1.73E+01	1.5743252	3	1.78E-03	2.68578639	3	6.43E-04
1.42E+02	1.80992323	9	6.58E-07	2.00900038	9	2.66E-05
4.64E-01	2.12536962	14	6.52E-11	2.2927321	14	4.95E-08
3.44E+02	0.77845496	5	9.95E-03	1.29845831	5	8.86E-03
1.01E-02	0.3412733	18	3.49E-03	0.95980964	18	3.05E-04
9.55E+00	0.75801687	18	1.50E-05	0.80094591	18	1.36E-03
2.36E+05	0.31969534	22	1.87E-03	0.74031465	22	8.78E-04
4.25E+01	0.66227302	10	1.86E-03	1.0657494	10	2.74E-03
2.25E+03	0.12966915	36	8.43E-03	0.73230231	36	2.98E-05
5.51E-01	1.40184531	10	5.19E-06	1.92102254	10	1.94E-05
3.02E+00	1.99691731	5	3.04E-05	3.00770479	5	2.15E-05
1.62E+02	1.03533934	14	6.19E-06	2.06577582	14	2.78E-07
6.27E-01	1.03532464	5	2.94E-03	1.38350163	5	6.57E-03
2.75E-02	0.63635644	22	1.32E-05	0.86960512	22	2.06E-04
1.16E-02	1.44789712	4	1.07E-03	1.90307199	4	2.29E-03
4.72E+02	0.80311923	8	1.77E-03	1.28983845	8	2.03E-03
1.98E+00	0.34434785	14	8.84E-03	0.6958179	14	9.22E-03

1.61E+10	0.35488058	26	3.99E-04	0.99161413	26	1.21E-05
4.51E+01	1.48142297	22	2.42E-11	1.95224195	22	1.09E-09
9.36E-01	2.3995864	11	3.91E-10	2.66955794	11	8.27E-08
2.06E+03	0.343035	14	8.97E-03	0.80538049	14	4.01E-03
5.28E+00	0.49593963	15	1.28E-03	0.69611467	15	7.30E-03
1.66E+05	0.46291409	21	2.74E-04	0.7656554	21	8.59E-04
3.92E-03	0.77869819	9	1.24E-03	1.97052889	9	3.27E-05
2.89E+01	0.37317729	17	2.99E-03	0.67424342	17	5.58E-03
1.97E+01	0.34684637	22	1.22E-03	1.08797324	22	1.78E-05
5.00E+07	1.01814685	24	8.79E-09	1.5779416	24	2.06E-08
1.07E-01	1.20736599	4	2.87E-03	1.91682871	4	2.20E-03
1.37E+05	0.12952016	36	8.46E-03	0.89229797	36	1.80E-06
8.56E-02	0.74609323	25	5.32E-07	1.26775073	25	5.42E-07
2.98E+02	0.24893947	28	1.91E-03	0.7420289	28	1.89E-04
3.65E+00	0.2283796	42	2.71E-04	0.38939516	42	7.04E-03
3.39E+00	0.52707203	11	3.81E-03	1.74922248	11	2.58E-05
3.71E-01	0.44771847	21	3.44E-04	1.04596799	21	4.20E-05
1.77E-02	0.52207357	12	2.78E-03	0.94558068	12	2.75E-03
5.11E+01	1.39309474	5	5.36E-04	2.10449056	5	5.18E-04
1.74E-03	0.24232212	63	4.45E-06	0.45070226	63	1.62E-04
1.03E+01	1.37012523	9	1.64E-05	1.56148098	9	2.90E-04
2.25E+05	0.46223958	17	9.87E-04	0.8867469	17	8.32E-04
2.08E-01	1.7423881	5	1.02E-04	2.50460392	5	1.26E-04
2.84E+02	1.91909537	8	1.03E-06	2.49662302	8	5.62E-06
3.64E+01	1.64598829	8	6.40E-06	2.32961375	8	1.27E-05
1.03E+03	0.37817604	29	1.18E-04	0.98037734	29	4.76E-06
9.03E+03	0.40838109	17	1.93E-03	1.46834181	17	4.55E-06
2.02E+03	0.5901463	14	6.67E-04	1.19692471	14	2.05E-04
1.52E-01	1.69117781	6	4.31E-05	2.2792635	6	1.08E-04
6.07E+01	1.0711224	5	2.48E-03	1.66911966	5	2.40E-03
1.88E+00	1.21282012	3	6.23E-03	1.68583839	3	8.81E-03
9.13E+00	1.51553064	4	8.08E-04	2.18388699	4	9.67E-04
1.60E+01	1.33296106	7	1.24E-04	1.21024318	7	4.78E-03
1.64E+01	0.80633979	7	2.97E-03	1.44264454	7	1.71E-03
1.70E+00	1.28330815	9	3.10E-05	1.81873699	9	7.34E-05
9.49E-02	1.0713824	4	5.02E-03	1.87674316	4	2.48E-03
4.09E+03	0.34334052	33	9.07E-05	1.11233462	33	1.33E-07
1.57E+02	0.23620335	39	3.65E-04	0.40002368	39	7.61E-03
8.94E-03	0.83292889	12	1.58E-04	0.95108919	12	2.65E-03
5.62E+01	0.41669641	11	9.82E-03	1.09346927	11	1.54E-03
1.99E+03	0.8697906	21	6.14E-07	1.31096362	21	2.42E-06
4.35E-01	0.34344688	28	3.03E-04	0.93449731	28	1.29E-05
6.17E-01	0.8431172	12	1.44E-04	1.289251	12	2.76E-04
1.19E+07	0.55227762	38	1.22E-07	0.943636	38	3.67E-07
4.95E+05	0.53194548	11	3.65E-03	1.09072973	11	1.57E-03
3.32E+01	1.4847621	9	7.09E-06	1.83470885	9	6.74E-05
5.20E-01	0.41328736	19	1.02E-03	0.64588561	19	4.74E-03

2.77E+01	0.17772768	35	2.96E-03	0.5439456	35	9.58E-04
2.02E+01	1.23405457	3	5.79E-03	1.84915602	3	5.75E-03
2.36E+01	0.84884055	12	1.36E-04	1.36092138	12	1.71E-04
4.84E+00	0.58619001	13	1.03E-03	1.12193558	13	5.53E-04
3.94E+00	1.41090225	19	1.17E-09	2.01440703	19	6.52E-09
4.08E+01	0.68071395	13	4.07E-04	1.13885909	13	4.90E-04
1.40E-01	0.5758913	8	8.07E-03	1.3336146	8	1.64E-03
1.89E+03	0.32444694	17	5.48E-03	0.68978401	17	4.86E-03
8.48E+00	0.90564423	9	4.90E-04	1.74578507	9	1.08E-04
1.09E+03	0.2744394	33	4.33E-04	0.53650726	33	1.50E-03
1.90E+04	0.97360796	23	3.56E-08	1.3086787	23	8.97E-07
3.03E+00	0.31778492	61	2.96E-07	0.57185022	61	6.22E-06
4.65E+02	0.71918642	14	1.72E-04	0.87689503	14	2.33E-03
3.99E+00	0.52916862	9	7.69E-03	1.38137969	9	7.57E-04
8.78E+01	1.37435967	5	5.86E-04	1.74310628	5	1.85E-03
4.16E-01	1.29421248	5	8.58E-04	2.40349635	5	1.80E-04
8.02E+03	0.27038705	20	5.98E-03	0.7877826	20	8.90E-04
4.61E+00	0.33983904	16	5.75E-03	0.78686524	16	2.67E-03
1.98E-01	0.59879821	8	6.93E-03	1.54396356	8	5.88E-04
2.74E+05	0.75398988	18	1.58E-05	1.46746786	18	2.56E-06
6.24E+01	2.3439693	2	5.64E-04	2.74563508	2	1.75E-03
9.68E-01	1.07360938	9	1.43E-04	1.8011445	9	8.06E-05
9.30E-01	1.07053625	5	2.48E-03	3.02621149	5	2.01E-05
1.93E-01	0.20850696	28	4.20E-03	0.487697	28	6.56E-03
7.74E+05	0.44825045	28	3.93E-05	0.80969639	28	7.37E-05
8.38E-01	1.2254599	6	5.31E-04	1.34455909	6	4.45E-03
2.35E-01	1.43327352	4	1.13E-03	1.87893715	4	2.47E-03
4.68E-01	0.76903446	8	2.22E-03	1.74498149	8	2.21E-04
1.28E-01	0.51707014	14	1.44E-03	1.13025106	14	3.40E-04
5.05E-02	0.93350533	4	8.85E-03	2.1750636	4	9.94E-04
7.25E+01	0.80373295	8	1.76E-03	1.11304551	8	4.82E-03
3.97E+03	1.92685303	6	1.21E-05	2.82069319	6	1.26E-05
4.39E-02	0.38999373	19	1.41E-03	0.78298708	19	1.23E-03
1.84E-01	1.43449912	5	4.41E-04	2.84105107	5	3.86E-05
1.08E+01	0.23140211	35	8.18E-04	0.62395133	35	2.44E-04
2.70E+01	0.01626322	130	6.69E-03	0.27587373	130	1.84E-03
1.27E+00	1.21089137	5	1.27E-03	2.42898241	5	1.65E-04
2.18E+03	1.07280199	10	7.10E-05	1.68422471	10	7.63E-05
9.30E-01	0.59258074	8	7.22E-03	1.25543752	8	2.41E-03
8.39E+01	1.08189599	4	4.81E-03	2.200004	4	9.21E-04
6.23E+03	0.52382082	13	1.92E-03	0.92674003	13	2.23E-03
1.86E-01	1.8449402	15	3.73E-10	2.95609067	15	9.13E-11
7.70E-01	2.18204207	2	8.92E-04	2.85407451	2	1.39E-03
5.65E-02	0.67833159	7	6.43E-03	1.62653953	7	7.55E-04
3.27E+04	1.56637939	11	5.03E-07	1.96613871	11	6.66E-06
3.95E+02	0.57776706	8	7.97E-03	1.37752312	8	1.33E-03

Worm-wide					
BC_02			BC_05		
gatc.num	FDR	gatc.num	polii	gatc.num	FDR
0.25766175	50	5.06E-01	0.59786165	50	2.29E-02
0.19274716	11	6.96E-01	0.26085226	11	9.12E-01
-0.09524582	10	3.08E+00	-0.57779593	10	2.42E+01
-0.15786214	24	4.01E+01	0.18541512	24	3.28E+00
-0.09815681	13	4.71E+00	0.05754657	13	2.74E+00
0.17426706	18	9.74E-01	0.76808583	18	4.75E-02
0.51135985	10	1.27E-01	0.95752311	10	5.47E-02
0.35725437	12	2.66E-01	0.75198499	12	9.99E-02
-0.22479687	13	1.06E+01	0.46391111	13	3.71E-01
-0.39364392	14	4.00E+01	-0.314244	14	2.15E+01
-0.47934913	12	4.07E+01	0.01345026	12	2.99E+00
0.67055993	4	1.41E-01	1.04351617	4	1.28E-01
0.60743203	7	1.15E-01	0.99730951	7	8.12E-02
0.60243049	10	7.90E-02	0.61177977	10	2.16E-01
0.86251576	2	1.27E-01	-0.72704476	2	2.39E+00
0.61398953	13	4.96E-02	0.7748301	13	8.03E-02
0.01680809	9	1.56E+00	-0.10125787	9	3.09E+00
0.04345809	21	3.70E+00	0.16617455	21	3.03E+00
0.20354001	19	7.81E-01	0.58196053	19	1.51E-01
0.0491157	13	1.84E+00	0.50005217	13	3.10E-01
-0.00333768	7	1.40E+00	0.33635498	7	5.95E-01
-0.44961368	7	8.75E+00	-0.11164013	7	2.30E+00
0.61816342	5	1.44E-01	0.10375708	5	9.84E-01
0.65239543	6	1.11E-01	1.68446341	6	1.53E-02
0.15869698	12	8.77E-01	-0.07823446	12	4.56E+00
0.01701562	6	1.18E+00	0.1656422	6	9.20E-01
1.04508939	1	1.15E-01	0.9121345	1	2.70E-01
0.20666889	16	7.14E-01	-0.16223279	16	1.40E+01
-0.55796539	12	6.52E+01	0.49071746	12	3.33E-01
-0.15748221	4	1.64E+00	0.09921327	4	8.99E-01
0.26276966	6	4.71E-01	-0.35843521	6	3.78E+00
0.29926415	16	3.55E-01	0.62544015	16	1.37E-01
0.12399899	3	6.75E-01	0.69253214	3	2.89E-01
-0.50980359	12	4.88E+01	0.35428904	12	6.23E-01
0.61563052	6	1.27E-01	1.33623684	6	3.92E-02
0.33811793	22	2.22E-01	0.6840987	22	5.85E-02
0.4863336	6	2.05E-01	0.94979402	6	1.11E-01
-0.58823117	4	5.84E+00	-0.75223273	4	5.20E+00
-0.39720976	126	6.91E+13	-0.22723624	126	1.23E+11
0.18760574	13	7.58E-01	0.57727242	13	2.12E-01
-0.87825747	21	2.25E+04	-0.72488209	21	2.34E+03

1.02527811	5	3.70E-02	0.90716285	5	1.45E-01
0.26473727	9	4.66E-01	0.6423252	9	2.05E-01
0.23764423	6	5.18E-01	0.54170312	6	3.34E-01
-0.86409475	10	1.74E+02	-0.51583376	10	1.89E+01
0.75972985	4	1.09E-01	0.84514721	4	1.93E-01
0.33089485	10	3.29E-01	0.70875551	10	1.47E-01
0.12494108	7	8.29E-01	-0.11735616	7	2.34E+00
0.29914662	5	4.18E-01	1.30845207	5	5.60E-02
-0.40523388	9	1.21E+01	0.6540226	9	1.97E-01
0.14303197	12	9.64E-01	0.21430798	12	1.19E+00
0.2640484	86	4.24E-01	0.46201139	86	1.32E-01
0.10707616	9	1.00E+00	-0.42793721	9	1.02E+01
-0.00097997	9	1.70E+00	0.54923709	9	2.88E-01
-0.17005082	12	6.33E+00	0.45056454	12	4.00E-01
0.37201906	32	1.04E-01	0.56328276	32	9.41E-02
1.09968188	8	1.10E-02	0.71570374	8	1.73E-01
0.09747141	15	1.53E+00	0.16453621	15	1.90E+00
-0.37402725	11	1.69E+01	0.39805938	11	5.06E-01
-0.98345237	11	5.24E+02	-0.20931722	11	6.83E+00
0.31708436	11	3.46E-01	0.69706499	11	1.41E-01
-0.45788752	14	6.19E+01	0.10352841	14	2.41E+00
0.30351281	19	3.27E-01	0.73560585	19	5.31E-02
-0.2717991	20	5.94E+01	-0.04953161	20	1.31E+01
0.64554442	16	2.61E-02	0.658134	16	1.13E-01
-0.03872005	2	9.16E-01	-0.7309981	2	2.40E+00
0.13217689	7	8.05E-01	-0.10037766	7	2.22E+00
-0.05639177	18	6.61E+00	-0.00622899	18	7.34E+00
-0.56500084	5	7.48E+00	0.61106296	5	2.94E-01
-0.29421846	11	1.08E+01	-0.35618776	11	1.28E+01
1.05318665	6	2.49E-02	0.24075842	6	7.51E-01
0.02554241	8	1.36E+00	-1.0656731	8	6.52E+01
-0.89091095	6	3.45E+01	1.23806703	6	5.10E-02
0.40138972	7	2.67E-01	0.21673069	7	8.54E-01
0.70085555	8	6.60E-02	0.68912507	8	1.89E-01
0.43488722	12	1.67E-01	0.82777831	12	7.05E-02
-0.02545698	9	1.91E+00	1.16501213	9	3.05E-02
0.22814195	8	5.50E-01	0.82868658	8	1.18E-01
-0.05614366	21	9.49E+00	0.41134254	21	4.87E-01
0.11882203	15	1.31E+00	0.55702011	15	2.15E-01
0.53453485	5	1.90E-01	0.36395523	5	5.30E-01
0.44181119	7	2.26E-01	-0.10973804	7	2.28E+00
0.36198049	6	3.26E-01	0.7528641	6	1.89E-01
0.57216013	6	1.49E-01	-0.04336636	6	1.62E+00
-0.15402591	9	3.57E+00	-0.60487552	9	1.94E+01
0.04900423	8	1.23E+00	0.03389394	8	1.67E+00
0.49000654	12	1.20E-01	0.26445006	12	9.42E-01
0.75073907	5	9.25E-02	1.46538709	5	3.86E-02

0.49052386	20	5.91E-02	0.80525677	20	2.92E-02
0.33794292	8	3.36E-01	0.04034752	8	1.64E+00
-0.22845397	5	2.43E+00	0.93126823	5	1.37E-01
1.4107505	5	1.02E-02	0.9495943	5	1.32E-01
-0.08199623	9	2.52E+00	0.151828	9	1.23E+00
0.3401428	2	3.99E-01	-0.14277859	2	1.04E+00
-0.05972831	30	2.95E+01	0.10561621	30	1.16E+01
-0.56954436	4	5.53E+00	-0.15753498	4	1.53E+00
-0.30107747	5	3.10E+00	0.10851477	5	9.73E-01
-0.19586268	21	3.55E+01	0.31137501	21	1.03E+00
-0.71084012	12	1.64E+02	-0.37804138	12	1.81E+01
-0.0802742	15	5.46E+00	0.63213195	15	1.41E-01
0.20226713	9	6.31E-01	0.29873216	9	7.19E-01
0.31148479	12	3.50E-01	0.45010477	12	4.01E-01
-0.42908765	42	8.16E+04	-0.31998753	42	1.56E+04
-0.67365475	7	2.19E+01	-1.6332274	7	2.25E+02
-0.02302142	4	1.10E+00	1.08513528	4	1.18E-01
0.22250659	7	5.56E-01	0.03496064	7	1.48E+00
-0.86626765	3	8.64E+00	-0.36545122	3	1.83E+00
-0.03149058	23	9.40E+00	0.51767728	23	2.07E-01
0.1556658	3	6.22E-01	0.91617011	3	1.96E-01
0.86963284	9	2.45E-02	0.41208087	9	4.75E-01
1.00688267	4	5.23E-02	1.26230295	4	8.18E-02
0.25392315	30	5.18E-01	0.29752914	30	1.60E+00
-0.27637975	2	1.54E+00	0.5405723	2	3.91E-01
0.15220422	12	9.12E-01	-0.00559652	12	3.27E+00
0.37785258	40	6.71E-02	0.46204101	40	2.54E-01
-0.03893483	19	6.41E+00	0.36457582	19	6.68E-01
0.09772504	8	9.87E-01	-0.17354792	8	3.34E+00
0.96246491	3	7.80E-02	0.67154074	3	3.00E-01
-0.03831372	2	9.15E-01	0.27219721	2	5.74E-01
0.73923839	16	1.29E-02	0.79664613	16	5.02E-02
0.00766416	7	1.34E+00	-0.2730303	7	3.74E+00
0.08855295	7	9.63E-01	0.06472602	7	1.35E+00
0.16439806	17	1.02E+00	0.65290307	17	1.08E-01
0.32287185	9	3.51E-01	0.16454644	9	1.17E+00
0.76688844	12	2.26E-02	0.18948963	12	1.33E+00
-0.00115004	22	6.24E+00	0.27301866	22	1.43E+00
0.78687358	5	8.20E-02	0.72559187	5	2.24E-01
0.4494511	8	2.04E-01	0.6766471	8	1.97E-01
0.02930469	15	2.49E+00	0.33309466	15	7.44E-01
0.61560749	9	8.45E-02	0.72759036	9	1.50E-01
0.20007103	14	7.16E-01	-0.02406852	14	4.70E+00
0.17393723	23	1.15E+00	-0.01669513	23	1.56E+01
0.18607372	33	1.35E+00	0.13870302	33	1.08E+01
0.32853732	11	3.24E-01	0.19972011	11	1.18E+00
-0.1245713	5	1.72E+00	0.61327129	5	2.93E-01

-0.39939199	8	9.17E+00	-0.76167419	8	2.37E+01
0.23759227	27	6.23E-01	0.5346392	27	1.55E-01
0.77983521	7	5.65E-02	1.43715166	7	2.16E-02
0.20809428	4	5.55E-01	0.26759066	4	6.35E-01
0.15648355	19	1.17E+00	0.0965508	19	4.16E+00
0.03416767	13	2.02E+00	0.64506631	13	1.52E-01
0.47997074	17	8.36E-02	0.99009838	17	1.34E-02
-0.18571564	16	1.38E+01	-0.71836144	16	3.67E+02
0.12269326	33	3.30E+00	0.02398033	33	3.92E+01
0.67104518	4	1.41E-01	1.76972799	4	2.87E-02
0.01151702	4	9.92E-01	-0.35368559	4	2.29E+00
0.02606928	19	3.65E+00	-0.11821504	19	1.80E+01
0.31553275	11	3.49E-01	1.14806907	11	2.04E-02
-1.00784122	11	6.01E+02	-0.79525247	11	8.41E+01
0.21522481	24	7.69E-01	0.20629938	24	2.75E+00
0.22384993	22	6.82E-01	0.56964601	22	1.42E-01
-0.14239301	16	9.93E+00	-0.3598802	16	4.47E+01
-0.30857658	16	3.48E+01	0.00468788	16	5.26E+00
0.36151064	18	2.06E-01	0.53296317	18	2.20E-01
0.53584541	16	5.97E-02	0.65839005	16	1.13E-01
0.45182009	22	7.25E-02	0.85334703	22	1.57E-02
0.33990272	14	2.78E-01	0.61271298	14	1.68E-01
1.19644565	5	2.09E-02	0.74196213	5	2.16E-01
0.06544427	11	1.43E+00	1.21518607	11	1.53E-02
0.0620395	31	6.63E+00	0.43152417	31	4.00E-01
0.42669419	4	2.91E-01	0.72125363	4	2.49E-01
0.1146735	21	1.89E+00	0.67603073	21	6.76E-02
0.03744596	9	1.41E+00	1.24036089	9	2.31E-02
0.42344919	9	2.15E-01	0.91431038	9	7.60E-02
0.32879286	51	1.14E-01	0.4013665	51	6.10E-01
1.08000741	3	5.76E-02	0.21180406	3	6.68E-01
0.06722422	9	1.22E+00	-0.24650722	9	5.26E+00
0.71495045	14	2.19E-02	0.82486176	14	5.52E-02
0.89070126	5	5.80E-02	0.22409865	5	7.39E-01
0.65600513	18	1.78E-02	0.59968535	18	1.42E-01
0.28469623	18	3.89E-01	0.37125232	18	6.29E-01
0.26646429	22	4.49E-01	0.80719925	22	2.25E-02
-0.35630938	10	1.21E+01	0.31771903	10	6.92E-01
0.27833778	36	3.63E-01	0.09633143	36	2.36E+01
0.15734664	10	8.17E-01	0.19888001	10	1.11E+00
0.42998997	5	2.70E-01	1.84779021	5	1.55E-02
-0.11783763	14	6.18E+00	-0.46337919	14	4.70E+01
0.75072257	5	9.25E-02	0.96359709	5	1.27E-01
0.42837928	22	9.13E-02	0.89915111	22	1.10E-02
-0.1558329	4	1.63E+00	-0.20642081	4	1.69E+00
0.36576255	8	2.97E-01	1.05984588	8	5.48E-02
0.38725039	14	2.01E-01	0.22973685	14	1.25E+00

-0.19957187	26	8.87E+01	-0.82128075	26	3.43E+04
-0.02085289	22	7.57E+00	-0.74488297	22	3.93E+03
-0.26734523	11	9.29E+00	0.07470462	11	2.02E+00
-0.03379096	14	3.49E+00	0.42172504	14	4.56E-01
-0.09085522	15	5.88E+00	-0.0814872	15	7.45E+00
0.5005174	21	4.92E-02	0.51344622	21	2.27E-01
0.06438469	9	1.23E+00	0.95077444	9	6.66E-02
0.40025614	17	1.57E-01	0.44102877	17	4.02E-01
0.32656594	22	2.49E-01	0.80656106	22	2.26E-02
-1.17798658	24	1.99E+06	-1.34458645	24	1.28E+06
-0.37138134	4	3.08E+00	0.13299793	4	8.38E-01
0.33742458	36	1.48E-01	0.34568802	36	1.12E+00
0.2420229	25	5.83E-01	0.5098227	25	2.08E-01
0.30584327	28	2.75E-01	0.40911184	28	5.04E-01
0.45687849	42	1.54E-02	0.44978529	42	2.94E-01
0.49561809	11	1.27E-01	0.21210198	11	1.12E+00
-0.04201514	21	8.30E+00	0.29307811	21	1.18E+00
0.45790345	12	1.45E-01	-0.16169547	12	6.70E+00
0.07671803	5	8.78E-01	0.23426893	5	7.21E-01
0.30723774	63	1.45E-01	0.34795161	63	1.97E+00
-0.81068921	9	8.73E+01	-0.86508495	9	5.03E+01
0.00256424	17	3.67E+00	0.68565965	17	8.85E-02
-0.42377491	5	4.67E+00	-0.70585736	5	6.75E+00
-0.06266513	8	2.03E+00	-0.17552629	8	3.36E+00
-0.71297477	8	3.74E+01	-0.39719848	8	7.04E+00
0.36246049	29	1.33E-01	0.34842072	29	9.28E-01
-1.26500716	17	8.44E+04	-0.32634344	17	4.65E+01
0.01678495	14	2.48E+00	-0.35999456	14	2.73E+01
0.64715564	6	1.13E-01	-0.16320733	6	2.23E+00
0.09014337	5	8.39E-01	0.46482979	5	4.17E-01
-0.92497782	3	1.01E+01	0.45382638	3	4.38E-01
0.08409806	4	8.01E-01	0.84755139	4	1.92E-01
-1.13919582	7	1.48E+02	-1.04589207	7	3.84E+01
-0.72869331	7	2.75E+01	0.55685256	7	3.06E-01
0.59637737	9	9.27E-02	1.07166392	9	4.28E-02
-0.29984677	4	2.49E+00	-0.00365626	4	1.11E+00
0.08323293	33	5.73E+00	0.43463201	33	3.83E-01
0.0686988	39	1.09E+01	0.11734077	39	2.42E+01
0.41322927	12	1.90E-01	0.48626368	12	3.40E-01
-0.04694283	11	2.69E+00	0.76710036	11	1.04E-01
0.47076073	21	6.52E-02	0.71481253	21	5.06E-02
0.29903675	28	2.98E-01	0.29211221	28	1.57E+00
0.28080205	12	4.21E-01	0.83534427	12	6.81E-02
-0.17295511	38	4.79E+02	-0.08434176	38	2.95E+02
0.49403383	11	1.28E-01	0.52256372	11	2.97E-01
-0.69081887	9	4.87E+01	-1.09907356	9	1.18E+02
0.68948549	19	1.15E-02	0.7078999	19	6.41E-02

0.35713284	35	1.14E-01	0.51338802	35	1.48E-01
0.91044988	3	8.92E-02	0.43199952	3	4.55E-01
0.44421223	12	1.58E-01	0.9798964	12	3.50E-02
-0.24034913	13	1.17E+01	0.13754646	13	1.85E+00
0.22252462	19	6.62E-01	0.08323317	19	4.56E+00
0.15291843	13	9.46E-01	1.00572793	13	2.58E-02
0.44408247	8	2.09E-01	-0.12550959	8	2.85E+00
-0.21000373	17	1.98E+01	0.22294295	17	1.55E+00
0.97951568	9	1.44E-02	0.94477575	9	6.80E-02
0.05707327	33	8.28E+00	0.62087331	33	4.69E-02
0.36314071	23	1.67E-01	0.52756154	23	1.91E-01
0.0925218	61	3.04E+01	0.20807194	61	3.16E+01
-0.29857945	14	2.10E+01	0.18080689	14	1.61E+00
0.30468193	9	3.83E-01	0.36429806	9	5.66E-01
0.62436363	5	1.41E-01	0.72843349	5	2.23E-01
0.02691234	5	1.04E+00	0.32539653	5	5.81E-01
0.61311673	20	1.94E-02	0.23500564	20	1.71E+00
0.37783414	16	1.96E-01	0.96492939	16	1.87E-02
-0.06620731	8	2.06E+00	0.22559109	8	8.83E-01
-1.23918431	18	1.22E+05	-1.45452596	18	9.10E+04
-1.28559893	2	1.41E+01	-0.61455885	2	2.03E+00
0.02550248	9	1.49E+00	0.33775219	9	6.24E-01
0.21850101	5	5.47E-01	1.86605268	5	1.49E-02
0.14934606	28	1.83E+00	0.72108859	28	2.46E-02
0.20857908	28	8.94E-01	0.74045721	28	2.04E-02
0.39758061	6	2.85E-01	0.19401426	6	8.52E-01
-0.39289275	4	3.28E+00	1.0306493	4	1.32E-01
0.31164919	8	3.78E-01	0.87008747	8	1.03E-01
-0.24178087	14	1.43E+01	0.14114015	14	1.98E+00
-0.50281682	4	4.54E+00	-0.5430876	4	3.38E+00
0.31205077	8	3.77E-01	-0.13480607	8	2.94E+00
-0.14835318	6	2.18E+00	-0.27445587	6	3.01E+00
0.05011049	19	2.96E+00	0.00887172	19	7.57E+00
-0.54922542	5	7.09E+00	0.78743157	5	1.93E-01
0.21810238	35	8.92E-01	0.45465846	35	2.98E-01
-0.31091087	130	2.30E+12	0.1732241	130	1.34E+04
-0.44481824	5	5.01E+00	0.19667076	5	7.89E-01
-1.2093335	10	1.07E+03	-0.75483248	10	4.88E+01
0.55755995	8	1.25E-01	0.36814249	8	5.49E-01
0.07025692	4	8.34E-01	1.25962126	4	8.22E-02
-0.26633581	13	1.38E+01	0.72900998	13	1.01E-01
0.34563457	15	2.59E-01	0.66076872	15	1.21E-01
0.47870622	2	2.95E-01	0.58844452	2	3.66E-01
0.90315596	7	3.40E-02	0.52347114	7	3.39E-01
0.11468811	11	1.08E+00	0.73704783	11	1.19E-01
0.85889403	8	3.25E-02	0.34674462	8	5.90E-01