

Table S1 Number of aligned mRNA reads to the *D. melanogaster* Refseq mRNA.

Samples	Barcode	Total # of post-filter reads	Mapped to dm3 genome and transcriptome
Control	ACTT	1,077,110	239,757
	TCGC	3,175,833	398,659
IPC	CTGG	3,118,626	592,440
	CGTC	3,833,784	417,340

Tables S2-S5

Available for download as Excel files at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.113.160663/-/DC1>

Table S2 List of all genes with aligned reads in laser-captured IPC and control samples.

Table S3 List of 193 IPC-enriched genes with their annotated molecular functions.

Table S4 Full list of biological functional clusters annotated by DAVID with IPC-enriched transcripts.

Table S5 List of 109 IPC-enriched genes and their mouse orthologs. The mouse orthologs that have higher expression levels in beta cells compared to other non-beta cell tissues (Ku et al.) are indicated.