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Data in Brief

# Identifying type 1 diabetes candidate genes by DNA microarray analysis of islet-specific CD4 + T cells

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ABSTRACT

Type 1 diabetes (T1D) is a T cell-mediated autoimmune disease resulting from the destruction of insulin-producing pancreatic beta cells and is fatal unless treated with insulin. During the last four decades, multiple insulin-dependent diabetes (*Idd*) susceptibility/resistance loci that regulate T1D development have been identified in humans and non-obese diabetic (NOD) mice, an established animal model for T1D. However, the exact mechanisms by which these loci confer diabetes risk and the identity of the causative genes remain largely elusive. To identify genes and molecular mechanisms that control the function of diabetogenic T cells, we conducted DNA microarray analysis in islet-specific CD4 + T cells from BDC2.5 TCR transgenic NOD mice that contain the *Idd9* locus from T1D-susceptible NOD mice or T1D-resistant C57BL/10 mice. Here we describe in detail the contents and analyses for these gene expression data associated with our previous study [1]. Gene expression data are available at the Gene Expression Omnibus (GEO) repository from the National Center for Biotechnology Information (accession number GSE64674).



| Specifications | |
|---|---|
| Organism/cell line/tissue | Mus musculus/islet-specific CD4 + T cells |
| Sex | Female |
| Sequencer or array type | Illumina MouseWG-6 v2.0 expression beadchip |
| Data format | Raw and processed |
| Experimental factors | Ex vivo and antigen-activated islet-specific CD4 + T cells |
| Experimental features | Analysis of gene expression levels in ex vivo and BDC2.5 mimotope-stimulated BDC2.5 CD4 + T cells containing insulin-dependent diabetes (*Idd*) locus 9 from diabetes-susceptible NOD or diabetes-resistant C57BL/10 mice |
| Consent | N/A |
| Sample source location | Hershey, PA, USA |

## 1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE64674.

## 2. Experimental design, materials and methods

### 2.1. Experimental design

Diabetes-free female BDC mice [2] and recently generated BDC-*Idd9*.905 NOD mice [1] were used as donors of splenic islet-specific CD4 + T cells that were pooled from two mice per group (6–9 weeks old; n = 6/group). CD4 + T cells transgenic for the islet-specific BDC2.5 TCR (CD4 + TCRVβ4 +) were isolated by flow cytometry immediately (ex vivo) or following splenocyte stimulation (48 h) with BDC2.5 mimotope p79 (p79-stimulated) [3]. We used three independent biological replicates for each condition for DNA microarray analysis.

### 2.2. Materials and methods

#### 2.2.1. RNA extraction

Total RNA was extracted from ex vivo or p79-stimulated CD4 + TCRVβ4 + BDC and BDC-*Idd9*.905 T cells [1,2] using the RNeasy kit (Qiagen). RNA quality and concentration were assessed using an Agilent 2100 Bioanalyzer with RNA Nano LabChip (Agilent, Santa Clara, CA). Labeled cRNA (750 ng/sample) was synthesized by TotalPrep Amplification (Ambion, Austin, TX) and used for hybridization to MouseWG-6

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v2.0 R3 Expression BeadChips for 18 h at 58 °C according to manufacturer's instructions. Following hybridization, Beadchips were washed and fluorescently labeled. Three independent replicate microarray hybridizations were processed per strain and per condition (12 hybridizations total). To collect intensity data, Beadchips were scanned with a BeadArray Reader (Illumina, San Diego, CA). A project was created with resultant scan data imported into GenomeStudio 1.0 (Illumina). Results were exported to GeneSpring Gx11 (Agilent Technologies).

*2.2.2. Microarray data analysis*

GeneSpring Gx11 software (Agilent Technologies, Santa Clara, CA) was used to analyze expression data, which was normalized to the median expression level of each gene. Expression of a transcript with detection p-value < 0.15 was considered present/marginal. Transcripts were subsequently filtered for signal level > 100 in at least 50% of the values in one of the six samples of each condition. Transcripts that failed to meet these requirements were excluded from further analysis. Differentially expressed genes were identified through volcano plots between non-averaged group comparison using fold-change of 1.4 or greater and asymptotic unpaired t-test p-value computation of $p < 0.05$ [4]. We subsequently subjected significantly differentially expressed gene sets to bioinformatics analyses to cluster them according to their biological functions and to discover T cell-specific gene networks using Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.7 [5] and Ingenuity Pathway Analysis (IPA) 8.6 (Ingenuity Systems, Redwood City, CA) software, respectively. Heat maps and hierarchical clustering of significantly differentially expressed genes were generated with R using the heatmap.2 function of the gplots package. Raw and processed gene expression data were deposited in Gene Expression Omnibus repository at the National Center for Biotechnology Information and are accessible through the accession number GSE64674.

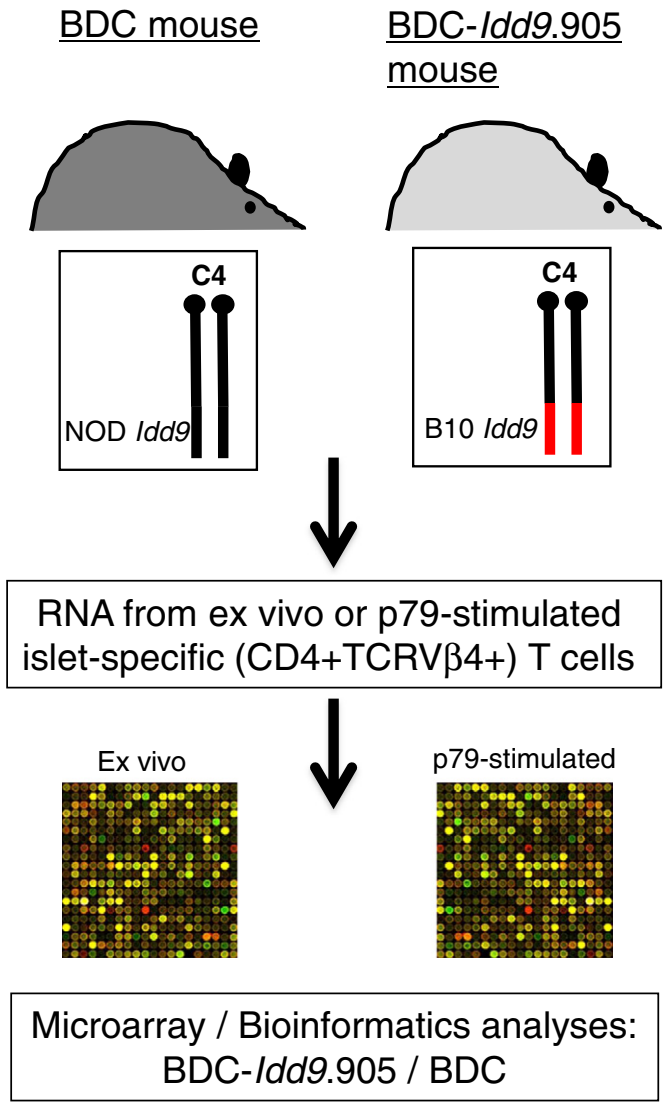


**Fig. 1.** Experimental design of gene expression analyses of islet-specific (CD4 + TCRVβ4 +) T cells containing NOD- or B10-derived *Idd9*.

## 3. Discussion

We described here unique datasets of ex vivo and antigen (p79)-stimulated islet-specific CD4 + T cells containing either the *Idd9* from T1D-susceptible NOD mice or T1D-resistant C57BL/10 mice (Fig. 1). These datasets show genome wide gene expression determined using Illumina MouseWG-6 v2.0 expression beadchip platform. We identified 55 genes and 80 genes that were differentially expressed in ex vivo and p79-stimulated CD4 + T cells, respectively (Figs. 2, 3). The majority of these genes were unique to either experimental condition, whereas 18 genes were differentially expressed under both conditions (Fig. 2). Notably, gene sets were highly enriched in genes within the *Idd9* locus and *Idd11* locus, which partially overlaps *Idd9* (Tables 1, 2). Bioinformatics analyses revealed that islet-specific CD4 + T cells containing the T1D-resistant *Idd9* were most significantly enriched for genes associated with cellular growth and development/differentiation. Of these genes, *Eno1*, *Rbbp4* and *Mtor* are encoded by *Idd9*, suggesting that they contribute to *Idd9*-dependent T1D susceptibility by regulating the diabetogenic function of islet-specific CD4 + T cells. The provided datasets, together with our previous gene expression validation by RT-qPCR and functional analyses of BDC and BDC-*Idd9*.905 CD4 + T cells [1], demonstrate the validity of using global gene expression analysis to discover T1D candidate genes and mechanisms that control T1D susceptibility.

## Acknowledgments

We thank Dr. Willard Freeman at the PSU College of Medicine Genome Sciences Facility for advice with the DNA microarray analysis. This work was supported by funds from the Pennsylvania Department of Health (RFA#67-27a) to HPW.

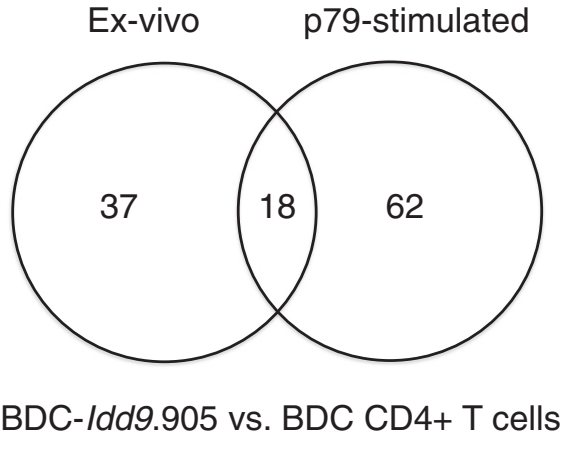


**Fig. 2.** Differentially expressed genes in BDC-*Idd9*.905 versus BDC CD4 + T cells. Venn diagram showing the number of commonly or uniquely differentially expressed genes in ex vivo or p79-stimulated islet-specific CD4 + T cells from BDC-*Idd9*.905 and BDC mice.

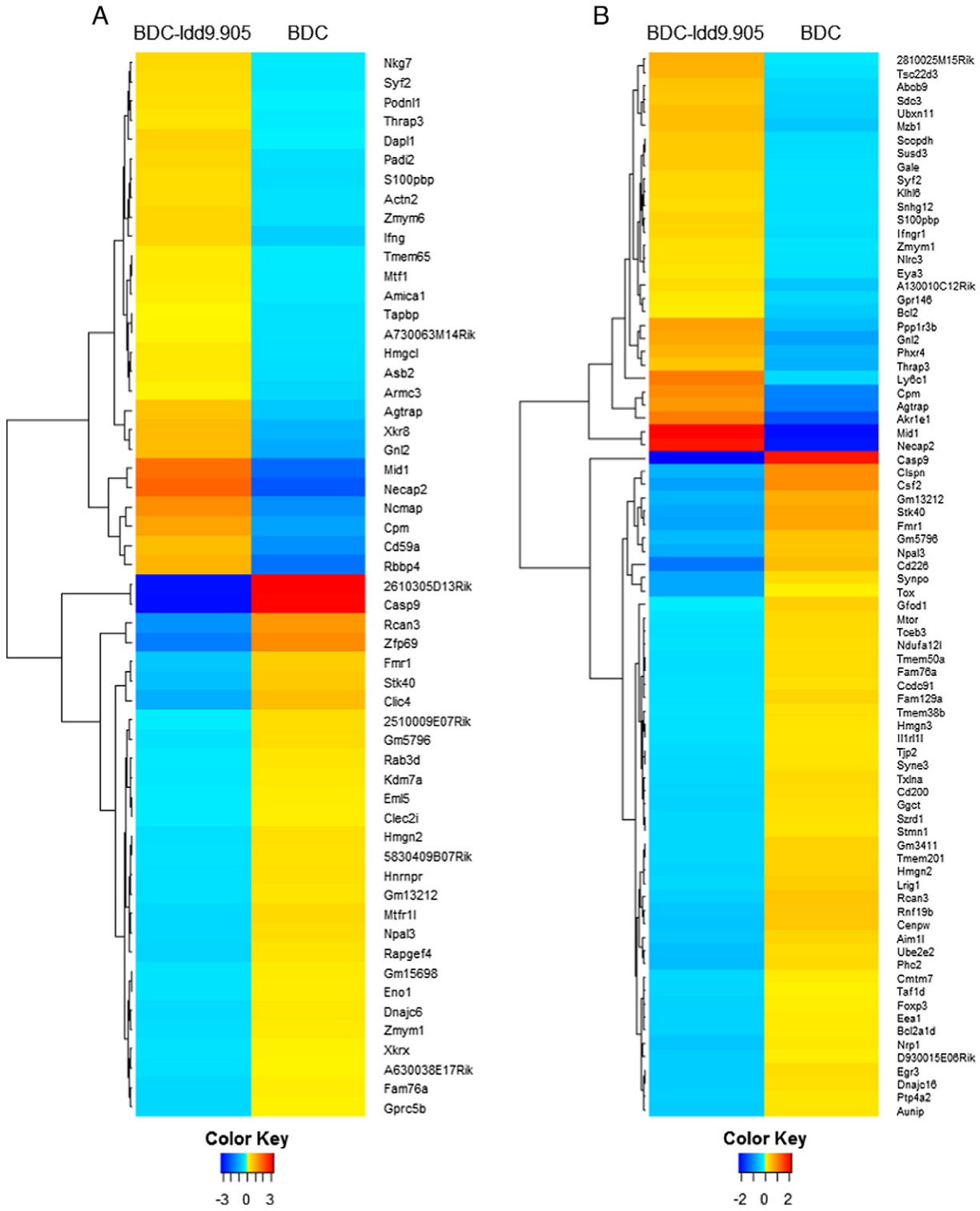


**Fig. 3.** Gene expression heat map and hierarchical clustering from microarray analysis. Columns show the expression patterns for significantly differentially expressed genes in ex vivo (A) or p79-stimulated (B) islet-specific CD4 + T cells from BDC-*Idd9*.905 vs. BDC mice. The red and blue colors represent high and low gene expression values within the indicated ranges, respectively.

**Table 1**
Differentially expressed transcripts between ex vivo BDC-*Idd9*.905 and BDC CD4 + TCRVβ4 + T cells detected by Illumina microarray probes.

| Probe ID | Gene symbol | Gene ID[a] | Chromosome | Idd region | p-Value | Fold change[b] | Regulation |
|---|---|---|---|---|---|---|---|
| 1570725 | Rcan3 | 53902 | 4 | | 2.47E−08 | 6.50 | Down |
| 7210706 | Casp9 | 12371 | 4 | | 1.33E−06 | 77.69 | Down |
| 1470608 | 2610305D13Rik | 112422 | 4 | Idd9.2 | 2.80E−06 | 78.00 | Down |
| 770133 | Xkr8 | 381560 | 4 | Idd11 | 1.18E−05 | 3.49 | Up |
| 5720706 | Fmr1 | 14265 | X | | 2.32E−05 | 2.53 | Down |

**Table 1** (*continued*)

| Probe ID | Gene symbol | Gene ID[a] | Chromosome | Idd region | p-Value | Fold change[b] | Regulation |
|---|---|---|---|---|---|---|---|
| 4810746 | Necap2 (synonym: 1110005F07Rik) | 66147 | 4 | | 3.57E−05 | 17.49 | Up |
| 1110349 | Ncmap (synonym: A330049M08Rik) | 230822 | 4 | | 5.81E−05 | 7.04 | Up |
| 4490356 | Zfp69 | 381549 | 4 | | 1.28E−04 | 8.79 | Down |
| 160519 | Tmem65 | 74868 | 15 | | 3.27E−04 | 1.46 | Up |
| 5360181 | Cpm | 70574 | 10 | | 3.27E−04 | 4.61 | Up |
| 610253 | Eno1 | 13806 | 4 | Idd9.3 | 8.39E−04 | 1.54 | Down |
| 3400491 | Clic4 | 29876 | 4 | | 0.00126461 | 3.54 | Down |
| 2190193 | Gnl2 | 230737 | 4 | | 0.001477347 | 3.87 | Up |
| 2850403 | Mid1 | 17318 | X | | 0.001548464 | 13.21 | Up |
| 610600 | Hmgn2 | 15331 | 4 | | 0.002030275 | 1.73 | Down |
| 270446 | S100pbp | 74648 | 4 | Idd9.1 | 0.002319395 | 1.87 | Up |
| 1470278 | Rab3d | 19340 | 9 | | 0.002501244 | 1.52 | Down |
| 5260433 | Agtrap | 11610 | 4 | Idd9.2 | 0.002749308 | 2.71 | Up |
| 7160392 | Rbbp4 | 19646 | 4 | Idd9.1 | 0.003758136 | 6.69 | Up |
| 4890079 | Padi2 | 18600 | 4 | | 0.004021732 | 1.89 | Up |
| 3420601 | Npal3 | 74552 | 4 | | 0.004041954 | 1.87 | Down |
| 6660020 | Zmym6 (synonym: 9330177P20Rik) | 100177 | 4 | Idd11 | 0.004275929 | 1.91 | Up |
| 5310274 | Rapgef4 | 56508 | 2 | | 0.005024596 | 1.85 | Down |
| 2030328 | Hnrnpr (synonym: 2610528B01Rik) | 74326 | 4 | | 0.005105765 | 1.77 | Down |
| 4850270 | Gm15698 | 217066 | 11 | | 0.005937492 | 1.56 | Down |
| 6660601 | Hmgcl | 15356 | 4 | | 0.008095779 | 1.63 | Up |
| 7160132 | Kdm7a (synonym: A630082K20Rik) | 338523 | 6 | | 0.0083255 | 1.53 | Down |
| 4480543 | Mtf1 | 17764 | 4 | | 0.009257403 | 1.47 | Up |
| 1990021 | Gm5796 (synonym: ENSMUSG00000068790) | 545007 | 14 | | 0.009987115 | 1.75 | Down |
| 6940537 | Dnajc6 | 72685 | 4 | | 0.010992913 | 1.71 | Down |
| 1400685 | Fam76a (BC008163) | 230789 | 4 | Idd11 | 0.015078585 | 1.67 | Down |
| 2030632 | Stk40 | 74178 | 4 | Idd11 | 0.015925948 | 2.75 | Down |
| 1440706 | Armc3 | 70882 | 2 | | 0.017203094 | 1.62 | Up |
| 6280477 | Ifng | 15978 | 10 | | 0.017631533 | 2.18 | Up |
| 430543 | A730063M14Rik | 100504703 | 10 | | 0.017646367 | 1.44 | Up |
| 6200619 | Xkrx | 331524 | X | | 0.019023608 | 1.46 | Down |
| 3360132 | Syf2 | 68592 | 4 | | 0.019146714 | 1.62 | Up |
| 2850398 | Asb2 | 65256 | 12 | | 0.0203302 | 1.66 | Up |
| 6980170 | Podnl1 | 244550 | 8 | | 0.023623548 | 1.50 | Up |
| 7200180 | 5830409B07Rik | 76020 | 4 | | 0.0246163 | 1.71 | Down |
| 430066 | Gprc5b | 64297 | 7 | | 0.026957931 | 1.60 | Down |
| 1090441 | Clec2i | 93675 | 6 | | 0.031066772 | 1.41 | Down |
| 870370 | 2510009E07Rik | 72190 | 16 | | 0.03157309 | 1.57 | Down |
| 1440019 | Cd59a | 12509 | 2 | | 0.03529127 | 4.79 | Up |
| 1570544 | Thrap3 (C730026O12Rik) | 230753 | 4 | Idd11 | 0.035571814 | 1.49 | Up |
| 460390 | Mtfr1l (synonym: 2410166I05Rik) | 76824 | 4 | | 0.036052007 | 1.93 | Down |
| 1570288 | Dapl1 | 76747 | 2 | | 0.036334574 | 1.65 | Up |
| 6200386 | Gm13212 (LOC433801) | 433801 | 4 | Idd9.2 | 0.03805429 | 1.67 | Down |
| 5390243 | Zmym1 | 68310 | 4 | Idd11 | 0.040785447 | 1.66 | Down |
| 1050678 | Actn2 | 11472 | 13 | | 0.04146113 | 1.79 | Up |
| 3850692 | Amica1 | 270152 | 9 | | 0.04214731 | 1.42 | Up |
| 6760736 | Eml5 | 319670 | 12 | | 0.0422112 | 1.42 | Down |
| 50255 | A630038E17Rik | 219065 | 14 | | 0.04455469 | 1.47 | Down |
| 4040035 | Nkg7 | 72310 | 7 | | 0.04593347 | 1.65 | Up |
| 3140386 | Tapbp | 21356 | 17 | | 0.04769256 | 1.42 | Up |

[a] Fold change in expression of BDC-*Idd9*.905/BDC samples.
[b] Gene ID: Entrez database.

**Table 2**
Differentially expressed transcripts between p79-stimulated BDC-*Idd9*.905 and BDC CD4 + TCRVβ4 + T cells detected by Illumina microarray probes.

| Probe ID | Gene symbol | Gene ID[a] | Chromosome | Idd region | p-Value | Fold change[b] | Regulation |
|---|---|---|---|---|---|---|---|
| 4810746 | Necap2 (synonym: 1110005F07Rik) | 66147 | 4 | | 1.04E−05 | 15.57 | Up |
| 5720706 | Fmr1 | 14265 | X | | 1.50E−05 | 2.81 | Down |
| 6200386 | Gm13212 (LOC433801) | 433801 | 4 | Idd9.2 | 4.05E−05 | 2.48 | Down |
| 2190193 | Gnl2 | 230 | 4 | | 1.23E−04 | 2.81 | Up |
| 5260433 | Agtrap | 11610 | 4 | Idd9.2 | 2.04E−04 | 3.93 | Up |
| 7210706 | Casp9 | 12371 | 4 | | 2.50E−04 | 17.66 | Down |
| 5360181 | Cpm | 70574 | 10 | | 2.53E−04 | 4.08 | Up |
| 5560131 | Syne3 (synonym: 4831426I19Rik) | 212073 | 12 | | 4.21E−04 | 1.46 | Down |
| 3890682 | Cenpw (synonym: 2610036L11Rik) | 66311 | 10 | | 4.84E−04 | 1.97 | Down |
| 130270 | Ndufa12l | 75597 | 13 | | 5.54E−04 | 1.45 | Down |
| 2030632 | Stk40 | 74178 | 4 | Idd11 | 6.77E−04 | 2.83 | Down |
| 70019 | Akr1e1 | 56043 | 13 | | 8.21E−04 | 6.03 | Up |
| 3420601 | Npal3 | 74552 | 4 | | 9.22E−04 | 2.27 | Down |
| 1980608 | Tmem201 | 230917 | 4 | | 0.001167733 | 1.64 | Down |
| 610600 | Hmgn2 | 15331 | 4 | | 0.001190718 | 1.69 | Down |

(*continued on next page*)

**Table 2** (*continued*)

| Probe ID | Gene symbol | Gene ID[a] | Chromosome | Idd region | p-Value | Fold change[b] | Regulation |
|---|---|---|---|---|---|---|---|
| 1850403 | Mtor (synonym: Frap1) | 56717 | 4 | Idd9.2 | 0.001898694 | 1.47 | Down |
| 1570544 | Thrap3 (C730026O12Rik) | 230753 | 4 | Idd11 | 0.00191536 | 2.23 | Up |
| 6370176 | Csf2 | 12981 | 11 | | 0.002062027 | 3.40 | Down |
| 3360132 | Syf2 | 68592 | 4 | | 0.002120117 | 1.50 | Up |
| 2450470 | Txlna | 109658 | 4 | Idd9.1 | 0.002173837 | 1.56 | Down |
| 6250133 | Ccdc91 | 67015 | 6 | | 0.002950219 | 1.46 | Down |
| 7650139 | Phc2 | 54383 | 4 | Idd9.1 | 0.003565085 | 1.83 | Down |
| 6510647 | Tceb3 | 27224 | 4 | | 0.003816067 | 1.50 | Down |
| 3170619 | Rnf19b | 75234 | 4 | Idd9.1 | 0.003891535 | 1.94 | Down |
| 270446 | S100pbp | 74648 | 4 | Idd9.1 | 0.005145121 | 1.47 | Up |
| 1780445 | Klhl6 | 239743 | 16 | | 0.005396708 | 1.53 | Up |
| 4120709 | Dnajc16 (synonym: 2900037O03Rik) | 214063 | 4 | | 0.005405837 | 1.62 | Down |
| 1570725 | Rcan3 | 53902 | 4 | | 0.006421643 | 1.91 | Down |
| 270139 | Cd200 | 17470 | 16 | | 0.00670664 | 1.49 | Down |
| 2850403 | Mid1 | 17318 | X | | 0.006896318 | 18.23 | Up |
| 2900139 | Ube2e2 | 218793 | 14 | | 0.007577249 | 1.79 | Down |
| 5820646 | Ptp4a2 | 19244 | 4 | Idd9.1 | 0.007635422 | 1.55 | Down |
| 3120392 | Stmn1 | 16765 | 4 | | 0.007748838 | 1.49 | Down |
| 4540626 | Tmem38b | 52076 | 4 | | 0.00839877 | 1.41 | Down |
| 1990021 | Gm5796 (synonym: ENSMUSG00000068790) | 545007 | 14 | | 0.009142185 | 2.11 | Down |
| 2650397 | Ubxn11 (synonym: D4Bwg1540e) | 67586 | 4 | | 0.009179465 | 1.90 | Up |
| 520286 | Phxr4 | 18689 | 9 | | 0.009703344 | 2.36 | Up |
| 7160626 | Il1rl1l | 17083 | 9 | | 0.010156409 | 1.41 | Down |
| 5080600 | Aim1l | 230806 | 4 | | 0.01032208 | 1.79 | Down |
| 1690255 | Susd3 | 66329 | 13 | | 0.011247533 | 1.66 | Up |
| 4920564 | Szrd1 (synonym: D4Ertd22e) | 213491 | 4 | | 0.011548025 | 1.50 | Down |
| 6350192 | Snhg12 (synonym: 2310005L22Rik) | 100039864 | 4 | Idd11 | 0.011811014 | 1.48 | Up |
| 2940441 | Nlrc3 (synonym: D230007K08Rik) | 268857 | 16 | | 0.012169471 | 1.43 | Up |
| 5820438 | Cd226 | 225825 | 18 | | 0.012342826 | 3.30 | Down |
| 5270575 | Gale | 74246 | 4 | | 0.012346829 | 1.62 | Up |
| 5690348 | Taf1d (synonym:4930553M18Rik) | 75316 | 9 | | 0.015596034 | 1.40 | Down |
| 940274 | A130010C12Rik | 320211 | 8 | | 0.015818644 | 1.74 | Up |
| 1030152 | Ifngr1 | 15979 | 10 | | 0.01632345 | 1.57 | Up |
| 1980768 | Cmtm7 | 102545 | 9 | | 0.016449802 | 1.42 | Down |
| 2480500 | Zmym1 (4933412A02Rik) | 68310 | 4 | Idd11 | 0.01667966 | 1.41 | Up |
| 7210672 | Mzb1 (synonym: 2010001M09Rik) | 69816 | 18 | | 0.01843534 | 2.00 | Up |
| 5570358 | Bcl2 | 12043 | 1 | | 0.019133182 | 1.52 | Up |
| 7380113 | Ggct (synonym: A030007L17Rik) | 110175 | 6 | | 0.019302472 | 1.55 | Down |
| 5670634 | Synpo | 104027 | 18 | | 0.021028133 | 2.04 | Down |
| 5360608 | Tjp2 | 21873 | 19 | | 0.02300658 | 1.44 | Down |
| 6510286 | Tmem50a | 71817 | 4 | | 0.0230189 | 1.49 | Down |
| 3800300 | LOC100041569 (Gm3411) | 100041569 | 14 | | 0.023209462 | 1.65 | Down |
| 1980370 | Gpr146 | 80290 | 5 | | 0.024589665 | 1.45 | Up |
| 5720017 | Eea1 | 216238 | 10 | | 0.024702739 | 1.46 | Down |
| 1400685 | Fam76a (BC008163) | 230789 | 4 | Idd11 | 0.025232932 | 1.50 | Down |
| 990671 | D930015E06Rik | 229473 | 3 | | 0.026054276 | 1.50 | Down |
| 6760762 | Sdc3 | 20970 | 4 | Idd9.1 | 0.028066363 | 1.80 | Up |
| 5310431 | Fam129a | 63913 | 1 | | 0.031280726 | 1.54 | Down |
| 3370196 | Gfod1 (AI850995) | 328232 | 13 | | 0.032448232 | 1.41 | Down |
| 4210152 | 2810025M15Rik | 69953 | 1 | | 0.033680663 | 1.80 | Up |
| 3180408 | Bcl2a1d | 12047 | 9 | | 0.036864646 | 1.49 | Down |
| 360743 | Nrp1 | 18186 | 8 | | 0.0391383 | 1.63 | Down |
| 2230132 | Eya3 | 14050 | 4 | Idd11 | 0.040735032 | 1.40 | Up |
| 6980315 | Clspn | 269582 | 4 | Idd11 | 0.040747937 | 3.01 | Down |
| 5080634 | Ppp1r3b | 244416 | 8 | | 0.043392483 | 2.59 | Up |
| 1570241 | Foxp3 | 20371 | X | | 0.044076834 | 1.45 | Down |
| 1090008 | Abcb9 | 56325 | 5 | | 0.045361392 | 1.79 | Up |
| 5340288 | Sccpdh | 109232 | 1 | | 0.04552452 | 1.65 | Up |
| 2070328 | Aunip (synonym: 2610002D18Rik) | 69885 | 4 | | 0.046391055 | 1.59 | Down |
| 6840382 | Tsc22d3 | 14605 | X | | 0.046913423 | 1.88 | Up |
| 670133 | Hmgn3 | 94353 | 9 | | 0.046961725 | 1.43 | Down |
| 3130020 | Lrig1 | 16206 | 6 | | 0.04753622 | 1.68 | Down |
| 20612 | Egr3 | 13655 | 14 | | 0.047545053 | 1.65 | Down |
| 5550671 | Ly6c1 | 17067 | 15 | | 0.049469374 | 2.70 | Up |
| 5690424 | Tox | 252838 | 4 | | 0.049562268 | 1.85 | Down |

[a] Fold change in expression of BDC-*Idd9*.905/BDC samples.
[b] Gene ID: Entrez database.

## References


[1] G.J. Berry, C. Frielle, T. Luu, A.C. Salzberg, D.B. Rainbow, L.S. Wicker, H. Waldner, Genome-wide transcriptional analyses of islet-specific CD4+ T cells identify Idd9 genes controlling diabetogenic T cell function. J. Immunol. 194 (2015) 2654–2663.

[2] J.D. Katz, B. Wang, K. Haskins, C. Benoist, D. Mathis, Following a diabetogenic T cell from genesis through pathogenesis. Cell 74 (1993) 1089–1100.

[3] V. Judkowski, C. Pinilla, K. Schroder, L. Tucker, N. Sarvetnick, D.B. Wilson, Identification of MHC class II-restricted peptide ligands, including a glutamic acid decarboxylase 65 sequence, that stimulate diabetogenic T cells from transgenic BDC2.5 nonobese diabetic mice. J. Immunol. 166 (2001) 908–917.

[4] I.V. Yang, E. Chen, J.P. Hasseman, W. Liang, B.C. Frank, S. Wang, V. Sharov, A.I. Saeed, J. White, J. Li, N.H. Lee, T.J. Yeatman, J. Quackenbush, Within the fold: assessing differential expression measures and reproducibility in microarray assays. Genome Biol. 3 (2002) (research0062).

[5] W. Huang da, B.T. Sherman, R.A. Lempicki, Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nat. Protoc. 4 (2009) 44–57.