

Overexpression of Dimethylarginine Dimethylaminohydrolase 1 Attenuates Airway Inflammation in a Mouse Model of Asthma

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Abstract

Levels of asymmetric dimethylarginine (ADMA), an endogenous inhibitor of nitric oxide synthase, are increased in lung, sputum, exhaled breath condensate and plasma samples from asthma patients. ADMA is metabolized primarily by dimethylarginine dimethylaminohydrolase 1 (DDAH1) and DDAH2. We determined the effect of DDAH1 overexpression on development of allergic inflammation in a mouse model of asthma. The expression of DDAH1 and DDAH2 in mouse lungs was determined by RT-quantitative PCR (qPCR). ADMA levels in bronchoalveolar lavage fluid (BALF) and serum samples were determined by mass spectrometry. Wild type and DDAH1-transgenic mice were intratracheally challenged with PBS or house dust mite (HDM). Airway inflammation was assessed by bronchoalveolar lavage (BAL) total and differential cell counts. The levels of IgE and IgG1 in BALF and serum samples were determined by ELISA. Gene expression in lungs was determined by RNA-Seq and RT-qPCR. Our data showed that the expression of DDAH1 and DDAH2 was decreased in the lungs of mice following HDM exposure, which correlated with increased ADMA levels in BALF and serum. Transgenic overexpression of DDAH1 resulted in decreased BAL total cell and eosinophil numbers following HDM exposure. Total IgE levels in BALF and serum were decreased in HDM-exposed DDAH1-transgenic mice compared to HDM-exposed wild type mice. RNA-Seq results showed downregulation of genes in the inducible nitric oxide synthase (iNOS) signaling pathway in PBS-treated DDAH1-transgenic mice versus PBS-treated wild type mice and downregulation of genes in IL-13/FOXA2 signaling pathway in HDM-treated DDAH1-transgenic mice versus HDM-treated wild type mice. Our findings suggest that decreased expression of DDAH1 and DDAH2 in the lungs may contribute to allergic asthma and overexpression of DDAH1 attenuates allergen-induced airway inflammation through modulation of Th2 responses.

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Introduction

Asthma is a chronic inflammatory lung disease characterized by airway hyperresponsiveness (AHR), airway inflammation, excess mucus production and pulmonary remodeling [1]. Arginine metabolism has been found to play a critical role in the pathogenesis of allergic asthma [1,2] and mounting evidence suggests that nitric oxide (NO) bioavailability plays an important role in the development of allergic inflammation [3,4]. Arginine is metabolized by arginase yielding urea and L-ornithine that is further metabolized to polyamines and prolines, which can modulate cell proliferation and collagen production [4]. Arginine is also metabolized by nitric oxide synthases (NOS) including neuronal NOS (nNOS), inducible NOS (iNOS) and endothelial NOS (eNOS) [5]. eNOS is expressed in bronchial epithelium and type II alveolar epithelium, nNOS is expressed in airway nervous

tissue, and iNOS is expressed in type II alveolar epithelium, lung fibroblasts, airway and vascular smooth muscle cells. The constitutive NO produced by nNOS and eNOS is important for smooth muscle relaxation, bronchodilation and determination of vascular tone and blood pressure while the inducible NO produced by iNOS has pro-inflammatory effects [5].

Asymmetric dimethylarginine (ADMA) is a by-product released from proteolysis of methylated proteins and ADMA competitively inhibits all three NOS by displacing L-arginine from NOS [6]. ADMA also competes with arginine for cellular uptake by cationic amino-acid transporters, affecting the cellular ADMA/arginine ratio [7,8]. Analysis of methylarginine metabolism in the cardiovascular system showed that the lung is a major source of ADMA [9]. ADMA has been shown to have profound effects on multiple tissues. Microarray studies showed that pathophysiologic

ical concentrations of ADMA elicit significant changes in the gene expression in coronary artery endothelial cells [10]. Treatment of primary mouse lung fibroblasts with ADMA induced arginase activity and collagen production [11]. ADMA infusion resulted in increased lung resistance and decreased compliance in response to methacholine in mice, which was associated with significantly increased pulmonary collagen deposition [11]. ADMA potentiates ovalbumin-induced airway inflammation in a mouse model of asthma [12]. In humans, plasma ADMA levels are increased in severe asthma patients compared to nonsevere asthma patients and control subjects [3]. Other studies showed that ADMA levels are increased in sputum and exhaled breath condensate from asthma patients [13–15]. A more recent study showed that lower L-arginine/ADMA ratios are associated with reduced lung function and increased respiratory symptom frequency in subjects with late-onset asthma [16].

DDAH activity is a key determinant of intracellular ADMA concentration [17]. Ninety percent of ADMA is metabolized by DDAH and the rest is excreted through the kidneys. DDAH metabolizes ADMA to generate citrulline and dimethylamine. There are two isoforms of DDAH in human, mouse, rat and other species, DDAH1 and DDAH2 [18–20]. Immunostaining of human lung tissues showed expression of DDAH1 and DDAH2 in both alveolar and bronchiolar epithelium [21]. One study showed that homozygous DDAH1-deficient mice die before birth while the heterozygous DDAH1-deficient mice have a 20% increased level of ADMA and develop severe endothelial dysfunction [22]. Another study showed that DDAH1-deficient mice are viable and have significantly increased ADMA levels

[23]. ADMA levels are decreased in DDAH1-transgenic mice by 50% compared to wild type mice. Further, DDAH1-transgenic mice display a significant increase in NOS activity and a decreased risk of endothelial dysfunction compared to the wild type mice [24–26]. DDAH1 is the major enzyme responsible for metabolizing ADMA whereas DDAH2 has no detectable role in degrading ADMA *in vivo* [23]. In this paper, we determined the role of DDAH1 in the development of AHR and airway inflammation.

Materials and Methods

Mice

Mice were maintained and handled under Institutional Animal Care and Use Committee-approved procedures (Cincinnati Children's Hospital Medical Center, Protocol Number: 2D10082) and the Guide for the Care and Use of Laboratory Animals (Institute of Laboratory Animal Resources, National Research Council). C57BL/6 wild type and DDAH1-transgenic mice were purchased from Jackson Laboratory (Bar Harbor, ME).

Immunization

C57BL/6 wild type and DDAH1-transgenic mice were immunized with intratracheal instillation of 100 μ g of house dust mite (HDM) (*Dermatophagoides pteronyssinus*) extract (Greer Laboratories, Lenoir, NC) in 50 μ l of PBS or 50 μ l of PBS alone 3 times per week for 3 weeks as previously described [27,28].

Analysis of AHR and airway inflammation

Twenty four hours after the last treatment, AHR in response to methacholine (0, 50, 100 and 200 mg/ml) was measured by flexiVent (SCIREQ, Montreal, Canada) as previously described

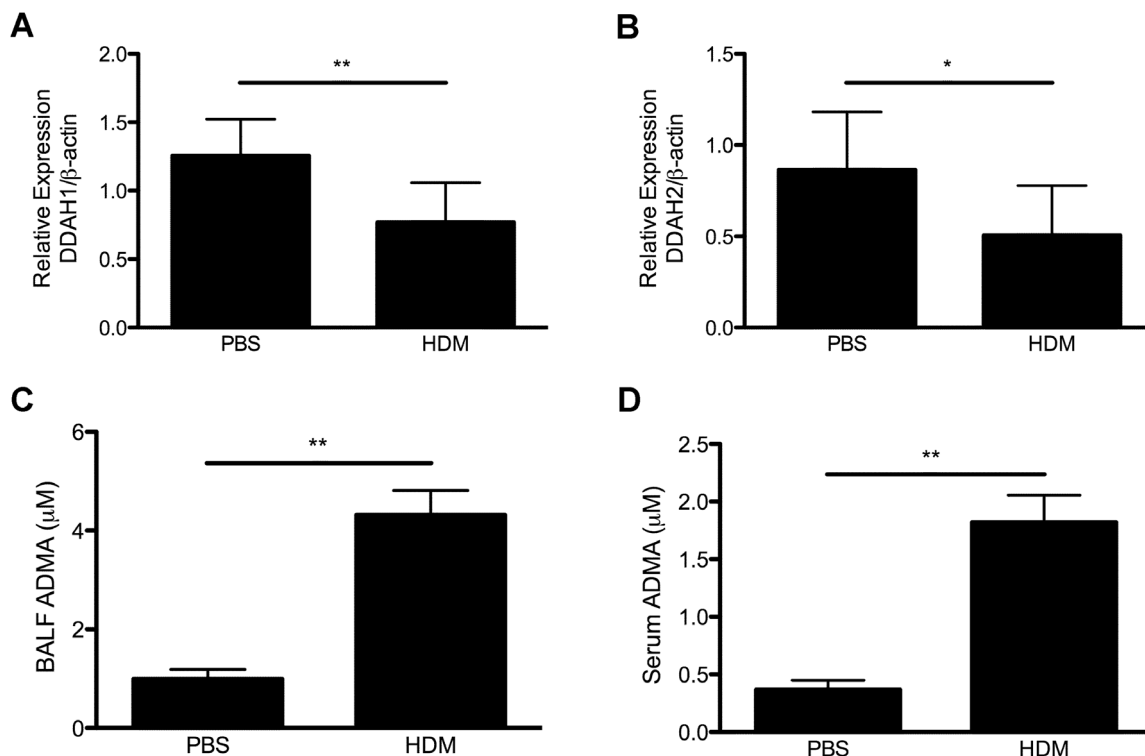


Figure 1. Expression of DDAH1 and DDAH2 in lungs and ADMA levels in BALF and serum samples from PBS or HDM-treated C57BL/6 mice. The mice were treated with PBS or HDM by 3 intratracheal challenges per week for 3 weeks. (A–B) DDAH1 and DDAH2 expression in lungs (n = 7–9). (C–D) ADMA levels in BALF and serum samples (n = 3). Data are shown as mean $\pm$ SD. *, $p < 0.05$; **, $p < 0.01$. doi:10.1371/journal.pone.0085148.g001

[29]. After AHR measurement, blood, bronchoalveolar lavage (BAL) samples and lung tissues were harvested as previously described [30]. The BAL total and differential cell counting as well as histological staining of lung sections by hematoxylin and eosin (H&E) or periodic acid Schiff (PAS) (Thermo Fisher Scientific, Waltham, MA) were performed as described by the manufacturer or as described previously [30]. ELISAs for total IgE and IgG1 or HDM-specific IgE and IgG1 in BAL fluid (BALF) and serum were done as previously described [31].

RNA-Seq and Bioinformatics Analysis

Total RNA was isolated from mouse lungs using Trizol reagent (Invitrogen, Carlsbad, CA), digested with RNase-free DNase and purified using an RNeasy MinElute kit (QIAGEN, Valencia, CA). Equal amounts of RNA were pooled from each mouse lung in an experimental group ($n = 4$ per group) and analyzed in duplicate. RNA-Seq was performed by the Genomics Sequencing Core in the University of Cincinnati. The RNA-Seq library was constructed using a PrepX SPIA RNA-Seq kit (IntegenX, Pleasanton, CA) and Apollo 324 NGS Library Prep System (IntegenX). 10 ng of total RNA was converted into cDNA suitable for mRNA

sequencing. The cDNA was then sheared by Covaris S2 (Covaris, Woburn, MA) under the conditions recommended by IntegenX, followed by Bioanalyzer assay of the size distribution with Agilent High Sensitivity DNA kit (Agilent, Santa Clara, CA). The properly sheared cDNA fragments were purified by Agencourt AMPure XP magnetic beads (Beckman Coulter, Brea CA). Using the IntegenX PrepX ILM DNA library kit for Illumina and Apollo 324 NGS Library Prep System, 500 ng of purified cDNA fragments were then put through end repair, addition of a single 'A' base and ligation of adapters, and indexed individually. The products were purified and enriched by PCR to create the final cDNA library targeting mRNAs. The size of the generated library was validated by Bioanalyzer and the library was quantified using the Kapa Library Quantification kit (Kapa Biosystems, Woburn, MA). Six individually indexed cDNA libraries were equal amount pooled for clustering in cBot system (Illumina, San Diego, CA). Libraries at the concentration of 6.5 pM were clustered onto a flow cell using Illumina's TruSeq SR Cluster Kit v3, and sequenced for 50 cycles using the TruSeq SBS kit on Illumina HiSeq system.

Sequence reads were aligned to the reference genome (mm10) using TopHat aligner [32]. The counts of reads aligning to each gene's coding region were summarized using ShortRead and associated Bioconductor packages for manipulating and analysis of next-generation sequencing data and custom-written R programs [33,34]. Statistical analysis to identify differentially expressed genes for each comparison was performed using the negative-binomial model of read counts as implemented in the DESeq Bioconductor package [35]. P-values were adjusted for multiple comparisons based on false discovery rates (FDR) [36]. Differential expressions with adjusted p-values of <0.05 were considered statistically significant.

Functional enrichment analysis was performed using the logistic regression based LRpath methodology [37]. The gene lists used in the functional enrichment analysis were from genes associated with Gene Ontology terms and KEGG pathways. The statistical significance of gene list enrichment was determined by the False Discovery Rate cut-off of 0.1. Genes that were both members of at least one statistically significant gene list and had differential expression p-values of <0.01 were considered to be differentially expressed for the purpose of network analysis. Ingenuity Pathways Analysis (IPA) (Ingenuity Systems, Mountain View, CA) was used to identify integrated and interconnected biological networks and upstream targets for the differentially expressed genes between two groups (with adjusted p-values of <0.05). RNA-Seq data have been deposited with the NCBI Gene Expression Omnibus (<http://www.ncbi.nlm.nih.gov/geo>) under accession number GSE49047.

RT-PCR

Total RNA was isolated from lung tissues using Trizol reagent (Invitrogen), digested with RNase-free DNase and purified using an RNeasy MinElute kit (QIAGEN). Reverse transcription was done using Oligo-dT First-Strand cDNA Synthesis Kit (GE Healthcare, Piscataway, NJ). Quantitative PCR (qPCR) was done using the SYBR Green Master Kit and LightCycler[®] 480 instrument (Roche Diagnostics, Indianapolis, IN). All primers used are listed in Table S1.

Mass Spectrometry (MS)

MS was performed by the Analytical & Mass Spectrometry of Small Molecules Core at the University of Cincinnati. The procedure to quantify ADMA was adapted from Schwedhelm *et al*

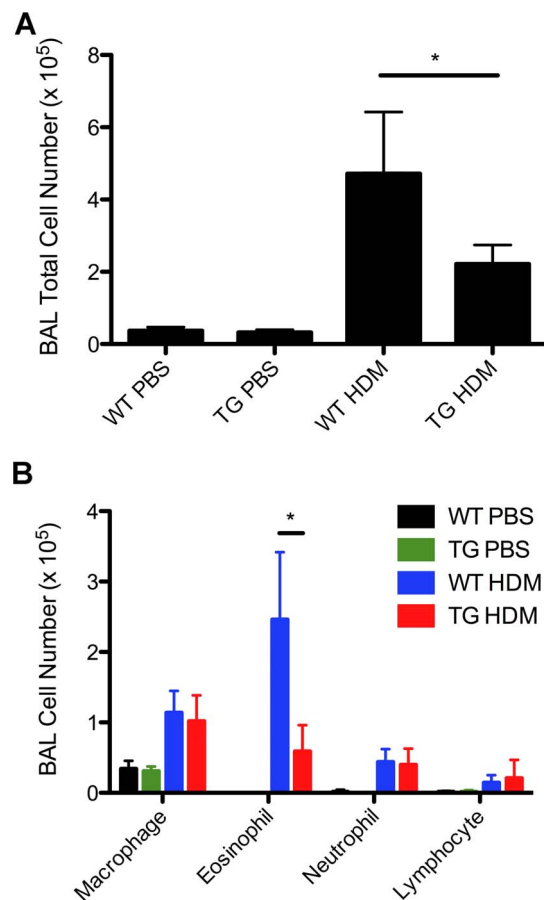


Figure 2. Airway inflammation in PBS or HDM-treated C57BL/6 wild type and DDAH1-transgenic mice. BAL total and differential cell counts in wild type and DDAH1-transgenic mice treated with PBS or HDM (3 intratracheal challenges per week for 3 weeks). WT: wild type; TG: DDAH1-transgenic. Data are shown as mean $\pm$ SD ($n = 5-9$). *, $p < 0.05$. doi:10.1371/journal.pone.0085148.g002

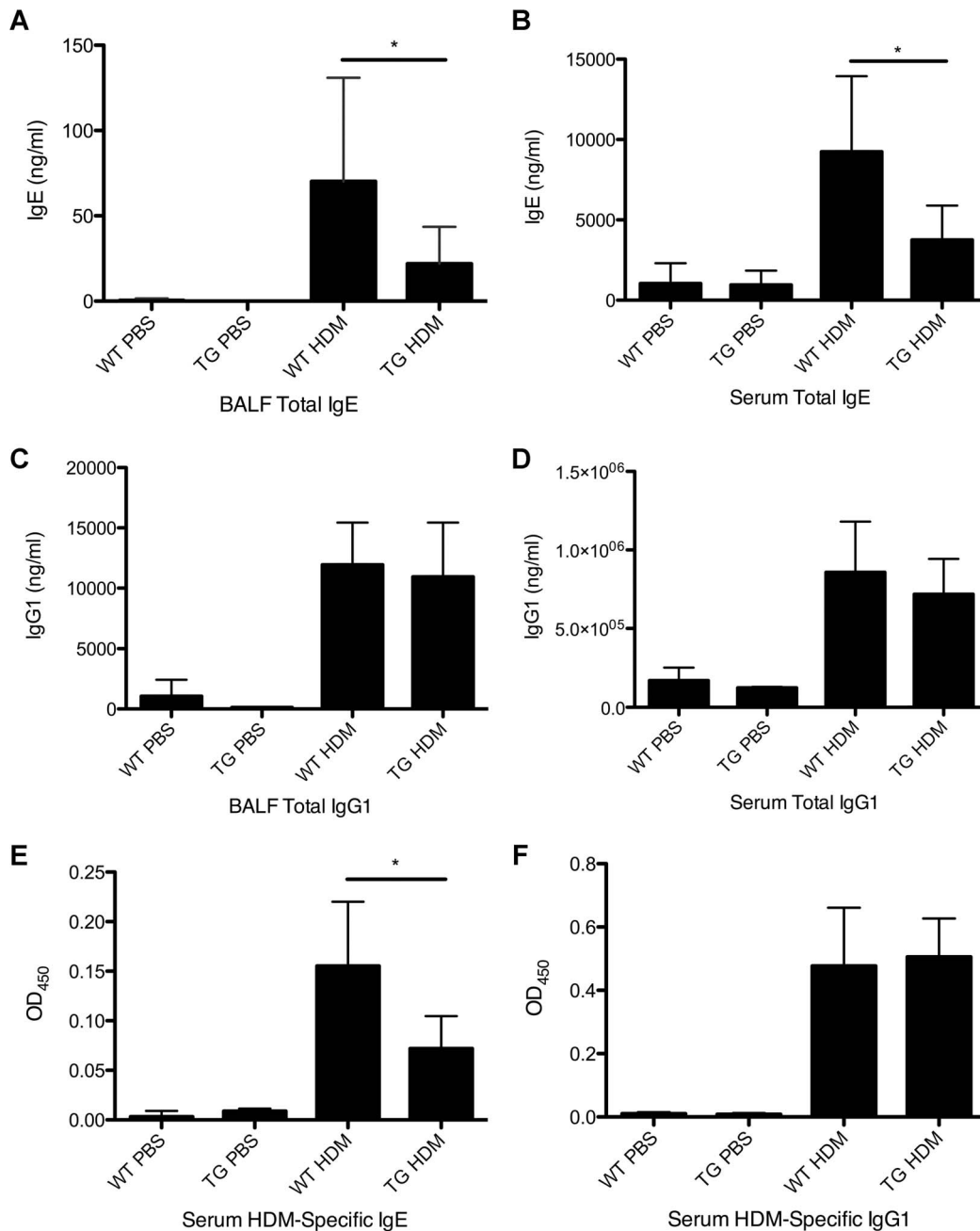


Figure 3. Levels of IgE and IgG1 in BALF and serum in PBS or HDM-treated C57BL/6 wild type and DDAH1-transgenic mice. (A) BALF total IgE. (B) Serum total IgE. (C) BALF total IgG1. (D) Serum total IgG1. (E) Serum HDM-specific IgE. (F) Serum HDM-specific IgG1. WT: wide type; TG: DDAH1-transgenic. Data are shown as mean ± SD (n = 5–9). *, p < 0.05. doi:10.1371/journal.pone.0085148.g003

[38]. In brief, BALF and serum samples were filtrated through 0.45 μ m filters to remove particles and 200 μ l aliquots were then ultra-filtrated through 3 kDa MWCO filters to remove proteins. The samples were derivatized by adding 200 μ l of 2 M HCl in 1-butanol for 20 min at 65°C. After evaporation, samples were reconstituted in 200 μ l of distilled deionized water and analyzed by nano liquid chromatography chip electrospray ionization ion trap MS (nanoLC-Chip ESI-IT-MS). For nanoLC-Chip ESI-MS/

MS analysis, the derivatized ADMA was separated in a microfluidic reverse phase chip column and detected by electrospray ionization with ion trap MS/MS detection. The tandem system consisted of an Agilent 1200 HPLC (Agilent Technologies, Santa Clara, CA), equipped with a capillary and nano pump, used for loading and flushing the on-chip nano column, a chip cube interface that contains the nano-chip column Zorbax SB C-18, 150 × 0.75 mm (Agilent Technologies), and an Agilent 6300 ion

Table 1. Genes Downregulated in the Lungs of PBS-treated DDAH1-transgenic Mice versus PBS-treated Wild Type Mice.

Symbol	Name	Fold Change
<i>Immune/Defense Response</i>		
Rag1	recombination activating gene 1	0.0020
Irg1	immunoresponsive gene 1	0.0042
Tlr6	toll-like receptor 6	0.0224
Saa3	serum amyloid A 3	0.0265
Clec4e	C-type lectin domain family 4, member e	0.0360
Ptafr	platelet-activating factor receptor	0.0656
Pram1	PML-RAR alpha-regulated adaptor molecule 1	0.1024
Clec4d	C-type lectin domain family 4, member d	0.1306
Cfd	complement factor D (adipsin)	0.1491
Cd4	CD4 antigen	0.2667
Tnfrsf1b	tumor necrosis factor receptor superfamily, member 1b	0.3327
Il1rn	interleukin 1 receptor antagonist	0.3365
Lilrb3	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	0.3596
Sell	selectin, lymphocyte	0.3826
Acs1l	acyl-CoA synthetase long-chain family member 1	0.4620
Cybb	cytochrome b-245, beta polypeptide	0.4694
Lcn2	lipocalin 2	0.4804
Tgtp1	T-cell specific GTPase 1	0.4907
Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member 4	0.4931
Tgtp2	T-cell specific GTPase 2	0.4986
Csf2rb	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0.5378
Ptprc	protein tyrosine phosphatase, receptor type, C	0.6052
<i>Cell Structure/Adhesion/Migration</i>		
Sprr2a2	small proline-rich protein 2A2	0.0179
Sprr2a1	small proline-rich protein 2A1	0.0179
Adipoq	adiponectin, C1Q and collagen domain containing	0.0702
S100a9	S100 calcium binding protein A9 (calgranulin B)	0.0736
Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.1651
S100a8	S100 calcium binding protein A8 (calgranulin A)	0.2070
H2-M2	histocompatibility 2, M region locus 2	0.2210
Sema4d	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	0.2948
Itgb2	integrin beta 2	0.4746
Myh6	myosin, heavy polypeptide 6, cardiac muscle, alpha	0.4752
Itgal	integrin alpha L	0.4913
Actc1	actin, alpha, cardiac muscle 1	0.5662
Csf3r	colony stimulating factor 3 receptor (granulocyte)	0.5942
<i>Cytokine/Chemokine</i>		
Ccl4	chemokine (C-C motif) ligand 4	0.0000
Ccl3	chemokine (C-C motif) ligand 3	0.0114
Cxcl2	chemokine (C-X-C motif) ligand 2	0.0236
Il1b	interleukin 1 beta	0.1342
<i>Transcriptional Factor</i>		
Tcf7	transcription factor 7, T-cell specific	0.4134
Stat1	signal transducer and activator of transcription 1	0.5833
<i>Other</i>		
Arpp21	cyclic AMP-regulated phosphoprotein, 21	0.0036
Gxylt2	glucoside xylosyltransferase 2	0.0112
1700071M16Rik	RIKEN cDNA 1700071M16 gene	0.0427

Table 1. Cont.

Symbol	Name	Fold Change
Trim30b	tripartite motif-containing 30B	0.0516
Cd177	CD177 antigen	0.0746
Niacr1	niacin receptor 1	0.0993
Mmp8	matrix metalloproteinase 8	0.1307
Slnf4	schlafen 4	0.1469
Acpp	acid phosphatase, prostate	0.2390
Steap4	STEAP family member 4	0.2412
F13a1	coagulation factor XIII, A1 subunit	0.2631
Gpnmb	glycoprotein (transmembrane) nmb	0.3398
Slpi	secretory leukocyte peptidase inhibitor	0.3547
Bpifa1	BPI fold containing family A, member 1	0.3796
Gp49a	glycoprotein 49 A	0.4032
Car3	carbonic anhydrase 3	0.4062
Gm1966	predicted gene 1966	0.5319
Ctss	cathepsin 5	0.6001
Fth1	ferritin heavy chain 1	0.6449

NCBI Gene Expression Omnibus accession numbers GSE49047 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE49047>).
doi:10.1371/journal.pone.0085148.t001

trap XCT system (Agilent Technologies). The mobile phase A consisted of 0.1% formic acid in water while B consisted of 0.1% formic acid in a 7:1 acetonitrile:water solution. A linear gradient from 2% to 25% B was carried out in 10 min and the column was then cleaned with 100% B for 5 min and then regenerated at original conditions for 10 min before the next injection. The flow rate was 0.3 μ l per min and the outlet of the column communicates directly with the nano electrospray needle. The analysis was carried out in the MRM mode by following the transition m/z 259.3 $\rightarrow$ 214. ADMA standards (Sigma-Aldrich, St. Louis, MO) were derivatized in the same way and quantification was carried out by the external calibration method.

Statistical analysis

All values are expressed as mean $\pm$ SD. The data were analyzed with a 2-tailed unpaired student's t-test with Welch's correction or 1-way ANOVA with Newman-Keuls' post test using Prism 5.0c for Mac OS X from GraphPad Software (San Diego, CA). A p-value of <0.05 was considered statistically significant.

Results

Expression of DDAH1 and DDAH2 is decreased in the lungs and ADMA levels are increased in BALF and serum from HDM-treated mice

Since ADMA levels are increased in allergic asthma and DDAH is responsible for the majority of ADMA metabolism, we hypothesized that the increased levels of ADMA are due to decreased expression of DDAH following allergen exposure. We determined the expression of DDAH1 and DDAH2 in the lungs in a mouse model of asthma. C57BL/6 mice were challenged by intratracheal instillation of 100 μ g HDM, 3 times per week for 3 weeks. This is a more clinically relevant protocol of chronic

allergen exposure with an increased dosage of HDM for the C57BL/6 mouse strain. As shown in Fig. 1A and 1B, HDM exposure resulted in decreased expression of DDAH1 and DDAH2 in mouse lungs, which correlated with increased levels of ADMA in BALF and serum (Fig. 1C and 1D).

Overexpression of DDAH1 attenuates HDM-induced airway inflammation

We next determined the effect of DDAH overexpression on airway inflammation and AHR in a HDM-induced asthma model using DDAH1-transgenic mice since DDAH1 is the major enzyme responsible for ADMA metabolism [23]. The mice were challenged by intratracheal instillation of 100 μ g HDM 3 times per week for 3 weeks. Twenty-four hours after the last treatment AHR was measured by flexiVent and airway inflammation was assessed by BAL cell counts. BAL total cell and eosinophil numbers were decreased in HDM-treated DDAH1-transgenic mice compared to HDM-treated wild type mice (Fig. 2A-2B). No significant differences in inflammatory cell infiltration in airways determined by H&E staining or in mucus production determined by PAS staining of lung sections were observed between HDM-treated DDAH1-transgenic mice and HDM-treated wild type mice (data not shown). No significant difference in AHR was observed in HDM-treated DDAH1-transgenic mice compared to HDM-treated wild type mice (data not shown).

IgE levels in BALF and serum are decreased in DDAH1-transgenic mice compared to wild type mice after HDM treatment

We next tested whether allergen sensitization was affected by the overexpression of DDAH1. As shown in Fig. 3A and 3B, the total IgE levels were decreased in BALF and serum in HDM-treated DDAH1-transgenic mice compared to HDM-treated wild

Table 2. Genes Upregulated in the Lungs of PBS-treated DDAH1-transgenic Mice versus PBS-treated Wild Type Mice.

Symbol	Name	Fold Change
<i>Muscle/Cell Structure</i>		
Myh2	myosin, heavy polypeptide 2, skeletal muscle, adult	181.3505
Myh8	myosin, heavy polypeptide 8, skeletal muscle, perinatal	109.1566
Myh4	myosin, heavy polypeptide 4, skeletal muscle	82.8001
Myh1	myosin, heavy polypeptide 1, skeletal muscle, adult	65.6757
Tnnt3	troponin T3, skeletal, fast	44.0881
Actn3	actinin alpha 3	26.0940
Mylpf	myosin light chain, phosphorylatable, fast skeletal muscle	14.9051
Neb	nebulin	10.4391
<i>Ion Homeostasis/Metabolism</i>		
Atp2a1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	45.0004
Ckm	creatine kinase, muscle	9.6517
Sod1	superoxide dismutase 1, soluble	1.8226
Errfi1	ERBB receptor feedback inhibitor 1	1.7924
Dpep1	dipeptidase 1 (renal)	1.6845
Sgms1	sphingomyelin synthase 1	1.6440
Glul	glutamate-ammonia ligase (glutamine synthetase)	1.4929
<i>Hemopoiesis</i>		
Hba-a2	hemoglobin alpha, adult chain 2	1.6691
Hba-a1	hemoglobin alpha, adult chain 1	1.6691
Beta-s	hemoglobin subunit beta-1-like	1.5436
Hbb-b1	hemoglobin, beta adult major chain	1.5242
Hbb-b2	hemoglobin, beta adult minor chain	1.5242
<i>MicroRNA</i>		
Mir5109	microRNA 5109	2.7839
<i>Other</i>		
Flrt2	fibronectin leucine rich transmembrane protein 2	11.5849
Gm13375	predicted gene 13375	8.1901
Gm3893	predicted gene 3893	5.6492
Rmrp	RNA component of mitochondrial RNAase P	4.8670
Angptl4	angiopoietin-like 4	2.7019
Efnb1	ephrin B1	2.3349
Zbtb16	zinc finger and BTB domain containing 16	2.2658
Cdkn1a	cyclin-dependent kinase inhibitor 1A (P21)	2.2030
Tsc22d3	TSC22 domain family, member 3	2.1869
6430548M08Rik	RIKEN cDNA 6430548M08 gene	2.1316
Krt7	keratin 7	2.0891
Bmp6	bone morphogenetic protein 6	1.8952
Gm10393	predicted gene 10393	1.8802
Lars2	leucyl-tRNA synthetase, mitochondrial	1.8365
Plxna2	plexin A2	1.8323
Eif3e	eukaryotic translation initiation factor 3, subunit E	1.7913
Cpm	carboxypeptidase M	1.7450
Rn45S	45S pre-ribosomal RNA	1.7382
Vps54	vacuolar protein sorting 54 (yeast)	1.5716
Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	1.5133
Tmbim6	transmembrane BAX inhibitor motif containing 6	1.4524
Sepp1	selenoprotein P, plasma, 1	1.3714
Sftpa1	surfactant associated protein A1	1.3527

NCBI Gene Expression Omnibus accession numbers GSE49047 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE49047>).
doi:10.1371/journal.pone.0085148.t002

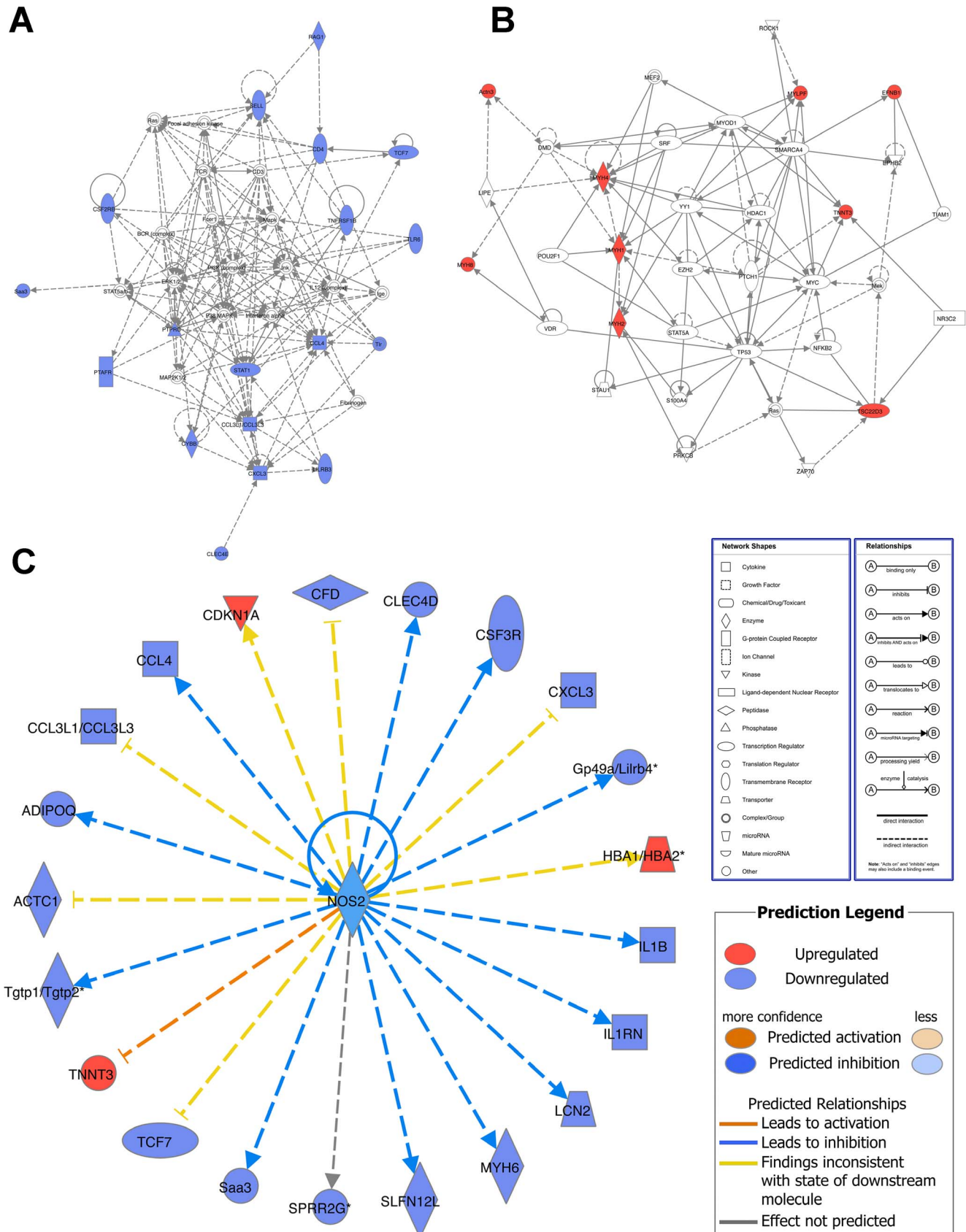


Figure 4. Network analysis of differentially expressed genes in the lungs of PBS-treated C57BL/6 wild type and PBS-treated DDAH1-transgenic mice. (A) Top network of the downregulated immune/defense response genes, cytokine/chemokine genes and transcriptional factor genes in PBS-treated DDAH1-transgenic mice. (B) Top network of the upregulated muscle/cell structure genes in PBS-treated DDAH1-transgenic mice. (C) Upstream target analysis of genes differentially expressed in PBS-treated wild type and DDAH1-transgenic mice. The genes with an adjusted p-value of <0.05 were included for analysis. doi:10.1371/journal.pone.0085148.g004

Table 3. Genes Downregulated in the Lungs of HDM-treated DDAH1-transgenic Mice versus HDM-treated Wild Type Mice.

Symbol	Name	Fold Change
Metabolism/Transport		
Fbp1	fructose biphosphatase 1	0.1302
Dhrs9	dehydrogenase/reductase (SDR family) member 9	0.1595
Arg1 *	arginase, liver	0.1808
Slc26a4	solute carrier family 26, member 4	0.2789
Cox15	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	0.2889
Chi3l4 *	chitinase 3-like 4	0.3373
Atp1a3	ATPase, Na ⁺ /K ⁺ transporting, alpha 3 polypeptide	0.3547
Slc5a1	solute carrier family 5 (sodium/glucose cotransporter), member 1	0.3701
Clca3	chloride channel calcium activated 3	0.3773
Kcnj15	potassium inwardly-rectifying channel, subfamily J, member 15	0.4207
Chi3l3 *	chitinase 3-like 3	0.4246
Slco4c1	solute carrier organic anion transporter family, member 4C1	0.4487
Man2b2	mannosidase 2, alpha B2	0.4520
Immune/Defense Response		
Ear11	eosinophil-associated, ribonuclease A family, member 11	0.2201
Chia *	chitinase, acidic	0.3222
Sod3	superoxide dismutase 3, extracellular	0.3353
Csf2ra	colony stimulating factor 2 receptor, alpha, low-affinity (granulocyte-macrophage)	0.3959
Ifitm2	interferon induced transmembrane protein 2	0.4031
Igf1	insulin-like growth factor 1	0.4424
Osmr	oncostatin M receptor	0.4612
Cytokine/Chemokine		
Ccl22	chemokine (C-C motif) ligand 22	0.2776
Tnfsf12	tumor necrosis factor (ligand) superfamily, member 12	0.3065
Ccl9	chemokine (C-C motif) ligand 9	0.4578
Il33 *	interleukin 33	0.4640
Extracellular Matrix		
Col6a2	collagen, type VI, alpha 2	0.3976
Muc5ac	mucin 5, subtypes A and C, tracheobronchial/gastric	0.4245
Muc4	mucin 4	0.4415
Col1a1	collagen, type I, alpha 1	0.4641
Transcriptional Factor		
Srebf2	sterol regulatory element binding factor 2	0.3294
Foxp4	forkhead box P4	0.3743
Nfic	nuclear factor I/C	0.4391
MicroRNA		
Mir5109	microRNA 5109	0.2007
Mir5107	microRNA 5107	0.4523
Other		
Syn2	synapsin II	0.0688
4833422F24Rik	RIKEN cDNA 4833422F24 gene	0.0775
LOC100048885	major urinary protein LOC100048885	0.1392
Corin	corin	0.1992
Zfp366	zinc finger protein 366	0.2274
Zfp385b	zinc finger protein 385B	0.2356
Epha7	Eph receptor A7	0.2597
Bahcc1	BAH domain and coiled-coil containing 1	0.2673
Actg2	actin, gamma 2, smooth muscle, enteric	0.2694

Table 3. Cont.

Symbol	Name	Fold Change
Phlda1	pleckstrin homology-like domain, family A, member 1	0.2729
Actc1	actin, alpha, cardiac muscle 1	0.2852
BC048546	cDNA sequence BC048546	0.2998
Trim65	tripartite motif-containing 65	0.3015
Bin2	bridging integrator 2	0.3016
Fcgbp	Fc fragment of IgG binding protein	0.3248
Prcc2a	proline-rich coiled-coil 2A	0.3288
Dusp8	dual specificity phosphatase 8	0.3328
Rhob	ras homolog gene family, member B	0.3346
Atn1	atrophin 1	0.3370
Rpph1	ribonuclease P RNA component H1	0.3560
Midn	midnolin	0.3735
Notch3	Notch gene homolog 3 (Drosophila)	0.3899
Sema5a	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	0.3949
Gm15401	predicted gene 15401	0.3967
Tgfb11i	transforming growth factor beta 1 induced transcript 1	0.4005
Taok2	TAO kinase 2	0.4159
Samd4b	sterile alpha motif domain containing 4B	0.4693

*Verified by RT-qPCR.

NCBI Gene Expression Omnibus accession numbers GSE49047 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE49047>).

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type mice but there was no difference in the levels of total IgG1 in BALF or serum (Fig. 3C and 3D). The level of HDM-specific IgE was decreased in serum from HDM-treated DDAH1-transgenic mice compared to HDM-treated wild type mice but the level of HDM-specific IgG1 in serum was unaffected (Fig. 3E and 3F).

Gene expression profiles are significantly different in the lungs of wild type and DDAH1-transgenic mice

To elucidate the potential mechanisms underlying attenuated HDM-induced airway inflammation in DDAH1-transgenic mice, we determined gene expression profiles in the lungs from C57BL/6 wild type and DDAH1-transgenic mice treated with PBS or HDM (intratracheal instillation of 100 µg of HDM in 50 µl of PBS or 50 µl of PBS alone 3 times per week for 3 weeks) by RNA-Seq.

There were 354 genes differentially expressed in the lungs of PBS-treated wild type and PBS-treated DDAH1-transgenic mice (Table S2). The top downregulated genes (with an adjusted p-value of <0.05) are shown in Table 1 (grouped and sorted by fold change), including immune/defense response genes (Rag1, Irg1, Tlr6, etc.), cell structure/adhesion/migration genes (Sprr2a2, Sprr2a1, Adipoq, etc.), cytokine/chemokine genes (Ccl4, Ccl3, Cxcl2 and Il1b), and transcriptional factors (Tcf7 and Stat1). The top upregulated genes (with an adjusted p-value of <0.05) are shown in Table 2 (grouped and sorted by fold change), including muscle/cell structure genes (Myh2, Myh8, Myh4, etc.), ion homeostasis/metabolism genes (Atp2a1, Ckm, Sod1, etc.) and hemopoiesis genes (Hba-a2, Hba-a1, Beta-s, etc.). For the downregulated immune/defense response genes, cytokine/chemokine genes and transcriptional factor genes, IPA analysis showed that the top network was associated with inflammatory response, immunological disease, and respiratory disease (Fig. 4A). The top network for the upregulated muscle/cell structure genes was associated with organ morphology, skeletal and muscular system

development and function, and cancer (Fig. 4B). The top upstream target for both downregulated and upregulated genes was iNOS (NOS2) (Fig. 4C).

There were 707 genes differentially expressed in the lungs of HDM-treated wild type and HDM-treated DDAH1-transgenic mice (Table S3). The top downregulated genes (with an adjusted p-value of <0.05) are shown in Table 3 (grouped and sorted by fold change), including metabolism/transport genes (Fbp1, Dhfr9, Arg1, etc.), immune/defense response genes (Ear11, Chia, Sod3, etc.), cytokine/chemokine genes (Ccl22, Tnfsf12, Ccl9 and Il33), extracellular matrix genes (Col6a2, Muc5ac, Muc4 and Col1a1) and microRNAs (Mir5109 and Mir5107). The top upregulated genes (with an adjusted p-value of <0.05) are shown in Table 4 (grouped and sorted by fold change), including ribosomal complex genes (Rps21, Rps12, Rpl30, etc.) and ribosomal pseudogenes (Gm11968, Gm12191, Gm13253, etc.). The top network for the downregulated immune/defense genes and cytokine/chemokine genes was associated with inflammatory response, cellular movement, and hematological system development and function (Fig. 5A). The top network for the upregulated ribosomal complex genes and ribosomal pseudogenes is associated with cellular development, cancer, and cellular assembly and organization (Fig. 5B). The top upstream targets for both downregulated and upregulated genes were IL-13 and FOXA2 (Fig. 5C).

The expression of IL-13, IL-4, IL-33, CCL11, ARG1, MMP-12, CHIA, CHI3L3 and CHI3L4 is decreased in the lungs from DDAH1-transgenic mice compared to wild type mice following allergen challenge

Based on RNA-Seq results, we verified the expression of some key cytokines, chemokines, matrix metalloproteinases and chitinases including IL-13, IL-4, IL-33, CCL11, MMP-12 and CHIA.

Table 4. Genes Upregulated in the Lungs of HDM-treated DDAH1-transgenic Mice versus HDM-treated Wild Type Mice.

Symbol	Name	Fold Change
<i>Ribosomal Complex</i>		
Rps21	ribosomal protein S21	5.4796
Rps12	ribosomal protein S12	5.4397
Rpl30	ribosomal protein L30	4.2587
Mrps16	mitochondrial ribosomal protein S16	4.1518
Rpl34	ribosomal protein L34	3.8427
Sec61b	Sec61 beta subunit	3.7764
Rps14	ribosomal protein S14	3.6956
Rpl36a	ribosomal protein L36A	3.6885
Rps15a	ribosomal protein S15A	3.6498
Rpl37a	ribosomal protein L37a	3.6295
Pttg1	pituitary tumor-transforming gene 1	3.5963
Rplp2	ribosomal protein, large P2	3.4879
Rps27	ribosomal protein S27	3.4532
Rpl27	ribosomal protein L27	3.4067
Rps28	ribosomal protein S28	3.3511
Mrpl20	mitochondrial ribosomal protein L20	3.2634
<i>Ribosomal Pseudogene</i>		
Gm11968	Rps15a pseudogene	4.4686
Gm12191	ribosomal protein L30 pseudogene	4.2620
Gm13253	ribosomal protein S15a pseudogene	4.0395
Rpl34-ps1	ribosomal protein L34, pseudogene 1	3.8391
Rplp2-ps1	ribosomal protein, large P2, pseudogene 1	3.3696
<i>Metabolism/Oxidative Process</i>		
Qdpr	quinoid dihydropteridine reductase	5.7248
Glx5	glutaredoxin 5 homolog (<i>S. cerevisiae</i>)	5.0037
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	4.9044
Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	4.7132
Sumf1	sulfatase modifying factor 1	4.4089
Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	4.2862
Cox17	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	4.1528
<i>Cytokine/Chemokine</i>		
Ccl20	chemokine (C-C motif) ligand 20	6.3854
Cxcl3	chemokine (C-X-C motif) ligand 3	3.9814
<i>Other</i>		
Dtwd1	DTW domain containing 1	14.2305
Flrt2	fibronectin leucine rich transmembrane protein 2	10.6123
1110038B12Rik	RIKEN cDNA 1110038B12 gene	8.9809
Scgb3a2	secretoglobin, family 3A, member 2	7.4584
Fpr2	formyl peptide receptor 2	6.5479
Fkbp14	FK506 binding protein 14	6.3078
Hbxip	hepatitis B virus x interacting protein	4.8871
BC002163	NADH dehydrogenase Fe-S protein 5 pseudogene	4.7683
S100a13	S100 calcium binding protein A13	4.6935
H3f3a	H3 histone, family 3A	4.6727
Commd1	COMM domain containing 1	4.6707
Osgp	O-sialoglycoprotein endopeptidase	4.2386
2010001M09Rik	RIKEN cDNA 2010001M09 gene	4.1526
Mettl7a2	methyltransferase like 7A2	4.1202

Table 4. Cont.

Symbol	Name	Fold Change
O610007C21Rik	RIKEN cDNA O610007C21 gene	3.9575
Tmbim4	transmembrane BAX inhibitor motif containing 4	3.9312
Snrpe	small nuclear ribonucleoprotein E	3.9247
Plac9	placenta specific 9	3.7440
Gngt2	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	3.5724
Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	3.5352
Gm9846	predicted gene 9846	3.4544
Ccdc84	coiled-coil domain containing 84	3.4251
S100a6	S100 calcium binding protein A6 (calcyclin)	3.3956
Vamp8	vesicle-associated membrane protein 8	3.3746
Shfm1	split hand/foot malformation (ectrodactyly) type 1	3.3414
Cd52	CD52 antigen	3.3025
Mettl7a1	methyltransferase like 7A1	3.2925
Pcolce2	procollagen C-endopeptidase enhancer 2	3.2669
Fam166a	family with sequence similarity 166, member A	3.2667
Neat1	nuclear paraspeckle assembly transcript 1 (non-protein coding)	3.2657

NCBI Gene Expression Omnibus accession numbers GSE49047 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE49047>).
doi:10.1371/journal.pone.0085148.t004

As shown in Fig. 6A and 6B, induction of IL-13 and IL-4 expression in the lungs was attenuated in HDM-treated DDAH1-transgenic mice compared to wild type mice. Expression of IL-33 was decreased in lungs from DDAH1-transgenic mice after HDM treatment compared to wild type mice (Fig. 6C). We found that the expression of CCL11 and MMP-12 was decreased in HDM-treated DDAH1-transgenic mice compared to HDM-treated wild type mice (Fig. 6D, 6E). The expression of ARG1, a key enzyme in arginine/NO metabolism, was significantly decreased in HDM-treated DDAH1-transgenic mice compared to HDM-treated wild type mice (Fig. 6F). The difference in expression of iNOS (NOS2) or FOXA2 was not significant between wild type and DDAH1-transgenic mice (Fig. 6G, 6H). The expression of acidic chitinase (CHIA) and chitinase like proteins (CHI3L3 and CHI3L4) was decreased in the lungs of HDM-treated DDAH1-transgenic mice compared to HDM-treated wild type mice (Fig. 7A–7C).

Discussion

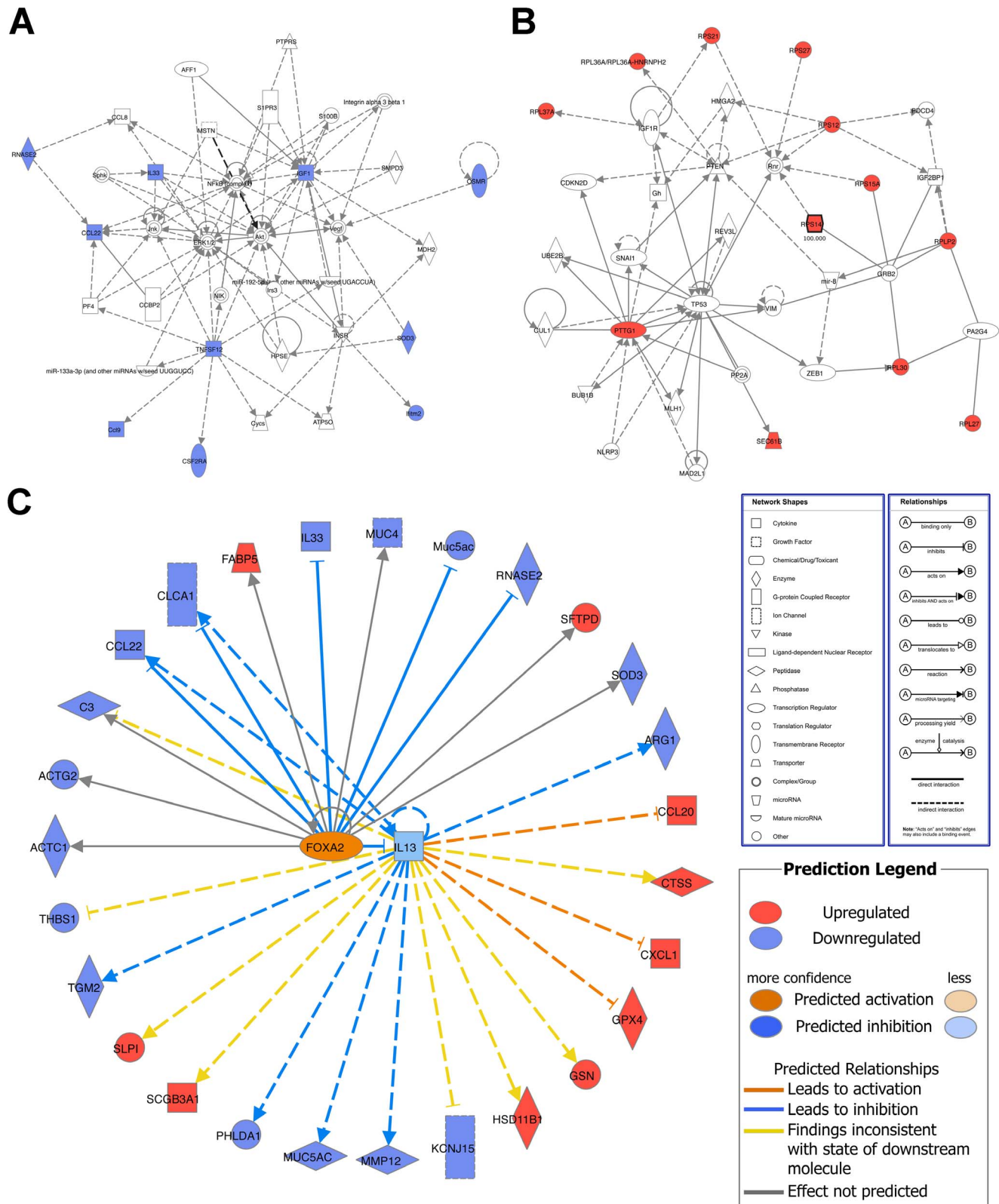
Our data reveal that expression of DDAH1 and DDAH2 is decreased in the lungs in a mouse model of asthma, and overexpression of DDAH1 attenuates allergen-induced airway inflammation. Asthma is a condition of decreased NO bioavailability. ADMA is an endogenous inhibitor of NOS, which is a major source of NO. DDAH1 and DDAH2 are responsible for metabolism of over 90% of ADMA *in vivo*, and our data support a role for DDAH downregulation in asthma pathogenesis.

The mechanism of the observed downregulation of DDAH may be epigenetic modulation. Studies using mouse trophoblast stem cells and trophoblastic tissues of postimplantation mouse embryos showed DNA methylation-dependent epigenetic regulation of DDAH2 gene expression. The CpG island in the DDAH2 promoter was hypermethylated in trophoblast stem cells but hypomethylated in differentiated cells [39]. We found that the

mouse DDAH1 promoter also contains a CpG island [40], but their methylation status and relationship to gene expression are unknown. Previous studies have shown that allergen exposure results in altered methylation status of IL-4 and IFN γ promoter CpG islands [41]. It is likely that allergen exposure results in hypermethylation of mouse DDAH1 and DDAH2 promoter CpG islands, which results in decreased expression of DDAH1 and DDAH2 in mouse lungs.

Our data showed that overexpression of DDAH1 attenuated allergen-induced airway inflammation although it had no significant effect on AHR. It is not surprising as studies showed uncoupled airway inflammation and AHR in allergen challenged C57BL/6 mice due to strain-dependent genomic factors [42]. The infiltration of eosinophils into the lungs was decreased in HDM-exposed DDAH1-transgenic mice, which is consistent with the result that expression of CCL11 was decreased in lungs from HDM-treated DDAH1-transgenic mice. The total IgE and HDM-specific IgE levels in BALF or serum were decreased in DDAH1-transgenic mice after HDM exposure, suggesting that overexpression of DDAH1 affected Ig class switch.

The RNA-Seq data showed that overexpression of DDAH1 results in decreased lung expression of multiple immune/defense response genes that are associated with a network of inflammatory responses. The top upstream target is iNOS. A previous study showed that increased ADMA levels increase the expression of iNOS in mouse lungs [12], suggesting the effect of DDAH1 overexpression on iNOS expression/activity may be mediated by altered ADMA levels. Following HDM exposure, the expression of ARG1 is significantly decreased in the lungs from DDAH1 transgenic mice, suggesting arginine/NO pathways play important roles in the effect of DDAH1 overexpression on allergic airway inflammation. We found the expression of genes involved in mucus production (Clca3, Muc5ac and Muc4) and collagen synthesis (Col6a2 and Col1a1) is also decreased. Another previous



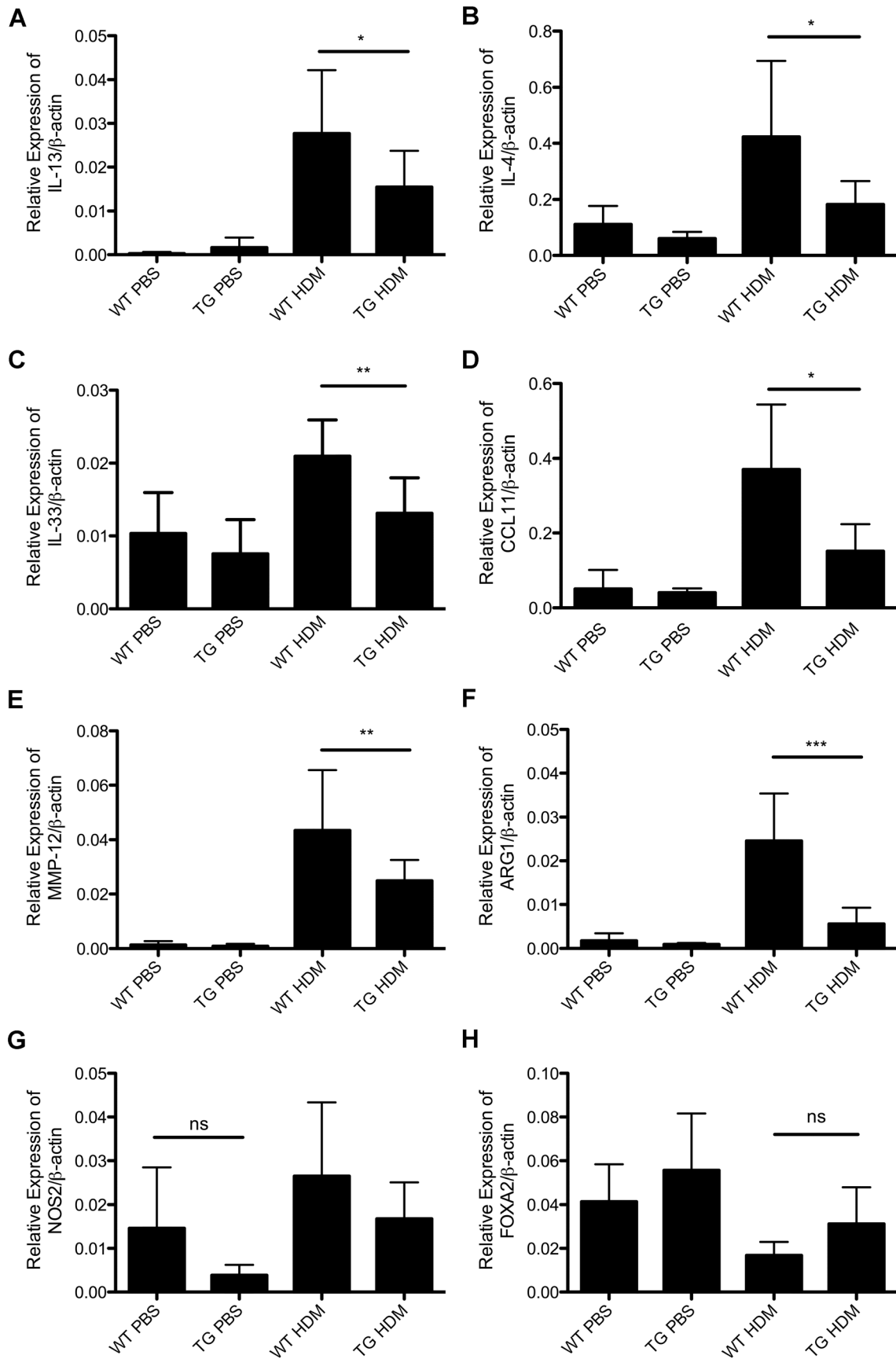


Figure 6. Expression of IL-13, IL-4, IL-33, CCL11, MMP-12, ARG1, NOS2 and FOXA2 in lungs from PBS or HDM-treated C57BL/6 wild type and DDAH1-transgenic mice. (A) IL-13. (B) IL-4. (C) IL-33. (D) CCL11 (E) MMP-12. (F) ARG1. (G) NOS2. (H) FOXA2. WT: wild type; TG: DDAH1-transgenic. Data are shown as mean $\pm$ SD (n = 5–9). *, p < 0.05; **, p < 0.01; ***, p < 0.001; ns, not significant. doi:10.1371/journal.pone.0085148.g006

study showed that increased levels of ADMA resulted in increased pulmonary collagen deposition [11], suggesting DDAH1 may regulate collagen synthesis through modulation of ADMA levels. Network analysis suggests that DDAH1 regulates mucus production gene expression through IL-13/FOXA2. RT-qPCR data

further showed that the expression of IL-13, IL-4 and CCL11 is decreased in HDM-treated DDAH1-transgenic mice, which is consistent with attenuated eosinophil infiltration in airways and decreased serum and BALF IgE levels. Although the difference in expression of iNOS and FOXA2 is not significant between the wild type and DDAH1-transgenic mice, overexpression of DDAH1 may directly or indirectly affect the activity of iNOS and FOXA2. Interestingly, the expression of acidic chitinase (CHIA) and chitinase like proteins (CHI3L3 and CHI3L4) was decreased in the lungs of HDM-treated DDAH1-transgenic mice. Acidic chitinase has been shown to play important roles in asthma [43]. CHI3L3 and CHI3L4 are rodent specific chitinase like proteins that are induced by Th2 cytokines or allergen challenge and have chemotactic activity [44–46]. Whether acidic chitinase and chitinase like proteins can modulate the expression of DDAH1 requires further studies. Overexpression of DDAH1 may have non-specific effects on gene expression. Generation of cell type specific transgenic mice with different expression levels of the DDAH1-transgene would help minimize the non-specific effects.

In summary, our data suggest that decreased expression of DDAH1 and DDAH2 in lungs may contribute to allergic asthma and overexpression of DDAH1 attenuates allergen-induced airway inflammation through modulation of Th2 responses.

Supporting Information

Table S1 Primers for PCR. (DOC)

Table S2 Genes differentially expressed in the lungs of PBS-treated wild type and PBS-treated DDAH1-transgenic mice. For RNA-Seq, equal amounts of RNA were pooled from each mouse lung in an experimental group (n = 4 per group) and analyzed in duplicate. The bioinformatics analyses were described in Materials and Methods. The differentially expressed genes with a p-value of <0.01 were shown. WT: wild type; TG: DDAH1-transgenic; Inf: infinity. (XLS)

Table S3 Genes differentially expressed in the lungs of HDM-treated wild type and HDM-treated DDAH1-transgenic mice. For RNA-Seq, equal amounts of RNA were pooled from each mouse lung in an experimental group (n = 4 per group) and analyzed in duplicate. The bioinformatics analyses were described in Materials and Methods. The differentially expressed genes with a p-value of <0.01 were shown. WT: wild type; TG: DDAH1-transgenic; Inf: infinity. (XLS)

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Author Contributions

Conceived and designed the experiments: GKKH WC. Performed the experiments: KGK AMG SAB BPD JALF WC. Analyzed the data: KGK JD MM JALF WC. Contributed reagents/materials/analysis tools: JD MM JALF. Wrote the paper: KGK MM JALF GKKH WC.

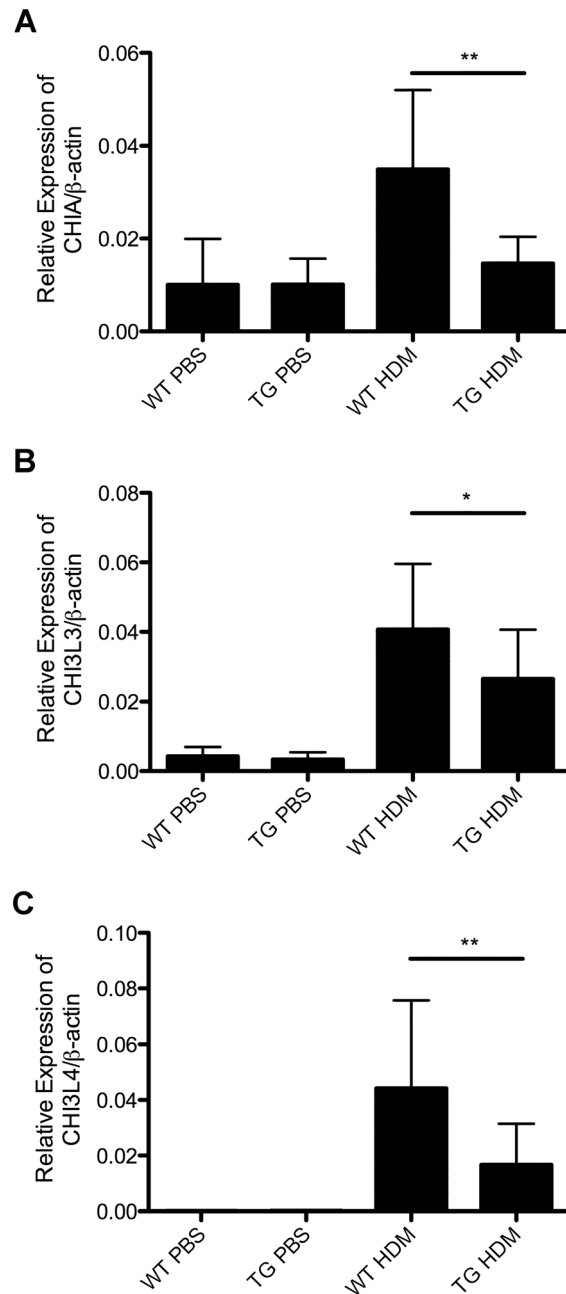


Figure 7. Expression of acidic chitinase (CHIA) and chitinase like proteins (CHI3L3 and CHI3L4) in the lungs of PBS or HDM-treated C57BL/6 wild type and DDAH1-transgenic mice. (A) CHIA. (B) CHI3L3. (C) CHI3L4. WT: wild type; TG: DDAH1-transgenic. Data are shown as mean $\pm$ SD (n = 5–9). *, p < 0.05; **, p < 0.01. doi:10.1371/journal.pone.0085148.g007

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Table S1. Primers for PCR

Primer	Sequence
IL-13 forward	5'-GCTTGCCTTGGTGGTCTCGCC-3'
IL-13 reverse	5'-GGGCTACACAGAACCCGCCA-3'
IL-4 forward	5'-CTGTAGGGCTTCCAAGGTGCTTCG-3'
IL-4 reverse	5'-CCATTTGCATGATGATGCTCTTTAGGC-3'
IL-33 forward	5'-TCCCAACAGAAGACCAAAG -3'
IL-33 reverse	5'- GATACTGCCAAGCAAGGAT-3'
CCL11 forward	5'-ATGAAAGGAGATGTGGGATTATT-3'
CCL11 reverse	5'-TTATCCTCAGTTACTCCTAACTCG-3'
MMP-12 forward	5'-TGGAGGTATGATGTGAGGCA-3'
MMP-12 reverse	5'-TTTGGTGACACGACGGA-3'
ARG1 forward	5'-CTCCAAGCCAAAGTCCTTAGAG-3'
ARG1 reverse	5'-AGGAGCTGTCATTAGGGACATC-3'
NOS2 forward	5'-GTTCTCAGCCCAACAATACAAGA-3'
NOS2 reverse	5'-GTGGACGGGTCGATGTCAC-3'
FOXA2 forward	5'-TCCGACTGGAGCAGCTACTAC-3'
FOXA2 reverse	5'-GCGCCCACATAGGATGACA-3'
DDAH1 forward	5'-GACGTCCTATTACAGGCA-3'
DDAH1 reverse	5'-CAATCAGGTTGGGTCCG-3'
DDAH2 forward	5'-GGTTGATGGAGTGCGTAAA-3'
DDAH2 reverse	5'-GCTCCTCGATGATTGGTC-3'
CHIA forward	5'-CAAGCTACTTCTCGTCACAGG-3'
CHIA reverse	5'-GGCAGGGGTTAATGTCATCAG-3'
CHI3L3 forward	5'-CAGGTCTGGCAATTCTTCTGAA-3'
CHI3L3 reverse	5'-GTCTTGCTCATGTGTGTAAGTGA-3'
CHI3L4 forward	5'-TCCACTTTGAACCACATTCCAA-3'
CHI3L4 reverse	5'-CCAGCACTAACAGTAGGGTCA-3'
β -actin forward	5'-TCATCACTATTGGCAACGA-3'
β -actin reverse	5'-TGTGTTGGCATAGAGGT-3'

Gene ID	Symbol	Name	Base Mean	Base Mean (TG PBS)	Base Mean (WT PBS)
399558	Flrt2	fibronectin le	1831,11083	3371,2199	291,0017632
17884	Myh4	myosin, heav	395,031505	780,635061	9,427950199
20210	Saa3	serum amyloi	474,62563	24,4877065	924,7635528
16365	Irg1	immunorespc	249,730771	2,0662853	497,3952561
17996	Neb	nebulin	581,916085	1062,09017	101,7420014
20202	S100a9	S100 calcium	364,872307	50,0028206	679,7417931
56619	Clec4e	C-type lectin	208,042421	14,4697322	401,6151101
100303744	Sprr2a2	small proline-	151,984355	5,33981539	298,6288936
20755	Sprr2a1	small proline-	151,984355	5,33981539	298,6288936
20302	Ccl3	chemokine (C	189,78794	4,27765572	375,2982234
20310	Cxcl2	chemokine (C	129,408288	5,97245481	252,8441204
17879	Myh1	myosin, heav	104,76918	206,395711	3,142650066
19782	Rmrp	RNA compon	455,142075	755,131758	155,1523919
19373	Rag1	recombinatio	127,379708	0,51657132	254,2428451
100861531	NA	NA	2045621,87	2597112,98	1494130,758
17882	Myh2	myosin, heav	76,7804883	152,718857	0,842119925
16176	Il1b	interleukin 1	256,563827	60,7114684	452,4161863
20201	S100a8	S100 calcium	429,268979	147,222486	711,315473
18843	Bpifa1	BPI fold conta	1022,10112	562,462807	1481,739433
21957	Tnnt3	troponin T3, s	130,003042	254,23946	5,766625006
16181	Il1rn	interleukin 1	680,716198	342,758046	1018,67435
17885	Myh8	myosin, heav	74,9502587	148,539722	1,360795052
16819	Lcn2	lipocalin 2	1936,15413	1256,59259	2615,715684
12350	Car3	carbonic anhy	1159,52642	669,932583	1649,12025
244183	Trim30b	tripartite mot	90,6604806	8,89778061	172,4231806
102436	Lars2	leucyl-tRNA s	546882,806	708154,949	385610,6637
11937	Atp2a1	ATPase, Ca++	221,335267	433,047353	9,623180528
12715	Ckm	creatine kinas	124,5712	225,752456	23,38994482
11537	Cfd	complement	154,821419	40,1879654	269,454872
74155	Errfi1	ERBB recepto	2633,9015	3381,3364	1886,466593
21938	Tnfrsf1b	tumor necros	449,013378	224,179802	673,8469536
14319	Fth1	ferritin heavy	15972,1558	12524,193	19420,11861
100503605	Beta-s	hemoglobin s	15605,1591	18940,1904	12270,12782
80885	Niacr1	niacin recept	105,138035	19,002806	191,2732638
27226	Pla2g7	phospholipas	154,285363	43,7169136	264,8538118
15129	Hbb-b1	hemoglobin, l	13163,7219	15897,3233	10430,12046
15130	Hbb-b2	hemoglobin, l	13163,7219	15897,3233	10430,12046
100042539	Gm3893	predicted gen	154,284335	262,16179	46,40688074
70574	Cpm	carboxypeptic	2294,57901	2917,30658	1671,851436

20568	Slpi	secretory leu	407,135108	213,203924	601,0662917
11474	Actn3	actinin alpha	53,5672396	103,180308	3,954170687
14605	Tsc22d3	TSC22 domain	758,413724	1040,87565	475,9517973
378460	Pram1	PML-RAR alpr	92,1065513	17,1048878	167,1082149
20343	Sell	selectin, lymph	470,667507	260,50782	680,8271944
17888	Myh6	myosin, heavy	811,819987	523,046831	1100,593143
93695	Gpnm	glycoprotein (	335,070529	169,96883	500,1722275
12575	Cdkn1a	cyclin-dependent	706,5353	971,893306	441,1772948
19204	Ptafr	platelet-activa	63,4271488	7,80660391	119,0476936
18845	Plxna2	plexin A2	1279,18822	1655,08264	903,2937989
13058	Cybb	cytochrome b	1604,48755	1025,11196	2183,863141
20655	Sod1	superoxide di	1227,46056	1585,18391	869,7372164
74100	Arpp21	cyclic AMP-re	72,4160835	0,51657132	144,3155956
15502	Dnaja1	DnaJ (Hsp40)	4977,52371	5994,08554	3960,961881
235320	Zbtb16	zinc finger an	901,007246	1250,22536	551,7891286
74145	F13a1	coagulation fa	182,812576	76,1677794	289,4573724
13641	Efnb1	ephrin B1	490,150728	686,346456	293,9550002
20303	Ccl4	chemokine (C	27,0053711	0	54,01074212
18733	Lilrb3	leukocyte imr	310,958209	164,483929	457,4324893
21414	Tcf7	transcription	420,77281	246,154156	595,3914646
12504	Cd4	CD4 antigen	184,950137	77,8801253	292,0201487
110257	Hba-a2	hemoglobin a	38581,0949	48253,1466	28909,04314
15122	Hba-a1	hemoglobin a	38581,0949	48253,1466	28909,04314
100039246	Gm10393	predicted gen	897,800413	1172,17182	623,4290078
20558	Slfn4	schlafen 4	91,6258879	23,4778458	159,77393
14081	Acsl1	acyl-CoA synt	573,879588	362,70155	785,0576259
21899	Tlr6	toll-like recep	35,3804243	1,54971397	69,21113457
57875	Angptl4	angiopoietin-	742,645131	1084,06992	401,2203452
100039796	Tgtp2	T-cell specific	681,813876	453,710547	909,9172044
21822	Tgtp1	T-cell specific	640,861095	421,903791	859,8183992
16414	Itgb2	integrin beta	597,0593	384,304417	809,814183
20354	Sema4d	sema domain	255,127127	116,170172	394,0840818
208449	Sgms1	sphingomyeli	1624,93489	2020,71525	1229,154532
100628584	Mir5109	microRNA 510	6803,66808	10011,1749	3596,161306
16408	Itgal	integrin alpha	646,06637	425,664876	866,4678649
14990	H2-M2	histocompatil	128,015496	46,3345224	209,6964697
13479	Dpep1	dipeptidase 1	1358,49147	1704,87661	1012,106326
17474	Clec4d	C-type lectin	76,1613523	17,5981772	134,7245274
20846	Stat1	signal transdu	1254,93443	924,671067	1585,197786
17907	Mylpf	myosin light c	51,0039426	95,5943705	6,413514601
110213	Tmbim6	transmembra	5261,37919	6232,02685	4290,731525

56318	Acpp	acid phosphatase	142,064372	54,8027827	229,3259611
14727	Gp49a	glycoprotein 49a	332,451568	191,055126	473,8480105
19264	Ptprc	protein tyrosine phosphatase	1905,08935	1436,49234	2373,686369
12161	Bmp6	bone morphogenetic protein 6	815,31147	1067,40097	563,2219722
434223	Gm1966	predicted gene	776,928153	539,530891	1014,325415
73504	1700071M16	RIKEN cDNA 1700071M16	38,5671439	3,15746199	73,97682588
110310	Krt7	keratin 7	540,401979	730,928145	349,8758118
433408	Gm13375	predicted gene	78,6230172	140,135573	17,11046194
12983	Csf2rb	colony stimulating factor 2 related beta	728,004927	509,204003	946,8058501
13040	Ctss	cathepsin S	1325,53561	994,303598	1656,767623
17394	Mmp8	matrix metalloproteinase 8	68,4110706	15,816327	121,0058142
14728	Lilrb4	leukocyte immunoglobulin like receptor family class B member 4	504,274198	333,07107	675,4773251
68891	Cd177	CD177 antigen	73,7803416	10,2501105	137,3105727
12986	Csf3r	colony stimulating factor 3 receptor	1135,14088	846,22173	1424,060035
20363	Sepp1	selenoprotein 1	11826,1521	13678,3644	9973,939754
16341	Eif3e	eukaryotic translation initiation factor 3 subunit e	817,550356	1049,30916	585,7915531
20387	Sftpa1	surfactant protein A1	23161,359	26633,3454	19689,37267
232313	Gxylt2	glucosyltransferase 2	24,6753072	0,54558835	48,80502605
234797	6430548M08	RIKEN cDNA 6430548M08	440,177156	599,232158	281,1221538
11464	Actc1	actin, alpha, cardiac	837,724361	605,697902	1069,75082
11450	Adipoq	adiponectin, C1q domain containing	43,3014673	5,68228457	80,92065012
14645	Glul	glutamate-aminotransferase	2495,45617	2988,83634	2002,076
117167	Steap4	STEAP family class 4 member	116,031696	45,0925254	186,9708663
245944	Vps54	vacuolar protein sorting 54	1508,43711	1843,73509	1173,139132
56492	Cldn18	claudin 18	8529,61137	9834,95112	7224,271621
73656	Ms4a6c	membrane-spanning 4 domain class A type 6c	192,524019	100,075145	284,972892
56726	Sh3bgrl	SH3-binding GRB1-like protein	5956,34643	6895,97148	5016,721385
11852	Rhob	ras homolog B	1187,56798	1471,01017	904,1257974
23844	Clca3	chloride channel, calcium-activated	130,94556	203,133651	58,75746863
56737	Alg2	asparagine-linked glycanase 2	282,162458	397,381333	166,9435839
211623	Plac9	placenta specific 9	679,866091	873,583147	486,1490343
15931	Ids	iduronate 2-sulphatase	4559,31351	5321,43246	3797,194573
22138	Ttn	titin	4200,74614	4963,30583	3438,186447
58210	Sectm1b	secreted and transmembrane 1b	19,069339	0	38,13867801
246728	Oas2	2'-5' oligoadenylate synthetase 2	111,555656	44,8661244	178,245187
14349	Fv1	Friend virus 1	67,4425155	118,195629	16,68940198
80719	Igsf6	immunoglobulin superfamily 6	148,926741	69,0403787	228,8131033
17476	Mpeg1	macrophage embryonic development 1	1615,6581	1275,85115	1955,465046
15139	Hc	hemolytic complement	10556,2114	12088,7375	9023,685261
66259	Camk2n1	calcium/calmodulin dependent kinase 2 nuclear 1	778,078719	983,93742	572,2200192
20410	Sorbs3	sorbin and SH3 domain containing 3	2799,84909	3312,27779	2287,420388

11770	Fabp4	fatty acid bin	165,330981	83,1386247	247,5233374
60533	Cd274	CD274 antige	715,490225	520,087095	910,8933561
13003	Vcan	versican	339,03655	214,202314	463,8707859
67547	Slc39a8	solute carrier	2515,53868	2968,02807	2063,049297
23880	Fyb	FYN binding p	330,496533	209,216439	451,776627
12772	Ccr2	chemokine (C	475,303287	316,436873	634,1697019
14009	Etv1	ets variant ge	474,556299	630,655957	318,4566415
22003	Tpm1	tropomyosin	2430,46211	2871,21498	1989,709239
60440	ligp1	interferon inc	425,706648	285,819473	565,5938225
56484	Foxo3	forkhead box	1028,92153	1271,06908	786,7739781
16601	Klf9	Kruppel-like f	1738,87536	2091,38632	1386,364408
19374	Rag2	recombinatio	29,4140917	2,66990769	56,15827574
320484	Rasal3	RAS protein a	132,85301	62,1856015	203,5204193
21835	Thrsp	thyroid horm	60,7755234	16,3619153	105,1891314
12475	Cd14	CD14 antigen	224,753241	127,95245	321,5540316
17329	Cxcl9	chemokine (C	234,542771	134,308203	334,7773388
237175	Gpr64	G protein-cou	68,6917881	115,769669	21,61390706
19293	Pvalb	parvalbumin	22,1164318	43,2931285	0,93973509
245049	Myrip	myosin VIIA a	199,238028	286,806394	111,6696619
229898	Gbp5	guanylate bin	138,729426	67,6647669	209,7940849
241431	Xirp2	xin actin-bind	237,725435	352,990951	122,4599202
236604	Pisd-ps1	phosphatidyls	1027,74711	789,242671	1266,251556
66884	Appbp2	amyloid beta	361,338917	486,138473	236,5393619
104759	Pld4	phospholipas	141,867665	69,4931809	214,2421487
408064	BC064078	cDNA sequen	44,4781803	80,2423159	8,714044743
18534	Pck1	phosphoenolp	71,7215106	24,6327916	118,8102295
81897	Tlr9	toll-like recep	60,7338385	17,5111261	103,9565508
100134861	BC090627	cDNA sequen	143,513876	72,4009599	214,6267921
76524	Cln6	ceroid-lipofus	121,553707	185,814174	57,29324116
13088	Cyp2b10	cytochrome P	2024,11149	2381,20577	1667,017216
12288	Cacna1c	calcium chan	422,322708	289,162849	555,4825661
20855	Stc1	stanniocalcin	121,180733	50,745793	191,6156734
56198	Heyl	hairy/enhanc	456,712651	319,211037	594,2142654
83921	Tmem2	transmembra	2051,19151	2415,86733	1686,515701
12765	Cxcr2	chemokine (C	1192,80932	938,44405	1447,174586
232664	Ccdc136	coiled-coil do	28,4186799	3,18647902	53,65088076
17896	Myl4	myosin, light	161,755433	86,0929675	237,4178983
12892	Cpox	coproporphyr	409,844571	540,343027	279,346116
12655	Chi3l3	chitinase 3-lik	4575,94153	5251,35859	3900,524477
74180	Muc5b	mucin 5, subt	6717,19737	5780,70212	7653,692628
66455	Cnpy4	canopy 4 hor	108,100697	169,092242	47,10915169

20230	Satb1	special AT-rich	405,980052	246,966632	564,9934709
55935	Fnbp4	formin binding	727,524711	547,84799	907,2014316
13033	Ctsd	cathepsin D	3006,3573	2527,97409	3484,740507
56644	Clec7a	C-type lectin	331,645848	217,191409	446,1002868
236794	Slc9a6	solute carrier	311,834289	424,730254	198,9383238
13819	Epas1	endothelial P	41845,322	46959,6174	36731,02664
109674	Ampd2	adenosine me	121,432936	58,5058331	184,3600389
12265	Ciita	class II trans	263,356976	163,201103	363,5128486
97064	Wwtr1	WW domain	2026,47594	2391,51897	1661,432908
232910	Ap2s1	adaptor-relat	153,449227	81,1536554	225,7447994
230379	Acer2	alkaline ceram	1579,44689	1872,77376	1286,120024
12236	Bub1b	budding uninl	74,3212886	26,1477535	122,4948237
70785	Dennd1c	DENN/MADD	88,3624583	35,5388235	141,1860931
230787	BC013712	cDNA sequen	171,683417	93,4643161	249,902518
18718	Pip4k2a	phosphatidyl	483,721265	344,37187	623,0706594
21925	Tnnc2	troponin C2, f	59,5865915	118,654508	0,518675127
16068	Il18bp	interleukin 18	194,458696	111,933004	276,9843873
21417	Zeb1	zinc finger E-k	1393,60715	1660,90462	1126,309678
13106	Cyp2e1	cytochrome P	763,747198	576,555318	950,9390775
22214	Ube2h	ubiquitin-con	1579,42677	1871,17748	1287,67605
16409	Itgam	integrin alpha	430,59366	299,285421	561,901898
21954	Tnni3	troponin I, ca	189,627039	107,82945	271,4246271
279572	Tlr13	toll-like recep	170,240005	93,9576055	246,5224037
69780	Smap2	stromal mem	491,084351	349,90907	632,2596325
50887	Hmgn5	high-mobility	232,220006	321,045186	143,3948253
57440	Ehd3	EH-domain co	222,537812	311,706074	133,3695496
18054	Ngp	neutrophilic g	35,3569549	0,54558835	70,16832142
68318	Aph1c	anterior phar	129,231294	64,1938528	194,2687346
242505	Rasef	RAS and EF ha	316,666793	424,492383	208,8412023
12508	Cd53	CD53 antigen	914,824199	674,826015	1154,822384
11931	Atp1b1	ATPase, Na+/	3667,71077	4204,66704	3130,754502
29817	Igfbp7	insulin-like gr	5564,62865	6350,88448	4778,37283
20309	Cxcl15	chemokine (C	17137,1059	19221,9684	15052,2434
381827	1700073E17R	Ribosomal pro	39,3510897	69,9517182	8,7504613
56338	Txnip	thioredoxin ir	3334,50777	3840,83956	2828,175977
192199	Rspo1	R-spondin ho	180,628036	259,776318	101,4797552
232201	Arhgap25	Rho GTPase a	146,165054	78,7158839	213,6142239
380928	Lmo7	LIM domain o	6754,84582	7663,16927	5846,522365
242122	Vtcn1	V-set domain	94,6401319	38,2320131	151,0482508
330812	Rnf150	ring finger pro	618,677295	776,949898	460,404691
50794	Klf13	Kruppel-like f	1299,92359	1560,80011	1039,047068

12359	Cat	catalase	5908,72969	6709,32121	5108,13817
117606	Boc	biregional cel	210,198965	125,479927	294,9180043
18648	Pgam1	phosphoglyce	496,021244	360,251966	631,7905214
20742	Spnb2	spectrin beta	30295,3123	33813,7151	26776,90939
235712	Mrgpra2b	MAS-related c	14,5170863	0	29,03417261
328833	Trem12	triggering rec	60,5837385	20,0359487	101,1315283
16401	Itga4	integrin alpha	1392,30625	1135,01883	1649,593665
239606	Slc2a13	solute carrier	106,829085	49,9970855	163,6610848
238276	Akap5	A kinase (PRK	5400,70803	6135,85822	4665,557847
239611	Muc19	mucin 19	157,919951	87,8805528	227,9593488
67006	Cisd2	CDGSH iron si	779,255175	1024,50766	534,0026908
231238	Sel1l3	sel-1 suppres	78,2693022	124,911056	31,62754825
98053	Gtf2f1	general transi	139,243851	203,760555	74,7271479
11475	Acta2	actin, alpha 2	682,510337	515,554021	849,4666526
330319	Wipf3	WAS/WASL ir	232,378937	319,489396	145,2684782
211151	Churc1	churchill dom	1461,64742	1188,82356	1734,471277
12389	Cav1	caveolin 1, ca	9831,11041	11049,835	8612,385772
100503468	Gm14023	predicted gen	41,4758164	10,0179743	72,93365837
16175	Il1a	interleukin 1 :	112,739089	31,830038	193,6481401
22782	Slc30a1	solute carrier	777,476156	996,682653	558,269659
18106	Cd244	CD244 natura	38,9684423	8,92679763	69,01008699
14415	Gad1	glutamic acid	14,0290105	0	28,05802096
229841	Cenpe	centromere p	94,801093	41,7957134	147,8064725
11909	Atf2	activating tra	1105,77641	1320,42171	891,1311111
26897	Acot1	acyl-CoA thio	322,348742	425,641594	219,055891
15481	Hspa8	heat shock pr	12808,9356	14363,4584	11254,41276
22627	Ywhae	tyrosine 3-mc	7567,41221	8843,52184	6291,302578
20531	Slc34a2	solute carrier	29821,4693	33282,5216	26360,41699
16822	Lcp2	lymphocyte c	358,92634	246,635975	471,2167053
16579	Kifap3	kinesin-associ	398,156452	513,452642	282,8602619
15519	Hsp90aa1	heat shock pr	8316,47981	9335,83322	7297,126394
12651	Chkb	choline kinase	133,543491	71,5419194	195,545062
100038947	LOC10003894	signal-regulat	132,809827	70,1605724	195,4590814
70350	Basp1	brain abunda	185,602701	111,184296	260,0211046
18738	Pitpna	phosphatidyli	1595,52281	1875,68154	1315,364088
21928	Tnfaip2	tumor necros	144,511942	78,779653	210,2442311
329251	Ppp1r12b	protein phosp	806,671144	626,320268	987,0220198
14461	Gata2	GATA binding	1144,71306	1410,84361	878,5825017
216984	Evi2b	ecotropic vira	408,378102	292,436379	524,3198247
20295	Ccl17	chemokine (C	77,1496389	123,129206	31,17007173
670558	H60c	histocompatil	19,7663102	37,976595	1,556025381

232334	Vgll4	vestigial like 4	129,181562	190,445769	67,91735538
66625	Sfrs18	serine/arginir	794,720067	618,746141	970,6939922
235461	Fam63b	family with se	2107,67568	2457,01927	1758,332081
103968	Plin1	perilipin 1	94,4598656	36,5777013	152,34203
93685	Entpd7	ectonucleosic	192,355562	268,122775	116,5883497
227525	Dclre1c	DNA cross-lin	1184,64962	957,02307	1412,276173
21885	Tle1	transducin-lik	444,077143	569,393165	318,7611215
16423	Cd47	CD47 antigen	2727,33226	3138,58297	2316,081552
668727	Mrgpra2a	MAS-related c	13,3821209	0	26,76424177
66676	Tmed7	transmembra	1530,73871	1797,37189	1264,105535
215821	D10Bwg1379i	DNA segment	471,774542	600,050369	343,4987138
338349	Cntln	centlein, cent	313,781256	415,199834	212,3626785
21858	Timp2	tissue inhibito	5635,79794	6375,11206	4896,483815
12491	Cd36	CD36 antigen	10091,4977	11277,4358	8905,559616
14164	Fgf1	fibroblast gro	1984,04623	2295,73397	1672,358477
78878	B230206F22R	RIKEN cDNA E	118,387407	58,4130469	178,361767
668101	Sirpb1b	signal-regulat	114,989888	59,0514214	170,9283539
69423	1700019M22	RIKEN cDNA 1	12,6443565	25,288713	0
20452	St8sia4	ST8 alpha-N-a	788,598069	622,146868	955,0492708
243277	Gpr133	G protein-cou	117,944139	60,3457173	175,5425617
66214	1190002H23F	RIKEN cDNA 1	743,596984	912,140082	575,053885
15212	Hexb	hexosaminida	301,212561	204,904031	397,5210904
16774	Lama3	laminin, alpha	1472,73417	1724,12302	1221,345319
13506	Dsc2	desmocollin 2	31,2292076	4,21962167	58,2387935
17898	Myl7	myosin, light	233,915311	152,590977	315,2396452
17395	Mmp9	matrix metall	50,2701227	15,6712419	84,86900355
213002	Ifitm6	interferon ind	24,7325726	3,18647902	46,27866627
107350	AW112010	expressed sec	391,729305	280,723606	502,7350039
52837	Tmx4	thioredoxin-r	618,50533	474,901442	762,1092189
66408	Aptx	aprataxin	103,274824	51,0416983	155,507949
72042	Cotl1	coactosin-like	237,830037	155,928618	319,7314559
114641	Rpl31	ribosomal prc	3958,69867	4501,29368	3416,103664
77569	Limch1	LIM and calpc	4952,71337	5564,83539	4340,591354
73327	1700040I03Ri	RIKEN cDNA 1	55,6154945	91,4965521	19,73443688
20250	Scd2	stearoyl-Coer	5901,54839	6626,49501	5176,601774
218975	Mapk1ip1l	mitogen-activ	1389,75081	1633,46762	1146,033993
381126	Fam59a	family with se	82,1861173	35,6839086	128,6883259
15516	Hsp90ab1	heat shock pr	12042,3793	13394,1452	10690,61347
21810	Tgfbf	transforming	377,813171	270,386444	485,2398985
11658	Alcam	activated leuk	5473,54954	6138,68707	4808,412006
22070	Tpt1	tumor proteir	6238,11694	7013,94508	5462,288806

18826	Lcp1	lymphocyte c	3740,6083	3243,55155	4237,665058
71373	Prr16	proline rich 1	35,4917995	8,38120929	62,60238964
17357	Marcksl1	MARCKS-like	99,3826291	49,9505216	148,8147365
319757	Smo	smoothened l	419,773505	305,008193	534,5388177
21673	Dntt	deoxynucleot	12,6223165	0	25,24463295
30960	Vapa	vesicle-associ	1259,99	1489,26966	1030,710336
20361	Sema7a	sema domain	369,084531	487,954733	250,2143282
12482	Ms4a1	membrane-sp	241,799283	159,974137	323,6244279
11991	Hnrnpd	heterogeneou	1309,76835	1538,7043	1080,832411
216080	Ube2d1	ubiquitin-con	314,590035	410,202829	218,9772407
11826	Aqp1	aquaporin 1	1853,25605	2241,6573	1464,8548
22612	Yes1	Yamaguchi sa	705,321476	855,479527	555,1634255
652925	4930420K17R	RIKEN cDNA 4	1413,5514	1656,58613	1170,51667
108100	Baiap2	brain-specific	385,536632	279,27849	491,7947751
14130	Fcgr2b	Fc receptor, l	204,813091	130,2917	279,3344815
85029	Rpph1	ribonuclease	1406,60955	2063,09909	750,1200054
22337	Vdr	vitamin D rec	101,090343	50,5831611	151,5975252
56434	Tspan3	tetraspanin 3	271,575585	358,743081	184,4080899
216233	Socs2	suppressor of	875,273157	1073,66899	676,8773279
17916	Myo1f	myosin IF	301,06338	187,97898	414,1477807
259301	Leap2	liver-expresse	35,1050386	8,35219226	61,85788488
215632	Psd4	pleckstrin anc	130,519862	73,5734526	187,4662724
12487	Cd28	CD28 antigen	115,420707	61,0363908	169,805023
72053	Tmub2	transmembra	107,441854	49,5500184	165,3336902
68371	Pbld1	phenazine bic	1219,56389	998,580913	1440,546876
50780	Rgs3	regulator of G	411,715821	285,308637	538,1230055
66396	Ccdc82	coiled-coil do	3733,32045	3250,28957	4216,351326
70686	Dusp16	dual specificit	442,731229	326,239916	559,2225417
213233	Tapbpl	TAP binding p	1169,22819	956,471747	1381,984638
109828	C7	complement c	2500,473	2852,78139	2148,164608
12774	Ccr5	chemokine (C	92,8957445	46,2764883	139,5150008
104099	Itga9	integrin alpha	1503,51741	1755,84812	1251,186708
66164	Nip7	nuclear impoi	1043,92837	850,168729	1237,688007
192232	Hps4	Hermansky-Pi	74,5080803	33,1533509	115,8628097
12577	Cdkn1c	cyclin-depenc	198,692923	271,210733	126,1751137
74480	Samd4	sterile alpha r	870,871034	1038,0087	703,7333676
102122	Fam192a	family with se	151,70934	90,5737424	212,844937
16400	Itga3	integrin alpha	1787,8548	2065,55809	1510,151498
14778	Gpx3	glutathione p	5838,33849	6560,4029	5116,274089
209039	Tenc1	tensin like C1	2376,50071	2708,50785	2044,493572
70882	Armc3	armadillo rep	34,6322511	8,70039655	60,56410569

227835	Gtdc1	glycosyltransf	985,083843	800,653462	1169,514223
20623	Snrk	SNF related ki	985,47706	1163,4478	807,5063226
18725	Pira2	paired-Ig-like	213,421629	138,05174	288,791518
18627	Per2	period homol	318,130883	423,447429	212,8143377
14268	Fn1	fibronectin 1	4324,17384	3787,91039	4860,437289
100113398	Adat3	adenosine de	18,1886987	1,03314265	35,34425479
68023	Pdf	peptide defor	167,480425	233,060035	101,9008151
67665	Dctn4	dynactin 4	1367,15451	1596,14695	1138,162068
19094	Mapk11	mitogen-activ	109,426269	166,056925	52,79561329
18613	Pecam1	platelet/endo	3963,29106	4500,16639	3426,415733
66105	Ube2d3	ubiquitin-con	3705,17286	4177,39302	3232,952702
192678	Rassf3	Ras associatic	1108,28339	1304,22816	912,3386187
54483	Mefv	Mediterranea	27,5148535	5,22374729	49,80595974
60344	Fign	fidgetin	241,593455	322,704892	160,4820182
18575	Pde1c	phosphodiect	19,2674707	2,15333637	36,38160505
18126	Nos2	nitric oxide sy	63,0343332	8,58432845	117,4843379
50934	Slc7a8	solute carrier	59,3514549	23,1063596	95,59655019
241919	Slc7a14	solute carrier	1524,43389	1277,18593	1771,681855
229731	Slc25a24	solute carrier	453,643775	567,773606	339,5139438
18722	Pira1	paired-Ig-like	209,039034	134,888543	283,189524
22317	Vamp1	vesicle-associ	38,6692814	10,2210935	67,11746927
50876	Tmod2	tropomodulin	1361,82084	1607,80742	1115,834256
20208	Saa1	serum amyloi	11,5026507	0	23,00530141
11656	Alas2	aminolevulini	343,689117	440,111326	247,2669085
100756	Usp30	ubiquitin spec	138,181648	79,4764031	196,8868923
69228	Zfp746	zinc finger pro	199,247846	269,428541	129,0671521
18197	Nsg2	neuron specif	16,033009	1,0911767	30,9748414
665562	Gm7689	predicted pse	3032,99478	3443,79462	2622,194936

Fold Change (WT PBS/TG PBS)	log2 Fold Change (WT PBS/TG PBS)	Fold Change (TG PBS/WT PBS)	log2 Fold Change (TG PBS/WT PBS)	p value
0,086319425	-3,534170937	11,58487793	3,534170937	8,67E-78
0,012077283	-6,371560312	82,80008316	6,371560312	3,04E-52
37,76440035	5,238954974	0,026479965	-5,238954974	5,89E-50
240,7195448	7,911209473	0,004154212	-7,911209473	1,41E-39
0,095794128	-3,383918968	10,43905324	3,383918968	1,02E-32
13,594069	3,764905445	0,073561492	-3,764905445	3,96E-26
27,75553167	4,794703424	0,036028854	-4,794703424	4,41E-22
55,9249472	5,805420084	0,017881108	-5,805420084	2,23E-20
55,9249472	5,805420084	0,017881108	-5,805420084	2,23E-20
87,73455564	6,455073278	0,011398017	-6,455073278	2,26E-20
42,33504121	5,403780388	0,023621094	-5,403780388	1,48E-16
0,015226334	-6,037287541	65,6756897	6,037287541	2,88E-15
0,205464	-2,283042455	4,867032657	2,283042455	3,27E-15
492,1737485	8,943023899	0,002031803	-8,943023899	8,09E-15
0,57530449	-0,797602364	1,738209969	0,797602364	2,42E-13
0,005514184	-7,502636792	181,3504849	7,502636792	2,52E-13
7,451906507	2,897609574	0,134193847	-2,897609574	2,81E-13
4,831568142	2,272491509	0,20697214	-2,272491509	1,47E-12
2,634377621	1,397462162	0,379596301	-1,397462162	1,70E-11
0,022681865	-5,462316944	44,08808609	5,462316944	3,43E-11
2,971992527	1,571430488	0,336474601	-1,571430488	1,01E-10
0,009161153	-6,770255175	109,1565714	6,770255175	1,63E-10
2,081594077	1,057688762	0,480401059	-1,057688762	2,20E-10
2,461621201	1,299608774	0,406236345	-1,299608774	1,38E-09
19,37822343	4,276364407	0,051604318	-4,276364407	2,73E-09
0,544528658	-0,876920117	1,836450636	0,876920117	5,80E-09
0,022222005	-5,491867186	45,00043947	5,491867186	1,61E-08
0,103608817	-3,27078132	9,651688267	3,27078132	1,65E-08
6,704864733	2,745208227	0,14914544	-2,745208227	3,28E-08
0,557905624	-0,841907	1,792417852	0,841907	3,64E-08
3,00583259	1,58776466	0,332686525	-1,58776466	5,13E-08
1,550608385	0,632834371	0,64490816	-0,632834371	5,18E-08
0,647835505	-0,626300557	1,54360172	0,626300557	8,27E-08
10,06552736	3,331350855	0,099348992	-3,331350855	8,88E-08
6,058383126	2,598932815	0,165060542	-2,598932815	1,49E-07
0,656092871	-0,60802805	1,524174465	0,60802805	2,57E-07
0,656092871	-0,60802805	1,524174465	0,60802805	2,57E-07
0,177016188	-2,498046795	5,649200852	2,498046795	2,72E-07
0,573080474	-0,803190354	1,744955632	0,803190354	3,06E-07

2,819208392	1,495290124	0,3547095	-1,495290124	6,58E-07
0,03832292	-4,705648706	26,09404516	4,705648706	7,40E-07
0,457260958	-1,128910351	2,186935014	1,128910351	8,85E-07
9,769617746	3,288302115	0,10235815	-3,288302115	9,26E-07
2,613461641	1,385961984	0,382634275	-1,385961984	1,02E-06
2,104196177	1,073269215	0,47524086	-1,073269215	1,24E-06
2,94272914	1,557154757	0,339820606	-1,557154757	2,35E-06
0,453935933	-1,1394394	2,202954045	1,1394394	2,49E-06
15,24961365	3,930700788	0,065575432	-3,930700788	2,78E-06
0,545769605	-0,873636045	1,832274996	0,873636045	3,57E-06
2,13036548	1,091100957	0,469403025	-1,091100957	4,42E-06
0,548666444	-0,86599875	1,822600983	0,86599875	4,55E-06
279,3720611	8,126043939	0,003579456	-8,126043939	7,50E-06
0,660811705	-0,597688854	1,513290387	0,597688854	8,82E-06
0,441351732	-1,179999237	2,265766572	1,179999237	1,14E-05
3,800260093	1,926098161	0,263139884	-1,926098161	1,14E-05
0,428289529	-1,22334169	2,334869131	1,22334169	1,18E-05
Inf	Inf	0		1,23E-05
2,781016309	1,475612205	0,359580775	-1,475612205	1,47E-05
2,418774783	1,274276443	0,413432456	-1,274276443	1,49E-05
3,749610669	1,906740805	0,266694355	-1,906740805	1,50E-05
0,599112083	-0,739102165	1,669136759	0,739102165	1,52E-05
0,599112083	-0,739102165	1,669136759	0,739102165	1,52E-05
0,531858042	-0,910886867	1,880200959	0,910886867	1,76E-05
6,805306222	2,766660081	0,146944159	-2,766660081	1,89E-05
2,164472765	1,114015648	0,462006275	-1,114015648	2,00E-05
44,66058626	5,480930285	0,022391108	-5,480930285	2,07E-05
0,370105599	-1,433991136	2,701931568	1,433991136	2,09E-05
2,005501547	1,003963079	0,498628386	-1,003963079	2,39E-05
2,037948976	1,027117931	0,490689419	-1,027117931	2,44E-05
2,107220594	1,075341351	0,474558764	-1,075341351	2,57E-05
3,39230005	1,762263782	0,294785245	-1,762263782	2,71E-05
0,608276961	-0,717199733	1,64398796	0,717199733	2,79E-05
0,359214713	-1,477081651	2,783850335	1,477081651	3,01E-05
2,035563455	1,025428196	0,491264469	-1,025428196	3,04E-05
4,525706946	2,178143168	0,220959954	-2,178143168	3,21E-05
0,593653712	-0,752306467	1,684483699	0,752306467	3,37E-05
7,655595586	2,93651462	0,13062341	-2,93651462	3,39E-05
1,714336959	0,777650704	0,583315896	-0,777650704	3,98E-05
0,067090923	-3,897738587	14,90514585	3,897738587	3,99E-05
0,688496957	-0,538477816	1,452439244	0,538477816	4,10E-05

4,184567822	2,06507863	0,238973304	-2,06507863	4,16E-05
2,480163814	1,310435414	0,403199173	-1,310435414	5,15E-05
1,652418398	0,724579028	0,605173606	-0,724579028	5,26E-05
0,527657356	-0,922326701	1,895169257	0,922326701	5,80E-05
1,880013602	0,9107431	0,531911045	-0,9107431	5,81E-05
23,42920549	4,550236126	0,042681772	-4,550236126	6,18E-05
0,478673333	-1,062886658	2,089107393	1,062886658	7,64E-05
0,122099347	-3,033872607	8,190051971	3,033872607	7,96E-05
1,859384144	0,894824858	0,537812481	-0,894824858	9,38E-05
1,666259306	0,736612932	0,600146686	-0,736612932	9,53E-05
7,650689962	2,93558986	0,130707166	-2,93558986	0,00012018
2,028027606	1,020077291	0,493089935	-1,020077291	0,00012794
13,39600899	3,743731344	0,074649099	-3,743731344	0,00014007
1,682845032	0,750902329	0,594231781	-0,750902329	0,00015001
0,729176345	-0,455660334	1,371410368	0,455660334	0,00015421
0,558264024	-0,840980508	1,791267138	0,840980508	0,00015837
0,739275235	-0,43581651	1,35267618	0,43581651	0,00017571
89,45393755	6,483073083	0,011178938	-6,483073083	0,00017702
0,469137296	-1,091917898	2,131572164	1,091917898	0,00017822
1,766145824	0,820604466	0,566204662	-0,820604466	0,00018187
14,24086547	3,831964922	0,070220451	-3,831964922	0,00019128
0,66985133	-0,578087163	1,492868574	0,578087163	0,00023774
4,146382674	2,051853271	0,241174074	-2,051853271	0,00024848
0,636283997	-0,652257259	1,571625257	0,652257259	0,00025729
0,734550842	-0,445065745	1,361376154	0,445065745	0,00029512
2,847589087	1,509740978	0,351174263	-1,509740978	0,00032279
0,727485808	-0,459008991	1,374597262	0,459008991	0,00032827
0,614629195	-0,702211799	1,626997235	0,702211799	0,000337
0,289255219	-1,789585105	3,457154562	1,789585105	0,0003547
0,420109276	-1,251163454	2,380333064	1,251163454	0,00036384
0,556500015	-0,845546368	1,796945145	0,845546368	0,00037757
0,713566245	-0,486880725	1,401411582	0,486880725	0,00038746
0,692721054	-0,529653572	1,443582513	0,529653572	0,00038856
Inf	Inf	0		0,00039069
3,972823362	1,99016465	0,251710159	-1,99016465	0,00040583
0,141201516	-2,824172519	7,082076948	2,824172519	0,00040613
3,314192469	1,728657389	0,301732627	-1,728657389	0,00040954
1,532674908	0,616051723	0,652454082	-0,616051723	0,00042788
0,746453899	-0,421874933	1,339667462	0,421874933	0,00045876
0,581561396	-0,781996589	1,719508907	0,781996589	0,00049004
0,69058833	-0,53410214	1,448040687	0,53410214	0,00049624

2,977236372	1,573973766	0,335881964	-1,573973766	0,00053383
1,751424646	0,808528918	0,570963759	-0,808528918	0,00054323
2,165573173	1,114748921	0,461771513	-1,114748921	0,00054844
0,695090899	-0,524726439	1,438660758	0,524726439	0,00055396
2,159374427	1,110613422	0,463097084	-1,110613422	0,00058379
2,004095465	1,002951233	0,498978226	-1,002951233	0,0005943
0,504960966	-0,985756224	1,980351091	0,985756224	0,0006336
0,692985114	-0,529103733	1,443032441	0,529103733	0,00064718
1,978849852	0,98466215	0,505344051	-0,98466215	0,00066434
0,618986011	-0,692021289	1,615545395	0,692021289	0,00068655
0,662892549	-0,593153058	1,508540112	0,593153058	0,00069418
21,03378925	4,39463687	0,047542551	-4,39463687	0,00071226
3,272790073	1,710521066	0,305549692	-1,710521066	0,00071273
6,428900848	2,6845721	0,155547585	-2,6845721	0,00076948
2,513074437	1,329453405	0,397918973	-1,329453405	0,00078622
2,492605304	1,317654455	0,401186661	-1,317654455	0,00082209
0,186697493	-2,421225537	5,356258306	2,421225537	0,0008296
0,021706334	-5,525740127	46,06950295	5,525740127	0,00083107
0,389355553	-1,360839894	2,568346574	1,360839894	0,00086337
3,100492243	1,63249728	0,322529431	-1,63249728	0,00087201
0,346920849	-1,527321551	2,882501885	1,527321551	0,00093761
1,604388108	0,682023178	0,623290583	-0,682023178	0,00094207
0,486567871	-1,039287034	2,055211736	1,039287034	0,00096042
3,08292333	1,624299011	0,324367457	-1,624299011	0,00100281
0,108596626	-3,202948819	9,208389251	3,202948819	0,00105776
4,823254758	2,270007013	0,207328879	-2,270007013	0,00113746
5,936599983	2,569636905	0,168446586	-2,569636905	0,0011581
2,964419151	1,56774945	0,337334213	-1,56774945	0,00118324
0,308336227	-1,697423692	3,243212809	1,697423692	0,00121475
0,700072726	-0,514423293	1,428423024	0,514423293	0,00124457
1,921002535	0,941859423	0,52056152	-0,941859423	0,00125217
3,775991311	1,916855445	0,264831118	-1,916855445	0,00129547
1,861509148	0,896472706	0,537198542	-0,896472706	0,00132921
0,698099471	-0,518495477	1,432460619	0,518495477	0,00142175
1,542100018	0,624896339	0,648466369	-0,624896339	0,00143064
16,83704191	4,073566789	0,059392856	-4,073566789	0,00145736
2,757692122	1,463461399	0,362622061	-1,463461399	0,00147512
0,516979219	-0,951821804	1,934313726	0,951821804	0,00147549
0,742764831	-0,429022588	1,346321148	0,429022588	0,00147965
1,324007443	0,404911232	0,755282763	-0,404911232	0,00150119
0,278600313	-1,843731214	3,58937141	1,843731214	0,00150177

2,287732012	1,193918063	0,437114135	-1,193918063	0,00151075
1,655936406	0,727647269	0,603887925	-0,727647269	0,00152635
1,378471607	0,463069552	0,72544113	-0,463069552	0,00156648
2,05394996	1,038401034	0,486866778	-1,038401034	0,00156878
0,468387457	-1,094225652	2,134984583	1,094225652	0,00157167
0,782183261	-0,354421433	1,27847277	0,354421433	0,00160176
3,151139454	1,655873602	0,317345524	-1,655873602	0,00160414
2,227392101	1,155355547	0,448955529	-1,155355547	0,00161558
0,694718683	-0,525499199	1,439431564	0,525499199	0,00166952
2,78169601	1,475964767	0,359492912	-1,475964767	0,00167595
0,686746073	-0,542151339	1,456142291	0,542151339	0,00169591
4,68471694	2,22796188	0,213460069	-2,22796188	0,001729
3,97272839	1,990130162	0,251716176	-1,990130162	0,00174828
2,673774638	1,418877872	0,374003099	-1,418877872	0,00174844
1,809296036	0,85542848	0,55270115	-0,85542848	0,00175181
0,004371306	-7,837720008	228,7645996	7,837720008	0,00178171
2,474555113	1,307169174	0,404113044	-1,307169174	0,00181151
0,678130259	-0,560365675	1,474642942	0,560365675	0,0018131
1,649345774	0,721893881	0,606301005	-0,721893881	0,00181559
0,688163503	-0,539176715	1,453143033	0,539176715	0,00182058
1,877478347	0,908796269	0,532629312	-0,908796269	0,00182112
2,517166007	1,331800365	0,397272169	-1,331800365	0,00189449
2,623762094	1,391636911	0,381132116	-1,391636911	0,00190863
1,806925534	0,853537052	0,553426238	-0,853537052	0,00191433
0,446649978	-1,162783404	2,238889621	1,162783404	0,00197085
0,427869589	-1,224756952	2,337160727	1,224756952	0,00199717
128,6103738	7,006863206	0,007775423	-7,006863206	0,00203556
3,026282522	1,597546678	0,330438415	-1,597546678	0,00206363
0,49197868	-1,023332297	2,032608404	1,023332297	0,00207808
1,711289072	0,775083481	0,58435481	-0,775083481	0,00209127
0,744590349	-0,425481177	1,343020361	0,425481177	0,00210945
0,752394859	-0,410438104	1,329089358	0,410438104	0,00215907
0,783075026	-0,352777557	1,277016846	0,352777557	0,00215918
0,125092872	-2,998928515	7,99406063	2,998928515	0,00224764
0,736343169	-0,441549811	1,358062438	0,441549811	0,0022566
0,390642827	-1,356077971	2,559883173	1,356077971	0,00228486
2,71373722	1,440281026	0,368495517	-1,440281026	0,00234195
0,762937912	-0,390362439	1,310722647	0,390362439	0,00235184
3,950831737	1,982156404	0,25311126	-1,982156404	0,00240041
0,59257964	-0,754919036	1,687536886	0,754919036	0,00249207
0,665714372	-0,587024779	1,502145727	0,587024779	0,00253016

0,761349474	-0,393369265	1,313457268	0,393369265	0,00254071
2,350320187	1,23285731	0,425473944	-1,23285731	0,00259722
1,753746212	0,810439988	0,570207931	-0,810439988	0,00269148
0,791894924	-0,336619081	1,262793799	0,336619081	0,00272055
Inf	Inf	0		0,00276277
5,047503865	2,33557011	0,198117728	-2,33557011	0,00276488
1,45336238	0,539394468	0,688059643	-0,539394468	0,00282756
3,273412506	1,710795418	0,305491593	-1,710795418	0,00282846
0,760375759	-0,395215556	1,315139243	0,395215556	0,00289156
2,59396808	1,375160727	0,385509755	-1,375160727	0,00290446
0,521228598	-0,940011853	1,918544001	0,940011853	0,00291975
0,253200551	-1,981647552	3,949438485	1,981647552	0,00296288
0,36674001	-1,447170429	2,726727311	1,447170429	0,00298117
1,647677291	0,720433708	0,606914962	-0,720433708	0,00298447
0,454689515	-1,137046359	2,19930297	1,137046359	0,00298592
1,458981242	0,544961335	0,685409772	-0,544961335	0,00299649
0,779413063	-0,359539984	1,283016731	0,359539984	0,00300414
7,280280021	2,863993942	0,137357354	-2,863993942	0,00302237
6,083817424	2,604976858	0,164370482	-2,604976858	0,00305554
0,560127797	-0,836172068	1,785306862	0,836172068	0,00313105
7,730665556	2,950592625	0,129354969	-2,950592625	0,00318484
Inf	Inf	0		0,00320818
3,536402667	1,822282554	0,282773229	-1,822282554	0,00321717
0,674883716	-0,567289151	1,481736745	0,567289151	0,00322288
0,514648696	-0,958340124	1,943073029	0,958340124	0,00324313
0,783544774	-0,351912379	1,276251254	0,351912379	0,00328705
0,711402391	-0,491262273	1,405674219	0,491262273	0,00334513
0,792019826	-0,33639155	1,262594656	0,33639155	0,00335644
1,91057572	0,934007435	0,523402443	-0,934007435	0,00341016
0,550898445	-0,860141705	1,815216597	0,860141705	0,00357134
0,781625616	-0,355450346	1,279384887	0,355450346	0,00357788
2,733293483	1,450640375	0,365858993	-1,450640375	0,00359429
2,785882078	1,478134192	0,358952738	-1,478134192	0,00363325
2,338649547	1,225675686	0,427597201	-1,225675686	0,00365012
0,70127261	-0,511952713	1,425978978	0,511952713	0,00367435
2,668763101	1,416171247	0,374705421	-1,416171247	0,0036781
1,575906243	0,656181706	0,634555516	-0,656181706	0,00369138
0,622735572	-0,683308404	1,605818015	0,683308404	0,00373521
1,792936385	0,842324301	0,557744273	-0,842324301	0,00373961
0,253149295	-1,981939628	3,950238137	1,981939628	0,00375032
0,040973273	-4,60917306	24,40615395	4,60917306	0,00379372

0,356623074	-1,487528046	2,804081043	1,487528046	0,00387298
1,568808155	0,64966894	0,637426569	-0,64966894	0,00402962
0,71563626	-0,482701607	1,397357927	0,482701607	0,00405194
4,164888025	2,058277709	0,240102494	-2,058277709	0,00419922
0,434831953	-1,201470138	2,299739	1,201470138	0,00422047
1,475697104	0,561396629	0,677645838	-0,561396629	0,00425538
0,559826041	-0,836949498	1,786269175	0,836949498	0,00428206
0,737938609	-0,438427295	1,355126277	0,438427295	0,00433929
Inf	Inf	0		0,00437601
0,703307724	-0,507772032	1,421852719	0,507772032	0,00440845
0,5724498	-0,804778911	1,746878068	0,804778911	0,00442693
0,51147101	-0,967275624	1,955145024	0,967275624	0,00443969
0,768062392	-0,380704585	1,301977561	0,380704585	0,00463401
0,78967948	-0,340660893	1,266336565	0,340660893	0,00470017
0,728463531	-0,457071347	1,372752317	0,457071347	0,00475196
3,053457686	1,610443853	0,327497579	-1,610443853	0,00477387
2,894567984	1,533348041	0,345474698	-1,533348041	0,00490742
0		Inf	Inf	0,0049394
1,53508652	0,61831997	0,65142908	-0,61831997	0,0049467
2,908948134	1,540497574	0,343766872	-1,540497574	0,00495082
0,630444705	-0,665558255	1,586181932	0,665558255	0,00501471
1,940035485	0,956083041	0,515454489	-0,956083041	0,00506529
0,708386411	-0,497391557	1,411658925	0,497391557	0,0050729
13,80189934	3,786794911	0,072453796	-3,786794911	0,00511817
2,065912754	1,046779328	0,484047547	-1,046779328	0,00517766
5,4155889	2,437118228	0,184652125	-2,437118228	0,00521409
14,52344924	3,860312221	0,068854167	-3,860312221	0,00521686
1,790854041	0,840647759	0,558392799	-0,840647759	0,00535186
1,604773437	0,682369631	0,623140923	-0,682369631	0,00545987
3,046684458	1,607240089	0,328225654	-1,607240089	0,00551071
2,05049888	1,035974956	0,487686197	-1,035974956	0,00558436
0,75891597	-0,39798794	1,317668937	0,39798794	0,00572058
0,780003549	-0,358447406	1,282045448	0,358447406	0,00586074
0,215685033	-2,213002026	4,636390318	2,213002026	0,00597439
0,781197566	-0,356240641	1,280085914	0,356240641	0,00598041
0,701595783	-0,51128802	1,425322137	0,51128802	0,00604504
3,606340529	1,85053563	0,2772894	-1,85053563	0,00605612
0,798155709	-0,325257872	1,252888364	0,325257872	0,0060872
1,794616221	0,843675356	0,557222201	-0,843675356	0,00613072
0,783296485	-0,35236961	1,276655799	0,35236961	0,00618016
0,778775531	-0,360720538	1,284067051	0,360720538	0,0061948

1,306489197	0,385695196	0,765410079	-0,385695196	0,00623656
7,469374348	2,900987405	0,133880022	-2,900987405	0,00625855
2,979242891	1,574945748	0,335655748	-1,574945748	0,00628332
1,75253921	0,809446722	0,570600643	-0,809446722	0,00633089
Inf	Inf	0		0,00636378
0,692091138	-0,530966064	1,444896409	0,530966064	0,00636685
0,512781844	-0,963582912	1,950147047	0,963582912	0,0063672
2,022979675	1,016481825	0,49432034	-1,016481825	0,00642477
0,702430228	-0,509573164	1,423628939	0,509573164	0,00644203
0,533826744	-0,905556512	1,873266958	0,905556512	0,00654425
0,653469556	-0,61380807	1,530293173	0,61380807	0,00655182
0,648949984	-0,623820804	1,540950804	0,623820804	0,00657197
0,706583646	-0,501067737	1,415260607	0,501067737	0,00661029
1,760947561	0,816351948	0,567876081	-0,816351948	0,00665041
2,143916157	1,100248487	0,466436151	-1,100248487	0,00669094
0,363588937	-1,459619791	2,750358709	1,459619791	0,00681895
2,996995878	1,5835171	0,333667459	-1,5835171	0,00682011
0,514039433	-0,96004906	1,945376047	0,96004906	0,00683606
0,630433902	-0,665582976	1,586209112	0,665582976	0,00683933
2,203160058	1,139574309	0,453893487	-1,139574309	0,00684585
7,40618546	2,888730677	0,135022274	-2,888730677	0,00691126
2,548015159	1,34937386	0,392462343	-1,34937386	0,00693727
2,782029226	1,476137576	0,359449854	-1,476137576	0,00697499
3,336702901	1,738423235	0,299697045	-1,738423235	0,00702275
1,442594043	0,528665372	0,693195709	-0,528665372	0,00707575
1,88610836	0,915412564	0,530192231	-0,915412564	0,0071228
1,297223288	0,375426828	0,770877311	-0,375426828	0,00714513
1,714145062	0,777489205	0,583381198	-0,777489205	0,00729044
1,444877637	0,53094732	0,69210013	-0,53094732	0,0074082
0,753007089	-0,409264647	1,328008745	0,409264647	0,00742369
3,014813911	1,592068955	0,331695431	-1,592068955	0,00748648
0,712582538	-0,488870965	1,403346205	0,488870965	0,00763545
1,455814553	0,541826591	0,686900676	-0,541826591	0,00763777
3,494754119	1,805190955	0,286143164	-1,805190955	0,00765914
0,465229058	-1,103986884	2,149478805	1,103986884	0,00773058
0,677964806	-0,560717711	1,475002818	0,560717711	0,00787088
2,349962929	1,232637998	0,425538628	-1,232637998	0,00787201
0,731110639	-0,45183835	1,367782039	0,45183835	0,00793584
0,779871933	-0,358690864	1,282261815	0,358690864	0,00797871
0,754841295	-0,405754744	1,324781787	0,405754744	0,00808525
6,961074169	2,799309947	0,14365599	-2,799309947	0,00812209

1,460699638	0,546659549	0,684603442	-0,546659549	0,00840918
0,694063218	-0,52686102	1,440790946	0,52686102	0,00844668
2,091907839	1,064819294	0,478032532	-1,064819294	0,00864968
0,502575582	-0,992587517	1,98975047	0,992587517	0,00866513
1,283144738	0,359683915	0,779335308	-0,359683915	0,00875799
34,21043052	5,096364354	0,029230851	-5,096364354	0,00884806
0,437229896	-1,193536044	2,287126311	1,193536044	0,00886219
0,713068475	-0,487887472	1,402389862	0,487887472	0,00887708
0,317936836	-1,653187919	3,145278832	1,653187919	0,00889417
0,761397565	-0,393278138	1,313374307	0,393278138	0,00903647
0,773916337	-0,369750481	1,292129333	0,369750481	0,00909784
0,699523783	-0,515554987	1,429543961	0,515554987	0,00911111
9,534527029	3,253161374	0,104881972	-3,253161374	0,00919544
0,497302713	-1,007803792	2,010847665	1,007803792	0,00928913
16,8954584	4,078563588	0,059187503	-4,078563588	0,00937909
13,68590899	3,774619353	0,073067854	-3,774619353	0,00938547
4,137239787	2,048668576	0,241707044	-2,048668576	0,00939307
1,38717614	0,472150989	0,720888985	-0,472150989	0,00954473
0,597974158	-0,741844957	1,67231307	0,741844957	0,00960856
2,09943348	1,070000078	0,476318973	-1,070000078	0,00965958
6,566564455	2,715138768	0,152286634	-2,715138768	0,00972073
0,694009893	-0,526971867	1,440901651	0,526971867	0,00972166
Inf	Inf	0		0,00974636
0,561828097	-0,83179932	1,779903864	0,83179932	0,00976344
2,477299986	1,308768581	0,403665283	-1,308768581	0,00977591
0,479040385	-1,061780808	2,087506671	1,061780808	0,0098102
28,38664122	4,827140251	0,035227838	-4,827140251	0,00983716
0,76142605	-0,393224167	1,313325175	0,393224167	0,00990743

Adjusted p value	WT PBS #1	WT PBS #2	TG PBS #1	TG PBS #2
1,60E-73	3,72959762	4,45296099	41,3016683	37,9513407
2,80E-48	0,10316364	0,20828233	10,4783492	11,0616883
3,62E-46	163,812147	183,755694	3,48429062	4,18647153
6,49E-36	19,7733043	18,592165	0,13617122	0
3,77E-29	0,41078679	0,49202382	4,07429802	3,80371161
1,22E-22	133,365753	144,635405	11,3739241	5,83086264
1,16E-18	16,8535636	14,9749952	0,31477769	0,63539968
4,18E-17	4,24329688	4,15943005	0,04967735	0,07520777
4,18E-17	4,24329688	4,15943005	0,04967735	0,07520777
4,18E-17	39,2862613	55,4953945	0,33456751	0,56278896
2,48E-13	23,7694881	22,8336797	0,08135067	0,82105868
4,43E-12	0,03449072	0,06963507	3,22023774	2,51146559
4,64E-12	88,701665	24,0811234	234,513574	223,433356
1,07E-11	2,94169533	4,66332343	0,01321079	0
2,90E-10	25706,765	25422,698	36763,055	37435,5959
2,90E-10	0	0,02756097	2,20148317	1,98803372
3,05E-10	34,5738665	33,4801421	4,64747129	3,01539524
1,51E-09	162,584413	199,516089	42,9276287	20,1886182
1,65E-08	135,485092	132,421881	40,6198493	44,2186954
3,16E-08	0,27778721	0,74778497	23,6564995	14,3573939
8,86E-08	38,4093395	35,7249022	7,70859151	12,9993375
1,37E-07	0,01688351	0,02726958	1,54767403	2,45876893
1,76E-07	306,653632	305,431851	112,271652	132,807638
1,06E-06	96,8074195	118,420969	36,9351734	36,1149293
2,02E-06	6,70522119	5,7175191	0,41332952	0,12835894
4,12E-06	10298,8091	9535,50799	16771,6951	13711,6063
1,09E-05	0,24139493	0,31678693	7,83704937	13,02791
1,09E-05	0,8069244	2,48814219	13,1375873	13,4480708
2,09E-05	26,6528251	31,6052979	4,19991571	3,08283962
2,24E-05	63,8344822	60,9396188	96,2766598	90,6000713
2,99E-05	13,2469952	14,1275196	5,09285339	2,57006575
2,99E-05	1022,84085	1073,47133	578,409742	551,221499
4,62E-05	1935,32248	1897,57926	2568,63026	2376,22709
4,82E-05	9,48966004	10,1177573	0,99551161	0,63938838
7,83E-05	12,6294299	14,9706161	2,4843603	1,34657911
0,000128	1696,61305	1629,26422	2209,74713	2027,2773
0,000128	1741,11437	1671,99902	2267,70771	2080,45179
0,000132	1,66476921	0,94346309	5,35458634	6,90548702
0,000145	34,007179	30,2389273	50,6739361	43,0995592

0,000304	65,1711204	71,7694309	21,2211027	19,3879511
0,000333	0,21572529	0,05807184	2,22774601	3,69604386
0,000389	20,4011706	17,7895881	32,7552528	36,8834872
0,000397	7,45140617	6,47242848	1,13989403	0,07422425
0,000427	29,6954248	28,8571864	10,3627997	8,39018678
0,000509	16,1575193	19,5659252	6,82122998	7,34738011
0,000942	12,95448	13,331049	4,12909277	3,34798676
0,000977	18,9565319	24,4942762	37,3110478	42,5291782
0,001069	6,33064841	6,72455908	0,62930555	0,09771501
0,001345	8,65390441	7,68759544	12,223412	12,7639618
0,00163	40,475814	51,2274249	18,8553292	17,1404293
0,001647	146,889561	121,083004	223,791931	184,839696
0,002659	1,80888175	0,79474519	0,0079551	0
0,003069	67,3760352	67,4960768	81,820457	88,4655854
0,003816	12,0362326	9,50713401	18,2958837	22,3605715
0,003816	7,34819205	7,36445375	1,0095811	2,19641038
0,003899	8,53847513	9,46845423	15,7654755	19,2688713
0,00397	6,29089823	10,0338014	0	0
0,004527	16,4755581	16,9927282	5,78093736	4,30261235
0,004527	24,8136301	28,2793365	10,2353539	8,14510024
0,004527	9,62537918	9,20874844	2,27729311	1,92493826
0,004527	2309,77647	2813,55444	3403,69353	3731,74562
0,004527	2326,30439	2833,68721	3428,04911	3758,44863
0,005153	22,6737084	18,8988041	34,6054997	30,7391043
0,005447	3,67154495	4,38406416	0,82359847	0,17972846
0,005675	21,6883203	18,5922483	8,60422907	6,97013618
0,005765	2,4752265	2,83721123	0,10165705	0
0,005765	17,6181514	24,4476174	41,8059946	52,8944728
0,006495	29,8940535	34,590419	13,7660589	13,104429
0,006513	27,8992042	33,1845088	12,796701	12,2507275
0,00676	30,3928196	26,0969901	10,7742739	11,5888904
0,007048	10,5293855	7,44998503	2,67710061	1,76744277
0,007141	30,5979644	23,4729521	36,9569702	37,2412791
0,00758	3760,65558	4488,10054	11361,2076	7897,5851
0,00758	16,2864624	15,6778074	6,67568631	6,4418586
0,007888	11,1408185	16,2386792	2,24869654	2,79331901
0,008125	51,0210349	39,0369415	63,6036092	63,0449031
0,008125	7,82867335	10,2737095	0,83059857	1,13770535
0,009309	26,2928267	28,7097687	13,8771064	12,9392539
0,009309	0,13748321	1,5544023	10,5023178	10,5998132
0,009451	160,902683	144,685534	179,317283	191,006516

0,009471	4,18196357	3,50391928	0,70990991	0,82098977
0,011587	33,4068389	39,0548895	9,92422088	14,3772094
0,011686	45,4696709	38,1702919	19,9032042	22,3007856
0,012618	19,2524979	27,3741117	38,2022416	35,6789517
0,012618	10,5178653	11,7057368	5,47438488	4,42211624
0,013247	2,77107419	2,70408695	0,13066782	0,06594042
0,016194	20,0269516	23,9957879	34,7744883	41,8812922
0,016685	1,49891438	0,96839504	10,9412835	6,03504809
0,019435	17,5359613	22,1133591	8,93045989	8,88273493
0,019532	115,636642	107,526685	59,8647076	52,1403842
0,02436	6,09342609	3,75904463	0,68241042	0,39874733
0,02565	42,3837068	52,6724863	16,9619592	22,0733926
0,02778	6,61656927	3,49020508	0,12984934	0,49145535
0,029435	35,629117	31,4844835	14,8501848	18,3676991
0,029942	441,253922	451,071034	506,502116	515,229633
0,030429	39,0007114	36,88157	54,5425369	58,85728
0,033204	679,019152	737,070763	789,273889	809,995072
0,033204	3,41072796	1,92810581	0	0,04869696
0,033204	4,12719702	4,68997384	7,72612756	7,96554668
0,033545	75,5722436	78,0372257	34,3537448	38,1911016
0,034933	8,42531013	4,69483927	0,78663194	0
0,042992	67,5706238	76,0526884	91,5863521	87,5782155
0,044498	6,28088088	5,60624396	1,76766719	0,65132964
0,045632	25,5754652	24,123302	32,5711031	32,6470148
0,051843	224,401655	221,90335	272,0797	236,103467
0,056168	11,6282378	14,373576	3,46448964	4,14719106
0,056588	184,321544	168,806156	213,484586	192,29562
0,057556	38,4530095	42,5720667	57,8780256	52,3461963
0,060022	2,82929665	1,17100324	5,46327272	6,05932915
0,06101	5,64018666	5,26832259	11,737424	9,98356294
0,062741	36,5946153	35,1291473	59,7770506	48,107849
0,063212	73,0481844	79,3757204	93,0997569	85,4689887
0,063212	3,3243405	3,25439145	4,41189521	3,53824425
0,063212	1,65400231	1,62454836	0	0
0,064564	4,32499253	4,88121285	1,18564814	0,75941553
0,064564	1,50434523	0,91115973	5,23509256	8,95650079
0,064564	12,26327	9,15687764	2,68480099	2,70972461
0,066883	44,9336401	45,0839146	24,6468332	24,4039621
0,071108	166,083524	164,529892	194,220696	176,045923
0,075323	16,605673	15,0113125	24,5556315	20,9196117
0,075646	61,7188124	68,158377	75,3949228	81,5337901

0,080709	36,9209971	40,1478869	9,34631646	12,2075159
0,081462	23,4248634	26,5443521	13,9976375	9,92352558
0,08158	2,88890912	3,28973482	1,37008257	1,0207804
0,081742	59,6890847	51,0896427	65,4728277	67,5395187
0,08546	15,0445762	18,6316338	6,51638023	6,51044021
0,086314	18,1049562	17,1670719	9,69646057	5,10383254
0,091302	5,65331726	9,38906628	12,9765398	11,9389087
0,092537	62,330542	58,7988409	72,9487771	73,002258
0,09426	17,815147	18,3328956	6,43209516	8,76963235
0,096668	26,5877007	27,7681369	41,4439855	32,1025419
0,097001	39,732141	45,0603811	51,1390316	55,5924416
0,098107	1,89672528	1,40822919	0,05193208	0,07862127
0,098107	5,27891392	5,76778731	0,91049919	1,886269
0,105134	11,9999793	8,23730532	1,61267126	1,02798445
0,106632	24,1298181	18,7588129	6,06184773	8,13769524
0,110281	13,1134369	9,89760981	5,03444441	2,72424727
0,110281	0,50197558	0,40538562	2,37114287	1,70138344
0,110281	0,11494997	0,09283133	3,02456932	4,92362432
0,113749	2,74648833	1,93635794	5,3283494	4,72425993
0,114072	5,66930501	8,18565876	1,6331531	2,08982672
0,121514	0,477172	1,27648753	1,90482229	2,31211588
0,121514	46,9207173	41,5904858	22,8585987	23,195339
0,123021	9,45204189	10,177711	18,5730179	15,1960039
0,127565	9,91818308	11,6967482	3,87509687	2,02296739
0,133633	0,37071365	1,69649264	5,76863422	10,0565027
0,142724	3,45205826	5,60767266	0,53885491	1,01973229
0,144332	3,46896549	2,51166128	0,43150309	0,40989066
0,146476	4,12722946	5,33291104	1,20662076	1,4535296
0,149374	3,15870241	2,19770362	8,08433723	6,45257564
0,15195	97,3677806	80,4234748	111,963946	100,320739
0,15195	5,77524535	6,01947014	2,64308332	2,48788642
0,156176	4,07656256	6,1363918	1,76535087	0,52264345
0,159203	11,6809154	14,4828558	6,55133184	5,21908524
0,169155	26,2185238	24,2791883	28,8213825	31,5163505
0,169155	51,2006346	43,7452488	24,4649513	26,8836684
0,170576	0,95147358	2,11307625	0,07571135	0,0764142
0,170576	26,8022187	26,8663135	7,88235492	8,35834019
0,170576	8,63911825	8,87236066	12,2856888	15,9185846
0,170576	256,767978	249,13795	291,557793	277,508712
0,170956	52,0421209	50,0618425	31,5128025	32,8512586
0,170956	1,98157996	3,29470448	6,5792641	9,18663704

0,170956	9,81724881	6,80443564	3,01117329	3,05222638
0,171668	18,1926338	20,4115322	9,48654637	9,97276433
0,17359	178,754553	177,220102	97,9320532	117,271509
0,17359	20,1491088	18,9594853	8,66711554	7,26361084
0,17359	3,23054772	4,84271389	6,5772415	7,79593215
0,175079	679,023828	690,83409	728,444692	733,927696
0,175079	4,15199283	5,92528422	1,25516285	1,41298576
0,175291	6,85283863	5,72304938	2,25943702	2,44990196
0,179726	31,6624074	35,3641223	38,7174929	41,7910903
0,179726	25,8849177	30,5683814	8,83235861	8,13434566
0,180815	32,6411425	28,4340789	39,9647945	34,4133935
0,182555	4,01732749	2,65028527	0,93649722	0,26659232
0,182555	6,09376179	5,0874591	1,2231643	1,12870328
0,182555	10,6576527	8,96965426	3,70849613	2,44864118
0,182555	17,2551128	18,5718031	8,0208809	8,50523122
0,183555	0,14999974	0	22,7895912	6,16790673
0,183555	20,0640167	19,3722178	5,71851121	7,5474736
0,183555	20,9709249	17,7586695	25,0378199	22,6972806
0,183555	59,4337684	49,929034	26,9484877	28,3767529
0,183555	28,7789836	25,0129457	34,4373274	30,9054632
0,183555	11,3942158	11,532168	5,90713633	4,32606622
0,189838	37,2873143	28,4847994	8,76750938	12,94961
0,189838	6,07697008	6,18154007	1,97539859	1,92727878
0,189838	22,4393416	21,0071718	10,0688888	10,009313
0,194398	8,81781383	6,19798849	16,123686	12,0301673
0,195946	3,51863799	3,75822254	6,64744847	7,53564875
0,198656	9,1193641	2,96028812	0	0,07658971
0,200335	4,26410064	3,21726372	0,7476417	1,3033693
0,200681	4,1455842	3,89778769	6,69737492	6,94826652
0,200904	38,934194	43,3194343	24,9027122	15,4548034
0,2016	128,687732	112,632008	140,284113	130,531402
0,204236	375,921363	410,287791	426,859045	445,409647
0,204236	727,379562	685,274367	760,409395	746,231169
0,211284	0,27084102	0,10936294	1,7241248	0,83139556
0,211284	97,8044241	98,6144944	115,385822	107,546346
0,21285	4,64099526	6,39898438	10,7126059	12,8484044
0,216899	5,74485086	8,90424505	2,12003933	2,38425958
0,216899	93,8347659	97,340042	106,736572	102,614203
0,220276	4,39427159	7,09745475	1,84807504	0,61043928
0,227556	4,45851579	5,02873619	7,68681949	5,72911605
0,229722	14,1191126	18,296133	20,2625368	20,4089309

0,229722	197,386488	202,288176	227,665036	211,095056
0,233687	7,52478376	5,77397066	2,24833194	2,4700182
0,240992	33,5989595	35,2328359	15,1005852	17,6191036
0,242418	248,574487	233,713335	243,091485	264,948732
0,24401	2,4714243	2,12893195	0	0
0,24401	2,30205857	2,17514379	0,46894359	0,27608986
0,247256	16,2899841	17,1967498	8,70095572	10,5000896
0,247256	2,23754391	2,75534926	1,10448368	0,19032093
0,251515	69,2205836	70,0833807	75,2530827	77,6808716
0,251515	2,57703609	2,42188519	0,53231382	1,06474255
0,251658	18,4516935	18,6995765	25,5187898	33,814024
0,25187	0,80518478	0,59451557	1,85500085	2,73935529
0,25187	5,06929357	3,60649736	10,1420639	9,61583831
0,25187	34,5461301	31,3861227	19,3538371	14,1747545
0,25187	3,72829994	3,17041973	5,67931794	6,95882388
0,25187	292,393861	249,512323	150,422738	159,472725
0,25187	294,123094	292,192642	331,046486	297,87813
0,252252	3,32206052	4,8479223	0,59361781	0,34949163
0,253872	6,78327096	12,7820848	2,23157997	0,49550517
0,258979	11,8883542	9,42449271	13,9987395	17,6821188
0,261876	1,29818829	2,36445708	0,28132872	0,11830848
0,261876	0,64252442	1,08966921	0	0
0,261876	2,35153824	1,42697434	0,50743952	0,38695793
0,261876	23,1826073	18,4277581	28,5983758	22,9995895
0,262367	15,5899602	12,4825374	22,1670659	23,3430989
0,264759	524,721908	542,921282	575,892345	562,304809
0,268006	302,208333	302,106892	327,523558	380,630043
0,268006	615,064918	645,429405	648,887297	679,495261
0,271122	14,7266771	13,3702077	7,39452819	4,94003641
0,282026	7,99686359	6,45810988	10,9818409	10,9244726
0,282026	265,873225	245,244556	281,032403	265,326755
0,282113	7,54746345	9,14277473	2,03488023	3,04262294
0,283698	13,9017617	12,8964147	3,87264955	4,15288775
0,283698	12,1985773	15,771168	4,65448634	5,32085862
0,283698	34,693051	35,9579527	44,6204054	39,6266429
0,283698	6,68738341	5,07186728	1,2092538	2,44095917
0,283698	16,6862982	15,0839394	8,82164215	8,02895307
0,284669	24,933722	29,1312629	32,7363079	39,6208285
0,284669	11,1784422	14,3702906	6,06715096	5,8411859
0,284669	5,25057459	6,84965215	17,1406181	22,6626573
0,286783	0,11054294	0	1,40739261	0,85227465

0,29158	5,30657488	5,19452798	11,4649625	13,086696
0,30214	20,9198319	21,7082553	13,4528773	9,33226679
0,302583	19,1132451	24,3046587	25,7407075	24,956323
0,312317	5,69276311	9,88218346	0,81283956	2,27884816
0,312637	1,99021144	1,85665738	3,71342284	3,67440724
0,313962	23,1842779	19,7441988	11,3213678	12,9292366
0,314672	6,15338832	8,40377491	11,5144623	10,2373746
0,317612	116,869704	124,645128	133,581118	139,606358
0,319034	2,01065028	2,30032901	0	0
0,319883	36,0833676	37,0080776	45,88899	41,0085989
0,319883	3,96703307	4,37702681	5,47961528	6,66688457
0,319883	2,73080564	3,23136108	4,42497066	5,29170473
0,332585	125,092827	144,694782	150,54337	143,004643
0,336026	219,521254	204,963076	217,459028	231,070557
0,338416	44,5311587	40,8732876	52,6272665	45,4271038
0,338669	1,79269611	2,86258897	0,85301655	0,43046765
0,345901	11,6566644	11,1507436	3,062396	3,5068975
0,345901	0	0	4,49208239	2,48626832
0,345901	14,6373219	17,2819732	8,23335282	9,11395764
0,345901	2,59348768	4,18889936	0,76789172	1,17114169
0,349043	53,2627089	72,2707177	90,8981607	75,7868605
0,350448	20,7054761	20,945673	9,94335805	8,02853161
0,350448	12,6262014	10,9504801	13,5962128	14,1781242
0,352256	1,85692614	0,77828227	0,09975405	0,06040805
0,355026	49,085	57,5420536	14,9326741	27,8819004
0,355074	3,0753053	2,32332669	0,67361155	0,16996621
0,355074	11,5119949	5,57811651	0,48855514	0,49309051
0,362923	64,690727	64,7899232	30,9212328	29,4872367
0,368891	14,1774381	15,3744706	7,58296683	7,79157092
0,370967	2,91145839	2,49727612	0,70605013	0,77457017
0,374558	16,2127847	22,7083909	9,29943896	6,61886513
0,382305	194,235415	231,833204	237,76737	231,304855
0,390258	71,4387002	62,70133	74,9555516	68,7689774
0,395371	1,68194154	1,35830293	4,21479335	7,47866622
0,395371	96,2019253	93,3611938	101,01676	101,595641
0,397527	25,389718	25,5230179	27,6681546	32,8133645
0,397527	3,42888808	1,94538223	0,55259948	0,68786624
0,39815	440,372913	410,874524	426,913657	462,798847
0,39958	18,2948153	17,8734291	8,91555363	7,93578664
0,400923	100,199585	93,360524	112,406992	94,3358676
0,400923	581,81309	637,607974	645,298641	662,031188

0,402202	98,1036351	96,9312606	63,7663402	60,9548324
0,402202	2,7536823	2,86458132	0,4753747	0,15992924
0,402202	7,39111778	11,1524585	2,53137274	2,66595344
0,402202	14,3550167	12,4781	6,64592234	6,14864979
0,402202	1,46196931	0,90517089	0	0
0,402202	57,7437835	67,4491121	73,9462749	77,068176
0,402202	7,41653681	7,83235688	10,4378252	14,3087589
0,404161	13,6246726	17,7678363	7,88085124	5,14417014
0,404161	15,5775943	16,100634	20,8548718	16,8962302
0,408148	14,7249222	15,8163576	27,951545	20,0087009
0,408148	53,366647	52,5739165	78,2071754	57,6373378
0,408148	11,2026165	8,53942471	12,0974606	13,2707941
0,40915	114,621057	121,837181	141,963179	137,611014
0,410257	12,0050172	14,5765814	7,2305367	5,41905402
0,411381	16,0466735	20,0077947	8,77608518	5,3490433
0,414005	197,698736	262,828931	670,665448	393,713301
0,414005	2,57473143	4,37038582	0,87010092	1,06198302
0,414005	10,8662623	10,4237938	18,6498649	15,9944036
0,414005	25,1101234	19,0726969	26,5834794	31,8009797
0,414005	12,9174314	8,66041517	3,65466777	4,50054973
0,416596	12,5311655	12,312573	2,3044992	0,5367444
0,416801	3,08096842	4,90465824	1,46743895	1,15826606
0,417707	4,59248686	3,26219245	0,81633335	1,52423639
0,419206	5,69512376	10,0384067	1,72338448	2,20604679
0,421007	81,629504	66,3969553	41,5348141	44,0713284
0,42241	6,44039431	8,26670602	2,50998187	3,97043331
0,42241	89,958354	91,3389541	56,5968293	60,0338935
0,429623	7,48918396	6,97108011	4,08559511	2,98321888
0,434698	72,6047951	60,4943252	36,6776154	40,1494131
0,434698	81,614477	76,6786826	91,2249132	84,4565692
0,436988	3,72487395	5,78707876	1,23452285	1,39793238
0,442861	17,7122808	17,5077332	18,8605297	22,3336183
0,442861	37,9959368	35,7113726	20,1332719	22,0975256
0,442861	3,17307955	4,94830809	1,30018153	0,65612571
0,445596	4,22398422	4,6867013	9,32156064	6,73355281
0,45093	10,5170392	8,41429373	11,9298425	11,3936329
0,45093	10,3280533	13,2799378	3,6729896	4,69564328
0,453178	31,1420851	30,9707943	35,1830171	35,7478258
0,45422	308,115091	364,925179	355,489189	365,119817
0,458869	45,7142614	40,9961871	51,2482269	44,809814
0,459546	2,13470068	1,75087892	0,02831066	0,42860213

0,474335	47,4292838	43,9811166	24,3196781	27,8529852
0,474997	19,1103076	14,1700853	19,3298766	20,6655641
0,484328	9,28924493	7,3566153	3,33183135	3,31142163
0,484328	3,2543031	4,02115379	5,07153215	6,9771561
0,488039	50,8414407	57,8539463	33,6358317	37,0369874
0,48971	1,25060025	3,74279363	0,12487991	0
0,48971	5,54139668	7,69502867	14,9132305	10,4782803
0,48971	30,631288	30,5378349	32,7598103	38,7381853
0,48971	3,18795518	1,13279318	7,21562467	4,18750015
0,496065	103,988262	102,950849	105,616703	120,991282
0,497202	122,427509	123,963647	134,929454	131,021309
0,497202	26,2531089	26,9303052	35,5601747	28,0993426
0,500324	1,11251577	0,89844588	0,1425323	0,03596386
0,503935	1,35372961	1,85851722	2,41292718	2,97056363
0,505117	0,14674082	0,39293763	0,00655527	0,01984836
0,505117	4,2664588	1,61770816	0,11040448	0,24514466
0,505117	2,77897388	1,95332409	0,67704167	0,2865564
0,511781	21,8637179	18,1498071	11,6307626	12,4327975
0,51371	9,57302515	10,4566555	13,3859969	14,5616444
0,513723	9,44457672	6,99368069	3,73924578	2,81754402
0,513723	1,67204544	0,78256662	0,08063589	0,22787647
0,513723	10,8272381	10,8848858	11,8008594	14,2682198
0,513723	3,42009294	4,14299977	0	0
0,513723	11,8080496	12,1848235	17,175116	18,4584929
0,513723	7,47805161	6,60999031	3,7577887	1,05174969
0,514013	3,86655043	3,19142992	5,06753854	7,18476946
0,514013	1,11065345	1,64439349	0	0,07928725
0,516222	494,550386	586,613672	598,698418	587,537718

Gene ID	Symbol	Name	Base Mean	Base Mean (TG HDM)	Base Mean (WT HDM)
117158	Scgb3a2	secretoglobin, famil	2270,05327	4003,3469	536,75963
399558	Flrt2	fibronectin leucine r	1414,45719	2585,3012	243,61315
100628584	Mir5109	microRNA 5109	3188,58705	1066,1175	5311,0566
20042	Rps12	ribosomal protein S	1562,63829	2639,9641	485,3125
100042173	Gm11968	Rps15a pseudogene	2123,74505	3470,7852	776,7049
66481	Rps21	ribosomal protein S	825,312698	1395,8819	254,74352
72338	Wdr89	WD repeat domain	3583,366	5480,9772	1685,7548
664903	Gm13253	ribosomal protein S	1356,36523	2174,4387	538,29174
20044	Rps14	ribosomal protein S	1726,12967	2717,0555	735,20387
267019	Rps15a	ribosomal protein S	3724,69075	5847,2806	1602,1009
665931	Rplp2-ps1	ribosomal protein, l	3495,00041	5390,3258	1599,675
104183	Chi3l4	chitinase 3-like 4	9901,13455	4994,4045	14807,865
57808	Rpl35a	ribosomal protein L	1898,04009	2899,5506	896,52956
393082	Mettl7a2	methyltransferase li	843,125071	1356,919	329,33115
20200	S100a6	S100 calcium bindin	1502,00699	2320,5952	683,41882
11846	Arg1	arginase, liver	537,713635	164,6458	910,78147
68436	Rpl34	ribosomal protein L	994,375119	1578,0813	410,66892
619547	Rpl34-ps1	ribosomal protein L	993,624262	1576,5796	410,66892
170658	BC002163	NADH dehydrogena	520,524741	860,57148	180,478
66212	Sec61b	Sec61 beta subunit	991,171753	1567,3106	415,03292
19942	Rpl27	ribosomal protein L	1478,00685	2285,2172	670,79649
23985	Slc26a4	solute carrier family	1185,29204	516,99025	1853,5938
20090	Rps29	ribosomal protein S	1866,09434	2802,3943	929,79436
19241	Tmsb4x	thymosin, beta 4, X	26004,6393	37124,741	14884,538
21664	Phlda1	pleckstrin homology	1024,88901	439,45941	1610,3186
23844	Clca3	chloride channel cal	11713,8932	6417,2665	17010,52
67248	Rpl39	ribosomal protein L	1642,6767	2491,6581	793,69529
27981	D4Wsu53e	DNA segment, Chr 4	1780,93336	2697,1303	864,73643
20657	Sod3	superoxide dismuta	2417,07405	1213,9489	3620,1992
100034726	Gm15772	ribosomal protein L	1392,64052	2108,3944	676,88659
19941	Rpl26	ribosomal protein L	1392,64052	2108,3944	676,88659
211623	Plac9	placenta specific 9	807,370449	1274,3655	340,37535
17313	Mgp	matrix Gla protein	4131,51559	5974,2258	2288,8054
67671	Rpl38	ribosomal protein L	1525,34941	2274,4739	776,22488
14694	Gnb2l1	guanine nucleotide	2059,98533	3025,0293	1094,9413
100043813	Gm9846	predicted gene 9846	7526,11501	11673,084	3379,1459
57294	Rps27	ribosomal protein S	7527,23145	11673,835	3380,6279
67186	Rplp2	ribosomal protein, l	4434,36084	6892,5805	1976,1412

17904	Myl6	myosin, light polype	1936,2386	2831,0651	1041,4121
16069	Igj	immunoglobulin join	12281,5928	17326,771	7236,4148
100040531	Dynlt1f	dynein light chain Tc	1827,41489	2669,0686	985,76115
100040563	Dynlt1c	dynein light chain Tc	1793,87186	2616,2169	971,52685
68222	Fam166a	family with sequenc	924,108667	1415,0481	433,16924
20005	Rpl9	ribosomal protein L	4574,44971	6447,3552	2701,5442
76846	Rps9	ribosomal protein S	2167,92268	3133,8335	1202,0119
22121	Rpl13a	ribosomal protein L	2774,786	3998,7446	1550,8274
100039246	Gm10393	predicted gene 1039	948,595901	1441,686	455,50578
11837	Rplp0	ribosomal protein, l	2149,51298	3093,2036	1205,8223
20102	Rps4x	ribosomal protein S	2123,46795	3059,0843	1187,8516
12655	Chi3l3	chitinase 3-like 3	63224,7182	37690,782	88758,654
75617	Rps25	ribosomal protein S	4882,03733	7258,7983	2505,2763
27425	Atp5l	ATP synthase, H+ tr	1344,73781	1980,9141	708,56152
16516	Kcnj15	potassium inwardly-	5677,8271	3362,9031	7992,7511
69816	2010001M09	RIKEN cDNA 201000	451,603284	727,91681	175,28976
78294	Rps27a	ribosomal protein S	4419,68972	6180,8282	2658,5512
17991	Ndufa2	NADH dehydrogena	330,57909	549,18176	111,97642
11852	Rhob	ras homolog gene fa	867,131459	434,84724	1299,4157
20088	Rps24	ribosomal protein S	3592,27884	5010,0246	2174,5331
19989	Rpl7	ribosomal protein L	3846,95118	5573,9104	2119,992
17938	Naca	nascent polypeptide	3170,54647	4456,9367	1884,1562
20918	Eif1	eukaryotic translati	2294,02403	3272,954	1315,0941
54127	Rps28	ribosomal protein S	713,015276	1098,2915	327,73904
19946	Rpl30	ribosomal protein L	4339,90815	7029,2405	1650,5758
666899	Gm12191	ribosomal protein L	4338,78879	7028,4838	1649,0938
13040	Ctss	cathepsin S	10982,3637	14944,143	7020,5845
19934	Rpl22	ribosomal protein L	2434,79508	3389,6559	1479,9343
66961	Neat1	nuclear paraspeckle	2659,23582	4071,6806	1246,791
19921	Rpl19	ribosomal protein L	4502,06982	6842,5591	2161,5805
20091	Rps3a	ribosomal protein S	5494,31191	7860,6763	3127,9475
67701	Wfdc2	WAP four-disulfide c	3164,54196	4363,6477	1965,4363
595136	Ndufs5	NADH dehydrogena	262,802146	433,60625	91,998044
21648	Dynlt1b	dynein light chain Tc	891,489852	1311,3696	471,61011
667250	Gm12657	predicted gene 1265	1020,59761	1504,2678	536,92747
81600	Chia	chitinase, acidic	3167,45351	1543,6391	4791,2679
16149	Cd74	CD74 antigen (invar	32362,6255	20725,965	43999,286
14109	Fau	Finkel-Biskis-Reilly n	1413,95651	1993,601	834,31207
227753	Gsn	gelsolin	5182,29417	7055,9616	3308,6268
93726	Ear11	eosinophil-associate	257,253729	92,810566	421,69689
55949	Eef1b2	eukaryotic translati	1139,296	1649,9904	628,60158

20068	Rps17	ribosomal protein S	2797,20946	3847,2993	1747,1197
17846	Commd1	COMM domain con	249,300936	410,67593	87,925945
77125	Il33	interleukin 33	4003,5885	2537,9545	5469,2225
17833	Muc5ac	mucin 5, subtypes A	1985,16911	1183,08	2787,2582
65019	Rpl23	ribosomal protein L	2934,66909	4010,9238	1858,4144
13498	Atn1	atrophin 1	742,202657	374,18933	1110,216
22320	Vamp8	vesicle-associated n	449,375947	693,30351	205,44838
228033	Atp5g3	ATP synthase, H+ tr	1847,24843	2589,9271	1104,5698
68212	Tmbim4	transmembrane BA	322,980988	514,96724	130,99474
53761	Prrc2a	proline-rich coiled-c	2367,45492	1171,4944	3563,4154
11464	Actc1	actin, alpha, cardiac	514,160553	228,2041	800,11701
66214	1190002H23F	RIKEN cDNA 119000	524,950925	793,06634	256,83551
19982	Rpl36a	ribosomal protein L	2665,83964	4194,4885	1137,1908
20308	Ccl9	chemokine (C-C mo	2932,93752	1842,1942	4023,6808
382073	Ccdc84	coiled-coil domain c	393,667858	609,40988	177,92584
16000	Igf1	insulin-like growth f	1719,14603	1054,6251	2383,667
20788	Sreb2	sterol regulatory ele	704,733798	349,21266	1060,2549
100310872	Dynlt1a	dynein light chain T	853,825995	1242,104	465,54797
66594	Uqcr11	ubiquinol-cytochr	482,280168	729,67925	234,88109
15078	H3f3a	H3 histone, family 3	4931,55687	8124,4243	1738,6894
70152	Mettl7a1	methyltransferase li	3051,80302	4681,6953	1421,9107
26961	Rpl8	ribosomal protein L	1038,29283	1487,7509	588,83477
20297	Ccl20	chemokine (C-C mo	167,474167	289,59536	45,352973
69185	Dtwd1	DTW domain contai	82,627204	154,4042	10,85021
20422	Shfm1	split hand/foot malf	512,39571	788,73824	236,05318
18029	Nfic	nuclear factor I/C	1342,84671	819,43572	1866,2577
69019	Spcs1	signal peptidase cor	880,856437	1265,2542	496,45866
12834	Col6a2	collagen, type VI, al	1114,05626	633,81658	1594,2959
100628611	Mir5107	microRNA 5107	2782,98445	1733,4854	3832,4835
12785	Cnbp	cellular nucleic acid	2179,88773	3005,8142	1353,9613
59090	Midn	midnolin	736,753662	400,7144	1072,7929
12309	S100g	S100 calcium bindin	622,23443	917,38174	327,08712
140474	Muc4	mucin 4	2126,40745	1302,5072	2950,3077
20655	Sod1	superoxide dismuta	848,111085	1227,3961	468,82605
12045	Bcl2a1b	B-cell leukemia/lym	1124,47594	1569,0692	679,88269
67427	Rps20	ribosomal protein S	5710,45758	8442,3843	2978,5309
218963	Gm1821	ubiquitin pseudoger	7914,08569	10403,928	5424,2439
100503670	Rpl5	ribosomal protein L	3900,03419	5201,0164	2599,0519
12864	Cox6c	cytochrome c oxida	638,21567	934,63395	341,79739
16592	Fabp5	fatty acid binding pr	1747,63332	2390,1428	1105,1238
110391	Qdpr	quinoid dihydropter	201,814847	343,60841	60,021283

66290	Atp6v1g1	ATPase, H+ transpor	675,465345	986,02484	364,90585
20342	Selenbp2	selenium binding pr	981,405336	1377,6162	585,19443
17992	Ndufa4	NADH dehydrogena	1201,23773	1724,8467	677,62873
19981	Rpl37a	ribosomal protein L	3125,74542	4901,1252	1350,3656
20568	Slpi	secretory leukocyte	4950,68385	6747,5795	3153,7882
14319	Fth1	ferritin heavy chain	24454,3246	36376,74	12531,909
23833	Cd52	CD52 antigen	1194,30842	1833,4448	555,17205
21743	Inmt	indolethylamine N-r	1872,36154	2526,3709	1218,3522
74614	4833422F24R	RIKEN cDNA 483342	115,048437	16,542199	213,55468
16785	Rpsa	ribosomal protein S	3427,5189	4528,9063	2326,1315
20335	Sec61g	SEC61, gamma subu	455,703548	684,11619	227,29091
66208	Nenf	neuron derived neu	491,257156	748,35732	234,15699
76933	Ifi2712a	interferon, alpha-in	859,162035	1204,9269	513,39717
76477	Pcolce2	procollagen C-endo	400,335947	613,02598	187,64592
68028	Rpl22l1	ribosomal protein L	658,226507	946,95308	369,49993
12631	Cfl1	cofilin 1, non-muscl	2932,41784	1995,3573	3869,4784
12047	Bcl2a1d	B-cell leukemia/lym	1024,89506	1413,1283	636,66186
22070	Tpt1	tumor protein, trans	7443,59155	9667,0743	5220,1088
215449	Rap1b	RAS related protein	2183,29075	2896,9538	1469,6277
11758	Prdx6	peroxiredoxin 6	2849,1884	3746,739	1951,6378
67941	Rps27l	ribosomal protein S	580,976935	838,8608	323,09307
621697	Gm6251	predicted gene 625	507,979127	736,03819	279,92006
80795	Selk	selenoprotein K	675,859906	972,14565	379,57416
215384	Fcgbp	Fc fragment of IgG b	552,633925	270,96795	834,2999
67115	Rpl14	ribosomal protein L	1058,98153	1479,5733	638,38978
20463	Cox7a2l	cytochrome c oxida	896,127303	1453,2133	339,0413
20085	Rps19	ribosomal protein S	1262,59654	1718,9896	806,20349
20356	Sema5a	sema domain, sever	880,696049	498,64292	1262,7492
14289	Fpr2	formyl peptide rece	120,995654	209,93063	32,060677
269261	Rpl12	ribosomal protein L	1595,95938	2246,9643	944,95443
12858	Cox5a	cytochrome c oxida	1133,73405	1545,5164	721,95172
20299	Ccl22	chemokine (C-C mo	318,063407	138,21409	497,91273
66448	Mrpl20	mitochondrial ribos	292,559654	447,87837	137,24094
13014	Cstb	cystatin B	1539,58282	2082,9003	996,26533
12866	Cox7a2	cytochrome c oxida	453,720651	668,63609	238,80521
21944	Tnfsf12	tumor necrosis fact	383,728474	180,04421	587,41274
20196	S100a13	S100 calcium bindin	178,370182	294,083	62,657365
20716	Serpina3n	serine (or cysteine)	1823,18195	1177,4914	2468,8725
12842	Col1a1	collagen, type I, alpl	1516,10032	961,17852	2071,0221
85029	Rpph1	ribonuclease P RNA	920,076234	483,08498	1357,0675
66576	Uqcrh	ubiquinol-cytochr	792,274618	1114,2191	470,33018

20341	Selenbp1	selenium binding pr	1884,15676	2663,344	1104,9695
22187	Ubb	ubiquitin B	6227,50326	8028,2145	4426,792
14605	Tsc22d3	TSC22 domain famil	683,081861	1043,4789	322,68478
12044	Bcl2a1a	B-cell leukemia/lym	814,119466	1121,79	506,44897
625249	Gpx4	glutathione peroxid	601,719068	858,96858	344,46956
268515	Bahcc1	BAH domain and co	265,23609	111,89908	418,5731
226139	Cox15	COX15 homolog, cyt	309,177475	138,61869	479,73626
56397	Morf4l2	mortality factor 4 lik	483,339201	707,88489	258,79351
18242	Oat	ornithine aminotrar	946,361968	1347,3523	545,37168
56455	Dynll1	dynein light chain L	1684,33194	2252,878	1115,7859
56612	Pfdn5	prefoldin 5	589,463404	837,2774	341,64941
73112	3110003A17F	RIKEN cDNA 31100C	660,23573	930,05296	390,4185
11906	Zfhx3	zinc finger homeobc	1836,99715	1229,2499	2444,7444
80876	Ifitm2	interferon induced t	1545,66257	888,13531	2203,1898
21346	Tagln2	transgelin 2	11872,3107	8297,9415	15446,68
100043160	Gm10012	cytochrome c oxida	984,741674	1410,3172	559,1661
330122	Cxcl3	chemokine (C-X-C r	212,985469	340,45911	85,511832
12512	Cd63	CD63 antigen	791,986011	1194,6056	389,36642
13024	Ctla2a	cytotoxic T lymphoc	1048,54131	1424,7062	672,37643
64138	Ctsz	cathepsin Z	1083,54461	1480,8006	686,28861
18703	Pigr	polymeric immunog	1780,28537	1184,1538	2376,4169
18477	Prdx1	peroxiredoxin 1	6867,15347	8748,9533	4985,3536
171567	Nme7	non-metastatic cells	688,489388	961,06567	415,91311
11974	Atp6v0e	ATPase, H+ transpor	378,634508	559,23081	198,0382
14870	Gstp1	glutathione S-transf	1093,70791	1469,5281	717,88774
66046	Ndufb5	NADH dehydrogena	274,933531	414,71812	135,14894
100042049	Gm15421	ribosomal protein L	493,891112	705,71016	282,07206
76293	Mfap4	microfibrillar-associ	6690,99704	4643,4528	8738,5412
19384	Ran	RAN, member RAS c	1258,1778	1782,5399	733,81568
238803	Zfp366	zinc finger protein 3	187,992486	69,658517	306,32646
12925	Crip1	cysteine-rich protei	2007,49117	2953,1592	1061,8231
20643	Snrpe	small nuclear ribonu	197,564376	314,89495	80,2338
20965	Syn2	synapsin II	70,004542	9,0102867	130,9988
58911	Sumf1	sulfatase modifying	349,834718	570,31464	129,3548
12856	Cox17	cytochrome c oxida	445,538809	718,14784	172,92978
67945	Rpl41	ribosomal protein L	8746,92015	12259,622	5234,2181
57423	Atp5j2	ATP synthase, H+ tr	274,489288	419,9838	128,99478
12867	Cox7c	cytochrome c oxida	1383,12206	1849,2223	917,0218
11927	Atox1	ATX1 (antioxidant p	346,686426	510,22087	183,15198
20198	S100a4	S100 calcium bindin	460,28228	660,22495	260,33961
71970	2410018M08	RIKEN cDNA 241001	978,947047	1365,7154	592,17872

74180	Muc5b	mucin 5, subtype B,	17355,0128	12420,918	22289,108
14962	Cfb	complement factor	1168,64034	1729,1357	608,14499
17381	Mmp12	matrix metalloprotei	5814,78832	4322,2177	7307,3589
668218	Bin2	bridging integrator	295,009197	136,7007	453,31769
26442	PsmA5	proteasome (prosor	275,195822	416,47074	133,92091
13033	Ctsd	cathepsin D	8332,34137	11046,379	5618,3034
68576	Hbxip	hepatitis B virus x in	125,47932	208,32972	42,628916
231997	Fkbp14	FK506 binding prote	99,6004674	171,94232	27,258613
18643	Pfn1	profilin 1	3506,07316	2459,9764	4552,1699
232400	BC048546	cDNA sequence BCC	286,534863	132,16639	440,90334
232975	Atp1a3	ATPase, Na ⁺ /K ⁺ tra	271,02126	141,91387	400,12865
14710	Gngt2	guanine nucleotide	220,313087	344,26007	96,3661
57436	Gabarapl1	gamma-aminobutyryl	311,830015	471,01676	152,64327
218490	Btf3	basic transcription f	1982,60616	2574,1825	1391,0298
66242	Mrps16	mitochondrial ribos	172,42392	277,91039	66,937446
338364	Trim65	tripartite motif-cont	256,978763	119,07306	394,88446
68662	Scgb3a1	secretoglobin, famil	1280,17981	1689,9707	870,38891
66169	Tomm7	translocase of outer	210,657154	328,41622	92,898091
100048885	LOC100048885	major urinary prote	119,849949	29,283432	210,41647
66142	Cox7b	cytochrome c oxida	417,281205	599,20129	235,36112
104158	Ces1d	carboxylesterase 1C	1732,71786	2483,6826	981,75312
19035	Ppib	peptidylprolyl isom	894,509254	1196,7978	592,22067
14121	Fbp1	fructose bisphosph	89,8561718	20,706923	159,00542
241494	Zfp385b	zinc finger protein 3	184,593184	70,386034	298,80033
13688	Eif4ebp2	eukaryotic translati	1467,03582	1014,855	1919,2166
16898	Rps2	ribosomal protein S	1654,47624	2147,8456	1161,1069
503845	Ear12	eosinophil-associat	1113,22247	729,1968	1497,2481
53876	Ear3	eosinophil-associat	1113,22247	729,1968	1497,2481
21825	Thbs1	thrombospondin 1	1868,1325	1310,7451	2425,5199
241452	Dhrs9	dehydrogenase/red	78,3051831	21,53947	135,0709
624713	Gm6525	ribosomal protein L	262,119948	396,2151	128,0248
242687	Wasf2	WAS protein family,	1622,08902	1096,0779	2148,1001
53419	Corin	corin	122,518016	40,709669	204,32636
76808	Rpl18a	ribosomal protein L	1996,83736	2623,9529	1369,7219
16852	Lgals1	lectin, galactose bin	496,216131	697,19784	295,23442
12266	C3	complement compo	18722,086	13558,311	23885,861
407819	BC031181	cDNA sequence BCC	382,792823	557,22914	208,3565
56040	Rplp1	ribosomal protein, l	3852,57365	5619,3861	2085,7612
66624	Spca2	signal peptidase cor	638,504584	881,55265	395,45652
20390	Sftpd	surfactant associate	4067,99874	5169,4298	2966,5677
15483	Hsd11b1	hydroxysteroid 11-b	722,223657	994,0197	450,42761

14869	Gstp2	glutathione S-transf	842,051847	1129,1915	554,91218
27207	Rps11	ribosomal protein S	1325,56949	1735,4034	915,73557
66059	Krtcap2	keratinocyte associa	237,442848	357,57711	117,30858
21817	Tgm2	transglutaminase 2,	3214,24752	2284,9548	4143,5403
381921	Taok2	TAO kinase 2	555,384872	326,259	784,51075
67963	Npc2	Niemann Pick type C	5918,8691	7428,5131	4409,2251
19823	Rnf7	ring finger protein 7	463,3061	664,00059	262,61161
73649	Cybrd1	cytochrome b reduc	1257,21696	858,68068	1655,7532
22166	Txn1	thioredoxin 1	3132,62674	3959,9318	2305,3217
230908	Tardbp	TAR DNA binding pr	829,517304	1110,2509	548,78374
109815	H47	histocompatibility 4	805,31588	1106,263	504,36872
67952	Tomm20	translocase of outer	1209,45366	1595,5397	823,36758
20055	Rps16	ribosomal protein S	4307,62652	5948,3546	2666,8984
381629	0610007C21R	RIKEN cDNA 06100C	149,635068	238,90282	60,367316
227394	Slco4c1	solute carrier organ	723,869828	448,388	999,35165
19073	Srgn	serglycin	2296,09481	1592,5908	2999,5988
21804	Tgfb1i1	transforming growth	535,987418	306,53248	765,44235
20832	Ssr4	signal sequence rec	330,76573	488,1776	173,35386
229600	BC028528	cDNA sequence BCC	317,757868	461,528	173,98773
22272	Uqcrq	ubiquinol-cytochr	319,771245	466,54278	172,99971
11468	Actg2	actin, gamma 2, sm	197,887866	83,988989	311,78674
73046	Glrx5	glutaredoxin 5 hom	114,438703	190,7546	38,122809
19167	Psma3	proteasome (prosor	662,989664	909,19233	416,787
69875	Ndufa11	NADH dehydrogena	229,156004	342,00949	116,30251
17160	Man2b2	mannosidase 2, alp	630,704589	392,67869	868,73048
18414	Osmr	oncostatin M recept	1179,68069	744,69639	1614,665
12982	Csf2ra	colony stimulating f	367,52635	208,48143	526,57127
22177	Tyrobp	TYRO protein tyrosi	1029,85385	1528,1981	531,50957
16599	Klf3	Kruppel-like factor 3	1237,66233	834,56771	1640,757
19899	Rpl18	ribosomal protein L	1294,85493	1682,7384	906,97149
268449	Rpl23a	ribosomal protein L	4927,82956	7441,4086	2414,2505
233033	Samd4b	sterile alpha motif d	647,93193	413,90108	881,96278
227613	Tubb2c	tubulin, beta 2C	2554,21704	3217,5755	1890,8586
18218	Dusp8	dual specificity phos	233,27145	116,50341	350,03949
12859	Cox5b	cytochrome c oxida	285,925933	418,75248	153,09938
68193	Rpl24	ribosomal protein L	2177,4405	2987,1753	1367,7057
66141	Ifitm3	interferon induced t	4144,6892	2960,901	5328,4774
74123	Foxp4	forkhead box P4	359,672483	195,89973	523,44523
67888	Tmem100	transmembrane pro	1740,96508	2279,2045	1202,7256
19231	Ptma	prothymosin alpha	8281,40717	11475,438	5087,3762
20537	Slc5a1	solute carrier family	275,033312	148,58406	401,48256

18131	Notch3	Notch gene homolo	374,456786	210,09985	538,81373
229722	5330417C22R	RIKEN cDNA 533041	829,760331	533,4566	1126,0641
15528	Hspe1	heat shock protein 1	1240,74455	1641,659	839,83012
14790	Grcc10	gene rich cluster, C1	320,193849	485,38039	155,00731
30939	Pttg1	pituitary tumor-tran	185,994978	291,05822	80,931735
68763	1110038B12R	RIKEN cDNA 111003	63,9390767	115,06588	12,81227
17436	Me1	malic enzyme 1, NA	1169,5031	807,72357	1531,2826
66246	Osgep	O-sialoglycoprotein	115,418841	186,77275	44,064934
66096	0910001L09R	RIKEN cDNA 091000	233,210703	347,85682	118,56459
13841	Epha7	Eph receptor A7	213,901911	88,200393	339,60343
66437	Fis1	fission 1 (mitochondr	370,560297	520,27575	220,84484
71750	R3hdm2	R3H domain contain	792,634936	510,15668	1075,1132
100038714	Gm15401	predicted gene 1540	392,041601	222,70104	561,38216
15312	Hmgn1	high mobility group	1699,32294	2595,2743	803,3716
15530	Hspg2	perlecan (heparan s	1640,43663	1138,5772	2142,296
216835	Usp43	ubiquitin specific pe	108,221806	31,975617	184,468
13007	Csrp1	cysteine and glycine	2332,08067	1653,5386	3010,6227
102436	Lars2	leucyl-tRNA synthet	330542,325	180162,82	480921,83
65098	Zfand6	zinc finger, AN1-typ	530,02961	739,86435	320,19487
18126	Nos2	nitric oxide synthase	121,169487	45,994844	196,34413
19695	Reg3g	regenerating islet-d	2325,81446	2909,0492	1742,5797
20103	Rps5	ribosomal protein S	878,340413	1232,8273	523,85352
22004	Tpm2	tropomyosin 2, beta	348,185573	202,47457	493,89657
19933	Rpl21	ribosomal protein L	1402,553	1821,0827	984,02331
66607	Ms4a4d	membrane-spanning	320,127832	468,77002	171,48564
16912	Psmb9	proteasome (prosor	322,632858	460,89968	184,36603
100861531	Rn45S	45S pre-ribosomal R	1346207,94	773780,53	1918635,3
54208	Arl6ip1	ADP-ribosylation fac	985,608096	1303,1198	668,09634
320878	Mical2	microtubule associa	1110,27777	745,84018	1474,7154
232910	Ap2s1	adaptor-related pro	220,632218	325,8719	115,39254
73694	2410091C18R	RIKEN cDNA 241009	1612,14747	1140,0478	2084,2472
66475	Rps23	ribosomal protein S	7245,57645	9522,5853	4968,5676
66230	Mrps28	mitochondrial ribos	245,459051	365,30742	125,61069
110253	Triobp	TRIO and F-actin bin	382,896194	215,82663	549,96576
319757	Smo	smoothened homol	296,143399	162,45158	429,83522
71679	Atp5h	ATP synthase, H+ tr	796,996677	1056,8096	537,18371
30049	Scd3	stearoyl-coenzyme 3	1241,68394	842,97501	1640,3929
65107	Lrp10	low-density lipoprot	977,153139	666,26098	1288,0453
71722	Cic	capicua homolog (D	847,748944	560,26957	1135,2283
76959	Chmp5	chromatin modifyin	508,701085	695,73114	321,67103
19290	Pura	purine rich element	304,498772	143,42341	465,57414

270084	Lpcat2	lysophosphatidylcho	258,533282	373,61552	143,45105
20024	Sub1	SUB1 homolog (S. ce	1404,07219	1793,1824	1014,962
233210	Prr12	proline rich 12	283,778624	157,58851	409,96874
232791	Cnot3	CCR4-NOT transcrip	478,79733	288,56443	669,03023
17776	Mast2	microtubule associa	491,746756	313,32322	670,17029
69189	1810033B17R	RIKEN cDNA 181003	106,93758	174,78237	39,092788
29817	Igfbp7	insulin-like growth f	4848,90605	3316,642	6381,1701
17749	Polr2k	polymerase (RNA) II	163,606445	250,96321	76,249676
20084	Rps18	ribosomal protein S	1573,20114	2226,5242	919,87804
66286	Sec11c	SEC11 homolog C (S	445,222299	613,50259	276,94201
20194	S100a10	S100 calcium bindin	477,018329	668,61659	285,42006
22003	Tpm1	tropomyosin 1, alph	1961,39696	1434,9925	2487,8014
94249	Slc24a3	solute carrier family	117,348346	44,868559	189,82813
98758	Hnrnpf	heterogeneous nucl	1707,69644	2372,4527	1042,9402
14463	Gata4	GATA binding prote	40,794346	6,4231311	75,165561
69241	Polr2d	polymerase (RNA) II	104,955288	171,03976	38,870819
64085	Clstn2	calsyntenin 2	159,298856	60,156102	258,44161
20602	Ncor2	nuclear receptor co	807,433763	524,6642	1090,2033
60594	Capn12	calpain 12	249,906909	371,85308	127,96074
20295	Ccl17	chemokine (C-C moi	300,726139	158,4989	442,95338
93706	Pcdhgc3	protocadherin gamr	1362,51945	985,85363	1739,1853
114585	D17H6S53E	DNA segment, Chr 1	1183,1884	822,64735	1543,7294
68052	Rps13	ribosomal protein S	1797,86365	2309,4375	1286,2898
14225	Fkbp1a	FK506 binding prote	2641,349	1918,0815	3364,6166
27392	Pign	phosphatidylinosito	378,265303	208,14884	548,38177
13682	Eif4a2	eukaryotic translati	1949,64704	2535,0988	1364,1953
13036	Ctsh	cathepsin H	2083,31944	2610,5213	1556,1176
20733	Spint2	serine protease inhi	902,387524	1194,728	610,04705
12226	Btg1	B-cell translocation	2247,19956	2839,056	1655,3432
233904	Setd1a	SET domain contain	447,481349	269,00713	625,95557
228003	Kbtbd10	kelch repeat and BT	698,759985	467,42784	930,09213
18555	Cdk16	cyclin-dependent ki	690,637505	446,35915	934,91586
66144	Atp6v1f	ATPase, H+ transpor	211,666847	315,44742	107,88627
11475	Acta2	actin, alpha 2, smoc	875,434783	598,51462	1152,3549
76743	Gje1	gap junction proteir	304,169704	165,35581	442,9836
230734	Yrdc	yrdC domain contain	104,361918	170,00099	38,722841
69576	2310010M20	RIKEN cDNA 231001	998,74135	704,62273	1292,86
97165	Hmgb2	high mobility group	954,683608	1256,4733	652,89388
18843	Bpifa1	BPI fold containing f	439,786487	603,47688	276,09609
67680	Sdhb	succinate dehydroge	312,191271	434,24041	190,14214
21803	Tgfb1	transforming growtl	285,209904	151,75286	418,66695

14297	Fxn	frataxin	1284,42172	904,75337	1664,0901
15081	H3f3b	H3 histone, family 3	4429,87522	5514,283	3345,4674
19679	Pitpnm2	phosphatidylinosito	627,035974	424,59397	829,47798
13056	Cyb561	cytochrome b-561	298,477538	426,3194	170,63567
11816	Apoe	apolipoprotein E	1563,67367	2080,1149	1047,2324
69051	Pycr2	pyrroline-5-carboxy	93,3888327	154,16297	32,614692
14268	Fn1	fibronectin 1	8613,87312	6512,2986	10715,448
22627	Ywhae	tyrosine 3-monooxy	5775,66623	4461,1343	7090,1982
17888	Myh6	myosin, heavy poly	506,754455	329,47832	684,03059
101214	Tra2a	transformer 2 alpha	720,368652	966,4072	474,3301
27367	Rpl3	ribosomal protein L	1737,73674	2182,5756	1292,8979
14470	Rabac1	Rab acceptor 1 (pre	307,064334	431,10662	183,02205
93692	Glrx	glutaredoxin	781,052159	526,01804	1036,0863
67832	Brix1	BRX1, biogenesis of	202,538	295,26963	109,80637
54405	Ndufa1	NADH dehydrogena	150,618476	232,20345	69,033498
67702	Rnf149	ring finger protein 1	678,830442	963,2384	394,42248
100042889	C920021L13R	RIKEN cDNA C92002	278,178634	403,072	153,28526
114641	Rpl31	ribosomal protein L	5313,66972	6497,3144	4130,0251
56312	Nupr1	nuclear protein 1	341,486443	490,34265	192,63024
67923	Tceb1	transcription elonga	241,379469	352,14407	130,61486
66489	Rpl35	ribosomal protein L	1084,10073	1646,8802	521,32121
70163	2210415F13R	RIKEN cDNA 221041	113,509103	40,264221	186,75399
24059	Slco2a1	solute carrier organ	4497,72376	3399,0299	5596,4176
382083	Snx22	sorting nexin 22	749,829591	1005,5686	494,09057
56094	Cts8	cathepsin 8	330,940792	195,6235	466,25808
238831	Ppwd1	peptidylprolyl isome	193,266071	92,271758	294,26038
233575	Pgap2	post-GPI attachmen	128,157592	52,74089	203,57429
67092	Gatm	glycine amidinotran	582,846121	376,39522	789,29702
12387	Ctnnb1	catenin (cadherin as	5854,52453	7154,423	4554,626
66373	Lsm5	LSM5 homolog, U6	111,721516	180,2601	43,182931
231162	Cytl1	cytokine-like 1	63,3000752	108,81979	17,780359
22218	Sumo1	SMT3 suppressor of	303,732672	434,05554	173,4098
68202	Ndufa5	NADH dehydrogena	77,6676433	131,65476	23,680525
69573	2310016C08R	RIKEN cDNA 231001	397,107672	585,00887	209,20648
66379	2310016M24	RIKEN cDNA 231001	213,665973	317,57746	109,75449
381318	Nsl1	NSL1, MIND kinetoc	790,087543	554,60698	1025,5681
18578	Pde4b	phosphodiesterase	1060,70059	737,26951	1384,1317
18102	Nme1	non-metastatic cells	245,086833	352,26276	137,9109
242050	Igsf10	immunoglobulin sup	400,496153	239,91241	561,0799
78929	Polr3h	polymerase (RNA) II	104,929949	172,41111	37,448788
103784	Wdr92	WD repeat domain	964,656995	1264,3437	664,97031

625054	Gm6548	eukaryotic translati	3849,27845	4730,375	2968,1819
20115	Rps7	ribosomal protein S	1152,72721	1515,6553	789,79915
378702	Serf2	small EDRK-rich fact	864,53805	1118,485	610,59114
23980	Pebp1	phosphatidylethano	549,490003	748,0946	350,8854
66317	Wdr61	WD repeat domain	164,369591	251,51953	77,219655
104725	1110002B05F	RIKEN cDNA 111000	545,634237	745,79734	345,47113
27428	Shroom3	shroom family mem	1190,21903	849,3553	1531,0828
100041953	Gm10094	predicted gene 1009	394,370142	532,9528	255,78748
328274	Zfp459	zinc finger protein 4	710,433869	493,14371	927,72403
16775	Lama4	laminin, alpha 4	659,467585	429,78194	889,15323
13653	Egr1	early growth respon	522,915138	355,72132	690,10896
109624	Cald1	caldesmon 1	2391,02301	1863,3834	2918,6626
66362	Exosc3	exosome componer	181,601918	287,07822	76,125612
244667	Disc1	disrupted in schizop	30,6704303	60,412841	0,92802
68107	Cntd1	cyclin N-terminal dc	194,533076	295,67224	93,393914
225908	Gm98	predicted gene 98	358,715699	212,06067	505,37073
21402	Skp1a	S-phase kinase-asso	610,849077	857,62242	364,07574
224116	Muc20	mucin 20	235,380725	115,49582	355,26563
114886	Cygb	cytoglobin	214,570776	122,62697	306,51458
14548	Mrps33	mitochondrial ribos	201,703464	294,45458	108,95234
18214	Ddr2	discoidin domain re	883,926209	621,04617	1146,8062
66824	Pycard	PYD and CARD domi	218,532124	329,63003	107,43422
241128	Fam124b	family with sequenc	103,087305	39,947142	166,22747
18769	Pkig	protein kinase inhib	257,704762	363,93023	151,4793
13627	Eef1a1	eukaryotic translati	23329,3585	27928,663	18730,054
13587	Ear2	eosinophil-associate	1362,5732	1004,9655	1720,1809
54683	Prdx5	peroxiredoxin 5	374,499093	528,17726	220,82093
66441	Magohb	mago-nashi homolo	42,7181839	76,844175	8,5921926
20147	Rs1	retinoschisis (X-link	72,6358483	24,537064	120,73463
17474	Clec4d	C-type lectin domain	124,616134	198,40321	50,829059
16400	Itga3	integrin alpha 3	1211,12986	856,72383	1565,5359
73824	Snhg6	small nucleolar RNA	56,8762271	101,13418	12,618275
66656	Eef1d	eukaryotic translati	316,426899	437,74763	195,10617
16656	Hivep3	human immunodef	542,449364	348,7127	736,18603
20358	Sema6a	sema domain, trans	755,507273	532,70958	978,30496
13207	Ddx5	DEAD (Asp-Glu-Ala-	7800,12841	9557,6529	6042,6039
26427	Creb3l1	cAMP responsive el	344,137185	148,49653	539,77783
17193	Mbd4	methyl-CpG binding	562,791115	371,96594	753,61629
55951	Brp44l	brain protein 44-like	718,484753	938,01281	498,95669
15161	Hcfc1	host cell factor C1	1375,49988	981,30579	1769,694
20447	St6galnac3	ST6 (alpha-N-acetyl-	173,318155	86,698678	259,93763

76938	Rbm17	RNA binding motif p	454,374268	622,88048	285,86806
54217	Rpl36	ribosomal protein L	422,588373	613,39372	231,78303
69126	1810022K09R	RIKEN cDNA 181002	193,998535	284,14681	103,85026
12018	Bak1	BCL2-antagonist/kill	348,57757	213,33866	483,81648
67267	2900010M23	RIKEN cDNA 290001	83,3682751	136,7999	29,936652
52686	Mettl2	methyltransferase li	865,923951	637,44435	1094,4036
69804	Tmem147	transmembrane pro	114,067683	178,54833	49,587037
59013	Hnrnp1	heterogeneous nucl	1535,19532	1995,1394	1075,2512
50790	Acsl4	acyl-CoA synthetase	4317,8677	3364,1266	5271,6088
208613	Tmem212	transmembrane pro	158,936703	236,95566	80,917749
213053	Slc39a14	solute carrier family	215,490596	117,60052	313,38067
20481	Ski	ski sarcoma viral on	1831,66168	1323,8346	2339,4888
66125	Sf3b5	splicing factor 3b, s	162,87144	243,86508	81,877799
93695	Gpnmb	glycoprotein (transr	3321,33817	4198,1864	2444,4899
93765	Ube2n	ubiquitin-conjugatir	672,622606	460,816	884,42921
15199	Hebp1	heme binding prote	142,71529	219,07512	66,355458
66121	Chchd1	coiled-coil-helix-coil	118,764546	182,68388	54,845213
319760	D130020L05R	RIKEN cDNA D13002	940,655703	619,20603	1262,1054
72042	Cotl1	coactosin-like 1 (Dic	601,725996	359,4776	843,9744
69066	1810010H24F	RIKEN cDNA 181001	78,0596845	128,45878	27,66059
217194	Klhl11	kelch-like 11 (Droso	143,711109	67,845558	219,57666
67097	Rps10	ribosomal protein S	1599,91262	2026,5278	1173,2974
69749	2410004N09F	RIKEN cDNA 241000	29,9700817	56,108077	3,8320863
93760	Arid1a	AT rich interactive d	2369,72665	1757,0032	2982,4501
225876	Kdm2a	lysine (K)-specific de	1444,71559	1051,2794	1838,1518
56620	Clec4n	C-type lectin domain	280,042887	403,12452	156,96125
227682	Trub2	TruB pseudouridine	157,720562	235,89939	79,541734
66578	2610039C10R	RIKEN cDNA 261003	176,194196	260,36643	92,021958
17329	Cxcl9	chemokine (C-X-C r	1375,52793	1750,8484	1000,2075
56619	Clec4e	C-type lectin domain	106,472819	166,81668	46,128956
14613	Gja5	gap junction proteir	372,815422	244,39222	501,23863
22785	Slc30a4	solute carrier family	658,857849	452,68693	865,02877
56224	Tspan5	tetraspanin 5	288,012134	170,32974	405,69453
27050	Rps3	ribosomal protein S	2138,19243	2878,1105	1398,2744
73095	Slc25a42	solute carrier family	411,273243	272,29063	550,25585
17841	Mup2	major urinary prote	71,0501809	17,269716	124,83065
66915	Myeov2	myeloma overexpre	161,76318	250,48077	73,045594
66148	Dnajc15	DnaJ (Hsp40) homol	149,517064	225,34654	73,687584
67865	Rgs10	regulator of G-prote	540,012415	783,40041	296,62442
17112	Tm4sf1	transmembrane 4 si	679,58732	888,02246	471,15218
66091	Ndufa3	NADH dehydrogena	245,024434	359,96005	130,08882

21925	Tnnc2	troponin C2, fast	109,495202	175,80747	43,182931
78286	Nav2	neuron navigator 2	1041,61721	718,893	1364,3414
22059	Trp53	transformation relat	340,867554	196,50472	485,23039
218977	Dlgap5	discs, large (Drosopl	692,908183	468,68449	917,13188
71147	Oxsm	3-oxoacyl-ACP synth	210,275302	72,696956	347,85365
12517	Cd72	CD72 antigen	235,094787	333,8726	136,31698
101401	Adamts9	a disintegrin-like an	242,823901	129,90214	355,74566
11668	Aldh1a1	aldehyde dehydroge	3899,31133	4775,3641	3023,2586
445007	Nup85	nucleoporin 85	122,566073	188,47285	56,659295
67281	Rpl37	ribosomal protein L	1829,50875	2640,1531	1018,8644
240752	Pik3c2b	phosphoinositide-3-	704,034708	508,75217	899,31724
26451	Rpl27a	ribosomal protein L	1568,74725	2119,4606	1018,0339
100503605	Beta-s	hemoglobin subunit	6206,01695	8327,9235	4084,1104
58223	Mmp19	matrix metalloprotei	1173,18687	852,39374	1493,98
52469	Ccdc56	coiled-coil domain c	177,491394	263,90284	91,079952
17308	Mgat1	mannoside acetylgl	435,538686	581,73319	289,34418
213006	Mfsd4	major facilitator sup	2353,20404	1797,1331	2909,275
75599	Pcdh1	protocadherin 1	1384,8331	987,17845	1782,4878
98386	Lbr	lamin B receptor	357,243115	490,8853	223,60093
100504265	Gm20139	predicted gene, 201	310,26039	190,3675	430,15328
434215	Lrrc32	leucine rich repeat c	465,524952	300,63649	630,41341
11838	Arc	activity regulated cy	25,8283763	1,5017144	50,155038
17470	Cd200	CD200 antigen	1407,23868	1047,7177	1766,7597
232210	8430410A17F	RIKEN cDNA 843041	80,3662345	129,91381	30,818655
20383	Srsf3	serine/arginine-rich	1072,55059	1372,2726	772,82861
16480	Jup	junction plakoglobir	1794,01242	1341,0926	2246,9322
192656	Ripk2	receptor (TNFRSF)-li	338,60343	213,75494	463,45192
223690	Ankrd54	ankyrin repeat dom	48,1318131	84,82737	11,436256
22186	Uba52	ubiquitin A-52 resid	1758,6279	2413,6257	1103,6301
19175	Psmb6	proteasome (prosor	346,380343	471,75794	221,00275
407831	Tmem204	transmembrane pro	463,205971	617,66731	308,74463
15016	H2-Q5	histocompatibility 2	973,23618	695,57359	1250,8988
100038993	Gm2002	predicted gene 200	171,674535	267,07548	76,27359
16158	Il11ra2	interleukin 11 recep	171,674535	267,07548	76,27359
654472	Gm12070	glyceraldehyde-3-ph	4280,92461	3279,9939	5281,8553
69038	1810006K21R	RIKEN cDNA 18100	79,4166247	130,45262	28,380628
66588	Cmpk1	cytidine monophos	803,511231	1215,038	391,98445
18103	Nme2	non-metastatic cells	899,045902	1152,184	645,90778
237029	4932411N23F	RIKEN cDNA 493241	72,1210686	32,537764	111,70437
56334	Tmed2	transmembrane em	2023,53169	2518,1385	1528,9249
100169	Phactr4	phosphatase and ac	590,658348	384,48544	796,83126

68943	Pink1	PTEN induced putat	307,154347	425,92064	188,38806
19881	Rom1	rod outer segment r	15,0842465	30,168493	0
64010	Sav1	salvador homolog 1	1062,42353	758,35769	1366,4894
171180	Syt12	synaptotagmin XII	631,805485	454,86749	808,74348
224904	2410015M20	RIKEN cDNA 241001	74,4511052	122,03565	26,866563
52837	Tmx4	thioredoxin-related	596,112621	400,58404	791,6412
56295	Higd1a	HIG1 domain family	147,726046	218,10837	77,34372
217124	Ppp1r9b	protein phosphatas	395,910429	245,56717	546,25368
20887	Sult1a1	sulfotransferase fan	242,360597	343,33417	141,38703
230815	Man1c1	mannosidase, alpha	485,323577	314,18693	656,46022
14797	Aes	amino-terminal enh	721,960789	499,62718	944,2944
100043636	AI662270	expressed sequence	252,84375	357,39424	148,29326
212503	Paox	polyamine oxidase (	60,3740392	103,28172	17,466356
21933	Tnfrsf10b	tumor necrosis facto	1321,35582	1010,3304	1632,3813
54611	Pde3a	phosphodiesterase	379,792543	247,30812	512,27696
68949	1500012F01R	RIKEN cDNA 150001	169,218765	252,2237	86,213825
210126	Lpp	LIM domain contain	4779,38135	3772,9487	5785,814
64294	Itm2c	integral membrane	681,666056	869,80549	493,52663
75422	Mettl5	methyltransferase li	188,159176	280,25633	96,062026
20388	Sftpb	surfactant associate	16096,0142	12412,122	19779,906
108143	Taf9	TAF9 RNA polymera	345,852324	475,02394	216,68071
67088	Cand2	cullin-associated an	557,618595	726,49878	388,73841
104718	Ttc7b	tetratricopeptide re	310,95871	184,16809	437,74933
171531	Mlph	melanophilin	516,47395	342,44327	690,50463
75613	Med25	mediator of RNA po	150,326619	71,934428	228,71881
57764	Ntn4	netrin 4	315,705736	192,55005	438,86142
66126	Elof1	elongation factor 1	189,12466	271,21302	107,0363
66643	Lix1	limb expression 1 ho	561,697419	392,87708	730,51776
68342	Ndufb10	NADH dehydrogena	260,011771	364,78028	155,24327
17153	Mal	myelin and lymphoc	353,587613	211,0044	496,17082
67160	Eef1g	eukaryotic translati	1405,33095	1765,8093	1044,8526
56615	Mgst1	microsomal glutathi	1900,32502	2325,8765	1474,7736
16854	Lgals3	lectin, galactose bin	2014,96739	2445,5565	1584,3783
240832	Tor1aip2	torsin A interacting	1904,46189	1418,6547	2390,2691
67268	2900073G15F	RIKEN cDNA 290007	1369,10314	1721,6544	1016,5518
13039	Ctsl	cathepsin L	1906,88121	2482,0817	1331,6807
14254	Flt1	FMS-like tyrosine ki	1302,91	985,01525	1620,8047
14422	B4galnt2	beta-1,4-N-acetyl-ga	2119,96693	1612,4729	2627,461
16504	Kcnc3	potassium voltage g	209,137108	125,6479	292,62631
16416	Itgb3	integrin beta 3	187,136533	267,45873	106,81433
68995	Mcts1	malignant T cell am	199,515589	287,98278	111,0484

11813	Apoc2	apolipoprotein C-II	33,1517164	61,035329	5,2681041
210356	Nckap5	NCK-associated prot	1542,37303	1160,3268	1924,4193
235169	Foxred1	FAD-dependent oxi	121,883913	189,25872	54,509108
20104	Rps6	ribosomal protein S	3073,04682	3736,0537	2410,0399
66204	Acyp1	acylphosphatase 1,	80,130111	136,59368	23,666539
50708	Hist1h1c	histone cluster 1, H	433,162483	575,07467	291,2503
12831	Col5a1	collagen, type V, alp	382,161329	235,33141	528,99125
19087	Prkar2a	protein kinase, cAM	474,524043	305,83414	643,21395
433102	Sfta2	surfactant associate	242,553104	337,55103	147,55518
100502825	Gm13826	predicted pseudoge	117,63028	185,60946	49,651099
18002	Nedd8	neural precursor cel	658,896156	851,02623	466,76608
238317	C130039O16F	RIKEN cDNA C13003	960,998134	697,46824	1224,528
20316	Sdf2	stromal cell derived	214,362533	306,74254	121,98252
100504715	Tmppe	transmembrane pro	598,89623	411,46763	786,32483
329065	Scd4	stearoyl-coenzyme ,	495,218139	316,99197	673,44431
12628	Cfh	complement compc	3377,35485	2668,02	4086,6897
230075	Ndufb6	NADH dehydrogena	215,330435	309,09431	121,56656
79221	Hdac9	histone deacetylase	282,273664	167,23296	397,31437
26365	Ceacam1	carcinoembryonic a	1047,77323	749,89988	1345,6466
241041	Gm4956	predicted gene 4956	151,794912	228,5542	75,035627
19179	Psmc1	protease (prosome,	355,281583	471,18995	239,37321
66384	Srp19	signal recognition p	615,338921	865,23602	365,44182
14181	Fgfbp1	fibroblast growth fa	35,3091203	64,062097	6,5561431
11433	Acp5	acid phosphatase 5,	482,674245	644,78954	320,55895
22401	Zmat3	zinc finger matrin ty	1152,35457	822,55969	1482,1494
19344	Rab5b	RAB5B, member RA	1068,24494	802,61928	1333,8706
110593	Prdm2	PR domain containi	1482,64571	1131,5004	1833,791
217431	Nol10	nucleolar protein 10	1883,21597	1433,5336	2332,8983
71712	Dram1	DNA-damage regula	2895,12228	3566,7664	2223,4781
101966	D8Ertd738e	DNA segment, Chr 8	158,385305	232,58472	84,185892
73689	Bloc1s2	biogenesis of lysoso	88,5568732	143,793	33,320744
100038607	Gm10636	predicted gene 1063	189,797969	98,659879	280,93606
434396	Gm5615	predicted gene 5615	270,774205	171,22647	370,32193
109828	C7	complement compc	1423,23329	1067,6621	1778,8045
27370	Rps26	ribosomal protein S	487,225438	635,2016	339,24928
66830	Nacc1	nucleus accumbens	747,73806	520,22907	975,24705
20715	Serpina3g	serine (or cysteine)	587,632633	395,23084	780,03443
212627	Prpsap2	phosphoribosyl pyrc	223,547898	356,12592	90,969873
13614	Edn1	endothelin 1	301,367234	414,28235	188,45212
170748	BC017612	cDNA sequence BCC	163,903913	275,83871	51,969119
68735	Mrps18c	mitochondrial ribos	87,7774548	141,05215	34,502763

118449	Synpo2	synaptopodin 2	157,310011	81,783097	232,83693
66055	0610009D07F	RIKEN cDNA 06100C	238,712371	331,9196	145,50514
239368	BC030476	cDNA sequence BCC	308,861305	190,30331	427,4193
16594	Klc2	kinesin light chain 2	69,561347	25,276251	113,84644
13733	Emr1	EGF-like module cor	376,03542	505,43949	246,63135
67676	Rpp21	ribonuclease P 21 su	118,139331	179,71546	56,563202
100504616	Gm15910	predicted gene 159:	2700,68081	2070,0054	3331,3562
14417	Gad2	glutamic acid decarbl	423,963182	284,24017	563,6862
26943	Serinc3	serine incorporator	12404,3267	14890,285	9918,3682
12827	Col4a2	collagen, type IV, al	2977,33542	2069,8266	3884,8442
13522	Adam28	a disintegrin and me	563,47478	384,68966	742,2599
74098	0610037L13R	RIKEN cDNA 061003	157,538514	236,46737	78,609656
68349	Ndufs3	NADH dehydrogena	209,482055	297,33349	121,63062
16156	Il11	interleukin 11	428,878197	295,67224	562,08416
56501	Elf4	E74-like factor 4 (et	1088,47773	798,34952	1378,6059
216350	Tspan8	tetraspanin 8	463,123317	615,15601	311,09062
54670	Atp8b1	ATPase, class I, type	228,336187	138,01954	318,65283
229603	Otud7b	OTU domain contain	1647,48569	1260,0234	2034,948
102791	Tcta	T-cell leukemia tran	147,451054	214,70034	80,201769
22323	Vasp	vasodilator-stimulat	358,520159	497,47764	219,56267
245240	9930111J21R	RIKEN cDNA 993011	1870,66477	1431,9502	2309,3793
20510	Slc1a1	solute carrier family	341,504008	219,75596	463,25206
331374	Dgkk	diacylglycerol kinase	13,1691762	26,338352	0
66965	Ctu2	cytosolic thiouridyla	218,85984	317,80118	119,9185
66510	Rnf181	ring finger protein 1	661,004085	858,83822	463,16995
14004	Chchd2	coiled-coil-helix-coil	3360,24334	5198,3137	1522,1729
16195	Il6st	interleukin 6 signal t	3070,88253	2383,8909	3757,8742
68634	Tm2d3	TM2 domain contain	150,444858	236,93033	63,95939
17714	Grpel2	GrpE-like 2, mitochc	354,163646	473,51838	234,80891
27059	Sh3d19	SH3 domain protein	853,276304	633,78541	1072,7672
75764	Slx1b	SLX1 structure-spec	583,465742	405,87705	761,05444
19224	Ptgs1	prostaglandin-endo	1117,43065	849,76958	1385,0917
68475	Ssna1	Sjogren's syndrome	129,053425	192,57339	65,533459
380928	Lmo7	LIM domain only 7	3673,73507	4480,5222	2866,9479
14433	Gapdh	glyceraldehyde-3-ph	4824,08528	3778,9986	5869,172
72199	Mms19	MMS19 (MET18 S. c	232,19515	326,38736	138,00294
546049	C330021F23R	RIKEN cDNA C33002	4697,84802	6004,3266	3391,3694
80889	Mesdc1	mesoderm developi	319,256128	212,32324	426,18901
11826	Aqp1	aquaporin 1	1513,51639	1878,1458	1148,8869
12332	Capg	capping protein (act	389,972	519,68244	260,26156
72179	Fbxl2	F-box and leucine-ri	73,3556384	120,29271	26,418568

14964	H2-D1	histocompatibility 2	12597,6791	14864,644	10330,714
22210	Ube2b	ubiquitin-conjugatir	894,585332	1124,9723	664,19839
70233	Cd2bp2	CD2 antigen (cytopl	157,199263	234,2148	80,183724
271457	Rab5a	RAB5A, member RA	639,75345	833,65533	445,85157
385493	AU015836	expressed sequence	14,7283135	0	29,456627
70335	Reep6	receptor accessory p	161,866777	85,924481	237,80907
14555	Gpd1	glycerol-3-phosphat	258,073477	147,20103	368,94592
71853	Pdia6	protein disulfide iso	1221,18997	1586,8114	855,56856
66477	Usmg5	upregulated during	203,401914	292,22336	114,58047
79196	Osbpl5	oxysterol binding pr	248,793701	344,75419	152,83321
68070	Pdzd2	PDZ domain contain	2898,83324	2243,5312	3554,1352
19300	Abcd4	ATP-binding cassett	448,462811	299,56272	597,3629
76205	Stard3nl	STARD3 N-terminal	266,784622	372,11181	161,45743
12417	Cbx3	chromobox homolo	763,175593	982,59148	543,75971
68528	1110017F19R	RIKEN cDNA 111001	97,314053	155,4293	39,198808
76916	4930455C21R	RIKEN cDNA 493045	458,446294	318,98966	597,90293
170706	Tmem37	transmembrane pro	151,270608	218,85339	83,687822
75415	Arhgap12	Rho GTPase activati	416,243722	562,6777	269,80975
67732	Iah1	isoamyl acetate-hyd	222,050143	312,10941	131,99088
76642	1700113A16F	RIKEN cDNA 170011	82,1596898	129,17463	35,144753
66229	Rpl7l1	ribosomal protein L	1478,96214	1121,1305	1836,7938
11958	Atp5k	ATP synthase, H+ tra	199,091796	295,34932	102,83427
105352	Dusp22	dual specificity phos	923,668477	692,14606	1155,1909
20017	Polr1b	polymerase (RNA) I	364,918766	242,02295	487,81458
18747	Prkaca	protein kinase, cAM	537,237473	350,16774	724,30721
19895	Rpia	ribose 5-phosphate	190,273716	270,14508	110,40235
14670	Gnl1	guanine nucleotide	137,730649	201,86575	73,59555
22688	Zfp26	zinc finger protein 2	864,555836	656,19244	1072,9192
26431	Git2	G protein-coupled r	821,011845	594,15151	1047,8722
80718	Rab27b	RAB27b, member R	644,263975	453,29191	835,23604
20393	Sgk1	serum/glucocorticoi	1239,11043	1522,9265	955,2944
12914	Crebbp	CREB binding protei	2285,22571	1752,2627	2818,1887
319722	E330033B04R	RIKEN cDNA E33003	425,816534	289,1149	562,51816
546546	Serpina3h	serine (or cysteine)	157,504971	82,146855	232,86309
56410	Cbln3	cerebellin 3 precurs	373,558284	249,94779	497,16877
56353	Rybp	RING1 and YY1 bind	656,146428	472,99509	839,29777
100038595	Gm16287	predicted gene 1628	253,544148	167,94098	339,14732
16527	Kcnk3	potassium channel,	228,737596	131,53806	325,93713
81500	Sil1	endoplasmic reticul	120,526792	181,67429	59,379293
67894	Fam45a	family with sequenc	343,215012	222,30227	464,12775
77771	Csrnp3	cysteine-serine-rich	310,797585	199,01403	422,58114

66520	2610001J05R	RIKEN cDNA 26100C	241,014451	340,14786	141,88104
231128	Fam193a	family with sequenc	646,228191	465,12859	827,32779
18032	Nfix	nuclear factor I/X	627,117386	433,92916	820,30561
100042498	2210403K04R	RIKEN cDNA 22104C	200,745235	281,05585	120,43462
14972	H2-K1	histocompatibility 2	18515,9078	22243	14788,816
66070	Cwc15	CWC15 homolog (S.	380,210801	527,27654	233,14506
71998	Slc25a35	solute carrier family	187,622361	110,12696	265,11776
94221	Gopc	golgi associated PDZ	425,471996	562,81973	288,12426
11946	Atp5a1	ATP synthase, H+ tr	2951,74929	3836,748	2066,7506
12111	Bgn	biglycan	8177,07446	6656,8421	9697,3068
110454	Ly6a	lymphocyte antigen	2436,85544	2949,3037	1924,4071
233073	U2af1l4	U2 small nuclear RN	75,6792118	120,53977	30,818655
381217	Fam189a2	family with sequenc	359,525327	477,81147	241,23918

Fold Change (WT HDM/TG HDM)	log2 Fold Change (WT HDM/TG HDM)	Fold Change (TG HDM/WT HDM)	log2 Fold Change (TG HDM/WT HDM)
0,134077721	-2,898858561	7,458360654	2,898858561
0,094230082	-3,407668493	10,61232232	3,407668493
4,98168029	2,316632436	0,200735483	-2,316632436
0,183832992	-2,44353239	5,439719987	2,44353239
0,223783628	-2,159823602	4,468602145	2,159823602
0,18249647	-2,454059533	5,479558028	2,454059533
0,307564652	-1,701038387	3,251348919	1,701038387
0,24755434	-2,014182853	4,039517142	2,014182853
0,270588467	-1,885827743	3,695649004	1,885827743
0,273990758	-1,867800865	3,649758143	1,867800865
0,296767776	-1,752593646	3,369638082	1,752593646
2,964890969	1,567979052	0,337280531	-1,567979052
0,309196036	-1,69340627	3,234194112	1,69340627
0,242705091	-2,042723722	4,12022671	2,042723722
0,294501529	-1,763652972	3,395568114	1,763652972
5,531762565	2,467739234	0,180774209	-2,467739234
0,260233053	-1,94212388	3,842709405	1,94212388
0,260480929	-1,940750347	3,839052652	1,940750347
0,209718783	-2,253472018	4,768290122	2,253472018
0,264805789	-1,916993431	3,776352482	1,916993431
0,2935373	-1,768384256	3,406722076	1,768384256
3,585355477	1,842116165	0,278912372	-1,842116165
0,3317857	-1,591676386	3,013993669	1,591676386
0,400933112	-1,318566522	2,49418162	1,318566522
3,664317082	1,873544348	0,272902147	-1,873544348
2,650742306	1,406396424	0,377252816	-1,406396424
0,31854101	-1,650448972	3,139313204	1,650448972
0,32061352	-1,641092833	3,119020063	1,641092833
2,982167832	1,576361452	0,335326533	-1,576361452
0,321043623	-1,639158754	3,114841502	1,639158754
0,321043623	-1,639158754	3,114841502	1,639158754
0,267093972	-1,904580681	3,744000639	1,904580681
0,383113314	-1,384156932	2,610193809	1,384156932
0,341276665	-1,550986323	2,930173971	1,550986323
0,36196057	-1,46609555	2,762731866	1,46609555
0,28948184	-1,78845525	3,454448132	1,78845525
0,289590174	-1,787915445	3,453155841	1,787915445
0,286705563	-1,802358196	3,487898835	1,802358196

0,367851711	-1,442803792	2,718486742	1,442803792
0,41764359	-1,2596558	2,394386085	1,2596558
0,369327766	-1,437026366	2,707622041	1,437026366
0,37134798	-1,429156363	2,692891985	1,429156363
0,306116264	-1,707848398	3,266732671	1,707848398
0,419015885	-1,254923158	2,386544368	1,254923158
0,383559602	-1,382477316	2,607156735	1,382477316
0,387828579	-1,366508977	2,57845877	1,366508977
0,315953523	-1,662215744	3,165022473	1,662215744
0,389829601	-1,359084453	2,565223366	1,359084453
0,388302996	-1,364745258	2,575308486	1,364745258
2,354916769	1,235676071	0,424643458	-1,235676071
0,345136514	-1,534760981	2,897404242	1,534760981
0,357694222	-1,483201279	2,79568396	1,483201279
2,376741403	1,248984942	0,420744133	-1,248984942
0,240810152	-2,054031879	4,152648842	2,054031879
0,430128643	-1,217159888	2,324885859	1,217159888
0,203896823	-2,2940888	4,904441306	2,2940888
2,98821184	1,579282427	0,334648296	-1,579282427
0,434036411	-1,204112019	2,30395417	1,204112019
0,380341951	-1,394631022	2,629212997	1,394631022
0,422746917	-1,242133862	2,365481473	1,242133862
0,401806482	-1,315427258	2,488760251	1,315427258
0,298408055	-1,744641616	3,351115974	1,744641616
0,234815668	-2,090399419	4,258659604	2,090399419
0,234630087	-2,091540069	4,262027993	2,091540069
0,469788367	-1,089917105	2,128618054	1,089917105
0,436603098	-1,195605729	2,290409769	1,195605729
0,306210416	-1,707404737	3,265728232	1,707404737
0,315902353	-1,662449413	3,165535145	1,662449413
0,397923465	-1,32943712	2,513046071	1,32943712
0,45041131	-1,150685039	2,220192915	1,150685039
0,212169553	-2,236710456	4,713211611	2,236710456
0,359631721	-1,475407815	2,780622343	1,475407815
0,3569361	-1,486262274	2,801621915	1,486262274
3,103878337	1,634072009	0,322177576	-1,634072009
2,122906484	1,086040821	0,471052309	-1,086040821
0,418495021	-1,256717636	2,389514689	1,256717636
0,468912246	-1,092610137	2,132595187	1,092610137
4,543630234	2,183845432	0,220088332	-2,183845432
0,380972867	-1,392239841	2,624858843	1,392239841

0,454115875	-1,138867623	2,202081131	1,138867623
0,214100557	-2,223639548	4,670702475	2,223639548
2,154972605	1,107669529	0,464043022	-1,107669529
2,355933753	1,236298972	0,424460152	-1,236298972
0,463338242	-1,109862332	2,158250514	1,109862332
2,966989931	1,569000031	0,337041926	-1,569000031
0,296332521	-1,754711131	3,374587427	1,754711131
0,426486844	-1,229426855	2,344738211	1,229426855
0,2543749	-1,974971775	3,931205484	1,974971775
3,041769082	1,604910634	0,328756054	-1,604910634
3,506146513	1,809886284	0,285213409	-1,809886284
0,323851231	-1,626596866	3,087837573	1,626596866
0,271115493	-1,883020534	3,688464969	1,883020534
2,184178409	1,127090704	0,457838058	-1,127090704
0,291964154	-1,776136841	3,425077995	1,776136841
2,260203136	1,176452441	0,442438108	-1,176452441
3,03612977	1,602233456	0,329366686	-1,602233456
0,374805949	-1,415784241	2,668047296	1,415784241
0,321896358	-1,635331842	3,106589982	1,635331842
0,21400771	-2,224265323	4,67272885	2,224265323
0,303717049	-1,7192002	3,29253825	1,7192002
0,395788553	-1,337198208	2,526601622	1,337198208
0,156608079	-2,674769455	6,385366615	2,674769455
0,070271472	-3,830917076	14,23052592	3,830917076
0,299279497	-1,740434651	3,3413582	1,740434651
2,277491261	1,187445518	0,439079621	-1,187445518
0,392378591	-1,349681769	2,54855903	1,349681769
2,515390095	1,330782156	0,397552651	-1,330782156
2,210854174	1,144603869	0,452313867	-1,144603869
0,450447447	-1,150569297	2,220014804	1,150569297
2,677200792	1,420725346	0,373524467	-1,420725346
0,356544175	-1,48784726	2,804701547	1,48784726
2,26509902	1,17957412	0,441481803	-1,17957412
0,381968003	-1,388476304	2,618020337	1,388476304
0,433303197	-1,206551213	2,307852807	1,206551213
0,352806837	-1,503049578	2,834412195	1,503049578
0,52136502	-0,939634304	1,918041989	0,939634304
0,499720003	-1,000808127	2,001120615	1,000808127
0,365701871	-1,451260087	2,734467825	1,451260087
0,46236728	-1,112888788	2,162782799	1,112888788
0,17467932	-2,517219273	5,724776115	2,517219273

0,370077748	-1,434099703	2,702134904	1,434099703
0,4247877	-1,235186103	2,354117128	1,235186103
0,392863159	-1,347901209	2,545415563	1,347901209
0,275521548	-1,85976294	3,629480184	1,85976294
0,467395481	-1,097284309	2,139515764	1,097284309
0,344503351	-1,537410081	2,902729388	1,537410081
0,302802712	-1,72354997	3,302480333	1,72354997
0,482253894	-1,052135206	2,073596526	1,052135206
12,90969109	3,690382574	0,077461187	-3,690382574
0,513618827	-0,961230008	1,946969128	0,961230008
0,332240213	-1,589701392	3,00987045	1,589701392
0,312894642	-1,676251139	3,195963959	1,676251139
0,426081587	-1,230798388	2,346968353	1,230798388
0,306097823	-1,707935309	3,266929471	1,707935309
0,390198778	-1,357718833	2,562796337	1,357718833
1,939240882	0,955492018	0,515665697	-0,955492018
0,450533671	-1,150293165	2,219589934	1,150293165
0,539988488	-0,888999443	1,851891331	0,888999443
0,507301051	-0,979085946	1,971216101	0,979085946
0,520889703	-0,940950178	1,919792223	0,940950178
0,385156946	-1,376481651	2,596344192	1,376481651
0,380306437	-1,394765736	2,629458516	1,394765736
0,39044989	-1,356790689	2,561148115	1,356790689
3,078961532	1,622443843	0,324784831	-1,622443843
0,431468845	-1,212671703	2,31766444	1,212671703
0,233304565	-2,09971356	4,286242753	2,09971356
0,468998473	-1,092344869	2,132203104	1,092344869
2,532371604	1,340489124	0,394886753	-1,340489124
0,15272034	-2,711035875	6,547916274	2,711035875
0,420547145	-1,249660552	2,377854686	1,249660552
0,467126546	-1,098114661	2,140747531	1,098114661
3,602474495	1,848988216	0,277586976	-1,848988216
0,306424573	-1,706396099	3,263445844	1,706396099
0,478306775	-1,063991869	2,090708418	1,063991869
0,35715274	-1,485386907	2,799922523	1,485386907
3,262602819	1,706023368	0,30650375	-1,706023368
0,213060139	-2,230667387	4,693510501	2,230667387
2,096722219	1,068135741	0,476934899	-1,068135741
2,154669579	1,107466648	0,464108284	-1,107466648
2,809169292	1,49014357	0,355977122	-1,49014357
0,422116443	-1,244287065	2,36901456	1,244287065

0,414880524	-1,26923216	2,410332472	1,26923216
0,551404304	-0,858817567	1,813551314	0,858817567
0,309239382	-1,693204034	3,233740776	1,693204034
0,451465063	-1,147313746	2,21501082	1,147313746
0,401026958	-1,318228875	2,493597951	1,318228875
3,740630598	1,903281501	0,267334604	-1,903281501
3,460833854	1,791119683	0,288947705	-1,791119683
0,365586999	-1,451713329	2,73532703	1,451713329
0,4047729	-1,304815393	2,470521126	1,304815393
0,495271351	-1,013708926	2,019095187	1,013708926
0,408048046	-1,293189062	2,4506918	1,293189062
0,419780938	-1,252291438	2,382194875	1,252291438
1,988809866	0,991905358	0,502813274	-0,991905358
2,480691616	1,3107424	0,403113387	-1,3107424
1,861507463	0,8964714	0,537199028	-0,8964714
0,396482498	-1,334670912	2,522179427	1,334670912
0,251166234	-1,993285572	3,981426906	1,993285572
0,325937211	-1,617334028	3,06807559	1,617334028
0,471940407	-1,083323395	2,118911592	1,083323395
0,463457808	-1,109490089	2,157693716	1,109490089
2,006848203	1,004931496	0,498293791	-1,004931496
0,569822859	-0,811414597	1,754931351	0,811414597
0,432762426	-1,20835285	2,310736653	1,20835285
0,354126061	-1,497665074	2,823853167	1,497665074
0,488515838	-1,03352276	2,047016541	1,03352276
0,325881456	-1,617580836	3,068600505	1,617580836
0,399699586	-1,323012018	2,501879002	1,323012018
1,881905888	0,912194482	0,5313762	-0,912194482
0,411668583	-1,280444742	2,429138487	1,280444742
4,397544897	2,136698307	0,227399611	-2,136698307
0,359554993	-1,475715651	2,781215724	1,475715651
0,254795446	-1,972588602	3,924716927	1,972588602
14,53880456	3,861836745	0,068781446	-3,861836745
0,226813041	-2,140424501	4,408917561	2,140424501
0,240799692	-2,05409455	4,152829238	2,05409455
0,426947751	-1,227868569	2,342206975	1,227868569
0,307142274	-1,703021001	3,255820134	1,703021001
0,495895917	-1,011890749	2,016552197	1,011890749
0,358966079	-1,478080573	2,78577854	1,478080573
0,394319554	-1,34256284	2,536014229	1,34256284
0,433603315	-1,205552309	2,306255431	1,205552309

1,794481492	0,843567043	0,557264037	-0,843567043
0,351704608	-1,507563856	2,843295129	1,507563856
1,69065034	0,757578312	0,591488362	-0,757578312
3,316132836	1,729501799	0,301556074	-1,729501799
0,321561389	-1,636833908	3,1098261	1,636833908
0,508610397	-0,975367142	1,966141484	0,975367142
0,204622345	-2,288964399	4,887051808	2,288964399
0,158533467	-2,65714066	6,307816363	2,65714066
1,85049336	0,887909959	0,540396427	-0,887909959
3,335971846	1,738107113	0,299762722	-1,738107113
2,819517627	1,495448362	0,354670597	-1,495448362
0,279922384	-1,83690124	3,572418851	1,83690124
0,324071852	-1,625614377	3,085735444	1,625614377
0,540377293	-0,887961041	1,850558882	0,887961041
0,240859813	-2,053734391	4,15179264	2,053734391
3,316320677	1,729583517	0,301538994	-1,729583517
0,515031946	-0,957266174	1,941627132	0,957266174
0,282866943	-1,821804507	3,53523105	1,821804507
7,185512559	2,845091071	0,139168917	-2,845091071
0,392791403	-1,348164741	2,545880567	1,348164741
0,39528123	-1,339048645	2,529844385	1,339048645
0,494837689	-1,014972709	2,020864665	1,014972709
7,678853017	2,940890833	0,130227782	-2,940890833
4,245165065	2,085820651	0,235562101	-2,085820651
1,891124005	0,919243967	0,528786054	-0,919243967
0,540591393	-0,887389551	1,849825972	0,887389551
2,053284043	1,037933218	0,487024678	-1,037933218
2,053284043	1,037933218	0,487024678	-1,037933218
1,850489354	0,887906835	0,540397597	-0,887906835
6,270855159	2,648662197	0,159467884	-2,648662197
0,323119441	-1,629860542	3,09483081	1,629860542
1,959805987	0,970710841	0,51025459	-0,970710841
5,019111371	2,327431959	0,199238456	-2,327431959
0,522007033	-0,93785885	1,915683001	0,93785885
0,4234586	-1,239707164	2,361505939	1,239707164
1,761713661	0,816979456	0,567629134	-0,816979456
0,373915302	-1,419216584	2,674402454	1,419216584
0,371172439	-1,429838505	2,694165553	1,429838505
0,448590931	-1,156527641	2,229202446	1,156527641
0,573867497	-0,801210431	1,742562536	0,801210431
0,453137508	-1,141979182	2,206835636	1,141979182

0,491424333	-1,0249588	2,034901271	1,0249588
0,52767879	-0,922268098	1,895092276	0,922268098
0,328065129	-1,607945839	3,048175225	1,607945839
1,813401438	0,858698334	0,551449877	-0,858698334
2,404564349	1,265775535	0,415875749	-1,265775535
0,59355419	-0,752548345	1,684766137	0,752548345
0,395499067	-1,338253804	2,528450972	1,338253804
1,928252605	0,94729406	0,518604252	-0,94729406
0,582161958	-0,780507526	1,717735049	0,780507526
0,494288058	-1,016576043	2,023111794	1,016576043
0,45592115	-1,133143757	2,193361723	1,133143757
0,516043292	-0,954435993	1,937821914	0,954435993
0,448342205	-1,157327779	2,230439134	1,157327779
0,252685659	-1,984584308	3,957486167	1,984584308
2,228765371	1,156244748	0,448678902	-1,156244748
1,883471115	0,913393908	0,530934609	-0,913393908
2,497100279	1,320253758	0,400464494	-1,320253758
0,355104083	-1,493686147	2,81607576	1,493686147
0,376981962	-1,407432599	2,65264681	1,407432599
0,370812103	-1,431239761	2,696783604	1,431239761
3,712233578	1,892287489	0,269379601	-1,892287489
0,199852635	-2,3229915	5,003686841	2,3229915
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0,340056394	-1,556154078	2,940688717	1,556154078
2,212318867	1,14555934	0,452014407	-1,14555934
2,16821918	1,116510603	0,461207985	-1,116510603
2,5257466	1,336709905	0,395922536	-1,336709905
0,347801482	-1,523664014	2,875203388	1,523664014
1,965996202	0,975260535	0,508647982	-0,975260535
0,538985442	-0,891681789	1,855337681	0,891681789
0,324434614	-1,624000345	3,082285171	1,624000345
2,130853984	1,091431736	0,469295413	-1,091431736
0,587665633	-0,766932564	1,701647917	0,766932564
3,004542775	1,587145461	0,332829344	-1,587145461
0,365608303	-1,451629261	2,735167644	1,451629261
0,457859181	-1,127024144	2,184077642	1,127024144
1,799613459	0,847687061	0,555674884	-0,847687061
2,67200584	1,417923161	0,374250679	-1,417923161
0,52769536	-0,922222796	1,895032769	0,922222796
0,443327409	-1,173555534	2,255669241	1,173555534
2,702056787	1,434057995	0,370088447	-1,434057995

2,564560314	1,358711502	0,389930389	-1,358711502
2,110882252	1,077846105	0,473735567	-1,077846105
0,511574042	-0,966985032	1,954751252	0,966985032
0,319352234	-1,646779552	3,131338672	1,646779552
0,278060295	-1,846530344	3,596342302	1,846530344
0,111347256	-3,166862088	8,980912822	3,166862088
1,895800345	0,922807036	0,527481706	-0,922807036
0,235928071	-2,083581012	4,238579986	2,083581012
0,340843087	-1,552820374	2,933901374	1,552820374
3,85036187	1,944994042	0,259715848	-1,944994042
0,424476526	-1,236243321	2,355842876	1,236243321
2,107417626	1,075476241	0,474514395	-1,075476241
2,520788248	1,333874934	0,39670131	-1,333874934
0,309551714	-1,691747649	3,230477998	1,691747649
1,881555315	0,911925704	0,531475207	-0,911925704
5,76902076	2,528326455	0,173339643	-2,528326455
1,820715087	0,864505181	0,549234752	-0,864505181
2,669373376	1,416501115	0,374619755	-1,416501115
0,432775101	-1,208310596	2,310668977	1,208310596
4,268829088	2,093840402	0,234256275	-2,093840402
0,599020367	-0,739323039	1,66939232	0,739323039
0,424920434	-1,234735371	2,353381762	1,234735371
2,439301698	1,286468205	0,40995339	-1,286468205
0,540350702	-0,888032036	1,85064995	0,888032036
0,365820416	-1,450792502	2,733581715	1,450792502
0,400013369	-1,321879877	2,499916445	1,321879877
2,479560117	1,310084204	0,40329734	-1,310084204
0,51268987	-0,963841703	1,950496896	0,963841703
1,977253841	0,983498097	0,505751957	-0,983498097
0,354103991	-1,497754993	2,824029174	1,497754993
1,828210377	0,870432095	0,546983002	-0,870432095
0,521766663	-0,938523324	1,916565527	0,938523324
0,343849267	-1,540151825	2,908251074	1,540151825
2,54818312	1,349468957	0,392436475	-1,349468957
2,645928262	1,403773947	0,377939196	-1,403773947
0,508306975	-0,976228067	1,967315124	0,976228067
1,945956715	0,96047962	0,513886045	-0,96047962
1,933244363	0,951024006	0,517265183	-0,951024006
2,02621804	1,01878943	0,493530301	-1,01878943
0,462349632	-1,112943855	2,162865354	1,112943855
3,246151657	1,698730403	0,30805708	-1,698730403

0,383953671	-1,380995854	2,604480894	1,380995854
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2,601514131	1,379351544	0,384391531	-1,379351544
2,31847787	1,213177956	0,431317466	-1,213177956
2,138910418	1,096876061	0,467527762	-1,096876061
0,223665505	-2,160585321	4,470962116	2,160585321
1,923985194	0,944097697	0,51975452	-0,944097697
0,303828099	-1,718672796	3,29133482	1,718672796
0,413145307	-1,275278817	2,420455913	1,275278817
0,451411308	-1,147485536	2,215274589	1,147485536
0,426881512	-1,228092415	2,342570416	1,228092415
1,733668606	0,793828151	0,576811506	-0,793828151
4,230760696	2,080917085	0,236364113	-2,080917085
0,439604206	-1,185722906	2,274773505	1,185722906
11,70232387	3,548723147	0,085453113	-3,548723147
0,227261897	-2,137572273	4,400209681	2,137572273
4,296182764	2,103055368	0,232764772	-2,103055368
2,07790686	1,055130988	0,481253525	-1,055130988
0,344116387	-1,5390315	2,905993548	1,5390315
2,794677869	1,482681999	0,357822993	-1,482681999
1,764141453	0,818966244	0,566847969	-0,818966244
1,876538509	0,908073896	0,532896072	-0,908073896
0,556971063	-0,84432572	1,795425412	0,84432572
1,754157282	0,810778109	0,570074309	-0,810778109
2,634565578	1,397565091	0,379569219	-1,397565091
0,538123107	-0,893991837	1,858310834	0,893991837
0,596094602	-0,746386785	1,677586068	0,746386785
0,510615847	-0,969689781	1,958419436	0,969689781
0,583061123	-0,778280964	1,715086053	0,778280964
2,326910725	1,218415861	0,429754347	-1,218415861
1,989809006	0,992629959	0,502560797	-0,992629959
2,094537233	1,06663153	0,47743243	-1,06663153
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1,925358054	0,945126765	0,519383913	-0,945126765
2,678972029	1,421679518	0,373277507	-1,421679518
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0,519624137	-0,944459647	1,924467953	0,944459647
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2,758873579	1,464079349	0,362466772	-1,464079349

1,839274803	0,879137046	0,543692546	-0,879137046
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0,400253121	-1,321015444	2,498418997	1,321015444
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1,589326322	0,668415371	0,629197407	-0,668415371
2,076101989	1,053877318	0,481671905	-1,053877318
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1,969678194	0,977959941	0,507697147	-0,977959941
0,371885101	-1,427071144	2,689002589	1,427071144
0,297297465	-1,750020931	3,363634462	1,750020931
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0,380292507	-1,394818581	2,629554833	1,394818581
0,635651105	-0,653692977	1,573190061	0,653692977
0,392848224	-1,347956055	2,545512332	1,347956055
0,37091314	-1,430846716	2,696048998	1,430846716
0,316550769	-1,659491193	3,159050924	1,659491193
4,638211841	2,213568714	0,215600329	-2,213568714
1,646474933	0,719380547	0,607358169	-0,719380547
0,491354405	-1,025164105	2,035190872	1,025164105
2,38344619	1,253049055	0,419560552	-1,253049055
3,189062295	1,67313228	0,313571799	-1,67313228
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2,096989986	1,068319972	0,476873999	-1,068319972
0,636616816	-0,651502829	1,570803621	0,651502829
0,239559008	-2,061547029	4,174336864	2,061547029
0,16339269	-2,61358465	6,120224822	2,61358465
0,399510634	-1,32369419	2,503062283	1,32369419
0,179868353	-2,47498672	5,559621704	2,47498672
0,357612485	-1,483530991	2,796322955	1,483530991
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1,84917996	0,886885633	0,54078025	-0,886885633
1,877375445	0,908717195	0,532658506	-0,908717195
0,391500082	-1,352915485	2,554277881	1,352915485
2,338686479	1,225698469	0,427590448	-1,225698469
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0,627472866	-0,672375022	1,593694412	0,672375022
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0,463223866	-1,110218509	2,158783415	1,110218509
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2,499569076	1,321679397	0,40006896	-1,321679397
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0,670639112	-0,57639147	1,491114941	0,57639147
1,7116816	0,775414362	0,584220804	-0,775414362
0,418081102	-1,258145264	2,391880418	1,258145264
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1,827351847	0,869754444	0,547239986	-0,869754444
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2,111153458	1,078031451	0,473674709	-1,078031451
1,83646961	0,876935022	0,544523032	-0,876935022
0,632226755	-0,661486006	1,58171098	0,661486006
3,634952405	1,861936474	0,275106766	-1,861936474
2,026035776	1,01865965	0,4935747	-1,01865965
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2,998172933	1,584083599	0,333536465	-1,584083599

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0,365481015	-1,452131627	2,736120232	1,452131627
2,267833061	1,181314445	0,440949564	-1,181314445
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1,716861328	0,779773517	0,582458224	-0,779773517
0,277723335	-1,848279696	3,600705722	1,848279696
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1,767206236	0,821470415	0,565864911	-0,821470415
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1,919267583	0,940555865	0,52103209	-0,940555865
0,302889063	-1,723138612	3,301538825	1,723138612
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2,347780229	1,231297367	0,425934245	-1,231297367
0,215326585	-2,215401643	4,644108387	2,215401643
3,236419087	1,694398436	0,30898347	-1,694398436
0,57896932	-0,788441194	1,727207238	0,788441194
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1,697464204	0,763381152	0,589114043	-0,763381152
1,748490263	0,806109762	0,571921973	-0,806109762
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0,353432492	-1,50049342	2,829394648	1,50049342
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2,050959844	1,036299245	0,487576587	-1,036299245
1,910876386	0,934234454	0,523320089	-0,934234454
2,381818449	1,25206345	0,419847281	-1,25206345
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7,22829747	2,853655879	0,138345164	-2,853655879
0,29162157	-1,777830661	3,429101626	1,777830661
0,326996736	-1,612651861	3,058134504	1,612651861
0,378637053	-1,401112495	2,641051611	1,401112495
0,530563366	-0,914403031	1,884789009	0,914403031
0,361397947	-1,468339782	2,767032871	1,468339782

0,245626255	-2,025463315	4,071226015	2,025463315
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1,956821494	0,968512156	0,511032817	-0,968512156
4,784982332	2,258513598	0,208987188	-2,258513598
0,408290401	-1,292332443	2,449237103	1,292332443
2,738566494	1,45342091	0,365154544	-1,45342091
0,633094894	-0,659506334	1,579542039	0,659506334
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0,490411612	-1,027934956	2,03910343	1,027934956
1,752687676	0,809568935	0,570552309	-0,809568935
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0,497382973	-1,007570975	2,010523187	1,007570975
1,618842246	0,694962403	0,617725416	-0,694962403
1,805638858	0,852509371	0,553820602	-0,852509371
0,455505454	-1,134459767	2,195363395	1,134459767
2,259594117	1,176063649	0,442557357	-1,176063649
2,096929128	1,068278102	0,476887839	-1,068278102
33,39851867	5,061712211	0,029941448	-5,061712211
1,68629369	0,753855822	0,593016511	-0,753855822
0,237223853	-2,075679016	4,215427701	2,075679016
0,563174274	-0,828346662	1,775649291	0,828346662
1,675448907	0,744547692	0,596854966	-0,744547692
2,168146046	1,116461939	0,461223543	-1,116461939
0,134817992	-2,890915052	7,417407612	2,890915052
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0,468466417	-1,093982465	2,134624731	1,093982465
0,49985586	-1,000415959	2,000576725	1,000415959
1,798370128	0,846689977	0,556059058	-0,846689977
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0,285588144	-1,807992007	3,501545919	1,807992007
1,610324756	0,687351667	0,620992751	-0,687351667
0,217555063	-2,200547501	4,596537469	2,200547501
0,322610859	-1,632133095	3,099709674	1,632133095
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0,442307891	-1,176877115	2,260868551	1,176877115
0		Inf	Inf
1,801906109	0,849523839	0,554967873	-0,849523839
1,777975986	0,830235838	0,562437293	-0,830235838
0,2201534	-2,183418971	4,542287337	2,183418971
1,976217504	0,98274174	0,506017176	-0,98274174
0,354611421	-1,495689093	2,819988135	1,495689093
2,224457251	1,153453373	0,449547861	-1,153453373
0,411805874	-1,279963686	2,428328644	1,279963686
2,089393799	1,06308443	0,478607719	-1,06308443
1,889998066	0,918384758	0,529101071	-0,918384758
0,414929075	-1,269063343	2,410050443	1,269063343
0,169113723	-2,563934363	5,913180692	2,563934363
1,615690632	0,692150981	0,61893037	-0,692150981
2,071411794	1,050614388	0,482762531	-1,050614388
0,341814919	-1,548712728	2,925559841	1,548712728
1,533499226	0,616827438	0,652103362	-0,616827438
0,567398842	-0,81756489	1,762428695	0,81756489
0,342764881	-1,544708793	2,917451743	1,544708793
1,593595825	0,672285773	0,627511684	-0,672285773
0,456146929	-1,132429491	2,192276077	1,132429491
0,535084747	-0,902160691	1,86886284	0,902160691
2,37690112	1,249081888	0,42071586	-1,249081888
2,016405891	1,011786075	0,495931898	-1,011786075
3,179545792	1,668820687	0,314510331	-1,668820687
2,279206984	1,188531947	0,438749094	-1,188531947
0,394657679	-1,341326274	2,533841486	1,341326274
1,859405365	0,894841323	0,537806343	-0,894841323
0,425580204	-1,232497049	2,349733352	1,232497049
2,351471422	1,233563799	0,42526564	-1,233563799
0,591713167	-0,757030095	1,690008023	0,757030095
0,634072171	-0,657281036	1,577107537	0,657281036
0,647860001	-0,626246007	1,543543357	0,626246007
1,68488441	0,75264962	0,593512525	-0,75264962
0,590450563	-0,760111824	1,693621893	0,760111824
0,53651768	-0,898302382	1,863871477	0,898302382
1,645461566	0,718492329	0,607732214	-0,718492329
1,629460567	0,704394439	0,613700031	-0,704394439
2,328939076	1,2196729	0,42938006	-1,2196729
0,399367526	-1,324211068	2,503959222	1,324211068
0,385607764	-1,374793994	2,593308778	1,374793994

0,086312373	-3,534288798	11,58582439	3,534288798
1,65851499	0,729892051	0,602949027	-0,729892051
0,288013725	-1,795790532	3,472056758	1,795790532
0,645076367	-0,632458132	1,550204056	0,632458132
0,173262324	-2,528970124	5,771595224	2,528970124
0,506456491	-0,981489762	1,974503276	0,981489762
2,247856562	1,168549979	0,444868243	-1,168549979
2,103146307	1,072549216	0,475478095	-1,072549216
0,437134435	-1,193851063	2,287625771	1,193851063
0,267503059	-1,902372706	3,738275009	1,902372706
0,548474379	-0,866503866	1,823239222	0,866503866
1,755675684	0,812026369	0,569581278	-0,812026369
0,397670708	-1,330353796	2,514643346	1,330353796
1,911024766	0,934346475	0,523279456	-0,934346475
2,124483805	1,087112346	0,470702576	-1,087112346
1,531731241	0,615163183	0,652856045	-0,615163183
0,393299252	-1,346300654	2,542593193	1,346300654
2,375813862	1,24842181	0,420908395	-1,24842181
1,794435014	0,843529676	0,557278471	-0,843529676
0,328305617	-1,606888662	3,045942405	1,606888662
0,508018498	-0,977047065	1,968432259	0,977047065
0,422360851	-1,243451977	2,367643679	1,243451977
0,102340438	-3,288551785	9,771308602	3,288551785
0,49715283	-1,008238675	2,011453901	1,008238675
1,801874641	0,849498644	0,554977565	-0,849498644
1,66189705	0,732831014	0,60172199	-0,732831014
1,62067191	0,69659206	0,617028032	-0,69659206
1,627376094	0,702547703	0,614486107	-0,702547703
0,623387652	-0,681798517	1,604138287	0,681798517
0,361957971	-1,466105908	2,762751703	1,466105908
0,23172716	-2,109500947	4,315419911	2,109500947
2,847520793	1,509706377	0,351182686	-1,509706377
2,162760958	1,112874219	0,462371949	-1,112874219
1,666074493	0,736452908	0,600213258	-0,736452908
0,534081279	-0,904868781	1,872374187	0,904868781
1,874649266	0,906620703	0,533433116	-0,906620703
1,973617306	0,980842271	0,506683842	-0,980842271
0,255442997	-1,968926712	3,91476773	1,968926712
0,454888122	-1,136416332	2,198342739	1,136416332
0,188404014	-2,408098393	5,307742544	2,408098393
0,244609981	-2,031444822	4,08814062	2,031444822

2,847005487	1,509445273	0,35124625	-1,509445273
0,438374663	-1,189763678	2,281153734	1,189763678
2,245989763	1,167351352	0,445238004	-1,167351352
4,504087335	2,171234802	0,222020562	-2,171234802
0,487954253	-1,035182197	2,049372443	1,035182197
0,314737546	-1,667778804	3,177250423	1,667778804
1,609346661	0,686475123	0,621370165	-0,686475123
1,983133509	0,987781806	0,504252485	-0,987781806
0,666096595	-0,586196689	1,50128376	0,586196689
1,876893538	0,90834682	0,53279527	-0,90834682
1,929503093	0,948229357	0,518268151	-0,948229357
0,332433413	-1,588862701	3,008121211	1,588862701
0,409071386	-1,289575469	2,444561107	1,289575469
1,901037987	0,926787361	0,526028415	-0,926787361
1,726820023	0,788117726	0,579099146	-0,788117726
0,505710118	-0,983617452	1,977417427	0,983617452
2,30875153	1,207112917	0,433134526	-1,207112917
1,615008077	0,69154138	0,61919195	-0,69154138
0,373552129	-1,420618509	2,677002541	1,420618509
0,441351841	-1,17999888	2,265766012	1,17999888
1,612751142	0,689523838	0,620058467	-0,689523838
2,108029546	1,075895088	0,474376653	-1,075895088
0		Inf	Inf
0,377338131	-1,4060702	2,650142984	1,4060702
0,539298252	-0,890844737	1,854261527	0,890844737
0,292820522	-1,771911429	3,41506119	1,771911429
1,576361659	0,656598565	0,634372191	-0,656598565
0,269950205	-1,889234784	3,704386893	1,889234784
0,495881307	-1,011933253	2,016611608	1,011933253
1,692634716	0,759270661	0,590794925	-0,759270661
1,875086184	0,906956907	0,53330882	-0,906956907
1,629961518	0,704837904	0,613511417	-0,704837904
0,34030381	-1,555104792	2,938550705	1,555104792
0,639869136	-0,644151215	1,562819558	0,644151215
1,553102464	0,635153013	0,643872522	-0,635153013
0,422819478	-1,241886258	2,36507553	1,241886258
0,564820939	-0,824134521	1,770472605	0,824134521
2,007265	1,005231095	0,498190324	-1,005231095
0,611713377	-0,70907227	1,634752546	0,70907227
0,500808844	-0,997668056	1,99676985	0,997668056
0,219619031	-2,186925019	4,553339461	2,186925019

0,694985672	-0,52494486	1,438878584	0,52494486
0,590413114	-0,760203329	1,693729317	0,760203329
0,342351226	-1,546450914	2,92097683	1,546450914
0,534815238	-0,902887523	1,869804613	0,902887523
Inf	Inf	0	0
2,767652104	1,468662606	0,361317088	-1,468662606
2,506408469	1,32562155	0,398977267	-1,32562155
0,539174702	-0,891175287	1,854686423	0,891175287
0,39209893	-1,35071039	2,550376764	1,35071039
0,443310666	-1,173610022	2,255754435	1,173610022
1,584170158	0,663727305	0,631245321	-0,663727305
1,994116302	0,995749554	0,501475265	-0,995749554
0,433894946	-1,204582313	2,304705341	1,204582313
0,553393475	-0,853622462	1,80703251	0,853622462
0,252197032	-1,987376797	3,965153721	1,987376797
1,874364633	0,906401637	0,533514121	-0,906401637
0,382392162	-1,386875143	2,615116364	1,386875143
0,47951029	-1,060366319	2,085460981	1,060366319
0,422899393	-1,241613607	2,364628604	1,241613607
0,272071647	-1,877941478	3,675502437	1,877941478
1,638340828	0,712235516	0,610373606	-0,712235516
0,348178443	-1,522101213	2,872090507	1,522101213
1,668998718	0,738982846	0,599161635	-0,738982846
2,015571623	1,01118905	0,49613717	-1,01118905
2,068457866	1,048555571	0,483451955	-1,048555571
0,408677984	-1,290963571	2,446914294	1,290963571
0,364576713	-1,455705681	2,742906949	1,455705681
1,635067954	0,709350596	0,611595376	-0,709350596
1,763644744	0,818559984	0,567007615	-0,818559984
1,842600781	0,881743529	0,542711156	-0,881743529
0,627275459	-0,672828974	1,594195956	0,672828974
1,608314064	0,685549157	0,621769107	-0,685549157
1,945656067	0,960256708	0,513965452	-0,960256708
2,834716986	1,503204706	0,352768903	-1,503204706
1,989090474	0,992108899	0,50274234	-0,992108899
1,774432325	0,827357553	0,563560518	-0,827357553
2,01944353	1,013957804	0,495185919	-1,013957804
2,477892128	1,309113383	0,403568819	-1,309113383
0,326844777	-1,613322454	3,059556314	1,613322454
2,08782282	1,061999285	0,478967847	-1,061999285
2,123373656	1,086358268	0,47094867	-1,086358268

0,417115771	-1,261480233	2,397415942	1,261480233
1,778707672	0,830829425	0,562205929	-0,830829425
1,890413648	0,91870195	0,528984755	-0,91870195
0,42850777	-1,222606732	2,333679973	1,222606732
0,66487507	-0,58884481	1,504041954	0,58884481
0,442168461	-1,177331971	2,261581475	1,177331971
2,407382862	1,267465602	0,415388851	-1,267465602
0,51192993	-0,96598174	1,953392333	0,96598174
0,538672491	-0,892519703	1,856415571	0,892519703
1,456742808	0,542746188	0,686462974	-0,542746188
0,652495405	-0,615960353	1,532577843	0,615960353
0,255672098	-1,967633372	3,911259811	1,967633372
0,504883607	-0,985977258	1,980654522	0,985977258

p value	Adjusted p value	WT HDM #1	WT HDM #2	TG HDM #1	TG HDM #2
9,17E-29	1,70E-24	58,7399828	68,5267406	595,812913	506,889435
4,32E-28	4,01E-24	4,13744577	2,81172439	46,5894171	37,8974963
2,95E-21	1,82E-17	5923,31717	6293,48938	1523,84032	1318,20355
1,70E-19	7,90E-16	88,3950463	98,8509466	607,802234	574,154295
2,56E-17	9,51E-14	82,2951741	105,435335	519,112916	457,770929
1,36E-15	4,21E-12	60,5480402	69,571726	378,584282	449,309789
6,35E-14	1,68E-10	46,7884603	65,582235	198,037527	228,348242
8,94E-14	2,02E-10	65,4305773	88,1844673	354,716703	368,777174
9,80E-14	2,02E-10	118,658843	127,709258	477,076782	578,34056
5,12E-13	9,50E-10	27,3638038	34,7978199	118,716343	145,400909
5,67E-13	9,56E-10	157,383657	227,614877	695,568429	819,613833
4,99E-12	7,72E-09	1049,29374	922,875586	345,724155	421,294855
6,37E-12	9,10E-09	113,327322	153,589571	461,856501	544,745793
1,30E-11	1,73E-08	16,7119145	20,2115261	84,5895347	92,2958707
1,81E-11	2,24E-08	86,7835005	102,897624	364,37762	384,117728
2,57E-11	2,98E-08	66,1646857	57,865145	11,8886151	13,9622101
2,83E-11	3,06E-08	46,3426657	56,7840944	233,536721	227,396574
2,97E-11	3,06E-08	89,0946165	109,168453	448,978587	436,331298
8,26E-11	7,75E-08	12,0296157	24,105555	94,5785243	108,236225
8,36E-11	7,75E-08	76,4673246	74,3462562	342,282705	316,211871
9,85E-11	8,71E-08	87,6353044	95,1523543	399,514157	322,566158
2,08E-10	1,70E-07	60,9853577	59,5961194	18,5676028	20,3210101
2,10E-10	1,70E-07	191,521238	281,655309	826,196258	840,237437
2,29E-10	1,77E-07	2101,86991	2338,69114	6412,61891	6437,69556
2,55E-10	1,89E-07	83,6794502	81,6919291	26,3437223	25,8411638
2,94E-10	2,10E-07	617,90809	547,440733	235,482559	271,564932
4,52E-10	3,11E-07	173,274181	227,671344	798,198902	668,501703
5,32E-10	3,53E-07	67,5722563	55,5445853	240,620781	201,453015
5,51E-10	3,53E-07	193,886734	162,569502	63,5404329	74,1209808
6,92E-10	4,14E-07	127,58279	133,044121	455,53355	484,765239
6,92E-10	4,14E-07	122,178731	127,408735	436,23839	464,231905
7,45E-10	4,32E-07	24,0083662	26,2969691	112,13152	106,306881
1,07E-09	6,02E-07	366,889968	397,405341	1152,06635	1160,95389
1,16E-09	6,31E-07	157,214013	197,536019	552,962666	656,791785
1,94E-09	1,03E-06	96,7366537	79,1893204	257,091017	302,326588
4,40E-09	2,27E-06	805,367161	1140,43065	3460,99985	4385,22497
4,55E-09	2,28E-06	452,527151	641,255623	1944,69861	2464,2942
4,85E-09	2,37E-06	371,41272	519,082842	1594,2897	2030,1162

5,45E-09	2,59E-06	193,086222	149,161301	494,754205	574,515423
5,84E-09	2,71E-06	367,217774	325,009417	988,827869	922,872286
1,05E-08	4,76E-06	51,5572793	48,7815592	151,196778	162,686886
1,26E-08	5,55E-06	72,1639687	68,5235144	208,788099	228,959597
1,31E-08	5,64E-06	42,3762083	35,1093341	152,047046	139,406962
1,41E-08	5,94E-06	365,144659	380,920018	986,72193	1075,60609
1,46E-08	6,01E-06	167,466704	174,863652	503,80484	530,002181
1,61E-08	6,51E-06	148,552311	154,125186	475,098723	428,791358
1,78E-08	7,04E-06	15,6305954	14,9017831	57,0067433	54,6667579
2,05E-08	7,93E-06	73,948401	102,293307	241,959367	285,480847
2,15E-08	8,14E-06	133,241694	138,288522	390,077133	419,770298
2,19E-08	8,14E-06	5952,40734	5624,46839	2488,67756	3190,5492
2,44E-08	8,88E-06	333,236551	397,560413	1085,14534	1375,80455
2,55E-08	9,09E-06	110,005625	164,033234	449,426962	446,092275
3,09E-08	1,08E-05	137,492174	123,39767	63,3031108	63,3454424
4,56E-08	1,56E-05	20,1549637	18,7006198	98,4571538	87,877808
4,62E-08	1,56E-05	243,090047	247,363625	638,6737	681,204635
4,77E-08	1,58E-05	20,4683803	21,8857348	124,14456	116,621032
4,87E-08	1,58E-05	65,0195446	52,5789436	26,7295251	18,5592196
5,30E-08	1,70E-05	230,712842	265,597957	604,447627	723,355125
5,57E-08	1,75E-05	208,600895	244,950726	615,052469	770,344032
7,26E-08	2,25E-05	28,9997491	24,9032313	70,02325	76,9191848
8,83E-08	2,69E-05	116,614249	101,821349	316,389721	310,403009
9,31E-08	2,79E-05	102,985351	98,1563316	429,589835	349,384225
2,11E-07	6,14E-05	208,628351	248,781444	945,285583	1318,61611
2,12E-07	6,14E-05	314,251909	374,142804	1423,49378	1986,2
2,87E-07	8,19E-05	494,28231	457,167482	1155,34773	1183,19485
3,01E-07	8,47E-05	28,3942937	37,7774932	83,1806592	93,4661179
3,15E-07	8,61E-05	36,1902012	42,1598812	168,630744	128,61665
3,16E-07	8,61E-05	267,873112	270,218922	841,982735	1129,12094
3,36E-07	9,03E-05	319,070656	344,464887	849,11187	1083,93089
3,43E-07	9,08E-05	280,077777	276,529692	656,000516	773,288898
3,82E-07	9,99E-05	11,5377024	24,040155	87,9699126	109,578807
5,08E-07	0,000131	64,1133828	58,9207147	190,645832	204,312068
5,17E-07	0,000131	59,5788357	50,9129791	194,087963	162,638611
5,87E-07	0,000147	286,180468	341,115747	131,004816	103,913684
6,12E-07	0,000151	3365,57824	2891,64446	1566,08265	1830,66431
7,01E-07	0,000171	76,1804778	88,2725866	202,982787	253,395495
8,42E-07	0,000202	116,629117	103,501722	266,994809	274,486792
8,48E-07	0,000202	74,8714848	48,9730385	19,8498521	11,3495786
8,92E-07	0,00021	31,0932836	33,9400609	104,920872	93,0454073

9,05E-07	0,00021	360,848337	377,101549	899,830968	982,480823
9,19E-07	0,00021	7,40368228	13,8082816	53,6659062	62,7603023
9,80E-07	0,000222	234,495879	189,012282	117,850248	108,27373
1,18E-06	0,000265	31,5255764	34,0316099	16,3103971	15,9499056
1,28E-06	0,000283	155,872377	192,950365	421,13001	454,731234
1,30E-06	0,000283	24,1717457	26,3365644	9,50672728	10,2333818
1,38E-06	0,000297	28,9525137	23,7112439	96,2867408	108,268627
1,45E-06	0,00031	159,196186	166,488763	459,029234	425,584126
1,57E-06	0,00033	21,3502827	11,6493135	65,4134262	82,3827706
1,63E-06	0,000336	60,5748069	43,1864745	15,3240893	23,7958691
1,64E-06	0,000336	65,4208219	50,7199376	15,03294	23,0366507
1,65E-06	0,000336	29,014079	27,3934753	91,8318774	109,3856
1,68E-06	0,000339	196,281771	266,210397	1144,41876	845,044597
1,76E-06	0,00035	129,618216	138,060475	74,7795866	67,2560635
1,77E-06	0,00035	14,8972612	15,8503094	51,1014359	70,9332329
1,99E-06	0,000382	32,5343249	28,3970262	17,4055127	13,678437
1,99E-06	0,000382	21,7856579	24,5717414	7,83836945	9,88183224
2,01E-06	0,000382	9,87193934	9,04146918	28,5496978	29,7024631
2,02E-06	0,000382	49,4582237	58,0734308	170,761959	217,334018
2,55E-06	0,000477	160,410823	163,321643	1033,17004	718,10345
2,69E-06	0,000499	72,9018275	78,180442	331,606622	245,051647
2,92E-06	0,000536	62,2738537	74,0344954	207,169324	193,105224
3,18E-06	0,000579	5,12013158	4,84020053	41,6893669	31,7970324
3,24E-06	0,000584	1,70813086	0	10,7213532	15,9384254
3,39E-06	0,000605	37,1902182	58,0861817	158,786377	213,72343
3,45E-06	0,000609	33,5120024	26,286625	17,350277	12,8412204
3,64E-06	0,000637	50,3498567	48,6538325	125,325148	166,328864
3,78E-06	0,000656	47,7628567	38,4179301	18,9297741	20,4874757
3,85E-06	0,000662	4937,35612	3848,48838	2099,15656	2469,00625
4,98E-06	0,000848	50,6634351	57,7817159	151,093239	128,426808
5,15E-06	0,000869	31,2550909	26,9585472	13,2595892	11,8036026
5,36E-06	0,000896	59,6445132	76,0855494	224,980895	218,258702
5,75E-06	0,000945	25,0478636	27,2796424	12,4112355	14,3762
5,76E-06	0,000945	75,7592938	69,5780415	232,229602	207,059751
5,87E-06	0,000956	84,7946563	93,1408356	213,058143	263,204255
5,94E-06	0,000958	511,264797	669,760338	1672,69831	2227,16263
6,10E-06	0,000976	343,352428	425,644372	812,65694	903,3678
6,29E-06	0,000998	128,30149	129,651147	282,83033	314,567147
7,10E-06	0,001117	64,761591	71,1094475	213,646213	217,274107
7,55E-06	0,001178	72,290796	75,7925855	177,240312	193,770885
7,70E-06	0,001191	4,60778714	4,05135378	34,3883735	22,7832885

8,59E-06	0,001312	33,4133525	33,4997165	107,47754	101,741236
8,63E-06	0,001312	39,4111238	30,2648477	82,9802188	105,494166
8,89E-06	0,001341	121,788202	152,668515	352,26039	460,711384
9,10E-06	0,001362	180,55652	274,855646	802,12203	1130,73072
9,60E-06	0,001425	341,484217	378,225016	786,76914	999,46255
1,00E-05	0,001475	699,645003	660,870531	1911,88503	2650,26267
1,11E-05	0,001622	99,4227242	120,698931	350,4915	494,748364
1,15E-05	0,001663	120,194974	118,601171	257,2988	315,391809
1,25E-05	0,001792	8,77263172	12,8966715	0,35908966	1,60147428
1,31E-05	0,001868	139,78605	112,182951	250,701506	313,641123
1,39E-05	0,001971	14,135319	15,2917409	52,848934	49,8426479
1,55E-05	0,002178	39,0471445	32,6152451	108,879478	154,852179
1,78E-05	0,00248	97,5082256	123,401203	279,889839	323,622326
1,79E-05	0,00248	13,42481	7,06200611	41,5932055	34,6001981
1,87E-05	0,002569	79,2566987	76,1694147	220,874019	239,514972
2,01E-05	0,002741	364,485636	294,224664	218,307105	172,557051
2,05E-05	0,002776	69,5122564	89,7512283	185,080496	226,606599
2,21E-05	0,002967	555,38885	612,032517	1193,41642	1314,25327
2,26E-05	0,003016	73,7591891	78,0904542	153,92878	192,894009
2,48E-05	0,003282	88,4976595	79,5679055	164,084129	208,176104
2,63E-05	0,003459	56,9549728	81,3463526	204,734507	214,533127
2,71E-05	0,00354	43,8653774	50,5611689	124,577424	163,738121
2,80E-05	0,003639	37,5876712	37,169778	115,740807	105,732437
2,83E-05	0,003648	10,8770671	10,2435219	2,50217118	5,42050913
3,09E-05	0,003927	66,0481405	70,5696721	157,378054	209,576747
3,09E-05	0,003927	29,3890083	29,7370778	175,136373	118,214076
3,17E-05	0,003996	116,561003	139,169477	300,660808	333,113441
3,29E-05	0,004127	11,6642913	11,7473018	4,38621595	6,31127152
3,35E-05	0,004174	2,97372929	2,0335962	18,9685789	18,5977792
3,44E-05	0,004252	139,942395	156,090575	461,555729	355,282133
3,52E-05	0,004319	90,169562	117,522045	239,539789	278,392699
3,80E-05	0,004641	27,1583563	27,9104943	7,17505165	10,5223316
3,94E-05	0,004747	21,8018116	19,6745518	67,5974141	88,5836034
3,94E-05	0,004747	174,833265	157,76344	395,234244	407,170846
4,04E-05	0,004826	26,6520065	36,327318	104,797984	100,861728
4,08E-05	0,004826	31,6341801	37,5616778	10,4693503	14,1769235
4,08E-05	0,004826	7,57186935	9,87340415	52,5556599	42,8373839
4,28E-05	0,005025	134,934571	104,013116	61,7319048	69,2351513
4,56E-05	0,005318	49,0054962	39,830436	22,1642706	25,2816816
4,86E-05	0,005631	371,842953	460,495569	165,3293	179,381545
4,94E-05	0,005691	80,1646458	91,8853468	245,38254	227,892333

5,00E-05	0,00571	72,7551423	59,3806643	155,169569	211,362608
5,02E-05	0,00571	345,697944	412,459693	728,605563	869,462154
5,35E-05	0,006051	16,3384364	9,98769436	56,461365	40,8137781
5,49E-05	0,006173	58,6761833	68,3481027	142,284768	184,520955
5,56E-05	0,006205	22,4626745	34,4059224	84,3615534	81,5071737
5,59E-05	0,006205	3,43022994	4,34348785	1,11312105	1,30597215
5,89E-05	0,006505	10,6907631	9,41656886	2,89120316	3,80842467
5,98E-05	0,006569	11,6181	9,41264529	34,3401209	31,8581452
6,35E-05	0,006936	26,6553384	24,1977053	83,0306947	61,9794081
6,66E-05	0,007192	57,7080473	53,1877334	127,547369	130,972228
6,67E-05	0,007192	46,1510756	54,421194	136,487439	149,899253
6,73E-05	0,007219	41,6888525	54,2679673	129,853472	136,428474
7,08E-05	0,007551	15,5902357	14,285875	9,11140598	8,23078613
7,30E-05	0,007736	317,138167	383,711664	155,990955	172,500321
7,42E-05	0,007819	1284,71745	971,84541	617,885479	774,495136
7,72E-05	0,008097	140,354541	159,913759	502,711048	376,590409
7,92E-05	0,008257	8,87715437	8,08391056	42,9886689	34,9599886
7,99E-05	0,008283	35,7094263	39,6369864	109,130581	159,033269
8,86E-05	0,009105	47,2536855	44,565994	106,670882	118,089663
8,88E-05	0,009105	55,2013938	44,1238864	124,038283	122,49343
9,45E-05	0,009631	64,4876424	59,5229375	35,6299231	35,7186877
0,0001051	0,010656	339,845182	364,084042	676,975751	754,873797
0,00010732	0,010804	10,76921	15,9159828	36,2203399	35,8406458
0,00010773	0,010804	28,5887887	21,6396242	79,1941575	83,7340352
0,0001103	0,010964	75,973987	115,380813	216,661381	241,392113
0,0001105	0,010964	11,6652856	15,2637491	41,3060947	54,9604386
0,00011644	0,011492	35,4581816	34,3968272	94,0841516	107,961115
0,00012056	0,011836	605,208803	555,053676	309,176912	402,516219
0,00012411	0,01212	34,5306118	29,9904651	103,76059	76,9353939
0,0001278	0,012415	13,6742873	8,83928618	2,22836098	3,62818896
0,00013245	0,012799	203,844438	268,902641	634,419854	897,581552
0,00013612	0,013085	8,57926081	23,3402993	86,3698222	62,0766587
0,00013808	0,013205	2,49218896	2,12761739	0	0,36592298
0,00014255	0,013564	4,69211265	5,24734166	30,8523046	20,0053959
0,00014452	0,013681	32,8318421	45,9837946	229,964809	152,073941
0,00014819	0,013957	993,836792	1325,52686	2717,61376	3614,0614
0,00015302	0,014339	26,7395173	27,4288825	110,805133	93,3980698
0,00015951	0,014872	196,396701	212,151382	493,933829	461,229349
0,00016153	0,014985	36,6624159	46,6334253	129,892077	140,254534
0,00016285	0,015032	51,4890202	53,0050767	149,202834	157,635564
0,00016411	0,015074	24,3492099	23,3521268	53,2917314	73,8444014

0,00016623	0,015168	156,33615	142,935325	87,3104088	105,191876
0,00016677	0,015168	22,8444803	19,7024077	81,569789	57,8778523
0,00017306	0,015663	207,587481	198,925963	162,110018	115,816886
0,00017671	0,015916	24,587067	21,5091793	6,39172338	9,63394464
0,00018079	0,016205	9,87729123	12,0655108	40,11123	39,252569
0,00018707	0,016687	274,577961	300,395374	568,841028	742,107939
0,00019201	0,017046	4,88420964	4,79693135	24,4599841	30,2526896
0,00019444	0,017179	0,52057937	1,49520084	8,50080944	6,58195432
0,00019805	0,017415	523,880278	524,836118	317,483553	338,252231
0,00020133	0,01762	11,0159824	7,95406594	2,50422619	4,01913913
0,00020489	0,017848	9,71113416	10,8319165	5,81858079	2,6374481
0,00020706	0,017952	10,4273624	13,7861976	56,7579297	44,0560453
0,00021281	0,018365	8,95353446	8,33494253	35,7528139	25,8635538
0,00021534	0,018497	119,192122	107,889866	226,233488	258,707698
0,0002194	0,01876	11,3485075	12,3062854	64,8397926	49,0411415
0,0002217	0,018869	13,5384771	12,4678974	4,31790603	4,73581324
0,0002252	0,019079	127,087945	156,007302	303,065817	336,272154
0,00023062	0,01945	4,05435409	12,3068852	38,4756964	30,20755
0,00023284	0,019548	4,57850093	3,45124397	0	1,28275336
0,00024255	0,020271	20,8088903	26,0469805	68,2381566	70,5843258
0,00026672	0,022191	50,2210628	49,8879776	170,057266	122,951844
0,00027336	0,022643	65,4751467	58,5348879	127,306263	161,790608
0,00027647	0,022798	10,795387	10,7554906	1,18725385	2,05914149
0,00027935	0,022934	9,51927383	6,96376433	1,48606066	2,96933648
0,00028247	0,023088	126,492197	90,7535005	70,7885154	60,9971008
0,00028781	0,023421	122,990688	110,615071	226,744094	271,840775
0,00029355	0,023681	325,935883	311,956248	175,222032	183,818193
0,00029355	0,023681	325,935883	311,956248	175,222032	183,818193
0,00029597	0,023773	44,5519035	39,5032597	27,9039033	24,490338
0,00030214	0,024163	4,98381285	4,64450726	1,49601572	0,2779982
0,00030986	0,024675	18,8142626	26,9174568	88,7448767	76,528004
0,00032312	0,025445	54,0957688	51,368913	29,1226284	33,0557403
0,00032332	0,025445	4,41210234	3,75907352	0,9768837	0,89900629
0,00032365	0,025445	90,907862	120,228134	255,707443	215,680089
0,00033275	0,025905	32,4603793	41,0626651	99,8695681	102,240787
0,00033314	0,025905	472,62259	460,71167	271,209026	341,323892
0,00033369	0,025905	18,9305927	20,8570555	67,4203703	56,0143801
0,00033765	0,026104	406,649311	482,699758	1132,73683	1651,58195
0,00034591	0,026631	13,8211633	14,3112333	36,6160476	36,0108892
0,00035295	0,026906	228,433157	220,409228	446,535307	457,575181
0,00035326	0,026906	31,6071482	26,5655159	77,4915032	70,3809769

0,00035384	0,026906	56,9844265	89,2448948	161,351114	186,870611
0,00035684	0,026968	163,5537	142,440529	308,895251	359,616992
0,00035755	0,026968	16,8939438	28,0920034	75,5466194	85,1584985
0,00036004	0,027046	129,949205	105,345244	70,8514562	78,4567471
0,00037713	0,028215	11,978879	10,1869027	4,80642824	5,81392414
0,00037948	0,028276	131,930749	138,6504	251,980218	276,138286
0,00038913	0,028867	24,9667166	21,7023005	76,3186076	59,7256536
0,00039193	0,028867	35,5907824	28,501808	19,9600899	18,278168
0,00039207	0,028867	216,698649	222,643541	384,43743	489,295345
0,0004015	0,029445	2,53064501	2,26067007	5,04859012	6,13345523
0,00041134	0,030036	48,2302722	37,2238113	120,159361	95,2691189
0,0004128	0,030036	17,9251923	15,3101792	36,0628001	38,1490917
0,00042187	0,030335	345,856114	514,557942	976,764171	1266,15161
0,0004222	0,030335	5,34714278	7,15008435	27,5908654	30,0608333
0,00042279	0,030335	38,5211335	44,8221204	20,4640609	22,9709656
0,00042346	0,030335	305,314951	334,158942	181,398086	212,338758
0,00043241	0,030857	27,352357	23,5471662	9,28459194	14,2051016
0,00043522	0,030939	9,81942028	21,6212978	45,0326263	59,4003162
0,00045433	0,032174	40,235156	37,9032696	109,599467	129,838841
0,00047115	0,033238	36,0423141	33,5761696	106,27183	110,554145
0,00048547	0,034119	22,3296218	25,0526681	6,14248127	8,66825865
0,00049536	0,034683	4,73604075	3,54239339	25,4895743	22,0808289
0,00051248	0,035746	28,3683004	30,3590954	77,5337802	70,9588444
0,00053373	0,037089	4,13802884	4,59843625	12,6697521	17,1345511
0,00054054	0,037394	28,4848578	22,5311428	12,988087	13,5309187
0,0005426	0,037394	30,7071267	35,956889	15,3985966	20,3181322
0,00054415	0,037394	30,2726239	26,9805408	14,1501525	12,0002305
0,0005502	0,037669	81,5471327	105,434931	250,362261	375,725862
0,00058525	0,039894	78,9126928	63,9848359	38,92833	44,7100153
0,00058699	0,039894	135,81678	132,109734	269,210948	305,508147
0,00059873	0,040416	378,369624	481,913968	1214,71425	1872,11198
0,00059903	0,040416	22,4856774	18,0064269	11,5170383	10,3441161
0,00060226	0,040487	122,500654	114,775443	207,640904	258,701822
0,00062791	0,042058	7,7498737	6,85585909	3,09723217	2,50982935
0,00063325	0,042264	18,7069448	34,408264	87,3345187	83,3432736
0,00065648	0,043451	184,062143	217,91868	427,737664	592,434632
0,00065657	0,043451	765,806095	876,625221	500,770484	558,873335
0,0006597	0,043451	12,2486593	11,6028749	4,62406403	5,68896018
0,0006604	0,043451	75,1148413	62,2173719	166,138207	133,529122
0,00067342	0,044151	393,52446	458,550597	1281,75398	951,088976
0,00068225	0,044572	11,1988759	9,35760058	5,08970565	3,6725732

0,00069124	0,044928	5,92638613	7,58415332	3,73606053	2,3990863
0,00069254	0,044928	36,4725688	31,6396195	16,7358887	20,4583605
0,00071752	0,046306	106,217893	112,633086	275,967419	219,799565
0,00071878	0,046306	29,6159162	25,3992016	77,1130801	121,389115
0,00072353	0,046451	3,91376571	3,62192656	11,8854184	19,4035525
0,00074602	0,04773	2,20953742	1,46655946	23,8769194	13,9270797
0,00077047	0,049125	47,5863194	38,6821039	26,7540371	25,615082
0,00077775	0,049311	3,19564939	2,34145405	10,4832743	16,4503014
0,00077871	0,049311	11,1954441	15,6698542	45,8508775	46,1359724
0,00078607	0,049392	3,46680026	4,99755109	1,32241631	1,24507741
0,0007867	0,049392	15,7375583	24,0013913	49,3960091	60,0882258
0,00078797	0,049392	22,8153324	24,0388263	11,9662936	13,7918096
0,0007957	0,049709	33,9076822	39,3989077	16,1928536	17,5847951
0,00080218	0,049945	53,3741926	79,458414	299,681869	201,943683
0,00081792	0,050755	15,3722138	14,9385991	8,55865401	10,0657428
0,00085317	0,052766	3,82507998	4,42997649	0,43288734	1,22856263
0,00086386	0,053249	171,908914	169,161721	98,313272	118,328441
0,00091043	0,055934	10597,059	14060,5664	5637,9021	5128,23248
0,00092318	0,056531	19,9792793	18,7912279	59,4141786	44,0840086
0,00093677	0,056778	6,16338135	3,82167553	1,45228819	1,22124121
0,00093688	0,056778	210,433335	239,329276	388,395833	483,183137
0,00093777	0,056778	53,692462	86,4945783	164,67949	221,649091
0,00093947	0,056778	11,7220193	10,5264679	5,86365574	4,66073761
0,0009592	0,057702	49,2917603	56,597587	119,775363	107,782268
0,00096097	0,057702	13,3504427	10,287044	43,4189439	30,8469763
0,00099228	0,059311	18,5570827	26,8599059	65,3578828	67,2572837
0,00099433	0,059311	28629,5394	36871,6053	14703,1256	16060,6545
0,00099737	0,059311	32,0625522	30,7288701	74,1857378	67,3691849
0,00101353	0,06008	22,095512	17,3043068	9,93099323	12,9771032
0,00101876	0,060151	10,8089151	17,8108952	42,4684274	52,2298695
0,00102122	0,060151	83,3138562	97,3552804	57,1846	57,6185367
0,0010378	0,060935	833,617839	954,493111	1701,21348	2277,55709
0,00105156	0,061548	18,5555059	16,4265001	63,2336007	54,1122338
0,00107112	0,062496	5,49260244	4,85069917	1,98718446	2,69373806
0,00107887	0,06275	11,1903402	10,5084599	4,85678475	4,61650365
0,00108508	0,062914	79,7711393	106,425205	215,363712	211,621528
0,00109744	0,063433	53,65494	41,719448	23,9861546	32,3479345
0,00111147	0,064044	50,0845744	36,344311	25,0100228	26,2889199
0,00111763	0,064199	18,2483625	16,6181677	9,2333578	10,6272907
0,00112493	0,06442	19,194859	27,3735093	59,0008918	58,6008855
0,0011556	0,065897	25,2757703	32,6297198	7,23876313	13,5330079

0,00115908	0,065897	5,83336448	4,5046231	12,7933387	18,1485167
0,00116139	0,065897	28,5422751	32,5091965	59,0603559	66,1574604
0,00119247	0,067455	6,60293514	5,40484793	2,88446249	2,42863494
0,00122576	0,069071	25,9330837	20,5101703	10,2153283	12,8198797
0,00122848	0,069071	10,0811169	8,40691058	5,53244032	4,4221897
0,00124075	0,069549	5,91743607	1,24725865	15,5119121	20,2928862
0,00124891	0,069796	492,618517	558,395676	272,729339	361,324549
0,00125655	0,070012	6,1630381	9,93445505	29,7650111	32,2821703
0,00126386	0,070209	151,300233	198,132591	401,45539	583,853514
0,00127122	0,070407	32,7717105	38,9952448	90,0778751	94,6977395
0,00130474	0,072048	50,2566786	38,3746308	138,044563	100,533985
0,00131432	0,072362	77,4327858	74,778716	52,6409676	48,8538383
0,0013199	0,072454	4,79987765	6,24392309	1,69334596	1,34766573
0,00133992	0,073336	36,1909293	28,4723116	98,3503866	70,8037397
0,00135214	0,073787	3,08303272	1,442551	0,36226464	0,07693496
0,00136098	0,073952	2,8452958	1,85222	10,6801874	12,9715915
0,00136312	0,073952	5,35675489	6,48998756	0,6053603	2,59980388
0,00138099	0,074702	12,5922685	11,2574787	5,54168082	7,6985443
0,00139248	0,075105	4,80219125	4,29360411	17,8823605	12,6151021
0,00143695	0,077279	101,936597	72,3345309	25,9634401	45,5381601
0,00145323	0,077928	38,9288198	35,6338727	26,3804462	22,4125517
0,00147389	0,078809	67,2020458	77,7893592	43,6922263	46,0442689
0,00149472	0,079692	206,698273	234,830944	397,351222	522,828155
0,00149973	0,079731	200,352778	210,106762	124,23255	146,825231
0,00151834	0,080389	8,35419908	7,88901066	2,38375767	4,73778337
0,00152077	0,080389	34,2218983	31,9438807	80,6294204	61,3928132
0,00154147	0,081251	91,2519497	100,447946	177,109526	195,90086
0,00154998	0,081468	44,5605478	39,455746	102,951498	86,8346414
0,00156224	0,081881	37,8916359	28,8318648	65,813004	65,6596995
0,00157479	0,082306	9,66961616	11,3948395	4,8258236	5,69233067
0,00159411	0,083082	34,3108705	38,904117	22,4855495	20,2277097
0,00164353	0,085308	35,1417882	26,8888519	14,604042	19,4221312
0,00164602	0,085308	20,9532512	13,4889877	57,5176815	57,689223
0,00169359	0,087529	41,8132369	47,6853686	27,3086851	26,6588599
0,0017007	0,087652	27,7705301	32,1189792	11,056412	14,9048066
0,00171489	0,088139	2,24382883	2,72566948	13,2204613	12,1505249
0,00172375	0,088349	95,9613624	107,944543	69,9884742	58,9933241
0,00173737	0,088802	27,6100444	21,3288025	57,7923599	50,4561567
0,00180126	0,091815	17,8700813	31,5460032	65,8480669	60,9251686
0,00183443	0,093249	15,5642718	19,7376066	38,4573985	55,3869309
0,00186752	0,094672	21,4722	18,7443796	6,5407822	10,2637625

0,00187804	0,094946	139,69428	163,66828	92,0469782	99,5687995
0,00190036	0,095813	182,692831	155,192937	334,273378	307,406725
0,0019453	0,097813	11,5186127	13,493354	8,46144344	6,41428351
0,00197345	0,098722	6,89874974	6,92441973	20,7959942	19,1682792
0,00197401	0,098722	87,6531922	80,5078374	159,312669	226,262756
0,00198811	0,098945	2,35284076	1,76597473	11,5306183	10,8290643
0,00198913	0,098945	125,826623	115,39034	76,3455848	92,8832353
0,0020075	0,099592	351,455305	333,383394	259,758688	238,135424
0,00203685	0,10074	12,2089014	10,1965221	6,62622057	5,80278282
0,00204152	0,10074	28,8634869	23,4286302	68,8739081	53,7407929
0,00211036	0,103858	93,176643	97,0311634	178,949339	192,951176
0,00211683	0,103858	14,2622484	27,0008453	55,588311	58,6719169
0,00212148	0,103858	78,9682153	77,5993515	43,5348184	48,3917979
0,00214756	0,104857	3,90692133	4,36230358	10,5859741	15,2125977
0,00216033	0,105069	12,6566606	15,2740694	57,3443612	51,8903655
0,00216323	0,105069	16,3239202	16,1646908	54,3233025	37,4651113
0,00218329	0,105767	9,94163826	7,96202904	30,3170706	23,8455129
0,00221912	0,107223	252,055419	264,67182	454,680902	487,057709
0,00223098	0,107516	23,0134887	37,8911599	73,7722752	107,863301
0,00226139	0,108385	10,7614748	16,3612473	47,0704506	38,4499163
0,00226164	0,108385	116,528082	114,742645	316,614599	528,24086
0,00226654	0,108385	18,3852845	15,546156	2,53566563	5,88989865
0,00228999	0,109225	149,574865	129,601833	91,6942087	103,755917
0,00230657	0,109734	20,6506669	18,235849	37,3869259	53,8768125
0,00231593	0,109875	17,6307333	19,7465443	9,36787581	8,83048509
0,00232139	0,109875	11,285879	13,526202	3,71079554	5,33260703
0,00232942	0,109975	21,2177252	13,9744051	4,64457355	5,7909966
0,00234678	0,110513	32,7800529	34,2641055	17,1348385	19,8982783
0,00237335	0,111252	124,260447	124,996434	221,14785	231,932864
0,00237446	0,111252	8,42514235	8,83022612	48,3674424	35,0832617
0,00241699	0,112959	3,10893845	0,67647348	9,91552	15,9911756
0,00245394	0,114398	11,177446	17,1209433	47,9814721	34,8769904
0,00249733	0,116129	2,84140878	5,65787422	34,5432482	21,0797577
0,00251249	0,116426	20,1608245	17,8721113	73,9848082	48,6992016
0,00251626	0,116426	6,09200262	23,4339717	45,4166473	56,4444005
0,00253043	0,116614	33,7968599	35,2697169	23,802463	19,4631467
0,00253289	0,116614	21,6701399	20,0398254	11,5394662	14,1127569
0,00255443	0,117314	13,9684441	8,68859565	30,1425969	36,0031302
0,00261943	0,119828	6,46074579	4,7791297	2,28113097	3,23582294
0,0026221	0,119828	1,86149573	1,16066827	10,0579386	5,84935191
0,00264151	0,12015	19,3631045	19,4782225	48,517608	36,9509112

0,00264327	0,12015	143,938493	147,510917	265,458089	272,300871
0,00264855	0,12015	74,0961214	89,816813	154,399213	211,33128
0,00267964	0,121006	20,206156	20,1988096	41,8552255	43,7796225
0,00268674	0,121006	36,2540514	23,8899627	82,5979136	64,1926534
0,00269039	0,121006	5,82188138	5,36120388	24,0540884	18,0049432
0,00269352	0,121006	36,9601419	14,9856495	62,353562	64,5418811
0,00271214	0,121549	21,4233157	19,043067	12,4188283	13,4746717
0,00272801	0,121965	34,1599858	31,7782505	66,4961223	92,1515851
0,0027378	0,122109	26,7842305	28,9445909	18,8250329	15,5213156
0,00274546	0,122157	13,887053	15,506111	7,05748385	9,42669544
0,00275783	0,122413	20,6700737	24,1750558	16,5763363	10,2818611
0,00277652	0,122949	75,2506698	70,0058203	62,5787825	44,5310398
0,00281299	0,124267	8,696864	6,19013423	40,0777403	24,3200029
0,00282849	0,124655	0,03533338	0,0362443	3,98925524	1,40722538
0,00287513	0,126269	6,42490268	2,19684719	18,0481237	12,7317685
0,00287872	0,126269	10,3942006	7,83686386	3,73339049	5,05259366
0,00290102	0,126725	28,5884716	21,945576	80,6721847	56,1338398
0,00290277	0,126725	8,44122136	8,19733059	1,68092194	4,57110043
0,00291573	0,126992	13,462973	12,9216924	7,90967771	4,29281216
0,00292895	0,127269	9,27742902	9,27669374	22,229084	35,7812261
0,00294942	0,127859	16,5479349	11,44505	8,49379166	8,87977888
0,00297252	0,12856	7,26350044	3,04202588	21,2194239	14,5905434
0,00298185	0,128664	7,79101043	4,04526684	1,59520125	1,64176295
0,00299016	0,128722	6,07490412	7,88744813	17,6407784	21,431087
0,00301985	0,1297	1082,66447	1019,13325	1663,48878	1956,80523
0,00303007	0,129838	246,831398	235,316132	171,18045	154,339475
0,0030562	0,130656	18,6722537	44,3269923	79,8854455	98,1430616
0,00308053	0,131183	0,59896077	1,59744633	10,086388	13,1769694
0,00308267	0,131183	1,75979596	2,35316132	0,69155504	0,28309166
0,00311289	0,132166	4,63438331	2,34523822	18,8010642	12,1877405
0,00313566	0,132829	30,1961634	34,2524862	18,5979292	22,3405608
0,00315383	0,133218	2,70547782	3,46903389	38,39789	19,2413004
0,00315921	0,133218	7,44529062	6,34783244	15,8510275	19,8049549
0,00318776	0,133921	7,09999236	9,15074816	4,80788457	4,15727646
0,00320049	0,133921	14,8675373	13,639734	9,7297985	8,19143023
0,00320218	0,133921	173,69379	170,550715	333,729975	295,994001
0,00320476	0,133921	18,7481314	28,3912903	7,65472905	7,50974614
0,00322588	0,134501	19,9190553	22,1134133	11,9055657	12,1634295
0,0032336	0,134521	57,4643092	53,0304492	118,482961	121,35832
0,0032532	0,135033	22,5631992	21,330522	12,3239679	15,7942342
0,00328286	0,13596	6,18824372	7,17153927	2,7118895	2,46370089

0,00335763	0,138149	21,8335647	15,8309158	52,4266226	41,7482979
0,00335796	0,138149	51,6295351	61,9800722	134,608333	214,861187
0,00336333	0,138149	22,1965002	29,3411636	80,5721982	83,7585694
0,00336831	0,138149	22,5047691	25,7648832	12,7179084	11,9958583
0,00337903	0,138149	5,43192834	7,16395836	33,0400448	34,0327393
0,00338038	0,138149	41,7285606	42,0136783	34,1266805	22,3264716
0,0033921	0,138323	7,50577887	4,12074333	20,6344173	27,0663914
0,0034215	0,139112	45,9628393	50,6151681	118,246484	89,6324389
0,00342643	0,139112	97,4988274	86,6054926	70,1830361	65,3394275
0,00345001	0,139763	10,750218	11,8150359	34,0413995	42,5965357
0,0035382	0,142833	6,7657725	5,36781039	2,69730945	2,53956265
0,00354119	0,142833	38,8870976	46,520686	27,2790528	28,8983324
0,00357941	0,144061	8,50099958	13,5931935	39,4729556	37,5793723
0,00359553	0,144397	73,3506469	56,5303947	143,924895	112,443903
0,00362373	0,145216	20,5395483	25,2486694	15,9590225	11,7946023
0,0036329	0,145269	4,7566856	7,62947686	26,9763994	20,9127485
0,00364245	0,145338	6,32301239	11,8646789	30,3970908	40,8012583
0,00368695	0,146798	23,5077222	27,9819796	12,3142572	17,0433187
0,00370741	0,147296	44,060855	58,4054927	24,21259	26,6508511
0,00371817	0,147408	2,75532853	2,31247882	11,9832697	15,1224443
0,003736	0,147799	10,3965427	7,80523131	3,31583041	3,14334252
0,00375951	0,148207	188,48595	220,285468	353,02838	467,108777
0,0037623	0,148207	0,42383737	1,30429265	11,7603938	18,2868884
0,00379196	0,148337	37,1308491	36,0501436	22,102397	27,7378611
0,00379452	0,148337	23,6190883	26,9228863	15,8796715	17,6781599
0,00379548	0,148337	17,7625303	8,01397912	43,2992911	31,8000911
0,00379758	0,148337	2,63598541	3,50781812	10,2930208	10,9442365
0,00381135	0,148563	7,97613017	6,29923185	21,8818192	24,5645623
0,00382824	0,148908	34,9354331	34,1188141	76,2220653	63,5602449
0,00384542	0,149263	2,58635016	1,15836445	5,99490142	9,36111202
0,00385585	0,149356	18,3810135	13,4677786	10,5467344	7,27848239
0,00390127	0,150286	14,3439072	17,1717178	9,87640838	9,29562822
0,00390217	0,150286	16,1420304	9,82214877	6,03399688	6,41902397
0,00391146	0,150286	66,5974207	81,8469103	145,58103	209,795974
0,00391226	0,150286	17,1834518	17,567106	11,6804894	8,22951792
0,00394579	0,151261	4,58803948	3,34474502	0	1,25868492
0,00395418	0,15127	7,88201654	10,7400696	46,1499272	28,3351446
0,00397491	0,151742	11,4700987	11,330036	39,0210767	41,6267981
0,00398287	0,151742	31,5657116	36,1445579	125,02353	82,6379033
0,00401369	0,152602	23,543252	25,9812764	55,5773379	52,7021443
0,00403209	0,152941	33,9173119	40,4554955	90,5646766	148,596011

0,00403909	0,152941	6,09970566	6,39298163	37,3012171	21,6276171
0,0040607	0,153446	11,0347179	11,6000361	5,48642936	8,32923245
0,00412867	0,155452	21,405736	19,3604577	6,68023867	12,3681305
0,00413052	0,155452	28,4198397	33,3443912	16,7656347	19,9038832
0,00418634	0,157233	7,01901562	11,3393275	1,91881361	2,57422479
0,00420659	0,157523	7,20147968	9,94880863	23,6719633	25,3330257
0,00421102	0,157523	5,86806905	5,94138147	1,8909319	3,09938515
0,00422751	0,157821	160,310434	139,012542	276,700145	268,319976
0,00425486	0,158203	0,80752895	4,27253005	10,5731032	9,67263764
0,00425664	0,158203	87,6331416	144,935196	278,480867	427,640428
0,00426332	0,158203	12,0588653	10,7434027	8,7254848	6,15645575
0,004294	0,158773	93,2461261	90,4020249	258,497088	183,57331
0,0042958	0,158773	597,952938	678,918343	1227,78993	1794,32871
0,00432622	0,15958	45,2848892	41,2940106	27,5522341	29,4646017
0,00437295	0,160984	13,2912564	12,1918665	46,2220414	39,0227387
0,00438686	0,161176	9,41988781	8,15648912	18,8213074	21,9109921
0,00441913	0,162041	55,8733017	63,8694435	43,9620311	41,9199286
0,00444402	0,162632	53,5937569	38,7409234	24,5256767	34,1408433
0,0045191	0,165054	4,54670579	7,8968702	17,5990329	14,4532453
0,00459455	0,16748	6,59159445	6,99929891	3,68710363	3,28326669
0,00461198	0,167678	18,5878119	14,725758	8,23676029	10,0329958
0,00464491	0,167678	2,23946858	0,97189391	0	0,10890292
0,00464609	0,167678	82,6120785	68,9806131	51,6235378	51,9040522
0,00465114	0,167678	2,47825871	1,94006193	8,36165929	13,0489233
0,00466126	0,167678	25,7388864	25,2262608	56,5298761	48,1277868
0,0046639	0,167678	46,4024915	43,6525754	29,6923206	32,3976958
0,00467172	0,167678	25,776045	23,2221496	14,040198	12,0381555
0,0046723	0,167678	0,34202637	0,85204989	5,70355993	4,77230241
0,0047006	0,168111	191,137353	253,417373	457,115325	675,851324
0,00471699	0,168111	21,6116145	21,1693663	50,0004626	55,6012497
0,00473077	0,168111	17,8466741	16,9840311	39,5804007	40,9388679
0,00473518	0,168111	112,506032	100,422803	64,5285036	72,0568505
0,00474093	0,168111	0,95869482	0,49170535	3,57086532	2,2078036
0,00474093	0,168111	0,95869482	0,49170535	3,57086532	2,2078036
0,00474777	0,168111	331,030114	313,087685	210,479119	251,630593
0,00477296	0,168681	3,77838545	7,19790522	32,7088437	26,6158746
0,00479902	0,169279	20,3045151	21,4287882	92,5608997	57,3455571
0,00482932	0,169879	59,7259577	50,2060793	114,440935	111,433099
0,00483434	0,169879	3,50983757	2,6937675	2,07775959	0
0,00486466	0,170622	77,6830583	77,4934746	156,568366	139,133383
0,00489193	0,171255	16,207257	18,6233997	7,72478964	11,7884257

0,00496383	0,173444	7,87296715	8,07593826	21,4483982	20,3006833
0,00503651	0,175653	0	0	2,64658023	1,93870041
0,00506669	0,176185	55,0637477	53,5733596	31,2493402	38,4542137
0,00507744	0,176185	23,4932262	25,8510246	19,2902485	12,9046475
0,00508682	0,176185	4,61842384	2,61808677	15,8151649	21,6669218
0,00508974	0,176185	13,727571	16,9343492	10,9853391	7,06656621
0,00510904	0,176322	2,59654129	5,52798175	11,8125737	15,1913474
0,0051127	0,176322	13,4780282	11,8908013	5,47466607	7,67647404
0,0051402	0,176941	10,9175246	9,82487793	28,9667409	29,1526768
0,00517045	0,177653	12,8445644	14,9524312	6,88972351	8,56293411
0,00521005	0,178683	36,6298649	39,9798767	22,0829217	24,9214953
0,00524278	0,179281	7,95086387	12,9022766	31,8016232	27,0681001
0,00524683	0,179281	1,58481502	0,48770183	7,17745193	6,61242001
0,00527168	0,179683	48,6369709	54,0064958	43,139218	30,5737679
0,00527797	0,179683	12,9403444	11,5503566	7,34951076	6,29062653
0,0052956	0,179954	13,8014196	9,82078167	43,3038778	35,9608374
0,0053142	0,180255	37,9296287	34,7354621	28,0473137	26,6545284
0,00533434	0,180608	24,2549518	24,601232	43,7251986	55,9310674
0,00536443	0,181296	12,2347719	8,03996785	41,1550418	26,5572258
0,00539323	0,181649	1099,16877	1022,66983	634,936702	902,578473
0,00539445	0,181649	9,0206985	11,2898615	28,0819602	23,7383786
0,00546116	0,183562	6,66372137	7,57775771	14,7482925	16,1484682
0,00548308	0,183849	14,0227122	11,5948913	5,1015353	7,3058928
0,00549408	0,183849	18,069754	13,0567916	7,9103833	9,79968448
0,00550498	0,183849	12,6469076	7,79206215	3,01549932	4,32959854
0,00550934	0,183849	18,6870791	17,841472	8,81251607	9,70825977
0,00561948	0,187188	10,2827855	10,1009394	25,8472944	33,8798754
0,00569858	0,189483	22,9475903	24,1762111	16,2975557	13,0674384
0,00571567	0,189711	30,6350982	18,9735212	64,7073917	68,5145166
0,00573672	0,19007	15,1283087	20,3974531	8,28039046	9,3340547
0,00575405	0,190304	62,7374088	70,6700205	111,527972	150,119027
0,00580023	0,19149	166,395493	148,027073	266,650921	305,331347
0,00583156	0,192183	100,208414	111,080517	166,106398	212,22223
0,00585211	0,192518	29,3714621	25,8369384	16,5571802	21,2262017
0,00587052	0,192782	58,2853806	56,3488883	119,62954	104,817197
0,00592346	0,194176	66,0621818	69,1979859	168,111351	123,964347
0,00597196	0,195421	26,9583848	24,8805592	19,2651032	17,1117187
0,00598759	0,195587	58,6810923	69,6388319	47,0573557	44,4650158
0,00605013	0,197283	5,626156	5,95737043	3,75083925	2,0135625
0,00607581	0,197773	1,54019667	2,13368495	4,70967313	6,02273307
0,00612406	0,198994	12,2557219	13,1089352	39,6892458	36,5535896

0,00613969	0,199154	1,59963341	0,14917029	10,2963697	12,1349958
0,00619795	0,200636	26,0188305	24,8425407	17,3675397	18,0719332
0,00621071	0,200636	4,07071894	1,13090932	11,0355356	9,2481933
0,0062231	0,200636	169,895694	176,301412	311,510798	310,039984
0,00622864	0,200636	1,27445541	5,81027487	31,9756045	16,9192792
0,0062506	0,200748	17,6350012	19,6574142	41,8457927	43,5903312
0,00625377	0,200748	7,12068969	5,57902565	2,46610232	4,0285916
0,0063171	0,202431	14,5817888	17,1943867	7,34542793	10,2090022
0,0063318	0,202552	28,833924	29,5772846	69,4050771	85,293803
0,00637365	0,20314	4,5088303	8,5001312	35,9118275	21,2622473
0,00638128	0,20314	74,2317351	80,836173	165,385842	162,463625
0,00638301	0,20314	18,8952243	14,6421766	10,4160374	11,5395856
0,00641097	0,20363	13,7496451	5,93857747	27,1424209	28,9587303
0,00642037	0,20363	12,1526833	10,9008757	6,58224551	7,33573017
0,00644135	0,203947	25,0311008	19,2113561	8,63112683	15,2953306
0,00646258	0,20427	97,0162758	90,9565586	74,019362	67,73692
0,00648983	0,204783	28,1812163	17,9792101	70,0406405	64,2009248
0,00654729	0,206245	4,34009236	2,80650352	1,44913662	1,99214363
0,00656658	0,206502	41,0663919	31,6190306	19,505316	27,0403103
0,00659839	0,207151	5,9948251	7,0512848	27,3793356	18,7973277
0,00661137	0,207209	13,8994225	18,0430064	30,8350197	42,3986381
0,00664446	0,207697	44,2043986	39,6491565	137,509205	91,5826348
0,00664935	0,207697	0,44115764	0,6033747	5,7687409	6,1355628
0,00671005	0,209006	18,2840187	21,3182437	52,2655449	40,2760212
0,00671379	0,209006	22,0145713	16,4497527	15,9529113	8,56493087
0,0067761	0,210166	43,511256	40,8098632	31,5694762	27,0410143
0,00678352	0,210166	13,0798992	10,1336968	8,42775936	8,03587289
0,00679321	0,210166	75,8117441	80,5402167	54,454396	56,8821927
0,00679635	0,210166	73,7812975	84,4354857	163,083634	131,620609
0,00684395	0,210643	6,38577355	18,5120104	43,0353478	38,5702523
0,0068474	0,210643	2,14824591	5,14180177	12,7242641	24,4452463
0,00684809	0,210643	11,3420736	11,9068601	3,70208231	5,75533269
0,00685721	0,210643	16,5733621	15,1920577	10,0468443	6,91054616
0,00687363	0,210799	60,8690066	70,2560678	45,2437069	46,1566289
0,00690466	0,211401	78,0376357	73,9564987	149,725962	179,076759
0,00695365	0,211936	21,9168429	23,4222656	12,3210138	15,708513
0,00698755	0,211936	47,8791446	30,4280068	20,949682	24,4240684
0,00700352	0,211936	7,22487202	2,77287354	27,7453023	16,4985305
0,00701835	0,211936	6,61585897	9,35642642	21,6497057	19,3404438
0,00702737	0,211936	5,43767642	5,57786387	44,5955162	23,1115052
0,00703926	0,211936	4,75255085	8,81263603	38,4769581	26,6933649

0,00704445	0,211936	3,89428871	2,72485235	1,33250726	1,3328365
0,00705176	0,211936	12,4978853	13,5791747	31,4686102	37,5031028
0,00705932	0,211936	15,834143	20,0058328	9,01623363	9,55829412
0,00706706	0,211936	3,51868815	3,32741805	1,10470094	0,65168841
0,00706739	0,211936	6,9280103	8,23787754	18,4523397	17,6708334
0,00706981	0,211936	12,8465105	9,977404	38,2796762	45,0729599
0,00707413	0,211936	102,285656	121,322761	82,5112676	78,9647664
0,00708206	0,211936	9,39630485	10,6258307	6,24337227	5,47604558
0,00712318	0,212733	285,665696	254,146519	483,527549	451,320367
0,00713161	0,212733	71,6122564	50,6519256	30,3041835	44,3868726
0,00715586	0,213114	15,822747	14,3637615	8,38704381	9,66815957
0,00718854	0,213744	6,27120805	4,00538097	20,8313678	14,5302901
0,00720958	0,214026	12,690322	13,2177572	35,8661811	37,4898315
0,00723092	0,214317	27,2827862	30,5039431	20,6847837	14,5917593
0,00726016	0,214808	21,1079634	25,9020802	16,4272927	15,2388847
0,00727064	0,214808	18,7961617	14,9286578	39,7448547	36,9573196
0,007382	0,217752	5,15798227	4,77940219	2,86295943	2,10777889
0,00740939	0,218212	23,945477	26,2824388	18,4460206	17,6261015
0,00748741	0,220161	3,54875982	6,18264608	13,0429566	17,5202008
0,00757543	0,222397	10,9248741	8,73941744	30,5789335	20,6806701
0,00767728	0,22503	51,9137717	44,7717585	33,3213689	35,7758114
0,00770997	0,225144	11,2597517	13,6569665	7,15070701	6,59406029
0,00771615	0,225144	0	0	0,25720645	0,63727432
0,00772496	0,225144	5,23748799	2,73230734	9,22073387	14,8144206
0,00773911	0,225144	34,1034315	33,0769748	78,5923421	65,4330973
0,0077507	0,225144	156,699194	177,495597	836,101609	488,900768
0,00776574	0,225144	75,4013824	63,3782481	47,2160754	54,1838987
0,00776611	0,225144	5,67215249	7,03836886	34,8388576	19,9532306
0,00783493	0,226674	7,59759379	4,21079782	11,9348943	15,20477
0,0078433	0,226674	15,8395749	17,5982562	12,6226764	10,2983312
0,00803087	0,231478	19,7340376	21,4920368	12,5560778	12,9388885
0,00803591	0,231478	49,9173569	47,1618226	37,338429	31,4755307
0,00804696	0,231478	4,67300317	10,2406095	25,4043468	26,2853088
0,00808296	0,232089	45,2490132	48,713215	93,3207204	76,9207898
0,00809323	0,232089	489,564667	466,506592	328,527693	382,802617
0,00812282	0,232578	3,93425832	3,08611321	9,6101088	9,48040464
0,00813644	0,232609	195,295943	222,628513	357,255891	501,682649
0,00818784	0,233577	13,214317	9,19977808	7,48571734	5,31535157
0,00820431	0,233577	37,6019757	45,4262446	84,6163565	73,2047821
0,00820803	0,233577	14,6472622	12,6680359	30,868786	32,0002465
0,00824111	0,234159	0,83080328	0,82283505	4,98880141	3,72177357

0,00825968	0,234327	590,155078	602,008068	935,831513	1049,87525
0,00828602	0,234716	28,9748187	33,442575	61,1483225	61,6259865
0,00837709	0,236934	2,45887621	2,43628151	9,83844443	6,70353207
0,00839109	0,236969	19,3303186	18,5147211	45,6071214	36,1819829
0,0084102	0,237147	1,10112947	0,87851356	0	0
0,00842453	0,237191	12,9721354	10,7853227	4,87763459	5,00672549
0,00845953	0,237815	13,6076144	12,9782973	4,41351496	7,84214451
0,00850731	0,238797	36,6611343	43,6746741	99,2420748	73,9511838
0,00855871	0,239877	33,3675598	33,9517704	111,742174	87,0134361
0,00860568	0,240527	4,73966379	2,85720444	9,11287813	10,4586529
0,00860783	0,240527	31,2915717	22,2877518	17,6210141	21,167885
0,00867097	0,241816	22,6587783	24,621126	13,063645	14,4276334
0,00869291	0,241816	14,2214931	11,1426954	36,6506375	30,5631306
0,00869603	0,241816	29,8744223	30,5401969	70,5106311	55,8855014
0,00870938	0,241816	5,92915871	2,31695884	23,2325487	13,7436607
0,00871915	0,241816	27,170383	30,3633719	19,9520382	15,6682836
0,00891005	0,246742	7,1279276	9,2553051	21,5824539	28,3200072
0,0089443	0,247321	5,98122793	4,82603832	15,1796021	10,7556354
0,00897278	0,24774	12,0894345	16,26375	40,7698614	37,3988635
0,00899889	0,248091	3,73390802	3,44715392	12,3255792	18,1462405
0,00904378	0,248647	64,6128353	76,0668878	48,8512136	50,919221
0,00904586	0,248647	25,4541916	44,1620686	143,121826	91,4833044
0,00908019	0,249222	39,4123239	40,7218357	29,8030738	25,7996194
0,00910545	0,2495	11,0627065	13,2784691	7,51043485	6,52927234
0,00911722	0,2495	36,7850008	22,0079836	16,7734484	15,6846761
0,00914038	0,249765	7,04258881	5,52435164	16,3505358	19,0034987
0,00919039	0,250352	3,31061158	2,12676388	6,97515966	10,0839186
0,00919692	0,250352	8,75214684	10,0339937	7,77377021	5,56849376
0,00920233	0,250352	23,5154455	16,7367705	12,008766	14,1661312
0,00929178	0,252415	11,2767824	12,1888468	6,97940185	7,78476949
0,0093161	0,252706	24,9433948	21,3069502	39,4106304	45,5475672
0,00939729	0,253644	36,9634511	38,2173209	24,6305278	29,4990269
0,00940073	0,253644	7,9155985	8,83487266	5,20610461	4,78366477
0,009405	0,253644	9,44004222	13,1253854	4,45194147	4,83643672
0,00941425	0,253644	9,69481981	11,3198868	6,61780276	5,65596546
0,00941903	0,253644	22,6256609	16,1537857	12,5998129	12,4674187
0,00944281	0,253916	14,147443	15,0796901	11,3433362	5,43365557
0,00945881	0,253978	6,98441705	10,0055678	4,05573396	3,95100379
0,00953174	0,255566	3,02448747	3,93347743	12,7122813	12,0866221
0,00956835	0,256178	24,0227262	14,6384594	9,87135567	11,2828255
0,00963494	0,257406	3,72305302	4,18947387	2,22126163	2,10358569

0,00966178	0,257406	8,29562324	7,51758692	25,224107	18,5319797
0,00967022	0,257406	15,0367798	14,8978342	10,0457618	9,4221371
0,00967084	0,257406	21,5714225	20,5848888	11,0618007	14,7064962
0,00968396	0,257406	6,07928221	7,51519244	16,8038102	20,1027644
0,00969746	0,257406	843,519141	951,729377	1715,62351	1418,48817
0,00975903	0,25867	18,39995	21,9791804	63,4092496	42,7513931
0,00982636	0,25974	12,9580097	15,9711004	8,26554826	5,71516822
0,00982739	0,25974	5,90908026	7,39144487	16,0667046	14,1696654
0,00984833	0,259923	82,4752469	87,6603411	212,143998	153,911055
0,00990067	0,260933	445,975106	371,502019	332,520335	313,707294
0,00998116	0,262335	130,788163	114,202791	184,707995	248,153508
0,00998754	0,262335	4,03577547	3,15933696	14,0231994	18,3292192
0,00999625	0,262335	9,68746169	9,30920962	20,8811766	22,6071015