# Gene Expression Profiling in C57BL/6 Mice Treated with the Anorectic Drugs Sibutramine and Phendimetrazine and Their Mechanistic Implications

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## Abstract

Recently, obesity has become a worldwide public health concern and the use of anorectic drugs has drastically increased. In this study, sibutramine and phendimetrazine, representative marketed anorectics, were repeatedly administered per os on a daily basis into C57BL/6 mice and the effects of these drugs on food intakes, body weight changes and gene expression profiles were monitored for up to following 7 days. Methamphetamine, which has a potent anorectic effect, was used as a positive control. Anorectic effects were sustained only for two days by phendimetrazine or methamphetamine, but for six days by sibutramine. The modulations of gene expressions in the hypothalamus and the striatum were investigated using microarrays on day 2 and day 7 post-administration, which corresponded to the anorectic period and a return of appetite respectively, for all three drugs tested. Differences in overall gene expression profiles in the stratum on day 2 for sibutramine and phendimetrazine seems to reflect difference between the two in terms of the onsets of drug tolerance. According to microarray findings, the Ankrd26 gene appears to have an important anorectic role, whereas the up-regulation of the olfaction system appeared to be involved in the drug tolerance of anorectics. The microarray data presented in this study demonstrates the usefulness of gene expression analysis for gathering information on the efficacy and safety of anorectic drugs.

*Keywords:* microarray, gene expression, anorectic drug, sibutramine, phendimetrazine, methamphetamine

#### Introduction

Obesity has increased and become a worldwide public health problem. Most of the drugs used to treat obesity are appetite suppressants that stimulate the central nervous system (CNS), and these often have side effects, such as, tolerance, addiction, and cardiovascular problems.

Sibutramine is a representative anti-obesity drug that inhibits serotonin (5-hydroxytryptamine, 5-HT) and noradrenaline reuptake (Stock, 1997). The mechanism underlying the anti-obesity effect of sibutramine is believed to involve satiety (Halford et al., 1998) and the stimulation of thermogenesis (Conneley et al., 1999; Liu et al., 2002). In fact, pre-treatment with serotonin or norepinephrine antagonists can reduce the anorectic effect of sibutramine (Grignaschi et al., 1999), which indicates that the anorectic effect of sibutramine is related to the inhibition of the reuptakes of norepinephrine (Balcioglu et al., 2000) and serotonin (Buckett et al., 1988; Gundlah et al., 1997). Sibutramine is an approved drug for the long-term treatment for obesity, but has been reported to increase mean systolic and diastolic blood pressures and heart rate (Eric Colman, 2005).

Phendimetrazine has also been widely prescribed as an anorectic for the treatment of obesity, and has been reported to have properties similar to methamphetamine, which is known to suppress appetite by activating catecholaminergic neurotransmission (Seiden *et al.*, 1993; Chen *et al.*, 2001). Methamphetamine is known to primarily block dopamine transporter, which inhibits dopamine reuptake, indicating that dopamine up-regulation has an anorectic effect (Mackler *et al.*, 1993). Because phendimetrazine and methamphetamine stimulate the central nervous system to produce euphoria, probably via the activation of dopaminergic systems in the brain (Nailles *et al.*, 2003), these drugs are restricted to short-term use (a few weeks) and prominently labeled to warn against the risk of addiction.

However, although many anorectics are available, evidence is still lacking concerning their efficacies, safeties, and molecular mechanisms. Recently, cDNA microarray studies on gene expression profile changes by amphetamine have been reported (Noailles *et al.*, 2003; Yamamoto *et al.*, 2005), but no such report has been issued on other anorectics. In this study, we employed

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microarray techniques to investigate the gene expression profiles of two representative anorectics, sibutramine and phendimetrazine and to compare these with that of methamphetamine in mouse brain. By comparing the gene expressional patterns of these drugs in different parts of mouse brain, we were able to identify genes whose expressions were specifically or commonly modulated by these drugs. We are in the belief that these identified genes would provide a molecular background and facilitate our understanding of the efficacies and safeties of anorectic drugs.

#### Methods

#### Animals

Mice were acclimated in the animal facility for seven days prior to commencing this study. Male C57BL/6 mice ( $20 \sim 25$  g, Orient Bio, Korea) were housed individually in standard animal cages. All animal experiments were performed in accordance with a program accredited by the Association for the Assessment and Accreditation of Laboratory Animal Care (AAALAC).

#### Drugs and food intake

Methamphetamine (Sigma), phendimetrazine (Dreampharma, Korea) and sibutramine (Knoll AG, Ludwigshafen, Germany) were dissolved in deionized water. The effects of these anorectic drugs on food intake and body weight were monitored on a daily basis for seven days. 64 C57BL/6 mice (n=16 mice/group) were used for the experiments. Vehicle, methamphetamine (5 mg/kg), phendimetrazine (60 mg/kg) or sibutramine (5 mg/kg) were repeatedly administered per os to the animals on a daily basis. And deionized water was used as vehicle control. After the drug administrations, food and water were freely provided for following 18 hours before monitoring daily food intake and body weight changes. On day 2 and day 7 post-administration, respectively, a half of the animals in each group were sacrificed for brain isolation and mRNA extraction.

#### RNA isolation and DNA microarray

Total RNA was extracted from brain tissues using Trizol reagent (Invitrogen) in accordance with the manufacturer's instructions. Quantity and purity (260/280 ratio) of RNA were monitored using a ND-1000 UV/VIS spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA). Differential gene expressions were profiled using mouse genome survey array chips (Applied Biosystems, Foster City, CA) containing 60-mer oligonu-

cleotide probes representing a set of 32,996 individual mouse genes and more than 1,000 control probes. Microarray experiments were performed according to the manufacturer's instructions. Digoxigenin (DIG)-UTPlabeled cRNA was generated from  $5 \mu g$  of total RNA and amplified using chemiluminescent reverse transcription in vitro transcription (RT-IVT) labeling kits (Applied Biosystems) Briefly, each microarray was prehybridized in hybridization buffer with blocking reagent at 55°C for 1 h. DIG-labeled cRNA targets (10  $\mu$  g) were fragmented to  $100 \sim 400$  bps and hybridized with each prehybridized microarray at 55°C for 16 h. Arrays were then washed with hybridization wash buffer followed by chemiluminescence rinse buffer. Chemiluminescent signals were generated by incubating arrays with anti-DIG alkaline phosphatase and chemiluminescence substrate. Images were collected for each microarray using a Model 1700 Chemiluminescent Microarray Analyzer (Applied Biosystems)

#### Analysis of microarray expression data

Signal intensities were imported into Avadis software (Strand and Stratagene, India). To minimize the effects of external variables, inter-array quantile normalization was performed. Average values of gene expression ratios obtained from three replicates were calculated. Differentially expressed genes (DEGs) were selected based on fold changes of  $\geq 2$  and a Welch' s t-test probability value of  $\leq 0.05$ . For further analysis, DEGs were categorized according to their biological functions using the PANTHER (Protein ANalysis THrough Evolutionary Relationships) classification system (Applied Biosystems, https://panther.appliedbiosystems.com).

# **Results and Discussion**

# Effect of anorectics on food intakes and body weights changes in C57BL/6 mice

To identify genes related to the effects of anorectic drugs, we repeatedly administered single doses of phendimetrazine (60 mg/kg.), sibutramine (5 mg/kg), or methamphetamine (5 mg/kg, positive control) *per os* to C57BL/6 mice for up to 7 days and monitored daily changes in food intake and body weight over seven days. Fig. 1 shows the effects of the three drugs on food intake (Fig. 1A, B) and body weight (Fig. 1C, D) as comparing to vehicle only (Fig. 1A, C) and baseline (Fig. 1B, D), respectively. Rates of food intake were significantly suppressed in all three treated groups. The phendimetrazine and methamphetamine treated groups showed a maximum anorectic effect and weight loss on

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**Fig. 1.** Effects of anorectic drugs on food intake and body weight in C57BL/6 mice. The food intake rates as compared with vehicle treated controls (a) and baseline (b). Body weight changes versus the vehicle treated controls (c) and baseline (d). The lines above symbols represent standard errors. The asterisks (\*) indicate significant differences between the vehicle controls and the three drug treatment groups and sharps (#) indicate significant differences between the drug treated groups and baseline ( $p \le 0.05$ ).

day 2 post-administration. After day 2, animals in these groups slowly recovered appetite and gained body weight to the control level. In contrast, the sibutramine-treated group, which exhibited the best anorectic effect and greatest weight loss at 2 days post-administration and drug effects were sustained up to day 6. However, on day 7 animals recovered their appetites in all treatment groups.

Phendimetrazine and methamphetamine show similar biochemical and behavioral properties (Crowin *et al.*, 1987; Evans and Johanson *et al.*, 1987; Jones and

Holtzman 1994), and have both been reported to release dopamine and norepinephrine (Rothman *et al.*, 2002). Moreover, the mechanism underlying the anorectic effect of these drugs has been attributed to the activation of catecholaminergic neurotransmission (Seiden, *et al.*, 1993; Chen *et al.*, 2001). On the other hand, sibutramine acts on serotonergic and noradrenergic pathways and has been demonstrated to effectively reduce body weight by reducing food intake and by modulating energy expenditure (Strack *et al.*, 2002). These previous observations may explain why the anorectic effects of

sibutramine differed from those of methamphetamine and phendimetrazine in the present study. To better understand the modes of action of these anorectic drugs, we employed microarray techniques and investigated genes specifically and commonly modulated by these anorectic agents.

## Genes differentially expressed in hypothalamus and striatum by sibutramine, phendimetrazine, and methamphetamine

Gene expression profiling was performed to examine the temporal effects of the three drugs on gene expression. Control of food intake and energy expenditure involves a complex network of neuropeptides, distributed throughout the central nervous system (CNS), but mainly in the hypothalamus (Schwartz *et al.*, 2000; Saper *et al.*, 2002). In the mammalian striatum, the basal ganglia nucleus subsumes many complex behaviors including feeding and sexual behavior (Alheid, G.F., 2003, Saint-Cyr, J.A., 2003). As described above, the three drugs showed a maximum effect on day 2 post-administration, though sibutramine had a sustained effect up to day 6. Based on these observations, total RNAs extracted from hypothalamus and striatum on days 2 and 7 were subjected to microarray analysis.

Table 1 shows the number of differentially expressed (fold change  $\geq 2$ , p-value  $\leq 0.05$ ) genes on days 2 and 7 in the hypothalamus and striatum. Methamphetamine had the greatest effect on gene expression on day 2 in both hypothalamus and striatum, suggesting that it has a substantial effect on feeding behavior. Phendimetrazine induced a smaller number of differentially expressed genes on day 2 in hypothalamus than methamphetamine, which concurs with a previous observation that phendimetrazine has a lower anorectic effect than the other two drugs. However, phendimetrazine still

**Table 1.** The number of differentially expressed genes (fold change  $\geq$ 2, p-value  $\leq$ 0.05) induced by the three anorectic drugs

	Н	ypothalam	us	Striatum				
	Meth	Phen	Sibu	Meth	Phen	Sibu		
Day 2	Up: 220 Down: 486 Total: 706	Up: 19 Down: 20 Total: 39	Up: 66 Down: 47 Total: 113	Up: 218 Down: 140 Total: 358	Up: 337 ) Down: 209 Total: 546	Up: 10 Down: 1 Total: 11		
Day 7	Up: 10 Down: 214 Total: 224	Up: 7 Down: 4 Total: 11	Up: 0 Down: 1 Total: 1	Up: 176 Down: 35 Total: 211	Up: 130 Down: 22 Total: 152	Up: 139 Down: 49 Total: 188		

Meth: methamphetamine, Phen: phendimetrazine, Sibu: sibutramine.

modulated large number of genes in the striatum on day 2, which implies that it stimulates the central nervous system like methamphetamine. In the case of sibutramine, gene expression patterns differed slightly from those of phendimetrazine and methamphetamine. Sibutramine highly modulated gene expression only on day 2



Fig. 2. Classification of genes differentially expressed in the hypothalamus and striatum on days 2 (a) and 7 (b) post-administration.

in the hypothalamus and did not showed significant gene modulation on day 2 in the striatum, which suggests its induction of anorexia differs mechanistically from those of phendimetrazine and methamphetamine. Nevertheless, all three anorectic drugs induced considerable differential gene expression in the striatum on day 7.

As described previously, all three drugs showed best efficacy on day 2, suggesting that genes modulated on day 2 in the hypothalamus are probably involved in anorectic effects. In fact, a large number of peptides and neurotransmitters in the hypothalamus affect energy balance. These include neuropeptide-Y (NPY), galanin, melanocyte stimulating hormone, and cocaine and amphetamine regulated transcript (CART) (Williams et al., 2000). Moreover, food deprivation is known to increase NPY mRNA in the hypothalamus of the goldfish and Coho and Chinook salmons (Silverstein et al. 1998;1999; Narnaware et al., 2000), and this effect can be reversed by re-feeding (Narnaware and Peter, 2001). Furthermore, CART was found to be a potent anorexigenic factor in mammals and to be most highly expressed in the hypothalamus (Gautvik et al., 1996). In addition, the actions of methamphetamine have been reported to be related to hypothalamic NPY and CART (Kuo 2003) and the anti-obesity actions of serotonin may be mediated by hypothalamic-NPY (Dryden et al., 1996).

A biological pathway analysis of gene expression profiles are considered as one of the most valuable tool in providing key information about the biological system and widely accepted by research community (Chung *et al*, 2007; Lee *et al*, 2008). To compare the biological

a. Hypothalamus



Fig. 3. Analysis of commonly modulated genes on day 2 post-administration in the hypothalamus (a) and striatum (b).

pathways induced by the anorectic agents, we classified differentially expressed genes by biological process. As shown in Fig. 2, even though the numbers of differentially expressed genes varied for the three drugs, the genes modulated by phendimetrazine and methamphetamine showed similar biological process classifications on days 2 and 7 post-administration in the striatum. However sibutramine revealed a quite different biological pathway. The results of our pathway analysis strongly suggested that the biologic impact of sibutramine differs markedly from those of phendimetrazine and methamphetamine. To obtain detailed information on gene expression profiles, we further analyzed and compared individual genes modulated by the three drugs.

# Analysis of gene expression profiles and safety considerations

To identify genes commonly and specifically expressed by the three drugs, Venn diagram analysis was employed (Fig. 3, 4). The numbers of genes commonly modulated by the three agents on day 2 was 16 in the hypothalamus and one in the striatum (Fig. 3). Since highest anorectic effects were observed on day 2 for all three drugs, commonly modulated genes on day 2, especially in the hypothalamus, might play a critical role in the anorectic effect of these drugs (Table 2).

Of the genes listed in Table 2, the ankyrin repeat domain 26 (Ankrd26) gene, which is up-regulated in the hypothalamus, revealed quite interesting information. The Ankrd26 gene is located at 10p12.1 in humans and

A. Hypothalamus



Fig. 4. Analysis of commonly modulated genes on day 7 post-administration in the hypothalamus (A) and striatum (B).

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Table 2. List of genes commonly modulated in the striatum on day 2 post-administration

#### a. Hypothalamus

Cana ID			Meth		Phen		Sib	
Gene_ID	Gene_symbol	Gene_name	р	Fold	р	Fold	р	Fold
mCG12278.3	Hip2	Huntingtin interacting protein 2	0.0000	-3.32	0.0002	-3.01	0.0016	-2.99
mCG5518_1	Reg3d	Regenerating islet-derived 3 delta	0.0038	-2.50	0.0008	-2.95	0.0177	-2.70
AK005238_1	Socs6	Suppressor of cytokine signaling 6	0.0021	2.31	0.0151	2.09	0.0087	2.08
mCG19763.1	LOC640437 Ankrd26	Ankyrin repeat domain 26	0.0028	2.41	0.0047	2.18	0.0068	2.30
mCG16888.2	Commd2	COMM domain containing 2	0,0073	2,52	0.0440	2,63	0,0070	2,39
mCG120273.1	LoC546387 Pcgf4	Polycomb group ring finger 4	0.0006	2.75	0.0379	2,16	0.0125	2,22
mCG141844	Pdzk2	PDZ domain containing 2	0.0000	3.32	0.0195	2.13	0.0094	2.48
b. Striatum								
Cana ID	Gene_symbol	Gene_name -	Meth		Phen		Sib	
Gene_ID			р	Fold	р	Fold	p	Fold
AK041983.1	Stk22s1	Serine/threonine kinase 22 substrate 1	0.0078	-2.62	0.0002	-2.63	0.0226	-2.60

Genes without any known function are not shown.

at chromosome 6 (qF1) in the mouse (Hahn *et al.*, 2006). Furthermore, Ankrd26 is present in many normal tissues, but little information has been reported about function of this gene. However, recently, it was reported that Ankrd26 gene mutant mice develop extreme obesity, insulin resistance, and an increase in body size (Bera *et al.*, 2008), which suggests that Ankrd26 plays a critical function in controlling obesity. In accordance with this previous report, our microarray data showed that Ankrd26 was up-regulated on day 2 when anorectic effects were significant. Thus, our data supports the notion that Ankrd26 plays a key role in controlling obesity.

In the present study, only small numbers of genes were found to be differentially expressed in the striatum. Nevertheless, phendimetrazine and methamphetamine modulated the expressions of more genes than sibutramine, which again suggests that these two drugs share a common biological mechanism.

The numbers of genes commonly modulated by the three drugs on day 7 differed from that observed on day 2. On day 7, only one gene was commonly expressed in the hypothalamus, whereas 77 were commonly expressed in the striatum. This observation agrees well with the previous observation on food intake and body weight as described earlier. As described above, on day 7 animals in all three treatment groups recovered their appetites almost to the control level. This earlier observation was matched by microarray results, which revealed no significant change in gene ex-

pression on day 7 for phendimetrazine and sibutramine in the hypothalamus, which predominantly controls appetite. In contrast with the hypothalamus, microarray data revealed that a significant number of genes were expressionally modulated by the three drugs on day 7 in the striatum. By comparing lists of differentially expressed genes on day 7 in the striatum, we identified 77 genes commonly modulated by anorectic drugs (Table 3).

Of these 77 common genes, we found that six, which were highly up-regulated, were related to the olfaction system, namely, olfactory receptor 1022 (Olfr1022), olfactory receptor 1330 (Olfr1330), olfactory receptor 1134 (Olfr1134), vomeronasal 1 receptor I5 (V1ri5), vomeronasal 1 receptor A4 (V1ra4), and vomeronasal 1 receptor C2 (V1rc2). The olfaction system is a sensory dimension that plays an important role in food intake (Janowitz et al., 1953; Le Magnen, 1981). It also has been reported that this system becomes more sensitive after fasting and less sensitive when satiated (Aime et al., 2007; Apelbaum et al., 2005; Pager et al., 1972). Accordingly, in the present study, olfaction system up-regulation appeared to stimulate appetite in tested animals on day 7. Since the up-regulation of olfactory genes was greater on day 7 than on day 2, and increased olfaction system activity appeared to account for recovered appetite after prolonged treatment with anorectics. The striatum has been postulated to mediate the reinforcing properties of food and drugs of abuse. Furthermore, the release of dopamine in the striatum is

Gane_UD         Gane_symbol         Carle_name         p         Fold         p         Fold         p         Fold           mCG21421,2         UgBa         UDP galactsyttmsforase & A         0.0000         -18,86         0.0000         -56,8         0.0000         -21,33           mCG10496,2         Tarc1         Tetratricoperitorie (astrowed 3 deta)         0.0016         -4,44         0.0001         -7,34         0.0007         -2,33           mCG13143,2         Dnase1         Decxyliboruclease I         0.0000         -4,26         0.0001         -3,03         0.0000         -5,74           mCG13672,2         Mt12         Malate dehydrogenase 2, NAD         0.0000         -2,46         0.0001         2,52         0.0187         2,137           mCG1001,01         Olf1022         Oltacry receptor 1022         0.028         2,42         0.0001         2,58         0.0001         2,56           mCG1049022         Apix         Aprataxin         0.0004         2,46         0.0007         2,47         0.0049         2,48         0.0001         2,56           mCG1042582,1         1/16         VArit pha subcombias         0.0000         2,51         0.0002         2,56         0.0001         3,33         0,463	0 10		-	Meth		Phen		Sib	
mCG214212         Ugl8a         UPP galactopythansfrase & A         0.0000         -5.96         0.0000         -5.97         0.0001         -6.937         0.0001         -6.937         0.0001         -5.96         0.0000         -5.96         0.0000         -7.94         0.0007         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.96         0.0000         -5.94         0.0000         -5.94         0.0000         -5.94         0.0000         -5.96         0.0000         -5.96         0.0000         2.61         0.0017         2.018         0.0012         2.06         0.0012         2.06         0.0012         2.06         0.0012         2.06         0.0012         2.06         0.0012         2.48         0.0022         2.36         0.0001         2.43         0.0012         2.43         0.0012         2.43         0.0012         2.44         0.0022         2.06         0.0002         2.023         0.0012	Gene_ID	Gene_symbol	Gene_name	р	Fold	р	Fold	р	Fold
mcG618618_1         Regonerating isst-derived 3 delta         0.0000         -5.06         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0000         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001         -7.34         0.0001	mCG21421.2	Ugt8a	UDP galactosyltransferase 8A	0,0000	-19,86	0,0000	-59,57	0,0000	-60,34
mCG10496.2         Tanct         Tertarticopeptide repeat, ankyin repeat         0,0016         -4,44         0,0001         -7,34         0,0077         -3,03           mCG13143.2         Dnase1         Descyriboruclease 1         0,0000         -2,26         0,0001         -3,03         0,0000         -5,74           mCG13672         Mih2         Malate delydrogenase 2, NAD         0,0000         -2,46         0,0001         -2,62         0,0017         2,13           mCG30021         Olifo22         Olifactory reception Tactor II A, 1         0,016         2,94         0,0032         2,36         0,0001         -2,33         0,0000         2,51           mCG1049022         Aptx         Aptxanin         0,0004         2,46         0,0072         2,18         0,0007         2,36         0,0001         2,46           mCG1042821         Viris         Vomeronasal 1 receptor, IS         0,0000         2,51         0,0002         2,50         0,0000         2,36         0,0000         2,36         0,0000         2,36         0,0000         2,36         0,0000         2,36         0,0000         3,37           mCG1037424         Chris         Vortein phosphatase 2 (formerly 4,0000         2,53         0,0000         3,00000         3,00000<	mCG5518_1	Reg3d	Regenerating islet-derived 3 delta	0,0000	-5,06	0,0000	-3,73	0,0001	-2,13
mcC613134.2         Dnase1         Deaxythonuclease I         0,0000         -4,26         0,0001         -5,33         0,0000         -5,74           mcG1876,2         Midr2         Malate dehydrogenase 2, NAD         0,0000         -2,46         0,0011         -3,03         0,0000         -3,37           mcG3002,1         Olfrl022         Olfrl02         Olfrl022         0,028         2,38         0,0001         2,52         0,0001         2,51           mcG1049922         Aptx         Aptxtrin         0,0001         2,47         0,0042         2,18         0,0007         2,48           mcG1049022         Aptx         Aptxtrin         ncceptor, I5         0,0000         2,51         0,0007         2,48         0,0007         2,48           mcG1042822,1         Vir5         Vormeronas1         receptor, I5         0,0000         2,51         0,0002         2,60         0,0002         2,88         0,0003         3,36           mcG1038744         Cln3         Ceroid Lipfolicionesis, neuronal 3, juvenile         0,0000         2,67         0,0085         2,28         0,0002         2,12         0,0023         4,29           mcG103876,1         Vir1330         Olfactor receptor 1330         0,125         2,89	mCG10496.2	Tanc1	Tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1	0 <u>.</u> 0016	-4.44	0 <u>.</u> 0001	-7.34	0.0077	-3.03
mCG1876.2         Mdn2         Malafie dehydrogenase 2, NAD         0,000         -2,46         0,0001         -5,03         0,0000         -3,37           mCG3862.2         Gtf2a1         General transcription factor II A, 1         0,0169         2,18         0,0000         2,82         0,0001         2,11           mCG104702         Otfactory receptor 1022         0,0028         2,36         0,0012         2,26         0,0007         2,18           mCG104022         Aprataxin         0,0004         2,46         0,0007         2,18         0,0007         2,18         0,0007         2,43           mCG104022         Aprataxin         0,0004         2,46         0,0007         2,18         0,0007         2,43         0,0011         2,66           mCG1042582,1         Vtri5         Vormeronasal 1 receptor, 15         0,0000         2,51         0,0002         2,06         0,0000         3,38           mCG1042582,1         Vtri5         Vormeronasal 1 receptor, 15         0,0000         2,51         0,0005         2,28         0,0008         2,28         0,0000         3,33         0,463         3,16           mCG104258,1         Virti3         Smapt         Smapt         Smapt         Smapt         Smapt <td< td=""><td>mCG13143.2</td><td>Dnase1</td><td>Deoxyribonuclease I</td><td>0.0000</td><td>-4,26</td><td>0.0002</td><td>-5.33</td><td>0.0000</td><td>-5.74</td></td<>	mCG13143.2	Dnase1	Deoxyribonuclease I	0.0000	-4,26	0.0002	-5.33	0.0000	-5.74
mC63627_2         GH2a1         General transcription factor II A, 1         0,0169         2,18         0,0000         2,62         0,0011         2,51           mC6103021         Olfratory receptor 1022         0,0238         2,36         0,0316         2,29         0,0107         2,14           mC61039023, Pp2Ca         Aptatxin         0,0004         2,46         0,0072         2,18         0,0067         2,43           mC61039023, Pp2Ca         Aptatxin         0,0004         2,47         0,0049         2,03         0,0011         2,66           mC61049022         Apta         Aprataxin         0,0007         2,51         0,0002         2,66         0,0009         2,74           mC6103748         Nufa4         NADH dehydrogenase (ubiquinone)         0,0000         2,67         0,0055         2,88         0,000         4,00         0,000         3,36           MC61038765, 1         Olfrator receptor subfamily 3, group C, polysa         2,88         0,001         3,33         0,463         3,16           mC61030873, Sapc1         Small nuclear Receptor subfamily 3, group C, polysaptide         0,0000         2,48         0,0000         3,28         0,0000         3,33         0,463         3,16           mC61030273, Bgfac	mCG1876_2	Mdh2	Malate dehydrogenase 2, NAD (mitochondrial)	0.0000	-2.46	0.0001	-3.03	0,0000	-3.37
mCG102001         Olfractory receptor 1022         0.0238         2.36         0.0316         2.29         0.0197         2.14           mCG147992         LOC381955         Expressed sequence Al326876         0.0028         2.42         0.0032         2.36         0.0000         2.56           mCG1049022         Aptx         Aprataxin         0.0001         2.47         0.0047         2.18         0.0067         2.43           mCG1049022         Aptx         Aprataxin         0.0001         2.47         0.0049         2.08         0.0000         2.56           mCG10475821         Virtic<	mCG3627 2	Gtf2a1	General transcription factor II A 1	0 0169	2 18	0 0000	2 62	0 0001	2 51
mcG147992         LOC381956         Expressed sequence Al326876         0.0028         2,42         0,0032         2,36         0,0000         2,56           mcG1049022         Aptx         Aprataxin         0.0004         2,46         0,0072         2,18         0,0067         2,43           mcG1049022         Aptx         Aprataxin         0.0001         2,47         0,0049         2,03         0,0011         2,66           mcG1049022         Mufa4         NADH dehydrogenase (ubiquinone)         0,0000         2,51         0,0002         2,06         0,0003         3,86           mcG10492582,1         Virit5         Vomeronasal 1 receptor, 15         0,0000         2,51         0,0002         2,06         0,0003         2,96           McG1039749         Cla3         Cercid Lipofuscinosis, neuronal 3, juvenile         0,0002         2,89         0,0012         5,12         0,0023         4,29           mcG1038786,1         Olfrator receptor subfamily 3, group C,         0,0022         2,89         0,0011         3,33         0,463         3,16           McG1038037,1         Hgfac         Hepatocyte growth factor activator         0,0004         3,00         0,017         2,74         0,0001         3,16         0,0001         3,16	mCG7000 1	Olfr1022	Olfactory receptor 1022	0.0238	2 36	0.0316	2 29	0 0197	2 14
mC61049022         Aprtaxin         0.0004         2.46         0.0072         2.18         0.0067         2.43           mC61037803.1         Ppp2ca         Protein phosphatase 2 (formery 2A), 0.000         2.47         0.0002         2.06         0.0009         2.74           mC61042582.1         Viri5         Virioforgenase (ubiquinone)         0.0000         2.53         0.0002         2.06         0.0009         2.74           mC61042582.1         Viriof         Virioforgenase (ubiquinone)         0.0000         2.53         0.0002         2.06         0.0008         2.96           mC61038764.1         Olri3.05         Genrid Lipotuscinosis, neuronal 3, juvenile         0.0002         2.67         0.0085         2.28         0.0008         2.96           MC6103876.1         Olri3.00         Olfactor receptor subiamily 3, group C, 0.0032         2.99         0.0011         3.33         0.0463         3.16           mC610267.3         Brafa         Melacotyte growth factor activator         0.0048         3.00         3.0000         5.53         0.0000         3.94           mC6103131         Ip-forge protein         2.07         0.0001         3.16         0.0005         3.94           mC6104274         Nudrabi         Nadhal dehydrogenase (u	mCG147992	LOC381955 Al326876	Expressed sequence Al326876	0.0028	2.42	0.0032	2,36	0.0000	2,56
mCG1037803,1         Ppp2ca         Protein phosphatase 2 (formerly 2A), 0,001         2,47         0,0049         2,03         0,0011         2,66           mCG1042582,1         V1ri5         Vineronasal 1 receptor, 15         0,0000         2,51         0,0002         2,06         0,0009         2,74           mCG1042582,1         V1ri5         Vineronasal 1 receptor, 15         0,0000         2,53         0,0004         4,00         0,0000         2,53         0,0005         2,28         0,0008         2,96           mCG1037449         Cin3         Ceroid Lipofuscinosis, neuronal 3, juvenile         0,0000         2,67         0,0085         2,28         0,0008         2,96           AK052337,1         Nr3c2         Muclear receptor subfamily 3, group C, notice 10,0000         2,95         0,0001         3,33         0,463         3,16           mcG1026173,1         Snapc1         Small nuclear RNA activation complex, notice 10,0002         3,07         0,0000         3,38         0,0000         3,38         0,0000         3,38         0,0000         3,36         0,0000         3,36         0,0000         3,36         0,0000         3,36         0,0000         3,36         0,0000         3,36         0,0000         3,36         0,0001         3,16         0,	mCG1049022	Aptx	Aprataxin	0.0004	2.46	0.0072	2,18	0.0067	2.43
mCG1042582,1         Viris         Vomeronasal 1 receptor, 15         0,0000         2,51         0,0002         2,06         0,0009         2,74           mCG12148,2         Ndufa         NADH dehydrogenase (ubiquinone)         0,0000         2,53         0,0000         4,00         0,0000         3,36           mCG1037449         Ch3         Ceroid LipOtuscinosis, neuronal 3, juvenile         0,0009         2,67         0,0085         2,28         0,0008         2,96           AK052337,1         Nr3c2         Nuclear receptor subfamily 3, group C, on032         2,89         0,0012         5,12         0,0023         4,29           mCG1038786,1         Olfr1330         Olfactor receptor 1330         0,0125         2,89         0,0001         3,33         0,0463         3,16           mCG1038786,1         Ufr1330         Olfactor receptor 1330         0,012         2,74         0,0021         2,13           mCG104876,3         Hgfac         Hepatocyte growth factor activator         0,0048         3,00         0,0001         2,54         0,0001         3,16           mCG1048243         Igh-X         Hepatocyte growth factor activator         0,0048         3,00         0,0001         2,51         0,0001         3,51         0,0001         2,56     <	mCG1037803.1	Ppp2ca	Protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	0.0001	2.47	0.0049	2.03	0.0011	2.66
mCG12148,2         Ndufa4         NADH dehydrogenase (ubiquinone)         0,0000         2,53         0,0000         4,00         0,0000         3,36           mCG1037449         Ch3         Ceroid Lipotuscinosis, neuronal 3, juvenile         0,0009         2,67         0,0085         2,28         0,0008         2,98           AK052337,1         Nr3c2         Nuclear receptor subfamily 3, group C, 0,0032         2,89         0,0012         5,12         0,0023         4,29           mCG1038766.1         Olf1330         Olfactor receptor 1330         0,0125         2,89         0,0001         3,33         0,0463         3,16           mCG1038767.3         Hgfac         Hepatocyte growth factor activator         0,0048         3,00         0,0000         5,53         0,0000         3,16         0,0015         3,94           mCG1031093,1         Igh-V         Immunoglobulin heavy chain variable regic         0,0002         3,07         0,0000         3,16         0,0001         3,11         0,0001         3,11         0,0000         3,19         0,0001         3,11         0,0000         3,16         0,0000         3,19           mCG1031093,1         Igh-V         Immunoglobulin heavy chain variable regic         0,0002         3,07         0,0000         3,16	mCG1042582 1	V1ri5	Vomeronasal 1 receptor 15	0 0000	2 51	0 0002	2 06	0 0009	2 74
mCG1037449         Cln3         Ceroid Lipofuscinosis, neuronal 3, juvenile         0,0009         2,67         0,0085         2,28         0,0008         2,96           K40523371         Nr3c2         Nuclear receptor subfamily 3, group C, 0,002         2,89         0,0012         5,12         0,0023         4,29           mCG1038786,1         Olfrator receptor subfamily 3, group C, 0,002         2,89         0,0001         3,33         0,0463         3,16           mCG1026173,1         Snapt         Snapt         Medicar RNA activation complex, 0,0000         2,95         0,0000         2,14         0,0021         2,13           mCG103203,1         Igh-V         Immunoglobulin heavy chain variable regic         0,0000         3,00         0,0000         5,53         0,0000         2,60         0,0000         3,16         0,0015         3,94           mCG104248         Polsphodiesterase 7B         0,0000         3,11         0,0000         2,60         0,0000         3,16         0,0000         2,60         0,0000         3,18           mCG104248         Spat1         NADH dehydrogenase (ubiquinone) 1, 0,0000         3,21         0,0005         2,51         0,0000         2,80         0,001         3,51           mCG1048476         Stac         Spermato	mCG12148.2	Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex 4	0.0000	2.53	0.0000	4.00	0.0000	3 <sub>.</sub> 36
AK052337,1         Nr3c2         Nuclear receptor subfamily 3, group C, member 2         0,0032         2,89         0,0012         5,12         0,0023         4,29           mCG1038786,1         Olfractor receptor 1330         0,0125         2,89         0,0001         3,33         0,0463         3,16           mCG1026173,1         Snapl         nuclear RNA activation complex, polypeptide 1         0,0000         2,95         0,0000         2,14         0,0001         3,22           mCG10301093,1         Igh-V         Hepatocyte growth factor activator         0,0048         3,00         0,0017         2,74         0,0021         2,13           mCG1031093,1         Igh-V         Immunoglobulin heavy chain variable regic         0,0001         3,11         0,0205         2,17         0,0001         2,56           mCG1042243         Spats1         NADH dehydrogenase (ubiquinone) 1, 0,0000         3,61         0,0001         3,21         0,0005         2,51         0,0000         3,16           mCG1048476         Stac         Src homology three (SH3) and cysteine rich 1         0,0000         3,28         0,0017         2,45         0,0000         3,17           mCG1048476         Stac         Src homology three (SH3) and cysteine rich domain         0,0000         3,57	mCG1037449	Cln3	Ceroid Lipofuscinosis, neuronal 3, juvenile (Batten, Spielmever-Voot disease)	0.0009	2.67	0.0085	2.28	0.0008	2.96
mCG1038786,1         Olfrator         receptor         1330         0,0125         2,89         0,0001         3,33         0,0463         3,16           mCG1026173,1         Snapc1         Small nuclear RNA activation complex, 0,0000         2,95         0,0000         2,14         0,0000         3,22           mCG3967,3         Hgfac         Hepatocyte growth factor activator         0,0048         3,00         0,0017         2,74         0,0021         2,13           mCG19062,3         Zfp207         Zinc finger protein 207         0,0000         3,03         0,0000         5,53         0,0001         3,94           mCG130193,1         Igh-V         Immunoglobulin heavy chain variable regic         0,0001         3,11         0,0225         2,17         0,0001         3,16         0,0000         3,60         0,0000         3,60         0,0000         3,60         0,0000         3,60         0,0000         3,60         0,0000         3,60         0,0000         3,61         0,0000         3,61         0,0000         3,61         0,0000         3,61         0,0000         3,61         0,0000         3,61         0,0000         3,61         0,0011         2,60         0,0000         3,61         0,0011         3,61         0,0114	AK052337.1	Nr3c2	Nuclear receptor subfamily 3, group C, member 2	0.0032	2.89	0.0012	5.12	0.0023	4.29
mCG1026179,1         Small nuclear         Small nuclear         RNA activation complex, 0,0000         2,95         0,0000         2,14         0,0000         3,22           mCG3967,3         Hgfac         Hepatocyte growth factor activator         0,0048         3,00         0,0017         2,74         0,0021         2,13           mCG19062,3         Zfp207         Zinc finger protein 207         0,0000         3,03         0,0000         3,16         0,0015         3,94           mCG19082,3         Zfp207         Xinc finger protein 207         0,0000         3,16         0,0000         3,16         0,0001         3,16         0,0001         3,16         0,0000         3,16         0,0000         3,16         0,0000         3,16         0,0000         3,16         0,0000         2,60         0,0000         3,11         0,0265         2,51         0,0000         2,51         0,0000         3,51           mCG1042243         Spats1         Spermatogenesis associated, serine-rich 1         0,0000         3,22         0,0017         2,45         0,0001         3,51           MCG10428476         Stac         Src homology three (SH3) and cysteine         0,0000         3,37         0,0014         2,70         0,0000         3,57         0,0000	mCG1038786_1	Olfr1330	Olfactor receptor 1330	0.0125	2,89	0.0001	3,33	0.0463	3,16
mcG3967.3 mcG19062.3         Hgfac Zfp207         Hepatocyte Innunoglobulin heavy chain variable regic McG1031093.1         0,0017 (a) (b) V         2,74 (b) (a) (b) (b) (b) (b) (b) (b) (b) (c) (c) (c) (c) (c) (c) (c) (c) (c) (c	mCG1026173_1	Snapc1	Small nuclear RNA activation complex,	0.0000	2.95	0.0000	2.14	0.0000	3.22
Increase	mCG3967 3	Hofac	Hepatocyte growth factor activator	0 0048	3 00	0 0017	2 74	0 0021	2 13
Index float_2       Entro imige proton feavy chain variable regic       0,0000       3,07       0,0000       3,16       0,0015       3,94         mCG1031093,1       Igh-V       Immunoglobulin heavy chain variable regic       0,0001       3,11       0,0000       3,16       0,0010       3,16       0,0001       2,56         mCG1031091,2       Pde7b       Phosphodiesterase 7B       0,0000       3,16       0,0000       2,60       0,0000       3,16       0,0000       3,16       0,0000       2,56         mCG1042243       Spats1       Spermatogenesis associated, serine-rich 1       0,0000       3,21       0,0005       2,51       0,0000       2,81         mCG59442,1       LOC635999       Protein (peptidyl-prolylcis/trans isomerase)       0,0000       3,28       0,0017       2,45       0,0001       3,51         mCG1030208,1       Capza1       Capping protein (actin filament) muscle       0,0000       3,39       0,0000       3,57       0,0000       4,04         Z-line, alpha 1       Capasing protein (actin filament) muscle       0,0000       3,63       0,0011       2,96       0,004       4,09         MCG124582,1       Cldn5       Claudin 5       0,0000       3,63       0,0012       2,96       0,0023       4,66 <td>mCG19062.3</td> <td>7fn207</td> <td>Zing finger protein 207</td> <td>0,0000</td> <td>3.03</td> <td>0,0000</td> <td>5 53</td> <td>0,0000</td> <td>4 99</td>	mCG19062.3	7fn207	Zing finger protein 207	0,0000	3.03	0,0000	5 53	0,0000	4 99
mind of 100 100 100 100 11       mind indication float       mind of 100 100 100 100 100 1000       100 100 100 100 1000       100 100 100 1000       100 100 100 1000       100 100 1000       100 100 1000       100 100 1000       100 100 1000       100 100 1000       100 100 1000       100 10000       100 1000       100 1000000	mCG1031093 1	Iah-V	Immunoglobulin heavy chain variable regio	0.0002	3.07	0,0000	3 16	0.0015	-1.00 3.0∕I
mCG57121.2       Ndufab1       NADH dehydrogenase (ubiquinone) 1, 0,0000       3,11       0,0000       2,60       0,0000       3,19         mCG57121.2       Ndufab1       NADH dehydrogenase (ubiquinone) 1, 0,0000       3,16       0,0000       2,60       0,0000       2,61         mCG57121.2       Ndufab1       NADH dehydrogenase (ubiquinone) 1, 0,0000       3,21       0,0005       2,51       0,0000       2,81         mCG50942.1       LOC628161       Spermatogenesis associated, serine-rich 1       0,0000       3,28       0,0017       2,45       0,0000       3,51         mCG1048476       Stac       Src homology three (SH3) and cysteine       0,0000       3,37       0,0014       2,70       0,0000       3,57       0,0000       4,04         mCG1048476       Stac       Src homology three (SH3) and cysteine       0,0000       3,39       0,0000       3,57       0,0000       4,04         mCG1030208,1       Capza1       Capza1       Capping protein (actin filament) muscle       0,0000       3,59       0,0077       2,86       0,0092       2,66         mCG121299,1       LOC632373       Alstrom syndrome 1 homolog (human)       0,0024       3,61       0,0114       3,93       0,0012       3,46         mCG121299,1 <td< td=""><td>mCG113012</td><td>Pde7b</td><td>Phosphodiesterase 78</td><td>0.0002</td><td>3.11</td><td>0.0000</td><td>2 17</td><td>0.0013</td><td>2.56</td></td<>	mCG113012	Pde7b	Phosphodiesterase 78	0.0002	3.11	0.0000	2 17	0.0013	2.56
mCG1042243 mCG59442,1         Spats1 LOC635999 Protein (peptidyl-prolylcis/trans isomerase) Protein (actin filament) muscle         0,0000         3,21         0,0001         2,51         0,0000         3,51           mCG1048476         Stac         Src homology three (SH3) and cysteine rich domain         0,0000         3,37         0,0014         2,70         0,0000         3,57         0,0000         4,04           mCG126582,1         Cldn5         Claudin 5         0,0000         3,59         0,0077         2,86         0,0092         2,66           mCG121996,1         V1ra4         Vomeronasal 1 receptor, A4         0,0000         3,63         0,0011         2,96         0,0004         3,70           mCG121996,1         V1ra4         Vomeronasal 1 receptor, A4         0,0002         4,00         0,0074         2,58         0,0023         4,05           mCG126802,2         Rnd2         Rho family GTPase 2         0,0028         4,	mCG57121.2	Ndufab1	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	0.0000	3.16	0.0000	2.60	0.0000	3 <sub>.</sub> 19
mCG59442.1         LOC635999 LOC628161         Protein (peptidyl-prolylcis/trans isomerase)         0,0000         3,28         0,0017         2,45         0,0001         3,51           mCG1048476         Stac         Src homology three (SH3) and cysteine         0,0000         3,37         0,0014         2,70         0,0000         3,17           mCG1048476         Stac         Src homology three (SH3) and cysteine         0,0000         3,37         0,0014         2,70         0,0000         4,04           mCG1030208.1         Capza1         Capping protein (actin filament) muscle         0,0000         3,59         0,0077         2,86         0,0092         2,66           mCG126582,1         Cldn5         Claudin 5         0,0000         3,63         0,0011         3,46         0,0166         4,09           Alms1         Nirka         Vira4         Vomeronasal 1 receptor, A4         0,0000         3,63         0,0014         3,93         0,0012         3,46           mCG12996,1         Vira4         Vomeronasal 1 receptor, A4         0,0002         4,00         0,0074         2,58         0,0023         4,05           mCG12996,1         Vira4         Vomeronasal 1 receptor, A4         0,0002         4,00         0,0074         2,58         0,	mCG1042243	Spats1	Spermatogenesis associated, serine-rich 1	0,0000	3,21	0,0005	2,51	0,0000	2,81
mCG1048476         Stac         Src homology three (SH3) and cysteine rich domain         0,0000         3,37         0,0014         2,70         0,0000         3,17           mCG1030208.1         Capza1         Capping protein (actin filament) muscle Z-line, alpha 1         0,0000         3,39         0,0000         3,57         0,0000         4,04           mCG126582.1         Cldn5         Claudin 5         0,0000         3,59         0,0077         2,86         0,0092         2,66           mCG127499.1         LOC623273         Alstrom syndrome 1 homolog (human)         0,0026         3,61         0,0114         3,46         0,0166         4,09           mCG121996.1         V1ra4         Vomeronasal 1 receptor, A4         0,0000         3,63         0,0014         3,93         0,0012         3,46           mCG16809.2         Rnd2         Rho family GTPase 2         0,0028         4,03         0,0003         9,85         0,0010         7,45           mCG1042759.1         Mrps26         Mitochondrial ribosomal protein S26         0,0003         4,14         0,0082         2,69         0,0170         3,73           mCG103054         Psg17         Pregnancy specific glycoprotein 17         0,0000         4,72         0,0001         3,73         0,0000 <td>mCG59442<sub>.</sub>1</td> <td>LOC635999 LOC628161 Pin4</td> <td>Protein (peptidyl-prolylcis/trans isomerase) NIMA-interacting, 4 (parvulin)</td> <td>0.0000</td> <td>3.28</td> <td>0.0017</td> <td>2.45</td> <td>0.0001</td> <td>3<u>.</u>51</td>	mCG59442 <sub>.</sub> 1	LOC635999 LOC628161 Pin4	Protein (peptidyl-prolylcis/trans isomerase) NIMA-interacting, 4 (parvulin)	0.0000	3.28	0.0017	2.45	0.0001	3 <u>.</u> 51
mCG1030208.1         Capza1         Capping protein (actin filament) muscle Z-line, alpha 1         0,0000         3.39         0,0000         3.57         0,0000         4.04           mCG126582.1         Cldn5         Claudin 5         0,0000         3.59         0,0077         2.86         0,0092         2.66           mCG127499.1         LOC623273         Alstrom syndrome 1 homolog (human)         0,0026         3.61         0,0114         3.46         0,0166         4.09           Alms1          Alms1         v         v         0,0002         3.63         0,0011         2.96         0,0004         3.70           mCG121996.1         V1ra4         Vomeronasal 1 receptor, A4         0,0000         3.63         0,0014         3.93         0,0012         3.46           mCG56416.2         Prox1         Prospero-related homeobox 1         0,0002         4.00         0,0074         2.58         0,0023         4.05           mCG1041193.1         Olfr1134         Olfactory receptor 1134         0,0100         4.10         0,0070         4.07         0,285         3.65           mCG1042759.1         Mrps26         Mitochondrial ribosomal protein S26         0,0003         4.14         0,0002         2.69         0,0170         <	mCG1048476	Stac	Src homology three (SH3) and cysteine rich domain	0.0000	3.37	0 <u>.</u> 0014	2.70	0.0000	3.17
mCG126582.1         Cldn5         Claudin 5         0,0000         3,59         0,0077         2,86         0,0092         2,66           mCG127499.1         LOC623273         Alstrom syndrome 1 homolog (human)         0,0026         3,61         0,0114         3,46         0,0166         4,09           Alms1         Alms1            0,0000         3,63         0,0001         2,96         0,0004         3,70           mCG121996.1         V1ra4         Vomeronasal 1 receptor, A4         0,0000         3,63         0,0011         2,96         0,0004         3,70           mCG115189         II16         Interleukin 1 family, member 6         0,0002         4,00         0,0074         2,58         0,0023         4,05           mCG16809.2         Rnd2         Rho family GTPase 2         0,0028         4,03         0,0003         9,85         0,0010         7,45           mCG1042759.1         Mrps26         Mitochondrial ribosomal protein S26         0,0003         4,14         0,0082         2,69         0,170         3,73           mCG1032176         V1rc2         Vomeronasal 1 receptor, C2         0,0024         4,80         0,0010         4,07         0,0213         4,60 <td< td=""><td>mCG1030208.1</td><td>Capza1</td><td>Capping protein (actin filament) muscle Z-line, alpha 1</td><td>0.0000</td><td>3.39</td><td>0.0000</td><td>3.57</td><td>0.0000</td><td>4.04</td></td<>	mCG1030208.1	Capza1	Capping protein (actin filament) muscle Z-line, alpha 1	0.0000	3.39	0.0000	3.57	0.0000	4.04
mCG127499.1       LOC623273       Alstrom syndrome 1 homolog (human)       0.0026       3.61       0.0114       3.46       0.0166       4.09         mCG121996.1       V1ra4       Vomeronasal 1 receptor, A4       0.0000       3.63       0.0001       2.96       0.0004       3.70         mCG115189       II16       Interleukin 1 family, member 6       0.0008       3.79       0.0014       3.93       0.0012       3.46         mCG56416.2       Prox1       Prospero-related homeobox 1       0.0002       4.00       0.0074       2.58       0.0023       4.05         mCG16809.2       Rnd2       Rho family GTPase 2       0.0028       4.03       0.00070       4.07       0.0285       3.65         mCG1041193.1       Olfactory receptor 1134       0.0100       4.10       0.0070       4.07       0.0285       3.65         mCG103054       Psg17       Pregnancy specific glycoprotein 17       0.0000       4.72       0.0001       3.73       0.0000       3.03         mCG141179.1       Snn       Stannin       0.0000       5.07       0.0000       15.12       0.0000       13.97         mCG140356       H2afz       H2A histone famile, member Z       0.0030       5.08       0.0001       5.39	mCG126582,1	Cldn5	Claudin 5	0,0000	3,59	0.0077	2,86	0,0092	2,66
mCG121996.1         V1ra4         Vomeronasal 1 receptor, A4         0,000         3,63         0,001         2,96         0,004         3,70           mCG115189         II1f6         Interleukin 1 family, member 6         0,0008         3,79         0,0014         3,93         0,0012         3,46           mCG56416.2         Prox1         Prospero-related homeobox 1         0,0002         4,00         0,0074         2,58         0,0023         4,05           mCG16809.2         Rnd2         Rho family GTPase 2         0,0028         4,03         0,0007         4,07         0,0285         3,65           mCG1041193.1         Olfactory receptor 1134         0,0100         4,10         0,0070         4,07         0,0285         3,65           mCG1042759.1         Mrps26         Mitochondrial ribosomal protein S26         0,0003         4,14         0,0082         2,69         0,0170         3,73           mCG1032176         V1rc2         Vomeronasal 1 receptor, C2         0,0024         4,80         0,0010         4,07         0,0213         4,60           mCG140356         H2afz         H2A histone famile, member Z         0,0030         5,08         0,0001         5,39         0,0276         5,99           mCG140356         <	mCG127499.1	LOC623273 Alms1	Alstrom syndrome 1 homolog (human)	0.0026	3.61	0.0114	3.46	0.0166	4.09
mCG115189       II1f6       Interleukin 1 family, member 6       0.0008       3.79       0.0014       3.93       0.0012       3.46         mCG56416.2       Prox1       Prospero-related homeobox 1       0.0002       4.00       0.0074       2.58       0.0023       4.05         mCG16809.2       Rnd2       Rho family GTPase 2       0.0028       4.03       0.0003       9.85       0.0010       7.45         mCG1041193.1       Olfactory receptor 1134       0.0100       4.10       0.0070       4.07       0.0285       3.65         mCG1042759.1       Mrps26       Mitochondrial ribosomal protein S26       0.0003       4.14       0.0082       2.69       0.0170       3.73         mCG1032176       V1rc2       Vomeronasal 1 receptor, C2       0.0024       4.80       0.0010       4.07       0.0213       4.60         mCG140356       H2afz       H2A histone famile, member Z       0.0000       5.07       0.0000       15.12       0.0000       13.97         mCG3861.4       Map2k1       Mitogen activated protein kinase kinase 1       0.0000       6.08       0.0000       18.40       0.0000       16.59         NM 177148.3       Hrbl       HIV-1       Bey binding protein-like       0.0000       9.10 <td>mCG121996_1</td> <td>V1ra4</td> <td>Vomeronasal 1 receptor, A4</td> <td>0.0000</td> <td>3,63</td> <td>0.0001</td> <td>2,96</td> <td>0.0004</td> <td>3,70</td>	mCG121996_1	V1ra4	Vomeronasal 1 receptor, A4	0.0000	3,63	0.0001	2,96	0.0004	3,70
mCG56416.2         Prox1         Prospero-related homeobox 1         0.0002         4.00         0.0074         2.58         0.0023         4.05           mCG16809.2         Rnd2         Rho family GTPase 2         0.0028         4.03         0.0003         9.85         0.0010         7.45           mCG1041193.1         Olfractory receptor 1134         0.0100         4.10         0.0070         4.07         0.0285         3.65           mCG1042759.1         Mrps26         Mitochondrial ribosomal protein S26         0.0003         4.14         0.0082         2.69         0.0170         3.73           mCG103054         Psg17         Pregnancy specific glycoprotein 17         0.0000         4.72         0.0001         3.73         0.0000         3.06           mCG1032176         V1rc2         Vomeronasal 1 receptor, C2         0.0024         4.80         0.0010         4.07         0.0213         4.60           mCG140356         H2afz         H2A histone famile, member Z         0.0030         5.08         0.0001         5.39         0.0276         5.99           mCG3861.4         Map2k1         Mitogen activated protein kinase kinase 1         0.0000         6.08         0.0000         18.40         0.0000         16.50	mCG115189	ll1f6	Interleukin 1 family, member 6	0.0008	3,79	0.0014	3,93	0.0012	3,46
mCG16809.2         Rnd2         Rho family GTPase 2         0.0028         4.03         0.0003         9.85         0.0010         7.45           mCG1041193.1         Olfr1134         Olfactory receptor 1134         0.0100         4.10         0.0070         4.07         0.0285         3.65           mCG1042759.1         Mrps26         Mitochondrial ribosomal protein S26         0.0003         4.14         0.0082         2.69         0.0170         3.73           mCG103054         Psg17         Pregnancy specific glycoprotein 17         0.0000         4.72         0.0010         4.07         0.0213         4.60           mCG1032176         V1rc2         Vomeronasal 1 receptor, C2         0.0024         4.80         0.0010         4.07         0.0213         4.60           mCG141179.1         Snn         Stannin         0.0000         5.07         0.0000         15.12         0.0000         13.97           mCG3861.4         Map2k1         Mitogen activated protein kinase kinase 1         0.0000         6.08         0.0000         18.40         0.0000         16.59           NM 177148.3         Hrbl         HIV-1 Rev binding protein-like         0.0000         9.10         0.0000         16.09	mCG56416 2	Prox1	Prospero-related homeobox 1	0 0002	4 00	0 0074	2 58	0 0023	4 05
International construction         Internation         Internaternati	mCG16809.2	Rnd2	Rho family GTPase 2	0.0028	4 03	0.0003	9.85	0.0010	7 45
Incomparison         Minor         Mitochondrial ribosomal protein         S26         Mitochondr	mCG1041193 1	Olfr1134	Olfactory receptor 1134	0.0100	4 10	0.0070	4 07	0.0285	3 65
mcG130054       Psg17       Pregnancy specific glycoprotein 17       0,0000       4,72       0,0001       3,73       0,0000       3,06         mcG1032176       V1rc2       Vomeronasal 1 receptor, C2       0,0024       4,80       0,0010       4,07       0,0213       4,60         mcG141179.1       Snn       Stannin       0,0000       5,07       0,0000       15,12       0,0000       13,97         mcG3861.4       Map2k1       Mitogen activated protein kinase kinase 1       0,0000       6,08       0,0000       18,40       0,0000       16,50         NM 177148.3       Hrbl       HIV-1       Bey binding protein-like       0,0000       910       0,0000       24.09       0,0000       16.09	mCG1042759 1	Mrps26	Mitochondrial ribosomal protein S26	0.0003	4 14	0.0082	2 69	0.0170	3 73
mCG1032176       V1rc2       Vomeronasal 1 receptor, C2       0.0004       4.80       0.0010       4.07       0.0213       4.60         mCG141179.1       Snn       Stannin       0.0000       5.07       0.0000       15.12       0.0000       13.97         mCG140356       H2afz       H2A histone famile, member Z       0.0030       5.08       0.0001       5.39       0.0276       5.99         mCG3861.4       Map2k1       Mitogen activated protein kinase kinase 1       0.0000       6.08       0.0000       18.40       0.0000       16.50         NM 177148.3       Hrbl       HIV-1 Rev binding protein-like       0.0000       9.10       0.0000       24.09       0.0000       16.09	mCG130054	Psq17	Pregnancy specific glycoprotein 17	0,0000	4 72	0.0001	3 73	0,0000	3.06
mcG1402102       Mod	mCG1032176	V1rc2	Vomeronasal 1 receptor C?	0.0024	1 80	0.0010	<u>∕</u> 107	0.0213	∆ 60
mCG140356       H2afz       H2A histone famile, member Z       0,0000       5,07       0,0000       15,12       0,0000       15,97         mCG140356       H2afz       H2A histone famile, member Z       0,0030       5,08       0,0001       5,39       0,0276       5,99         mCG3861,4       Map2k1       Mitogen activated protein kinase kinase 1       0,0000       6,08       0,0000       18,40       0,0000       16,50         NM 177148.3       Hrbl       HIV-1       Rev binding protein-like       0,0000       9,10       0,0000       24,09       0,0000       16,09	mCG141170 1	Snn	Stannin	0.002-	5.07	0,0000	15 10	0,0210	13.07
mCG3861.4 Map2k1 Mitogen activated protein kinase kinase 1 0,0000 6,08 0,0000 18,40 0,0000 16,50 NM 177148.3 Hrbl HIV-1 Rev binding protein-like 0,0000 910 0,0000 24,09 0,0000 16,09	mCG1/0356	H2afz	H2A histone famile member 7	0.0000	5.02	0.0001	5 20	0.0000	5 00
NM 177148.3 Hrbl HIV-1 Rev binding protein-like 0.0000 9.10 0.0000 24.09 0.0000 16.00	mCG3861 /	Man2k1	Mitogen activated protain kinase kinase 1	0,0000	8 09.00	0.0001	18 /0	0,0270	16 50
	NM 177148.3	Hrbl	HIV-1 Rev binding protein-like	0,0000	9 10	0,0000	24 09	0,0000	16.09

## Table 3. List of genes commonly modulated in the striatum on day 7 post-administration

Genes without any known function are not shown.

known to be implicated in the mechanisms of drug addiction and neuroadaptation (Rompre and Wise, 1989; Robinson and Berridge, 1993). Accordingly, our striatal microarray data appears to reflect the importance of the striatum in drug tolerance.

In summary, we investigated gene expression profiles in the hypothalamus and striatum of C57BL/6 mice after administering sibutramine, phendimetrazine, or methamphetamine. We identified genes whose expressions were highly modulated by these drugs both in the hypothalamus and striatum. Analyses of gene expressions in these brain regions showed that sibutramine utilizes a biological pathway that differs from that utilized by phendimetrazine and methamphetamine. Further analysis of the genes commonly modulated by these three drugs resulted in the identification of Ankrd26, which probably accounts for the biological effects of these drugs. In addition, microarray data revealed the implication of the olfaction systems in the hypothalamus, which might explain why these anorectic drugs tend to lack efficacy after prolonged use. Our findings demonstrate that genes related to the olfaction system were significantly up-regulated at 7 days post-administration as compared with 2 days post-administration in the striatum, and since the appetites of drug-treated animals completely recovered to the control level on day 7, it would appear that olfactory genes play roles in the anorectic drug tolerance

Our microarray experiments also revealed that sibutramine and the two other anorectics induced different gene expressions, and suggested that the biologic pathway induced by sibutramine differed from those induced by phendimetrazine and methamphetamine. In addition, sibutramine induced gene expressional changes on day 2 in striatum, a brain region implicated in drug tolerance. Our microarray data revealed that sibutramine also up-regulated genes related to olfaction system on day 7 in the striatum like phendimetrazine and methamphetamine. This observation suggests that sibutramine may invoke drug tolerance and that the prolonged use of sibutramine should be viewed with caution.

The microarray data presented in this study demonstrates that gene expression analysis can improve our understanding of the biological effect of anorectic drugs. Further studies involving microarray and clinical data are likely to provide profound information on drug efficacy and safety.

#### Acknowledgments

This research was supported by a grant (06141KFDA472) from the Korea Food & Drug Administration in 2006.

# Note

This article has been approved for publication by KFDA, but the views presented in this article do not necessarily reflect those of the KFDA.

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