Erratum

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Genetic Differentiation of Hypothalamus Parentally Biased Transcripts in Populations of the House Mouse Implicate the Prader–Willi Syndrome Imprinted Region as a Possible Source of Behavioral Divergence

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In the original version of table 1, the locus H19 (chr7:142575532–142578146) imprinting status was accidentally listed in the hypothalamus (HYP) column, but should be in the vomeronasal organ (VNO) column. The conclusions and the original data, deposited at ArrayExpress (www.ebi.ac.uk/arrayexpress), accession number E-MTAB-3288, are not affected.

Table 1. List of Imprinted Transcripts Identified in This Study.

Region in mm10	Gene Name	Liver	HYP	VNO	Status	SNPs $F_{st} > 0.8$
chr1:63273269–63314575	Zdbf2	–	pat > 0.95	–	Known	—
chr1:63445904–63596515	Adam23	+	pat > 0.55	+	Known[a,b]	—
chr2:152669461–152708668	H13 (short)	–	pat > 0.8	pat > 0.95	Known	—
chr2:152669461–152708668	H13 (long)	mat > 0.7	mat > 0.8	mat > 0.6	Known	—
chr2:152780668–152831682	Bcl2l1	+	pat > 0.55	+	Known[a]	—
chr2:157556362–157566361	Blcap	+	mat > 0.62	+	Known	—
chr2:157560110–157562519	Nnat	–	pat > 0.99	pat > 0.75	Known	—
chr6:4674350–4747204	Sgce	–	pat > 0.95	pat > 0.95	Known	—
chr6:4747306–4760516	Peg10	–	pat > 0.95	–	Known	—
chr6:4903320–5165661	Ppp1r9a	–	mat > 0.55	+	Known	—
chr6:5383386–5433021	Asb4	–	mat > 0.8	–	Known	—
chr6:30401909–30455174	Klhdc10	+	mat > 0.55	+	Known[a]	—
chr6:30738050–30748466	Mest	–	pat > 0.95	pat > 0.95	Known	—
chr6:30804784–30807552	Copg2os2	–	pat > 0.95	–	Known	—
chr6:30809559–30896760	Copg2	+	mat > 0.7	+	Known	—
chr6:58833700–58920396	Herc3	–	mat > 0.65	+	Known	—
chr6:58905233–58907126	Nap1l5	–	pat > 0.99	pat > 0.95	Known	—
chr7:6671269–6672888	AK003710	–	mat > 0.9	–	New	—
chr7:6675443–6696432	Zim1	–	mat > 0.9	–	Known	—
chr7:6703901–6730554	Peg3	pat > 0.95	pat > 0.99	pat > 0.99	Known	—
chr7:6730741–6967220	Usp29	–	pat > 0.99	–	Known	—
chr7:59228750–59306727	Ube3a	+	mat > 0.8	+	Known	—
chr7:59262923–59263934	AK038761	–	pat > 0.99	–	New[c]	—
chr7:59281852–59290247	A230073K19Rik	–	pat > 0.99	–	New[c]	1
chr7:59307924–59324149	C230091D08Rik	+	mat > 0.8	+	Known[a]	—
chr7:59327318-59328016	AK020709	–	pat > 0.95	–	New	—
chr7:59937467–59975759	D7Ertd715e	–	pat > 0.99	–	New[c]	4
chr7:59976740–59980676	AK139082	–	pat > 0.99	–	New[c]	1
chr7:59982501–60140219	Snrpn/Snurf	pat > 0.99	pat > 0.99	pat > 0.99	Known	1
chr7:61010256–61012230	AK046019	–	pat > 0.99	–	Known	—
chr7:61072752–61089737	AK038418	–	pat > 0.95	–	New	—
chr7:61089568–61221965	DOKist4	–	pat > 0.99	–	Known[a]	—
chr7:61529410–61615327	B230209E15Rik	–	pat > 0.95	–	New	—
chr7:61705850–61927574	A230057D06Rik	–	pat > 0.95	–	New	—

(continued)

Table 1. Continued

Region in mm10	Gene Name	Liver	HYP	VNO	Status	SNPs $F_{st} > 0.8$
chr7:61751446–61753692	AK031915/AK046509	–	pat > 0.99	+	New	—
chr7:61930789–61982715	ENSMUST00000181804	–	pat > 0.99	–	New	—
chr7:61930944–61934821	AK048029	–	pat > 0.99	–	New	—
chr7:62348277–62349927	Ndn	–	pat > 0.99	pat > 0.95	Known	—
chr7:62376979–62381640	Magel2	–	pat > 0.99	–	Known	—
chr7:128439777–128461513	Tial1	+	mat > 0.65	+	New	—
chr7:128611365–128696436	Inpp5f	+	pat > 0.8	+	Known	—
chr7:142575532–142578146	H19	–	–	mat > 0.99	Known	—
chr7:142650768–142658804	Igf2	–	mat > 0.55	pat > 0.8	Known	—
chr7:143107254–143427042	Kcnq1	–	–	pat > 0.99	Known	—
chr7:143458339–143461050	Cdkn1c	–	–	mat > 0.95	Known	—
chr9:89909775–90026979	Rasgrf1	–	pat > 0.95	–	Known	—
chr10:13090788–13131695	Plagl1	–	pat > 0.99	pat > 0.99	Known	—
chr11:11814101–11890408	Ddc	+	mat > 0.55	–	Known	—
chr11:11930499–12037420	Grb10	–	pat > 0.95	mat > 0.95	Known	—
chr11:22972005–22976496	Zrsr1	pat > 0.95	pat > 0.95	pat > 0.95	Known	—
chr11:22899728–22982284	Commd1/Murr	+	mat > 0.85	+	Known	—
chr12:108860030–108893211	Wars	+	pat > 0.55	+	Known[a,b]	—
chr12:109032182–109068217	Begain	–	pat > 0.75	–	Known	—
chr12:109453455–109463336	Dlk1	–	pat > 0.95	–	Known	—
chr12:109542023–109568594	Meg3	–	mat > 0.95	mat > 0.95	Known	—
chr12:109589193–109600330	Rtl1	–	mat > 0.8	–	Known	—
chr12:109603945–109661711	Rian	–	mat > 0.99	mat > 0.99	Known	—
chr12:109734825–109749457	Mirg	–	mat > 0.99	–	Known	—
chr13:107413865–107414767	ENSMUST00000061241	mat > 0.65	mat > 0.65	+	New	
chr15:72506991–72508007	AK039650	–	mat > 0.95	–	Known[a]	—
chr15:72589620–73061204	Trappc9	+	mat > 0.7	+	Known	—
chr15:72805600–72810324	Peg13	pat > 0.99	pat > 0.99	pat > 0.99	Known	5
chr15:73098490–73099318	DQ715667	–	mat > 0.7	+	Known[a]	—
chr15:73101625–73184947	Eif2c2	+	mat > 0.7	+	Known[a]	—
chr17:77674376–77674702	ENSMUST00000168236	mat > 0.55	mat > 0.55	mat > 0.6	New	—
chr18:12972252–12992948	Impact	pat > 0.8	pat > 0.95	pat > 0.75	Known	—

NOTE.—Expression status is designed as "+" when expressed but not imprinted in a given tissue, as "–" when not expressed, and as the degree of maternal (mat) or paternal (pat) bias when imprinted. Chromosomal regions with clustered transcripts are separated by horizontal lines.

[a] First described by DeVeale et al. (2012).

[b] Confirmed by pyrosequencing in DeVeale et al. (2012).

[c] Confirmed by pyrosequencing in this study.