

Supplemental Table S2
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr1:33428882-33429004	<i>Prim2</i>	185387	C57BL/6	intra	A_51_P338998	0.0513 (P)	0.0448 (P)	0.0738 (P)	0.998 (P)	0.707 (P)	0.836 (P)
chr1:33476141-33476727	<i>Prim2</i>	137896	C57BL/6	intra	A_51_P338998	0.0513 (P)	0.0448 (P)	0.0738 (P)	0.998 (P)	0.707 (P)	0.836 (P)
chr1:33499231-33499713	<i>Prim2</i>	114858	C57BL/6	intra	A_51_P338998	0.0513 (P)	0.0448 (P)	0.0738 (P)	0.998 (P)	0.707 (P)	0.836 (P)
chr1:33585109-33585169	<i>Prim2</i>	29191	BALB/c	intra	A_51_P338998	0.0513 (P)	0.0448 (P)	0.0738 (P)	0.998 (P)	0.707 (P)	0.836 (P)
chr1:33600588-33600898	<i>Prim2</i>	13587	C57BL/6	intra	A_51_P338998	0.0513 (P)	0.0448 (P)	0.0738 (P)	0.998 (P)	0.707 (P)	0.836 (P)
chr1:38834245-38834666	<i>Chst10</i>	8250	C57BL/6	intra	A_51_P445562	35.28 (P)	20.88 (P)	35.87 (P)	1 (P)	0.909 (P)	0.791 (P)
chr1:57749504-57749558	<i>2810022L02Rik</i>	30090	BALB/c	intra	A_52_P538470	10.77 (P)	11.78 (P)	2.183 (A)	0.999 (A)	0.941 (A)	1.051 (A)
chr1:58749011-58749071	<i>Casp8</i>	9056	BALB/c	intra	A_51_P247799	0.996 (P)	0.945 (P)	0.967 (P)	0.998 (P)	1.322 (P)	1.211 (P)
chr1:58777847-58778072	<i>Casp8</i>	22913	C57BL/6	intra	A_51_P247799	0.996 (P)	0.945 (P)	0.967 (P)	0.998 (P)	1.322 (P)	1.211 (P)
chr1:109401592-109402066	<i>Serpinc8</i>	-15747	C57BL/6	distal	A_52_P544885	1.48 (P)	0.478 (P)	1.357 (P)	0.995 (P)	0.401 (P)	1.026 (P)
chr1:122290855-122291258	<i>Marco</i>	41273	BALB/c	distal	A_51_P371750	0.0779 (P)	0.0956 (P)	0.0863 (P)	1 (P)	0.81 (P)	0.352 (P)
chr1:122308958-122309018	<i>Marco</i>	23317	C57BL/6	intra	A_51_P371750	0.0779 (P)	0.0956 (P)	0.0863 (P)	1 (P)	0.81 (P)	0.352 (P)
chr1:122371709-122371770	<i>Marco</i>	-39434	C57BL/6	distal	A_51_P371750	0.0779 (P)	0.0956 (P)	0.0863 (P)	1 (P)	0.81 (P)	0.352 (P)
chr1:133539104-133539235	<i>5430435G22Rik</i>	21915	BALB/c	intra	A_52_P244682	0.0695 (P)	0.0194 (P)	0.0432 (P)	0.995 (P)	0.25 (P)	0.604 (P)
chr1:133540665-133540799	<i>5430435G22Rik</i>	20352	C57BL/6	intra	A_52_P244682	0.0695 (P)	0.0194 (P)	0.0432 (P)	0.995 (P)	0.25 (P)	0.604 (P)
chr1:133553009-133553065	<i>Slc26a9</i>	-18531	BALB/c	distal	A_52_P258557	0.561 (A)	0.354 (A)	0.223 (A)	0.991 (P)	0.489 (P.A)	0.51 (P)
chr1:133559814-133559910	<i>Slc26a9</i>	-11706	BALB/c	distal	A_52_P258557	0.561 (A)	0.354 (A)	0.223 (A)	0.991 (P)	0.489 (P.A)	0.51 (P)
chr1:157549961-157550607	<i>Qsox1</i>	24770	C57BL/6	intra	A_52_P302304	9.433 (P)	16.4 (P)	11.21 (P)	0.992 (P)	1.55 (P)	1.319 (P)
chr1:157554929-157555080	<i>Qsox1</i>	20050	C57BL/6	intra	A_52_P302304	9.433 (P)	16.4 (P)	11.21 (P)	0.992 (P)	1.55 (P)	1.319 (P)
chr1:157577435-157577492	<i>Qsox1</i>	-2409	BALB/c	distal	A_52_P302304	9.433 (P)	16.4 (P)	11.21 (P)	0.992 (P)	1.55 (P)	1.319 (P)
chr1:161072415-161072474	<i>Rfwd2</i>	3230	BALB/c	intra	A_51_P411598	0.0874 (P)	0.088 (P)	0.0779 (P)	0.987 (P)	0.871 (P)	0.912 (P)
chr1:161132832-161133097	<i>Rfwd2</i>	63750	C57BL/6	intra	A_51_P411598	0.0874 (P)	0.088 (P)	0.0779 (P)	0.987 (P)	0.871 (P)	0.912 (P)
chr1:161154201-161154255	<i>Rfwd2</i>	85013	BALB/c	intra	A_51_P411598	0.0874 (P)	0.088 (P)	0.0779 (P)	0.987 (P)	0.871 (P)	0.912 (P)
chr1:161173713-161173898	<i>Rfwd2</i>	104591	C57BL/6	intra	A_51_P411598	0.0874 (P)	0.088 (P)	0.0779 (P)	0.987 (P)	0.871 (P)	0.912 (P)
chr1:161181010-161181534	<i>Rfwd2</i>	112057	C57BL/6	intra	A_51_P411598	0.0874 (P)	0.088 (P)	0.0779 (P)	0.987 (P)	0.871 (P)	0.912 (P)
chr1:161220409-161220798	<i>Rfwd2</i>	151389	BALB/c	distal	A_51_P411598	0.0874 (P)	0.088 (P)	0.0779 (P)	0.987 (P)	0.871 (P)	0.912 (P)
chr1:173418157-173418737	<i>Cd244</i>	22591	BALB/c	intra	A_51_P205209	0.122 (P)	0.0895 (P)	0.0947 (P)	0.987 (P)	0.908 (P)	0.325 (P)
chr1:173424681-173424758	<i>Ly9</i>	19253	BALB/c	distal	A_51_P497171	0.851 (P)	0.728 (P)	0.604 (P)	0.995 (P)	1.581 (P)	1.351 (P)
chr1:173434392-173434437	<i>Ly9</i>	9610	C57BL/6	intra	A_51_P497171	0.851 (P)	0.728 (P)	0.604 (P)	0.995 (P)	1.581 (P)	1.351 (P)
chr1:173472612-173472668	<i>Slamf7</i>	13042	BALB/c	intra	A_52_P429609	0.17 (P)	0.0779 (P)	0.0585 (P)	0.999 (P)	0.823 (P)	0.778 (P)
chr1:173480500-173480622	<i>Slamf7</i>	5087	BALB/c	intra	A_52_P429609	0.17 (P)	0.0779 (P)	0.0585 (P)	0.999 (P)	0.823 (P)	0.778 (P)
chr1:173509929-173510843	<i>Cd48</i>	-8269	C57BL/6	distal	A_52_P460230	0.953 (P)	0.591 (P)	0.627 (P)	0.999 (P)	0.872 (P)	1.008 (P)
chr1:173521917-173521962	<i>Cd48</i>	3199	BALB/c	intra	A_52_P460230	0.953 (P)	0.591 (P)	0.627 (P)	0.999 (P)	0.872 (P)	1.008 (P)
chr10:6828900-6829688	<i>Iyd</i>	-23023	C57BL/6	distal	A_51_P411200	1.207 (A)	1.103 (A)	1.287 (A)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:7018786-7019486	<i>Ppp1r14c</i>	-39141	C57BL/6	distal	A_51_P124741	0.0184 (A)	0.0205 (P.A)	0.0135 (A)	1 (P)	0.663 (P)	0.914 (P)
chr10:7456811-7457022	<i>BC013529</i>	14178	C57BL/6	distal	A_52_P267543	0.781 (P)	0.693 (P)	0.649 (P)	0.993 (P)	0.957 (P)	0.931 (P)
chr10:7465903-7466014	<i>BC013529</i>	5136	BALB/c	intra	A_52_P267543	0.781 (P)	0.693 (P)	0.649 (P)	0.993 (P)	0.957 (P)	0.931 (P)
chr10:7554662-7554765	<i>Zc3h12d</i>	32081	C57BL/6	intra	A_52_P648688	0.0925 (P)	0.0513 (P)	0.044 (P)	0.999 (P)	0.574 (P)	0.557 (P)

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chr10:7556446-7556491	<i>Zc3h12d</i>	33836	BALB/c	intra	A_52_P648688	0.0925 (P)	0.0513 (P)	0.044 (P)	0.999 (P)	0.574 (P)	0.557 (P)
chr10:8453154-8453214	<i>Sash1</i>	123059	BALB/c	intra	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:8499529-8500702	<i>Sash1</i>	76127	BALB/c	intra	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:8516559-8516781	<i>Sash1</i>	59572	BALB/c	intra	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:8533747-8533799	<i>Sash1</i>	42469	C57BL/6	intra	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:8565556-8566318	<i>Sash1</i>	10305	BALB/c	intra	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:8569257-8569687	<i>Sash1</i>	6770	C57BL/6	intra	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:8600425-8600804	<i>Sash1</i>	-24372	BALB/c	distal	A_51_P245875	1.302 (P)	0.555 (P.A)	0.423 (A)	0.994 (P)	1.001 (P)	0.521 (P)
chr10:18209707-18210091	<i>Nhs1</i>	-6409	C57BL/6	distal	A_51_P332169	1.503 (P)	1.627 (P)	1.856 (P)	0.966 (P)	1.748 (P)	1.108 (P)
chr10:18262232-18262290	<i>Hebp2</i>	-26769	C57BL/6	distal	A_51_P159612	21.81 (P)	38.89 (P)	58.11 (P)	1 (P)	15.46 (P)	29.42 (P)
chr10:18264292-18264337	<i>Hebp2</i>	-28823	C57BL/6	distal	A_51_P159612	21.81 (P)	38.89 (P)	58.11 (P)	1 (P)	15.46 (P)	29.42 (P)
chr10:84777151-84777599	<i>Btbd11</i>	-40634	BALB/c	distal	A_51_P217509	0.151 (A)	0.365 (P.A)	0.152 (A)	0.96 (P)	0.847 (P)	1.01 (P)
chr10:84813063-84813163	<i>Btbd11</i>	-4896	C57BL/6	distal	A_51_P217509	0.151 (A)	0.365 (P.A)	0.152 (A)	0.96 (P)	0.847 (P)	1.01 (P)
chr10:85015114-85015305	<i>Btbd11</i>	-13052	C57BL/6	intra	A_51_P217509	0.151 (A)	0.365 (P.A)	0.152 (A)	0.96 (P)	0.847 (P)	1.01 (P)
chr10:85038563-85039091	<i>Btbd11</i>	10566	BALB/c	intra	A_51_P217509	0.151 (A)	0.365 (P.A)	0.152 (A)	0.96 (P)	0.847 (P)	1.01 (P)
chr10:85073454-85073867	<i>Btbd11</i>	45451	BALB/c	intra	A_51_P217509	0.151 (A)	0.365 (P.A)	0.152 (A)	0.96 (P)	0.847 (P)	1.01 (P)
chr10:85077536-85077897	<i>Btbd11</i>	49507	C57BL/6	intra	A_51_P217509	0.151 (A)	0.365 (P.A)	0.152 (A)	0.96 (P)	0.847 (P)	1.01 (P)
chr10:88105615-88105792	<i>Spic</i>	7119	BALB/c	intra	A_52_P361323	6.522 (P)	5.929 (P)	3.593 (P)	0.991 (P)	1.012 (P)	0.376 (P)
chr10:92874018-92874212	<i>Lta4h</i>	-9106	C57BL/6	distal	A_51_P101955	1.032 (P)	0.857 (P)	1.232 (P)	1 (P)	0.967 (P)	1.334 (P)
chr10:92886703-92886763	<i>Lta4h</i>	3512	BALB/c	intra	A_51_P101955	1.032 (P)	0.857 (P)	1.232 (P)	1 (P)	0.967 (P)	1.334 (P)
chr10:92893443-92893580	<i>Lta4h</i>	10290	BALB/c	intra	A_51_P101955	1.032 (P)	0.857 (P)	1.232 (P)	1 (P)	0.967 (P)	1.334 (P)
chr10:92894786-92895269	<i>Lta4h</i>	11806	C57BL/6	intra	A_51_P101955	1.032 (P)	0.857 (P)	1.232 (P)	1 (P)	0.967 (P)	1.334 (P)
chr10:92900457-92900512	<i>Lta4h</i>	17263	BALB/c	intra	A_51_P101955	1.032 (P)	0.857 (P)	1.232 (P)	1 (P)	0.967 (P)	1.334 (P)
chr10:92912661-92912967	<i>Lta4h</i>	29592	C57BL/6	intra	A_51_P101955	1.032 (P)	0.857 (P)	1.232 (P)	1 (P)	0.967 (P)	1.334 (P)
chr10:92916395-92916703	<i>Hal</i>	-2318	C57BL/6	distal	A_51_P172155	1293 (P)	647.5 (P)	1155 (P)	0.997 (P.A)	0.68 (P.A)	1.318 (P)
chr10:92931309-92931538	<i>Hal</i>	12556	C57BL/6	intra	A_51_P172155	1293 (P)	647.5 (P)	1155 (P)	0.997 (P.A)	0.68 (P.A)	1.318 (P)
chr10:92947751-92947804	<i>Hal</i>	28910	C57BL/6	distal	A_51_P172155	1293 (P)	647.5 (P)	1155 (P)	0.997 (P.A)	0.68 (P.A)	1.318 (P)
chr10:93014816-93014876	<i>Ccdc38</i>	44415	C57BL/6	intra	A_51_P127507	1.207 (A)	1.103 (A)	1.283 (A)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:104598765-104598953	<i>Tmtc2</i>	379702	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104626764-104627103	<i>Tmtc2</i>	351627	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104634539-104634758	<i>Tmtc2</i>	343912	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104635908-104635968	<i>Tmtc2</i>	342623	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104671761-104672161	<i>Tmtc2</i>	306600	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104706006-104706340	<i>Tmtc2</i>	272388	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104747765-104747995	<i>Tmtc2</i>	230681	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104759614-104759674	<i>Tmtc2</i>	218917	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104789057-104789197	<i>Tmtc2</i>	189434	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104839643-104839694	<i>Tmtc2</i>	138892	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)

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chr10:104840547-104840607	<i>Tmtc2</i>	137984	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104840635-104840749	<i>Tmtc2</i>	137869	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104842784-104842934	<i>Tmtc2</i>	135702	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104883498-104883558	<i>Tmtc2</i>	95033	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104927384-104927444	<i>Tmtc2</i>	51147	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104951824-104951878	<i>Tmtc2</i>	26710	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104968996-104969374	<i>Tmtc2</i>	9376	C57BL/6	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:104976330-104976386	<i>Tmtc2</i>	2203	BALB/c	intra	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:105001660-105002240	<i>Tmtc2</i>	-23389	C57BL/6	distal	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:105014390-105014549	<i>Tmtc2</i>	-35909	C57BL/6	distal	A_51_P288916	0.0226 (P.A)	0.0232 (P.A)	0.0222 (A)	0.993 (P)	0.484 (P)	0.664 (P)
chr10:122672434-122672816	<i>Fam19a2</i>	4571	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122708405-122708511	<i>Fam19a2</i>	40404	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122710469-122710529	<i>Fam19a2</i>	42445	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122822800-122823015	<i>Fam19a2</i>	154853	BALB/c	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122827614-122827671	<i>Fam19a2</i>	159588	BALB/c	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122849206-122849328	<i>Fam19a2</i>	181213	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122858308-122858831	<i>Fam19a2</i>	190515	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122859610-122860125	<i>Fam19a2</i>	191813	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122868108-122868477	<i>Fam19a2</i>	200238	BALB/c	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122904978-122905047	<i>Fam19a2</i>	236958	BALB/c	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:122957032-122957347	<i>Fam19a2</i>	289135	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:123131977-123132288	<i>Fam19a2</i>	464078	BALB/c	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr10:123135244-123135391	<i>Fam19a2</i>	467263	C57BL/6	intra	A_51_P317620	69.92 (P)	38.73 (P)	14.5 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr11:3092678-3093978	<i>Sfi1</i>	117	BALB/c	prom	A_52_P389274	16.38 (P)	14.46 (P)	11.82 (P)	0.974 (P)	0.984 (P)	0.783 (P)
chr11:3128842-3128985	<i>Eif4enif1</i>	18782	C57BL/6	intra	A_52_P1115466	1.48 (P)	1.256 (P)	1.054 (P)	0.957 (P)	0.962 (P)	0.997 (P)
chr11:5857646-5857691	<i>Ykt6</i>	1853	C57BL/6	intra	A_52_P583155	1.141 (P)	1.268 (P)	1.144 (P)	0.973 (P)	1.374 (P)	1.345 (P)
chr11:5911639-5911781	<i>Camk2b</i>	54041	BALB/c	intra	A_51_P318933	0.0639 (A)	0.0785 (A)	0.0636 (A)	0.992 (P)	0.98 (P)	1.54 (P)
chr11:5932196-5932242	<i>Camk2b</i>	33532	C57BL/6	intra	A_51_P318933	0.0639 (A)	0.0785 (A)	0.0636 (A)	0.992 (P)	0.98 (P)	1.54 (P)
chr11:46600295-46600496	<i>Havcr1</i>	16749	C57BL/6	intra	A_51_P371740	0.19 (A)	0.507 (P.A)	0.541 (P)	0.806 (P)	0.287 (P)	0.165 (P.A)
chr11:46707379-46707893	<i>Timd4</i>	53413	BALB/c	distal	A_52_P609868	8.529 (P)	6.422 (P)	4.34 (P)	0.967 (P.A)	0.844 (P.A)	0.771 (P.A)
chr11:88799550-88799596	<i>Coil</i>	9534	BALB/c	intra	A_51_P483839	0.682 (P)	0.906 (P)	0.763 (P)	0.999 (P)	0.83 (P)	0.788 (P)
chr11:88801073-88801240	<i>Coil</i>	11118	BALB/c	intra	A_51_P483839	0.682 (P)	0.906 (P)	0.763 (P)	0.999 (P)	0.83 (P)	0.788 (P)
chr11:88804568-88804628	<i>Coil</i>	14559	BALB/c	intra	A_51_P483839	0.682 (P)	0.906 (P)	0.763 (P)	0.999 (P)	0.83 (P)	0.788 (P)
chr11:90494121-90494462	<i>Tom11</i>	9399	BALB/c	intra	A_51_P299866	6.307 (P)	3.763 (P)	3.706 (P)	0.998 (P)	0.673 (P)	0.616 (P)
chr11:90523839-90524032	<i>Tom11</i>	-20266	C57BL/6	distal	A_51_P299866	6.307 (P)	3.763 (P)	3.706 (P)	0.998 (P)	0.673 (P)	0.616 (P)
chr11:90527633-90527930	<i>Tom11</i>	-24112	BALB/c	distal	A_51_P299866	6.307 (P)	3.763 (P)	3.706 (P)	0.998 (P)	0.673 (P)	0.616 (P)
chr11:90538382-90538517	<i>Tom11</i>	-34780	BALB/c	distal	A_51_P299866	6.307 (P)	3.763 (P)	3.706 (P)	0.998 (P)	0.673 (P)	0.616 (P)
chr11:90543530-90543948	<i>Tom11</i>	-40070	C57BL/6	distal	A_51_P299866	6.307 (P)	3.763 (P)	3.706 (P)	0.998 (P)	0.673 (P)	0.616 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe_ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr11:90546847-90546916	<i>Tom11l</i>	-43212	BALB/c	distal	A_51_P299866	6.307 (P)	3.763 (P)	3.706 (P)	0.998 (P)	0.673 (P)	0.616 (P)
chr12:15770109-15770577	<i>Trib2</i>	71992	C57BL/6	distal	A_52_P220810	0.0942 (A)	0.13 (A)	0.13 (A)	0.891 (P)	2.108 (P)	2.32 (P)
chr12:15784239-15784299	<i>Trib2</i>	58066	BALB/c	distal	A_52_P220810	0.0942 (A)	0.13 (A)	0.13 (A)	0.891 (P)	2.108 (P)	2.32 (P)
chr12:15823593-15823638	<i>Trib2</i>	18719	BALB/c	intra	A_52_P220810	0.0942 (A)	0.13 (A)	0.13 (A)	0.891 (P)	2.108 (P)	2.32 (P)
chr12:15826824-15826870	<i>Trib2</i>	15488	BALB/c	intra	A_52_P220810	0.0942 (A)	0.13 (A)	0.13 (A)	0.891 (P)	2.108 (P)	2.32 (P)
chr12:45187434-45187920	<i>Nrcam</i>	-11597	C57BL/6	distal	A_51_P306247	42.4 (P)	62.66 (P)	46.83 (P)	0.942 (P)	2.449 (P)	1.539 (P)
chr12:45213241-45213388	<i>Nrcam</i>	14081	C57BL/6	intra	A_51_P306247	42.4 (P)	62.66 (P)	46.83 (P)	0.942 (P)	2.449 (P)	1.539 (P)
chr12:79919494-79919852	<i>6330442E10Rik</i>	6,444	C57BL/6	intra	A_52_P220783	0.944 (P)	0.755 (P)	0.55 (P)	0.998 (P)	1.048 (P)	0.69 (P)
chr12:79968891-79969672	<i>Plekhh1</i>	21248	C57BL/6	intra	A_51_P287617	5.628 (P)	2.767 (P)	1.726 (P)	0.998 (P)	3.051 (P)	1.466 (P)
chr12:79994386-79994739	<i>Plekhh1</i>	46529	C57BL/6	intra	A_51_P287617	5.628 (P)	2.767 (P)	1.726 (P)	0.998 (P)	3.051 (P)	1.466 (P)
chr12:79995677-79995722	<i>Plekhh1</i>	47666	BALB/c	intra	A_51_P287617	5.628 (P)	2.767 (P)	1.726 (P)	0.998 (P)	3.051 (P)	1.466 (P)
chr12:80002205-80002717	<i>Pigh</i>	6012	BALB/c	intra	A_52_P260516	1.281 (P)	0.796 (P)	0.657 (P.A)	0.998 (P)	1.084 (P)	0.913 (P)
chr13:56269324-56269539	<i>Neurog1</i>	-7632	C57BL/6	distal	A_51_P298790	0.756 (P)	1.002 (P)	0.844 (P)	0.979 (P)	0.988 (P)	1.208 (P)
chr13:56313994-56314118	<i>Cxcl14</i>	-7883	BALB/c	distal	A_51_P209183	17.13 (P)	11.67 (P)	8.816 (P)	0.952 (P)	0.582 (P)	0.313 (P)
chr13:56347924-56348198	<i>Cxcl14</i>	-41888	C57BL/6	distal	A_51_P209183	17.13 (P)	11.67 (P)	8.816 (P)	0.952 (P)	0.582 (P)	0.313 (P)
chr13:62858842-62859176	<i>Fbp2</i>	8984	C57BL/6	intra	A_51_P499020	1.207 (A)	1.103 (A)	1.212 (A)	0.996 (A)	1.061 (A)	1.101 (A)
chr13:67930408-67930468	<i>Zfp459</i>	-10007	BALB/c	distal	A_51_P452576	7.655 (P)	18.46 (P)	8.513 (P)	0.937 (P.A)	16.26 (P)	3.322 (P)
chr13:76579670-76579730	<i>Ttc37</i>	14964	C57BL/6	intra	A_51_P373208	1.925 (P)	1.301 (P)	2.197 (P)	0.939 (P)	1.047 (P)	1.024 (P)
chr13:109314064-109314489	<i>Erccl8</i>	34792	BALB/c	intra	A_52_P471227	1.302 (P)	1.725 (P)	1.352 (P)	0.998 (P)	1.692 (P)	1.174 (P)
chr13:109326652-109326712	<i>Elov17</i>	-8496	BALB/c	distal	A_52_P354682	0.0586 (A)	0.053 (P.A)	0.135 (P)	0.996 (P)	0.528 (P)	0.933 (P)
chr13:109416087-109416140	<i>Elov17</i>	80934	C57BL/6	distal	A_52_P354682	0.0586 (A)	0.053 (P.A)	0.135 (P)	0.996 (P)	0.528 (P)	0.933 (P)
chr14:19624572-19624712	<i>Plau</i>	-570	C57BL/6	prom	A_52_P302433	20.23 (P)	20.66 (P)	12.96 (P)	0.974 (P)	1.459 (P)	0.912 (P)
chr14:50788103-50788154	<i>Ear6</i>	12478	C57BL/6	distal	A_52_P157726	0.863 (A)	1.668 (A)	18.53 (P)	0.996 (A)	4.279 (P)	56.62 (P)
chr14:50809903-50810041	<i>Mett11d1</i>	3091	C57BL/6	intra	A_51_P465273	1.097 (P)	1.126 (P)	0.945 (P)	1 (P)	1.378 (P)	1.159 (P)
chr14:50884020-50884348	<i>E130112L23Rik</i>	-22665	BALB/c	distal	A_52_P251615	1.953 (P)	1.757 (P)	1.368 (P)	0.99 (P)	0.841 (P)	0.577 (P)
chr14:51053374-51053423	<i>Rpgrip1</i>	20526	BALB/c	intra	A_52_P507488	0.21 (P)	0.157 (P)	0.157 (P)	1 (P)	1.19 (P)	1.146 (P)
chr14:51060437-51060883	<i>Rpgrip1</i>	27787	C57BL/6	intra	A_52_P507488	0.21 (P)	0.157 (P)	0.157 (P)	1 (P)	1.19 (P)	1.146 (P)
chr14:51081511-51082058	<i>Rpgrip1</i>	48912	BALB/c	intra	A_52_P507488	0.21 (P)	0.157 (P)	0.157 (P)	1 (P)	1.19 (P)	1.146 (P)
chr14:51104658-51105062	<i>Supt16h</i>	14331	C57BL/6	intra	A_51_P280532	0.652 (P)	0.746 (P)	0.829 (P)	0.999 (P)	0.972 (P)	0.947 (P)
chr14:65636120-65636251	<i>Adra1a</i>	46761	BALB/c	intra	A_52_P424778	5.283 (P)	1.378 (P)	1.222 (P)	0.999 (P)	0.187 (A)	0.174 (A)
chr14:65651727-65652060	<i>Adra1a</i>	39645	BALB/c	intra	A_52_P424778	5.283 (P)	1.378 (P)	1.222 (P)	0.999 (P)	0.187 (A)	0.174 (A)
chr14:65710648-65711641	<i>Adra1a</i>	121777	C57BL/6	distal	A_52_P424778	5.283 (P)	1.378 (P)	1.222 (P)	0.999 (P)	0.187 (A)	0.174 (A)
chr14:78033582-78034116	<i>1190002H23Rik</i>	1941	C57BL/6	intra	A_51_P226269	0.0526 (P)	0.0628 (P.A)	0.153 (P)	0.994 (P)	0.493 (P)	0.972 (P)
chr14:78037674-78038068	<i>1190002H23Rik</i>	-2081	BALB/c	distal	A_51_P226269	0.0526 (P)	0.0628 (P.A)	0.153 (P)	0.994 (P)	0.493 (P)	0.972 (P)
chr14:78042149-78042203	<i>1190002H23Rik</i>	-6386	BALB/c	distal	A_51_P226269	0.0526 (P)	0.0628 (P.A)	0.153 (P)	0.994 (P)	0.493 (P)	0.972 (P)
chr15:74776186-74776280	<i>Ly6e</i>	-6670	C57BL/6	distal	A_51_P148814	1.38 (P)	1.447 (P)	0.724 (P)	0.982 (P)	1.379 (P)	0.728 (P)
chr15:74783393-74783628	<i>Ly6e</i>	607	C57BL/6	intra	A_51_P148814	1.38 (P)	1.447 (P)	0.724 (P)	0.982 (P)	1.379 (P)	0.728 (P)
chr15:74790167-74790537	<i>Ly6e</i>	7449	C57BL/6	distal	A_51_P148814	1.38 (P)	1.447 (P)	0.724 (P)	0.982 (P)	1.379 (P)	0.728 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr15:90288150-90288496	<i>Cpne8</i>	218832	C57BL/6	distal	A_51_P427563	39.53 (P)	48.38 (P)	59.57 (P)	0.924 (P)	1.123 (P)	0.967 (P)
chr15:90314666-90314836	<i>Cpne8</i>	192404	C57BL/6	distal	A_51_P427563	39.53 (P)	48.38 (P)	59.57 (P)	0.924 (P)	1.123 (P)	0.967 (P)
chr15:90335420-90335501	<i>Cpne8</i>	171694	C57BL/6	intra	A_51_P427563	39.53 (P)	48.38 (P)	59.57 (P)	0.924 (P)	1.123 (P)	0.967 (P)
chr15:90478475-90478535	<i>Cpne8</i>	28650	C57BL/6	intra	A_51_P427563	39.53 (P)	48.38 (P)	59.57 (P)	0.924 (P)	1.123 (P)	0.967 (P)
chr16:28833304-28834357	<i>1600021P15Rik</i>	15587	C57BL/6	intra	A_52_P85893	8.062 (P)	22.48 (P)	11.8 (P)	0.998 (P)	4.831 (P)	1.653 (P)
chr16:38842237-38842369	<i>Igsf11</i>	20584	BALB/c	intra	A_52_P578581	0.314 (P.A)	0.214 (A)	0.365 (P.A)	0.984 (P)	2.145 (P)	1.204 (P)
chr16:38873534-38873736	<i>Igsf11</i>	51916	BALB/c	intra	A_52_P578581	0.314 (P.A)	0.214 (A)	0.365 (P.A)	0.984 (P)	2.145 (P)	1.204 (P)
chr16:38944175-38944451	<i>Igsf11</i>	122594	C57BL/6	intra	A_52_P578581	0.314 (P.A)	0.214 (A)	0.365 (P.A)	0.984 (P)	2.145 (P)	1.204 (P)
chr16:85665872-85665932	<i>Adamts1</i>	26409	C57BL/6	distal	A_52_P489295	30.23 (P)	12.25 (P)	19.74 (P)	0.987 (P.A)	0.661 (P.A)	1.274 (P)
chr17:3293172-3293498	<i>Tiam2</i>	10280	C57BL/6	intra	A_51_P256066	0.0958 (P)	0.0616 (P.A)	0.118 (P)	0.979 (P)	0.254 (P)	0.735 (P)
chr17:3334336-3334651	<i>Tiam2</i>	51439	C57BL/6	intra	A_51_P256066	0.0958 (P)	0.0616 (P.A)	0.118 (P)	0.979 (P)	0.254 (P)	0.735 (P)
chr17:3353108-3353259	<i>Tiam2</i>	70129	C57BL/6	intra	A_51_P256066	0.0958 (P)	0.0616 (P.A)	0.118 (P)	0.979 (P)	0.254 (P)	0.735 (P)
chr17:3355433-3355486	<i>Tiam2</i>	72405	BALB/c	intra	A_51_P256066	0.0958 (P)	0.0616 (P.A)	0.118 (P)	0.979 (P)	0.254 (P)	0.735 (P)
chr17:3359059-3359104	<i>Tiam2</i>	76027	BALB/c	intra	A_51_P256066	0.0958 (P)	0.0616 (P.A)	0.118 (P)	0.979 (P)	0.254 (P)	0.735 (P)
chr17:3360576-3360633	<i>Tiam2</i>	77550	C57BL/6	intra	A_51_P256066	0.0958 (P)	0.0616 (P.A)	0.118 (P)	0.979 (P)	0.254 (P)	0.735 (P)
chr17:3486560-3486832	<i>Tfb1m</i>	27499	C57BL/6	intra	A_51_P215324	1.298 (A)	1.117 (A)	1.019 (A)	0.984 (A)	1.076 (P.A)	1.808 (A)
chr17:3489017-3489250	<i>Tfb1m</i>	25061	C57BL/6	intra	A_51_P215324	1.298 (A)	1.117 (A)	1.019 (A)	0.984 (A)	1.076 (P.A)	1.808 (A)
chr17:3505060-3505778	<i>Tfb1m</i>	8776	C57BL/6	intra	A_51_P215324	1.298 (A)	1.117 (A)	1.019 (A)	0.984 (A)	1.076 (P.A)	1.808 (A)
chr17:30301717-30302316	<i>Btdb9</i>	1252	C57BL/6	intra	A_52_P542860	11.81 (P)	11.91 (P)	10.83 (P)	0.995 (P)	1.257 (P)	1.22 (P)
chr17:30462176-30462337	<i>Dnahc8</i>	108309	C57BL/6	intra	A_51_P326631	4.678 (P)	6.926 (P)	14.15 (P)	0.996 (P)	1.919 (P)	1.858 (P)
chr17:33787792-33788060	<i>Psmb9</i>	9701	C57BL/6	distal	A_51_P369803	0.992 (P)	1.061 (P)	0.748 (P)	0.994 (P)	1.07 (P)	0.656 (P)
chr17:33914667-33915150	<i>H2-Eb1</i>	1311	C57BL/6	intra	A_51_P393226	1.578 (P)	1.823 (P)	1.974 (P)	0.997 (P)	1.085 (P)	1.507 (P)
chr17:33917083-33917555	<i>H2-Eb1</i>	3722	C57BL/6	intra	A_51_P393226	1.578 (P)	1.823 (P)	1.974 (P)	0.997 (P)	1.085 (P)	1.507 (P)
chr17:33948318-33948367	<i>H2-Ea</i>	3883	C57BL/6	distal	A_51_P222741	319.1 (P)	319.9 (P)	402.8 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:34637963-34638443	<i>Msh5</i>	16475	C57BL/6	intra	A_52_P326240	56.31 (P)	50.51 (P)	39.06 (P)	0.994 (P)	1.019 (P)	0.666 (P)
chr17:43287601-43287829	<i>Rcan2</i>	22720	C57BL/6	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43292477-43292537	<i>Rcan2</i>	27512	C57BL/6	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43295716-43295900	<i>Rcan2</i>	30813	C57BL/6	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43343826-43344046	<i>Rcan2</i>	78941	BALB/c	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43395146-43395209	<i>Rcan2</i>	130182	BALB/c	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43417114-43417163	<i>Rcan2</i>	152233	C57BL/6	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43475365-43475425	<i>Rcan2</i>	210489	BALB/c	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43485699-43486569	<i>Rcan2</i>	221228	BALB/c	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr17:43490290-43490887	<i>Rcan2</i>	225683	BALB/c	intra	A_52_P414464	17.43 (P)	6.779 (P)	19.66 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr18:9209850-9210313	<i>Fzd8</i>	-2080	C57BL/6	distal	A_51_P312517	5.553 (P)	5.943 (P)	4.713 (P)	0.937 (P)	0.956 (P)	0.574 (P.A)
chr18:9214393-9214977	<i>Fzd8</i>	2524	C57BL/6	intra	A_51_P312517	5.553 (P)	5.943 (P)	4.713 (P)	0.937 (P)	0.956 (P)	0.574 (P.A)
chr18:58681880-58682279	<i>Slc27a6</i>	470	C57BL/6	intra	A_51_P211616	8.848 (P)	10.22 (P)	30.23 (P)	0.997 (A)	0.909 (A)	2.456 (P)
chr18:58686133-58686695	<i>Slc27a6</i>	4805	C57BL/6	intra	A_51_P211616	8.848 (P)	10.22 (P)	30.23 (P)	0.997 (A)	0.909 (A)	2.456 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe_ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr19:5687110-5687363	<i>Pcnxl3</i>	1437	BALB/c	intra	A_51_P487892	1.089 (P)	1.138 (P)	1.101 (P)	0.995 (P)	0.888 (P)	0.956 (P)
chr19:10054676-10054898	<i>Best1</i>	13891	BALB/c	intra	A_51_P508781	0.111 (P)	0.142 (P)	0.19 (P)	0.997 (P)	0.71 (P)	0.826 (P)
chr19:10059640-10059975	<i>Best1</i>	8870	C57BL/6	intra	A_51_P508781	0.111 (P)	0.142 (P)	0.19 (P)	0.997 (P)	0.71 (P)	0.826 (P)
chr19:17402472-17402791	<i>Gcnt1</i>	21004	C57BL/6	intra	A_52_P21550	0.0663 (P)	0.0708 (P)	0.0554 (P)	0.994 (P)	0.862 (P)	0.853 (P)
chr19:17411445-17411968	<i>Gcnt1</i>	11929	BALB/c	intra	A_52_P21550	0.0663 (P)	0.0708 (P)	0.0554 (P)	0.994 (P)	0.862 (P)	0.853 (P)
chr19:17417594-17417742	<i>Gcnt1</i>	5968	BALB/c	intra	A_52_P21550	0.0663 (P)	0.0708 (P)	0.0554 (P)	0.994 (P)	0.862 (P)	0.853 (P)
chr19:17424366-17424594	<i>Gcnt1</i>	-844	C57BL/6	prom	A_52_P21550	0.0663 (P)	0.0708 (P)	0.0554 (P)	0.994 (P)	0.862 (P)	0.853 (P)
chr19:24146132-24146183	<i>Tjp2</i>	94987	BALB/c	distal	A_52_P679101	0.0519 (P)	0.0503 (P)	0.0802 (P)	0.974 (P)	0.65 (P)	1.109 (P)
chr19:24221222-24221543	<i>Tjp2</i>	19762	C57BL/6	intra	A_52_P679101	0.0519 (P)	0.0503 (P)	0.0802 (P)	0.974 (P)	0.65 (P)	1.109 (P)
chr19:24229262-24229401	<i>Tjp2</i>	11813	BALB/c	intra	A_52_P679101	0.0519 (P)	0.0503 (P)	0.0802 (P)	0.974 (P)	0.65 (P)	1.109 (P)
chr19:24310167-24310227	<i>Tjp2</i>	-69052	C57BL/6	distal	A_52_P679101	0.0519 (P)	0.0503 (P)	0.0802 (P)	0.974 (P)	0.65 (P)	1.109 (P)
chr19:24331447-24331788	<i>Fxn</i>	16065	BALB/c	intra	A_52_P329256	0.85 (P)	1.005 (P)	1.193 (P)	0.999 (P)	0.955 (P)	0.865 (P)
chr19:24337430-24337560	<i>Fxn</i>	10188	BALB/c	intra	A_52_P329256	0.85 (P)	1.005 (P)	1.193 (P)	0.999 (P)	0.955 (P)	0.865 (P)
chr19:25277140-25278032	<i>Kank1</i>	-26713	BALB/c	distal	A_51_P338705	20.66 (P)	5.575 (P)	7.342 (P)	0.912 (P.A)	0.355 (P.A)	0.576 (P.A)
chr19:25346036-25346164	<i>Kank1</i>	41801	C57BL/6	intra	A_51_P338705	20.66 (P)	5.575 (P)	7.342 (P)	0.912 (P.A)	0.355 (P.A)	0.576 (P.A)
chr19:25390590-25390638	<i>Kank1</i>	86315	C57BL/6	intra	A_51_P338705	20.66 (P)	5.575 (P)	7.342 (P)	0.912 (P.A)	0.355 (P.A)	0.576 (P.A)
chr19:25499075-25499142	<i>Kank1</i>	194810	BALB/c	intra	A_51_P338705	20.66 (P)	5.575 (P)	7.342 (P)	0.912 (P.A)	0.355 (P.A)	0.576 (P.A)
chr19:25499563-25499613	<i>Kank1</i>	195289	BALB/c	intra	A_51_P338705	20.66 (P)	5.575 (P)	7.342 (P)	0.912 (P.A)	0.355 (P.A)	0.576 (P.A)
chr19:47809044-47809476	<i>6330577E15Rik</i>	24168	BALB/c	intra	A_51_P437188	1.013 (P)	0.989 (P)	1.068 (P)	1 (P)	0.859 (P)	0.905 (P)
chr19:47919990-47920050	<i>Gsto2</i>	906	BALB/c	intra	A_51_P396852	0.946 (P)	0.898 (P)	1.006 (P)	0.996 (P)	1.026 (P)	1.08 (P)
chr19:47932361-47932413	<i>Gsto2</i>	13274	BALB/c	intra	A_51_P396852	0.946 (P)	0.898 (P)	1.006 (P)	0.996 (P)	1.026 (P)	1.08 (P)
chr19:47956327-47956551	<i>Itrip1</i>	16171	C57BL/6	intra							
chr19:47958144-47958529	<i>Itrip1</i>	14273	C57BL/6	intra							
chr19:47961787-47962003	<i>Itrip1</i>	10715	BALB/c	intra							
chr2:118831692-118831737	<i>Fam82a2</i>	16679	C57BL/6	intra	A_52_P333749	1.389 (P)	2.232 (P)	1.463 (P)	0.968 (P)	2.362 (P)	1.351 (P)
chr2:118870105-118870259	<i>Dnajc17</i>	30033	C57BL/6	intra	A_52_P521419	1.771 (P)	2.002 (P)	1.796 (P)	0.982 (P)	1.928 (P)	1.936 (P)
chr2:118921263-118922015	<i>Ppp1r14d</i>	-346	C57BL/6	prom	A_52_P40345	1.414 (A)	1.103 (A)	1.242 (A)	0.996 (A)	1.363 (A)	1.101 (A)
chr2:118931167-118931543	<i>Spint1</i>	2515	C57BL/6	intra	A_51_P341108	0.0282 (P)	0.0803 (P)	0.207 (P)	0.839 (P)	1.733 (P)	2.425 (P)
chr2:118933687-118934010	<i>Spint1</i>	5008	C57BL/6	intra	A_51_P341108	0.0282 (P)	0.0803 (P)	0.207 (P)	0.839 (P)	1.733 (P)	2.425 (P)
chr2:120043669-120043809	<i>Vps39</i>	823	BALB/c	intra	A_52_P274184	1.379 (P)	1.176 (P)	1.129 (P)	1 (P)	1.18 (P)	1.181 (P)
chr2:121917801-121918164	<i>Sord</i>	-8298	C57BL/6	distal	A_51_P273596	0.147 (P)	0.131 (P)	0.152 (P)	0.971 (P)	1.075 (P)	1.191 (P)
chr2:129008854-129009320	<i>Il1a</i>	-7674	C57BL/6	distal	A_52_P100926	1.584 (A)	1.103 (A)	1.252 (A)	0.996 (A)	1.061 (A)	1.101 (A)
chr2:129060442-129060527	<i>Il1b</i>	2076	BALB/c	intra	A_51_P212782	10.84 (P)	1.819 (P)	1.285 (P)	0.997 (P)	0.416 (P.M)	0.41 (M)
chr2:129084712-129085352	<i>Il1b</i>	-22452	C57BL/6	distal	A_51_P212782	10.84 (P)	1.819 (P)	1.285 (P)	0.997 (P)	0.416 (P.M)	0.41 (M)
chr2:129095204-129095388	<i>Il1b</i>	-32716	C57BL/6	distal	A_51_P212782	10.84 (P)	1.819 (P)	1.285 (P)	0.997 (P)	0.416 (P.M)	0.41 (M)
chr2:165163847-165163893	<i>Slc13a3</i>	529	BALB/c	intra	A_51_P233768	0.0413 (P.A)	0.0331 (P.A)	0.0137 (A)	0.999 (P)	0.812 (P)	0.411 (P)
chr2:165165074-165165182	<i>Slc13a3</i>	-729	BALB/c	prom	A_51_P233768	0.0413 (P.A)	0.0331 (P.A)	0.0137 (A)	0.999 (P)	0.812 (P)	0.411 (P)
chr2:180916370-180916541	<i>9230112E08Rik</i>	2632	C57BL/6	distal	A_52_P661972	0.995 (P)	1.051 (P)	0.764 (P)	0.992 (P)	1.003 (P)	0.883 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr2:180924755-180925097	9230112E08Rik	11103	C57BL/6	distal	A_52_P661972	0.995 (P)	1.051 (P)	0.764 (P)	0.992 (P)	1.003 (P)	0.883 (P)
chr3:54505131-54505191	Postn	56122	BALB/c	distal	A_51_P489192	2.843 (P)	5.466 (P)	16.52 (P)	1 (P.A)	1.374 (P.A)	1.969 (P)
chr3:117362502-117362562	D3Bwg0562e	-10325	BALB/c	distal	A_52_P470466	20.58 (P)	9.399 (P)	22.85 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr3:117363368-117363427	D3Bwg0562e	-11190	BALB/c	distal	A_52_P470466	20.58 (P)	9.399 (P)	22.85 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr3:117378454-117378604	D3Bwg0562e	-26322	BALB/c	distal	A_52_P470466	20.58 (P)	9.399 (P)	22.85 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr3:117390058-117390183	D3Bwg0562e	-37913	BALB/c	distal	A_52_P470466	20.58 (P)	9.399 (P)	22.85 (P)	0.996 (A)	1.061 (A)	1.101 (A)
chr3:126918409-126918466	Ank2	482605	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:126932154-126932803	Ank2	468564	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:126961500-126961737	Ank2	439424	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:126964886-126964946	Ank2	436127	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:126990100-126990231	Ank2	410877	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:126997578-126997623	Ank2	403442	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127002910-127003059	Ank2	398058	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127058579-127058783	Ank2	342362	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127064288-127064344	Ank2	336727	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127115515-127116082	Ank2	285244	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127144143-127144203	Ank2	256870	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127144544-127144604	Ank2	256469	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127152673-127152718	Ank2	248347	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127157369-127157422	Ank2	243647	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127161553-127161690	Ank2	239421	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127181064-127181574	Ank2	219724	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127183561-127183610	Ank2	217457	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127204193-127204468	Ank2	196712	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127220202-127220609	Ank2	180637	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127228341-127228401	Ank2	172672	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127234728-127235174	Ank2	166092	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127242061-127242747	Ank2	158639	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127260837-127261164	Ank2	140042	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127261581-127261716	Ank2	139394	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127308653-127309047	Ank2	92193	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127347726-127347863	Ank2	53248	C57BL/6	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127384454-127384514	Ank2	16559	BALB/c	intra	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127401141-127401603	Ank2	-329	C57BL/6	prom	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127443926-127443972	Ank2	-42906	C57BL/6	distal	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127474127-127474259	Ank2	-73150	BALB/c	distal	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:127492535-127492881	Ank2	-91665	C57BL/6	distal	A_52_P137678	6.139 (P)	20.19 (P)	38.64 (P)	0.999 (P.A)	0.701 (A)	1.033 (A)
chr3:131987012-131987072	Dkk2	-35553	BALB/c	distal	A_51_P241068	8.107 (P)	2.121 (P.A)	1.483 (A)	0.99 (A)	1.343 (A)	1.038 (A)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr3:142400177-142400232	<i>Gbp5</i>	-34114	BALB/c	distal	A_52_P327664	1.205 (P)	1.169 (P)	0.22 (P)	1 (P)	1.078 (P)	0.269 (P)
chr3:142401448-142401499	<i>Gbp5</i>	-32845	BALB/c	distal	A_52_P327664	1.205 (P)	1.169 (P)	0.22 (P)	1 (P)	1.078 (P)	0.269 (P)
chr3:142548523-142548645	<i>Gbp2</i>	-9461	C57BL/6	distal	A_51_P203955	0.743 (P)	0.62 (P)	0.164 (P)	1 (P)	0.945 (P)	0.419 (P)
chr4:46555277-46556225	<i>Trim14</i>	1049	C57BL/6	intra	A_52_P252348	1.145 (P)	0.858 (P)	0.671 (P)	0.995 (P)	1.364 (P)	0.826 (P)
chr4:46594578-46596131	<i>Coro2a</i>	27636	C57BL/6	intra	A_51_P281033	0.209 (P)	0.122 (P)	0.286 (P)	0.997 (P)	1.112 (P)	0.749 (P)
chr4:46610429-46610801	<i>Coro2a</i>	12376	C57BL/6	intra	A_51_P281033	0.209 (P)	0.122 (P)	0.286 (P)	0.997 (P)	1.112 (P)	0.749 (P)
chr4:46620908-46622454	<i>Coro2a</i>	1322	C57BL/6	intra	A_51_P281033	0.209 (P)	0.122 (P)	0.286 (P)	0.997 (P)	1.112 (P)	0.749 (P)
chr4:46645788-46645910	<i>Tbc1d2</i>	25450	C57BL/6	intra	A_52_P218765	1.5 (P)	0.761 (P)	1.427 (P)	0.993 (P)	0.578 (P)	1.006 (P)
chr4:46661251-46661373	<i>Tbc1d2</i>	9966	C57BL/6	intra	A_52_P218765	1.5 (P)	0.761 (P)	1.427 (P)	0.993 (P)	0.578 (P)	1.006 (P)
chr4:66324635-66324996	<i>Tlr4</i>	10644	C57BL/6	intra	A_51_P300806	1.542 (P)	1.752 (P)	1.756 (P)	0.994 (P)	0.886 (P)	0.728 (P)
chr4:75614171-75614231	<i>Ptprd</i>	306762	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75643880-75643940	<i>Ptprd</i>	277053	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75666515-75667215	<i>Ptprd</i>	254098	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75709451-75709627	<i>Ptprd</i>	211424	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75749082-75749313	<i>Ptprd</i>	171765	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75762858-75763384	<i>Ptprd</i>	157842	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75781594-75781862	<i>Ptprd</i>	139235	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75852063-75852194	<i>Ptprd</i>	68834	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75857675-75858015	<i>Ptprd</i>	63118	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75903639-75904077	<i>Ptprd</i>	17105	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75909398-75909566	<i>Ptprd</i>	11481	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75970799-75971683	<i>Ptprd</i>	-50278	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:75998019-75998274	<i>Ptprd</i>	-77184	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:76002246-76002407	<i>Ptprd</i>	-81364	C57BL/6	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:76014633-76014693	<i>Ptprd</i>	-93700	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:76042627-76042753	<i>Ptprd</i>	-121727	BALB/c	intra	A_52_P605266	44.94 (P)	141.5 (P)	223.7 (P)	0.996 (A)	1.061 (A)	1.418 (A)
chr4:95020698-95021255	<i>Fggy</i>	-28563	C57BL/6	distal	A_52_P141141	0.15 (P)	0.117 (P)	0.117 (P)	0.98 (P)	1.262 (P)	1.344 (P)
chr4:95049158-95049994	<i>Fggy</i>	37	C57BL/6	prom	A_52_P141141	0.15 (P)	0.117 (P)	0.117 (P)	0.98 (P)	1.262 (P)	1.344 (P)
chr4:95071653-95071921	<i>Fggy</i>	22248	BALB/c	intra	A_52_P141141	0.15 (P)	0.117 (P)	0.117 (P)	0.98 (P)	1.262 (P)	1.344 (P)
chr4:95074879-95075609	<i>Fggy</i>	25705	C57BL/6	intra	A_52_P141141	0.15 (P)	0.117 (P)	0.117 (P)	0.98 (P)	1.262 (P)	1.344 (P)
chr4:95255640-95255700	<i>Fggy</i>	206145	C57BL/6	intra	A_52_P141141	0.15 (P)	0.117 (P)	0.117 (P)	0.98 (P)	1.262 (P)	1.344 (P)
chr4:95281652-95281871	<i>Fggy</i>	232237	BALB/c	intra	A_52_P141141	0.15 (P)	0.117 (P)	0.117 (P)	0.98 (P)	1.262 (P)	1.344 (P)
chr4:117954421-117954479	<i>Mpl</i>	952	BALB/c	intra	A_51_P341746	0.664 (A)	1.498 (P.A)	0.399 (A)	0.939 (P)	0.664 (P)	1.237 (P)
chr4:117998531-117998591	<i>Tie1</i>	-10834	BALB/c	distal	A_51_P177171	13.28 (P)	15.13 (P)	11.09 (P)	0.958 (A)	1.114 (A)	1.424 (P.A)
chr4:118000679-118000739	<i>Tie1</i>	-12982	C57BL/6	distal	A_51_P177171	13.28 (P)	15.13 (P)	11.09 (P)	0.958 (A)	1.114 (A)	1.424 (P.A)
chr4:136116934-136117007	<i>Ephb2</i>	-8920	BALB/c	distal	A_52_P315155	0.583 (A)	0.636 (A)	0.648 (A)	0.983 (P.A)	0.921 (A)	0.59 (A)
chr4:136120484-136120813	<i>Ephb2</i>	-12598	BALB/c	distal	A_52_P315155	0.583 (A)	0.636 (A)	0.648 (A)	0.983 (P.A)	0.921 (A)	0.59 (A)
chr4:136127607-136127655	<i>Ephb2</i>	-19581	BALB/c	distal	A_52_P315155	0.583 (A)	0.636 (A)	0.648 (A)	0.983 (P.A)	0.921 (A)	0.59 (A)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe_ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr4:136157517-136157754	<i>C1qb</i>	574	C57BL/6	prom	A_51_P351860	0.146 (P)	0.139 (P)	0.127 (P)	0.995 (P)	1.095 (P)	1.003 (P)
chr4:136160301-136161004	<i>C1qb</i>	-2723	BALB/c	distal	A_51_P351860	0.146 (P)	0.139 (P)	0.127 (P)	0.995 (P)	1.095 (P)	1.003 (P)
chr4:136188412-136188847	<i>C1qa</i>	-17794	BALB/c	distal	A_51_P181451	0.383 (P)	0.322 (P)	0.217 (P)	0.999 (P)	0.845 (P)	0.654 (P)
chr4:139992658-139992703	<i>Rcc2</i>	19063	C57BL/6	intra	A_51_P299670	1.033 (P)	1.134 (P)	1.525 (P)	0.999 (P)	1.032 (P)	0.948 (P)
chr4:140001888-140002184	<i>Padi6</i>	12669	BALB/c	intra	A_51_P448094	0.781 (A)	0.84 (A)	0.717 (A)	0.992 (P.A)	1.291 (P.A)	1.686 (P)
chr4:140037365-140037761	<i>Padi4</i>	8716	BALB/c	intra	A_51_P255875	0.0265 (P)	0.0263 (P.A)	0.0111 (A)	0.989 (P)	0.62 (P)	0.446 (P)
chr4:140053810-140053855	<i>Padi4</i>	-7553	C57BL/6	distal	A_51_P255875	0.0265 (P)	0.0263 (P.A)	0.0111 (A)	0.989 (P)	0.62 (P)	0.446 (P)
chr4:140066734-140066816	<i>Padi3</i>	15949	BALB/c	intra	A_51_P450549	0.443 (P.A)	0.471 (P.A)	0.243 (A)	0.999 (P)	0.484 (P)	1.076 (P)
chr4:140075656-140075701	<i>Padi3</i>	7046	C57BL/6	intra	A_51_P450549	0.443 (P.A)	0.471 (P.A)	0.243 (A)	0.999 (P)	0.484 (P)	1.076 (P)
chr4:140086347-140087247	<i>Padi1</i>	31057	C57BL/6	intra	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140088960-140089479	<i>Padi1</i>	28634	BALB/c	intra	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140098544-140098705	<i>Padi1</i>	19229	C57BL/6	intra	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140100052-140100287	<i>Padi1</i>	17684	C57BL/6	intra	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140102179-140102439	<i>Padi1</i>	15545	C57BL/6	intra	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140117495-140117765	<i>Padi1</i>	224	BALB/c	prom	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140150659-140150706	<i>Padi1</i>	-32829	BALB/c	distal	A_51_P439403	0.756 (P)	1.04 (P)	0.71 (P)	0.999 (P)	0.846 (P)	1.19 (P)
chr4:140834500-140834615	<i>Fblim1</i>	43550	BALB/c	distal	A_51_P309370	0.126 (P)	0.0827 (P)	0.0597 (P)	0.991 (P)	0.974 (P)	1.032 (P)
chr4:140848488-140848640	<i>Fblim1</i>	29544	BALB/c	distal	A_51_P309370	0.126 (P)	0.0827 (P)	0.0597 (P)	0.991 (P)	0.974 (P)	1.032 (P)
chr4:140887217-140887262	<i>Tmem82</i>	2903	C57BL/6	intra	A_52_P112110	1.56 (P)	1.1 (P)	1.057 (P)	1 (P)	0.821 (P)	0.716 (P)
chr4:140902197-140902509	<i>Slc25a34</i>	6106	BALB/c	intra	A_51_P333344	0.779 (P)	1.003 (P)	0.716 (P.A)	0.99 (P)	1.004 (P)	1.336 (P)
chr4:146455519-146455683	<i>2610305D13Rik</i>	30707	C57BL/6	distal	A_51_P347875	0.0885 (A)	0.0809 (A)	0.0973 (A)	0.989 (P)	1.321 (P)	1.044 (P)
chr4:147309756-147309900	<i>Mtor (Frap1)</i>	17413	C57BL/6	intra	A_51_P282179	1.22 (P)	1.381 (P)	1.166 (P)	0.998 (P)	1.254 (P)	1.122 (P)
chr4:147344719-147345290	<i>Angptl7</i>	-744	BALB/c	prom	A_51_P220150	71.66 (P)	44.62 (P)	31.07 (P)	0.998 (A)	1.089 (A)	1.144 (A)
chr4:153165776-153166060	<i>Prdm16</i>	314642	BALB/c	intra	A_51_P514139	0.0185 (A)	0.0169 (A)	0.0196 (A)	0.988 (P)	1.051 (P)	0.79 (P)
chr4:153374889-153374938	<i>Prdm16</i>	105646	C57BL/6	intra	A_51_P514139	0.0185 (A)	0.0169 (A)	0.0196 (A)	0.988 (P)	1.051 (P)	0.79 (P)
chr4:153377867-153377925	<i>Prdm16</i>	102664	C57BL/6	intra	A_51_P514139	0.0185 (A)	0.0169 (A)	0.0196 (A)	0.988 (P)	1.051 (P)	0.79 (P)
chr4:153397287-153397825	<i>Prdm16</i>	83004	C57BL/6	intra	A_51_P514139	0.0185 (A)	0.0169 (A)	0.0196 (A)	0.988 (P)	1.051 (P)	0.79 (P)
chr4:153416659-153417244	<i>Prdm16</i>	63608	BALB/c	intra	A_51_P514139	0.0185 (A)	0.0169 (A)	0.0196 (A)	0.988 (P)	1.051 (P)	0.79 (P)
chr4:153521279-153522015	<i>Actrt2</i>	-10114	C57BL/6	distal	A_51_P214725	0.524 (A)	0.979 (P.A)	0.81 (A)	0.84 (P.A)	0.884 (P.A)	0.429 (A)
chr5:31235102-31235151	<i>Preb</i>	1735	BALB/c	intra	A_51_P135037	0.987 (P)	1.238 (P)	0.954 (P)	0.996 (P)	1.692 (P)	1.746 (P)
chr5:35229612-35229843	<i>A930005104Rik</i>	-2951	C57BL/6	distal	A_51_P148744	0.143 (P)	0.13 (P)	0.0878 (P)	0.999 (P)	1.309 (P)	0.928 (P)
chr5:53010351-53010409	<i>Pi4k2b</i>	-19459	C57BL/6	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:53012858-53013017	<i>Pi4k2b</i>	-16902	C57BL/6	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:53013951-53014431	<i>Pi4k2b</i>	-15648	C57BL/6	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:53026418-53026767	<i>Pi4k2b</i>	-3247	C57BL/6	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:53049276-53049634	<i>Pi4k2b</i>	19597	BALB/c	intra	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:53058948-53058993	<i>Pi4k2b</i>	29113	BALB/c	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:53061668-53062228	<i>Pi4k2b</i>	32090	C57BL/6	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe_ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr5:53063596-53064069	<i>Pi4k2b</i>	33975	BALB/c	distal	A_51_P230987	7.234 (P)	5.022 (P)	6.078 (P)	0.999 (P)	0.655 (P)	1.066 (P)
chr5:66959934-66959982	<i>Uchl1</i>	4580	C57BL/6	intra	A_51_P475049	0.0211 (P)	0.0207 (P)	0.0318 (P)	0.998 (P)	0.901 (P)	0.713 (P)
chr5:67640239-67640299	<i>Slc30a9</i>	54177	BALB/c	distal	A_51_P465809	1.548 (P)	1.499 (P)	1.248 (P)	0.99 (P)	1.418 (P)	1.384 (P)
chr5:67676687-67677026	<i>Slc30a9</i>	90765	BALB/c	distal	A_51_P465809	1.548 (P)	1.499 (P)	1.248 (P)	0.99 (P)	1.418 (P)	1.384 (P)
chr5:67680207-67680368	<i>Slc30a9</i>	94196	C57BL/6	distal	A_51_P465809	1.548 (P)	1.499 (P)	1.248 (P)	0.99 (P)	1.418 (P)	1.384 (P)
chr5:104720508-104721242	<i>Pkd2</i>	21019	C57BL/6	intra	A_51_P419613	25.9 (P)	22.17 (P)	18.67 (P)	1 (P)	0.867 (P)	1.007 (P)
chr5:104725504-104725800	<i>Pkd2</i>	25796	C57BL/6	intra	A_51_P419613	25.9 (P)	22.17 (P)	18.67 (P)	1 (P)	0.867 (P)	1.007 (P)
chr5:104733382-104733438	<i>Pkd2</i>	33554	C57BL/6	intra	A_51_P419613	25.9 (P)	22.17 (P)	18.67 (P)	1 (P)	0.867 (P)	1.007 (P)
chr6:5104955-5105188	<i>Ppp1r9a</i>	251752	C57BL/6	intra	A_52_P239536	10.8 (P)	8.688 (P)	5.637 (P)	0.988 (P)	0.841 (P)	0.445 (P)
chr6:5333111-5334506	<i>Asb4</i>	-6638	C57BL/6	distal	A_52_P594756	0.0642 (P.A)	0.0262 (P.A)	0.0366 (P.A)	0.997 (P)	0.82 (P)	1.696 (P)
chr6:29688651-29688794	<i>Smo</i>	3068	C57BL/6	intra	A_51_P258766	7.301 (P)	10.08 (P)	14.44 (P)	0.984 (P)	1.338 (P)	1.968 (P)
chr6:29716478-29716561	<i>Ahcyl2</i>	-2016	BALB/c	distal	A_51_P176396	1.345 (P)	2.348 (P)	2.071 (P)	0.827 (P)	2.708 (P)	1.955 (P)
chr6:93630855-93630915	<i>Magi1</i>	-28060	C57BL/6	distal	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93691281-93691444	<i>Magi1</i>	-88537	BALB/c	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93694981-93695577	<i>Magi1</i>	-92454	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93704332-93704392	<i>Magi1</i>	-101537	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93713202-93713457	<i>Magi1</i>	-110504	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93735273-93735333	<i>Magi1</i>	-132478	BALB/c	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93755446-93756328	<i>Magi1</i>	130353	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93768673-93769578	<i>Magi1</i>	117115	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93814158-93814213	<i>Magi1</i>	72055	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:93823430-93823772	<i>Magi1</i>	62639	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:94029111-94029381	<i>Magi1</i>	-150093	C57BL/6	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:94085475-94085534	<i>Magi1</i>	163862	BALB/c	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:94115136-94115260	<i>Magi1</i>	134169	BALB/c	intra	A_51_P406346	9.72 (P)	7.492 (P)	6.942 (P)	1 (P.A)	0.657 (P.A)	1.294 (P)
chr6:122566409-122566463	<i>Apobec1</i>	1552	C57BL/6	intra	A_51_P160754	2.923 (P)	1.163 (P)	1.119 (P)	1 (P)	0.386 (P)	0.54 (P)
chr6:122593442-122593497	<i>Dppa3</i>	1430	C57BL/6	intra	A_51_P195044	0.0522 (P)	0.0133 (P.A)	0.0121 (A)	0.998 (P)	0.273 (P)	0.385 (P)
chr6:122599007-122599338	<i>Dppa3</i>	7133	BALB/c	distal	A_51_P195044	0.0522 (P)	0.0133 (P.A)	0.0121 (A)	0.998 (P)	0.273 (P)	0.385 (P)
chr6:129559721-129559770	<i>Klrd1</i>	2293	BALB/c	intra	A_51_P280947	0.785 (P)	0.209 (A)	0.185 (A)	0.99 (P)	0.463 (P)	0.326 (P.A)
chr6:134647920-134648332	<i>Loh12cr1</i>	41635	BALB/c	intra	A_51_P498947	0.551 (P)	2.057 (P)	1.48 (P)	1 (P)	3.096 (P)	1.703 (P)
chr6:134652859-134653242	<i>Loh12cr1</i>	46539	C57BL/6	intra	A_51_P498947	0.551 (P)	2.057 (P)	1.48 (P)	1 (P)	3.096 (P)	1.703 (P)
chr6:134666768-134667057	<i>Loh12cr1</i>	60361	C57BL/6	intra	A_51_P498947	0.551 (P)	2.057 (P)	1.48 (P)	1 (P)	3.096 (P)	1.703 (P)
chr6:134684992-134685037	<i>Dusp16</i>	73307	BALB/c	intra	A_51_P242634	6.056 (P)	3.482 (P)	3.614 (P)	0.989 (P)	0.487 (P)	0.454 (P)
chr6:134711215-134711398	<i>Dusp16</i>	46953	BALB/c	intra	A_51_P242634	6.056 (P)	3.482 (P)	3.614 (P)	0.989 (P)	0.487 (P)	0.454 (P)
chr6:134723586-134723979	<i>Dusp16</i>	34372	C57BL/6	intra	A_51_P242634	6.056 (P)	3.482 (P)	3.614 (P)	0.989 (P)	0.487 (P)	0.454 (P)
chr6:136898012-136898210	<i>Arhgdib</i>	7791	C57BL/6	intra	A_52_P515247	0.933 (P)	0.974 (P)	0.984 (P)	0.997 (P)	0.991 (P)	0.836 (P)
chr6:136920044-136920089	<i>Pde6h</i>	1325	BALB/c	intra	A_52_P68261	0.125 (A)	0.13 (A)	0.119 (A)	0.999 (P)	0.863 (P)	0.836 (P)
chr6:136962558-136962606	<i>Pde6h</i>	43841	C57BL/6	distal	A_52_P68261	0.125 (A)	0.13 (A)	0.119 (A)	0.999 (P)	0.863 (P)	0.836 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe_ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr6:136920044-136920089	<i>Pde6h</i>	1325	BALB/c	intra	A_52_P68261	0.125 (A)	0.13 (A)	0.119 (A)	0.999 (P)	0.863 (P)	0.836 (P)
chr6:136962558-136962606	<i>Pde6h</i>	43841	C57BL/6	distal	A_52_P68261	0.125 (A)	0.13 (A)	0.119 (A)	0.999 (P)	0.863 (P)	0.836 (P)
chr7:4064078-4064123	<i>Eps8l1</i>	198	BALB/c	intra	A_52_P37757	0.0861 (A)	0.0787 (A)	0.0899 (A)	0.979 (P)	0.939 (P)	0.963 (P)
chr7:4073211-4073587	<i>Eps8l1</i>	9597	BALB/c	intra	A_52_P37757	0.0861 (A)	0.0787 (A)	0.0899 (A)	0.979 (P)	0.939 (P)	0.963 (P)
chr7:4073898-4074764	<i>Eps8l1</i>	10529	BALB/c	intra	A_52_P37757	0.0861 (A)	0.0787 (A)	0.0899 (A)	0.979 (P)	0.939 (P)	0.963 (P)
chr7:4081211-4081948	<i>Eps8l1</i>	17777	BALB/c	intra	A_52_P37757	0.0861 (A)	0.0787 (A)	0.0899 (A)	0.979 (P)	0.939 (P)	0.963 (P)
chr7:4468706-4470122	<i>Isoc2b</i>	-190	C57BL/6	prom	A_51_P343356	0.188 (P)	0.153 (P)	0.118 (P)	0.987 (P)	1.058 (P)	1.079 (P)
chr7:4476223-4476274	<i>Isoc2b</i>	-3958	C57BL/6	distal	A_51_P343356	0.188 (P)	0.153 (P)	0.118 (P)	0.987 (P)	1.058 (P)	1.079 (P)
chr7:15421071-15421190	<i>C5ar1</i>	-3416	BALB/c	distal	A_51_P279542	0.37 (P)	0.136 (P)	0.173 (P)	0.998 (P)	0.705 (P)	0.588 (P)
chr7:28818237-28818282	<i>Ryr1</i>	15653	BALB/c	intra	A_52_P391110	13.91 (P)	16.15 (P)	32.57 (P)	1 (P)	2.332 (P)	7.618 (P)
chr7:28863980-28864027	<i>Fam98c</i>	936	BALB/c	intra	A_51_P223111	1.008 (P)	1.251 (P)	1.072 (P)	1 (P)	1.089 (P)	1.185 (P)
chr7:29665315-29665376	<i>Zfp74</i>	-2524	BALB/c	intra	A_51_P223624	1.336 (P)	1.188 (P)	1.236 (P)	0.999 (P)	1.014 (P)	0.987 (P)
chr7:29692014-29692149	<i>Zfp568</i>	-582	C57BL/6	prom							
chr7:37961808-37962602	<i>Pop4</i>	18262	BALB/c	distal	A_52_P206492	0.1 (P)	0.244 (P)	0.168 (P)	0.999 (P)	1.369 (P)	1.266 (P)
chr7:80210572-80210730	<i>Unc45a</i>	3063	C57BL/6	intra	A_51_P124993	2.327 (P)	2.42 (P)	2.17 (P)	0.999 (P)	1.216 (P)	1.093 (P)
chr7:99033917-99034043	<i>Dgat2</i>	23925	C57BL/6	intra	A_51_P396003	11.39 (P)	16.61 (P)	26.17 (P)	0.99 (P)	3.568 (P)	1.908 (P)
chr7:99037518-99037643	<i>Dgat2</i>	20324	BALB/c	intra	A_51_P396003	11.39 (P)	16.61 (P)	26.17 (P)	0.99 (P)	3.568 (P)	1.908 (P)
chr7:99064892-99065884	<i>Dgat2</i>	-7483	C57BL/6	distal	A_51_P396003	11.39 (P)	16.61 (P)	26.17 (P)	0.99 (P)	3.568 (P)	1.908 (P)
chr7:119504588-119504967	<i>Thumpd1</i>	7136	C57BL/6	distal	A_51_P392518	0.01 (A)	0.01 (A)	0.0122 (P)	0.996 (P)	1.37 (P)	1.136 (P)
chr7:119506866-119506918	<i>Thumpd1</i>	5022	BALB/c	distal	A_51_P392518	0.01 (A)	0.01 (A)	0.0122 (P)	0.996 (P)	1.37 (P)	1.136 (P)
chr7:119994863-119995241	<i>Abca14</i>	-61	C57BL/6	prom	A_51_P511142	1.207 (A)	1.103 (A)	1.325 (A)	0.996 (A)	1.061 (A)	1.101 (A)
chr7:120010482-120010849	<i>Abca14</i>	15552	BALB/c	intra	A_51_P511142	1.207 (A)	1.103 (A)	1.325 (A)	0.996 (A)	1.061 (A)	1.101 (A)
chr7:125348874-125348919	<i>Il4ra</i>	5477	BALB/c	intra	A_51_P464478	1.04 (P)	2.457 (P)	0.963 (P)	0.999 (P)	3.548 (P)	1.028 (P)
chr7:125398313-125398366	<i>Il21r</i>	3730	C57BL/6	intra	A_51_P362877	0.724 (P)	0.369 (P)	0.188 (P)	0.99 (P)	1.492 (P)	1.226 (P)
chr7:142430532-142430685	<i>Igf2</i>	30411	BALB/c	distal	A_51_P516826	1.098 (M.A)	0.797 (M.A)	1.281 (M.A)	0.923 (P)	8.246 (M.A)	0.87 (M.A)
chr8:73561622-73562051	<i>Gdf15</i>	-1209	C57BL/6	distal	A_52_P532982	0.0791 (P)	0.0582 (P)	0.116 (P)	0.988 (P)	0.439 (P)	0.847 (P)
chr8:124746984-124747033	<i>Slc7a5</i>	-31389	BALB/c	distal	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124747942-124748185	<i>Slc7a5</i>	-32444	BALB/c	distal	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124755205-124755348	<i>Slc7a5</i>	38500	BALB/c	distal	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124757601-124757653	<i>Slc7a5</i>	36149	C57BL/6	distal	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124758800-124759357	<i>Slc7a5</i>	34698	BALB/c	distal	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124760437-124760974	<i>Slc7a5</i>	33071	BALB/c	distal	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124768035-124768493	<i>Slc7a5</i>	25512	C57BL/6	intra	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124774258-124775049	<i>Slc7a5</i>	19123	C57BL/6	intra	A_51_P273639	3.167 (P)	5.188 (P)	8.51 (P)	0.998 (P)	1.539 (P)	0.757 (P)
chr8:124798597-124798956	<i>BC048644</i>	4853	C57BL/6	intra							
chr8:124823004-124823197	<i>Car5a</i>	7859	C57BL/6	intra	A_51_P240287	0.693 (A)	0.834 (A)	0.672 (A)	0.973 (P.A)	0.938 (P.A)	1.524 (P)
chr8:127227407-127227452	<i>Galnt2</i>	109842	BALB/c	intra	A_52_P496890	1.505 (P)	1.316 (P)	1.496 (P)	0.999 (P)	1.081 (P)	1.224 (P)
chr8:127276982-127277478	<i>Pgbd5</i>	42796	BALB/c	intra	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)

Supplemental Table S2 (continued)
Annotated List of Mouse Strain-Specific DMR

Center of DMR (Mouse Assembly mm8)	Gene Symbol	Distance to TSS	De- methylated in	Position Relative to Gene	Agilent Probe_ID	BMM BALB/c 0 h	BMM BALB/c 4 h	BMM BALB/c 18 h	BMM C57BL/6 0 h	BMM C57BL/6 4 h	BMM C57BL/6 18
chr8:127283682-127283870	<i>Pgbd5</i>	36250	C57BL/6	intra	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)
chr8:127301989-127302034	<i>Pgbd5</i>	18014	C57BL/6	intra	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)
chr8:127317898-127318260	<i>Pgbd5</i>	1947	BALB/c	intra	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)
chr8:127359130-127359175	<i>Pgbd5</i>	-39127	C57BL/6	distal	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)
chr8:127361009-127361074	<i>Pgbd5</i>	-41016	C57BL/6	distal	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)
chr8:127364656-127364799	<i>Pgbd5</i>	-44702	BALB/c	distal	A_51_P167313	0.0115 (A)	0.056 (P)	0.0181 (A)	1 (P)	0.479 (P)	0.651 (P)
chr9:49187501-49188250	<i>Ttc12</i>	50224	C57BL/6	distal	A_52_P327118	7.06 (P)	6.109 (P)	6.619 (P)	0.998 (P)	1.103 (P)	1.541 (P)
chr9:49192161-49192634	<i>Ttc12</i>	45702	C57BL/6	intra	A_52_P327118	7.06 (P)	6.109 (P)	6.619 (P)	0.998 (P)	1.103 (P)	1.541 (P)
chr9:49237091-49237345	<i>Ttc12</i>	882	BALB/c	intra	A_52_P327118	7.06 (P)	6.109 (P)	6.619 (P)	0.998 (P)	1.103 (P)	1.541 (P)
chr9:50769119-50769184	<i>Snf1lk2</i>	-7910	C57BL/6	distal	A_52_P575296	1.375 (P)	1.42 (P)	1.321 (P)	0.966 (P)	1.106 (P)	1.236 (P)
chr9:51783122-51783240	<i>Rdx</i>	-17455	C57BL/6	distal	A_51_P430950	0.971 (P)	0.975 (P)	1.053 (P)	1 (P)	0.981 (P)	1.028 (P)
chr9:51850201-51850259	<i>Rdx</i>	49594	C57BL/6	distal	A_51_P430950	0.971 (P)	0.975 (P)	1.053 (P)	1 (P)	0.981 (P)	1.028 (P)
chr9:51851802-51851859	<i>Rdx</i>	51195	C57BL/6	distal	A_51_P430950	0.971 (P)	0.975 (P)	1.053 (P)	1 (P)	0.981 (P)	1.028 (P)
chr9:72207341-72207401	<i>BC065403</i>	966	BALB/c	intra							
chr9:102967337-102967700	<i>Rab6b</i>	-2380	C57BL/6	distal	A_51_P276418	0.0133 (A)	0.0122 (A)	0.0138 (A)	0.988 (P)	0.797 (P)	0.99 (P)
chr9:102971565-102971612	<i>Rab6b</i>	1690	BALB/c	intra	A_51_P276418	0.0133 (A)	0.0122 (A)	0.0138 (A)	0.988 (P)	0.797 (P)	0.99 (P)
chrX:119220336-119220381	<i>3110007F17Rik</i>	-142	C57BL/6	prom	A_52_P321978	0.0515 (A)	0.0578 (A)	0.0497 (A)	0.992 (P)	0.518 (P)	0.825 (P)