Table 2, supplement. Distribution of macroH2A1 on genes with altered expression in *macroH2A1* knockout liver

Gene	Location (bp)		Relative concentration[1]		
	From start	From end	Newborn[2]	Adult Male	Adult Female
Lpl	-13,626		0.7 ± 0.01	8.1 ± 0.52	7 ± 0.46
	-11,280		0.6 ± 0.04	5 ± 0.02	5.4 ± 0.17
	-6,826		0.3 ± 0.02	5.2 ± 0.02	5.1 ± 0.3
	-4,147		1 ± 0.01	4.6 ± 0.0	4.8 ± 0.55
	-1,260		0.5 ± 0.01	3.8 ± 0.14	3.7 ± 0.38
	-450		0.3 ± 0.02	1.5 ± 0.13	1.7 ± 0.05
	-294		0.2 ± 0.01	1 ± 0.01	1.2 ± 0.03
	-188		0.2 ± 0.02	0.7 ± 0.06	0.7 ± 0.05
	+72	-26,326	0.1 ± 0.02	0.4 ± 0.07	0.4 ± 0.03
	+3,225	-23,173	0.4 ± 0.02	1.3 ± 0.1	1.2 ± 0.18
	+7,038	-19,360		0.5 ± 0.07	0.5 ± 0.06
	+13,129	-13,269		0.8 ± 0.05	0.9 ± 0.06
	+17,719	-8,679	0.2 ± 0.02	0.8 ± 0.03	0.8 ± 0.04
	+23,905	-2,493		0.8 ± 0.04	0.7 ± 0.03
	+25,948	-381	0.2 ± 0.01	1.1 ± 0.01	1.1 ± 0.18
Krt1-23	-2,893		0.4 ± 0.04	3.8 ± 0.08	3.1 ± 0.05
	-1,857		0.6 ± 0.01	5.7 ± 0.47	5 ± 0.49
	-845		0.4 ± 0.03	5.7 ± 0.46	6.3 ± 1.42
	-496		0.2 ± 0.01	4.5 ± 0.28	3.4 ± 0.18
	-109		0.2 ± 0.03	1.8 ± 0.11	1.2 ± 0.06
	+63			2.9 ± 0.16	2.2 ± 0.17
	+579	-14,558	0.2 ± 0.09	4.4 ± 0.38	3.6 ± 0.44
	+2,011	-13,126		1.4 ± 0.25	1.3 ± 0.18
	+4,496	-10,641	0.2 ± 0.04	5.4 ± 0.07	5.4 ± 0.52
	+9,468	-5,669	0.1 ± 0.05	5.8 ± 0.08	4.6 ± 0.04
	+11,673	-3,464	0.1 ± 0.03	4.4 ± 0.3	3.9 ± 0.9
	+14,853	-284	0.2 ± 0.1	5.5 ± 0.01	5.2 ± 0.81
Serpina7	-4,505		0.8 ± 0.15	3.3 ± 0.24	3.2 ± 0.5
	-2,163		0.7 ± 0.11	2.3 ± 0.22	3.5 ± 0.43
	-1,739		0.5 ± 0.1	1.1 ± 0.01	2.7 ± 0.18
	-1,260		0.5 ± 0.1	2.1 ± 0.11	2.8 ± 0.13
	-948		0.6 ± 0.14	3.8 ± 0.02	3.9 ± 0.42
	-342		0.4 ± 0.01	2.2 ± 0.34	2.1 ± 0.14
	-136		0.4 ± 0.07	2.9 ± 0.76	2.8 ± 0.28

Serpina7	+238	-3,289	0.5 ± 0.11	2.2 ± 0.03	2.4 ± 0.21
	+937	-2,590	0.7± 0.14	3.3 ± 0.36	3 ± 0.64
	+2,252	-1,275	0.7 ± 0.03	2.9 ± 0.68	3.7 ± 0.39
	+3,300	-227	0.5 ± 0.15	2.5 ± 0.02	2.1 ± 0.71
Scd2	-6,284		2.0± 0.75	5.6 ± 0.34	5.7 ± 1.48
	-4,653		1.3 ± 1.59	5.6 ± 0.11	4.7 ± 0.51
	-2,145		1.8 ± 0.5	6.4 ± 0.21	5.6 ± 0.63
	-1,285		1.1 ± 0.43	7 ± 0.31	6 ± 0.33
	-370		0.4 ± 0.02	4.4 ± 0.69	4.8 ± 0.61
	+730		0.5 ± 0.04	3.1 ± 1.0	3.6 ± 0.42
	+6,437		0.6 ± 0.29	3.8 ± 0.52	4.1 ± 0.31
	+12,587			4.6± 0.21	4.5 ± 0.79
ATP11a	-10,661			4.1 ± 0.02	3.8 ± 0.49
	-7,700			2.7 ± 0.06	2.5 ± 0.26
	-1,150			1.5 ± 0.29	1.6 ± 0.25
	-529			0.3 ± 0.03	0.4 ± 0.06
	+598	-107,276		0.3 ± 0.04	0.4 ± 0.03
	+11,093	-96,781		0.3 ± 0.01	0.3 ± 0.01
	+19,802	-88,072		0.6 ± 0.07	0.5 ± 0.04
	+22,554	-85,320		0.5 ± 0.1	0.6 ± 0.08
	+40,661	-67,213		0.4 ± 0.04	0.4 ± 0.05
	+52,371	-55,503		0.4 ± 0.01	0.5 ± 0.01
	+65,228	-42,646		0.4 ± 0.08	0.4 ± 0.07
	+77,423	-30,451		0.7 ± 0.16	0.8 ± 0.12
	+89,380	-18,494		1.1 ± 0.25	1.2 ± 0.26
	+100,664	-7,210		0.5 ± 0.09	0.5 ± 0.09
	+110,661	+2,768		0.6 ± 0.11	0.8 ± 0.17
Sucnr1	-4,981			1.7 ± 0.21	1.7 ± 0.44
	-891			1.7 ± 0.05	1.6 ± 0.2
	+109	-5,582		1.5 ± 0.02	1.5 ± 0.13
	+2,615	-3,076		1 ± 0.01	1 ± 0.11
	+5,543	-148		2 ± 0.08	2.0 ± 0.58
GTPbp4	-4,919			1.1 ± 0.09	1.9 ± 0.7
	-830			0.2 ± 0.0	0.3 ± 0.08
	+3,655	-19,888		0.3 ± 0.0	0.2 ± 0.04
	+8,950	-14,593		0.1 ± 0.01	0.1 ± 0.03
	+16,398	-7,145		0.1 ± 0.01	0.1 ± 0.03
	+22,616	-927		0.2 ± 0.01	0.1 ± 0.01

[1] Ratio of the concentration in the macroH2A1-enriched Thiopropyl Sepharose eluted fraction divided by the concentration in the starting material of adult liver as determined by real-time PCR.

[2] 3-Day liver, mixed sexes.

Table 3, supplement. Primer sequences

Primer Name	**Location**	**Forward Primer**	**Reverse Primer**	**PRODUCT SIZE**	**Annealing Temp**
LPL					
LPL LTR#4	(-)13,626	TCTCACTATATGAGTGGACAGATCG	TGGAGTTGCTCCAGTTGTGG	73 bp	64^{0}c
LPL LTR #5	(-)11,280	ATGCTCCTGCTTCTCTCAGC	CAGGAGGGTGTGTAGCTTGC	63 bp	60^{0}c
LPL#38	(-)6,826	TAGGATGGCAAGTTGACAGG	AGCATGAGGATGCTCTGTAGG	86 bp	64^{0}c
LPL#37	(-)4,147	GGCTGCATCCTCTCTATCTGG	CACTGTTAACCAAGACTGTGTGG	66 bp	60^{0}c
LPL#30	(-)1,260	GTTGGAGCCAGTAATGAACG	GTCTCGCCATCTCATCTTGC	69 bp	60^{0}c
LPL #44	(-)450	TGCCAAGATACAAAGCAGACC	GGGACCTTAGGACACATATTGC	63 bp	64^{0}c
LPL #7	(-)294	TGTGTGTGAGTGTGAAAGTGTTAGG	GTTTTCTAAGGGGAAGAAGTTTTGC	66 bp	60^{0}c
LPL #10	(-)188	ATCAGTGTAAACCCCTCCTCTCTGC	TGTTTAGACTCCAGTTTGCCTACCG	83 bp	60^{0}c
LPL #8	(+)72	AGACTCTCGATTTCTCCTCCTACTCC	GGGAGGGCAGAACAGTTACAAGG	68 bp	60^{0}c
LPL #42	(+)3,225	CAGCACAGTTGGATGAATGC	AGGTGAGCTTGACTAATCTGAGG	84 bp	64^{0}c
LPL #45	(+)7,038	TGTCATCTCATTCCTGGATTAGC	GATCACCACGAAGGTCTTGC	78 bp	60^{0}c
LPl #21	(+)13,129	GATGAGCAGGATGAGTTACTGG	ATGAGAGTTCTAGCTTAGATTGTGG	67 bp	60^{0}c
LPL #4	(+)17,719	AGGCTTCTGTCTGGACTTCCT	CAAGGCAGTGCTGTAGGTCA	86 bp	60^{0}c
LPL #43	(+)23,905	TCTATAATCTGCACCACACAAGC	CAGCACTGTCAGGAGGAAGC	61 bp	64^{0}c
LPL #34	(+)25,948	GCTGGAATGTTAGCCCTTGC	GAAATCGGTCACCTTTGTCC	72 bp	60^{0}c
Keratin1-23					
Krt1-23 #11	(-)2,893	AGAGCCCATGGAGTTCAAGC	AGGCAAGACAACCCTCACC	60 bp	64^{0}c
Krt1-23 #10	(-)1,857	AAACTCCTGGACCCTGTGG	GGGCCACTTGGTATCTCTGC	61 bp	64^{0}c
Krt1-23 #7	(-)845	ACTCTCAACCTCTGCCTTGG	GTGGTCTGACATGTGTGATGC	55 bp	64^{0}c
Krt1-23 #12	(-)496	ACGGCAGCAGACACAAAGG	GCGGAAGGAAACAGAGAGG	55 bp	64^{0}c
Krt1-23 #13	(-)109	CGTGGTTCTAAACAACAACAGC	TGTTTCCTCTTGGTCAATCC	69 bp	64^{0}c
Krt1-23 #14	(+)63	GCGTCAGAGAGCTGAGATAGC	CTGTGGCTGGAGTTCATGG	62 bp	64^{0}c

Krt1-23 #3	(+)579	GAACCAGACTGTGTGCATGG	TGGGTGAGCAGTACTTGAGC	72 bp	64^{0}c
Krt1-23 #2	(+)2,011	TGCGTGATACCAACTCAATAGC	TCCATGGGACTAAGACATGC	60 bp	64^{0}c
Krt1-23 #4	(+)4,496	TGTGAGTCCTTGCTCTGATCC	TCGTTGGAGGTGTTTGAGC	65 bp	64^{0}c
Krt1-23 #5	(+)9,468	GCCTTCCATGACCTTGTCC	AGACAATGAGAGAAGTCCAAAGG	64 bp	64^{0}c
Krt1-23 #9	(+)11,673	CATTGCTCATCTTGCATTCG	GTGGTCTGATGGAGTGATGC	80 bp	64^{0}c
Krt1-23 #6	(+)14,853	ACCAGTGACCTCTCCGATGG	TGAGTGATGGCCTTGATCG	66 bp	64^{0}c
Serpina7					
Serpina7#11	(-)4,505	AAAGACCCAGGACTTACAAACC	AAGCAAAGTAGCTTCCTTCTGG	60 bp	64^{0}c
Serpina7#10	(-)2,163	AGCCCAGATAGTTCCCTACTCC	TGATTTCCCACATGGCTACC	78 bp	64^{0}c
Serpina7#15	(-)1,739	CCCAAGTCTCTTGTCTGTAAACC	AGTTCTTCCTGTCAGTGTTAGGC	67 bp	64^{0}c
Serpina7#14	(-)1,260	TGACCTAAGAGTGGACGAAGG	AGCTCCTAGCAGGACAGAGG	63 bp	64^{0}c
Serpina7#13	(-)948	CCAAAGGAGGCTGAAGTCC	TCCTTACTCATCTACCCAGTTGC	55 bp	64^{0}c
Serpina7#6	(-)342	AATAGAGGGAGTGCTTGTTCTGC	AAAGGCAGTTTATGAGTGTGACG	55 bp	64^{0}c
Serpina7#12	(-)136	CATGTCACTGGTCTTTAGTGAGG	GGTGTGTTCAGCAAGAAATAAGG	61 bp	64^{0}c
Serpina7#4	(+)238	GTATCGGAGGCTCTCTGTGG	AAGCAACAGATATGCTCACAGG	71 bp	64^{0}c
Serpina7#3	(+)937	AAACCTGTGCTTGGGAAGTC	GCAGTGTATCCAAATGTACACAGG	82 bp	64^{0}c
Serpina7#8	(+)2,252	CTGTCCTTGCTCAATAACATGG	GGGCTACAACACACAGTGTCC	71 bp	64^{0}c
Serpina7#5	(+)3,300	TGCTACACATTGGTGAAGAGG	TTCCTGCTGATCCAGAGACC	71 bp	64^{0}c
Scd2					
Scd2#6	(-)6,284	GAAGGAACCTGCACACTGC	TAGTTGTGCGATGGTGAAGC	60 bp	64^{0}c
Scd2#9	(-)4,653	TTGGGATATGTGGTCTAACAGG	CGGGAACAATTCAAGTGTGG	63 bp	64^{0}c
Scd2#8	(-)2,145	GGCTTAAGAAACATCACCAACC	GCCCTTACATTCCCTCAACC	73 bp	64^{0}c
Scd2#7	(-)1285	TTCAGCATTCTTGGCTATGG	CAACTCTCTGGCTTGTGACC	71 bp	64^{0}c
Scd2 #4	(-)370	GCTCTCTGTTGGTGGTAGCC	GACCACTTGCAACTCCATCC	77 bp	64^{0}c
Scd2#2	(+)730	CTGCACATTTCCGTGTTCC	GATGCAATAACGGCCATACC	76 bp	64^{0}c
Scd2 #5	(+)6,437	AGCAGCCGAATCACTAAAGG	CACCTAACTTGTGCCCTTCC	80 bp	64^{0}c
Scd2#3	(+)12,587	GCCTATGTCCCAGATGACG	CTGACGCATCCATTCAACC	62 bp	64^{0}c
ATP11a					
ATP11a #2	(-)10,661	GCTGTGCTGGTCGTTATGC	GCATGTGAAGCTCCTGTGC	81 bp	64^{0}c
ATP11a #3	(-)7,700	AGCACTTGCCCTCAACAAGG	CCTACCCAAGCAATCTCACC	69 bp	64^{0}c
ATP11a #12	(-)1,150	CACAGCAAGTCCAGGAAGC	GAGCACCAGCTACAGACACC	73 bp	64^{0}c
ATP11a#18	(-)529	ACGTGTTTGGTTTGGTCTCC	GATCCTCAGGTGGCTACAGG	78 bp	64^{0}c
ATP11a #4	(+)598	GACAGCTTGTCTTCCCTAAGC	GCTCCTCAAACCTGTGACC	79 bp	64^{0}c
ATP11a #7	(+)11,093	CTGTGTAGGCTTCGGTCTCC	GGCAGGAGGAAGGTACATGG	58 bp	64^{0}c
ATP11a #6	(+)19,802	AGGTGGCTTGTTCTGGAAGC	AAGTCTAAGGCGAGCACAGC	58 bp	64^{0}c

ATP11a #13	(+)22,554	CAGCCTTGGAGCAGATAACC	CCTTGAAGGCAGTGTCTTGG	88 bp	64^0c
ATP11a #8	(+)40,661	TTGTACCACCATTGGTCTCC	GTGGCATGTCACTGAGTTGG	78 bp	64^0c
ATP11a#10	(+)52,371	TGGGACTTCTGTGATCTGTCC	CTGGGTATGCCAATCTCTGG	59 bp	64^0c
ATP11a #11	(+)65,228	CCACCAGAGGAACAATAGCC	CATGCACATCCTGTGAGTCC	83 bp	64^0c
ATP11a #15	(+)77,423	CACGTACCTGAGGCTGAAGG	CATGCAGACAGCTTCTCACC	82 bp	64^0c
ATP11a #16	(+)89,380	AAGCCTGAGTGAGGCGTAGC	CACACAACAGCTCCAACTGC	72 bp	64^0c
ATP11a #17	(+)100,664	CACTGGACACGCACTACTGG	GGAGAAGGCAATGTAGAAGAGC	77 bp	64^0c
ATP11a #14	(+)110,661	TCCATTCCTGAGCACAAGC	CTTTGGGTGTGCCATTCC	58 bp	64^0c
Succinate Receptor					
Sucnr1 #5	(-)4,981	CAGTCCCAAATCCAGACACC	AATCCAGGACATTGCTGTGG	74 bp	64^0c
Sucnr1 #4	(-)891	GGTGGTGGTCAGAACTTTCC	GTTCATGGACCTCTCCAAGG	85 bp	64^0c
Sucnr1 #1	(+)109	CCGACAGCAGAATGGTAAGG	TTGGTCTTCTTTGGTGTGACC	63 bp	64^0c
sucnr1 #6	(+)2,615	AACAGACCCAGAGCAGTTGG	AATATCCACACTTAGCCCTTGC	55 bp	64^0c
Sucnr1 #3	(+)5,543	AGCTAGTTGCAAATGCTGAATGC	AACACGCTTATCGACCTGACC	55 bp	64^0c
GTPbp4					
GTPbp4 #1	(-)4,919	GGTTTGGCGATATTTGTGG	CCAATCAACTCTTTCCATGC	59 bp	64^0c
GTPbp4b #2	(-)830	TGGCAACACCTGAGAAAGG	AAGCCACCCATTTCTTTACC	85 bp	64^0c
GTPbp4b #3	(+)3,655	GGCTTGACAGGGTCTTTGG	CAAACCTGCAGCTCTGATCC	57 bp	64^0c
GTPbp4b #4	(+)8,950	TGTAGAAACGCTGGGTTTGG	GAAGCACATTTCCCAACAGG	56 bp	64^0c
GTPbp4b #5	(+)16,398	GTAGGCAAGAACAGCCTTCC	TGCTTTGCAACCTCCTTACC	81 bp	64^0c
GTPbp4b #6	(+)22,616	TGGTGGTCTGAGAGAGAGTGG	ACCAAAGCCAGTATGTCAACC	57 bp	64^0c

cDNA Primers

Serpina7#1	TTGTGGGATAGAATTTGGCTAC	TTTGTGTCACCAGAACATCCTC	163 bp	60^0c
Serpina7#2	AAGGCTGTGCTACACATTGG	CGGATAACAGGGTGAAGAGG	104 bp	64^0c
Lpl	GAGCGAGAACATTCCCTTCA	TCTGAGTCTCTCCGGCTTTC	203 bp	55^0c
Krt1-23	TCGATACTCCTGCCGTCTCC	TGACTCAGATCCATCCATCG	205 bp	60^0c
ATP11a	GGCATATCTGCACTGACTGG	ATTGCATTCACCAAGTGACG	167 bp	64^0c
CD36	GCAAAGTTGCCATAATTGAGTCC	GTCTGTGCCATTAATCATGTCG	86 bp	60^0c
Scd2	TGGGATAATATTCCTGACCTACC	ACGTCATCTGGGACATAGGC	163 bp	64^0c
Thrsp	GAGTGCATCTGTGGACTTGG	GAGTAACTGCGACATGACACC	198 bp	60^0c
GTPbp4	AATGATGGAAATCCGACAGC	TGTCCACACCAAGACTACGC	164 bp	60^0c
Succinate recep	GGTCCACATGAATCAGAAGG	ACACGCTTATCGACCTGACC	261 bp	60^0c
Androgen recep	CTGCTCAGTAGAGTGAATGTTGC	GCCTTCTCCATGGTTCTCC	196 bp	60^0c

Figure 1, supplement

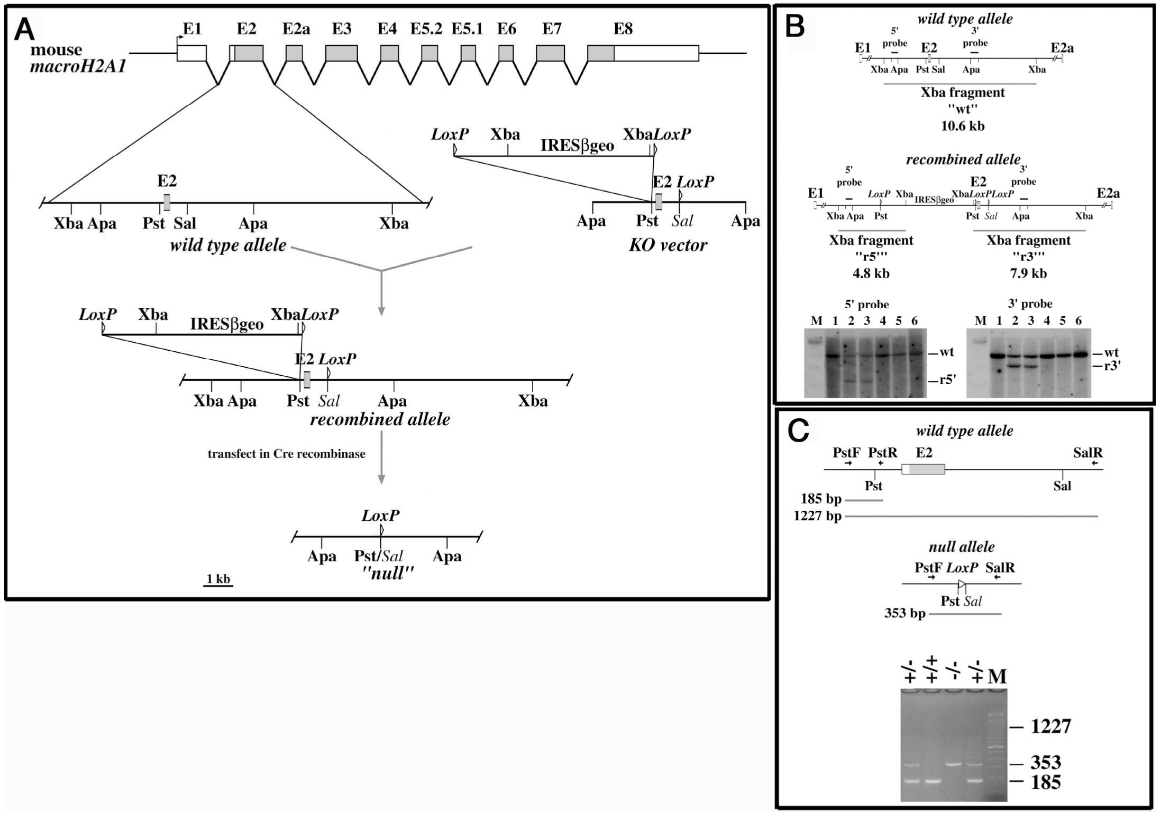

Fig. 1, supplement. Strategy used for making a *macroH2A1* knockout and identifying recombined and knockout alleles. (**A**) Diagram of exon structure of *macroH2A1* is at top; exon 5.2 is used in macroH2A1.2 and exon 5.1 in macroH2A1.1. Below on the left is a map of the wild type allele around exon 2 (E2) and on the right is a diagram of our KO vector; the cloning vector is not shown. The bottom half shows a map of the recombined allele before and after Cre mediated recombination between *lox*P sites. **(B)** Southern blots with 5' and 3' probes showing homologous recombination in 2 ES cell clones, lanes 2 and 3. **(C)** PCR genotype assay. PCRs with 1 forward primer, PstF, and 2 reverse primers, PstR and SalR, were used. Wild type allele produces a fragment of 185 bp (the 1227 bp fragment is usually not seen) while null allele produces a fragment of 353 bp.