

# Supporting Information

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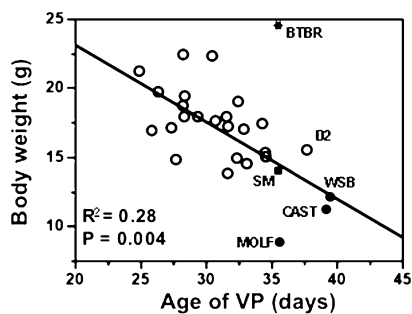


Fig. S1. Correlation between the age of vaginal patency (VP) and body weight at 38 d among inbred strains.

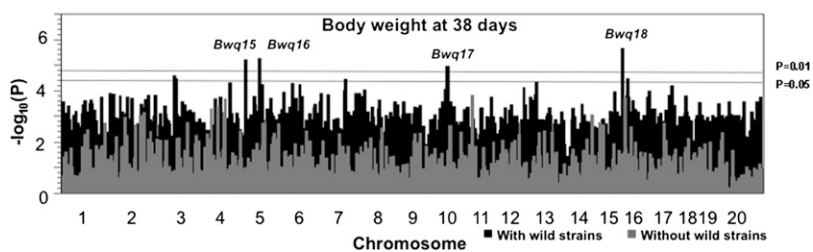


Fig. S2. Haplotype association mapping for body weight at 38 d. Dashed lines represent  $P = 0.01$  and  $P = 0.05$  in the permutation test ( $n = 1,000$ ). Black bars are scans including wild-derived strains; gray bars are scans without wild-derived strains.

**Table S1. Lifespan parameters of inbred strains**

Strain	Female (d)							Male (d)						
	Normal death	Censored	Mean	SEM	Median	95% CI	25~75% death	Normal death	Censored	Mean	SEM	Median	95% CI	25~75% death
129S1/SvlmJ	32	0	787	28	781	673~869	666~923	32	0	878	23	879	809~959	798~991
A/J	32	0	631	23	654	610~694	531~745	30	2	618	23	623	555~681	537~708
AKR/J	31	1	276	17	251	224~266	214~321	32	0	293	12	288	245~325	238~327
BALB/cByJ	32	0	734	27	771	715~819	669~839	32	0	664	36	711	527~758	508~804
BTBR T+ tf/J	32	0	580	24	604	547~644	533~662	32	0	592	28	568	456~694	441~722
BUB/BnJ	24	8	611	45	625	457~722	456~768	25	7	586	52	493	354~855	354~873
C3H/HeJ	29	3	727	23	777	659~813	622~820	32	0	719	25	721	630~820	621~834
C57BL/10J	32	0	829	41	888	692~908	653~993	27	5	720	39	792	733~849	677~852
C57BL/6J	29	3	858	33	866	782~952	776~999	32	0	894	20	901	859~929	832~958
C57BLKS/J	32	0	739	38	853	672~873	584~888	32	0	815	31	823	784~889	770~912
C57BR/cdJ	32	0	806	36	876	792~905	775~926	32	0	831	24	849	754~907	733~938
C57L/J	32	0	713	14	725	706~737	700~744	32	0	703	17	732	660~755	658~766
CAST/EiJ	17	8	578	53	671	475~748	475~763							
CBA/J	30	2	636	32	652	532~777	475~786	32	0	647	30	665	539~750	520~793
DBA/2J	32	0	580	39	650	413~707	355~785	32	0	595	40	698	492~745	391~758
FVB/NJ	29	3	705	50	760	602~869	564~944	25	7	620	37	591	562~693	553~708
KK/HIJ	32	0	575	24	593	551~614	524~646	32	0	635	24	633	548~693	539~707
LP/J	32	0	786	38	808	721~875	708~956	32	0	806	20	815	723~834	721~859
MOLF	32	0	681	30	695	590~736	579~792	32	0	587	23	639	557~651	538~668
MRL/MpJ	31	1	534	22	554	452~603	415~640							
NOD.B10Sn-H2/J	32	0	617	35	661	556~740	529~755	31	1	670	40	696	550~773	501~878
NON/ShiLtJ	31	1	724	25	750	631~819	617~840	32	0	821	25	845	799~904	786~915
NZO/HILtJ	32	0	548	33	569	405~682	393~691	31	1	467	35	423	286~568	283~637
NZW/LacJ	32	0	730	26	730	617~813	604~835	32	0	802	42	780	642~977	600~1,003
P/J	32	0	676	32	686	560~792	553~813							
PL/J	32	0	462	24	408	386~512	380~520	32	0	471	23	463	365~538	365~557
PWD/PhJ	32	0	786	36	854	697~921	673~941	27	5	717	48	813	578~901	575~905
RIIS/J	32	0	786	19	792	735~842	715~860	32	0	847	19	860	799~926	772~940
SJL/J	30	2	510	30	488	393~560	373~609	16	16	496	32	514	392~568	470~574
SM/J	32	0	732	26	753	712~786	691~789	31	1	731	31	783	741~818	711~833
SWR/J	31	1	644	37	654	548~743	516~812	32	0	655	46	714	411~812	377~852
WSB/EiJ	32	0	853	64	954	713~1,131	650~1,169	32	0	809	64	953	662~1,050	430~1,101
Total	984	33	672	7	693	677~708	533~833	883	45	684	8	720	706~736	532~849

Data updated since 2009 (1).

1. Yuan R, et al. (2009) Aging in inbred strains of mice: Study design and interim report on median lifespans and circulating IGF1 levels. *Aging Cell* 8:277-287.

**Table S2. Cross-strains comparison of ages of vaginal patency**

Strain	Abbreviation		Mean	SEM	No.
PWD/PhJ	PWD*	A	42.9	0.7	43
WSB/EiJ	WSB*	B	39.5	0.8	42
CAST/EiJ	CAST*	A B C D	39.2	2.0	10
DBA/2J	D2	B C	37.7	0.7	51
MOLF/EiJ	MOLF*	C D E F	35.6	0.9	29
C57BL/6J	B6	C D E F	35.6	0.2	29
BTBR <i>T<sub>+</sub> tff/J</i>	BTBR	C D E	35.5	0.3	47
SM/J	SM	C D E F H	35.5	1.2	20
LP/J	LP	C D E F G H	34.6	0.8	26
SJL/J	SJL	D E F H	34.5	1.0	51
PL/J	PL	E F G H I J	33.1	0.3	16
C57BR/cdJ	BR	E F G H I	32.9	0.7	28
BALB/cByJ	cBy	F G H I	32.5	0.4	50
RHIS/J	R3	E F G H I J K L	32.4	0.3	19
NZW/LacJ	NZW	E F G H I J K L M	31.7	0.7	20
C57BL/10J	B10	G I J L	31.7	0.6	60
C57BLKS/J	BKS	G H I J K L	31.6	0.4	38
P/J	P	C D E F G H I J K L M N O P	31.0	0.4	4
A/J	A	I J K L M	30.7	0.6	50
KK/Hij	KK	I J K L M N	30.5	0.5	37
C3H/HeJ	C3H	J K L M N O	29.4	0.5	53
MRL/MpJ	MRL	K M N O P	28.5	0.3	35
CBA/J	CBA	M N O P	28.4	0.5	55
129S1/SvImJ	129S1	M N O P	28.4	0.4	47
AKR/J	AKR	K L M N O P	28.3	0.5	25
NOD.B10Sn-H2/J	NOD.B10	K M N O P	28.3	0.7	34
SWR/J	SWR	N O P	27.7	0.4	74
C57L/J	L	K L M N O P	27.4	0.4	13
BUB/BnJ	BUB	P	26.4	0.4	60
FVB/NJ	FVB	P	25.9	0.4	74
NON/ShiLtJ	NON	O P	24.9	0.6	11

\*Wild-derived inbred strains. Strains connected by different letters are significantly different ( $P < 0.05$ ).  $P$  values were adjusted by the Tukey HSC method.

**Table S3. Lifespan parameters of B6 and B6.C3H-Igf1 mice**

Strain	Female			Male		
	Mean (SEM)	Median (95% CI)	No.	Mean (SEM)	Median (95% CI)	No.
B6	810 (32)	839 (756~909)	32	866 (28)	872 (796~951)	32
B6.C3H-Igf1	656 (24)	683 (606~745)	70	831 (24)	888 (825~924)	60

CI, confidence interval.

**Table S4. Haplotype groups of *Vpq1***

HAM ID	SNP Score	SNP name	Position Chr (bp)	CAST	MOLF	PWD	WSB	SM	BTBR	B10	B6	BLK	D2	KK	PL	R3	A	AK	cBy	C3	BR	CBA	FVB	L	LP	MRL	NOD	NON	NZW	SJL	SWR	129S1	BUB	
<i>Vpq1</i>	5.54	rs13477738	4 62690603	2	2	2	2	2	3	3	3	3	3	3	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
	5.54	NES09402911	4 62730288	2	2	2	2	2	3	3	3	3	3	3	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
	5.54	NES09401593	4 62761940	2	2	2	2	2	3	3	3	3	3	3	3	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Haplotype group				H-I					H-II					H-III																				

Score of each quantitative trait locus (QTL) is  $-\log_{10}P$ . SNP positions are from National Center for Biotechnology Information (NCBI) build 37. Haplotypes of each SNP were determined using the Hidden Markov Model (HMM) method. The combination of haplotypes of SNPs for each haplotype association mapping (HAM) ID defines the haplotype groups, which are used in Fig. 3. Chr, chromosome.

**Table S5. Haplotype groups of *Vpq2***

HAM ID	SNP Score	SNP name	Position Chr (bp)	CAST	MOLF	PWD	WSB	SM	129S1	LP	NZW	SJL	C3	CBA	BTBR	B10	B6	BLK	D2	KK	P	PL	R3	BR	L	A	AK	cBy	BUB	FVB	MRL	NOD	NON	SWR
<i>Vpq2</i>	5.27	16-37537086	16 37682809	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	3	3	0	0	0	0	0	0	0	0	0
	5.27	NES12101893	16 37705326	1	1	1	1	1	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	3	3	0	0	0	0	0	0	0	0	0
Haplotype group				H-I					H-II					H-III					H-IV															

Score of each QTL is  $-\log_{10}P$ . SNP positions are from NCBI build 37. Haplotypes of each SNP were determined using the HMM method. The combination of haplotypes of SNPs for each HAM ID defines the haplotype groups, which are used in Fig. 3.

**Table S6. Haplotype groups of *Vpq3***

HAM ID	SNP Score	SNP name	Position Chr (bp)	CAST	MOLF	PWD	WSB	SM	A	BR	L	SJL	D2	PL	R3	B10	B6	BLK	129S1	LP	NZW	BTBR	KK	P	AK	cBy	BUB	C3	CBA	FVB	MRL	NOD	NON	SWR
<i>Vpq3</i>	5.4	NES12227206	16 74844038	3	3	3	3	2	2	2	2	2	2	2	2	0	0	0	1	1	1	1	1	1	4	4	4	4	4	4	4	4	4	4
Haplotype group				H-I					H-II					H-III					H-IV					H-V										

Score of each QTL is  $-\log_{10}P$ . SNP positions are from NCBI build 37. Haplotypes of each SNP were determined using the HMM method. The combination of haplotypes of SNPs for each HAM ID defines the haplotype groups, which are used in Fig. 3.

**Table S7. Candidate genes in *Vpq1*, *Vpq2*, and *Vpq3***

	Candidate genes	Location*
<i>Vpq1</i>	<i>Zfp618</i>	Chr4: 62,626,607–62,800,742
	<i>Whrn</i>	Chr4: 63,075,944–63,157,025
<i>Vpq2</i>	<i>Sema5b</i>	Chr16: 35,541,231–35,664,818
	<i>Hcls1</i>	Chr16: 36,935,101–36,963,300
	<i>Fbxo40</i>	Chr16: 36,963,546–36,990,553
	<i>Stxbp5l</i>	Chr16: 37,115,028–37,385,048
	<i>Polq</i>	Chr16: 37,011,872–37,095,483
	<i>Loc100043217</i>	Chr16: 35,894,376–35,921,294
<i>Vpq3</i>	<i>Robo1</i>	Chr16: 72,663,394–73,046,340
	<i>Nrip1</i>	Chr16: 76,287,645–76,374,072

\*NCBI build 37. We extended 2 Mb at each side of *Vpq1*, 2, and 3 to search for candidate genes.