

Supplementary Figure 1. Progeria in *Zmpste24*-deficient mice. *a*) Photograph of a 4-month-old *Zmpste24*^{-/-} mouse showing a strong progeric phenotype with alopecia, wrinkled skin, lordokyphosis and reduced body weight. *b*) Survival curve of *Zmpste24*^{-/-} mice (open diamonds, n=45). All wild-type animals (solid squares, n=40) stayed alive during this study. *Zmpste24* deficiency causes premature death. *c*) Wound healing assay in *Zmpste24*^{-/-} (open diamonds, n=11) and control (solid squares, n=11) mice. *Zmpste24* deficiency causes a delay in wound healing. *d*) Susceptibility to 5-fluorouracil (5FU) treatment of *Zmpste24*^{-/-} (open diamonds, n=5) and control (solid squares, n=4) mice. All *Zmpste24*-null mice but no control mouse died within 5 days after treatment. Error bars represent SEM.

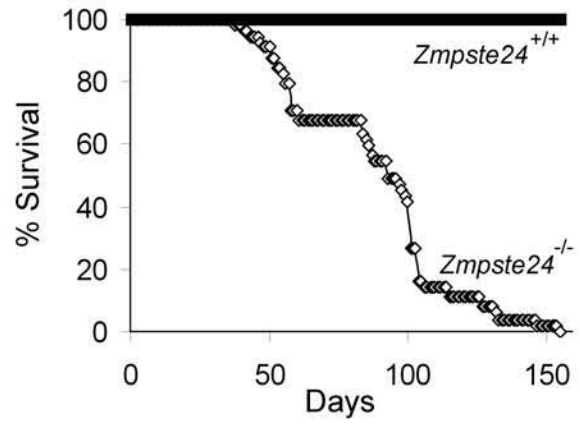
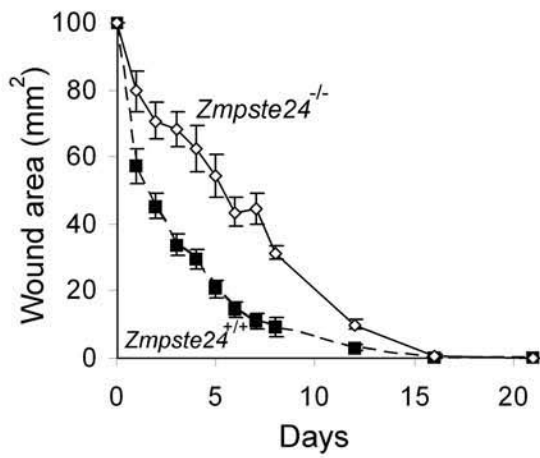
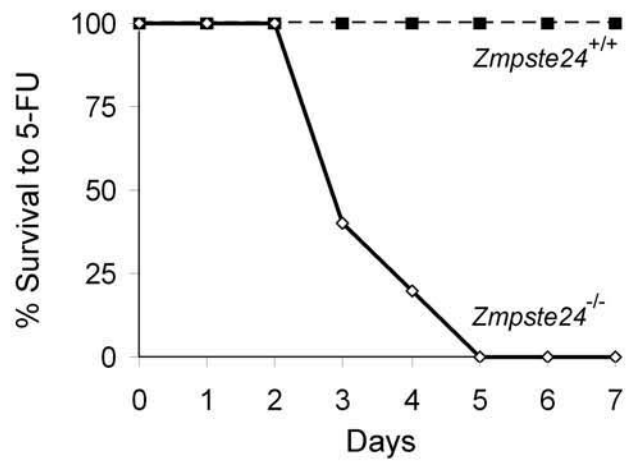
Supplementary Figure 2. *p21* overexpression in tissues from *Zmpste24*-null mice. *a*) *p21* *in situ* hybridization in liver and kidney from *Zmpste24*-null and control mice. Hepatocytes and kidney epithelial cells from *Zmpste24*-deficient mice showed increased levels of *p21* mRNA as compared with the corresponding controls. *b*) Western-blot analysis revealed increased levels of p21 protein in livers from severely affected *Zmpste24*-deficient mice.

Supplementary Figure 3. *p21* overexpression in *Zmpste24*-deficient mice increases with age and phenotype severity. Percentage of *Zmpste24*^{-/-} mice showing *p21* overexpression in <50 (n=6), 50-100 (n=12) and 101-150 (n=12) day-old mice. Clear and dark grey indicate mild and severe phenotype, respectively.

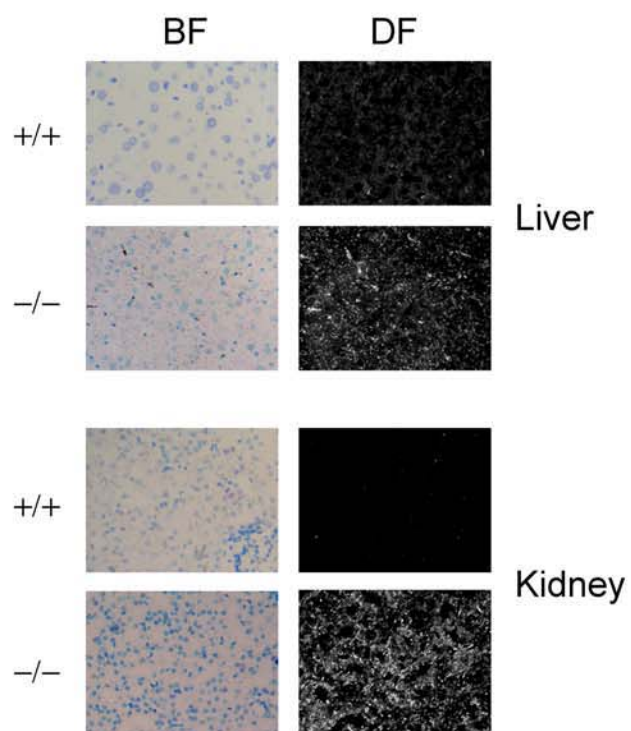
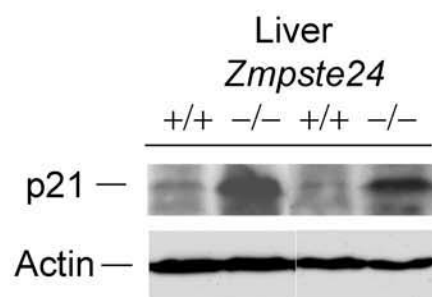
Supplementary Figure 4. Heterochromatin alterations in *Zmpste24*-deficient mice. Representative electron micrographs showing nuclei of wild-type and *Zmpste24*^{-/-} hepatocytes. Note the reduced size, irregular shape and heterochromatin accumulation in the mutant nucleus. The mean size of nuclei from wild-type cells was 10.3 ± 1.2 μm while the size of nuclei from *Zmpste24*-deficient cells was 8.8 ± 1.1 μm. Scale bar, 5 μm. *b*) Nuclear abnormalities in *Zmpste24*^{+/+}, *Zmpste24*^{-/-}, *Zmpste24*^{-/-}*Lmna*^{+/-} and *Zmpste24*^{-/-}*p53*^{-/-} adult fibroblasts. *Top*. Photographs of 4%-formaldehyde-fixed adult fibroblasts stained with DAPI showing large abnormalities in *Zmpste24*^{-/-} and *Zmpste24*^{-/-}*p53*^{-/-} nuclei and partial rescue of the normal nuclear shape in *Zmpste24*^{-/-}*Lmna*^{+/-} fibroblasts. *Bottom*. Frequency (%) of cells with nuclear abnormalities observed in each genotype. Error bars represent SEM and * indicates *p*-value <0.05.

Supplementary Figure 5. Lack of increased apoptosis in *Zmpste24*-null mice. Apoptosis assay of *Zmpste24*^{-/-} (n=3) and control fibroblasts (n=3). Annexin V immunofluorescence and propidium iodide staining showed no significant differences in the levels of apoptosis between *Zmpste24*-deficient and wild-type adult fibroblasts. Error bars represent SEM.

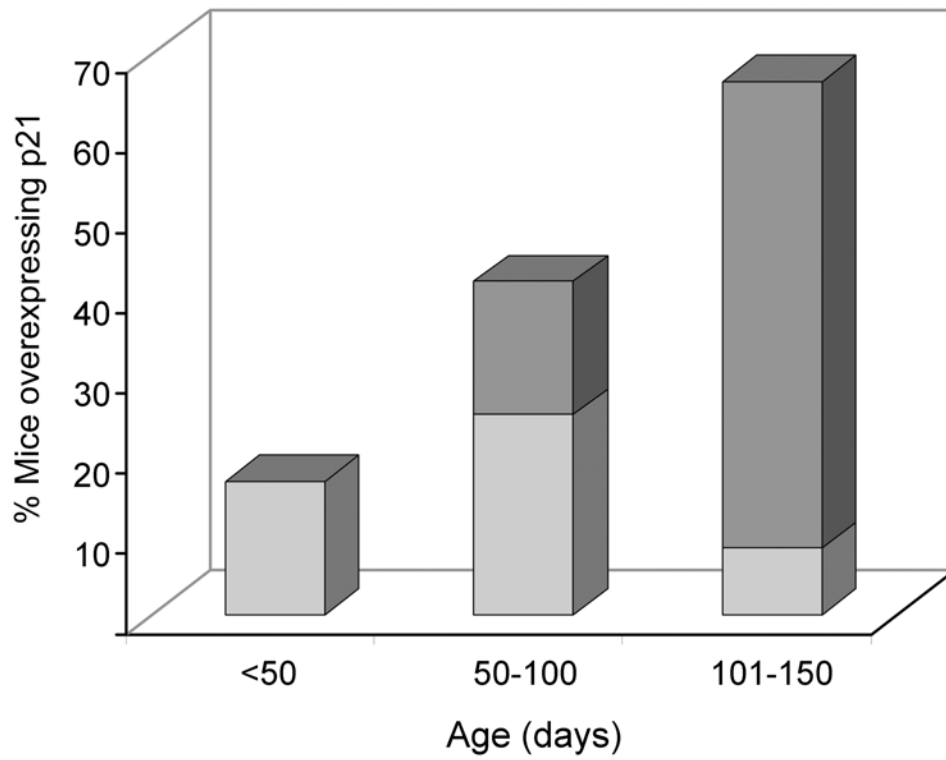
Supplementary Figure 6. Retinoblastoma protein levels (pRb) are decreased in liver from *Zmpste24*-deficient mice. Western-blot analysis of liver extracts (120 μg/lane) from 3-month-old *Zmpste24*^{-/-} mice and control littermates showing a reduction of pRb levels in *Zmpste24*-null mice. β-actin was used as loading control.

a**b****c****d**

Supplementary figure 1

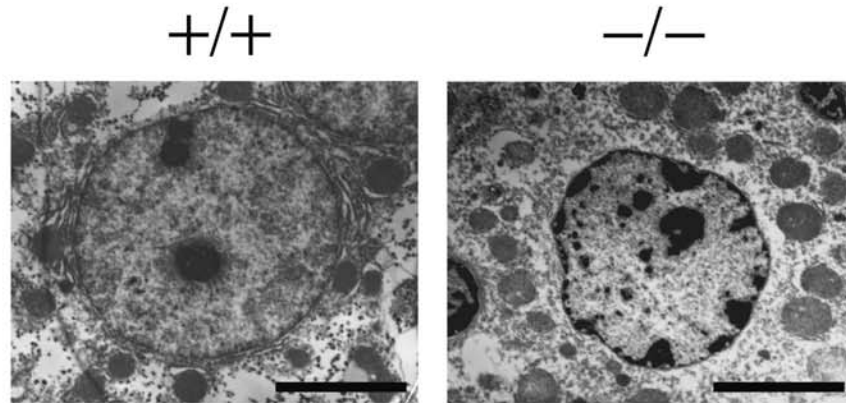
a**b**

Supplementary figure 2



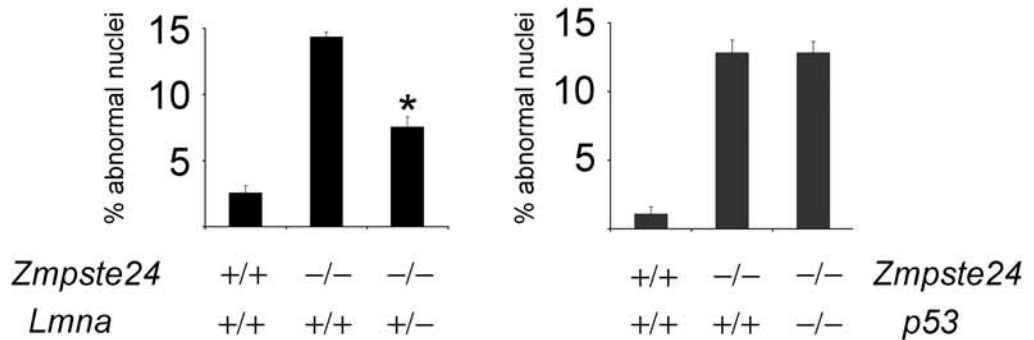
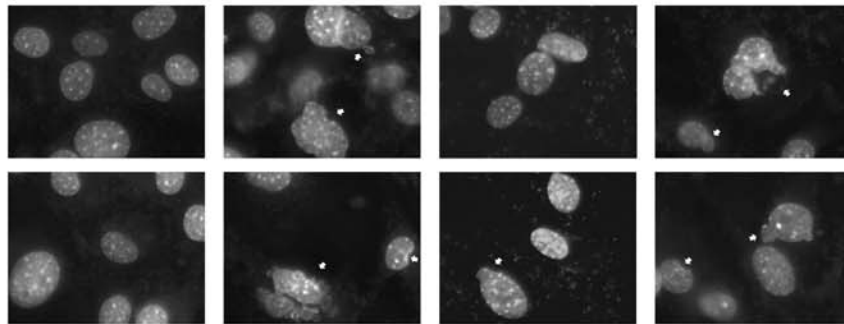
Supplementary figure 3

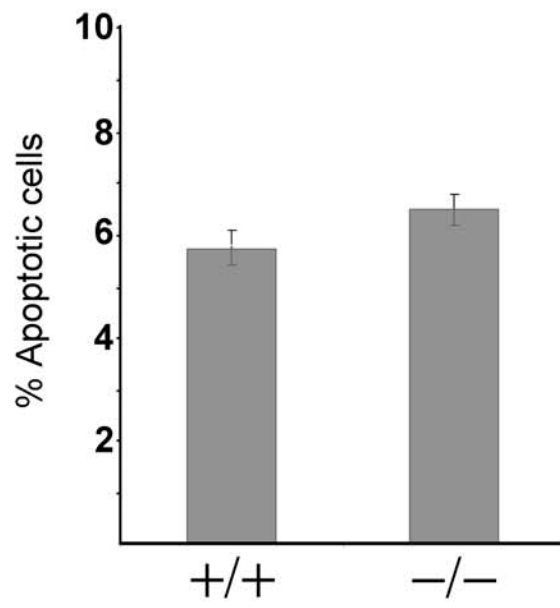
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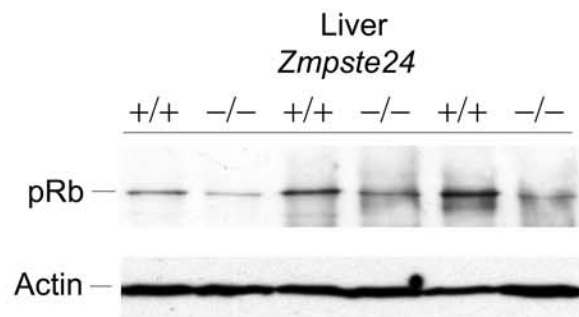
b

<i>Zmpste24</i>	+/+	-/-	-/-	-/-
<i>Lmna</i>	+/+	+/+	+/-	+/+
<i>p53</i>	+/+	+/+	+/+	-/-





Supplementary figure 5



Supplementary figure 6

Supplementary Table 1. Affymetrix U74Av2 probes showing a greater than 5-fold increase or decrease in liver from Zmpste24/Face1-deficient mice were sorted by p-value and fold-change, and the top 50 up- and down-regulated sequences were selected. Expression data of the same genes in liver of Lmna-deficient mice and in heart of Zmpste24-deficient mice are also shown.

Id	Accession	Name	Gene symbol	control liver Signal	Face1-liver Signal	Face1-liver fold	Face1-liver Change	p-value	Lmna-liver Signal	Lmna-fold	Lmna-Change	p-value	control heart Signal	Face1-heart Signal	Face1-heart Fold	Face1-heart Change	p-value
102779_at	X54149	growth arrest and DNA-damage inducible 45 beta	Gadd45b	16,4	547,7	35,753	I	0	307,6	27,0958	I	0	76,3	124,6	1,777685	I	0,00012
102292_at	U00937	growth arrest and DNA-damage inducible 45 alpha	Gadd45a	19	695,8	31,779	I	0	31,4	1,68179	NC	0,04102	112,3	112,3	1,433955	I	0,00027
103460_at	AI849939	HIF-1 responsive RTP801	RTP801	65,9	2962	26,355	I	0	2501,2	27,2843	I	0	439,5	747,1	1,693491	I	1E-06
98088_at	X13333	CD14 antigen	Cd14	47,5	1938	25,634	I	0	557,4	8,39773	I	0	192	323,9	1,765406	I	1E-06
95731_at	AI843106	p53 regulated PA26 nuclear protein	Pa26	78,5	2004,1	23,425	I	0	1038,6	13,2691	I	1E-06	407,4	2133,9	4,626753	I	0
92202_g_at	AI553024	expressed sequence AI467657	AI467657	16,1	374,2	22,943	I	1E-06	404,8	20,1122	I	0	65,2	953,8	10,55606	I	1E-06
101979_at	AF055638	growth arrest and DNA-damage inducible 45 gamma	Gadd45g	243,4	4769,4	22,785	I	1E-06	1539,7	6,36429	I	0	36,5	178,9	3,732132	I	8E-06
94881_at	AW048937	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	25,1	507,4	22,009	I	0	255,1	8,87656	I	0	223,1	711,7	3,031433	I	0
93129_at	U45665	cut-like 2 (Drosophila)	Cutl2	5,5	116,4	20,821	I	1E-06	13,1	1,05702	NC	0,41123	7,4	6,3	-1,071773	NC	0,91678
100010_at	U36340	Kruppel-like factor 3 (basic)	Klf3	55,3	881,6	20,393	I	1E-06	221,8	5,42642	I	5E-06	4,6	47	6,498019	I	0,00211
104712_at	L00039	myelocytomatosis oncogene	Myc	10,4	156,8	16,45	I	1E-06	93,3	6,72717	I	1E-06	13	22,5	1,647182	NC	0,16083
94378_at	U94828	regulator of G-protein signaling 16	Rgs16	530,5	8694,8	15,78	I	0	2698,1	4,75683	I	0	71,2	56,4	-1,164734	NC	0,52981
96146_at	D83745	B-cell translocation gene 3	Btg3	22,5	225	14,32	I	1E-06	159,7	4,43828	I	0	89,4	195,2	2,411616	I	1,3E-05
98320_at	Y12657	cytochrome P450, 26, retinoic acid A1	Cyp26a1	23,2	359,9	13,833	I	1E-06	73,2	1,93187	I	6E-06	4,4	21,4	3,116658	NC	0,00679
104155_f_at	U19118	activating transcription factor 3 similar to Serine/threonine-protein kinase pim-3	Atf3	27,8	492	13,548	I	0	86,2	2,67586	I	7E-06	77,4	638,6	6,543216	I	0
96841_at	AW046627	casein kinase 1, delta	Csnk1d	82,7	1128,9	12,641	I	0	389,1	3,68075	I	3E-06	81,1	288,7	2,928171	I	2E-06
103065_at	M73696	solute carrier family 20, member 1	Slc20a1	75,3	1314,4	12,641	I	0	1244,3	13,5479	I	0	21,7	34,4	1,310393	NC	0,5
100431_at	U42467	leptin receptor	Lepr	76,4	662,4	11,876	I	1E-06	688,1	8,57419	I	1E-06	23,1	21	1,257013	NC	0,17013
98067_at	U09507	cyclin-dependent kinase inhibitor 1A (P21)	Cdkn1a	53,8	589,1	11,081	I	0	265,7	5,24157	I	3,7E-05	279	555,7	2,42839	I	0
94288_at	J03482	H1 histone family, member 2	H1f2	278,8	2889,1	10,267	I	0	345,6	1,25701	I	0,00166	396,2	3233,2	8,282119	I	0
96156_at	AA874329	ESTs		28,6	334,3	9,4479	I	1E-06	78,5	2,28153	I	5E-06	157,9	527,1	2,86791	I	0
97181_f_at	M10062	intracisternal A particles	Iap	240,9	2558,6	9,2535	I	0	859,2	2,88786	I	0	236,6	1062,3	4,346939	I	1E-06
104052_at	AI840921	similar to CG9578 gene product	LOC226591	107,8	944,3	9,1896	I	0	333,2	3,27161	I	0	154,3	131,4	-1,172835	NC	0,6596
101583_at	M64292	B-cell translocation gene 2, anti-proliferative	Btg2	134,2	1674	9,1261	I	0	978,8	7,83536	I	2E-06	245,1	800,4	2,445281	I	1,5E-05
93907_f_at	M17551	intracisternal A particles	Ccr4	114,1	1437,3	9,0631	I	0	705,9	4,11246	I	0	162,4	545,7	4,14106	I	0
93909_f_at	X04120			89,5	656,4	8,7543	I	0	317,4	3,36359	I	1E-06	67,6	316,2	5,735821	I	5E-06
97838_at	AA684508	RNA, U22 small nucleolar	Rnu22	45,5	344,9	8,6338	I	1E-06	215,1	4,82323	I	1E-06	58,7	187,2	4,346939	I	0
160547_s_at	AI839138	thioredoxin interacting protein	Txnip	267	2180,9	8,1117	I	0	1770,6	7,67411	I	0	914,1	910,2	1,079228	NC	0,5
93284_at	D78135	cold inducible RNA binding protein	Cirbp	88	685,9	7,6211	I	0	347,4	3,22657	I	3E-06	140,4	1149,5	6,916298	I	0
98254_f_at	AW209004	intracisternal A particles	Iap	412,2	4755,6	7,5685	I	0	1339,9	2,82843	I	0	389,8	2041,3	3,630077	I	1E-06
161436_s_at	AV345565	adenosine deaminase, RNA-specific, B1	Adarb1	40,5	293	7,5162	I	1E-06	68,9	1,82766	I	0,00024	53,9	123,1	1,658639	I	5E-06
103334_at	AF028242	calcitonin gene-related peptide receptor component protein	Crcp	110	518,1	7,4643	I	1E-06	243,2	2,31338	I	1,9E-05	47,7	74,8	1,569168	NC	0,03783
161951_f_at	AV360914	fibrosin	Fbs	43,9	311	7,0616	I	1E-06	129,6	2,42839	I	4E-06	95,5	54,4	-1,515717	NC	0,71893
104389_at	AW049360	RIKEN cDNA 1700017B05 gene	1700017B05Rik	32,3	395,4	6,8685	I	1E-06	100,1	2,15846	I	0,00029	67	46	-1,189207	NC	0,64579
99027_at	L35049	Bcl2-like	Bcl2l	151,3	1080,2	6,8211	I	0	334,4	1,60214	I	0,00044	202,4	801,3	3,160165	I	1E-06
96614_at	AA763368	ESTs, Moderately similar to Y247 HUMAN Hypothetical		137,4	890,1	6,6807	I	0	631,8	4,99332	I	0	257,1	480,6	1,892115	I	6E-06
100599_at	M94087	activating transcription factor 4	Atf4	371,5	2991,7	6,4086	I	1E-06	1063,1	2,44528	I	1E-06	259,3	733,6	2,445281	I	5E-06
103098_at	AW045765	brain-specific angiogenesis inhibitor 1-associated protein 2	Baiap2	126,7	865,9	6,4086	I	1E-06	117,5	1,6358	I	0,00022	36,5	142,2	3,317278	NC	0,06981
98295_at	AF047726	cytochrome P450, 2c39	Cyp2c39	498,6	2642,7	6,2767	I	1E-06	2869	7,06162	I	0	14,6	83,8	3,506423	NC	0,0394
95721_at	AW120722	MAP kinase-activated protein kinase 2	Mapkapk2	230,3	2037,6	6,105	I	0	495,1	1,82766	I	0	1707,1	2458,2	1,484524	I	0
94928_at	X87128	tumor necrosis factor receptor superfamily, member 1t	Tnfrsf1b	113,3	706,5	6,0629	I	0	298,8	2,80889	I	0	48,6	52	-1,132884	NC	0,68658
101007_at	AI845732	MAP kinase-interacting serine/threonine kinase 2 similar to Orphan nuclear receptor NR1D1 (V-erbA)	Mknk2	331,7	2195,9	5,6962	I	0	575,4	2,07053	I	0	388	1214,7	2,657372	I	1E-06
98507_at	AI834950		LOC217166	120,6	846,3	5,6569	I	1E-06	123,3	1,11729	NC	0,5	106,4	325,3	2,657372	I	0
93670_at	AW048233	Ets2 repressor factor	Erf	59,8	327,9	5,4642	I	0	113,6	1,64718	I	2,3E-05	71,6	148,4	1,827663	I	0,00013
99633_at	AB017608	neurochondrin	Ncdn-pending	50,8	293,3	5,3517	I	1E-06	67,4	1,43396	NC	0,01368	101,8	50,4	-1,931873	NC	0,90785
160307_at	AW121695	phosphatidylinositol 4-kinase type 2 alpha	Pi4k2a-pending	89,6	559,8	5,2054	I	1E-06	105,8	1,07923	NC	0,12316	62,1	201,3	3,363586	I	0,00025
97410_at	AW049193	fibrosin	Fbs	107,5	747,9	5,1694	I	0	224,3	1,60214	I	7,9E-05	115,1	95,6	-1,265757	NC	0,8843
93488_at	AI840579	Mus musculus, Similar to hypothetical protein FL110534.		40,9	250,4	5,1337	I	0	163,4	3,50642	I	1E-06	47	105,7	1,717131	I	2,1E-05
160273_at	AA960603	zinc finger protein 36, C3H type like 2	Zfp36l2	211,7	1367,3	5,0982	I	0	1013,3	4,11246	I	0	196,7	258	1,385109	I	5,9E-05

Id	Accession	Name	Gene symbol	control liver Signal	Face1-liver Signal	Face1-liver fold	Face1-liver Change	p-value	Lmna-liver Signal	Lmna-fold	Lmna-Change	p-value	control heart Signal	Face1-heart Signal	Face1-heart Fold	Face1-heart Change	p-value
93775_at	AI841894	DNA segment, Chr 12, ERATO Doi 647, expressed	D12Erd647e	515	80,5	-5,028	D	1	233,9	-2,8879	D	0,99998	860,8	142	-5,028053	D	1
160829_at	U44088	T-cell death associated gene	Tdag	325,5	54	-5,169	D	1	207,9	-1,181	NC	0,5	59,6	99,1	1,347234	I	0,00014
96605_at	AI787183	RIKEN cDNA 0610011104 gene	0610011104Rik	960,1	103,3	-5,205	D	1	218,5	-2,3457	D	1	53,8	64,6	1,385109	NC	0,5
97316_at	AJ011864	RIKEN cDNA 1300002P22 gene	1300002P22Rik	180,3	30,2	-5,242	D	1	706,8	3,65533	I	0	9,5	0,8	-4,531536	NC	0,99683
94398_s_at	AF040094	inositol polyphosphate-5-phosphatase, 75 kDa	Inpp5b	150	21,8	-5,242	D	1	72,4	-2,0562	NC	0,98979	18,8	11,4	-1,049717	NC	0,5
103422_at	M63695	CD1d1 antigen	Cd1d1	617,2	96,2	-5,242	D	1	384,2	-1,6358	NC	0,99122	33,6	15,4	-1,94531	NC	0,89142
93793_at	AW122780	LIM and SH3 protein 1	Lasp1	214,6	29,8	-5,426	D	1	55,9	-2,8879	D	0,99995	96,6	110,2	-1,494849	NC	0,90472
101045_at	U96116	hydroxysteroid (17-beta) dehydrogenase 10	Hsd17b10	1823,6	300,9	-5,54	D	1	2215	-1,0497	NC	0,47019	697,5	1169,3	1,526259	I	3E-06
160569_at	AI848235	RIKEN cDNA 2310008M10 gene	2310008M10Rik	223,8	43,2	-5,618	D	1	95,4	-2,3295	D	0,99999	282,8	109,2	-2,928171	D	1
96231_at	AW123780	RIKEN cDNA 2010012D11 gene	2010012D11Rik	587,1	153,8	-5,618	D	1	148,4	-3,4343	D	0,99999	116	74,7	-2	D	0,99982
160376_at	AW125508	RIKEN cDNA 1110029F20 gene	1110029F20Rik	944,7	192,3	-5,618	D	1	212	-4,1125	D	1	1486,4	610,6	-3,09513	D	1
93434_at	AF026074	sulfotransferase-related protein SULT-X1	Sult-x1	180,4	28,5	-5,856	D	1	26,7	-7,4643	D	0,99999	25,8	18,7	-1,156688	NC	0,58877
102820_at	M60358	cytochrome P450, 2b13, phenobarbital inducible, type aldehyde dehydrogenase family 3, subfamily A2	Cyp2b13	191,8	46,9	-5,938	D	1	119,4	-1,6586	NC	0,92765	6	3,6	-1,464086	NC	0,37529
99559_at	U14390	sulfotransferase family 1B, member 1	Sult1b1	141,7	24,5	-5,979	D	1	112,7	-1,2226	NC	0,5	8,4	8,7	1,591073	NC	0,5
101877_at	AI854432	Mus musculus, RIKEN cDNA 4930445G01 gene, clone		599,1	50	-6,021	D	1	379,6	-1,5801	D	0,99947	178	159,9	-1,006956	NC	0,5
95646_at	U01170	carnitine palmitoyltransferase 2	Cpt2	1795,8	241,3	-6,021	D	1	946,8	-1,6472	D	0,99991	1616,1	246,2	-5,278032	D	0,99999
160479_at	M29394	catalase 1	Cas1	723	128,3	-6,105	D	1	615,1	-1,2142	NC	0,71259	152,4	115,5	-1,474269	MD	0,99718
102096_f_at	AI255271	major urinary protein 1	Mup1	1870,9	324,7	-6,32	D	1	125,4	-12,381	D	1	13,9	20,1	1,60214	NC	0,39674
161815_f_at	AV355798	major urinary protein 1	Mup1	3178	365	-6,821	D	1	397,4	-6,7272	D	1	12,4	8,2	-1,265757	NC	0,47019
93662_s_at	AI386093	zeta-chain (TCR) associated protein kinase (70kD)	Zap70	602,9	71,9	-6,964	D	1	22,4	-19,835	D	1	5,1	7,9	-1,385109	NC	0,5
97987_at	U66900	insulin-like growth factor binding protein, acid labile subunit	Igfals	468	77,1	-7,062	D	1	44,9	-10,126	D	1	9,5	11,7	1,06437	NC	0,0173
97402_at	M88694	thioether S-methyltransferase	Temt	1289,3	191,3	-7,516	D	1	336,2	-3,605	D	1	90,9	288,8	2,732081	I	0,00015
101991_at	D16215	flavin containing monooxygenase 1	Fmo1	793,3	117,6	-7,568	D	1	533	-1,5476	NC	0,99507	128,9	62,5	-1,777685	D	0,99999
97531_at	X95280	G0/G1 switch gene 2	G0s2	200,3	19,5	-7,621	D	1	29,6	-6,6346	D	1	327,3	115,5	-2,531513	D	1
100068_at	M74570	aldehyde dehydrogenase family 1, subfamily A1	Aldh1a1	2507	295,9	-8,112	D	1	1106,7	-2,2815	D	1	62,8	126,1	2,013911	I	1,8E-05
99535_at	AW047630	carbon catabolite repression 4 homolog (S. cerevisiae)	Ccr4	341,4	33,3	-8,168	D	1	126,3	-2,4116	D	1	206,7	257,7	1,006956	NC	0,5
101635_f_at	M16360	major urinary protein 5	Mup5	5864,4	372,8	-8,282	D	1	336,6	-11,314	D	1	3,3	6,8	-1,36604	NC	0,63178
101682_f_at	M16358	major urinary protein 4	Mup4	4040,6	318,7	-8,456	D	1	592,8	-16,336	D	1	6,1	4,1	-1,453973	NC	0,76132
93766_at	U32170	regucalcin	Rgn	1463,6	164,7	-8,515	D	1	767,2	-1,6818	D	0,99999	2,1	7,7	3,160165	NC	0,22724
160297_at	AW121431	Mus musculus, similar to CG15881 gene product (H.		67,7	5,4	-8,754	D	1	59,5	-1,1329	NC	0,49254	53,3	21,4	-1,866066	NC	0,99122
96134_at	AA755260	deleted in polyposis 1-like 1	Dp111	3728,9	365,6	-8,815	D	1	714,5	-4,9588	D	1	35	35,5	1,292353	NC	0,5
103963_f_at	AA914345	interferon-inducible GTPase	Iigp-pending	331,9	41,9	-9,646	D	1	199,3	-1,8921	D	0,99973	110,2	78,7	-1,547565	NC	0,99451
94414_at	X07092	ornithine transcarbamylase	Otc	1080,4	131,1	-10,34	D	1	773,7	-1,2658	NC	0,85675	8,6	3,6	-1,414214	NC	0,39674
104165_at	AJ132098	vanin 1	Vnn1	591,6	64,7	-11,16	D	1	249,6	-1,8532	D	1	28,2	14,9	-2,042024	NC	0,5
101532_g_at	AI527354	hypothetical protein MGC36398	MGC36398	2738,3	158,6	-11,63	D	1	3362,6	1,25701	NC	0,0248	34	7,7	-3,784231	NC	0,02271
104344_at	M58588	kallikrein B, plasma 1	Klkb1	217,2	10,4	-12,21	D	1	78,6	-3,8637	D	1	1,6	2,6	1,274561	NC	0,22164
102013_at	AF030513	retinol dehydrogenase type 6	Rdh6	103,8	7,3	-12,64	D	1	114,4	1,18921	NC	0,08612	3,1	3,1	-1,148698	NC	0,86504
92556_at	D45850	hydroxysteroid (17-beta) dehydrogenase 5	Hsd17b5	2551,2	239,7	-12,82	D	1	434,6	-4,6268	D	1	18,5	20,1	-1,125058	NC	0,5
101910_f_at	M16359	major urinary protein 1	Mup1	9987,3	421,5	-13	D	1	571,5	-14,123	D	1	12,2	3,7	-2,056228	NC	0,5
160951_at	AI645694	RIKEN cDNA 4632419J12 gene	4632419J12Rik	204,8	13,1	-13,83	D	1	3,6	-26,538	D	1	41,5	6,7	-7,412704	NC	0,90785
97288_at	AW260404	PDZ domain containing 1	Pdzk1	115,3	4,4	-14,42	D	1	17,1	-4,4383	D	0,99998	5,8	1,9	-2,114036	NC	0,5
96269_at	AA716963	similar to Isopenentenyl-diphosphate delta-isomerase	LOC207933	332,3	20,5	-15,35	D	1	27,2	-10,778	D	1	17	19,3	1,125058	NC	0,36119
94075_at	Y14660	fatty acid binding protein 1, liver	Fabp1	6809,6	376,5	-16	D	1	3869,2	-1,9588	D	0,99999	4,4	2,2	-1,356604	NC	0,5
96090_g_at	AI255972	RIKEN cDNA 4931406C07 gene	4931406C07Rik	411,9	22,4	-16,68	D	1	216,2	-2,3295	D	0,99996	21,3	30,1	1,613284	NC	0,5
92539_at	M16465	S100 calcium binding protein A10 (calpactin)	S100a10	1308	40	-18,77	D	1	246,7	-5,1694	D	1	786,2	202,1	-3,784231	D	1
101909_f_at	M16357	major urinary protein 3	Mup3	10462,6	335,7	-19,03	D	1	742	-14,825	D	1	12,2	2,7	-2,411616	NC	0,5
101753_s_at	X51547	P lysozyme structural	Lzp-s	112,4	3,9	-28,44	D	1	8,1	-11,158	D	1	576,2	230,2	-2,8481	D	1
99126_at	L04961	inactive X specific transcripts	Xist	180,3	2,4	-41,64	D	1	2,3	-69,551	D	1	17	18,8	1,257013	NC	0,16544
160375_at	AJ006474	carbonic anhydrase 3	Car3	379,6	3,4	-51,27	D	1	23,9	-10,853	D	1	299,1	9,1	-32,22258	D	1

Supplementary Table 2. Analysis of potential alternative splicing forms of mouse p53 mRNA in wild-type (+/+) and *Zmpste24*-deficient (-/-) mice. 0.2 g of liver cDNA were used as template for PCR reactions using 25 pmol of each of the indicated oligonucleotides. Only PCR products of the expected size were obtained in both wild-type and *Zmpste24*-deficient livers. "+" indicates presence of the corresponding band.

Oligonucleotides used	Expected size (bp)	+/+	-/-
Ex1F: 5'-tgctcacctggctaaagttctg-3' Ex3R: 5'-caggatatcttctggaggaagt-3'	248	+	+
Ex1F: 5'-tgctcacctggctaaagttctg-3' Ex5R: 5'-acgacctcgcgatgtgctgt-3'	652	+	+
Ex1F: 5'-tgctcacctggctaaagttctg-3' Ex7R: 5'-gtaaggataggctcggcggttcat-3'	892	+	+
Ex1F: 5'-tgctcacctggctaaagttctg-3' Ex9R: 5'-tgagggtgaaatactctccatcaagtg-3'	1125	+	+
Ex1F: 5'-tgctcacctggctaaagttctg-3' Ex11R: 5'-caactgggccaggaaccac-3'	1485	+	+
Ex2F: 5'-gccatggaggagtcacagtcg-3' Ex11R: 5'-caactgggccaggaaccac-3'	1326	+	+
Ex4F: 5'-ctgcccaggatgttgagga-3' Ex11R: 5'-caactgggccaggaaccac-3'	1197	+	+
Ex6F: 5'-ggctcctccccagcatcttacc-3' Ex11R: 5'-caactgggccaggaaccac-3'	778	+	+
Ex8F: 5'-gaaccttctgggacgggacag-3' Ex11R: 5'-caactgggccaggaaccac-	556	+	+
Ex10F: 5'- gatgccatgctacagaggagtct-3' Ex11R: 5'-caactgggccaggaaccac-3'	288	+	+