## **Supplementary material**

## List of analyzed genes in the liver

Symbol	Description	
Hk1	Hexokinase 1	
Nfil3	Nuclear factor, interleukin 3 regulated	
Acsl1	Acyl-CoA synthetase long-chain family member 1	
Pfkp	Phophofructokinase, platelet	
Dsp	Desmoplakin	
Akt1	V-akt murine thymoma viral oncogene homolog 1	
Atm	Ataxia telangiectasia mutated homolog (human)	
ld4	Inhibitor of DNA binding 4	
Нр	Haptoglobin	
Pde1alpha	Phosphodiesterase 1A, calmodulin-dependent	
18SrRNA	Rat 18S rRNA sequence	
Pgk1	Phosphoglycerate kinase 1	
Actb	Actin, beta	

Table S1 shows symbol and description of the analyzed genes in the liver

## List of analyzed genes in the testicle

Symbol	Description
Abl1	C-abl oncogene 1, receptor tyrosine kinase
Apex1	APEX nuclease (multifunctional DNA repair enzyme)
Atm	Ataxia telangiectasia mutated homolog (human)
Atrx	Alpha thalassemia/mental ratardation syndrome X-linked (RAD54 homolog S. cerevisiae)
Bard1	BRCA1 associated RING domain 1
Bax	Bcl2-associated X protein

Bbc3	Bcl-2 binding component 3
Blm	Bloom syndrome, RecQ helicase-like
Brca1	Breast cancer 1
Brca2	Breast cancer 2
Cdc25a	Cell division cycle 25 homolog A (S. pombe)
Cdc25c	Cell division cycle 25 homolog C (S. pombe)
Cdkn1a	Cyclin-dependent kinase inhibitor 1A
Check1	CHK1 checkpoint homolog (S. pombe)
Check2	CHK2 checkpoint homolog (S. pombe)
Csnk2a2	Casein kinase 2, alpha prime polypeptide
Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)
Ddb2	Damage specific DNA binding protein 2
Ddit3	DNA-damage inducible transcript 3
Ercc1	Excission repair cross-complementing rodent repair deficiency, complementation group 1
Ercc2	Excission repair cross-complementing rodent repair deficiency, complementation group 2
Exo1	Exonuclease 1
Fanca	Fanconi anemia, complementation group A
Fancc	Fanconi anemia, complementation group C
Fancd2	Fanconi anemia, complementation group D2
Fancg	Fanconi anemia, complementation group G
Fen1	Flap structure-specific endonuclease 1
Gadd45a	Growth arrest and DNA-damage-inducible, alpha
Gadd45g	Growth arrest and Dna-damage-inducible, gamma
Hus1	HUS1 checkpoint homolog (S. pombe)
Lig1	Ligase I, DNA, ATP-dependent

Mbd4	Methyl-CpG binding domani protein 4
Mgmt	O-6-methylguanine-DNA methyltransferase
Mif	Macrophage migration inhibitory factor
Mlh1	MutL homolog 1 (E. coli)
Mlh3	MutL homolog 3 (E. coli)
Мрд	N-methylpurine-DNA glycosylase
Mre11a	MRE11 meiotic recombination 11 homolog A (S. cerevisiae)
Msh2	MutS homolog 2 (E.coli)
Msh3	MutS homolog 3 (E.coli)
Nbn	Nibirin
Nthl1	Nth (endonuclease III)-like 1 (E.coli)
Ogg1	8-oxoguanine DNA glycosylase
Parp1	Poly (ADP-ribose) polymerase 1
Parp2	Poly (ADP-ribose) polymerase 2
Pcna	Proliferating cell nuclear antigen
Pms1	Postmeiotic segregation increased 1 (S. cerevisiae)
Pms2	PMS2 postmeiotic segregation increased 2 (S. cerevisiae)
Pold3	Polymerase (DNA-directed), delta 3, accessory subunit
Pole	Polymerase (DNA directed), epsilon
Polh	Polymerase (DNA directed), eta
Poli	Polymerase (DNA directed), iota
Ppm1d	Protein phosphatase 1D magnesium-dependent, delta isoform
Ppp1r15a	Protein phosphatase 1, regulatory (inhibitor) subunit 15A
Prkdc	Protein kinase, DNA activated, catalytic polypeptide
Pttg1	Pituitary tumor-transforming 1

Rad1	RAD1 homolog (S. pombe)
Rad17	RAD17 homolog (S. pombe)
Rad18	RAD18 homolog (S. cerevisiae)
Rad21	RAD21 homolog (S. pombe)
Rad50	RAD50 homolog (S. cerevisiae)
Rad51	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)
Rad51c	RAD51 homolog c (S. cerevisiae)
Rad51b	RAD51 paralog b
Rad52	RAD52 homolog (S. cerevisiae)
Rad9	RAD9 homolog (S. pombe)
Rev1	REV1 homolog (S. cerevisiae)
Rnf8	Ring finger protein 8
Rpa1	Replication protein A1
Sirt1	Sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)
Smc1a	Structural maintenance of chromosome 1A
Smc3	Structural maintenance of chromosome 3
Sumo1	SMT3 suppresso of mif two 3 homolog 1 (S. cerevisiae)
Terf1	Telomeric repeat binding factor (NIMA-interacting)1
Topbp1	Topoisomerase (DNA) II binding protein 1
Тр53	Tumor protein 53
Tp53bp1	Tumor protein p53 binding protein 1
Ung	Uracil-DNA glycosylase
Wrn	Werner syndrome
Wrnip1	Werner helicase interacting protein 1
Хрс	Xeroderma pigmentosum, complementation group C

Xrcc1	X-ray repair complementing defective repair in Chinese hamster cells 1
Xrcc2	X-ray repair complementing defective repair in Chinese hamster cells 2
Xrcc6	X-ray repair complementing defective repair in Chinese hamster cells 6

Table S2 shows symbol and description of the analyzed genes in the testicle

P-value for all t	the genes analy	zed in the testicle
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Gene	Fold	
Symbol	Regulation	p-value
		0,143347795
Abl1	-1,54	5
		0,151726647
Apex1	-1,59	6
Atm	-1,66	0,198130388
		0,079080803
Atrx	-1,76	64
		0,100847531
Bax	-2,02	3
		0,011589042
Bbc3	-5,49	80
		0,085064475
Blm	-1,85	35
		0,150153595
Brca1	-1,75	4
Brca2	-1,55	0,308506315
		0,068921061
Cdc25a	-1,67	06
		0,076802933
Cdc25c	-1,75	94
		0,050389420
Cdkn1a	-2,07	37
		0,065205141
Chek2	-2,35	99
		0,169318727
Ddb2	-1,72	6
		0,157855559
Ddit3	-1,79	3

		0,304819835
Ercc2	-1,61	5
		0,169331591
Exo1	-1,58	5
_	1.01	0,218952361
Fancc	-1,91	9
Eaned?	1.52	0,235667183
	-1,52	2
Fancg	-1,58	0,044551593
Fon1	1.57	0,262962991
	-1,57	0.057079706
Gadd45g	-2 62	0,057978706
	_,0_	0 099871361
Lig1	-1,94	95
		0,044873915
Mbd4	-1,79	44
		0,039260375
Mgmt	-1,84	1
		0,155479245
Mif	-1,76	7
		0,110737442
Mlh1	-2,11	8
MILO	1.02	0,070064983
IVIITIS	-1,95	75
Mpg	-1.85	0,226063912
	-1,03	9
Ogg1	-1,61	0,18214759
Dana	1 74	0,022247833
FCIIA	-1,74	0.400500007
Pms1	-1 73	0,162582667
	-1,75	0 162786507
Pole	-1.67	0,102780507
	.,	0 118083861
Polh	-1.81	5
	,	0.003227466
Ppm1d	-1,67	353
		0,158936494
Pttg1	-1,75	3

		0,129766861
Rad1	-1,53	3
Pod17	1.6	0,332052841
rau i i	-1,0	0.000701441
Rad18	-1,66	0,028701441 61
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	0.250399989
Rad51	-1,69	6
		0,220790690
Rad52	-1,53	5
Ded0	1 70	0,134382498
Rady	-1,72	I
Rev1	-1,64	0,161923206
Rnf8	-1.63	0,455249258 7
	-1,00	0 165877474
Sirt1	-1,66	3
		0,059192267
Smc3	-1,74	38
Ung	-1,77	0,156993114
		0,080142782
Wrn	-1,56	5
Vroot	1.6	0,146863589
	-1,0	0 216062094
Xrcc2	-1,52	0,210903004
		0,112869336
Xrcc6	-1,71	1
Check1	-1,24	0,39552
Csnk2a2	-1,21	0,783206
Dclre1a	-1,31	0.608092
Ercc1	-1,4	0.377563
Fanca	-1,24	0.620050
Gadd45a	-1,43	0.253278
Hus1	-1,3	0.593755
Mre11a	-1,45	0.182590
Msh2	1,07	0.724642
Meh2	-1 24	0.358648

Nbn	1,23	0.506336
Nthl1	-1,35	0.481611
Parp1	-1,44	0.363357
Parp2	-1,34	0.246076
Pms2	-1,32	0.390605
Pold3	-1,36	0.166457
Poli	-1,33	0.501038
Ppp1r15a	-1,26	0.623647
Prkdc	-1,42	0.304382
Rad21	-1,23	0.746137
Rad50	-1,42	0.393958
Rad51c	-1,16	0.901608
Rad51b	-1,22	0.567819
Rpa1	-1,38	0.245941
Smc1a	-1,39	0.604607
Sumo1	1,08	0.756822
Terf1	-1,41	0.209488
Topbp1	-1,17	0.481340
Тр53	-1,05	0.995145
Tp53bp1	-1,49	0.366596
Wrnip1	-1,33	0.488990
Хрс	-1,26	0.720942

**Table S3** shows the fold regulation and p value for all the genes analyzed in the testicle.