

## Supplements

Verification of SHR vs. PD5 transcriptomic data (heart)	
Primer	Sequence (5'-3')
Nr4a3_e5F	CACTACAACAGGAGCCCTCG
Nr4a3_e5-6R	TGGTCGGTGGGACAGTATCT
Nr4a3_e6F	AGCTGGGCAGAAAAGATCCC
Nr4a3_e7R	TGAAGTCGGTGCAGGACAAG
Nr4a1_e3F	ATCTGCCTGGCAAACAAGGA
Nr4a1_e4R	GGCTGCTTGGGTTTTGAAGG
Nr4a1_e5-6F	CCTGGCCTACCGATCTAAGC
Nr4a1_e6R	AGGCAAAGGCAGGAACATCA
KCNA5_e1F	CACTTTCCTCTGGCCCTACG
KCNA5_e1R	CGCACGAGCAACTCAAAGT
Per1_e17F	TTGACACCTCTTCTGTGGCG
Per1_e18R	ACACATAGCAGGGGTTTCG

Supplementary table 1: Primers used in qPCR verification of the transcriptomic data.

Verification of SHR vs. PD vs. BN transcriptomic data (liver)	
Primer	Sequence (5'-3')
Acs15_1660F	GTACTGGACAAGGATGGCTGG
Acs15_1795R	CAATCTTCTCTGGAGCGATGT
Acsm1_1288F	GCCATTTTACCCTTTGACATACA
Acsm1_1436R	TCAGATGTCTTCTCTGGGCTATT
Acsm2a_1712F	GCACCCTACAAGTACCCAG
Acsm2a_1833R	GCCTGGGCTTATCCTGATGT
Acsm3_c14F	TCTCTCCCATTAAAGCAGGTCT
Acsm3_c2309R	CATGGGGCAGAGATTGGTT
Acsm3_1210F	AACCCTCTCCAAGTTCCCAT
Acsm3_1351R	CACTTCAGGGTTGATGGGTTC
Acsm4_1218F	ATACGAGGGCTACGGACAGA
Acsm4_1367R	TCCTTGCCCGATGGTAGGAT
Acsm5_1503F	GCCATCCGCATCAAACCTAC
Acsm5_1628R	CTCGTCCATATGTGCTCGGT
Apo13_250F	GATCCCACACCAGGAAGCAAG
Apo13_393R	AGGCTTCGTCTTTGGTCAAC
Casp12_976F	GATGAGGAATGTGTGTTGAGCC
Casp12_1117R	TGGAAATGAAGAGAGACCAC
Cd36_1199F	TACGTCGTATGGTGTGCTGG
Cd36_1332_R	GCTCATCTTCGTTAGGATTCAAGC
Ces2e_1365F	TGGTGATGAGCTTCCTTATGTGA
Ces2e_1511R	GGTAGACCCTCACTGTTGGGA
Cyp2b1_929F	CACCACACTCCGCTATGGTT
Cyp2b1_1042R	TCATCAAGGGTTGGTAGCCG
Cyp7b1_1146F	AATTGGACAGCTTGGTCTGC
Cyp7b1_1237R	ATCCTCTTGCACTTCACGGA
Lep_102F	TGTTCAAGCTGTGCCTATCCA
Lep_244R	GCCCCGGAATGAAGTCCAAA
Ppia_c59F	TGTTCTTCGACATCACGGCT
Ppia_c178R	ATCCTTTCTCCCCAGTGCTC
Rgs16_302F	AGAAGATCCGATCAGCCACC
Rgs16_422R	GTCTTGGTCAGTTCTCGGGT
Rpl41_55F	TCTTAGCGCCATCTTCCTTG
Rpl41_170R	ATGGTTTACTTGGACCTCTGCC
Scd1_867F	CCCCTACGACAAGAACATTCAA
Scd1_950R	TGATGGTAGTTGTGGAAGCCC
Sirt3_413F	TGCGGCTCTACACACAGAAC
Sirt3_560R	TCACGTCAGCCCGTATGTCT
Ugt2a3_915F	AGTGTTTTCGCTGGGGTCAA
Ugt2a3_1034R	GCTGGCTTCTTGCCCTGAGTA

Supplementary table 2: Primers used in qPCR verification of the transcriptomic data.

Verification of SHR vs. PD5 transcriptomic data (liver)	
Primer	Sequence (5'-3')
Aox1_e19F	GGATTCTGAGACACGGGCAA
Aox1_e20R	ACACTCCAGCTTCCGTCTCG
Aox1_e32-33F	ATAGGCCAGGTTGAAGGTGC
Aox1_e33R	TTTGAGTGTTCGGATGGGGG
Doc2a_e3-4F	CCTGCAAGGCCAATAAGCTAAA
Doc2a_e5R	GCACTCGGATCTCCCAATA
Gca_e5-6F	ATCGCGTCATGGGTTACAG
Gca_e7R	GCAAGTGGTCTCTTCGCCTA
Ifih1_e11-12R	TGTTCACTCTGAGTCATGGGC
Ifih1_e11F	TTCACAAAAACGCGGCAGAG
Ifih1_e5F	AGAAGAAGCAGGCGTGTGAA
Ifih1_e6R	GGGTATCGCCGCTTAATCCA
Ingig1_e1-2F	CCGCTGTGTGTCGGCTTATTG
Ingig1_e2-3R	CTAATTTGGCACTGGCATGGT
Ingig1_e3F	GGACGTTGATCGATCCCGA
Ingig1e_4R	CAAGGGAGCCAAGAACGGAT
Lmod2_e2-3F	AGCTACGGAGGGTGAAGTT
Lmod2_e3R	GACTAGTGTCTGAAGCTGGGAG
Nox4_e7-8R	TCAACAAGCCACCCGAAACA
Nox4_e7F	GTGTCTGCATGGTGGTGGTA
Ppia_59F	TGTTCTTCGACATCACGGCT
Ppia_178R	ATCCTTTCTCCCCAGTGCTC
RGD1559600_e1-2F	GGGCTACTCAAGATGCAGGT
RGD1559600_e2R	TACCAATGCGATCTGAGGCT
Slc17a2_e1F	GACCTCCGTTTGGGAATGGT
Slc17a2_e2R	TTCCCTCTGCCCAAATCAC
Slc17a2_e5-6F	AGGCTCAGGAGCAGCATTTG
Slc17a2_e7R	TCGTGAACCACAGGACACAG
Tenm3_e17F	TCACCAAACCTGGCCTACAC
Tenm3_e18R	CAGGTCCAAGCACGACTCAT
Tenm3_e25-26F	AAAGCTCAGGGTCAACGGAC
Tenm3_e26R	CCGCCATCAGCTTGCTACTA

Supplementary table 3: Primers used in qPCR verification of the transcriptomic data.

Acsm3 sequencing	
Primer	Sequence (5'-3')
Acsm3_prome1F	ccaatTTTctaaaggggacca
Acsm3_prome1R	ctggacttgctgggtTTTgt
Acsm3_e2aF	tgaaaagcagtaggccaggt
Acsm3_e2aR	gatccacttgggcacttgtc
Acsm3_e2F	gcccaaagtaaagccattca
Acsm3_e2R	aagcttcccacgattTTTcct
Acsm3_e3F	cttagctgcattgggggtct
Acsm3_e3R	tgtagccactgtgactaccc
Acsm3_e4F	cctgacctctgagTTTTctgc
Acsm3_e4R	aaatgctgccccaaacacact
Acsm3_e5F	caaacagatttctcccctggt
Acsm3_e5R	ttgttgagctcactgagttgg
Acsm3_e6F	agaaaaggcccaaagcagat
Acsm3_e6R	CCAGCCAGAACctggaatac
Acsm3_e7F	ccgtgcctacagtacacaacc
Acsm3_e7R	cctcccaatctccgtgttta
Acsm3_e8F	aaagcccacaaagacaggaa
Acsm3_e8R	ctggacacagcagccatcta
Acsm3_e9F	atctgcatatggcctccagt
Acsm3_e9R	ccatacctTTTtagtatccctcca
Acsm3_e10F	tagacacaccagccatgtg
Acsm3_e10R	ctcacccaattctcctttgg
Acsm3_e11F	TTTgtgcaatgataacttgggta
Acsm3_e11R	TTTgtggccttctgcttct
Acsm3_e12F	aaatgactggacaaaagagtcaca
Acsm3_e13R	tgcattgtaacacacaggactga
Acsm3_e14F	gattcccaccacaatgggtc
Acsm3_e14R	aggggctgactTTTaaacctc
Acsm3_e15F	gggtaactggcatgacctga
Acsm3_e15R	TTTAAGGCATCACGGCATCT
Acsm3_e15bF	TGAAATCATATAATCACTGAATCCTT
Acsm3_e15bR	agatgagcatttgggtagtca

Supplementary table 4: Primers used for *Acsm3* sequencing.

GST pull-down	
Primer	Sequence (5'-3')
<b>BTB domain</b>	
Plzf_c-1F_EcoRI	caaa <b>GAATTC</b> cATGGATCTGACAAAGATGGGT
Plzf_c454R_HindIII	caaa <b>AAGCTT</b> agATCGAGCCTTACGGTCCTCT
<b>ZF domain</b>	
Plzf_c1142F_EcoRI	caaa <b>GAATTC</b> tgAGAGGGAGCTGTTCAGCAAG
Plzf_c1997R_HindIII	caaa <b>AAGCTT</b> gGTCTTCTCTATCCTCCAGTCAGG
<b>ALL (<i>Plzf</i> complete sequence)</b>	
Plzf_c-1F_EcoRI	caaa <b>GAATTC</b> cATGGATCTGACAAAGATGGGT
Plzf_c2021R_Sall	caaa <b>GTCGAC</b> gCACACATAACACAGGTAGAGGTATGTC

Supplementary table 5: Primers for construct preparation for GST pull-down assay. Restriction sites for EcoRI, HindIII and Sall are marked in bold letters.

<b>Construct name</b>	<b>Primer</b>	<b>Sequence (5'-3')</b>
full	Plzf_XSreg_m_F	CAAgtcgacATGTCATTCAACCCCTGCTT
	Plzf_Sreg_m_R	CAAgtcgacAGCACACACAAGATGTGATCG
out	Plzf_outreg_m_F	caaGTCGACacagtgccgtctgacctcat
	Plzf_outreg_m_R	caaGTCGACgccttctcaccccaagtga
A	Plzf_i2_rc2F_Acc65I	caaaGGTACctcagccatttggtagccatt
	Plzf_corereg_m_R	caaGTCGAcctccaggctcagaagagtt
R	Plzf_i2_rc1bF_Acc65I	caaaGGTACCgaaggccctccttaatcc
	Plzf_corereg_m_R	caaGTCGAcctccaggctcagaagagtt
L	Plzf_i2_rc2F_Acc65I	caaaGGTACctcagccatttggtagccatt
	Plzf_i2_rc2R_XhoI	caaaCTCGAgcccagaagaggatgacaag

Supplementary table 6: Primers for construct preparation for luciferase assay. For cloning, restriction enzymes XhoI (restriction site CTCGAG) and Acc65I (restriction site GGTACC) were used.

Crude nutrients	%
Dry matter	95.1
Crude protein (Nx6,25)	20.8
Crude fat	30.2
Crude fibre	5.0
Crude ash	5.6
N free extracts	33.4
Starch	22.1
Sugar	13.0

Fatty acids	%
C 4:0	0.12
C 6:0	0.11
C 8:0	0.50
C 10:0	0.45
C 12:0	2.81
C 14:0	1.77
C 16:0	8.57
C 16:1	0.4
C 17:0	0.13
C 18:0	2.63
C 18:1	8.83
C 18:2	1.60
C 18:3	0.12
C 20:0	0.07
C 20:1	0.01
C 20:4	0.02
Cholesterol (mg/kg)	171

Supplementary table 7: The individual components of the high fat diet.

			PD	SHR	BN
Class	Sub-Class	Total Cholesterol of all factions [mg/dL]	52.15 ± 4.19	34.96 ± 1.47	45.84 ± 2.02
CM (>80nm)		G01 fraction cholesterol [mg/dL]	4.33 ± 0.91	0.05 ± 0.01	0.31 ± 0.13
		G02 fraction cholesterol [mg/dL]	1.77 ± 0.27	0.02 ± 0.01	0.17 ± 0.08
VLDL (30-80nm)	large VLDL	G03 fraction cholesterol [mg/dL]	3.00 ± 0.28	0.07 ± 0.02	0.42 ± 0.17
		G04 fraction cholesterol [mg/dL]	3.46 ± 0.22	0.18 ± 0.06	0.81 ± 0.21
		G05 fraction cholesterol [mg/dL]	3.02 ± 0.15	0.36 ± 0.09	1.43 ± 0.18
	medium VLDL	G06 fraction cholesterol [mg/dL]	1.32 ± 0.10	0.30 ± 0.04	1.23 ± 0.07
	small VLDL	G07 fraction cholesterol [mg/dL]	0.36 ± 0.04	0.08 ± 0.01	0.59 ± 0.07
LDL (16-30nm)	large LDL	G08 fraction cholesterol [mg/dL]	0.65 ± 0.07	0.28 ± 0.03	1.33 ± 0.15
	medium LDL	G09 fraction cholesterol [mg/dL]	0.97 ± 0.12	1.04 ± 0.08	2.84 ± 0.13
	small LDL	G10 fraction cholesterol [mg/dL]	1.94 ± 0.25	2.18 ± 0.13	2.62 ± 0.18
	very small LDL	G11 fraction cholesterol [mg/dL]	0.96 ± 0.16	0.08 ± 0.03	0.59 ± 0.12
		G12 fraction cholesterol [mg/dL]	2.29 ± 0.60	2.99 ± 0.11	1.38 ± 0.30
		G13 fraction cholesterol [mg/dL]	1.49 ± 0.43	2.31 ± 0.09	1.29 ± 0.23
HDL (8-16nm)	very large HDL	G14 fraction cholesterol [mg/dL]	1.46 ± 0.44	2.65 ± 0.13	1.59 ± 0.23
		G15 fraction cholesterol [mg/dL]	3.34 ± 0.78	3.65 ± 0.20	3.98 ± 0.42
	large HDL	G16 fraction cholesterol [mg/dL]	12.62 ± 1.11	9.73 ± .61	13.65 ± 0.91
	medium HDL	G17 fraction cholesterol [mg/dL]	6.17 ± 0.32	5.02 ± 0.30	6.95 ± 0.42
	small HDL	G18 fraction cholesterol [mg/dL]	1.74 ± 0.11	2.15 ± 0.10	2.49 ± 0.09
	very small HDL	G19 fraction cholesterol [mg/dL]	0.73 ± 0.04	0.99 ± 0.04	1.26 ± 0.03
		G20 fraction cholesterol [mg/dL]	0.53 ± 0.05	0.86 ± 0.02	0.90 ± 0.03

Supplementary table 8: Serum levels of lipoprotein particles in PD, SHR and BN rat strains. CM chylomicrons, VLDL very low density lipoproteins, LDL low density lipoproteins, HDL high density lipoproteins. Data are expressed as arithmetic mean ± SEM.



	PD		SHR		BN	
	before HFD	after HFD	before HFD	after HFD	before HFD	after HFD
<b>MCP-1 (pg/ml)</b>	1393.23 ± 67.96	1329.75 ± 97.29	1523.29 ± 114.08	1255.53 ± 82.87	1685.23 ± 81.22	1543.65 ± 59.30
<b>IL-1a (pg/ml)</b>	1008.78 ± 16.40	894.33 ± 62.47	842.58 ± 84.58	874.05 ± 37.53	832.18 ± 92.09	947.68 ± 48.82
<b>IL-1b (pg/ml)</b>	336.80 ± 13.03	265.78 ± 20.30	300.61 ± 26.98	260.04 ± 16.72	429.16 ± 11.86	422.00 ± 33.15
<b>IL-2 (pg/ml)</b>	8620.72 ± 238.68	7510.59 ± 573.11	6572.68 ± 1014.59	7474.38 ± 395.77	6384.21 ± 530.29	7332.76 ± 285.40
<b>IL-4 (pg/ml)</b>	534.67 ± 15.88	447.08 ± 39.38	441.98 ± 50.47	436.83 ± 21.64	390.92 ± 11.72	441.93 ± 7.49
<b>IL-5 (pg/ml)</b>	1201.16 ± 17.56	1140.29 ± 34.31	1091.19 ± 78.88	1110.75 ± 21.12	1074.01 ± 39.13	1089.06 ± 12.02
<b>IL-6 (pg/ml)</b>	1406.31 ± 87.79	1236.42 ± 152.73	1088.86 ± 174.99	1318.95 ± 138.50	1216.76 ± 160.18	1519.78 ± 53.86
<b>IL-7 (pg/ml)</b>	297.92 ± 8.83	245.09 ± 14.77	266.28 ± 30.68	234.74 ± 15.01	362.93 ± 30.50	376.42 ± 30.04
<b>IL-10 (pg/ml)</b>	301.85 ± 3.71	259.49 ± 18.16	256.42 ± 23.74	251.43 ± 11.09	242.57 ± 18.52	242.84 ± 4.38
<b>IL-12(p70) (pg/ml)</b>	1886.65 ± 86.96	1471.49 ± 144.58	1703.01 ± 155.78	1519.70 ± 111.68	1434.92 ± 191.49	1458.04 ± 27.45
<b>IL-13 (pg/ml)</b>	620.76 ± 42.16	612.38 ± 53.06	358.18 ± 113.99	493.57 ± 69.41	392.96 ± 74.20	604.58 ± 39.89
<b>IL-17 (pg/ml)</b>	124.50 ± 2.81	108.84 ± 7.66	93.86 ± 16.06	100.05 ± 3.68	94.93 ± 9.52	103.51 ± 1.81
<b>IL-18 (pg/ml)</b>	7941.55 ± 668.54	10624.25 ± 3463.23	6000.48 ± 444.75	6090.49 ± 212.29	6752.79 ± 1066.55	5875.92 ± 84.23
<b>G-CSF (pg/ml)</b>	35.15 ± 3.40	30.39 ± 5.19	23.16 ± 5.46	32.16 ± 3.60	28.11 ± 2.69	34.89 ± 2.26
<b>GM-CSF (pg/ml)</b>	265.49 ± 9.30	225.43 ± 14.73	244.21 ± 25.46	218.71 ± 11.16	366.36 ± 22.47	370.96 ± 28.16
<b>GRO/KC (pg/ml)</b>	327.39 ± 12.18	333.06 ± 39.43	364.91 ± 25.62	287.98 ± 17.57	401.15 ± 28.78	418.37 ± 26.86
<b>IFN-g (pg/ml)</b>	852.52 ± 27.98	741.64 ± 74.58	690.52 ± 92.76	738.01 ± 46.00	727.35 ± 68.16	862.10 ± 22.10
<b>M-CSF (pg/ml)</b>	162.56 ± 9.33	137.79 ± 17.20	130.36 ± 20.69	146.88 ± 8.42	132.07 ± 20.04	147.86 ± 5.05
<b>MIP-1a (pg/ml)</b>	80.56 ± 1.27	62.45 ± 1.96	97.80 ± 4.25	71.62 ± 4.92	104.76 ± 6.04	104.65 ± 6.59
<b>MIP-3a (pg/ml)</b>	74.79 ± 6.58	72.67 ± 12.78	38.30 ± 4.55	46.03 ± 3.40	37.04 ± 4.59	44.20 ± 1.21
<b>RANTES (pg/ml)</b>	1403.23 ± 145.83	1368.75 ± 182.06	1664.14 ± 284.34	1065.89 ± 116.06	857.33 ± 60.55	592.81 ± 51.27
<b>TNF-a (pg/ml)</b>	1970.42 ± 115.57	1712.45 ± 193.45	1476.37 ± 325.72	1657.04 ± 175.62	1284.17 ± 162.68	1632.29 ± 111.98
<b>VEGF (pg/ml)</b>	301.27 ± 7.11	227.19 ± 22.91	241.02 ± 39.87	213.14 ± 12.03	323.71 ± 59.18	331.62 ± 22.99

Supplementary table 9: Serum cytokine levels in PD, SHR and BN strain before and after HFD. Data are expressed as arithmetic mean ± SEM.

	PD		SHR		BN	
	before HFD	after HFD	before HFD	after HFD	before HFD	after HFD
<b>Adiponectin (ug/ml)</b>	0.40 ± 0.09	0.46 ± 0.04	0.42 ± 0.02	0.54 ± 0.15	0.48 ± 0.07	0.33 ± 0.03
<b>C-Peptide (pg/ml)</b>	642.72 ± 22.57	899.16 ± 133.65	554.20 ± 82.29	610.21 ± 91.62	539.77 ± 63.48	805.05 ± 113.48
<b>GIP (pg/ml)</b>	57.38 ± 7.13	39.98 ± 7.12	16.72 ± 3.61	30.95 ± 9.51	20.99 ± 4.05	21.62 ± 9.66
<b>GLP-1 (pg/ml)</b>	312.41 ± 25.59	268.45 ± 44.27	234.83 ± 58.82	214.96 ± 28.47	205.76 ± 21.67	198.20 ± 36.52
<b>Glucagon (pg/ml)</b>	58.67 ± 6.22	36.69 ± 7.14	50.75 ± 15.70	35.98 ± 3.81	46.99 ± 11.80	38.69 ± 6.66
<b>PP (pg/ml)</b>	66.60 ± 4.17	48.97 ± 11.11	57.07 ± 1.60	44.41 ± 6.42	58.13 ± 11.32	56.47 ± 8.52

Supplementary table 10: Serum levels of Adiponectin, C-Peptide, GIP (gastric inhibitory peptide), GLP-1 (glucagon like peptide 1) and PP (pancreatic polypeptide) in PD, SHR and BN strain before and after HFD. Data are expressed as arithmetic mean ± SEM.

<b>SHR vs. BN pathway enrichment analysis</b>	<b>Genes total</b>	<b>Upregulated in BN</b>	<b>Downregulated in BN</b>	<b>-log(p value)</b>
GPCRs, Class A Rhodopsin-like	4	0	Ptger4,Ednra,Ntsr1,Ednrb	5,10
Oxidative Stress	9	Maoa,Gpx1,Ugt1a6,Xdh	Nfix,Gpx3,Txnrd1,Sod3,Mapk10	3,37
Tryptophan metabolism	12	Ddc,Echs1,Gcdh,Cyp7b1,Cyp2a1,Cyp2a2,Aldh1a1,Aldh9a1	Cyp2j4,Ogdh,Aox1,Cyp2f4	3,02
TNF-alpha NF-kB Signaling Pathway	29	Psm12,Psm1,Rpl30,Kpna3,Papola,Kpna6,Chuk,Cul1,Mtif2,Rpl4,Rps6kb1	Rela,Tradd,Tifa,Cdc37,Stat1,Pml,Gsk3b,Ywhag,Tnip1,Src,Csnk2b,Btrc,Nkiras2,Polr1a,LOC681193,Dap,Bag4,Traf4	2,86
Glucuronidation	7	Pgm1,Ugt1a5,Ugt2a3,Ugt1a6,Ugt1a3,Ugt1a1,Ugt1a2	0	2,73
Complement Activation, Classical Pathway	6	0	C1qa,C1qb,C1qc,C1r,C6,C7	2,70
Fatty Acid Omega Oxidation	5	Adh6,Adh1,Adh4,Aldh1a1,Adh7	0	2,37
Retinol metabolism	9	Cd36,Aldh1a1,Adh4,Adh1	Scarb1,Rxra,Abcg5,Lrat,Rbp1	2,22
Cytoplasmic Ribosomal Proteins	16	Rpl3,Rpl7,Rpl4,Rpl14,Rpl19,RGD1562923,Rpl32,Rpl35a,Rpl39,Rps4x,Rps8,Rps25,Rps6kb1,Rpl30	Rpl34,Fau	2,12
ErbB signaling pathway	10	Egf,Nrg4,Nck1,Rps6kb1	Nrg1,Pleg1,Src,Araf,Gsk3b,Eif4ebp1	2,07
TCA Cycle	7	Idh3B,Sdhb,Idh2,Pdhx,Pdhb	Pc,Ogdh	1,96
Fatty Acid Biosynthesis	6	Echs1,Acs15	Ech1,Acaa2,Pc,Echdc2	1,93
Selenium metabolism Selenoproteins	9	Gpx1,Selenbp1,Rpl30	Dio1,Txnrd1,Gpx3,Seli,Fabp1,Rela	1,93
Folic Acid Network	7	Xdh,Kmo,Gpx1	Mthfr,Fads2,Gpx3,Txnrd1	1,88
Steroid Biosynthesis	4	Hsd3b5,F13b,Cyp17a1,Hsd17b7	0	1,88
Nucleotide Metabolism	5	Adss	Dhfr,Polg,Srm,Oaz1	1,71
Selenium Micronutrient Network	7	Xdh,Kmo,Gpx1	Mthfr,Fads1,Fads2,Gpx3	1,65
Endochondral Ossification	11	Bmpr1a,Vegfa,Serpinh1	Igf1,Ghr,Tgfb1,Fgfr3,Stat1,Plat,Plau,Mgp	1,63
Eukaryotic Transcription Initiation	8	Gtf2b,Polr2b,Mnat1	Ilk,Gtf2h4,Polr2e,Polr1a,Polr2j	1,59
Metapathway biotransformation	21	Fmo5,Ugt1a1,Ugt1a2,Ugt1a5,Ugt1a3,Ugt1a6,Tpmt,Cyp7b1,Cyp17a1,Cyp27a1,Akr1d1,Mgst2,Chst9	Ephx1,Gstt1,Cyp2u1,Cyp4b1,Ephx2,Gpx3,Gstk1,Gsto1	1,58
Urea cycle and metabolism of amino groups	5	Arg1,Otc,Oat,Cps1	Srm	1,52
Glycogen Metabolism	7	Agl,Pgm1,Ppp2r5a,Ppp2r3a	Gsk3b,Ppp2r1a,Ppp2r4	1,51

Type II interferon signaling (IFNG)	7	0	Stat1,Stat2,Irf9,Oas1a,Cxcl10,Icam1,Irf2	1,51
Estrogen metabolism	4	Ugt1a1,Ugt1a3,Ugt1a2	Sts	1,49
Focal Adhesion	26	Egf,Hgf,Cav2,Met,Map2k6,Rock1,Vegfa,Farp2,Pik3r4, Ppp1r12a,Myk	Igf1,Pelo,Itgb2,Src,Ilk,Actn1,Pdgfra,Araf,Pxn,Capn1,Gsk3b,Itga9,Itga2b, Tln1,Parvb	1,38
MAPK Cascade	6	Map2k6	Mapk10,Mbp,Sipa1,Rras,Araf	1,37
EGFR1 Signaling Pathway	24	Egf,Gja1,Eppk1,Ptpn12,Plscr1,Appl2,Pkn2,Cav2,Nck1	Stat1,Stat2,Ap2a1,Epn1,Tnip1,Pxn,Araf,Plcg1,Ptpn6,Src,Ptk2b,Git1,Rgs16, Inpp11,Arf4	1,33
Integrin-mediated cell adhesion	15	Rock1,Cav2,Capn2,Map2k6	Araf,Src,Capn5,Capn9,Tln1,Capn1,Itga9,Itgb2,Mapk10,Pxn,Ilk	1,31

Supplementary table 11: Differentially expressed genes in the liver after HFD. Pathway enrichment analysis using Transcriptomic analysis console software. Pathway enrichment analysis SHR vs. BN comparison. Significantly pathways were selected based on a p-value < 0.05.

SHR vs. PD pathway enrichment analysis	Genes total	Upregulated in PD	Downregulated in PD	-log(p value)
Tryptophan metabolism	11	Ddc,Acac1,Echs1,Cyp2a1,Cyp2a2,Aldh1a1	Cyp2j4,Ogdh,Acmsd,Cyp7b1,Inmt	5,15
Beta Oxidation Meta Pathway	8	Echs1,Acac1,Lipc,Acs15	Lpl,Tpi1,Crat,Cpt1a	4,20
Fatty Acid Beta Oxidation	8	Echs1,Acs15,Lipc,Acac1	Crat,Cpt1a,Gk,Lpl	4,00
Fatty Acid Beta Oxidation	7	Echs1,Acs15,Lipc	Lpl,Cpt1a,Crat,Tpi1	3,85
Retinol metabolism	8	Rxra,Aldh1a1,Adh1,Retsat	Cd36,Lpl,Lrat,Aldh1a3	3,64
Fatty Acid Biosynthesis	6	Echs1,Acs15,Scd1,Acaa2,Acaca	Echdc1	3,50
Prostaglandin Synthesis and Regulation	7	0	Ptgs1,Anxa3,Hsd11b1,Ednrb,Ednra,Tbxas1,Ptger3	3,44
Selenium Micronutrient Network	7	Kmo,Sod1,Gpx1	Mthfr,Fads1,Fads2,Tbxas1	3,35
Complement Activation, Classical Pathway	5	0	C1qa,C1qb,C1qc,C1r,C1s	3,29
Triacylglyceride Synthesis	6	Lipc	Gk,Agpat2,Lpl,Agpat5,Agpat3	2,98
Fatty Acid Omega Oxidation	4	Adh1,Aldh1a1,Adh7	Cyp3a2	2,69
Type II interferon signaling (IFNG)	6	Icam1	Stat1,Irf9,Cybb,Ifit2,Cxcl9	2,44
TCA Cycle	5	Sdha,Idh3B,Pdhb	Idh2,Ogdh	2,13
Folic Acid Network	5	Sod1,Kmo,Gpx1	Mthfr,Fads2	2,06
Urea cycle and metabolism of amino groups	4	Gamt,Otc	Asl,Arg1	1,96
Adipogenesis	12	Rxra,Scd1,Fzd1,Nampt	Lpl,Rbl2,Stat1,Stat6,Ilf6st,Hif1a,Irs1,Agpat2	1,79
Cholesterol metabolism	4	Lipc	Hmgcs1,Dhcr7,Lpl	1,75
Lipid Droplet Metabolism	4	0	Gk,Agpat3,Agpat2,Agpat5	1,62
Nuclear Receptors	5	Rorc,Rxra,Esr1	Nr2f2,Nr1i3	1,58
Aflatoxin B1 metabolism	2	Akr7a3,Ephx1	0	1,58
Oxidative Stress	4	Gpx1,Junb,Sod1	Mapk10	1,51
Focal Adhesion	15	Fn1,Vegfa,Farp2	Pelo,Ilk,Actn1,Met,Pdgfra,Pxn,Capn1,Rac1,Itgb5,Itga2b,Tln1,Parvb	1,49
Glucocorticoid Metabolism	2	0	Cyp17a1,Hsd11b1	1,44
Fatty Acid Beta Oxidation 3	2	Echs1,Acac1	0	1,33

Supplementary table 12: Differentially expressed genes in the liver after HFD. Pathway enrichment analysis using Transcriptomic analysis console software. Pathway enrichment analysis SHR vs. PD comparison. Significantly pathways were selected based on a p-value < 0.05.

BN vs. PD pathway enrichment analysis	Genes total	Upregulated in BN	Downregulated in BN	-log(p value)
GPCRs, Class A Rhodopsin-like	7	P2ry2,Avpr1a,Ednrb	Adra2c,Cckbr,Galr3,Gpr27	6,00
Proteasome Degradation	15	Psm2,Psm12,Psm4,Psm3,Psm13,Psm6,Psm5,Nedd4,Psmc6,Psmc4,Psm4,Psm1,Psm2	Psm9,Psm8	2,94
Fatty Acid Biosynthesis	8	Acs15,Echdc1	Scd1,Acaa2,Pc,Acly,Acaca,Echdc2	2,41
Cytoplasmic Ribosomal Proteins	20	Rpl3,Rpl7,Rpl4,Rpl19,RGD1562923,Rpl22,Rpl24,Rpl35a,Rpl37,Rpl39,Rps23,Rps11,Rps4x,Rps8,Rps21,Rps25,Rps6kb1,Rpl10	Rpl13,Rpl30	2,06
Glucuronidation	7	Ugt1a5,Ugt2a3,Ugt1a6,Ugt1a3,Ugt1a1,Ugt1a2	Ugt2b17	1,94
Fatty Acid Omega Oxidation	5	Cyp2e1,Cyp3a2,Adh6,Adh1,Adh4	0	1,77
Nucleotide Metabolism	6	Prps2,Adss	Dhfr,Polg,Srm,Oaz1	1,72
Cholesterol metabolism	7	Hmgcs1,Idi1,Fdft1,Lss,Nsdhl	Scarb1,Lipc	1,71
GPCRs, Other	3	Alg6	Cckbr,Gpr183	1,66
G1 to S cell cycle control	15	Cdk7,Cdk2,Creb3,Orc3,Mnat1,E2f6,Orc2,Creb1,Atm,Orc4,Prim1	Cdkn1a,Tp53,Ccnb1,Creb3l1	1,64
TGF-beta Receptor Signaling Pathway	28	Arrb2,Ap2b1,Fnta,Cav1,Pard3,Cull1,Anapc1,Anapc4,Cdc16,Anapc5,Ctcf,Cops5,Map2k6,Smurf2,Snx2,Cdk2,Rbl2,Rock1,Xpo1,Pias1	Gipc1,Esr1,Tp53,Atf3,Junb,Trap1,Cdkn1a,Nfyb	1,63
Estrogen metabolism	5	Comt,Ugt1a1,Ugt1a3,Ugt1a2	Sts	1,63
Aflatoxin B1 metabolism	3	0	Akr7a3,Gstt1,Ephx1	1,53
EGFR1 Signaling Pathway	32	Egf,Raf1,Shoc2,Sos1,Pik3cb,Gja1,Eppk1,Plscr1,Cblb,Eps15,Sh3bgr1,Reps2,Appl2,Mta2,Asap1,Pkn2,Creb1,Hat1,Itch,Cav1,Cav2,Nck1,Rasa1	Stat3,Stat2,Map2k2,Ap2a1,Araf,Ptpn6,Rgs16,Inpp11,Ptpn11	1,53
Cholesterol Biosynthesis	5	Idi1,Hmgcs1,Fdft1,Lss,Nsdhl	0	1,50
Signaling of Hepatocyte Growth Factor Receptor	9	Itga1,Rasa1,Sos1,Raf1,Met,Hgf	Ptpn11,Stat3,Map2k2	1,49
EPO Receptor Signaling	7	Ptpcr,Raf1,Sos1,Rasa1	Map2k2,Stat3,Ptpru	1,43

Supplementary table 13: Differentially expressed genes in the liver after HFD. Pathway enrichment analysis using Transcriptomic analysis console software. Pathway enrichment analysis BN vs. PD comparison. Significantly pathways were selected based on a p-value < 0.05.



Pathway enrichment analysis dexamethasone admission	Total	Upregulated after dexamethasone	Downregulated after dexamethasone	-log(p value)
Glutathione metabolism	12	Gpx3	Anpep,Idh1,Gsr,Gclc,Gstm3,Gsta5,Gsta2,Gstm2,Gstt1,Gstt2,Gclm	7,00
Tryptophan metabolism	18	Ddc,Acmsd,Kynu,Tdo2,Cyp2f4,Aldh9a1	Cyp2j4,Mdm2,Acat1,Gedh,Cat,Cyp7b1,Aox1,Inmt,Cyp1a2,Cyp2a2,Aldh1a1,Aldh2	7,00
Complement and Coagulation Cascades	19	Cd59	C1s,C2,C9,Masp1,Cfi,C3ar1,F10,Plg,Kng1,C7,C8b,C1qa,C1r,C4a,Mbl1,F13b,Klkb1,Serpinc1	7,00
Oxidative Stress	12	Gpx3	Nfkb1,Hmox1,Nqo1,Cat,Txnrd1,Gclc,Gsr,Cyba,Junb,Sod1,Sod3	7,00
Complement Activation, Classical Pathway	9	0	C1qa,C1qc,C1r,C1s,C2,C5,C7,C8b,C9	6,00
Type II interferon signaling (IFNG)	13	Socs1	Ifngr2,Jak1,Socs3,Stat1,Prkcd,Psb9,Tap1,Cybb,Ii1b,Icam1,Cxcl9,Irf8	6,00
Spinal Cord Injury	22	Zfp36,Mbp,Arg1,Vim	Plxna2,Cd47,Ii1b,Tgfb1,Rtn4,C5,Cxcl1,Ceng1,Ntn1,Ccr2,Pla2g2a,Icam1,Cdk4,Cend1,Casp3,Rhoc,Lilrb3,Nox4	4,96
Fatty Acid Beta Oxidation	11	Pnpla2,Cpt2,Crat	Gedh,Acs15,Acs11,Decr1,Lipc,Cpt1a,Gk,Acat1	4,46
IL-5 Signaling Pathway	16	Nfkb1a,Pik3r1,Socs1,Foxo3,Cdkn1b	Prkcb,Nfkb1,Mapk9,Pla2g4a,Hcls1,Prkcd,Icam1,Itgb2,Itgam,Jak1,Stat1	4,26
Apoptosis	17	Nfkb1a,Cflar,Pik3r1	Mdm2,Nfkb1,Fas,Casp4,Casp3,Tnfrsf1a,Tnfrsf1b,Bid,Casp7,Irf7,Nfkb1e,Xiap,Tnfrsf10,Casp6	3,96
Fatty Acid Biosynthesis	8	Scd1,Acly,Acaca	Acs15,Acs11,Decr1,Mecr,Echdc2	3,78
IL-2 Signaling Pathway	16	Pik3r1,Foxo3,Sos1,Socs1,Crk,Prkez	Jak1,Socs3,Cd53,Icam1,Nmi,Itm2b,Hsp90aa1,Nfkb1,Mapk9,Stat1	3,72
Apoptosis Modulation by HSP70	7	0	Map3k1,Casp3,Bid,Casp6,Casp7,Nfkb1,Tnfrsf1a	3,58
Aflatoxin B1 metabolism	4	0	Cyp1a2,Akr7a3,Gstt1,Ephx1	3,30
Beta Oxidation Meta Pathway	9	Crat,Cpt2,Pnpla2	Acs11,Cpt1a,Acat1,Gedh,Lipc,Acs15	3,23
Nuclear receptors in lipid metabolism and toxicity	9	Ppard,Nr1h4,Nr1i2,Cyp26a1	Abca1,Abcb1a,Cyp8b1,Cyp2b2,Cyp1a2	3,23
MAPK Signaling Pathway	34	Crk,Dusp1,Ntrk1,Map2k6,Map3k6,Atf4,Sos1,Rasgrp3,Map3k5,Cacnb4	Mapk9,Arrb2,Stk4,Casp3,Flna,Tnfrsf1a,Hspb1,Tgfb1,Cdc25b,Rac2,Prkcd,Ii1b,Map3k8,Fgfr2,Rras2,Nfkb1,Ntf3,Tgfb2,Fas,Pla2g4a,Nras,Cacnb2,Fgf1,Pak1	3,02



Hexoses metabolism in proximal tubules	12	Slc2a5,Pgk1,Gpi,Pdhh,Pklr,Aldob,Pdk1,Acly,Pfkl,Tkfc,Mdh1	Sord	3,02
IL-3 Signaling Pathway	18	Tec,Pik3r1,Sos1,Crk,Ppp2ca,Foxo1	Jak1,Stat1,Stat6,Prkcb,Src,Socs3,Rac2,Pak1,Nfkb1,Hspb1,Tnfrsf1b,Mapk9	2,97
Folic Acid Network	8	Cbs,Gpx3	Cat,Sod1,Fads2,Kmo,Gsr,Txnrd1	2,87
Adipogenesis	21	Ppard,Cyp26a1,Mef2d,Scd1,Agt,Cdkn1a,Gadd45b,Bmp1,Foxo1,Socs1,Ilf6st,Rora,Agpat2,Lpin1	Fas,Tgfb1,Cfd,Stat1,Stat6,Socs3,Mbnl1	2,84
FAS pathway and Stress induction of HSP regulation	9	Cflar	Fas,Hspb1,Casp3,Casp7,Pak1,Casp6,Lmnb1,Map3k1	2,74
Fructose Metabolism in Proximal Tubules	6	Gpi,Tkfc,Pfkl,Aldob,Slc2a5	Sord	2,73
Retinol metabolism	9	Sult1a1,Cyp26a1	Scarb1,Aldh1a1,Adh1,Lrat,Rbp1,Rdh5,Retsat	2,65
Fatty Acid Omega Oxidation	5	0	Adh1,Cyp3a2,Cyp1a2,Aldh1a1,Aldh2	2,65
Keap1-Nrf2	5	0	Nqo1,Nfe2l2,Gclc,Gclm,Hmox1	2,65
Metapathway biotransformation	22	Fmo1,Fmo2,Fmo3,Sult1a1,Cyp26a1,Cyp27a1,Gpx3	Cyp1a2,Akr7a3,Ephx1,Gstt1,Comt,Tpmt,Cyp7b1,Cyp8b1,Cyp17a1,Akr1d1,Gstm3,Gsto1,Gstt2,Mgst2,Gsr	2,63
Toll-like receptor signaling pathway	16	Pik3r1,Nfkb1a,Map2k6	Irak4,Nfkb1,Map3k8,Irf7,Cxcl9,Tlr7,Mapk9,Ill1b,Ccl5,Stat1,Cd80,Tlr3,Lbp	2,63
Lipid Droplet Metabolism	7	Plin2,Pnpla2,Dgat2,Agpat2,Lpin1	Acs11,Gk	2,61
IL-4 Signaling Pathway	12	Pik3r1,Prkcz,Pawr,Sos1,Socs1	Jak1,Stat6,Nfkb1,Socs3,Stat1,Src,Prkcd	2,55
EPO Receptor Signaling	7	Pdk1,Socs1,Ptpru,Sos1	Src,Stat1,Ptprc	2,50
Nuclear factor, erythroid-derived 2, like 2 signaling pathway	40	Map3k5,Map2k6,Prkcz,Pik3r1,Atf4,Bach1,G6pd,Dnajb9,Herpud1,Fmo1,Cdkn1a,Slc35b1	Nras,Rras2,Nfe2l2,Map3k1,Mapk9,Prkcd,Prkcb,Mdm2,Hmox1,Gclm,Gsta2,Gclc,Gsta3,Gstm2,Gstm3,Gsto1,Gstt1,Gstt2,Mgst2,Nqo1,Sod1,Sod3,Aox1,Txnrd1,Akr7a3,Ephx1,Scarb1,Gsr	2,47
Fatty Acid Beta Oxidation 1	7	Crat,Cpt2,Pnpla2	Cpt1a,Acs15,Lipc,Acs11	2,40
Triacylglyceride Synthesis	7	Dgat2,Lpin1,Agpat2,Pnpla2	Gk,Acs11,Lipc	2,40
One Carbon Metabolism	7	Ftcd,Ahcy,Ahcy2,Mat1a	Shmt1,Dhfr,Tyms	2,40
Insulin Signaling	23	Pik3r1,Map3k5,Crk,Foxo1,Sos1,Map2k6,Pfkl,Prkcz,Prkaa2,Socs1,Mapk4,Foxo3,Map3k6	Socs3,Prkcd,Prkcb,Rac2,Enpp1,Map3k8,Sgk1,Mapk9,Flot1,Sgk2	2,39

TNF-alpha NF-kB Signaling Pathway	25	Trpc4ap,Prkcz,PPP2ca,Nfkbia,Cflar,Fkbp5,Usp2	Flna,Nfkb1,Hspb1,Tnfrsf1b,Tnfrsf1a,Casp7,Stat1,Bcl3,Unc5cl,Src,Casp3,Nfkbie,Hsp90aa1,Map3k1,Map3k8,Nsmaf,Akap8,Dap	2,38
B Cell Receptor Signaling Pathway	22	Sos1,Pik3r1,Tec,Crk,Foxo1,Nfkbia,Mapk4,Rasgrp3,Itrp1	Hcls1,Actr2,Arpc2,Pik3ap1,Nedd9,Casp7,Sh3bp2,Lcp2,Prkcd,Cdk4,Prkcb,Ptpre,Stat1	2,20
IL-6 Signaling Pathway	16	Il6,Tec,Sos1,Pik3r1,PPP2ca,Map2k6	Jak1,Tyk2,Stat1,Nfkb1,Prkcd,Socs3,ErbB3,Casp3,Fgr,Hspb1	2,13
T Cell Receptor Signaling Pathway	19	Pik3r1,Crk,Sos1,Itrp1	Fyb,Map3k1,Stat1,Pak1,Src,Cd4,Sh3bp2,Rac2,Nfam1,Lcp2,Nedd9,Evl,Ptpre,Cd2ap,Dock2	2,13
PI3K-AKT-NFKB pathway	14	Nfkbia,Pik3r1,PPP2ca	Fas,Cfb,Irak4,Mdm2,Nfkbie,Abca1,Igfbp2,Nfkb1,Psmb9,Sod1,Tap1	2,12
PKC-SCP2	17	Ahcy,St8sia1,Slc6a9,G6pd,Prkcz	Amacr,Pdzk1,Slc10a1,Rtn4,Gne,Nqo1,Pla2g4a,Sod1,Sod3,Prkcb,Prkcd,Nox4	2,10
Senescence and Autophagy	16	Cdkn1a,Irf1,Map1lc3b,Cdkn1b,Ulk1	Col3a1,Cdc25b,Mdm2,Tgfb1,Cdk4,Src,Igfbp7,Rnasel,Lamp1,Ill1b,Irf7	2,07
GPCRs, Class A Rhodopsin-like	8	P2ry1,Avpr1b	Cmklr1,Ptger3,Gpr81,Adra2b,C3ar1,Ccr5	2,03
Selenium Micronutrient Network	7	Gpx3	Gsr,Cat,Kmo,Sod1,Fads1,Fads2	1,98
Cytokines and Inflammatory Response (BioCarta)	6		Cxcl1,Ill1b,Tgfb1,Csf1,Cd4,RT1-Db1	1,79
Estrogen metabolism	4	Sult1a1	Cyp1a2,Comt,Nqo1	1,70
Integrin-mediated cell adhesion	14	Mapk4,Sos1,Mapk6,Crk,Tnfrsf1	Rac2,Cav2,Src,Capn5,Itga4,Itgal,Itgam,Itgb2,Pak1	1,63
p53 signal pathway	6		Mdm2,Fas,Cdk4,Bid,Casp3,Ei24	1,57
Methylation	3	Mat1a	Comt,Tpmt	1,55
ErbB signaling pathway	8	Nrg4,Crk,Sos1,Cdkn1b,Cdkn1a	Nrg1,ErbB3,Src	1,55
Myometrial Relaxation and Contraction Pathways	19	Itpr3,Pde4d,Prkcz,Grk5,Itrp1,Atp2a2,Atf7,Ywhaq	Prkcb,Igfbp2,Arrb2,Gsto1,Rgs10,Rgs18,Ill1b,Adcy9,Prkcd,Dgkz,Nfkb1	1,52
Mitochondrial LC-Fatty Acid Beta-Oxidation	4	Cpt2	Ehhadh,Cpt1a,Acs1l	1,50
Kit Receptor Signaling Pathway	1		Src,Stat1,Fgr,Prkcb	1,41
Glycolysis and Gluconeogenesis	0	Pik3r1,Crk,Ptpre,Tec,Socs1,Sos1		1,37
p38 MAPK Signaling Pathway	7	Pfkfb3,Aldob,Pklr,Gp130,Pdgfra,Mdh1	Hspb1,Stat1,Pla2g4a	1,33

1 i, b  
6 Map2k6,Mef2d,Map35  
k

Nucleotide Metabolism	4	Polg	Dhfr,Adss,Rrm2b	1,32
EGFR1 Signaling Pathway	21	Pik3r1,Sos1,Prkcz,Pkn2,Foxo1,Crk,Socs1,Dusp1	Nras,Jak1,Stat1,Map3k1,Prkcb,Plscr1,Pld1,Sh3bgr1,Asap1,Pak1,Src,Cav2,Soes3	1,32
Steroid Biosynthesis	3	0	Hsd17b2,F13b,Cyp17a1	1,31

Supplementary table 14: Differentially expressed genes in the liver after HFD. Pathway enrichment analysis using Transcriptomic analysis console software. Pathway enrichment analysis BN vs. PD comparison. Significantly pathways were selected based on a p-value < 0.05.

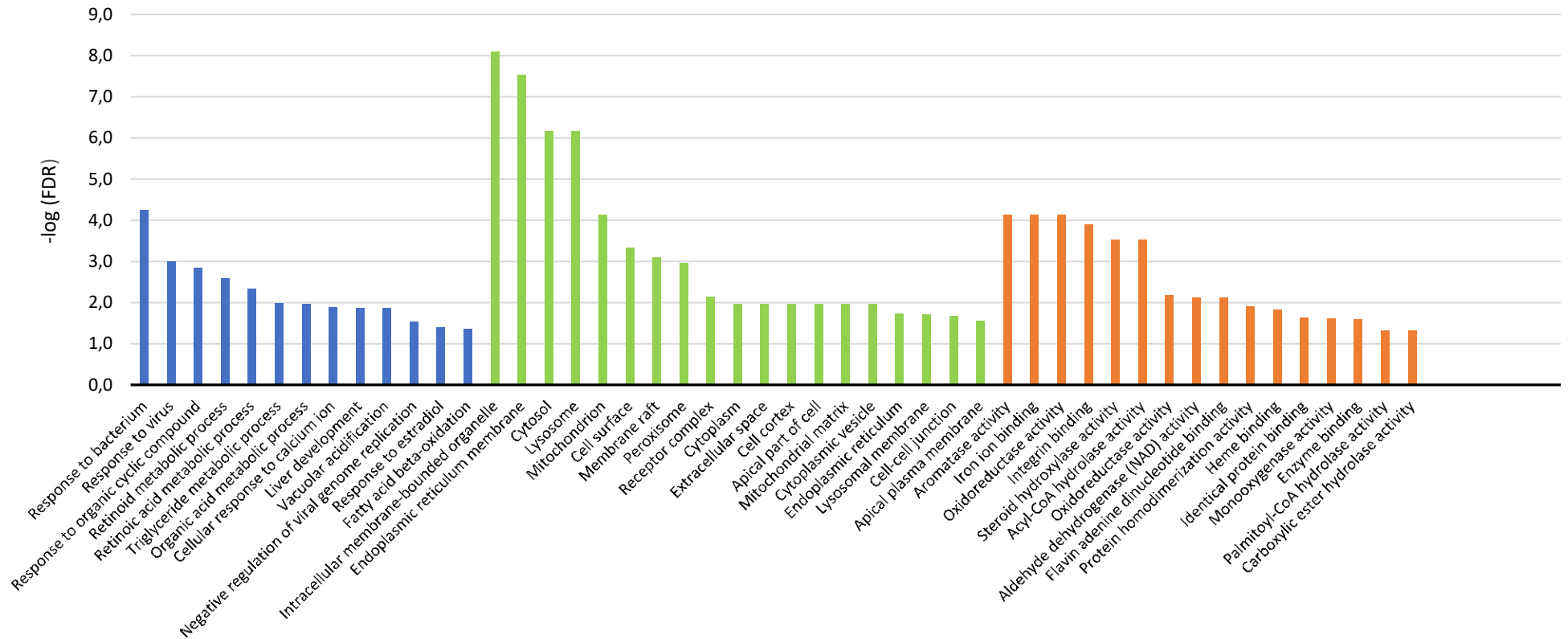
Strain - Pathway enrichment analysis	Genes total	Upregulated in PD5	Downregulated in PD5	-log(p value)
Oxidative Stress	3	Txnrd2,Gclc,Sod1	0	4,14
Keap1-Nrf2	2	Gclc,Gclm	0	3,17
Glutathione metabolism	2	Gclc,Gclm	0	2,75
Lipid Droplet Metabolism	2	Acs11,Dgat2	0	2,59
Triacylglyceride Synthesis	2	Dgat2,Acs11	0	2,53
Folic Acid Network	2	Sod1,Txnrd2	0	2,47
Tryptophan metabolism	2	Aox1	Dhcr24	2,04
IL-2 Signaling Pathway	2	Hsp90aa1	Icam1	1,67
Spinal Cord Injury	2	Nox4	Icam1	1,42
The effect of Glucocorticoids on target gene expression	1	Hsp90aa1	0	1,36
Mitochondrial LC-Fatty Acid Beta-Oxidation	1	Acs11	0	1,33

Supplementary table 15: Differentially expressed genes in the liver after. Pathway enrichment analysis using Transcriptomic analysis console software. Pathway enrichment analysis SHR vs. PD5, comparison for the factor strain. Significantly pathways were selected based on a p-value < 0.05.

<b>Interaction - pathway enrichment analysis</b>	<b>Upregulated in SHR + DEX</b>	<b>Downregulated in SHR + DEX</b>	<b>-log(p value)</b>
Insulin induced PI3K-Akt and MAPK in hepatocytes	0	Pfkfb2	1,47
PI3K-AKT-NFKB pathway	0	Pfkfb2	1,09
Regulation of Actin Cytoskeleton	0	Baiap2	0,87
PKC-SCP2	0	St3gal5	0,00

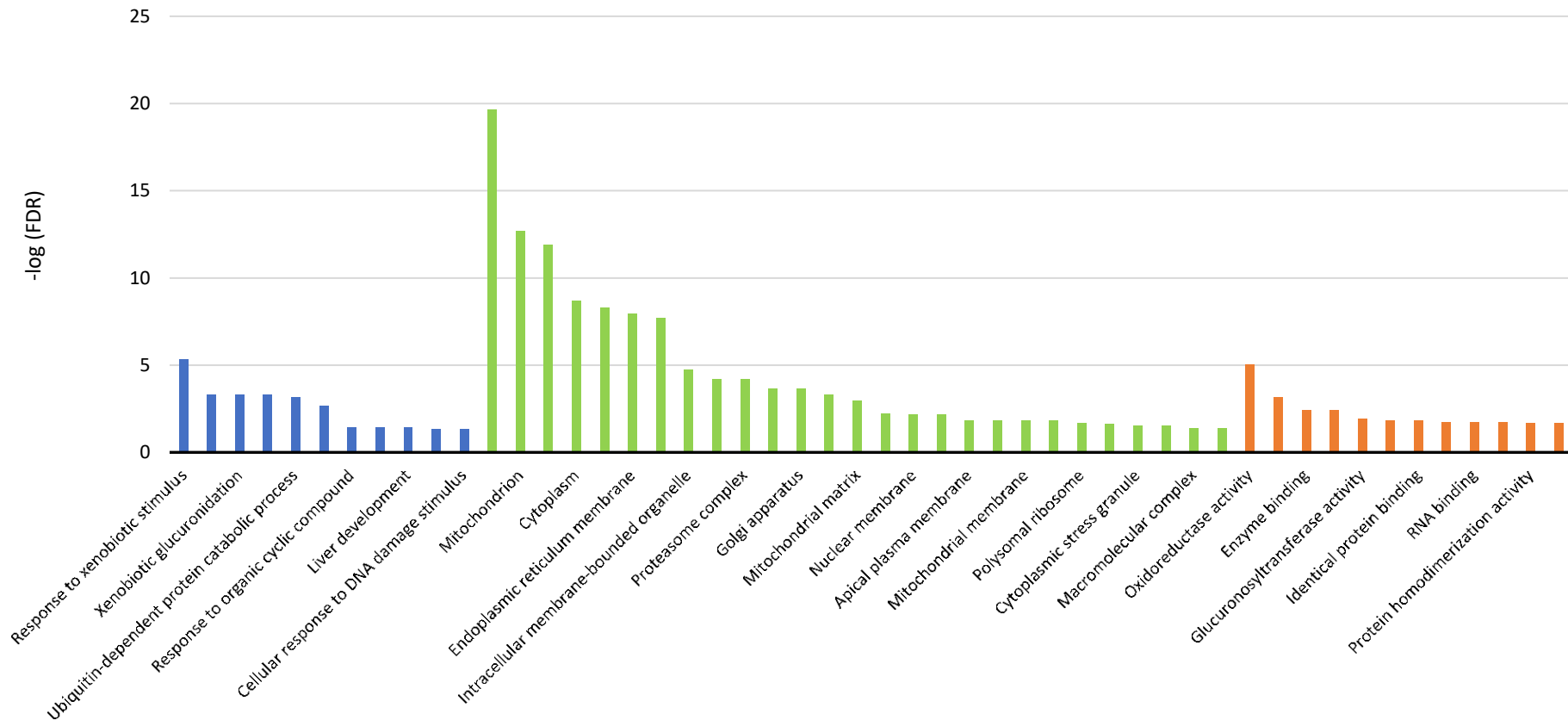
Supplementary table 16: Differentially expressed genes in the liver. Pathway enrichment analysis using Transcriptomic analysis console software. Pathway enrichment analysis SHR vs. PD5, comparison for the factor interaction (strain x diet). None of the enriched pathways reached significance level of  $p < 0.05$ .

### PD vs. SHR GO term enrichment analysis



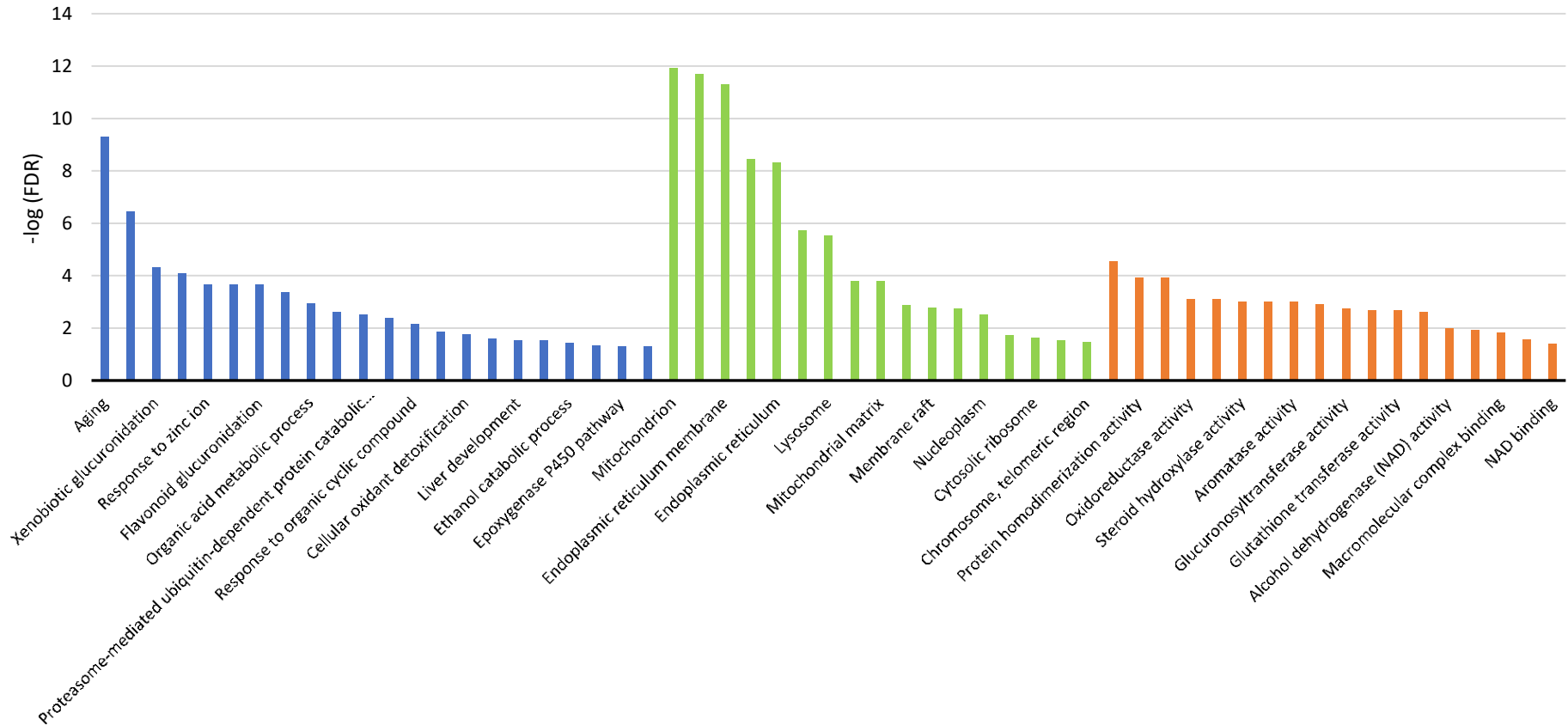
Supplementary figure 1: PD vs. SHR. Gene Ontology (GO) term enrichment analysis. Significantly enriched GO terms were selected based on a FDR < 0.05. GO terms of the categories of Biological Processes, Cellular Components, and Molecular Functions are depicted in blue, green, and orange, respectively.

### PD vs. BN GO term enrichment analysis



Supplementary figure 2: PD vs. BN. Gene Ontology (GO) term enrichment analysis. Significantly enriched GO terms were selected based on a FDR < 0.05. GO terms of the categories of Biological Processes, Cellular Components, and Molecular Functions are depicted in blue, green, and orange, respectively.

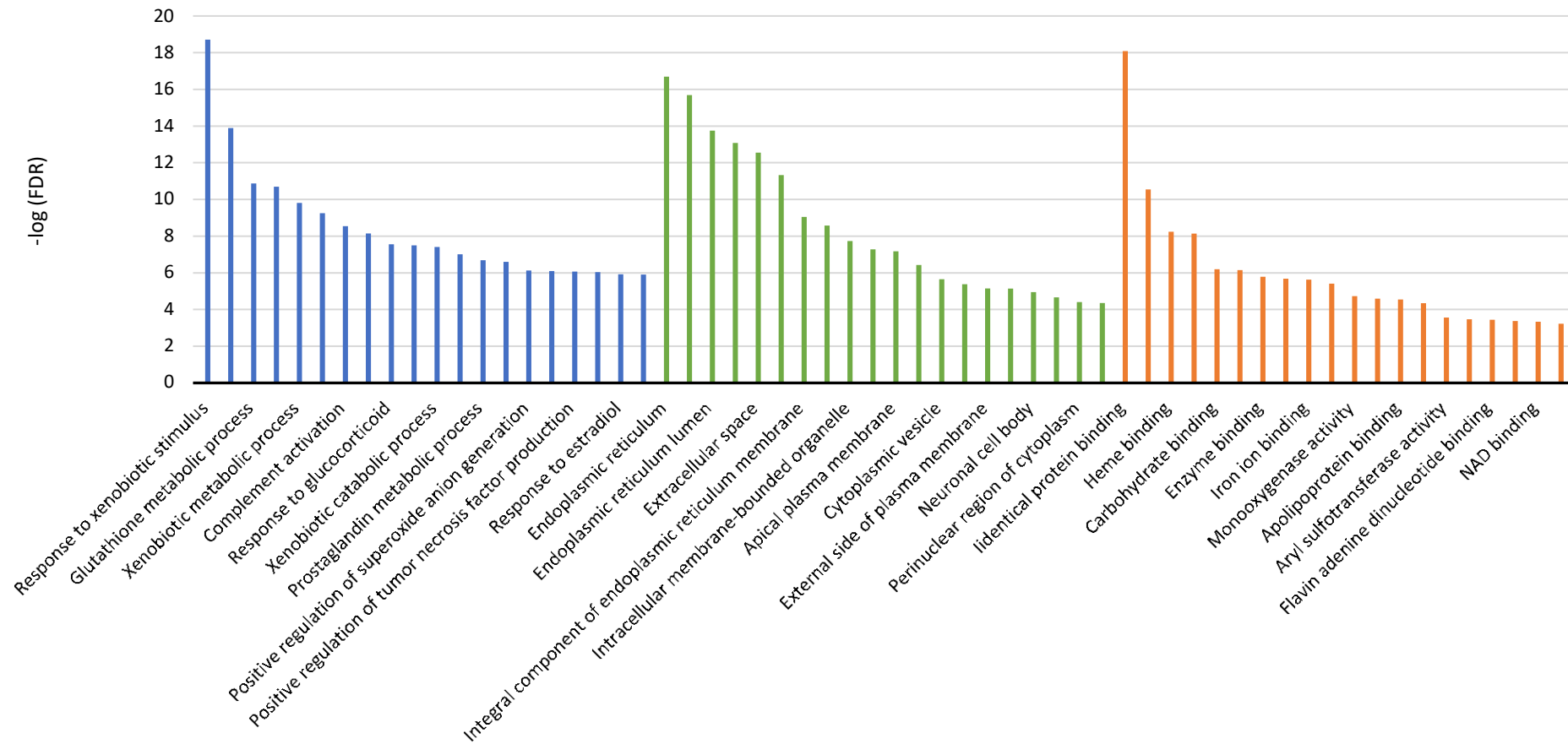
### SHR vs. BN GO term enrichment analysis



Supplementary figure 3: SHR vs. BN Gene Ontology (GO) term enrichment analysis. Significantly enriched GO terms were selected based on a FDR < 0.05. GO terms of the categories of Biological Processes, Cellular Components, and Molecular Functions are depicted in blue, green, and orange, respectively.

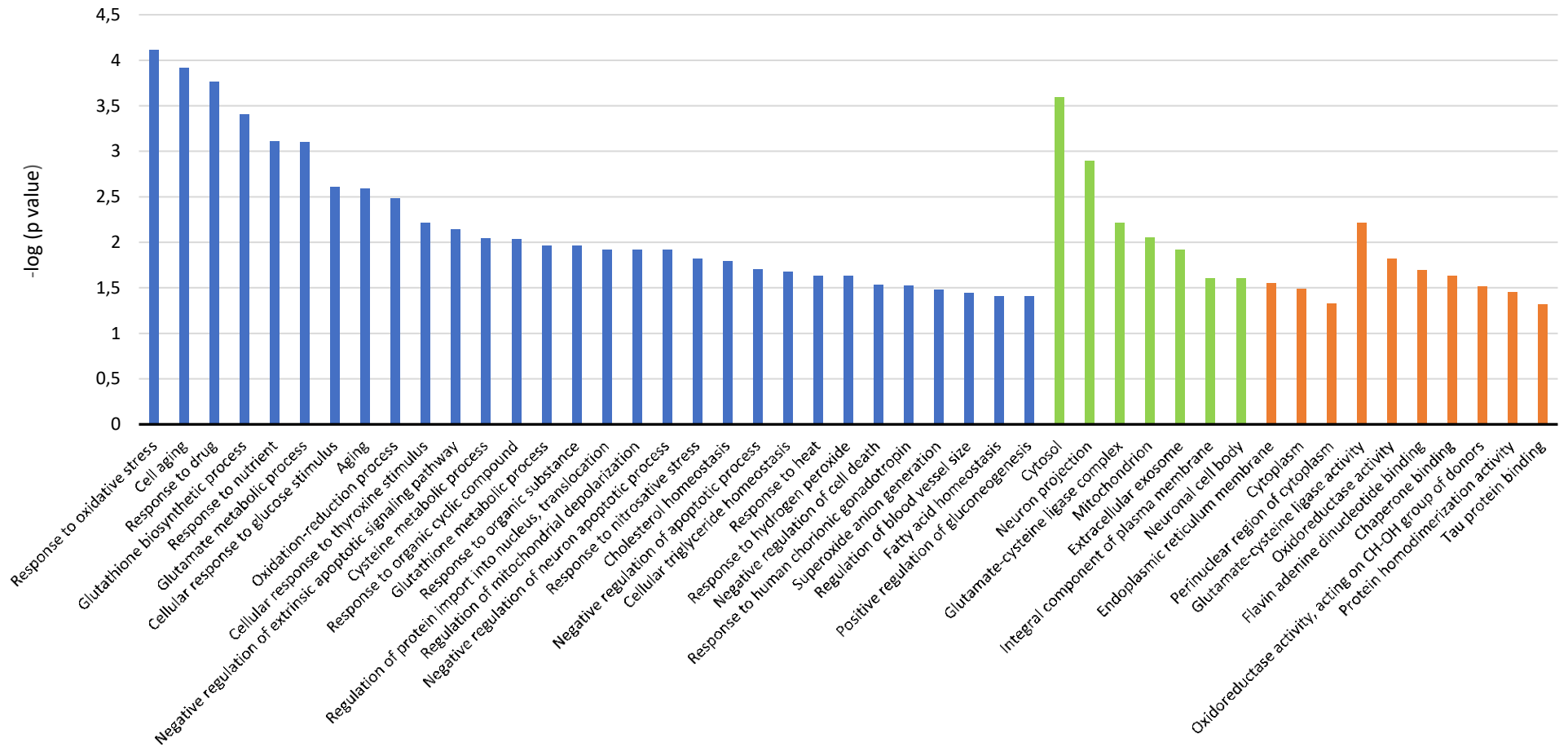


## Dexamethasone vs. standard diet GO term enrichment analysis



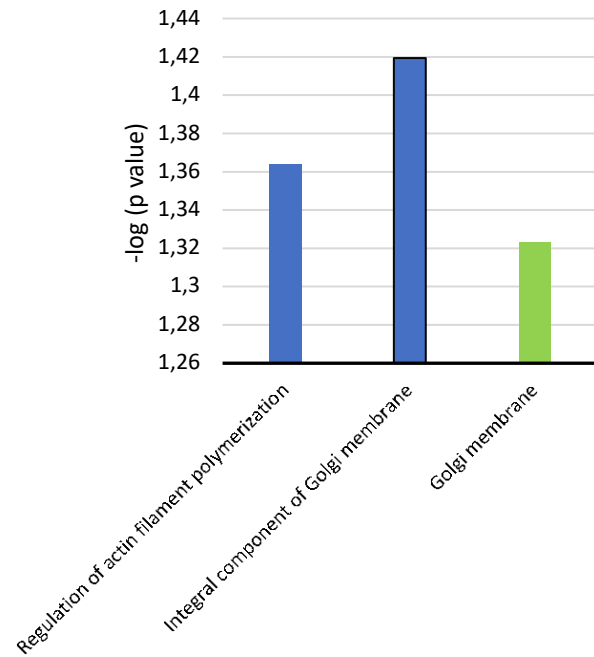
Supplementary figure 4: SHR vs. PD5 (Dexamethasone vs. standard diet. Gene Ontology (GO) term enrichment analysis. Top 20 significantly enriched GO terms for each category were selected based on a  $\text{FDR} < 0.05$ . GO terms of the categories of Biological Processes, Cellular Components, and Molecular Functions are depicted in blue, green, and orange, respectively.

### Strain (SHR vs. PD5) GO term enrichment analysis



Supplementary figure 5: SHR vs. PD5 (strain). Gene Ontology (GO) term enrichment analysis. Significantly enriched GO terms were selected based on a  $p < 0.05$  since none of the enriched pathways reached FDR threshold of  $< 0.05$ . GO terms of the categories of Biological Processes, Cellular Components, and Molecular Functions are depicted in blue, green, and orange, respectively.

### Interaction (strain x dexamethasone) GO term enrichment analysis



Supplementary figure 6: SHR vs. PD5 (interaction dexamethasone x strain). Gene Ontology (GO) term enrichment analysis. None of the significantly enriched GO terms reached a significance threshold of  $p < 0$ . GO terms of the categories of Biological Processes, Cellular Components are depicted in blue, green, respectively. No genes were enriched in the Molecular function category.

Majority protein IDs	Gene names	Razor + unique peptides	Unique peptides	Sequence coverage [%]	Q-value	Score	Intensity
Q9WVK3	Pecr	12	12	12	32,433	0	323,31
Q60587	Hadhb	28	28	28	51,414	0	323,31
Q6AXY0	Gsta6	9	7	7	25,808	0	207,82
Q9WUL0	Top1	20	20	20	90,759	0	161,03
P04176	Pah	26	26	26	51,821	0	323,31
P04905	Gstm1	26	24	21	25,914	0	323,31
P62630;M0R757;F1M6C2	Eef1a1;LOC100360413;LOC100360150	18	18	18	50,113	0	225,81
P14942;A0A8I6AQP1	Gsta4	12	10	10	25,51	0	227,92
P08010	Gstm2	31	31	17	25,702	0	323,31
Q10758	Krt8	38	30	28	54,018	0	323,31
O09171	Bhmt	22	22	19	44,976	0	323,31
P22791	Hmgcs2	26	26	25	56,885	0	323,31
P19112	Fbp1	19	19	19	39,609	0	323,31
P04762	Cat	25	25	25	59,756	0	323,31
A0A8I6AUI8;Q64119	Myl6	7	7	7	20,554	0	88,102
P63018;M0RCB1;A0A8I6AQL9	Hspa8;LOC102549957	29	27	27	70,87	0	323,31
Q02253	Aldh6a1	23	23	23	57,807	0	323,31
Q03336	Rgn	14	14	14	33,389	0	252,74
P02770	Alb	23	23	23	68,73	0	323,31
P10860	Glud1	28	28	28	61,415	0	323,31
Q5XIC0	Eci2	10	10	10	43,021	0	323,31

Supplementary table 17: PLZF-ALL GST pull-down assay. Significant proteins were selected based on FDR<1%, intensity >23. Peptides with larger intensities in GST control group than in PLZF-ALL sample were not further considered