

Supplementary Material

Table S1: Protein analysis in ClueGO plugins and the number of genes involved within the process biologic category between SHRP vs. SHRC groups.

<i>Process Biologic</i>	
<i>Term</i>	Nr. Genes
<i>cellular response to epidermal growth factor stimulus</i>	3.00
<i>collagen fibril organization</i>	3.00
<i>structural constituent of cytoskeleton</i>	22.00
<i>mitochondrial electron transport. cytochrome c to oxygen</i>	2.00
<i>protein homotetramerization</i>	3.00
<i>cellular response to interleukin-4</i>	4.00
<i>cerebellar cortex development</i>	4.00
<i>regulation of mitotic spindle organization</i>	3.00
<i>acute-phase response</i>	5.00
<i>stress response to metal ion</i>	2.00
<i>positive regulation of axon guidance</i>	2.00
<i>endothelial cell chemotaxis</i>	2.00
<i>dendritic cell chemotaxis</i>	3.00
<i>glial cell proliferation</i>	7.00
<i>hydrogen peroxide metabolic process</i>	5.00
<i>platelet activation</i>	6.00
<i>chondroitin sulfate proteoglycan metabolic process</i>	2.00
<i>regulation of transepithelial transport</i>	2.00
<i>response to lead ion</i>	4.00
<i>sarcomere organization</i>	6.00
<i>mesenchyme migration</i>	4.00
<i>regulation of protein dephosphorylation</i>	9.00
<i>establishment or maintenance of epithelial cell apical/basal polarity</i>	4.00
<i>regulation of cholesterol metabolic process</i>	2.00
<i>lactate metabolic process</i>	3.00
<i>response to hydrogen peroxide</i>	16.00
<i>regulation of oxidative stress-induced intrinsic apoptotic signaling pathway</i>	5.00
<i>ventricular system development</i>	2.00
<i>energy derivation by oxidation of organic compounds</i>	19.00
<i>intermediate filament organization</i>	11.00
<i>positive regulation of blood vessel endothelial cell migration</i>	5.00
<i>regulation of calcium-mediated signaling</i>	5.00
<i>thioester biosynthetic process</i>	2.00
<i>structural constituent of synapse</i>	7.00
<i>cellular response to reactive oxygen species</i>	11.00
<i>regulation of NIK/NF-kappaB signaling</i>	6.00
<i>actin filament fragmentation</i>	2.00
<i>response to platinum ion</i>	2.00
<i>negative regulation of extrinsic apoptotic signaling pathway</i>	6.00
<i>ribonucleoside metabolic process</i>	2.00
<i>cellular response to cadmium ion</i>	2.00

<i>positive regulation of viral process</i>	4.00
<i>cellular oxidant detoxification</i>	9.00
<i>regulation of response to oxidative stress</i>	10.00
<i>negative regulation of vascular associated smooth muscle cell proliferation</i>	6.00
<i>ATP-dependent protein folding chaperone</i>	8.00
<i>positive regulation of epithelial cell migration</i>	9.00
<i>purine-containing compound biosynthetic process</i>	11.00
<i>chaperone-mediated protein folding</i>	8.00
<i>negative regulation of striated muscle cell apoptotic process</i>	2.00
<i>regulation of wound healing</i>	7.00
<i>purine ribonucleoside triphosphate biosynthetic process</i>	7.00
<i>structural constituent of postsynapse</i>	5.00
<i>supramolecular fiber organization</i>	44.00
<i>peroxidase activity</i>	6.00
<i>fatty acid beta-oxidation</i>	7.00
<i>regulation of polysaccharide biosynthetic process</i>	2.00
<i>structural constituent of postsynaptic intermediate filament cytoskeleton</i>	2.00
<i>intermediate filament cytoskeleton organization</i>	11.00
<i>pyrimidine nucleoside triphosphate biosynthetic process</i>	2.00
<i>negative regulation of exocytosis</i>	4.00
<i>male meiosis I</i>	4.00
<i>blood vessel endothelial cell migration</i>	7.00
<i>dopamine receptor signaling pathway</i>	5.00
<i>response to reactive oxygen species</i>	20.00
<i>regulation of vascular associated smooth muscle cell proliferation</i>	9.00
<i>response to inorganic substance</i>	43.00

Table S2: Protein analysis in ClueGO plug-ins and the number of genes involved within the process biological category between SHR_T vs SHR_C groups.

<i>Process Biological</i>	
<i>Term</i>	Nr. Genes
<i>collagen fibril organization</i>	4.00
<i>regulation of cholesterol metabolic process</i>	3.00
<i>cellular response to epidermal growth factor stimulus</i>	4.00
<i>tricarboxylic acid metabolic process</i>	2.00
<i>negative regulation of blood vessel endothelial cell migration</i>	2.00
<i>acute-phase response</i>	6.00
<i>fatty acid beta-oxidation using acyl-CoA dehydrogenase</i>	3.00
<i>regulation of protein dephosphorylation</i>	5.00
<i>positive regulation of bone resorption</i>	2.00
<i>response to lead ion</i>	4.00
<i>cardiac epithelial to mesenchymal transition</i>	2.00
<i>sarcomere organization</i>	4.00
<i>actomyosin structure organization</i>	11.00
<i>response to heat</i>	10.00
<i>cellular oxidant detoxification</i>	7.00
<i>regulation of reactive oxygen species metabolic process</i>	9.00
<i>nucleus localization</i>	2.00
<i>hydrogen peroxide metabolic process</i>	5.00
<i>superoxide metabolic process</i>	6.00
<i>positive regulation of gliogenesis</i>	5.00
<i>ATP-dependent protein folding chaperone</i>	7.00
<i>response to ATP</i>	2.00
<i>negative regulation of extrinsic apoptotic signaling pathway</i>	6.00
<i>cellular response to fatty acid</i>	5.00
<i>positive regulation of sterol transport</i>	2.00
<i>mesenchyme migration</i>	4.00
<i>myofibril assembly</i>	8.00
<i>protein refolding</i>	5.00
<i>gluconeogenesis</i>	5.00
<i>face morphogenesis</i>	2.00
<i>regulation of superoxide metabolic process</i>	4.00
<i>negative regulation of ion transmembrane transport</i>	7.00
<i>collagen biosynthetic process</i>	4.00
<i>cerebellar Purkinje cell layer development</i>	4.00
<i>negative regulation of striated muscle cell apoptotic process</i>	2.00
<i>structural constituent of synapse</i>	4.00
<i>fibrinolysis</i>	3.00
<i>negative regulation of hyaluronan biosynthetic process</i>	2.00
<i>chaperone cofactor-dependent protein refolding</i>	5.00
<i>protein localization to chromatin</i>	2.00
<i>positive regulation of lamellipodium organization</i>	2.00
<i>cellular response to butyrate</i>	2.00
<i>regulation of dopamine biosynthetic process</i>	2.00

<i>regulation of wound healing</i>	8.00
<i>regulation of cellular response to oxidative stress</i>	7.00
<i>actin filament fragmentation</i>	3.00
<i>protein folding chaperone</i>	8.00
<i>regulation of response to oxidative stress</i>	8.00

Table S3. The protein of comparison SHRP vs. SHRC. 138 proteins were identified, with 73 *upregulated* and 2 *downregulated* significantly in the first group of the comparison and unique from each group with $p < 0.05^{**}$.

<i>c</i> cession ^a	<i>Description</i>	<i>Score</i>	<i>SHRP:SHRC_</i> <i>Ratio</i> ^b	<i>SHRP:SHRC_</i> <i>P</i> ^c	<i>Up /</i> <i>intermediate /</i> <i>Down</i> ^d
Q9ER34	Aconitate hydratase_ mitochondrial	83	1.67	< 0.01	↑
P68035	Actin_ alpha cardiac muscle 1	5542	1.07	< 0.01	↑
P68136	Actin_ alpha skeletal muscle	5242	1.07	< 0.01	↑
P62738	Actin_ aortic smooth muscle	5534	1.07	< 0.01	↑
P60711	Actin_ cytoplasmic 1	4354	1.12	< 0.01	↑
P63259	Actin_ cytoplasmic 2	4358	1.12	< 0.01	↑
P63269	Actin_ gamma-enteric smooth muscle	5534	1.07	< 0.01	↑
Q9Z1P2	Alpha-actinin-1	719	1.30	< 0.01	↑
Q9QXQ0	Alpha-actinin-4	431	1.31	< 0.01	↑
Q07936	Annexin A2	474	1.38	< 0.01	↑
P15999	ATP synthase subunit alpha_ mitochondrial	175	1.54	< 0.01	↑
P10719	ATP synthase subunit beta_ mitochondrial	87	1.38	< 0.01	↑
P47853	Biglycan	227	1.72	< 0.01	↑
P02454	Collagen alpha-1(I) chain	47	1.88	< 0.01	↑
P47875	Cysteine and glycine-rich protein 1	1148	1.45	< 0.01	↑
P36201	Cysteine-rich protein 2	176	1.63	< 0.01	↑
P48675	Desmin	467	1.26	< 0.01	↑
Q4V8H8	EH domain-containing protein 2	225	1.45	< 0.01	↑
P62630	Elongation factor 1-alpha 1	298	1.62	< 0.01	↑
P70623	Fatty acid-binding protein_ adipocyte	436	1.60	< 0.01	↑
P06399	Fibrinogen alpha chain	112	1.32	< 0.01	↑
Q9WVH8	Fibulin-5	52	1.32	< 0.01	↑
P11762	Galectin-1	260	1.75	< 0.01	↑
P08010	Glutathione S-transferase Mu 2	217	1.58	< 0.01	↑
P0DMW0	Heat shock 70 kDa protein 1A	849	1.28	< 0.01	↑
P55063	Heat shock 70 kDa protein 1-like	597	1.31	< 0.01	↑
P63018	Heat shock cognate 71 kDa protein	852	1.36	< 0.01	↑
P42930	Heat shock protein beta-1	848	1.54	< 0.01	↑
P14659	Heat shock-related 70 kDa protein 2	691	1.39	< 0.01	↑
Q6IG12	Keratin_ type II cytoskeletal 7	193	1.67	< 0.01	↑
Q10758	Keratin_ type II cytoskeletal 8	193	1.70	< 0.01	↑
P18666	Myosin regulatory light chain 12B	975	1.27	< 0.01	↑
Q64122	Myosin regulatory light polypeptide 9	4053	1.34	< 0.01	↑
Q9JLT0	Myosin-10	71	1.49	< 0.01	↑
Q62812	Myosin-9	68	1.52	< 0.01	↑
P10111	Peptidyl-prolyl cis-trans isomerase A	1750	1.42	< 0.01	↑
P62963	Profilin-1	3064	1.19	< 0.01	↑
P02770	Serum albumin	7160	1.09	< 0.01	↑
P31232	Transgelin	9127	1.40	< 0.01	↑
P68370	Tubulin alpha-1A chain	237	1.67	< 0.01	↑
Q6P9V9	Tubulin alpha-1B chain	237	1.67	< 0.01	↑
Q6AYZ1	Tubulin alpha-1C chain	237	1.68	< 0.01	↑
Q68FR8	Tubulin alpha-3 chain	111	1.84	< 0.01	↑

Q5XIF6	Tubulin alpha-4A chain	107	1.73	< 0.01	↑
Q6AY56	Tubulin alpha-8 chain	46	2.20	< 0.01	↑
P85108	Tubulin beta-2A chain	94	1.49	< 0.01	↑
Q3KRE8	Tubulin beta-2B chain	94	1.49	< 0.01	↑
Q4QRB4	Tubulin beta-3 chain	94	1.48	< 0.01	↑
Q6P9T8	Tubulin beta-4B chain	467	1.48	< 0.01	↑
P69897	Tubulin beta-5 chain	94	1.49	< 0.01	↑
P31000	Vimentin	1733	1.23	< 0.01	↑
Q5RKI0	WD repeat-containing protein 1	192	1.32	< 0.01	↑
P07150 *	Annexin A1	94	1.52	0.01	↑
P85125	Caveolae-associated protein 1	150	1.51	0.01	↑
P06761	Endoplasmic reticulum chaperone BiP	248	1.22	0.01	↑
P0DMW1	Heat shock 70 kDa protein 1B	845	1.30	0.01	↑
Q00715	Histone H2B type 1	122	1.48	0.01	↑
P15650	Long-chain specific acyl-CoA dehydrogenase_ mitochondrial	93	1.51	0.01	↑
P02600	Myosin light chain 1/3_ skeletal muscle isoform	809	1.28	0.01	↑
P16409	Myosin light chain 3	787	1.30	0.01	↑
P13832	Myosin regulatory light chain RLC-A	975	1.26	0.01	↑
P85973	Purine nucleoside phosphorylase	155	1.31	0.01	↑
Q7M0E3	Dextrin	1706	1.22	0.02	↑
P20760	Ig gamma-2A chain C region	643	1.13	0.02	↑
Q62736	Non-muscle caldesmon	274	1.72	0.02	↑
P21807	Peripherin	195	1.35	0.02	↑
P12346	Serotransferrin	1002	1.14	0.02	↑
P63102	14-3-3 protein zeta/delta	142	1.34	0.03	↑
Q01129	Decorin	150	1.55	0.03	↑
P05065	Fructose-bisphosphate aldolase A	202	1.26	0.03	↑
Q6P6Q2	Keratin_ type II cytoskeletal 5	76	1.70	0.03	↑
P04636	Malate dehydrogenase_ mitochondrial	346	1.40	0.03	↑
Q5XI73	Rho GDP-dissociation inhibitor 1	327	1.36	0.04	↑
P14668 *	Annexin A5	145	1.25	0.95	----
P04797	Glyceraldehyde-3-phosphate dehydrogenase	1896	1.13	0.95	----
A6YP92	Homeobox protein ARX	33	1.75	0.95	----
P11598	Protein disulfide-isomerase A3	100	1.42	0.95	----
P16636	Protein-lysine 6-oxidase	251	1.46	0.95	----
P50398	Rab GDP dissociation inhibitor alpha	112	1.79	0.95	----
Q64119	Myosin light polypeptide 6	13395	1.09	0.94	----
P25113	Phosphoglycerate mutase 1	276	1.55	0.94	----
P50137	Transketolase	50	1.40	0.94	----
P48037	Annexin A6	120	1.15	0.93	----
P34058	Heat shock protein HSP 90-beta	106	1.67	0.93	----
P23565	Alpha-internexin	69	1.31	0.90	----
P62632	Elongation factor 1-alpha 2	51	2.03	0.90	----
P02680	Fibrinogen gamma chain	682	1.19	0.90	----
P20761	Ig gamma-2B chain C region	130	1.19	0.90	----
P04692	Tropomyosin alpha-1 chain	736	1.19	0.90	----
P68511	14-3-3 protein eta	63	1.34	0.89	----
O88989	Malate dehydrogenase_ cytoplasmic	103	1.34	0.89	----
P11506	Plasma membrane calcium-transporting ATPase 2	71	1.40	0.89	----

P07943	Aldose reductase	254	1.17	0.88	----
Q68FY0	Cytochrome b-c1 complex subunit 1_ mitochondrial	160	1.35	0.87	----
P70490	Lactadherin	112	1.27	0.87	----
P58775	Tropomyosin beta chain	736	1.17	0.87	----
Q4FZU2	Keratin_type II cytoskeletal 6A	76	1.54	0.86	----
Q08163	Adenylyl cyclase-associated protein 1	165	1.15	0.85	----
P16617	Phosphoglycerate kinase 1	73	1.55	0.84	----
P11980	Pyruvate kinase PKM	40	1.51	0.83	----
Q61E24	Inactive ubiquitin carboxyl-terminal hydrolase 54	36	1.13	0.82	----
P50399	Rab GDP dissociation inhibitor beta	52	1.65	0.81	----
P09495	Tropomyosin alpha-4 chain	50	1.22	0.81	----
Q6IG05	Keratin_type II cytoskeletal 75	76	1.45	0.79	----
P47819	Glial fibrillary acidic protein	52	1.45	0.78	----
P01836	Ig kappa chain C region_ A allele	701	1.22	0.78	----
Q6IG00	Keratin_type II cytoskeletal 4	52	1.49	0.77	----
P09117	Fructose-bisphosphate aldolase C	79	1.51	0.74	----
Q63610	Tropomyosin alpha-3 chain	50	1.17	0.74	----
P15800	Laminin subunit beta-2	47	1.22	0.73	----
P24090	Alpha-2-HS-glycoprotein	275	1.15	0.72	----
P14480	Fibrinogen beta chain	941	1.08	0.72	----
P51886	Lumican	1267	1.00	0.72	----
P20759	Ig gamma-1 chain C region	31	1.39	0.70	----
P01026	Complement C3	57	1.12	0.69	----
P13437	3-ketoacyl-CoA thiolase_ mitochondrial	85	1.16	0.67	----
P45592	Cofilin-1	297	1.06	0.67	----
P61983	14-3-3 protein gamma	53	1.09	0.65	----
P07632	Superoxide dismutase [Cu-Zn]	125	1.07	0.65	----
P04764	Alpha-enolase	138	1.05	0.62	----
P62260	14-3-3 protein epsilon	148	1.09	0.59	----
P11884	Aldehyde dehydrogenase_ mitochondrial	90	1.05	0.59	----
P20059	Hemopexin	409	1.02	0.58	----
P68255	14-3-3 protein theta	164	1.08	0.53	----
P35213	14-3-3 protein beta/alpha	164	1.03	0.43	----
P62982	Ubiquitin-40S ribosomal protein S27a	274	0.93	0.42	----
P04906	Glutathione S-transferase P	114	0.95	0.39	----
Q66HD0	Endoplasmic	51	0.90	0.37	----
Q63429	Polyubiquitin-C	274	0.92	0.35	----
P12839	Neurofilament medium polypeptide	79	0.92	0.34	----
P0CG51	Polyubiquitin-B	274	0.90	0.33	----
Q63598	Plastin-3	90	0.86	0.32	----
P62986	Ubiquitin-60S ribosomal protein L40	274	0.90	0.29	----
Q68FU3	Electron transfer flavoprotein subunit beta	536	0.68	0.19	----
P06866	Haptoglobin	335	0.88	0.17	----
P11517	Hemoglobin subunit beta-2	3388	0.86	0.06	----
P01946	Hemoglobin subunit alpha-1/2	14931	0.62	< 0.01	↓
P02091	Hemoglobin subunit beta-1	10419	0.76	< 0.01	↓
P26772	10 kDa heat shock protein_ mitochondrial	416			SHR _P
Q5XI78	2-oxoglutarate dehydrogenase_ mitochondrial	90			SHR _P
P17764	Acetyl-CoA acetyltransferase_ mitochondrial	180			SHR _P

<i>Q5XIK1</i>	Actin-related protein T1	73			SHR _P
<i>P11030</i>	Acyl-CoA-binding protein	271			SHR _P
<i>P17475</i>	Alpha-1-antiproteinase	149			SHR _P
<i>P10759</i>	AMP deaminase 1	101			SHR _P
<i>Q5M9H0</i>	Ankyrin repeat and SAM domain-containing protein 3	98			SHR _P
<i>D3ZAF6</i>	ATP synthase subunit f_ mitochondrial	55			SHR _P
<i>Q925T8</i>	BMP/retinoic acid-inducible neural-specific protein 1	95			SHR _P
<i>P0DP29</i>	Calmodulin-1	145			SHR _P
<i>P0DP30</i>	Calmodulin-2	145			SHR _P
<i>P0DP31</i>	Calmodulin-3	145			SHR _P
<i>Q08290</i>	Calponin-1	92			SHR _P
<i>P18418</i>	Calreticulin	109			SHR _P
<i>P24268</i>	Cathepsin D	117			SHR _P
<i>Q5U3Z0</i>	Cilia- and flagella-associated protein 298	158			SHR _P
<i>P11442</i>	Clathrin heavy chain 1	71			SHR _P
<i>P05371</i>	Clusterin	93			SHR _P
<i>Q4KM47</i>	Cyclin-dependent kinase 10	102			SHR _P
<i>P14841</i>	Cystatin-C	264			SHR _P
<i>P11240</i>	Cytochrome c oxidase subunit 5A_ mitochondrial	587			SHR _P
<i>P10818</i>	Cytochrome c oxidase subunit 6A1_ mitochondrial	631			SHR _P
<i>Q62871</i>	Cytoplasmic dynein 1 intermediate chain 2	109			SHR _P
<i>Q5BK18</i>	Cytosolic iron-sulfur assembly component 3	92			SHR _P
<i>Q8K5A9</i>	Death domain-containing membrane protein NRADD	70			SHR _P
<i>P06214</i>	Delta-aminolevulinic acid dehydratase	75			SHR _P
<i>Q62952</i>	Dihydropyrimidinase-related protein 3	103			SHR _P
<i>Q62967</i>	Diphosphomevalonate decarboxylase	95			SHR _P
<i>Q66HC9</i>	Dynein intermediate chain 2_ axonemal	95			SHR _P
<i>Q00911</i>	Early growth response protein 4	140			SHR _P
<i>P13803</i>	Electron transfer flavoprotein subunit alpha_ mitochondrial	189			SHR _P
<i>P05197</i>	Elongation factor 2	108			SHR _P
<i>P14604</i>	Enoyl-CoA hydratase_ mitochondrial	46			SHR _P
<i>Q5RKI1</i>	Eukaryotic initiation factor 4A-II	92			SHR _P
<i>P50609</i>	Fibromodulin	125			SHR _P
<i>Q9WUH4</i>	Four and a half LIM domains protein 1	413			SHR _P
<i>P10860</i>	Glutamate dehydrogenase 1_ mitochondrial	253			SHR _P
<i>Q99MZ4</i>	Glutathione hydrolase 7	121			SHR _P
<i>Q63406</i>	Guanine nucleotide exchange factor DBS	61			SHR _P
<i>P10824</i>	Guanine nucleotide-binding protein G(i) subunit alpha-1	104			SHR _P
<i>P04897</i>	Guanine nucleotide-binding protein G(i) subunit alpha-2	157			SHR _P
<i>P08753</i>	Guanine nucleotide-binding protein G(k) subunit alpha	104			SHR _P
<i>P59215</i>	Guanine nucleotide-binding protein G(o) subunit alpha	104			SHR _P
<i>P38406</i>	Guanine nucleotide-binding protein G(olf) subunit alpha	104			SHR _P

P63095	Guanine nucleotide-binding protein G(s) subunit alpha isoforms short	104			SHR _P
Q63803	Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	104			SHR _P
P29348	Guanine nucleotide-binding protein G(t) subunit alpha-3	104			SHR _P
Q63210	Guanine nucleotide-binding protein subunit alpha-12	101			SHR _P
Q6Q7Y5	Guanine nucleotide-binding protein subunit alpha-13	101			SHR _P
Q9Z136	Hamartin	51			SHR _P
P62959	Histidine triad nucleotide-binding protein 1	223			SHR _P
Q99MK2	Histone acetyltransferase KAT5	156			SHR _P
Q00729	Histone H2B type 1-A	1001			SHR _P
Q9ESM2	Hyaluronan and proteoglycan link protein 2	59			SHR _P
P20762	Ig gamma-2C chain C region	127			SHR _P
P01835	Ig kappa chain C region_ B allele	2149			SHR _P
Q99NA5	Isocitrate dehydrogenase [NAD] subunit alpha_mitochondrial	82			SHR _P
Q6IFW6	Keratin_type I cytoskeletal 10	74			SHR _P
P25030	Keratin_type I cytoskeletal 20	65			SHR _P
P70615	Lamin-B1	53			SHR _P
Q99MZ8	LIM and SH3 domain protein 1	97			SHR _P
Q5XI07	Lipoma-preferred partner homolog	326			SHR _P
A1A5P5	LisH domain-containing protein ARMC9	128			SHR _P
P04642	L-lactate dehydrogenase A chain	122			SHR _P
P42123	L-lactate dehydrogenase B chain	214			SHR _P
P30904	Macrophage migration inhibitory factor	169			SHR _P
P02761	Major urinary protein	48			SHR _P
O35763	Moesin	109			SHR _P
P16884	Neurofilament heavy polypeptide	96			SHR _P
P19527	Neurofilament light polypeptide	89			SHR _P
O08658	Nuclear pore complex protein Nup88	54			SHR _P
Q05982	Nucleoside diphosphate kinase A	480			SHR _P
P19804	Nucleoside diphosphate kinase B	447			SHR _P
Q63371	P2Y purinoceptor 6	95			SHR _P
P27657	Pancreatic triacylglycerol lipase	58			SHR _P
P52944	PDZ and LIM domain protein 1	213			SHR _P
Q66HS7	PDZ and LIM domain protein 3	128			SHR _P
Q62920	PDZ and LIM domain protein 5	93			SHR _P
Q9Z1Z9	PDZ and LIM domain protein 7	118			SHR _P
Q63716	Peroxiredoxin-1	105			SHR _P
Q9Z221	Polyamine-modulated factor 1-binding protein 1	106			SHR _P
D4ABH7	Pre-miRNA 5'-monophosphate methyltransferase	148			SHR _P
P04785	Protein disulfide-isomerase	91			SHR _P
Q9QZQ5	Protein NOV homolog	256			SHR _P
P05964	Protein S100-A6	1473			SHR _P
P98106	P-selectin	57			SHR _P
P49432	Pyruvate dehydrogenase E1 component subunit beta_mitochondrial	53			SHR _P
P29315	Ribonuclease inhibitor	58			SHR _P

P57760	Serine/threonine-protein kinase 16	110			SHR _P
Q9QWN8	Spectrin beta chain_ non-erythrocytic 2	54			SHR _P
G3V7P1	Syntaxin-12	92			SHR _P
Q63635	Syntaxin-6	91			SHR _P
Q5XHX6	Thioredoxin domain-containing protein 2	55			SHR _P
Q6IE14	Transmembrane protease serine 11B-like protein	106			SHR _P
P02767	Transthyretin	216			SHR _P
P27435	Tryptase	591			SHR _P
Q9EQT5	Tubulointerstitial nephritis antigen-like	310			SHR _P
Q498R7	UPF0587 protein C1orf123 homolog	79			SHR _P
Q6AY86	Vacuolar protein sorting-associated protein 26A	104			SHR _P
O54975	Xaa-Pro aminopeptidase 1	107			SHR _P
P80299	Bifunctional epoxide hydrolase 2	47			SHR _C
Q4V8E4	Cilia- and flagella-associated protein 36	83			SHR _C
O55096	Dipeptidyl peptidase 3	45			SHR _C
Q91XQ4	DNA-directed RNA polymerase II subunit GRINL1A	69			SHR _C
Q62862	Dual specificity mitogen-activated protein kinase kinase 5	67			SHR _C
Q5EZ72	Ectonucleotide pyrophosphatase/phosphodiesterase family member 7	42			SHR _C
Q66H04	F-box only protein 43	68			SHR _C
P13255	Glycine N-methyltransferase	44			SHR _C
Q5XHZ0	Heat shock protein 75 kDa_ mitochondrial	47			SHR _C
P06762	Heme oxygenase 1	60			SHR _C
E9PU28	Inosine-5'-monophosphate dehydrogenase 2	79			SHR _C
Q99J82	Integrin-linked protein kinase	75			SHR _C
P18588	Interferon-induced GTP-binding protein Mx1	61			SHR _C
P56574	Isocitrate dehydrogenase [NADP]_ mitochondrial	74			SHR _C
Q5U2U7	mRNA cap guanine-N7 methyltransferase	99			SHR _C
A7E3N2	Neutrophil cytosol factor 2	52			SHR _C
O88767	Protein/nucleic acid deglycase DJ-1	229			SHR _C
Q9JK11	Reticulon-4	39			SHR _C
P42346	Serine/threonine-protein kinase mTOR	52			SHR _C
D3ZVU1	SprT-like domain-containing protein Spartan	72			SHR _C
P01048	T-kininogen 1	55			SHR _C

^a identification of proteins in the Uniprot database (<http://www.uniprot.org/>).

^b Significant difference in expression proteins up regulation, down regulation and intermediates.

^c p value (p<0.05).

^d Up regulated (↑), Intermediate (----, present in both comparison groups), down regulated (↓) and unique each comparison group (SHR_P and SHR_C).

**Adapted with permission from ref 15.

Table S4. The protein of comparison SHR_T vs. SHR_C. 123 proteins were identified, with 7 *upregulated* and 22 *downregulated* significantly in the first group of the comparison and unique from each group with p<0.05.

<i>Accession ^a</i>	<i>Description</i>	<i>Score</i>	<i>SHR_T: SHR_C Ratio</i> <i>^b</i>	<i>SHR_T: SHR_C</i> <i>^c</i> <i>__P</i>	<i>Up / intermediate /</i> <i>Down / Unique</i>
P68035	Actin_ alpha cardiac muscle 1	5542	1.32	< 0.01	↑
P63269	Actin_ gamma-enteric smooth muscle	5534	1.32	< 0.01	↑
P47853	Biglycan	227	1.57	< 0.01	↑
P06761	Endoplasmic reticulum chaperone BiP	248	1.34	< 0.01	↑
P70490	Lactadherin	112	3.16	< 0.01	↑
Q6AY56	Tubulin alpha-8 chain	46	1.86	< 0.01	↑
Q9JLT0	Myosin-10	71	1.31	0.02	↑
P21807	Peripherin	195	1.38	0.95	----
Q6AYZ1	Tubulin alpha-1C chain	237	1.15	0.95	----
P01026	Complement C3	57	1.43	0.94	----
P48675	Desmin	467	1.13	0.94	----
P16636	Protein-lysine 6-oxidase V=2	251	1.42	0.94	----
Q68FR8	Tubulin alpha-3 chain	111	1.23	0.93	----
P58775	Tropomyosin beta chain	736	1.20	0.92	----
P06762	Heme oxygenase 1	60	1.54	0.89	----
Q62736	Non-muscle caldesmon	274	1.39	0.89	----
P68370	Tubulin alpha-1A chain	237	1.14	0.89	----
Q5XIF6	Tubulin alpha-4A chain	107	1.19	0.89	----
Q6P9V9	Tubulin alpha-1B chain	237	1.12	0.87	----
P01836	Ig kappa chain C region_ A allele	701	1.25	0.86	----
P23565	Alpha-internexin	69	1.20	0.85	----
P20761	Ig gamma-2B chain C region	130	1.19	0.85	----
Q63598	Plastin-3	90	1.52	0.85	----
P11762	Galectin-1	260	1.22	0.84	----
P07943	Aldose reductase OS=Rattus norvegicus	254	1.21	0.83	----
Q5XI73	Rho GDP-dissociation inhibitor 1	327	1.19	0.83	----
P04692	Tropomyosin alpha-1 chain	736	1.19	0.83	----
P12839	Neurofilament medium polypeptide	79	1.12	0.81	----
P14668	Annexin A5	145	1.15	0.80	----
P18666	Myosin regulatory light chain 12B	975	1.13	0.79	----
P13832	Myosin regulatory light chain RLC-A	975	1.11	0.78	----
Q6IG00	Keratin_ type II cytoskeletal 4	52	1.72	0.77	----
P04764	Alpha-enolase	138	1.16	0.75	----
P63102	14-3-3 protein zeta/delta	142	1.17	0.74	----
P07150	Annexin A1	94	1.20	0.74	----
P11598	Protein disulfide-isomerase A3	100	1.22	0.74	----
O88989	Malate dehydrogenase_ cytoplasmic	103	1.23	0.73	----
P47819	Glial fibrillary acidic protein	52	1.43	0.72	----
Q6IG05	Keratin_ type II cytoskeletal 75	76	1.31	0.71	----
E9PU28	Inosine-5'-monophosphate dehydrogenase 2	79	1.54	0.70	----
P09495	Tropomyosin alpha-4 chain	50	1.27	0.70	----
P25113	Phosphoglycerate mutase 1	276	1.25	0.68	----
Q3KRE8	Tubulin beta-2B chain	94	1.05	0.68	----
P14480	Fibrinogen beta chain	941	1.05	0.67	----

D3ZVU1	SprT-like domain-containing protein Spartan	72	1.13	0.67	----
P05065	Fructose-bisphosphate aldolase A	202	1.07	0.66	----
Q6P6Q2	Keratin_ type II cytoskeletal 5	76	1.16	0.66	----
Q63610	Tropomyosin alpha-3 chain	50	1.21	0.66	----
P69897	Tubulin beta-5 chain	94	1.03	0.66	----
Q4QRB4	Tubulin beta-3 chain	94	1.04	0.65	----
P08010	Glutathione S-transferase Mu 2	217	1.14	0.64	----
P55063	Heat shock 70 kDa protein 1-like	597	1.03	0.64	----
P85108	Tubulin beta-2A chain	94	1.04	0.64	----
Q61G12	Keratin_ type II cytoskeletal 7	193	1.09	0.63	----
Q4FZU2	Keratin_ type II cytoskeletal 6A	76	1.17	0.61	----
Q62812	Myosin-9	68	1.03	0.60	----
P11980	Pyruvate kinase PKM	40	1.12	0.59	----
P62632	Elongation factor 1-alpha 2	51	1.28	0.58	----
P31232	Transgelin	9127	1.02	0.58	----
P34058	Heat shock protein HSP 90-beta	106	1.17	0.56	----
Q6P9T8	Tubulin beta-4B chain	467	1.01	0.56	----
P56574	Isocitrate dehydrogenase [NADP]_ mitochondrial	74	1.20	0.55	----
P48037	Annexin A6	120	0.99	0.52	----
P15999	ATP synthase subunit alpha_ mitochondrial	175	1.04	0.52	----
Q10758	Keratin_ type II cytoskeletal 8	193	1.04	0.52	----
P85973	Purine nucleoside phosphorylase	155	0.98	0.50	----
P14659	Heat shock-related 70 kDa protein 2	691	0.99	0.49	----
P20059	Hemopexin	409	0.99	0.46	----
P62630	Elongation factor 1-alpha 1	298	0.98	0.45	----
P70623	Fatty acid-binding protein_ adipocyte	436	0.94	0.40	----
P16409	Myosin light chain 3	787	0.95	0.40	----
P45592	Cofilin-1	297	0.96	0.38	----
P04636	Malate dehydrogenase_ mitochondrial	346	0.90	0.38	----
P04906	Glutathione S-transferase P	114	0.81	0.35	----
P07632	Superoxide dismutase [Cu-Zn]	125	0.78	0.34	----
P63018	Heat shock cognate 71 kDa protein	852	0.96	0.33	----
P62982	Ubiquitin-40S ribosomal protein S27a	274	0.82	0.31	----
P06399	Fibrinogen alpha chain	112	0.90	0.30	----
Q63429	Polyubiquitin-C	274	0.84	0.30	----
Q9JK11	Reticulon-4	39	0.27	0.30	----
Q08163	Adenylyl cyclase-associated protein 1	165	0.90	0.28	----
Q9ER34	Aconitate hydratase_ mitochondrial	83	0.86	0.27	----
P24090	Alpha-2-HS-glycoprotein	275	0.77	0.27	----
Q9WVH8	Fibulin-5	52	0.97	0.27	----
P0CG51	Polyubiquitin-B	274	0.84	0.25	----
Q07936	Annexin A2	474	0.88	0.24	----
P62986	Ubiquitin-60S ribosomal protein L40 2	274	0.83	0.24	----
P02680	Fibrinogen gamma chain	682	0.90	0.23	----
P0DMW1	Heat shock 70 kDa protein 1B	845	0.92	0.23	----
P02600	Myosin light chain 1/3_ skeletal muscle isoform	809	0.88	0.23	----
P31000	Vimentin	1733	0.96	0.21	----

P15650	Long-chain specific acyl-CoA dehydrogenase_ mitochondrial	93	0.84	0.18	----
P13437	3-ketoacyl-CoA thiolase_ mitochondrial	85	0.58	0.15	----
Q5RKI0	WD repeat-containing protein 1	192	0.89	0.15	----
Q66HD0	Endoplasmic	51	0.50	0.14	----
P12346	Serotransferrin	1002	0.90	0.13	----
P62963	Profilin-1	3064	0.90	0.11	----
P0DMW0	Heat shock 70 kDa protein 1A	849	0.86	0.10	----
Q9QXQ0	Alpha-actinin-4	431	0.88	0.08	----
Q4V8H8	EH domain-containing protein 2	225	0.61	0.06	----
P10719	ATP synthase subunit beta_ mitochondrial	87	0.84	0.05	----
P47875	Cysteine and glycine-rich protein 1	1148	0.84	0.04	↓
Q7M0E3	Dextrin	1706	0.81	0.04	↓
P02454	Collagen alpha-1(I) chain	47	0.63	0.03	↓
P06866	Haptoglobin	335	0.76	0.03	↓
P50399	Rab GDP dissociation inhibitor beta	52	0.23	0.01	↓
P68136	Actin_ alpha skeletal muscle	5242	0.84	< 0.01	↓
P62738	Actin_ aortic smooth muscle	5534	0.87	< 0.01	↓
P60711	Actin_ cytoplasmic 1	4354	0.77	< 0.01	↓
P63259	Actin_ cytoplasmic 2	4358	0.77	< 0.01	↓
Q9Z1P2	Alpha-actinin-1	719	0.78	< 0.01	↓
P36201	Cysteine-rich protein 2	176	0.55	< 0.01	↓
P04797	Glyceraldehyde-3-phosphate dehydrogenase	1896	0.65	< 0.01	↓
P42930	Heat shock protein beta-1	848	0.76	< 0.01	↓
P01946	Hemoglobin subunit alpha-1/2	14931	0.43	< 0.01	↓
P02091	Hemoglobin subunit beta-1	10419	0.32	< 0.01	↓
P11517	Hemoglobin subunit beta-2	3388	0.32	< 0.01	↓
P20760	Ig gamma-2A chain C region	643	0.68	< 0.01	↓
P51886	Lumican	1267	0.45	< 0.01	↓
Q64119	Myosin light polypeptide 6	13395	0.79	< 0.01	↓
Q64122	Myosin regulatory light polypeptide 9	4053	0.74	< 0.01	↓
P10111	Peptidyl-prolyl cis-trans isomerase A	1750	0.72	< 0.01	↓
P02770	Serum albumin	7160	0.74	< 0.01	↓
P26772	10 kDa heat shock protein_ mitochondrial	124			SHR _T
B0BN56	28S ribosomal protein S31_ mitochondrial	262			SHR _T
Q7TP48	Adipocyte plasma membrane-associated protein	74			SHR _T
P17475	Alpha-1-antiproteinase	87			SHR _T
Q78E60	Aryl hydrocarbon receptor nuclear translocator 2	81			SHR _T
Q701R3	Beta-galactoside alpha-2_6-sialyltransferase 2	84			SHR _T
Q08290	Calponin-1	62			SHR _T
P11442	Clathrin heavy chain 1	27			SHR _T
P56745	Claudin-1	133			SHR _T
Q62952	Dihydropyrimidinase-related protein 3	154			SHR _T
Q9Z1Z3	Epsin-2	43			SHR _T
Q9ERW3	Fibroblast growth factor 13	84			SHR _T

P50609	Fibromodulin	241	SHR _T
Q9WUH4	Four and a half LIM domains protein 1	573	SHR _T
P10860	Glutamate dehydrogenase 1_mitochondrial	113	SHR _T
P97879	Glutamate receptor-interacting protein 1	85	SHR _T
Q0VGK3	Glycerate kinase	118	SHR _T
Q510D1	Glyoxalase domain-containing protein 4	57	SHR _T
Q63406	Guanine nucleotide exchange factor DBS	29	SHR _T
P01835	Ig kappa chain C region_ B allele	209	SHR _T
D4AD37	Inositol monophosphatase 3	95	SHR _T
Q566E5	KDEL motif-containing protein 2	131	SHR _T
O35806	Latent-transforming growth factor beta-binding protein 2	66	SHR _T
Q5XI07	Lipoma-preferred partner homolog	119	SHR _T
P42123	L-lactate dehydrogenase B chain	137	SHR _T
Q5BK54	Lymphocyte activation gene 3 protein	78	SHR _T
P08494	Matrix Gla protein	185	SHR _T
D3ZSK5	N-lysine methyltransferase SETD6	313	SHR _T
Q05982	Nucleoside diphosphate kinase A	283	SHR _T
P19804	Nucleoside diphosphate kinase B	256	SHR _T
Q66HS7	PDZ and LIM domain protein 3	56	SHR _T
O08561	Phosphatidylinositol 4-kinase beta	26	SHR _T
O88422	Polypeptide N-acetylgalactosaminyltransferase 5	61	SHR _T
Q9ERS0	Potassium channel subfamily K member 13	71	SHR _T
Q9QZQ5	Protein NOV homolog	253	SHR _T
P83900	Rap guanine nucleotide exchange factor 5	132	SHR _T
I6L9G5	Reticulocalbin-3	69	SHR _T
D3ZA76	Serine protease HTRA3	197	SHR _T
P57760	Serine/threonine-protein kinase 16	155	SHR _T
O70142	SHC-transforming protein 2	86	SHR _T
Q9QWN8	Spectrin beta chain_ non-erythrocytic 2	36	SHR _T
P17246	Transforming growth factor beta-1 proprotein	64	SHR _T
P46462	Transitional endoplasmic reticulum ATPase	67	SHR _T
O08700	Vacuolar protein sorting-associated protein 45	128	SHR _T
P35213	14-3-3 protein beta/alpha	164	SHR _C
P62260	14-3-3 protein epsilon	148	SHR _C
P68511	14-3-3 protein eta	63	SHR _C
P61983	14-3-3 protein gamma	53	SHR _C
P68255	14-3-3 protein theta	164	SHR _C
P11884	Aldehyde dehydrogenase_mitochondrial	90	SHR _C
P80299	Bifunctional epoxide hydrolase 2	47	SHR _C
P85125	Caveolae-associated protein 1	150	SHR _C

Q4V8E4	Cilia- and flagella-associated protein 36	83	SHR _c
Q68FY0	Cytochrome b-c1 complex subunit 1_mitochondrial	160	SHR _c
Q01129	Decorin	150	SHR _c
O55096	Dipeptidyl peptidase 3	45	SHR _c
Q91XQ4	DNA-directed RNA polymerase II subunit GRINL1A	69	SHR _c
Q62862	Dual specificity mitogen-activated protein kinase kinase 5	67	SHR _c
Q5EZ72	Ectonucleotide pyrophosphatase/phosphodiesterase family member 7	42	SHR _c
Q68FU3	Electron transfer flavoprotein subunit beta	536	SHR _c
Q66H04	F-box only protein 43	68	SHR _c
P09117	Fructose-bisphosphate aldolase C	79	SHR _c
P13255	Glycine N-methyltransferase	44	SHR _c
Q5XHZ0	Heat shock protein 75 kDa_mitochondrial	47	SHR _c
Q00715	Histone H2B type 1	122	SHR _c
A6YP92	Homeobox protein ARX	33	SHR _c
P20759	Ig gamma-1 chain C region	31	SHR _c
Q6IE24	Inactive ubiquitin carboxyl-terminal hydrolase 54	36	SHR _c
Q99J82	Integrin-linked protein kinase	75	SHR _c
P18588	Interferon-induced GTP-binding protein Mx1	61	SHR _c
P15800	Laminin subunit beta-2	47	SHR _c
Q5U2U7	mRNA cap guanine-N7 methyltransferase	99	SHR _c
A7E3N2	Neutrophil cytosol factor 2	52	SHR _c
P16617	Phosphoglycerate kinase 1	73	SHR _c
P11506	Plasma membrane calcium-transporting ATPase 2	71	SHR _c
O88767	Protein/nucleic acid deglycase DJ-1	229	SHR _c
P50398	Rab GDP dissociation inhibitor alpha	112	SHR _c
P42346	Serine/threonine-protein kinase mTOR	52	SHR _c
P01048	T-kininogen 1	55	SHR _c
P50137	Transketolase	50	SHR _c

^a identification of proteins in the Uniprot database (<http://www.uniprot.org/>).

^b Significant difference in expression proteins up regulation, down regulation and intermediates.

^c p value (p<0.05) .

^d Up regulated (↑), Intermediate (----, present in both comparison groups), down regulated (↓) and unique each comparison group (SHR_T and SHR_c).

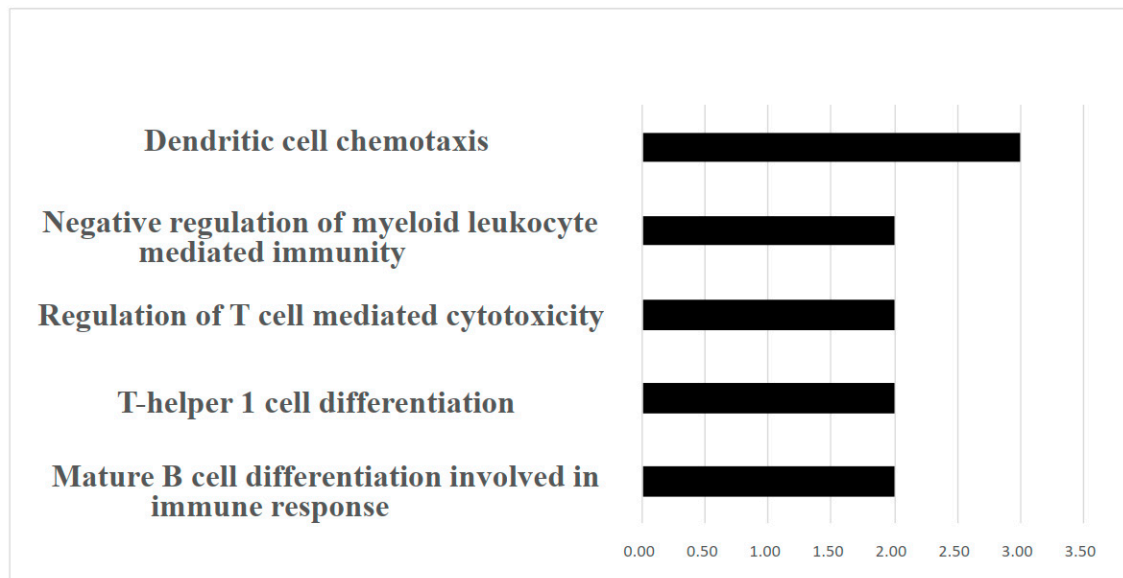


Figure S1: Protein analysis in ClueGO plugins and the number of genes involved within the sistem immune category between SHR_P vs. SHR_C groups.

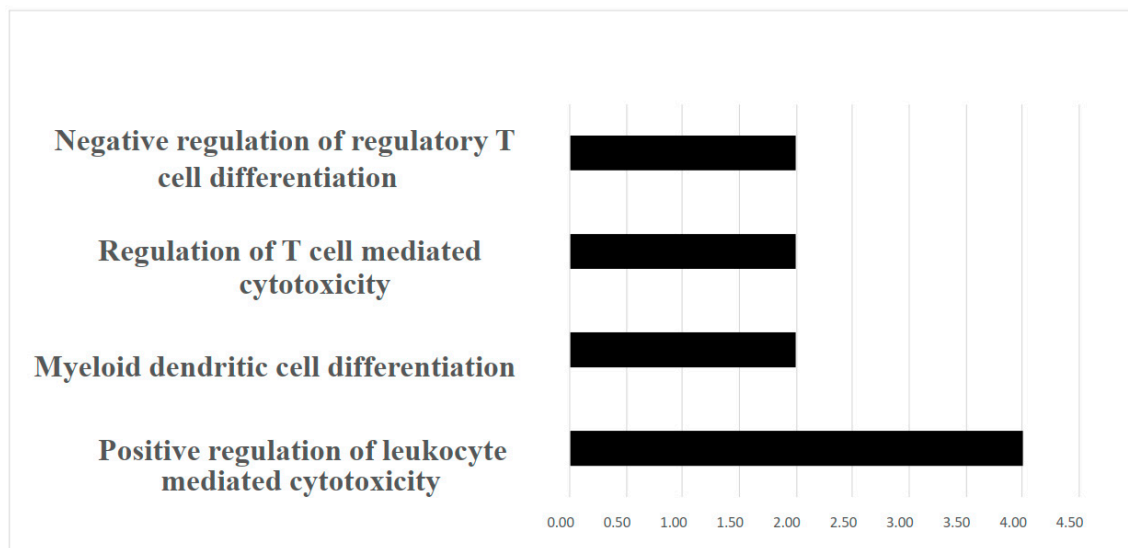


Figure S2 : Protein analysis in ClueGO plug-ins and the number of genes involved within the sistem immune category between SHR_T vs. SHR_C groups