Table S1 *GeXP analysis*

Function	Gene	H	I	N	H vs. I	H vs. N	I vs. N
Cytoskeleton/skeleton rearrangement	**α-tubulin**	0.199 ± 0.058	0.013 ± 0.008	0.012 ± 0.005	**0.014**	**0.015**	0.435
	β-tubulin	0.536 ± 0.359	0.213 ± 0.015	0.177 ± 0.133	0.130	0.112	0.383
	Actin	3.475 ± 1.458	1.904 ± 0.053	3.502 ± 2.066	0.101	0.494	0.236
	Actin-related protein 2/3	0.968 ± 0.017	0.898 ± 0.035	0.663 ± 0.166	0.088	0.116	0.142
	Gelsolin	0.950 ± 0.101	0.546 ± 0.033	0.923 ± 1.021	**0.006**	0.488	0.347
	Profilin	0.818 ± 0.048	0.824 ± 0.067	0.907 ± 0.694	0.465	0.443	0.446
	Prolidase	0.146 ± 0.150	0.013 ± 0.003	0.055 ± 0.042	0.133	0.206	0.197
	B-thymosin	0.339 ± 0.019	0.175 ± 0.022	0.277 ± 0.029	**0.006**	0.075	**0.033**
	Villin	0.540 ± 0.100	0.676 ± 0.102	0.783 ± 0.562	0.133	0.325	0.416
	Radial Spoke Protein	0.864 ± 0.130	0.229 ± 0.106	0.253 ± 0.111	**0.007**	**0.008**	0.424
Signal transduction	**Calmodulin**	0.469 ± 0.065	0.126 ± 0.039	0.159 ± 0.092	**0.003**	**0.036**	0.353
	YWHAQ	0.989 ± 0.081	0.884 ± 0.080	0.805 ± 0.473	0.137	0.339	0.426
Chaperone	**Cyclophilin**	2.097 ± 0.090	1.328 ± 0.004	1.645 ± 0.228	**0.002**	0.096	0.150
	Hsp70	0.098 ± 0.029	0.361 ± 0.077	0.588 ± 0.534	0.053	0.209	0.328
	Hsp90	2.139 ± 1.038	2.135 ± 0.184	2.041 ± 1.163	0.498	0.466	0.464
Protein synthesis/degradation	**Apoptosis-linked gene 2l**	0.019 ± 0.008	0.139 ± 0.025	0.140 ± 0.042	**0.038**	0.074	0.496
	Cyclophilin NIMA-interacting 4	0.040 ± 0.005	0.020 ± 0.004	0.040 ± 0.026	**0.008**	0.493	0.240

	Elongation factor - Tu	0.249 ± 0.027	0.118 ± 0.025	0.025 ± 0.013	**0.010**	**0.001**	**0.037**
	Polyubiquitin	0.691 ± 0.071	0.547 ± 0.039	0.949 ± 0.802	**0.031**	0.364	0.304
	Ribosomal Protein S9	0.121 ± 0.019	0.043 ± 0.002	0.060 ± 0.005	**0.009**	**0.012**	**0.046**
	Ubiquitin Conjugating Enzyme	0.235 ± 0.042	0.086 ± 0.004	0.392 ± 0.475	**0.012**	0.361	0.265
Oxidative stress	**Ferritin**	1.594 ± 0.323	1.102 ± 0.009	1.065 ± 0.160	0.059	**0.048**	0.398
Detoxification	**Glutathione-S-Transferase**	0.580 ± 0.022	0.041 ± 0.012	0.029 ± 0.022	**< 0.001**	**< 0.001**	0.297

* Average expression with standard deviations are shown. *P*-values show pair-wise *t*-test between the healthy (H), intermediate (I), and necrotic (N) groups. *P*-values < 0.05 are in bold.