Chemical genomic profiling unveils the *in vitro* and *in vivo* antiplasmodial mechanism of açaí (*Euterpe oleracea* Mart.) polyphenols

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Table S1 – Sensitive mutant yeast strains depleted under total phenolics (1) treatment.

			TP		
ORF	**Gene**	**Protein ID**	**log2FoldChange**	**pvalue**	**Process**
YBL069W	AST1	P35183	-3,00989	0,009216	protein transport
YAR023C	unknown	D6VPM8	-2,25249	0,0006	unknown
YLL003W	SFI1	Q12369	-2,06444	0,006149	cell cycle progression
YAL017W	PSK1	P31374	-2,04111	0,005236	protein phosphorylation
YHL015W	RPS20	P38701	-1,84055	0,008569	RNA modification and translation
YML010W-A	unknown	Q6B0Y1	-1,83123	0,001358	unknown
YMR018W	PEX9	Q04364	-1,81627	0,000698	protein import for peroxisome
YCR017C	CWH43	P25618	-1,73376	0,000595	cell wall assembly/GPI biosynthesis
YCL058C	FYV5	P25585	-1,57698	0,002022	signaling
YMR204C	INP1	Q03694	-1,57039	0,003732	peroxisome inheritance
YMR230W	RPS10B	P46784	-1,53678	0,001565	RNA export and translation
YGL157W	ARI1	P53111	-1,50278	7,94E-05	oxireduction
YHL023C	NPR3	P38742	-1,4926	0,00037	signaling
YFL049W	SWP82	P43554	-1,46713	0,009164	transcription regulation
YMR271C	URA10	P30402	-1,46672	0,002199	ribonucleotides biosynthesis
YER044C	ERG28	P40030	-1,46511	0,001549	lipid metabolism
YER071C	TDA2	P40045	-1,38	0,001858	cytoskeleton organization
YER036C*	ARB1	P40024	-1,36015	0,009498	ribosome biogenesis and transport
YLR428C	unknown	O13564	-1,35653	0,000926	unknown
YMR207C	HFA1	P32874	-1,3407	0,002794	lipid metabolism
YCR053W	THR4	P16120	-1,31124	0,003309	AA biosynthesis
YNR013C	PHO91	P27514	-1,3081	0,004094	ion transport
YBL035C	POL12	P38121	-1,30419	0,004748	DNA replication
YOL150C	unknown	Q08293	-1,30041	0,001477	unknown
YPR119W	CLB2	P24869	-1,30011	0,002362	protein phosphorylation/cell cycle
YIL053W	GPP1	P41277	-1,23148	0,005322	response to osmotic stress
YCR024C-A	PMP1	P32903	-1,21954	0,004522	ion transport
YKR050W	TRK2	P28584	-1,20432	0,000486	ion transport
YFL031W	HAC1	P41546	-1,19712	0,001506	unfolded protein response/transcription regulation
YPR167C	MET16	P18408	-1,13406	0,005196	oxireduction
YKR018C	unknown	P36114	-1,13193	0,007639	unknown
YOR132W	VPS17	P32913	-1,09145	0,006946	vesicle transport
YER097W	unknown	P40062	-1,03611	0,008503	unknown
YPR075C	OPY2	Q06810	-1,03551	0,001841	signaling
YPL006W	NCR1	Q12200	-1,03369	0,004371	lipid metabolism
YCR032W	BPH1	P25356	-1,02783	0,004942	cell wall organization
YCL035C	GRX1	P25373	-1,02432	0,006681	response to oxidative stress
YGL252C	RTG2	P32608	-1,01761	0,003385	transcription regulation
YCR052W	RSC6	P25632	-0,99924	0,00826	transcription regulation
YHR016C	YSC84	P32793	-0,99431	0,006581	cytoskeleton organization
YFL004W	VTC2	P43585	-0,98317	0,001928	vacuolar transport

YBR103W	SIF2	P38262	-0,97773	0,009337	signaling
YNL022C	RCM1	P53972	-0,97595	0,007339	RNA modification
YOL141W	PPM2	Q08282	-0,96816	0,007268	RNA modification
YJL171C	unknown	P46992	-0,96689	0,007395	unknown
YER092W	IES5	P40060	-0,96485	0,004248	telomere maintenance
YKR041W	unknown	P36134	-0,92104	0,002953	unknown
YFR014C	CMK1	P27466	-0,87737	0,005333	signaling
YPR189W	SKI3	P17883	-0,85451	0,009877	RNA degradation
YIL023C	YKE4	P40544	-0,85284	0,00611	ion transport
YLL009C	COX17	Q12287	1,29817	0,000727	aerobic respiration

ORFs marked with * represent essential genes

Table S2 – Sensitive mutant yeast strains depleted under non-anthocyanin phenolics (2) treatment.

			NAP		
ORF	**Gene**	**Protein ID**	**log2FoldChange**	**pvalue**	**Gene ontology**
YMR044W	IOC4	Q04213	-2,50373	1,75E-05	chromatin organization
YCR059C	YIH1	P25637	-1,29308	1,86E-05	protein phosphorylation
YAL053W	FLC2	P39719	-1,55199	6,25E-05	lipid metabolism
YCR065W	HCM1	P25364	-1,00563	0,0001	transcription regulation
YCR051W	unknown	P25631	-1,05881	0,000125	unknown
YCR049C	unknown	P25629	-1,22856	0,000137	unknown
YLR025W	SNF7	P39929	1,158644	0,00015	protein degradation
YAR028W	unknown	P39548	-1,78479	0,000208	unknown
YOR374W	ALD4	P46367	-1,09686	0,000238	monocarboxylic acid metabolism
YMR207C	HFA1	P32874	-1,42527	0,000277	lipid metabolism
YFR014C	CMK1	P27466	-1,07409	0,000278	signaling
YCR082W	AHC2	P25649	-1,37753	0,000306	histone acetylation
YCR002C	CDC10	P25342	-1,69566	0,000362	cell cycle
YDR068W	unknown	P54858	1,287375	0,000399	unknown
YFL027C	GYP8	P43570	-1,31164	0,000581	vesicle transport
YMR218C*	TRS130	Q03660	-1,50952	0,000601	endosomal transport
YMR084W	unknown	A2P2R3	-1,0953	0,000853	unknown
YBR219C	unknown	P38317	-1,25534	0,001255	unknown
YHR009C	TDA3	P38758	-1,38673	0,00133	endosomal transport
YNL140C	unknown	P53910	-1,16283	0,001589	unknown
YER007C-A	VID28	P89886	-1,43867	0,001647	ribosome biogenesis
YEL026W	SNU13	P39990	-1,1394	0,001671	RNA modification
YFL031W	HAC1	P41546	-1,03349	0,001869	unfolded protein response/transcription regulation
YKL157W	APE2	P32454	-0,82714	0,001935	peptide catabolism
YMR144W	FDO1	P40214	-1,61338	0,00198	yeast mating
YJL007C	unknown	P47080	-1,00179	0,002297	unknown
YIL154C	IMP2'	P32351	-0,83364	0,002327	transcription regulation
YBR057C	MUM2	P38236	-1,03262	0,0024	cell cycle/DNA replication
YAR003W	SWD1	P39706	-1,52401	0,002615	chromatin organization
YJR064W*	CCT5	P40413	-1,27372	0,0028	protein folding
YIL142W*	CCT2	P39076	-2,02489	0,002921	protein folding
YDR219C	MFB1	Q04922	-0,96579	0,003298	protein degradation
YKL164C	PIR1	Q03178	-1,00759	0,003518	cell wall organization/protein transport
YIL009C-A	EST3	Q03096	-1,3971	0,003632	telomere maintenance
YKR050W	TRK2	P28584	-0,81496	0,003718	ion transport
YIR018W	YAP5	P40574	-0,90611	0,004499	transcription regulation
YER121W	unknown	P40076	-0,99279	0,004655	unknown
YKR018C	unknown	P36114	-1,18662	0,004849	unknown
YDR390C*	UBA2	P52488	-1,19621	0,004944	protein sumoylation
YIL141W	unknown	P40461	-1,01421	0,005015	unknown
YJL172W	CPS1	P27614	-0,83284	0,005113	protein degradation
YMR026C	PEX12	Q04370	-1,88709	0,005124	protein import to peroxisome

YGL218W	unknown	P53084	-0,79706	0,005292	unknown
YBR137W	unknown	P38276	-0,81766	0,005298	unknown
YNR057C	BIO4	P53630	-1,95844	0,005492	biotin biosynthesis
YIL017C	VID28	P40547	-0,91135	0,005495	transcription regulation/protein degradation
YJR116W	unknown	P47153	-1,37086	0,005773	unknown
YFR030W	MET10	P39692	-0,71096	0,006122	sulfate assimilation
YJL140W	RPB4	P20433	-1,14835	0,006258	transcription regulation
YCL035C	GRX1	P25373	-0,97205	0,006305	response to oxidative stress
YAL019W	FUN30	P31380	-1,21014	0,006494	chromatin organization
YJL182C	unknown	P46986	-0,84505	0,006506	unknown
YAR050W	FLO1	P32768	-1,06777	0,006524	response to oxidative stress
YCL004W*	PGS1	P25578	-1,06198	0,007057	lipid metabolism
YCR084C	TUP1	P16649	-0,80358	0,007425	transcription regulation
YFR035C	unknown	P43608	-0,91414	0,007469	unknown
YBR164C	ARL1	P38116	-1,14691	0,007623	vesicle transport
YER087W	AIM10	P39965	-1,0392	0,007903	unknown
YAL016W	TPD3	P31383	-1,2793	0,007904	cell cycle
YNL239W	LAP3	Q01532	-0,77652	0,008292	transcription regulation
YML053C	unknown	Q04978	-1,15255	0,008355	unknown
YCR063W	BUD31	P25337	-0,9003	0,008484	cell cycle progression
YPR122W	AXL1	P40851	-1,15161	0,008655	mating/cell cycle
YOR357C	SNX3	Q08826	-0,9141	0,008685	endosomal transport
YHR033W	unknown	P38690	-1,03916	0,009233	unknown
YBR027C	unknown	P38220	-0,94287	0,009373	unknown
YER174C	GRX4	P32642	-0,75323	0,009499	response to oxidative stress/chromatin organization

ORFs marked with * represent essential genes