Supplementary table S1 - General and case-study specific modifications applied to the Yeast 6.06 model

General modifications			
Modification	Details	Source/Justification	
Added reaction r_4039	acetate_m + succinyl_CoA_m<>succinate_m + acetyl_CoA_m	imported from Yeast 7.11 (more recent consensus model)	
Modified r_0718	NADP_m + S_malate_m>NADPH_m + pyruvate_m + carbon_dioxide_m	updated according to Yeast 7.11 (more recent consensus model)	
Modified r_0773	NADH_m + H_m + ubiquinone_6_m> NAD_m + ubiquinol_6_m	updated according to Yeast 7.11 (more recent consensus model)	
Modified r_0226	4 H_c + 1 ADP_m + 1 phosphate_m> 3 H_m + 1 H2O_m + 1 ATP_m	updated according to Yeast 7.11 (more recent consensus model)	
Modified r_2129	H_m < H_c	updated according to Yeast 7.11 (more recent consensus model)	
Modified r_1110	ADP_c + ATP_m <> ATP_c + ADP_m	updated according to Yeast 7.11 (more recent consensus model)	
Modified r_0470	NAD_c + H2O_c + L_glutamate_c> H_c + NADH_c + ammonium_c + 2_oxoglutarate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0303	citrate_c> H2O + cis_aconitate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0338	ubiquinone_6_m + S_dihydroorotate_c> ubiquinol_6_m + orotate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0339	oxygen_c + S_dihydroorotate_c> hydrogen_peroxide_c + orotate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_2127	NAD_c + S_dihydroorotate_c> NADH_c + orotate_c	updated according to Yeast 7.11 (more recent consensus model)	
Modified r_1254	H_e + pyruvate_e <> H_c + pyruvate_c	updated according to Yeast 7.11 (more recent consensus model)	
Gene rule update r_0530	(YPL252C AND YDR376W) or (YPL252C AND YDR376W AND YER141W)	updated according to Yeast 7.11 (more recent consensus model)	
Updated biomass reaction r_4041	Add 1.0E-6 * chitin_c and 1.0E-6* heme_a_m to reactants	updated according to Yeast 7.11 (more recent consensus model)	
gene rule update r_0076	(YER037W or YGL224C)	updated according to Yeast 7.11 (more recent consensus model)	
gene rule update r_0078	(YER037W or YGL224C)	updated according to Yeast 7.11 (more recent consensus model)	
gene rule update r_1619	YER037W	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0333	phosphate_c + 2_deoxyuridine_c <> uracil_c + 2_deoxy_D_ribofuranose_1_phosphate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0944	phosphate_c + adenosine_c<> alpha_D_ribose_1_phosphate_c + adenine_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0945	phosphate_m + adenosine_m <> adenine_m + alpha_D_ribose_1_phosphate_m	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0946	phosphate_c + 2_deoxyadenosine_c <> 2_deoxy_D_ribofuranose_1_phosphate_c + adenine_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0947	phosphate_c + 2_deoxyguanosine_c <> guanine_c + 2_deoxy_D_ribofuranose_1_phosphate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0948	phosphate_c + 2_deoxyinosine_c <> hypoxanthine_c + 2_deoxy_D_ribofuranose_1_phosphate_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_0952	phosphate_c + xanthosine_c <> alpha_D_ribose_1_phosphate_c + 9H_xanthine_c	updated according to Yeast 7.11 (more recent consensus model)	
Removed r_1044	phosphate_c + thymidine_c <> 2_deoxy_D_ribofuranose_1_phosphate_c + thymine_c	updated according to Yeast 7.11 (more recent consensus model)	
Added reaction r_4045	H2O_c + uridine_c> uracil_c + D_ribose_c	imported from Yeast 7.11 (more recent consensus model)	
gene rule update r_0888	(YMR105C or YKL127W)	updated according to Yeast 7.11 (more recent consensus model)	
gene rule update r_0907	( (YMR278W or YMR105C) or YKL127W)	updated according to Yeast 7.11 (more recent consensus model)	
I		As corrected in Pereira R, Nielsen J, Rocha I (2016) Improving the flux	
1		distributions simulated with genome-scale metabolic models of Saccharomyces	
Modified r_0110	H_c + coenzyme_A_c + acetate_c < H2O_c + acetyl_CoA_c	cerevisiae. Metab Eng Commun 3: 153–163. doi:10.1016/j.meteno.2016.05.002.	
I		As corrected in Pereira R, Nielsen J, Rocha I (2016) Improving the flux	
	NAD_c + zymosterol_intermediate_1c_c> H_c + NADH_c + carbon_dioxide_c +	distributions simulated with genome-scale metabolic models of Saccharomyces	
Added reaction r 0234x	zymosterol intermediate 2 c	cerevisiae. Metab Eng Commun 3: 153-163. doi:10.1016/j.meteno.2016.05.002	
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		As corrected in Pereira R, Nielsen J, Rocha I (2016) Improving the flux	
		distributions simulated with genome-scale metabolic models of Saccharomyces	
Added reaction r_0939x	prephenate_c + NAD_c> NADH_c + 3_4_hydroxyphenylpyruvate_c + carbon_dioxide_c	cerevisiae. Metab Eng Commun 3: 153–163. doi:10.1016/j.meteno.2016.05.002	
Inactivated r_1840	3_hydroxy_3_methylglutaryl_CoA_c <> 3_hydroxy_3_methylglutaryl_CoA_m	No data supporting such reaction	
		As corrected in Pereira R, Nielsen J, Rocha I (2016) Improving the flux	
1		distributions simulated with genome-scale metabolic models of Saccharomyces	
Modified r 1117	H_c+L_aspartate_c>H_m+L_aspartate_m	cerevisiae. Metab Eng Commun 3: 153–163. doi:10.1016/j.meteno.2016.05.002	
	Fig. 5 - 2-species - 2 min - s copporate in	23. 23. 23. 23. 23. 23. 23. 23. 23. 23.	

Modifications for PHB production			
Added reaction R_phaA	2 acetyl_CoA_c> coenzyme_A_c + acetoacetyl_CoA_c	Acetoacetyl-CoA thiolase from Ralstonia eutropha	
Added reaction R_phaB	H_c + NADPH_c + acetoacetyl_CoA_c> 3hbcoa_c + NADP_c	Acetoacetyl-CoA reductase from Ralstonia eutropha	
Added reaction R_phaC	3hbcoa_c> phb_c + coenzyme_A_c	PHB synthase from Ralstonia eutropha	
Added reaction R_EX_phb_e_	phb_c>	PHB drain reaction required for simulation purposes	

Modifications for 3-HP production				
Added reaction R_MCR	2* H_c + 2* NADPH_c + 1* malonyl_CoA_c> 1* coenzyme_A_c + 2* NADP_c + 1* 3hp_c	Malonyl-CoA reductase from Chloroflexus aurantiacus		
Added reaction R_EX_3hp_e_	M_3hp_c>	3-HP drain reaction required for simulation purposes		
Added reaction R gapN	glyceraldehyde 3 phosphate c+H2O c+NADP c> H c+NADPH c+3 phosphoglycerate c	Glyceraldehyde-3-phosphate dehydrogenase from Streptococcus mutans		

Modifications for santalene production			
Added reaction R_SANSYN	farnesyl_diphosphate_c> diphosphate_c + santalene_c	Santalene synthase from Clausena lansium	
Added reaction R_EX_santalene_e_	santalene_c>	santalene drain reaction required for simulation purposes	