



Figure S9 Metabolic pathways corresponding to transcripts decreased in accumulation 5hPBM in all three strains (down_all_three), in LVP (lvp_down), in CTM (ctm_down) and in Rex-D (rexd_down) are visualized by LinkinPath (Ingriswang et al., 2011). Multi-library corresponds to pathways elicited by transcripts increased in accumulation in more than one tested condition.