Table S2. The commonly altered genes in the pathways of energy metabolism and its regulation in 6-month-old $PML^{-/-}$, $HBsAg^{tg/0}$ and $PML^{-/-}HBsAg^{tg/0}$ male mice.

Oxiadative phosphorylation	Glycolysis and gluconeogenesis	Fatty acid metabolism	Tricarboxylic acid cycle
ATP synthases (Atp5a1, Atp5b, Atp5c1 Atp5f1, Atp5h and Atp5j2) **Cytochrome c oxidases** (COX2, Cox5a, Cox5b and Cox4i1) **NADH dehydrogenases (ubiquinone)** (Ndufa4, Ndufa9, Ndufb2, Ndufb4, Ndufb11, Ndufs1, Ndufs3, Ndufs7 and Ndufs8) **Ubiquinol cytochrome c reductases** (Uqcrc2, Uqcrh and Uqcrq)	**Fructose-bisphosphate aldolase A** (Aldoa) **Enolases** (Eno2 and Eno3) **Phosphoglycerate mutase 1** (Pgam1) **Cytoplasmic malate dehydrogenase** (Mdh1) **Fructose-1,6-bisphosphatase 1** (Fbp1)	**Acetyl-CoA acyltransferases** (Hadha and Hadhb) **Mitochondrial enoyl-CoA hydratase** (Echs1) **Peroxisomal acyl-coenzyme A oxidases** (Acox1 and Acox2) **Enoyl-CoA hydratase** (Ehhadh) **Very long-chain acyl-CoA synthetase** (Slc27a2)	**Citrate synthase** (Cs) **Fumarate hydratase 1** (Fh1) **Isocitrate dehydrogenase 2** (Idh2) **Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex** (Dlst) **Succinate-Coenzyme A ligase, GDP-forming beta subunit** (Suclg2)