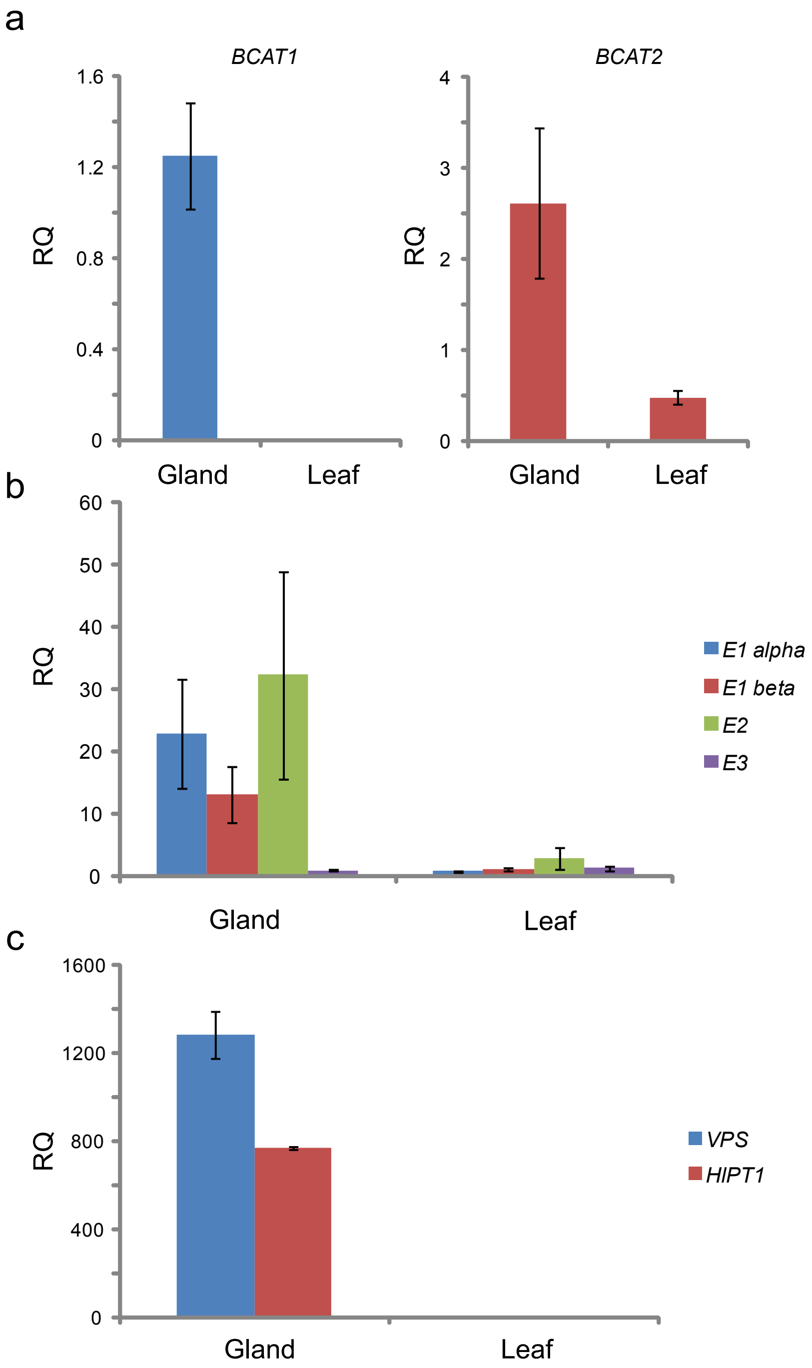

Figure S1 – Relative abundance of select metabolic transcripts in lupulin gland and leaf samples as determined by qRT-PCR. Data is presented using relative quantitation (RQ) based on $\Delta\Delta C_T$ values. Samples are normalized using β-tubulin.
a) qRT-PCR analysis of *HlBCAT1* and *HlBCAT2*. A single gland sample was used as reference.
b) qRT-PCR analysis of genes encoding enzymes of the BCKDH complex (ketoacid dehydrogenase E1α and E1β, dihydrolipoyl acyltransferase (E2), and dihydrolipoyl dehydrogenase (E3)). A single leaf sample was used as reference.
c) qRT-PCR analysis of *VPS* and *HlPT1*. A single leaf sample was used as reference. Data represents the mean and standard error, n=3. Transcript abundance between panels a, b and c is not directly comparable in this figure.