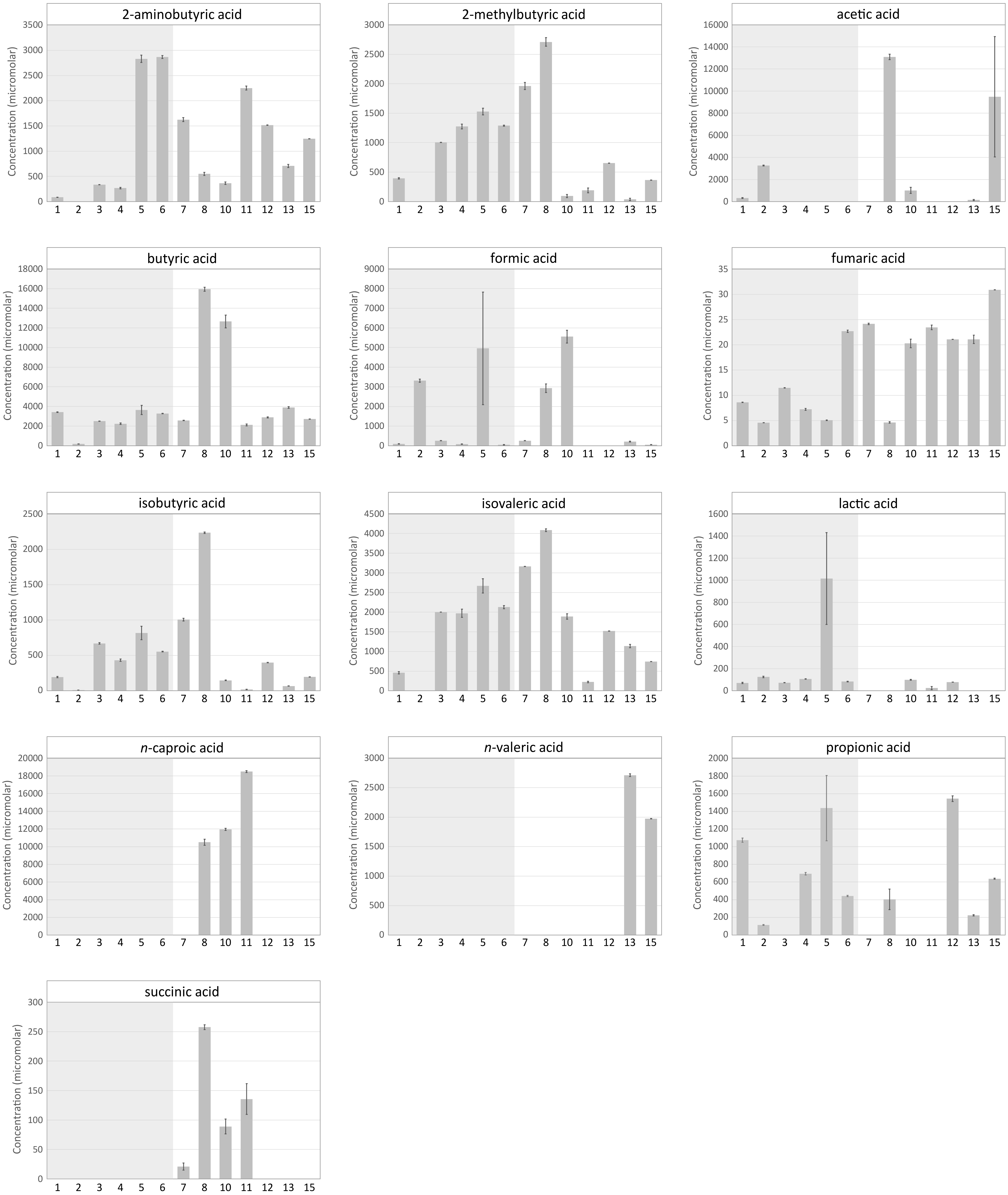
SUPPLEMENTARY FIGURE LEGENDS

Fig 1. Concentrations of short chain fatty acids produced were measured using proton NMR after growth of bacterial cells in PYG-mod-YG for 48 hours at 37°C. Results reported are mean values of triplicate measurements. Concentrations (µM) are shown on the y-axis. Strains: 1, *M. lornae* UPII 199-6^T; *M. lornae* 2, DNF00751; 3, *M. hutchinsoni* KA00182^T; 4, *M. hutchinsoni* UPII 135-E; 5, *M. vaginalis* BV3C16-1^T; 6, *M. vaginalis* HL562; 7, *M. cerevisiae* DSM 20462; 8, *M. elsdenii* DSM 20460; 10, *M. indica* DSM 25563; 11, *M. massiliensis* DSM 26228; 12, *M. micronuciformis* DSM 17226; 13, *M. paucivorans* DSM 16981; 15, *M. sueciensis* DSM 17042. Data for 9, *M. hexanoica* MH and 14, *M. stantonii* AJH120 not presented.

Fig 2. Molecular phylogenetic analysis by neighbor joining method based on 16S rRNA gene sequences showing the phylogenetic positions of *M. lornae*, *M. hutchinsoni* and *M. vaginalis* with closely related members of the family *Veillonellaceae.* The genital tract isolates clustered within the *Megasphaera* clade. Bootstrap values (based on 1000 replications) greater than or equal to 70% are shown as percentages at each node. Bar, 0.02 substitutions per nucleotide position. *Selenomonas sputigena* ATCC 35185 (NR_025115) from the family *Selenomonadaceae* was added as an outgroup.

Supplementary Fig. 1



Supplementary Fig. 2