

**Supplementary Figure 1.** Flow chart of study participants (OBU – open bay unit; SFR – single-family room; TCH – Tallinn Children’s hospital; MOB – mother’s own breast milk; SSC – skin-to-skin contact; NICU – neonatal intensive care unit).

**Supplementary Figure 2.** Species distribution of *Enterobacteriaceae* colonising neonates and their parents admitted to NICU (**panel A**) (\* $p = 0.001$ ; \*\* $p < 0.001$ ; other *Enterobacteriaceae* included *Citrobacteriaceae* (n=10) and *Pantoeaceae* (n=17), equally present in routine care group (RCG) and intervention group (IG), while *Raoultella*, *Serratia*, *Enterobacter asburiae*, and *Enterobacter aerogenes* were isolated only in RCG; and *Escherichia hermannii* (one isolate) in IG), and timing of colonization of different materials / locations with *Enterobacteriaceae* (**panel B**).

**Supplementary Figure 3.** The spread of similar genotypes (PFGE) within the same family group. Only family groups, where the same PFGE type was isolated from more than one location, are presented. Asterisks represent hospital strains.