

Similar bases in a 6 bp tag

Figure S2: Matrix of similarities between all possible primer combinations using 6 bp inline tags. For some primers, several tagging-sequences are shown, due to nucleotide degeneracy in the primer sequence. All tagging combinations are suitable because they show at least 2 bp differences when a 6 bp tag is used for demultiplexing. With each primer combination 6*6*2 = 72 samples can be uniquely tagged and additionally indexed using the P5 or P7 tail (parallel sequencing approach, see Elbrecht & Leese 2015).