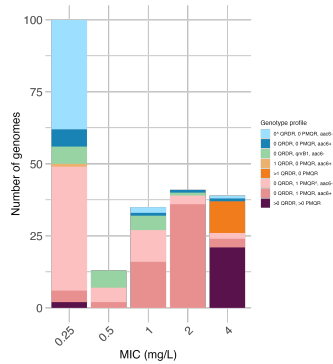
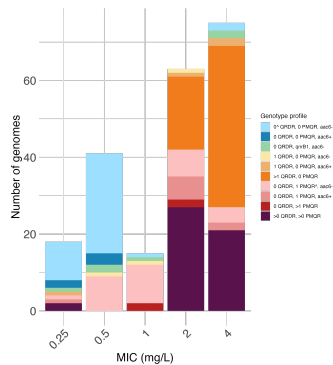


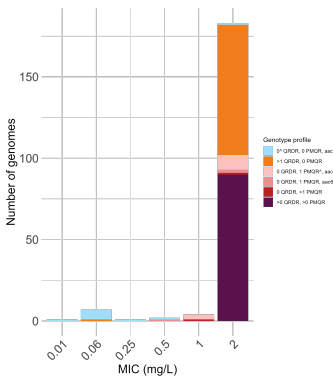
I) MBIRA (n=228) – MIC distribution vs. genotype profile



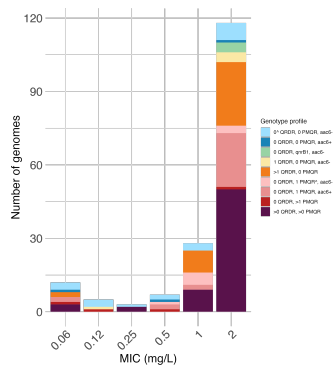
K) Controlling Superbugs study & Victorian CPE program (n=212) – MIC distribution vs. genotype profile



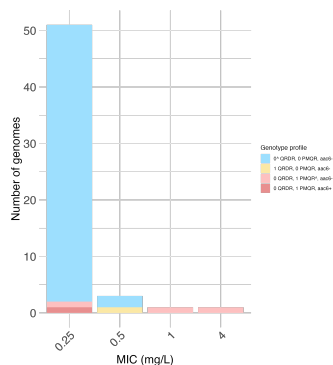
M) IRCCS Ospedale San Raffaele (n=198) – MIC distribution vs. genotype profile



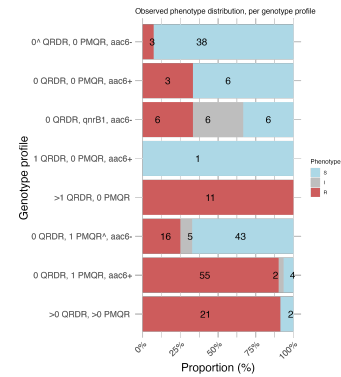
O) HRYC & CIBERINFEC (n=173) – MIC distribution vs. genotype profile



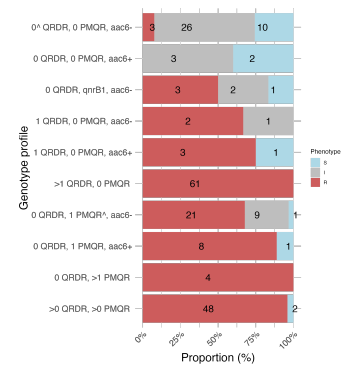
Q) SCHARKI (n=56) – MIC distribution vs. genotype profile



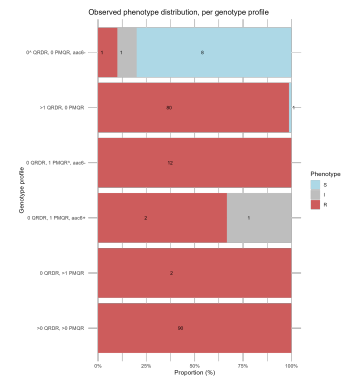
J) MBIRA (n=228) – observed phenotype vs. genotype profile



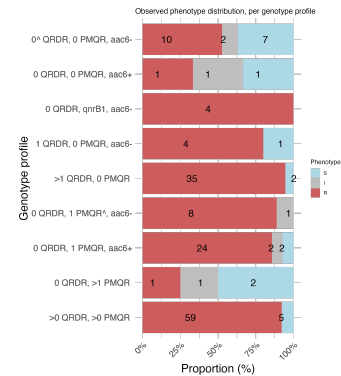
L) Controlling Superbugs study & Victorian CPE program (n=212) – observed phenotype vs. genotype profile



N) IRCCS Ospedale San Raffaele (n=198) – observed phenotype vs. genotype profile



P) HRYC & CIBERINFEC (n=173) – observed phenotype vs. genotype profile



R) SCHARKI (n=56) – observed phenotype vs. genotype profile

