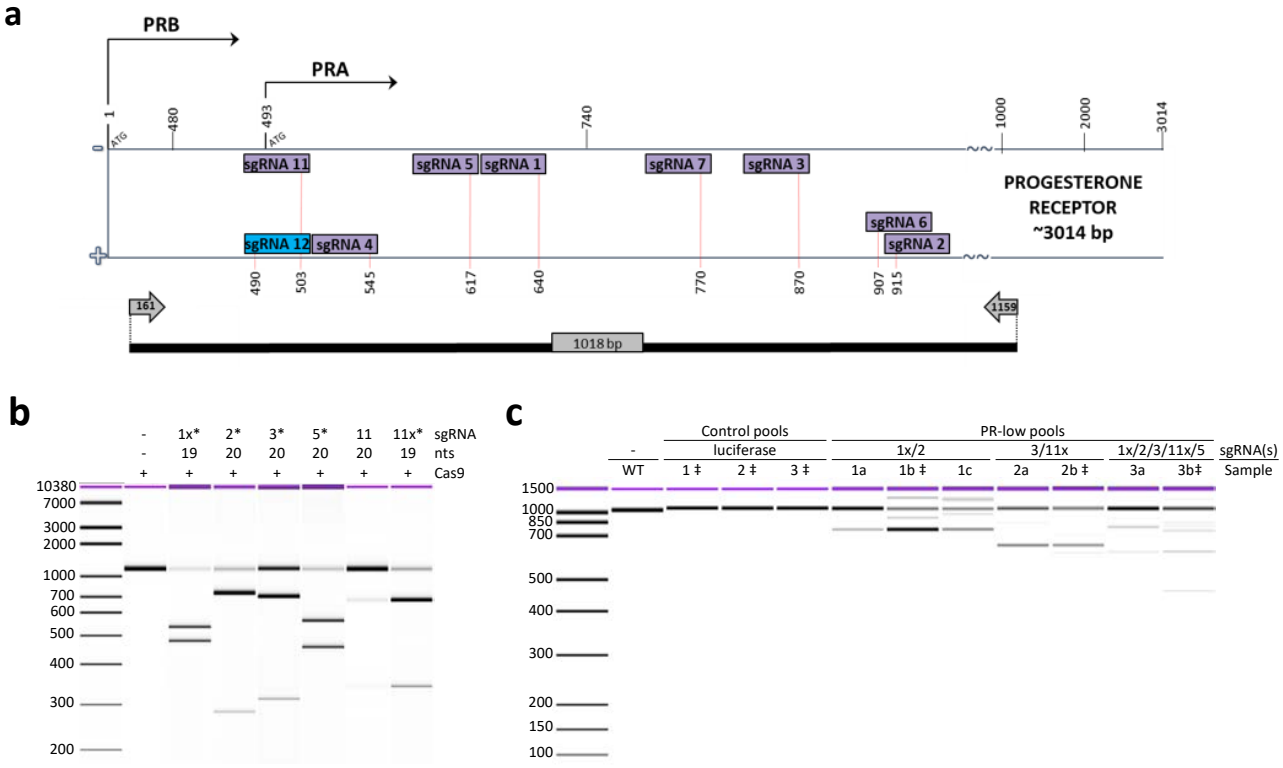

SUPPLEMENTARY FIGURE 1. <u>Design, selection and screening of sgRNAs</u>. a) Schematic representation of the *PGR* gene showing the pre-selected sgRNAs targeting exon 1 of isoform B only (blue box) or isoforms A and B (purple box). The red lines denote the Cas9 cleavage site. Grey arrows represent thethe forward primer at position 161 and the reverse primer at position 1'159 used for amplifying the *PGR* gene for *in vitro* tests and screenings . The black line below the *PGR* gene represents the PCR product of about 1'018 bp. **b,** Bioanalyzer gel image showing the *in vitro* testing of pre-selected sgRNAs (not all shown). Five sgRNAs were selected (*) based on their efficiency to cleave a synthetic target fragment of *PGR*. sgRNAs representing 19-mers (x) and 20-mers were tested. **c,** Bioanalyzer gel image showing the amplification of the *PGR* gene in control and PR-low pools. The expected size of the intact wild-type (WT) allele is 1'018 bp. PCR products smaller than 1018 bp correspond to the expected sizes when 2 sgRNAs result in the removal of the fragment between them leading to larger deletions and shorter PCR products. The size of bands was determined by the Bioanalyzer software. In PR-low pools bands at around 1'018 bp may correspond to intact WT allele and/or allele with indel mutations. Three control pools and PR-low pools were selected for RNA-seq (‡).