Figure S1

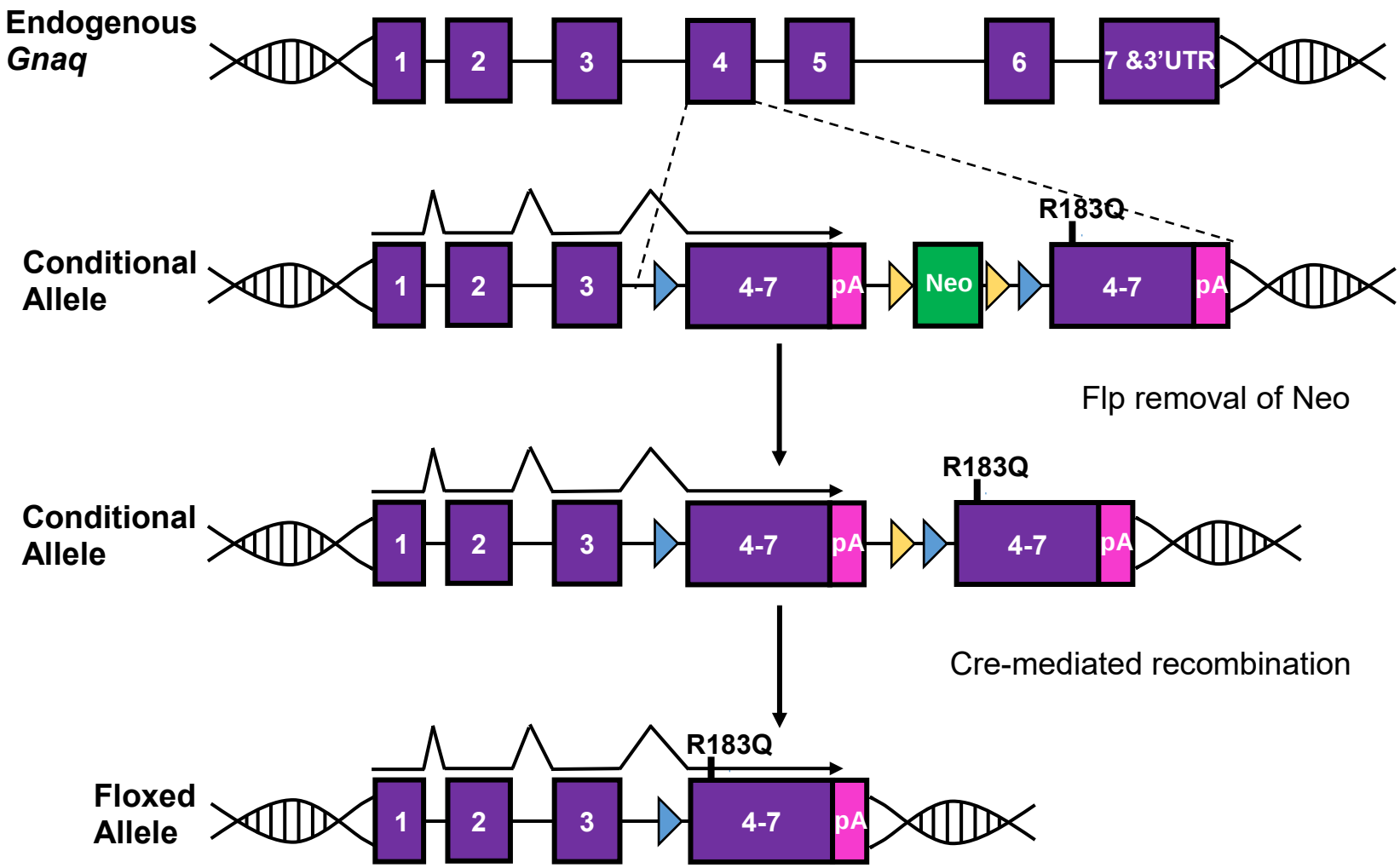
Endogenous
Gnaq
1
2
3
4
5
6
7 &3'UTR
Conditional
Allele
R183Q
4-7
pA
Neo
Flp removal of Neo
Cre-mediated recombination
Floxed
Allele

Figure S1. *Gnaq*RQ Mouse Gene Targeting Approach

Homologous recombination was used to replace the endogenous exon 4 of *Gnaq* with a construct allowing for Cre recombinase-dependent expression of p.R183Q GNAQ. The following elements were present in the targeting construct: 1) a cDNA block of mouse *Gnaq* exons 4-7 encoding the WT form of the protein, 2) a neomycin resistance cassette (green box) flanked by FRT sites (yellow triangles) for FRT-mediated recombination, 3) loxP sites (blue triangles) for Cre mediated recombination of the WT *Gnaq* cDNA block and the FRT site, and 4) a cDNA block of mouse *Gnaq* exons 4-7 encoding the p.R183Q mutant form of the protein. The 3'UTR and poly(A) site from Bovine growth hormone 1 (BGH1, pink block denoted pA) was ligated to the 3' end of exon 7 to provide a way to distinguish transcripts from the conditional allele from the endogenous *Gnaq*.

Figure S2

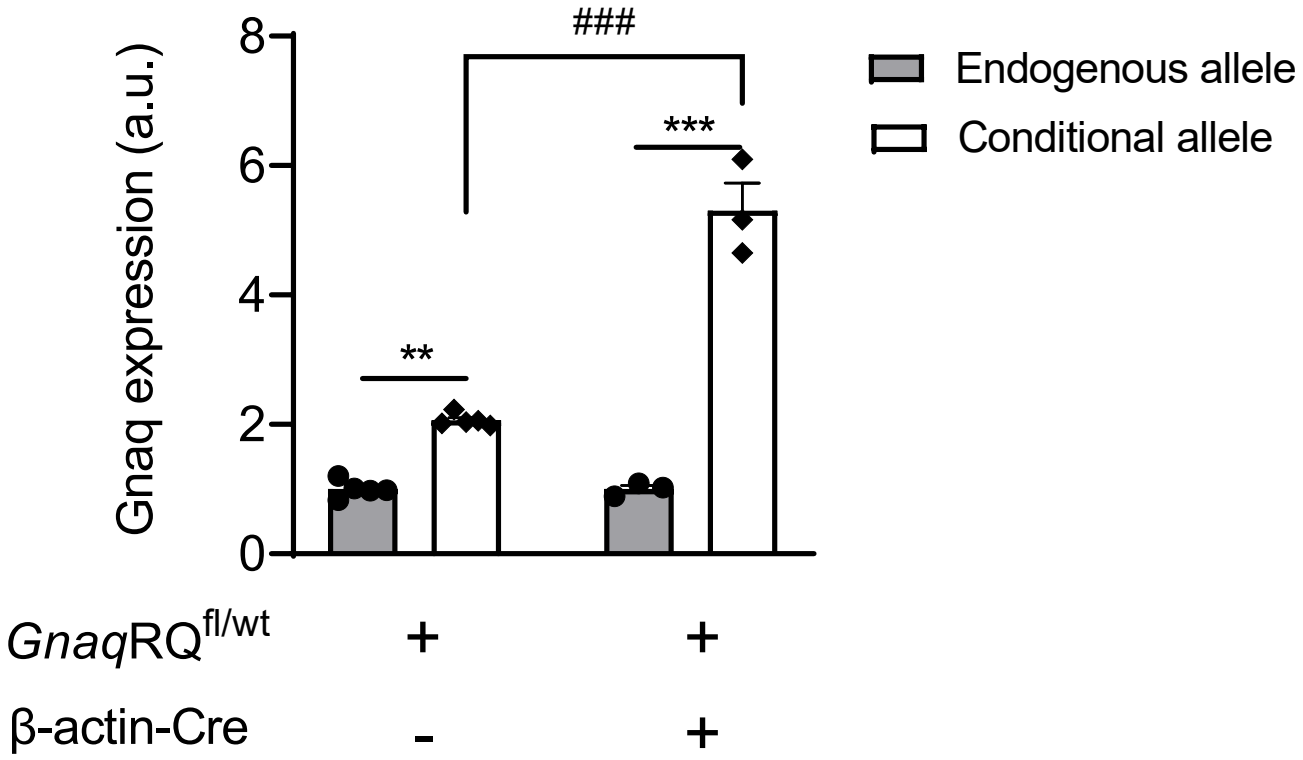

Figure S2. *Gnaq* transcript levels in embryos from *Gnaq*RQ$^{fl/wt}$ x *Gnaq*RQ$^{fl/wt}$;β-actin-Cre+ cross. qRT-PCR results from e14.5 embryonic mouse tissue from *Gnaq*RQ$^{fl/wt}$ and *Gnaq*RQ$^{fl/wt}$;β-actin-Cre+ littermates using allele specific primers revealed that *Gnaq* conditional allele transcripts were significantly higher than transcripts from the endogenous allele in both groups (p^{***} = 0.0002 and p^{**} = 0.007 conditional *vs* endogenous allele, for *Gnaq*RQ$^{fl/wt}$ and *Gnaq*RQ$^{fl/wt}$;β-actin-Cre+, respectively, two tailed paired *t*-test) with a greater increase in *Gnaq*RQ$^{fl/wt}$;β-actin-Cre+ ($p^{###}$ <0.001 *Gnaq*RQ$^{fl/wt}$;β-actin-Cre+ vs *Gnaq*RQ$^{fl/wt}$, two tailed unpaired *t*-test).