

## Supplemental Figure Legends

### Supplemental Figure 1 related to Figure 1.

**A.** Olfr231 expression in the G9a single KO versus G9a/GLP dKO. Olfr231 ISH (red) at E18.5. Top-most panels are more anterior, bottom panels are posterior. DAPI nuclear dye is blue. **B.** MOR28 immunofluorescence (red) illustrating that unlike in Foxg1-Cre; G9a flox/flox MOE, this OR is expressed. **C.** OMP is expressed at normal levels by chromogenic ISH, suggesting OSNs are normal. **D.** MOR28-IRES-Cre mediated deletion of G9a with R26R mT/mG (Muzumdar et al., 2007) Cre-labeling of neurons illustrate that olfactory bulb targeting is not altered in the absence of G9a.

**Supplemental Figure 2 related to Figure 2:** **A.** Histogram depicting total number of OR genes detected in E18.5 MOE by RNA-seq per genotype, where all are Foxg1-Cre<sup>+</sup> and 3=G9a flox/+, 2=G9aflox/flox, 1=G9aflox/flox;GLPflox/+, and 0=G9aflox/flox;GLPflox/flox. **B.** Boxplot of OR genes with outliers and without outliers (inset) for the same dosage series illustrating the decrease in median (shown as solid differently colored horizontal bar within boxplot). **C.** Cartoon depiction of 3 different hypothetical MOEs with 5 different OSN frequencies and resulting Gini coefficients. **D.** Gini coefficients calculated from Fig. 4D are plotted and show a simple upward trend toward perfect inequality, illustrating that the diversity of OSNs in the dKO is severely diminished compared to control MOE. **E.** RNA-seq values across two genotypes for a set of marker

genes specific to the following stages: mature OSN (Adcy3, OMP, Slc17a6 (Vglut2), Cnga2), immature neuron (Gap43), progenitor cells (NeuroD1 and Ascl1), and transient OR-choice/immature neuron (Atf5 and Lsd1). **F.** ATF5 (red) and ADCY3 (green) are expressed at similar levels in control and G9a/GLP double KO MOEs at E18.5. **G.** Lsd1 IF illustrating its expression pattern is the same between control and double G9a/GLP double KO MOEs at E18.5 **H.** VGLUT2-positive mature OSN axons target the olfactory bulb in G9a/GLP double KO MOEs at E18.5, suggesting that OSN maturation is not impaired.

**Supplemental Figure 3 related to Figure 3:** **A.** Boxplot depiction of all Refseq OR expression levels as RPKM from SUV4-20 control and dKO RNA-seq experiments. Outliers are shown as individual circles. Median values for each genotype are colored bars, either green (double heterozygote: Foxg1-Cre+; SUV4-20H1fl/+; SUV4-20H2 +/-) or red (double knockout: Foxg1-Cre+; SUV4-20H1 fl/fl; SUV4-20H2 -/-). **B.** Lorenz curve for double heterozygote control versus double knockout SUV4-20 mutant (as shown in Figure 4D). **C.** qRT-PCR from cDNA of control and SUV4-20 dKO MOE at PND21 illustrating the similarity in expression level for Olfr231 and other OR genes. Values for the above experiments represent the mean of technical duplicates; error bar is +/-SEM. **D.** MOR28 IF in the Foxg1-Cre+ control and SUV4-20 dKO MOE at PND21 illustrating the prevalence of this OSN type in the absence of SUV4-20, in contrast to the loss of MOR28 in the G9a/GLP dKO (data not shown). DAPI nuclear stain is blue. **E.** Representative ChIP-qPCR in PND21 SUV4-20 double

knockout illustrates depletion of H4K20me3 at all loci assayed. **F.** ChIP-qPCR in PND21 SUV4-20 double knockout illustrates maintenance of H3K9me3 at all loci assayed despite loss of H4K20me3. Values represent the mean of technical duplicates; error bars are mean +/-SEM.

**Supplemental Figure 4 related to Figure 4:** **A.** Olfr231 FISH (red) in GLP heterozygote and GLP KO MOE at E18.5. **B.** Quantitative RT-PCR from E18.5 MOE cDNA illustrating Olfr231 is upregulated in both G9a and GLP single KOs, and there is a synergistic effect from the removal of both genes. Ubiquitously expressed genes such as TBP remain relatively constantly expressed. Normalized to Act-B. Values represent the mean of technical duplicates; error bars are mean +/-SEM. **C.** G9a immunofluorescence (red) indicating it is expressed in every cell in the MOE at E18.5, indicating that GLP must be coexpressed with G9a (DAPI is shown in blue).

Table S1 related to Figure 1. Non-chemoreceptor genes misregulated in the G9a/GLP double knockout MOE.

Downregulated genes				Upregulated genes			
gene	cont_fpk m	dko_fpk m	cuffdiff_p_val	gene	cont_fpk m	dko_fpk m	cuffdiff_p_val
Ttr	66.9947	1.01025	0.0003	Lce1g	3.34612	16.5146	0.0043
Ambn	144.032	4.36029	0.00005	Sprr2d	0	3.03183	0.00005
Enam	34.7472	0.435202	0.00005	Tbx18	0.75721	6.4342	0.00005
Amtn	22.3772	0	0.00005	Pla2g2f	2.37024	13.3765	0.0001
Abpb	18.9729	0	0.00005	Kremen2	0.65967	6.2253	0.0079
Gm1006	25.1943	0.363092	0.00565	Ivl	1.4299	9.72708	0.00005
Bpil3	13.3564	0	0.00005	Lce1e	2.85627	16.2442	0.00375
Odam	32.5018	1.58375	0.00035	Cxcl14	11.2525	54.2732	0.00005
Car6	14.7257	0.309201	0.00565	Ggct	3.14498	18.4711	0.00005
Serpina3n	23.6058	1.2586	0.00005	Dhrs2	3.01362	19.6933	0.0002
Dspp	31.709	2.57553	0.00005	Casp14	2.5689	17.5257	0.00005
Krt76	42.8591	4.02448	0.00005	Krtap14	0	4.26381	0.00005
Sult1e1	20.3228	1.63968	0.0001	Krt79	0.595468	7.4448	0.0016
5430413K10Rik	657.044	81.4107	0.00005	Krt10	165.101	882.976	0.00005
Dcpp3	41.5419	4.608	0.00025	Krtap15	0	4.41197	0.00005
Abpa	6.35306	0	0.00005	Lce1a2	4.76775	30.8184	0.00135
Rsc1a1	6.11259	0.00162905	0.01185	Il1f5	2.00706	15.934	0.00005
Rspo4	12.8765	1.06473	0.0002	Twist2	2.70956	20.5417	0.0016
Lcn13	5.66824	0	0.00005	Lce1d	11.6936	74.7501	0.00005
4833413D08Rik	41.4009	5.39757	0.00005	Lce1a1	6.7046	45.6865	0.00015
Foxf1a	15.112	1.50601	0.02715	Lce1i	3.22069	26.6162	0.0006
Muc5b	26.3138	3.25083	0.00005	Flg2	0.78783	12.5662	0.00005
Expi	203.021	30.9041	0.00005	Lce1b	4.73736	52.8095	0.00015
Sult1c1	11.3124	0.973546	0.00035	Lce1c	5.53744	61.6205	0.00005
Scgb1c1	67.6346	12.4039	0.00035	Cyp2b19	0.55726	17.6213	0.00075
Atp2a3	20.153	3.1582	0.00005	Krt77	0.18003	18.6752	0.0153
E030002O03Rik	468.406	93.232	0.00005	Stfa3	29.544	710.325	0.00005
Pglyrp1	184.271	39.1801	0.00005	2310050C09Rik	0	49.3986	0.00005
Csn3	12.0558	1.83271	0.00025	Lce1m	1.08784	104.321	0.0049
Cxcl17	30.4136	5.84761	0.02045	Hba-a1	0.0091495	347.98	0.00695
Ccl21c	3.36526	0.000572025	0.03075				
Reg3g	389.651	89.2604	0.00005				



Figure S1

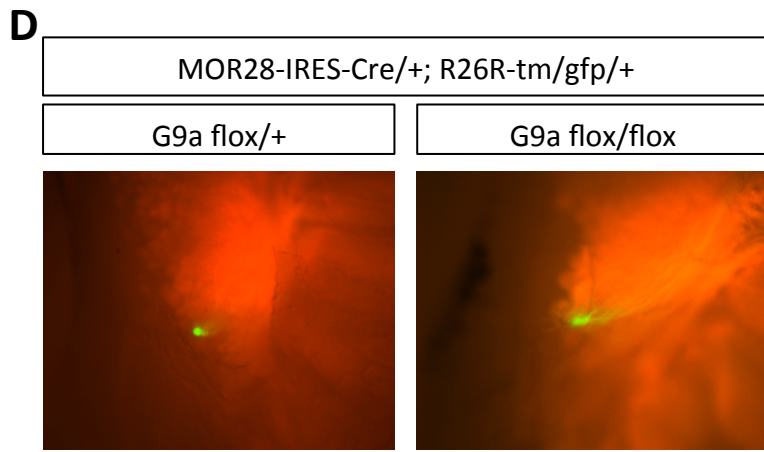
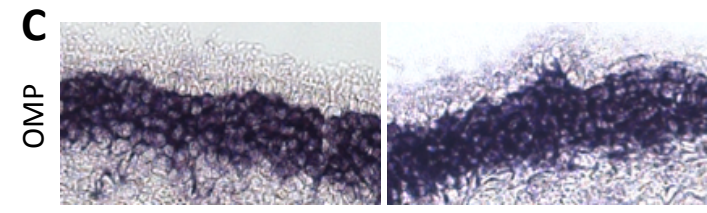
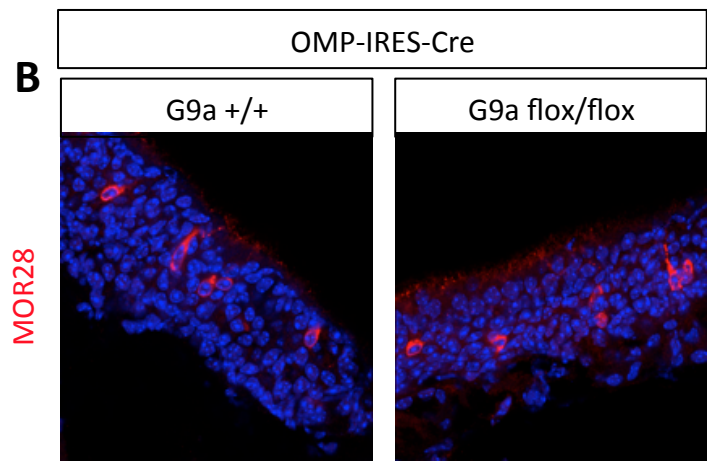
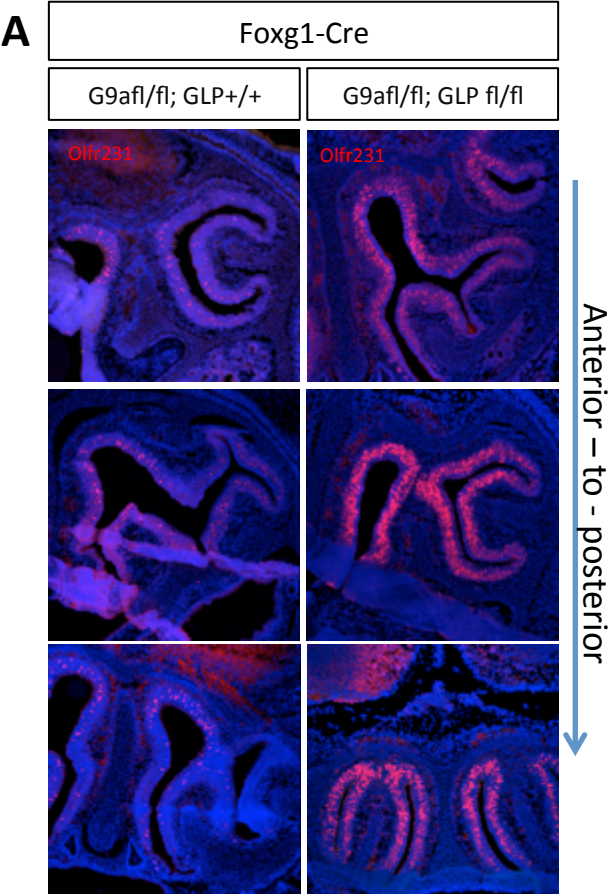


Figure S2

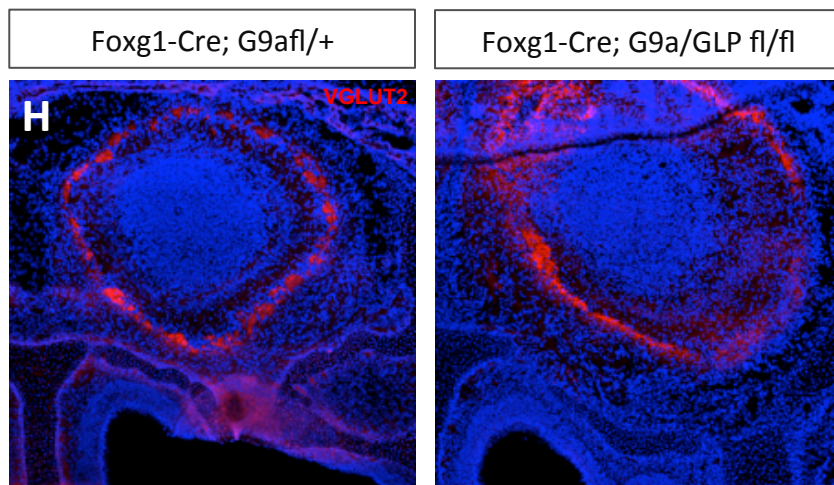
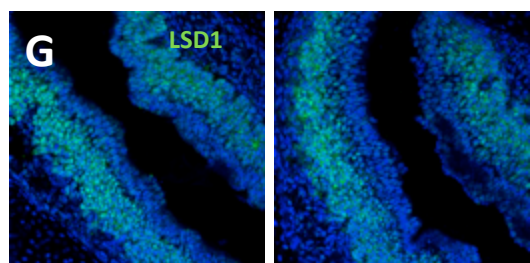
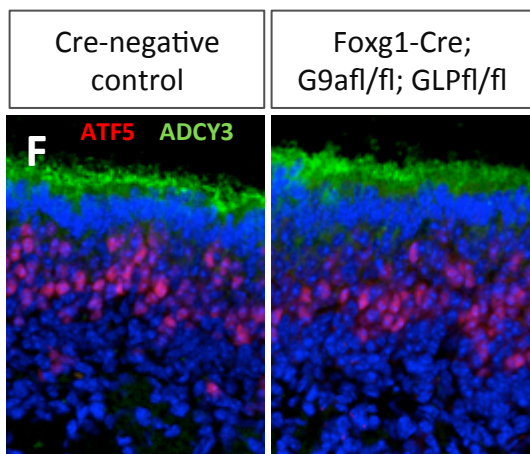
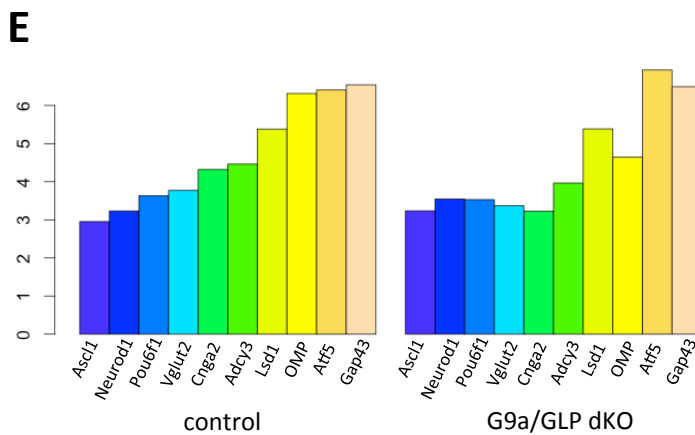
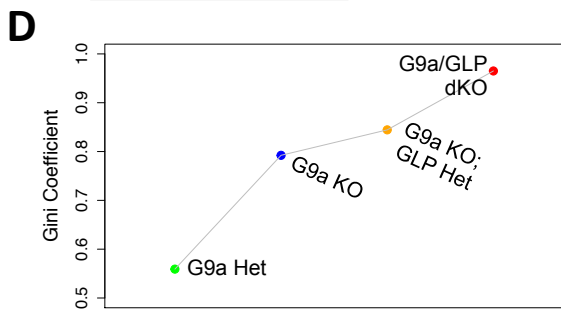
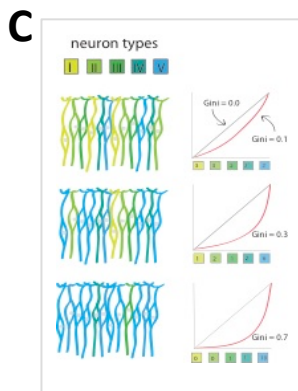
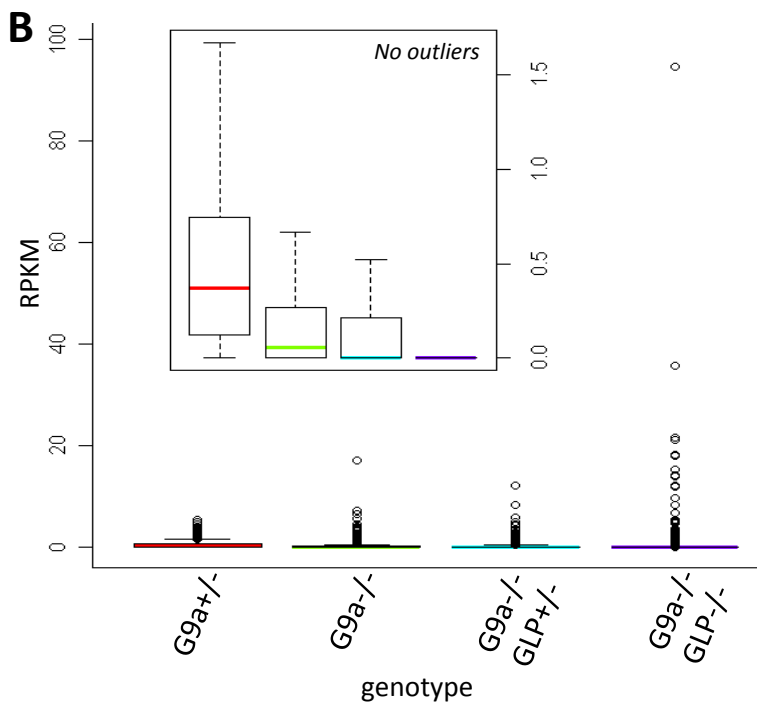
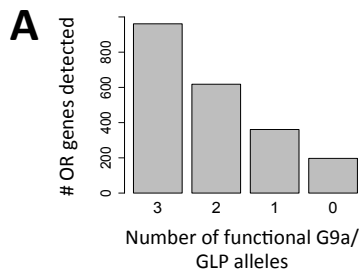
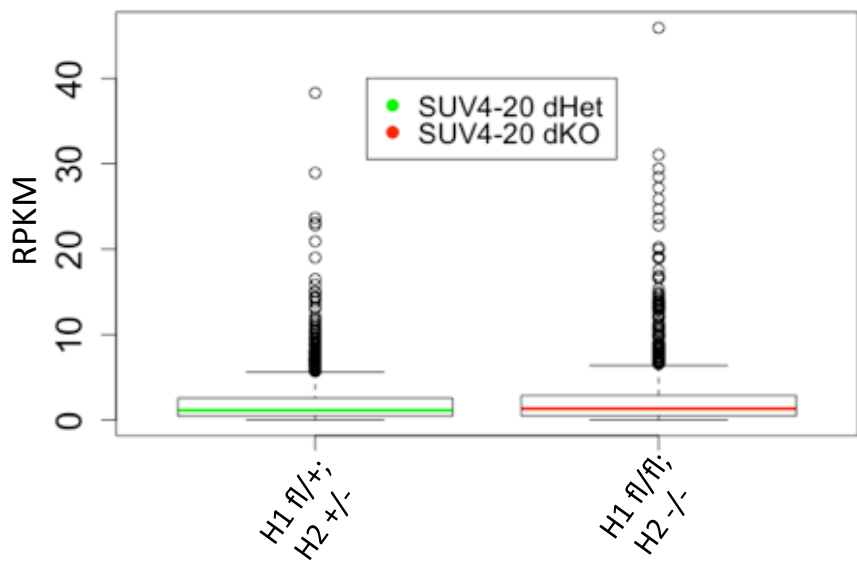
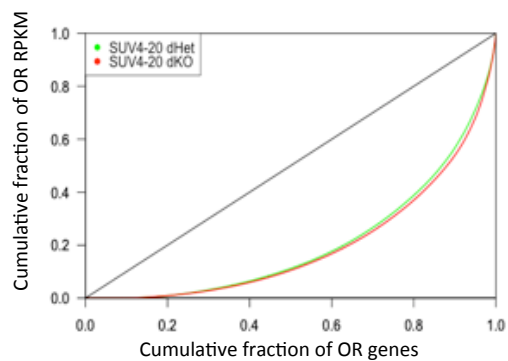


Figure S3

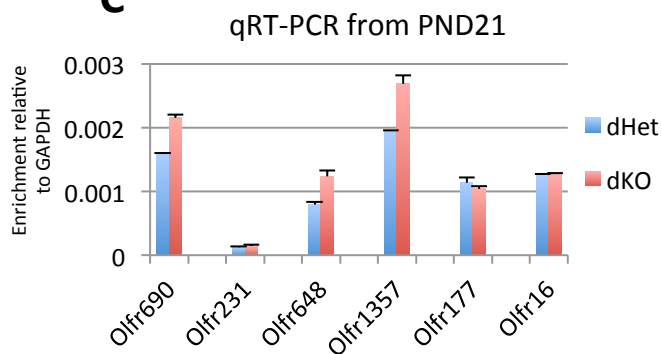
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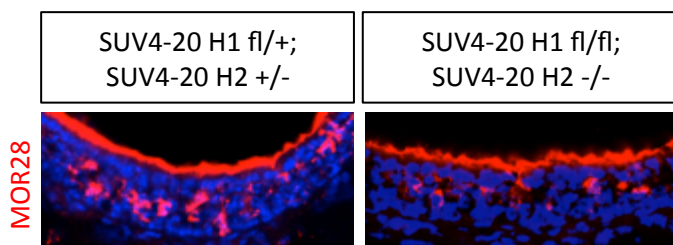
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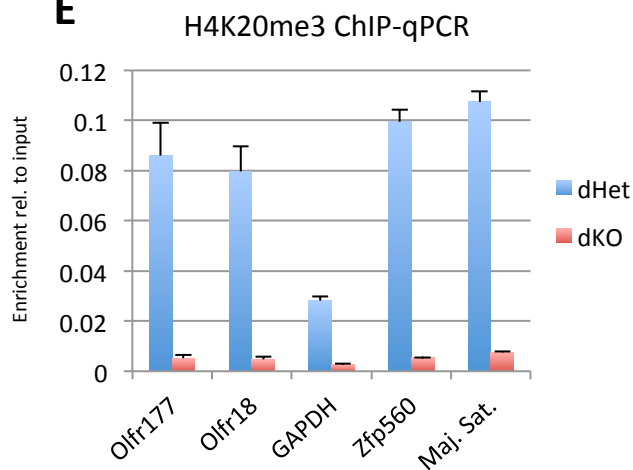
**C**



**D**



**E**



**F**

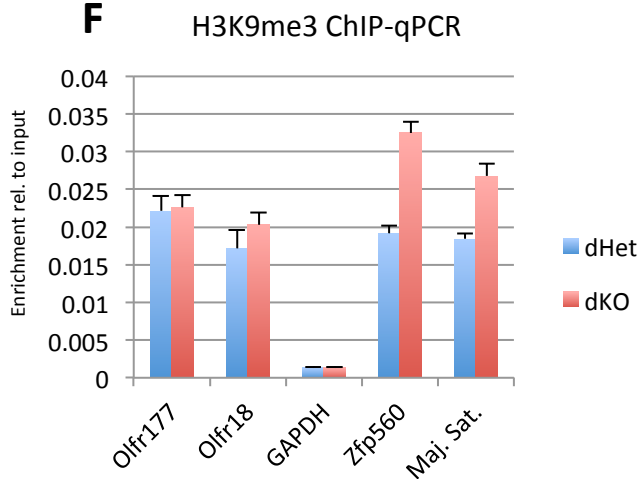




Figure S4

