

Supplementary Information

Olfactory receptors contribute to progression of kidney fibrosis

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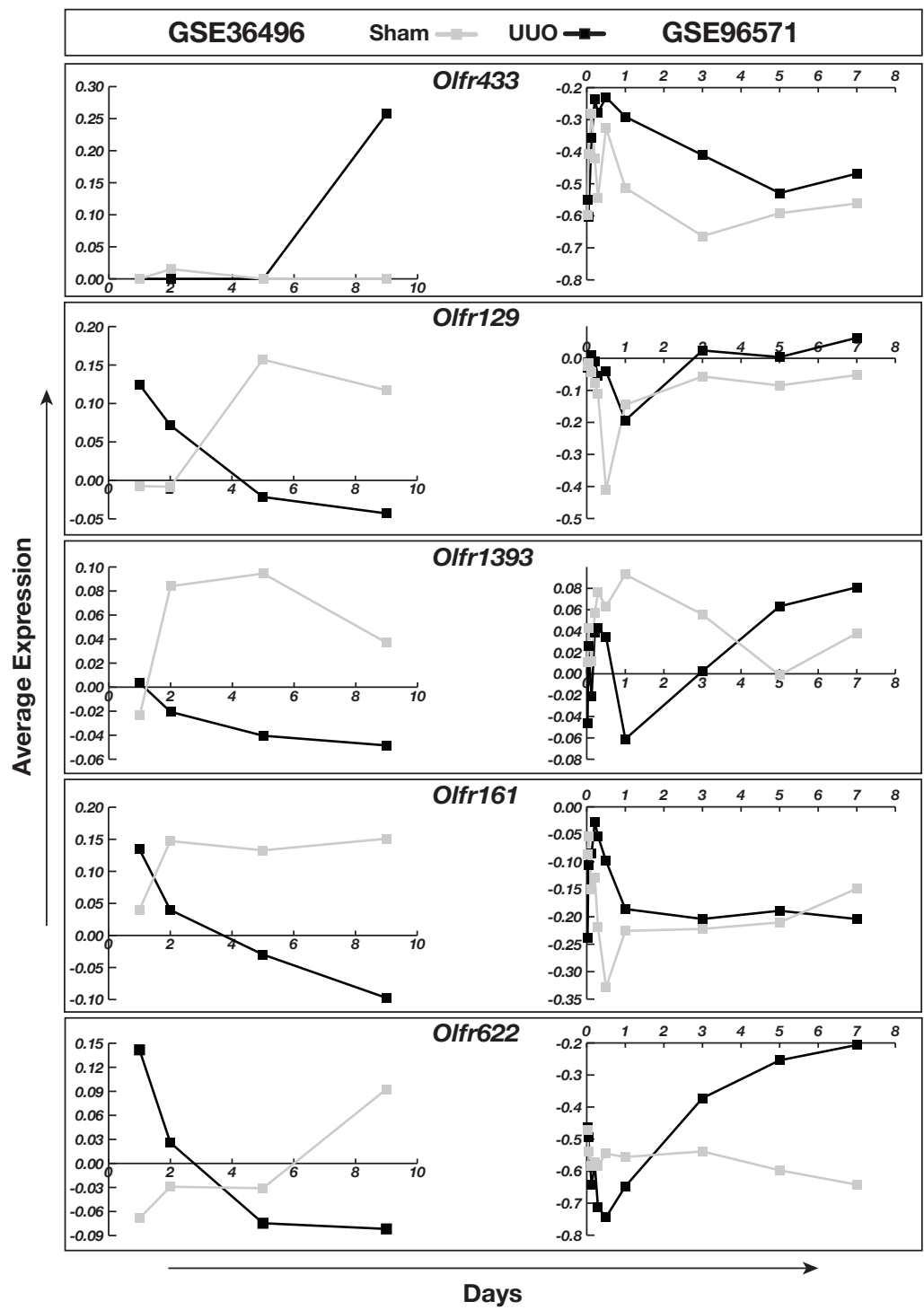
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Supplementary Figure 1. Expression patterns of common ORs between GSE36496 and GSE96571 datasets. The expression patterns of common ORs (*Olf433*, *Olf129*, *Olf1393*, *Olf161*, and *Olf622*) between GSE36496 and GSE96571 datasets. The right and left sides represent the expression patterns of ORs in GSE36496 and GSE96571 datasets, respectively.

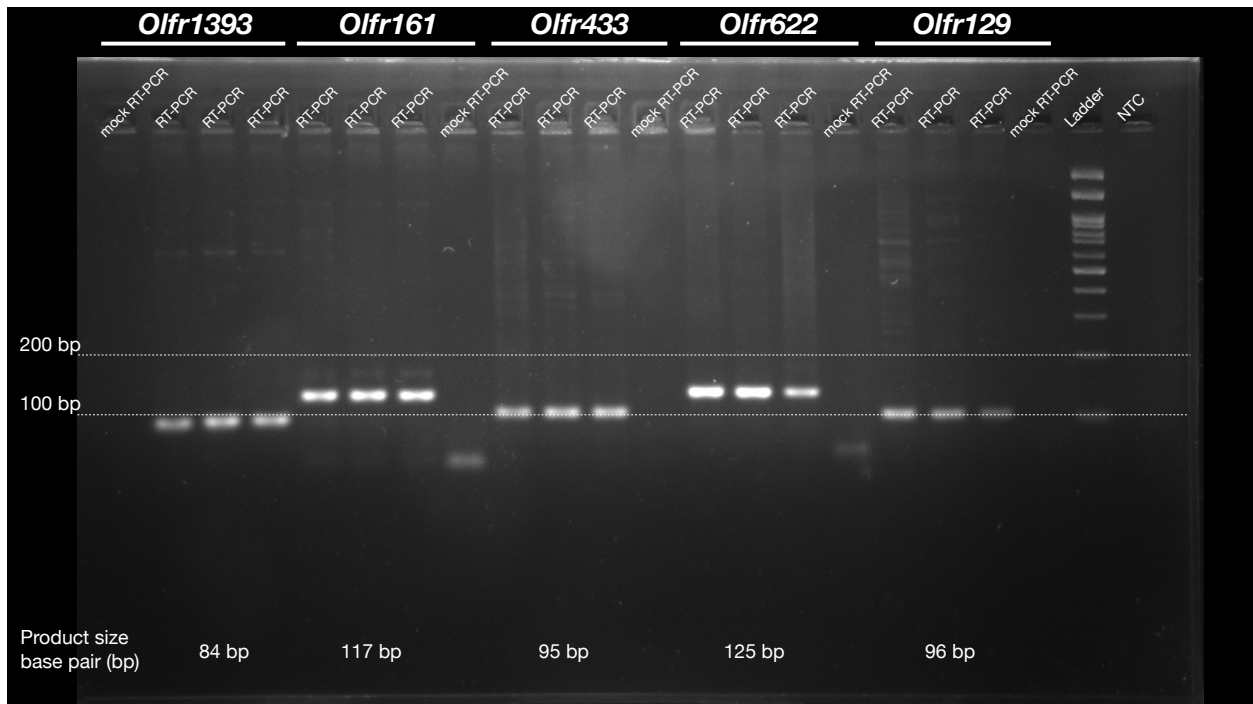
Gene	Sham (FC)	UUO (FC)	Result
<i>Cebpb</i>	0.582	3.462 *	Up-regulation
<i>Hnf4a</i>	0.612	0.213 *	Down-regulation
<i>Serpina3n</i>	0.705 *	19.549 *	Up-regulation
<i>Tgfb1</i>	0.763 *	4.464 *	Up-regulation

Supplementary Table 1. Expression profile of selected genes confirms that our model recapitulates the findings of Wu et al. studies. Expression of each gene is normalized to two housekeeping genes (*Hprt* and *Tfrc*) and is shown as fold change (FC).

* P-value < 0.05

Supplementary Data 1. PCR products sequencing of *Olf433*, *Olf161*, *Olf129*, *Olf622*, and *Olf1393*. The results were uploaded in figshare repository¹.

Supplementary Data 2. Expression value of *Olf433*, *Olf161*, *Olf129*, *Olf622*, and *Olf1393* in mouse model of UUO over 21 days of treatment. The Cycle of threshold (Ct) alongside the amplification of each read were uploaded in figshare repository².



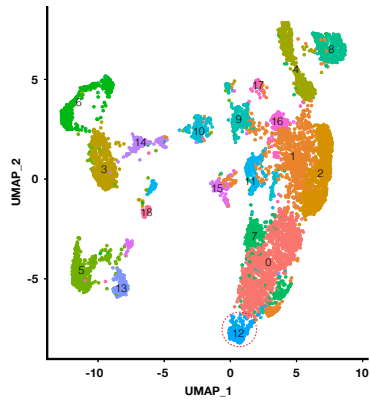
Supplementary Figure 2. The gel-electrophoresis of RT-qPCR products alongside their mock reactions. For each primer three different samples and mock reactions as well as non-template control (NTC) were loaded.

Gene	Gene ID	Forward primer	Reverse primer
<i>Olf433</i>	258712	CTCCGACCTCTTGCCTTCC	CCTGAATCTGCCTGAACCAA
<i>Olf129</i>	258324	GGTATAACTGAGTGCTGCCTACTG	CCCACGATTCATTCGGGTGTAT
<i>Olf1393</i>	258463	CGTCCACTGCACTATACT	GTTCAAGAAGCCTCCTACC
<i>Olf161</i>	258859	GTCTTGGGAAACCTGCTCATCAT	AGTGGTGGAGGAGAAGCATAACAT
<i>Olf622</i>	259087	CCTGGCTTGGAGAATGTTCACTGT	ATAGGCTGGTGGAGACTTGGCTC
<i>Cebpb</i>	12608	CAACCTGGAGACGCAGCACAAG	GCTTGAACAAGTCCGCAGGGT
<i>Hnf4a</i>	15378	ACTCCTCTCCTGCTATGCCA	GGGATGGTGACTCCTACCCT
<i>Serpina3n</i>	20716	CAACCCTGAACATCGGGAGT	TGCAGTCTACAGAGCTGAAACC
<i>Tgfb1</i>	21803	ATTCCTGGCGTTACCTTG	GCTGATCCCGTTGATTTC
<i>Hprt</i>	15452	CGTCGTGATTAGCGATGATG	AGTCTTTCAGTCCTGTCCATAA
<i>Tfrc</i>	22042	TGCATTGCGGACTGTAGAG	CCCACCAAACAAGTTAGAGAAT

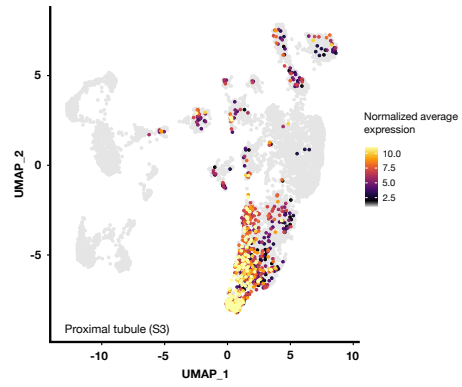
Supplementary Table 2. The sequence of primers.

a

GSE119531
Normal samples

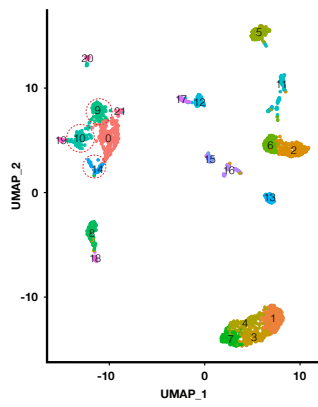


Slc7a13

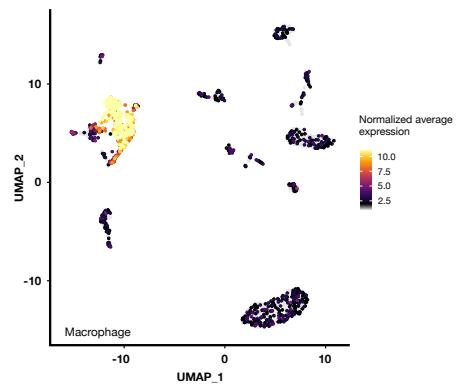


b

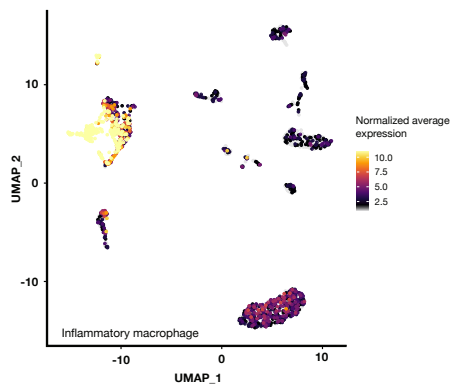
GSE140023
UUO day-2



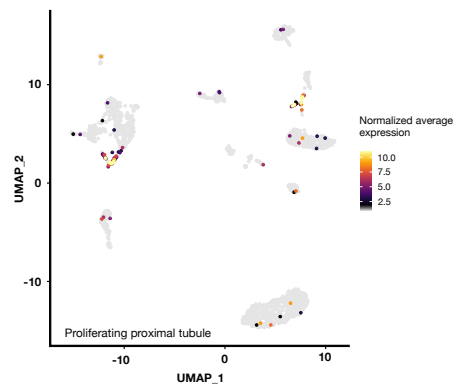
Lyz2



CD74

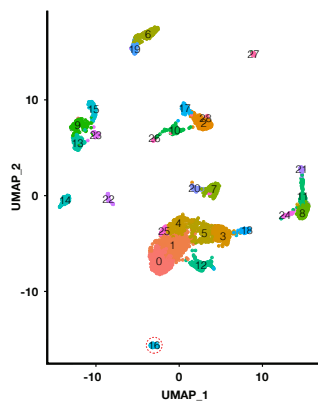


Mki67

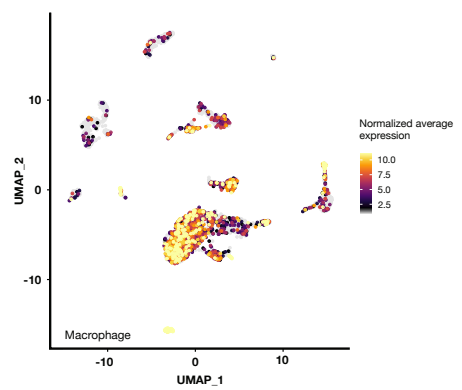


c

GSE140023
UUO day-7



Irf8



Supplementary Figure 3. The expression of selected marker genes related to normal and UUO kidneys. Expression of the proximal tubule third segment (S3) cell marker in normal kidney cells (GSE119531) along with its uniform manifold approximation and projection (UMAP) plot (a). Expression of macrophage, inflammatory macrophage, and proliferating proximal tubule cell marker in UUO day-2 and macrophage cell marker in UUO day-7 samples (GSE140023), with their related UMAP plots (b and c).

References

1. Motahharynia, A. *et al.* Supplementary Data 1: PCR products sequence. *Figshare* (2021)
doi:<https://doi.org/10.6084/m9.figshare.12753749.v11>.
2. Motahharynia, A. *et al.* Supplementary Data 2: RT-qPCR results. *Figshare* (2021)
doi:<https://doi.org/10.6084/m9.figshare.16755340.v2>.