

**Supporting Information**

**SARS-CoV-2 Receptor ACE2 is Enriched in a Subpopulation of Mouse Tongue Epithelial cells in Nongustatory papillae but Not in Taste Buds or Embryonic Oral Epithelium**

Zhonghou Wang<sup>1,2</sup>, Jingqi Zhou<sup>3</sup>, Brett Marshall<sup>1,2</sup>, Romdhane Rekaya<sup>2,4</sup>, Kaixiong Ye<sup>3,4</sup>, Hong-Xiang Liu<sup>1,2\*</sup>

<sup>1</sup> Regenerative Bioscience Center, University of Georgia, Athens, Georgia 30602, USA

<sup>2</sup> Department of Animal and Dairy Science, College of Agricultural and Environmental Sciences, University of Georgia, Athens, Georgia 30602, USA

<sup>3</sup> Department of Genetics, Franklin College of Arts and Sciences, University of Georgia, Athens, Georgia 30602, USA

<sup>4</sup> Institute of Bioinformatics, University of Georgia, Athens, Georgia, 30602, USA

**Table of Contents**

***SARS-CoV-2 receptor ACE2 is enriched in a subpopulation of mouse tongue epithelial cells in non-gustatory papillae, but not in taste buds or embryonic oral epithelium..... 1***

**Table S-1..... 2**

**Table S-2..... 6**

Table S-1

Table for top 10 significant genes for each cluster (13 clusters in total) identified in dataset from Schaum et al. (7538 cells in total). pct. 1 : The percentage of cells where the gene is detected in the cluster. pct. 2 : The percentage of cells where the gene is detected in the cells in addition to this cluster. avg\_logFC: the difference (log scaled fold change) between this cluster and the rest of cells.

gene	cluster	pct.1	pct.2	avg_logFC	p_val	p_val_adj
Gltscr2	0	1	0.988	0.46962156	2.71E-270	4.03E-266
Rpl3	0	1	1	0.29459527	5.89E-254	8.74E-250
Ccnd2	0	0.902	0.574	0.70067911	4.91E-251	7.29E-247
Cox7a2l	0	0.999	0.981	0.42084125	1.53E-239	2.27E-235
Dusp6	0	0.798	0.454	0.75069428	6.31E-238	9.36E-234
Eef2	0	1	1	0.32342224	6.80E-238	1.01E-233
Npm1	0	1	0.992	0.43433172	6.83E-236	1.01E-231
Tgif1	0	0.879	0.594	0.61919128	1.45E-231	2.16E-227
Klf9	0	0.957	0.817	0.56154669	1.61E-231	2.39E-227
Rpl18a	0	1	1	0.25246291	1.81E-231	2.69E-227
Krt4	1	0.996	0.911	3.55069607	0	0
Krt13	1	0.999	0.81	2.01708437	0	0
2610528A11Rik	1	0.94	0.387	1.86617384	0	0
Krt23	1	0.626	0.149	1.55623627	0	0
Fabp5	1	1	0.982	1.54286544	0	0
Aldh3a1	1	0.967	0.684	1.39367184	0	0
Pir	1	0.971	0.676	1.23036923	0	0
1110032A04Rik	1	0.684	0.064	1.1769939	0	0
Krt32	1	0.951	0.251	1.15218617	0	0
Calml3	1	0.994	0.883	0.99408609	0	0
Krt16	2	0.996	0.858	2.66961595	0	0
Krt24	2	0.98	0.551	2.16134043	0	0
Defb4	2	0.614	0.116	2.09207394	0	0
Krt6a	2	1	0.995	1.85095867	0	0
Sbsn	2	0.988	0.809	1.70336197	0	0
Ctnnbip1	2	0.979	0.718	1.69115677	0	0
Fam25c	2	0.995	0.804	1.60700513	0	0

Spink5	2	0.972	0.514	1.58123329	0	0
Lypd3	2	0.991	0.824	1.42714279	0	0
Dsg1a	2	0.947	0.348	1.36076104	0	0
Ube2c	3	0.979	0.14	2.35606481	0	0
Tubb5	3	0.999	0.771	2.17485269	0	0
Hmgb2	3	1	0.804	1.99616428	0	0
Stmn1	3	1	0.697	1.84232023	0	0
Tuba1b	3	0.995	0.8	1.77443461	0	0
Birc5	3	0.988	0.085	1.68431103	0	0
Cdc20	3	0.953	0.158	1.67750797	0	0
2810417H13Rik	3	0.934	0.073	1.62690193	0	0
Cenpa	3	0.952	0.117	1.59187524	0	0
Top2a	3	0.969	0.085	1.57030348	0	0
Tchh	4	0.809	0.193	2.42475762	0	0
Dapl1	4	0.997	0.827	1.98061817	0	0
Krt78	4	0.857	0.156	1.33694821	0	0
Csrp2	4	0.917	0.243	1.02070574	0	0
Aox4	4	0.831	0.204	0.98756096	0	0
Alcam	4	0.92	0.106	0.95617787	0	0
Ptgs1	4	0.925	0.26	0.75627333	0	0
Pcdh19	4	0.806	0.117	0.60150922	0	0
Dsc1	4	0.681	0.095	0.60045065	0	0
Otop2	4	0.766	0.058	0.59770482	0	0
Wfdc2	5	0.97	0.568	0.92392794	6.11E-138	9.07E-134
Rpl13	5	1	1	0.27061578	5.70E-126	8.46E-122
Krt15	5	1	0.926	0.88771569	1.00E-119	1.49E-115
Rps18	5	1	1	0.260998	1.35E-102	2.01E-98
Ung	5	0.261	0.041	0.26327348	2.77E-100	4.11E-96
Moxd1	5	0.887	0.564	0.5301687	3.61E-92	5.35E-88
Siva1	5	0.881	0.601	0.51280138	1.88E-87	2.80E-83
Rpl3	5	1	1	0.26085961	5.78E-86	8.58E-82
5730469M10Rik	5	0.929	0.626	0.57261026	1.50E-85	2.23E-81
Cdca7	5	0.66	0.3	0.46368973	2.31E-85	3.43E-81
Jakmip2	6	0.791	0.073	0.92339269	0	0
Notum	6	0.759	0.054	0.76334601	0	0
Runx2	6	0.55	0.048	0.41076475	0	0
Dcn	6	0.998	0.559	2.14335351	9.53E-284	1.41E-279
Rbp1	6	0.753	0.155	0.89498505	4.06E-265	6.03E-261

Stra6	6	0.35	0.022	0.31070869	1.70E-258	2.53E-254
Otop3	6	0.746	0.163	0.63290751	2.54E-244	3.78E-240
Igfbp2	6	1	0.947	1.26687491	3.17E-199	4.71E-195
Otop2	6	0.531	0.087	0.42093327	7.56E-194	1.12E-189
Ptn	6	0.691	0.171	0.56803314	4.39E-186	6.52E-182
Cpe	7	0.756	0.153	0.81289018	1.57E-264	2.33E-260
Glul	7	0.859	0.285	1.00640118	3.08E-204	4.58E-200
Osr2	7	0.475	0.075	0.50349394	7.50E-178	1.11E-173
Aknad1	7	0.648	0.159	0.57483163	6.61E-174	9.81E-170
Igfbp7	7	0.989	0.619	0.99041543	2.01E-166	2.99E-162
Tgfb1	7	0.892	0.351	0.78685324	1.61E-162	2.39E-158
Ndufa4l2	7	0.942	0.43	1.13188597	8.05E-158	1.20E-153
Serpinb10-ps	7	0.984	0.681	0.89364467	1.51E-134	2.25E-130
Cpxm2	7	0.673	0.21	0.50611633	3.86E-131	5.73E-127
Cst3	7	1	0.951	0.70185449	3.60E-129	5.34E-125
Gm12824	8	0.703	0.134	0.81868875	5.03E-193	7.48E-189
Fxyd3	8	1	0.994	0.89389478	8.17E-162	1.21E-157
Tgfb1	8	0.91	0.359	1.28529336	2.18E-157	3.23E-153
S100a6	8	1	0.975	1.17631917	6.55E-137	9.72E-133
Krt14	8	1	0.997	1.07560052	7.04E-128	1.04E-123
Plxna2	8	0.864	0.413	0.94428634	3.10E-126	4.60E-122
Igfbp3	8	0.882	0.424	1.36686614	1.33E-110	1.98E-106
Col17a1	8	0.975	0.658	0.95875554	3.40E-110	5.05E-106
Frem2	8	0.384	0.073	0.39698108	4.96E-95	7.36E-91
Wnt10a	8	0.929	0.568	0.75886206	4.70E-92	6.98E-88
Cenpa	9	0.974	0.179	1.29184876	3.54E-241	5.25E-237
Ccnb2	9	0.887	0.157	1.05083709	2.45E-220	3.63E-216
Cdca8	9	0.898	0.229	0.83469547	5.51E-152	8.18E-148
Cdca3	9	0.85	0.206	0.762794	7.54E-137	1.12E-132
Cdkn3	9	0.628	0.12	0.58418549	7.03E-129	1.04E-124
Ptms	9	1	0.976	0.87976807	1.17E-125	1.74E-121
Hmgb1	9	1	0.976	1.06004176	1.50E-122	2.23E-118
Hmgn2	9	0.989	0.556	1.10278805	3.52E-122	5.22E-118
D2Ertd750e	9	0.786	0.218	0.66749888	1.69E-119	2.51E-115
Lmna	9	1	0.999	0.70001283	1.04E-112	1.55E-108
Fxyd4	10	0.916	0.105	1.69680309	0	0
2310043J07Rik	10	0.797	0.051	1.20013996	0	0
Msx1	10	0.614	0.029	0.67308279	0	0
Foxq1	10	0.932	0.144	1.63264722	2.00E-301	2.96E-297

Hhip	10	0.522	0.037	0.53849118	7.54E-253	1.12E-248
Cpm	10	0.725	0.093	1.08374066	1.36E-231	2.02E-227
Lamb1	10	0.414	0.029	0.34291634	5.00E-201	7.42E-197
Sparc	10	0.873	0.208	1.15400192	3.72E-174	5.53E-170
Msx2	10	0.693	0.122	0.95242259	4.08E-173	6.05E-169
Al118078	10	0.741	0.145	0.8088096	1.44E-171	2.14E-167
Krt85	11	0.949	0.078	3.65411083	0	0
Cpm	11	0.964	0.092	1.66794209	0	0
Saa1	11	0.713	0.014	1.56874326	0	0
Sprr2k	11	0.677	0.043	1.45032898	0	0
Cybrd1	11	0.81	0.037	1.06856133	0	0
Cryba4	11	0.795	0.01	1.05700904	0	0
Heph11	11	0.856	0.012	0.98045953	0	0
Hoxc13	11	0.944	0.083	0.88714707	0	0
Wnt3	11	0.954	0.027	0.85732176	0	0
Ttc36	11	0.841	0.054	0.70841751	0	0
Cd207	12	0.944	0.011	4.27157282	0	0
Vim	12	1	0.009	3.85999326	0	0
Cd83	12	1	0.007	3.28991622	0	0
Tyrobp	12	1	0.006	3.08509353	0	0
Ccl22	12	0.889	0.007	3.00885414	0	0
Cd52	12	1	0.005	2.96223882	0	0
Ctss	12	1	0.003	2.66282587	0	0
Pgf	12	0.833	0.007	2.58216353	0	0
Tnfaip2	12	0.972	0.017	2.51440348	0	0
Srgn	12	0.972	0.004	2.46604194	0	0

Table S-2.

Table for top 10 significant marker genes for each cluster (6 clusters in total) identified in dataset from Schaum et al. (1432 cells in total). pct. 1 : The percentage of cells where the gene is detected in the cluster. pct. 2 : The percentage of cells where the feature is detected in the cells in addition to this cluster. avg\_logFC: the difference (log scaled fold change) between this cluster and the rest of cells.

gene	cluster	pct.1	pct.2	avg_logFC	p_val	p_val_adj
Krt15	0	0.964	0.83	0.87692567	3.54E-66	6.05E-62
Ccnd2	0	0.938	0.779	0.78619454	5.80E-55	9.92E-51
5730469M10Rik	0	0.906	0.621	0.69573778	2.24E-52	3.83E-48
Ifitm3	0	0.962	0.783	0.51320421	1.74E-48	2.97E-44
Ptrf	0	0.966	0.986	0.56105847	4.95E-48	8.47E-44
Wfdc2	0	0.837	0.523	0.6345341	4.03E-46	6.89E-42
Col17a1	0	0.962	0.761	0.52250693	2.45E-44	4.19E-40
Lamb3	0	0.926	0.692	0.57956932	9.49E-44	1.62E-39
Cav1	0	0.801	0.526	0.66417101	1.62E-41	2.78E-37
Crip1	0	0.984	0.985	0.46403567	3.40E-41	5.81E-37
Cdk1	1	0.806	0.057	1.4920684	1.34E-180	2.29E-176
Birc5	1	0.87	0.103	1.26280857	1.52E-170	2.59E-166
Kif22	1	0.733	0.039	1.1303087	3.76E-168	6.43E-164
Pbk	1	0.672	0.022	0.93759916	8.96E-167	1.53E-162
Cep55	1	0.692	0.029	0.50996347	4.72E-164	8.07E-160
Plk1	1	0.648	0.019	0.97491183	6.36E-163	1.09E-158
Ccna2	1	0.806	0.082	1.43930692	2.16E-162	3.69E-158
Hmmr	1	0.761	0.052	0.74711712	4.09E-162	6.99E-158
Ccnb1	1	0.842	0.098	1.80087348	5.26E-162	8.99E-158
Cdc25c	1	0.684	0.028	0.93922622	5.57E-162	9.53E-158
Gm12824	2	0.764	0.175	0.78825051	2.83E-82	4.84E-78
Nrp2	2	0.731	0.152	0.93211646	2.12E-80	3.63E-76
Plxna2	2	0.981	0.625	1.11191045	2.49E-72	4.26E-68
Cux1	2	0.995	0.856	0.96546231	2.52E-71	4.31E-67
Npnt	2	0.572	0.119	0.70142895	1.74E-61	2.98E-57
Foxq1	2	0.596	0.132	0.77963828	3.14E-61	5.36E-57
Cxcr7	2	0.75	0.276	1.05749045	2.33E-56	3.98E-52

Hhip	2	0.317	0.025	0.54111971	2.47E-56	4.22E-52
Slc39a6	2	0.981	0.79	0.95931634	2.93E-55	5.01E-51
Igfbp3	2	0.918	0.518	1.32381523	4.35E-53	7.43E-49
1110032A04Rik	3	0.616	0.044	1.22381668	6.82E-118	1.17E-113
Krt32	3	0.921	0.217	1.21970994	3.95E-113	6.74E-109
Tmprss4	3	0.816	0.14	1.06206775	6.26E-109	1.07E-104
Krt4	3	0.984	0.525	3.58076916	2.57E-98	4.39E-94
Ces1b	3	0.905	0.248	1.37286341	4.67E-94	7.98E-90
Gsta2	3	0.726	0.121	0.52276524	4.41E-90	7.53E-86
Krt13	3	0.995	0.816	2.16033635	2.36E-89	4.03E-85
Fabp5	3	1	0.953	1.63260252	9.06E-86	1.55E-81
Rnase1	3	0.4	0.023	0.32200061	3.49E-78	5.96E-74
Pir	3	0.963	0.692	1.39857155	1.59E-75	2.72E-71
Notum	4	0.792	0.036	1.03457412	8.12E-176	1.39E-171
Runx2	4	0.804	0.05	0.62856596	1.92E-158	3.28E-154
Lhx6	4	0.613	0.012	0.38968852	7.58E-157	1.30E-152
Otop2	4	0.768	0.064	1.50555682	5.03E-141	8.59E-137
Otop3	4	0.893	0.137	1.31924287	4.89E-126	8.35E-122
Lgr6	4	0.53	0.024	0.31231378	1.73E-109	2.96E-105
Jakmip2	4	0.607	0.044	0.56153634	8.48E-109	1.45E-104
Rbp1	4	0.815	0.129	0.56376416	2.64E-104	4.51E-100
Lef1	4	0.935	0.2	0.76533009	8.95E-102	1.53E-97
Alcam	4	0.863	0.21	1.16903579	4.18E-94	7.15E-90
Cldn17	5	0.888	0.025	1.19502891	1.10E-209	1.87E-205
Prss53	5	0.836	0.039	1.67750979	1.76E-170	3.01E-166
Lypd5	5	0.836	0.046	1.88282536	1.24E-159	2.13E-155
2310042E22Rik	5	0.879	0.065	1.38001488	6.08E-148	1.04E-143
Defb4	5	0.595	0.019	0.60840486	2.07E-129	3.54E-125
Krtap3-3	5	0.741	0.047	0.37326788	8.37E-129	1.43E-124
Sdr9c7	5	0.698	0.05	0.55000323	7.07E-112	1.21E-107
Serpib7	5	0.517	0.018	0.59858342	1.69E-107	2.89E-103
Serpib11	5	0.569	0.027	0.76299276	4.50E-107	7.69E-103
Cnfn	5	0.836	0.101	2.02499136	1.82E-104	3.11E-100