Supplementary

Table S1 Datasets, platforms, and sample counts used in the study

Database	Platform	Platform access number	Total number
GSE164690	Illumina NextSeq 500	GPL18573	18 patients 134,606 cells
TCGA-HNSC	RNA_Seq	–	500 samples
GSE65858	Illumina HumanHT-12 V4.0 expression beadchip	GPL10558	270 samples
User data	–	–	6 samples (3N 3T)

Table S2 Cell counts after $CD45^-$ selection and marker-based filtering

Cells	Endothelial cells	Epithelial cells	Fibroblasts	Immune cells
Count	7,912	14,587	4,684	11,195

Table S3 Malignant clone cell counts based on CNV clustering

Clone	Count
1	2,911
2	1,427
3	845
4	1,818
5	876
6	3,398
7	1,021
8	1,240
9	412

CNV, copy number variation.

https://dx.doi.org/10.21037/tcr-2025-1019

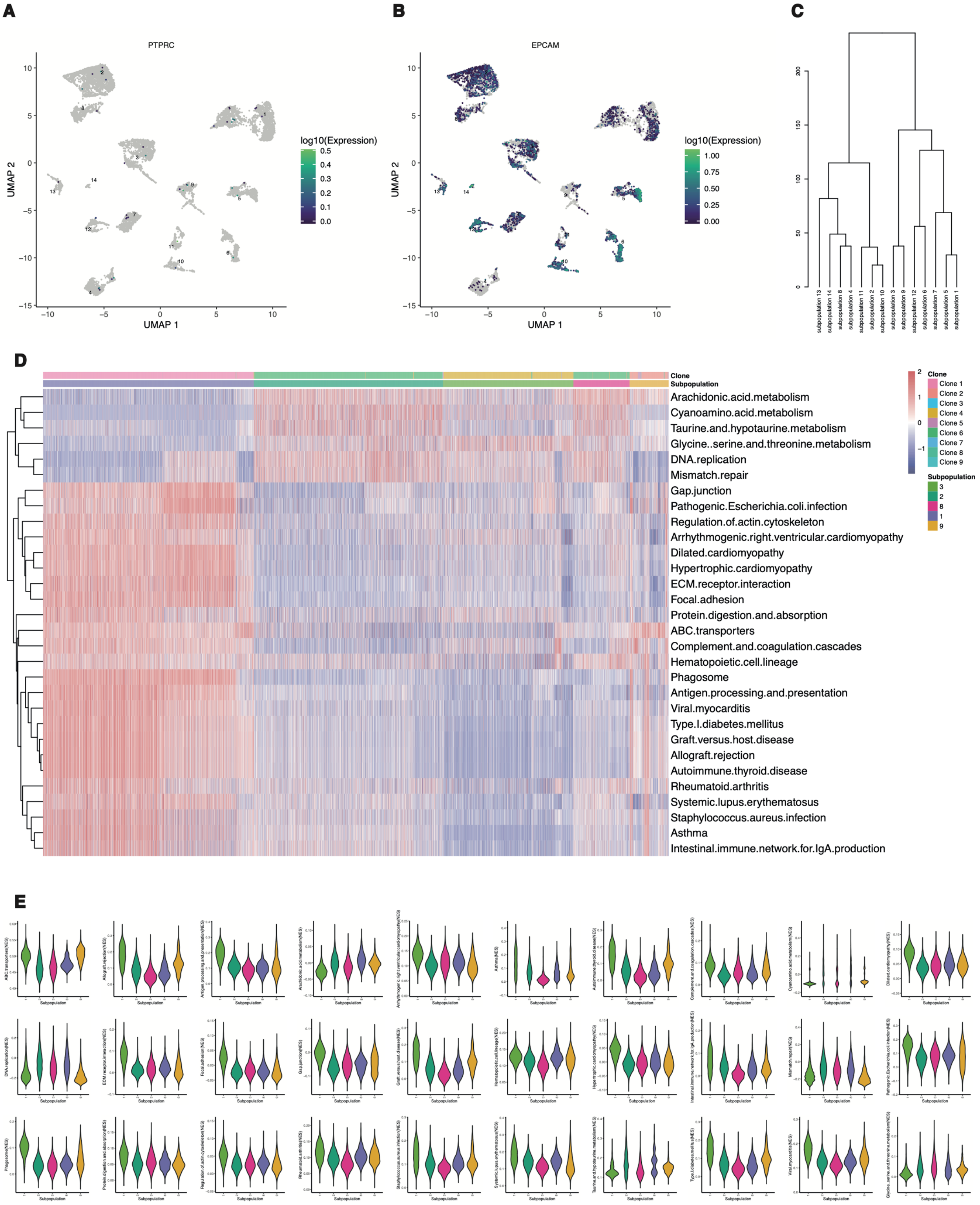

Figure S1 The functional status of HNSCC clones is illustrated. (A,B) Differential expression of immune cell marker and epithelial cell marker in epithelial cells. (C) Clustering relationships among 14 functional subgroups. (D) Top 30 significant pathway enrichment heat map for functional subsets 1, 2, 3, 8, and 9 in KEGG pathway. (E) Distribution of enrichment scores among the top 30 significantly enriched pathways among the five functional subsets.

Table S4 IQR of functional subpopulation proportions across clones

Subpopulation	IQR
Subpopulation 3	11
Subpopulation 9	10
Subpopulation 1	7
Subpopulation 8	7
Subpopulation 2	6
Subpopulation 4	3
Subpopulation 6	2
Subpopulation 11	2
Subpopulation 5	1
Subpopulation 7	1
Subpopulation 10	1
Subpopulation 12	1
Subpopulation 14	1
Subpopulation 13	0

IQR, interquartile range.

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Table S5 ANOVA of KEGG pathway enrichment across functional subsets 1, 2, 3, 8, and 9

Path	F	P	P.adj
ABC.transporters	1007.756	0.00E+00	0.00E+00
Allograft.rejection	1962.144	0.00E+00	0.00E+00
Antigen.processing.and.presentation	2087.139	0.00E+00	0.00E+00
Arachidonic.acid.metabolism	808.108	0.00E+00	0.00E+00
Arrhythmogenic.right.ventricular.cardiomyopathy	735.815	0.00E+00	0.00E+00
Asthma	1059.701	0.00E+00	0.00E+00
Autoimmune.thyroid.disease	2015.805	0.00E+00	0.00E+00
Complement.and.coagulation.cascades	877.784	0.00E+00	0.00E+00
Cyanoamino.acid.metabolism	802.707	0.00E+00	0.00E+00
Dilated.cardiomyopathy	1554.351	0.00E+00	0.00E+00
DNA.replication	537.159	0.00E+00	0.00E+00
ECM.receptor.interaction	1681.411	0.00E+00	0.00E+00
Focal.adhesion	1774.63	0.00E+00	0.00E+00
Gap.junction	1076.573	0.00E+00	0.00E+00
Graft.versus.host.disease	1987.863	0.00E+00	0.00E+00
Hematopoietic.cell.lineage	484.092	0.00E+00	0.00E+00
Hypertrophic.cardiomyopathy	1395.756	0.00E+00	0.00E+00
Intestinal.immune.network.for.IgA.production	693.653	0.00E+00	0.00E+00
Mismatch.repair	415.751	0.00E+00	0.00E+00
Pathogenic.Escherichia.coli.infection	726.28	0.00E+00	0.00E+00
Phagosome	2573.787	0.00E+00	0.00E+00
Protein.digestion.and.absorption	443.042	0.00E+00	0.00E+00
Regulation.of.actin.cytoskeleton	793.504	0.00E+00	0.00E+00
Rheumatoid.arthritis	579.213	0.00E+00	0.00E+00
Staphylococcus.aureus.infection	699.505	0.00E+00	0.00E+00
Systemic.lupus.erythematosus	853.208	0.00E+00	0.00E+00
Taurine.and.hypotaurine.metabolism	440.694	0.00E+00	0.00E+00
Type.I.diabetes.mellitus	1820.86	0.00E+00	0.00E+00
Viral.myocarditis	1680.002	0.00E+00	0.00E+00
Glycine..serine.and.threonine.metabolism	408.302	6.4228533959362e-323	4.84184332924422e-322
Histidine.metabolism	407.958	1.18575755001899e-322	8.64614880222181e-322
Bacterial.invasion.of.epithelial.cells	404.499	4.00983678164756e-320	2.83193487539744e-319
Leishmaniasis	404	9.29979765166978e-320	6.36895083397493e-319
Protein.processing.in.endoplasmic.reticulum	396.195	4.86999999996738e-314	3.23711764703133e-313
Tryptophan.metabolism	390.495	7.5e-310	0.00E+00

Table S5 (*continued*)

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Table S5 (*continued*)

Path	F	P	P.adj
TGF.beta.signaling.pathway	389.224	0.00E+00	4.05E-308
Valine..leucine.and.isoleucine.degradation	380.187	2.96E-302	1.81E-301
Toxoplasmosis	379.301	1.33E-301	7.91E-301
Lysine.degradation	358.187	6.09E-286	3.53E-285
Spliceosome	349.25	2.83E-279	1.60E-278
Protein.export	345.34	2.38E-276	1.31E-275
Cell.adhesion.molecules	338.562	2.86E-271	1.54E-270
Steroid.hormone.biosynthesis	334.167	5.73E-268	3.01E-267
Metabolic.pathways	330.262	4.97E-265	2.55E-264
Pentose.phosphate.pathway	317.663	1.61E-255	8.09E-255
Huntington.disease	310.808	2.51E-250	1.23E-249
Base.excision.repair	308.644	1.10E-248	5.29E-248
PPAR.signaling.pathway	300.943	7.95E-243	3.74E-242
Alzheimer.disease	299.576	8.75E-242	4.04E-241
Osteoclast.differentiation	297.642	2.61E-240	1.18E-239
Fatty.acid.degradation	293.517	3.68E-237	1.63E-236
Lysine.biosynthesis	283.803	1.00E-229	4.35E-229
Nucleotide.excision.repair	283.613	1.40E-229	5.97E-229
Vibrio.cholerae.infection	279.618	1.63E-226	6.82E-226
Hepatitis.C	275.516	2.33E-223	9.57E-223
Peroxisome	268.707	4.12E-218	1.66E-217
Sulfur.metabolism	265.462	1.32E-215	5.23E-215
Proteasome	262.651	1.96E-213	7.64E-213
Oxidative.phosphorylation	259.357	6.96E-211	2.67E-210
Primary.immunodeficiency	254.446	4.47E-207	1.68E-206
Citrate.cycle..TCA.cycle.	248.77	1.15E-202	4.19E-202
Pathways.in.cancer	248.769	1.15E-202	4.19E-202
Nucleocytoplasmic.transport	243.66	1.10E-198	3.95E-198
Propanoate.metabolism	237.561	6.31E-194	2.23E-193
RNA.degradation	232.449	6.30E-190	2.19E-189
Vitamin.B6.metabolism	232.058	1.27E-189	4.35E-189
Basal.transcription.factors	224.028	2.53E-183	8.53E-183
Amoebiasis	223.641	5.10E-183	1.70E-182
Glutathione.metabolism	222.657	3.03E-182	9.92E-182

Table S5 (*continued*)

Table S5 (*continued*)

Path	F	P	P.adj
Glycosaminoglycan.biosynthesis...chondroitin.sulfate...dermatan.sulfate	222.305	5.74E-182	1.85E-181
Neuroactive.ligand.receptor.interaction	218.63	4.46E-179	1.42E-178
One.carbon.pool.by.folate	216.875	1.08E-177	3.39E-177
Wnt.signaling.pathway	215.958	5.69E-177	1.76E-176
Apoptosis	209.824	3.95E-172	1.21E-171
Homologous.recombination	209.223	1.18E-171	3.56E-171
Small.cell.lung.cancer	201.329	2.10E-165	6.24E-165
Adipocytokine.signaling.pathway	200.909	4.52E-165	1.33E-164
Aldosterone.regulated.sodium.reabsorption	199.295	8.63E-164	2.50E-163
Glycerolipid.metabolism	194.351	7.31E-160	2.09E-159
Selenocompound.metabolism	192.622	1.73E-158	4.89E-158
Cardiac.muscle.contraction	190.8	4.89E-157	1.36E-156
Glycolysis...Gluconeogenesis	189.059	1.19E-155	3.28E-155
Retinol.metabolism	188.555	3.01E-155	8.20E-155
Olfactory.transduction	182.511	2.01E-150	5.41E-150
Colorectal.cancer	180.469	8.61E-149	2.29E-148
Notch.signaling.pathway	178.203	5.60E-147	1.47E-146
Salivary.secretion	175.204	1.41E-144	3.66E-144
Linoleic.acid.metabolism	173.63	2.59E-143	6.65E-143
Parkinson.disease	172.788	1.23E-142	3.12E-142
Glycosylphosphatidylinositol..GPI..anchor.biosynthesis	170.994	3.38E-141	8.49E-141
Tyrosine.metabolism	168.792	1.98E-139	4.92E-139
Phototransduction	167.636	1.68E-138	4.13E-138
Terpenoid.backbone.biosynthesis	166.611	1.12E-137	2.72E-137
Cell.cycle	165.458	9.51E-137	2.29E-136
Metabolism.of.xenobiotics.by.cytochrome.P450	162.455	2.49E-134	5.92E-134
Chronic.myeloid.leukemia	157.783	1.46E-130	3.44E-130
Drug.metabolism...cytochrome.P450	156.968	6.64E-130	1.55E-129
RIG.I.like.receptor.signaling.pathway	156.685	1.12E-129	2.58E-129
Amyotrophic.lateral.sclerosis	156.206	2.74E-129	6.25E-129
B.cell.receptor.signaling.pathway	154.953	2.82E-128	6.37E-128
Glycosphingolipid.biosynthesis...lacto.and.neolacto.series	153.603	3.49E-127	7.81E-127
Alanine..aspartate.and.glutamate.metabolism	149.465	7.79E-124	1.73E-123

Table S5 (*continued*)

https://dx.doi.org/10.21037/tcr-2025-1019

Table S5 (*continued*)

Path	F	P	P.adj
Inositol.phosphate.metabolism	148.358	6.13E-123	1.35E-122
Natural.killer.cell.mediated.cytotoxicity	147.602	2.52E-122	5.48E-122
Ubiquitin.mediated.proteolysis	144.779	4.90E-120	1.05E-119
Autophagy...animal	142.769	2.10E-118	4.48E-118
Bladder.cancer	141.757	1.39E-117	2.94E-117
Leukocyte.transendothelial.migration	139.335	1.30E-115	2.72E-115
MAPK.signaling.pathway	137.476	4.23E-114	8.77E-114
mRNA.surveillance.pathway	133.332	1.00E-110	2.05E-110
Malaria	128.366	1.14E-106	2.32E-106
Nitrogen.metabolism	128.34	1.19E-106	2.40E-106
N.Glycan.biosynthesis	127.436	6.54E-106	1.31E-105
Collecting.duct.acid.secretion	126.162	7.19E-105	1.43E-104
Non.homologous.end.joining	125.768	1.51E-104	2.97E-104
Gastric.acid.secretion	121.601	3.89E-101	7.58E-101
Non.small.cell.lung.cancer	119.84	1.08E-99	2.09E-99
NOD.like.receptor.signaling.pathway	117.897	4.23E-98	8.10E-98
Valine..leucine.and.isoleucine.biosynthesis	116.532	5.58E-97	1.06E-96
Butanoate.metabolism	114.98	1.05E-95	1.98E-95
ErbB.signaling.pathway	114.118	5.37E-95	1.00E-94
Neurotrophin.signaling.pathway	109.638	2.59E-91	4.80E-91
p53.signaling.pathway	108.856	1.14E-90	2.09E-90
Thyroid.cancer	108.036	5.40E-90	9.84E-90
Renal.cell.carcinoma	105.819	3.63E-88	6.56E-88
Prostate.cancer	105.428	7.62E-88	1.37E-87
Toll.like.receptor.signaling.pathway	104.96	1.85E-87	3.29E-87
Epithelial.cell.signaling.in.Helicobacter.pylori.infection	104.241	7.27E-87	1.28E-86
Prion.disease	104.163	8.42E-87	1.48E-86
Other.glycan.degradation	103.996	1.16E-86	2.02E-86
Phenylalanine.metabolism	103.54	2.75E-86	4.74E-86
Primary.bile.acid.biosynthesis	102.785	1.16E-85	1.99E-85
Ribosome	99.434	6.76E-83	1.15E-82
Pyruvate.metabolism	99.32	8.41E-83	1.42E-82
Ribosome.biogenesis.in.eukaryotes	97.204	4.72E-81	7.90E-81
Pyrimidine.metabolism	96.885	8.67E-81	1.44E-80
alpha.Linolenic.acid.metabolism	96.153	3.50E-80	5.77E-80

Table S5 (*continued*)

Table S5 (*continued*)

Path	F	P	P.adj
Vitamin.digestion.and.absorption	95.93	5.35E-80	8.76E-80
Cytokine.cytokine.receptor.interaction	93.991	2.15E-78	3.50E-78
Glycosaminoglycan.biosynthesis...heparan.sulfate...heparin	88.699	5.26E-74	8.49E-74
Glycosaminoglycan.biosynthesis...keratan.sulfate	88.456	8.37E-74	1.34E-73
Aminoacyl.tRNA.biosynthesis	88.253	1.23E-73	1.96E-73
Ether.lipid.metabolism	87.384	6.49E-73	1.03E-72
Endometrial.cancer	85.153	4.63E-71	7.27E-71
Porphyrin.metabolism	83.264	1.72E-69	2.68E-69
Nicotinate.and.nicotinamide.metabolism	82.222	1.27E-68	1.97E-68
Arginine.and.proline.metabolism	80.843	1.78E-67	2.74E-67
African.trypanosomiasis	80.47	3.63E-67	5.54E-67
Pantothenate.and.CoA.biosynthesis	76.415	8.68E-64	1.32E-63
Mucin.type.O.glycan.biosynthesis	74.66	2.52E-62	3.80E-62
Cytosolic.DNA.sensing.pathway	73.258	3.73E-61	5.58E-61
Maturity.onset.diabetes.of.the.young	72.422	1.86E-60	2.77E-60
RNA.polymerase	71.804	6.10E-60	9.01E-60
T.cell.receptor.signaling.pathway	71.781	6.37E-60	9.35E-60
SNARE.interactions.in.vesicular.transport	71.557	9.81E-60	1.43E-59
Endocytosis	71.421	1.27E-59	1.84E-59
Drug.metabolism...other.enzymes	70.732	4.80E-59	6.91E-59
Adherens.junction	70.247	1.22E-58	1.75E-58
Pancreatic.cancer	70.067	1.72E-58	2.44E-58
Riboflavin.metabolism	66.612	1.33E-55	1.88E-55
Axon.guidance	64.689	5.42E-54	7.61E-54
Vasopressin.regulated.water.reabsorption	64.594	6.51E-54	9.08E-54
Circadian.rhythm	64.543	7.17E-54	9.94E-54
Vascular.smooth.muscle.contraction	62.924	1.63E-52	2.25E-52
Progesterone.mediated.oocyte.maturation	62.412	4.37E-52	5.99E-52
Purine.metabolism	60.328	2.43E-50	3.31E-50
Lysosome	59.955	5.00E-50	6.77E-50
Sphingolipid.metabolism	59.942	5.13E-50	6.90E-50
Phenylalanine..tyrosine.and.tryptophan.biosynthesis	59.69	8.35E-50	1.12E-49
Fatty.acid.elongation	56.734	2.52E-47	3.35E-47
Glycerophospholipid.metabolism	56.599	3.27E-47	4.32E-47

Table S5 (*continued*)

Table S5 (*continued*)

Path	F	P	P.adj
Acute.myeloid.leukemia	56.36	5.19E-47	6.82E-47
Dorso.ventral.axis.formation	55.479	2.84E-46	3.71E-46
Long.term.depression	53.665	9.49E-45	1.23E-44
Glyoxylate.and.dicarboxylate.metabolism	52.951	3.77E-44	4.87E-44
Calcium.signaling.pathway	51.608	5.08E-43	6.52E-43
Glycosphingolipid.biosynthesis...globo.and.isoglobo.series	51.448	6.92E-43	8.84E-43
Starch.and.sucrose.metabolism	50.944	1.83E-42	2.32E-42
Ascorbate.and.aldarate.metabolism	49.251	4.86E-41	6.14E-41
Galactose.metabolism	48.81	1.14E-40	1.43E-40
Insulin.signaling.pathway	48.5	2.08E-40	2.60E-40
Chagas.disease	47.584	1.22E-39	1.51E-39
Tight.junction	47.539	1.34E-39	1.65E-39
Long.term.potentiation	45.455	7.59E-38	9.32E-38
Basal.cell.carcinoma	44.025	1.21E-36	1.48E-36
Melanoma	43.343	4.54E-36	5.52E-36
Neomycin..kanamycin.and.gentamicin.biosynthesis	41.818	8.74E-35	1.06E-34
Biosynthesis.of.unsaturated.fatty.acids	40.204	2.00E-33	2.40E-33
Glycosphingolipid.biosynthesis...ganglio.series	39.448	8.67E-33	1.04E-32
Fc.gamma.R.mediated.phagocytosis	39.264	1.24E-32	1.47E-32
Folate.biosynthesis	38.266	8.59E-32	1.02E-31
Bile.secretion	37.815	2.06E-31	2.42E-31
Other.types.of.O.glycan.biosynthesis	36.982	1.04E-30	1.22E-30
Proximal.tubule.bicarbonate.reclamation	36.942	1.12E-30	1.30E-30
Chemokine.signaling.pathway	35.71	1.22E-29	1.41E-29
Fructose.and.mannose.metabolism	34.478	1.34E-28	1.55E-28
Phosphatidylinositol.signaling.system	33.226	1.52E-27	1.74E-27
Glioma	32.647	4.66E-27	5.32E-27
Shigellosis	31.306	6.30E-26	7.15E-26
Pancreatic.secretion	31.124	8.97E-26	1.01E-25
JAK.STAT.signaling.pathway	30.866	1.48E-25	1.66E-25
mTOR.signaling.pathway	30.666	2.18E-25	2.44E-25
Fat.digestion.and.absorption	30.065	7.00E-25	7.79E-25
Amino.sugar.and.nucleotide.sugar.metabolism	27.521	9.75E-23	1.08E-22
Hedgehog.signaling.pathway	27.236	1.69E-22	1.86E-22

Table S5 (*continued*)

Table S5 (*continued*)

Path	F	P	P.adj
Biotin.metabolism	26.428	8.12E-22	8.91E-22
beta.Alanine.metabolism	25.388	6.10E-21	6.66E-21
VEGF.signaling.pathway	24.824	1.82E-20	1.98E-20
Steroid.biosynthesis	22.733	1.05E-18	1.14E-18
Melanogenesis	21.911	5.14E-18	5.53E-18
Renin.angiotensin.system	21.377	1.45E-17	1.55E-17
Caffeine.metabolism	20.776	4.62E-17	4.93E-17
Lipoic.acid.metabolism	19.864	2.70E-16	2.86E-16
Ubiquinone.and.other.terpenoid.quinone.biosynthesis	17.773	1.53E-14	1.62E-14
Cysteine.and.methionine.metabolism	17.075	5.88E-14	6.18E-14
Oocyte.meiosis	16.742	1.12E-13	1.17E-13
Pentose.and.glucuronate.interconversions	14.195	1.50E-11	1.56E-11
Type.II.diabetes.mellitus	14.149	1.64E-11	1.70E-11
Glycosaminoglycan.degradation	13.659	4.20E-11	4.33E-11
GnRH.signaling.pathway	13.044	1.36E-10	1.40E-10
Carbohydrate.digestion.and.absorption	12.586	3.27E-10	3.34E-10
Taste.transduction	11.697	1.79E-09	1.82E-09
Thiamine.metabolism	11.323	3.65E-09	3.70E-09
Sulfur.relay.system	10.786	1.01E-08	1.02E-08
Fc.epsilon.RI.signaling.pathway	5.814	1.14E-04	1.15E-04
Fatty.acid.biosynthesis	1.713	0.144	0.144

Table S6 Clone-module associations based on Monocle3 co-expression analysis

Clone	Modules
Clone 1	1, 19
Clone 2	6, 14
Clone 3	20
Clone 4	13
Clone 5	18
Clone 6	5
Clone 7	16, 17
Clone 8	6, 8
Clone 9	24

Table S7 Functional subpopulation-module associations based on Monocle3 co-expression analysis

Subpopulation	Modules
Subpopulation 1	19, 5, 17
Subpopulation 2	1
Subpopulation 3	13
Subpopulation 4	9
Subpopulation 5	16
Subpopulation 6	15
Subpopulation 7	6, 14
Subpopulation 8	1
Subpopulation 9	14, 12
Subpopulation 10	10
Subpopulation 11	10, 6
Subpopulation 12	10, 15, 3, 1
Subpopulation 13	21, 7
Subpopulation 14	21

https://dx.doi.org/10.21037/tcr-2025-1019

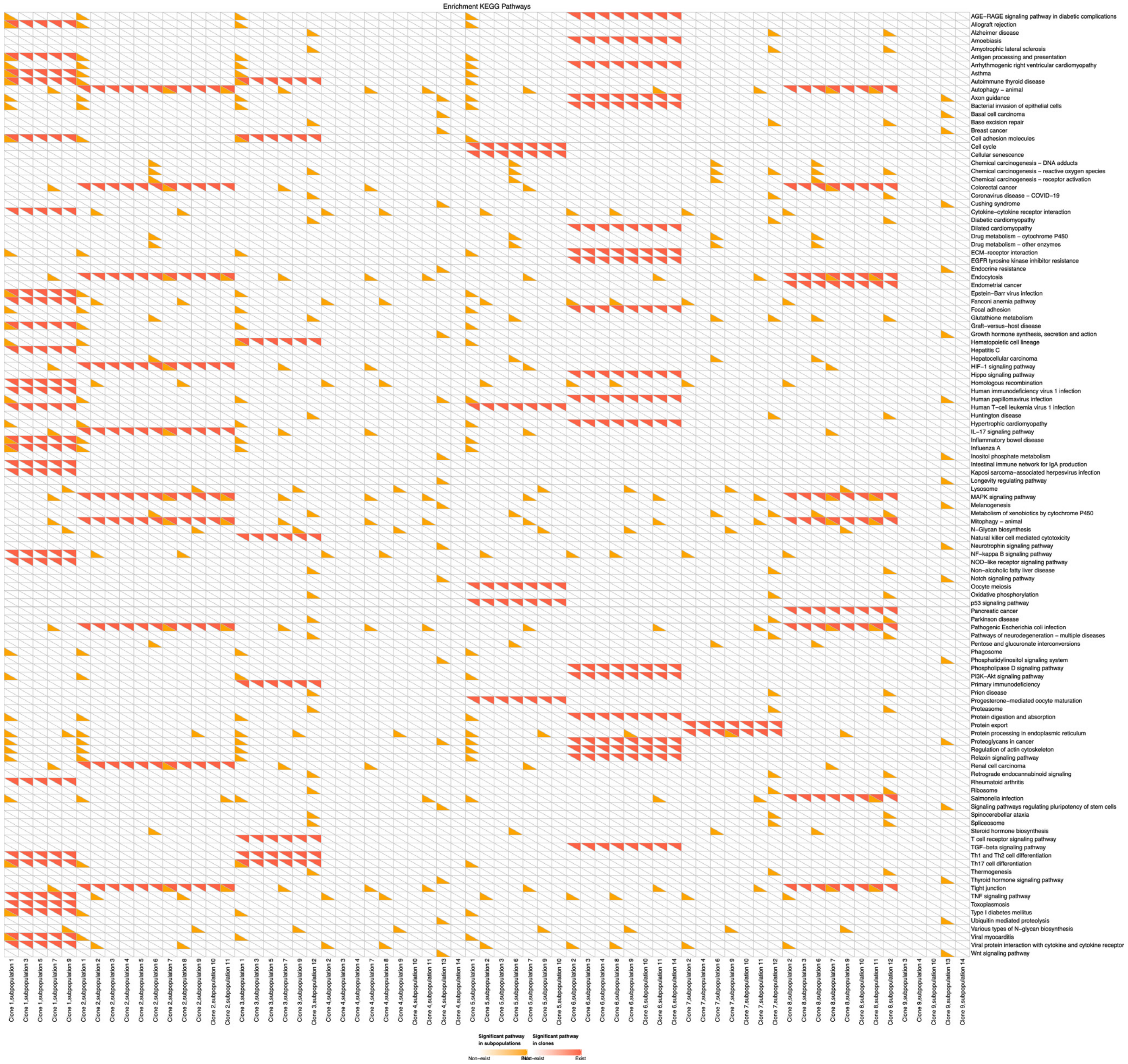


Figure S2 Significant pathways in clones and subpopulations.

Table S8 Shared regulator genes between Clone 1 and functional Subpopulation 1

Item	Gene
1	*ABCD1*
2	*AC006262.2*
3	*AC022034.2*
4	*AIM2*
5	*APOL1*
6	*APOL2*
7	*APOL3*
8	*APOL4*
9	*APOL6*
10	*B2M*
11	*BATF2*
12	*BST2*
13	*BTN3A2*
14	*C19orf66*
15	*CASP1*
16	*CASP7*
17	*CD38*
18	*CERS4*
19	*CIITA*
20	*CMPK2*
21	*CXCL10*
22	*CXCL11*
23	*CXCL9*
24	*DDX58*
25	*DDX60*
26	*DDX60L*
27	*DTX3L*
28	*EIF2AK2*
29	*EPSTI1*
30	*ETV7*
31	*FBXO6*
32	*GBP1*
33	*GBP2*
34	*GBP3*
35	*GBP4*
36	*GBP5*
37	*GBP7*
38	*GSDMD*
39	*HELZ2*
40	*HERC5*
41	*HERC6*
42	*HLA-A*
43	*HLA-C*
44	*HLA-DMA*
45	*HLA-DMB*
46	*HLA-DPA1*
47	*HLA-DPB1*
48	*HLA-DQA1*
49	*HLA-DQB1*
50	*HLA-DRA*
51	*HLA-DRB1*
52	*HLA-E*
53	*HLA-F*
54	*IFI16*
55	*IFI27*
56	*IFI35*
57	*IFI44*
58	*IFI44L*
59	*IFI6*
60	*IFIH1*
61	*IFIT1*
62	*IFIT2*
63	*IFIT3*
64	*IFIT5*
65	*IFITM3*
66	*IL15RA*
67	*IRF7*
68	*ISG15*

Table S8 (*continued*)

Table S8 (*continued*)

Item	Gene
69	*ISG20*
70	*LAP3*
71	*LGALS3BP*
72	*LY6E*
73	*MCUB*
74	*MSRB1*
75	*MX1*
76	*MX2*
77	*NEXN*
78	*NLRC5*
79	*NMI*
80	*NNMT*
81	*NT5C3A*
82	*OAS2*
83	*OAS3*
84	*OASL*
85	*OGFR*
86	*PARP12*
87	*PARP14*
88	*PARP9*
89	*PCDHGA4*
90	*PLSCR1*
91	*PML*
92	*PSMB8*
93	*PSMB9*
94	*RAMP3*
95	*RNF213*
96	*RSAD2*
97	*RTP4*
98	*SAMD9*

Table S8 (*continued*)

Table S8 (*continued*)

Item	Gene
99	*SAMD9L*
100	*SELENOP*
101	*SERPING1*
102	*SH3KBP1*
103	*SHISA5*
104	*SP100*
105	*SP110*
106	*SP140L*
107	*SPATS2L*
108	*STAT1*
109	*STAT2*
110	*TAP1*
111	*TAP2*
112	*TMEM140*
113	*TNFSF10*
114	*TRIM22*
115	*TRIM69*
116	*TXNIP*
117	*TYMP*
118	*UBB*
119	*UBE2L6*
120	*USP18*
121	*WARS*
122	*XAF1*
123	*XRN1*
124	*ZBP1*
125	*ZC3HAV1*
126	*ZNFX1*

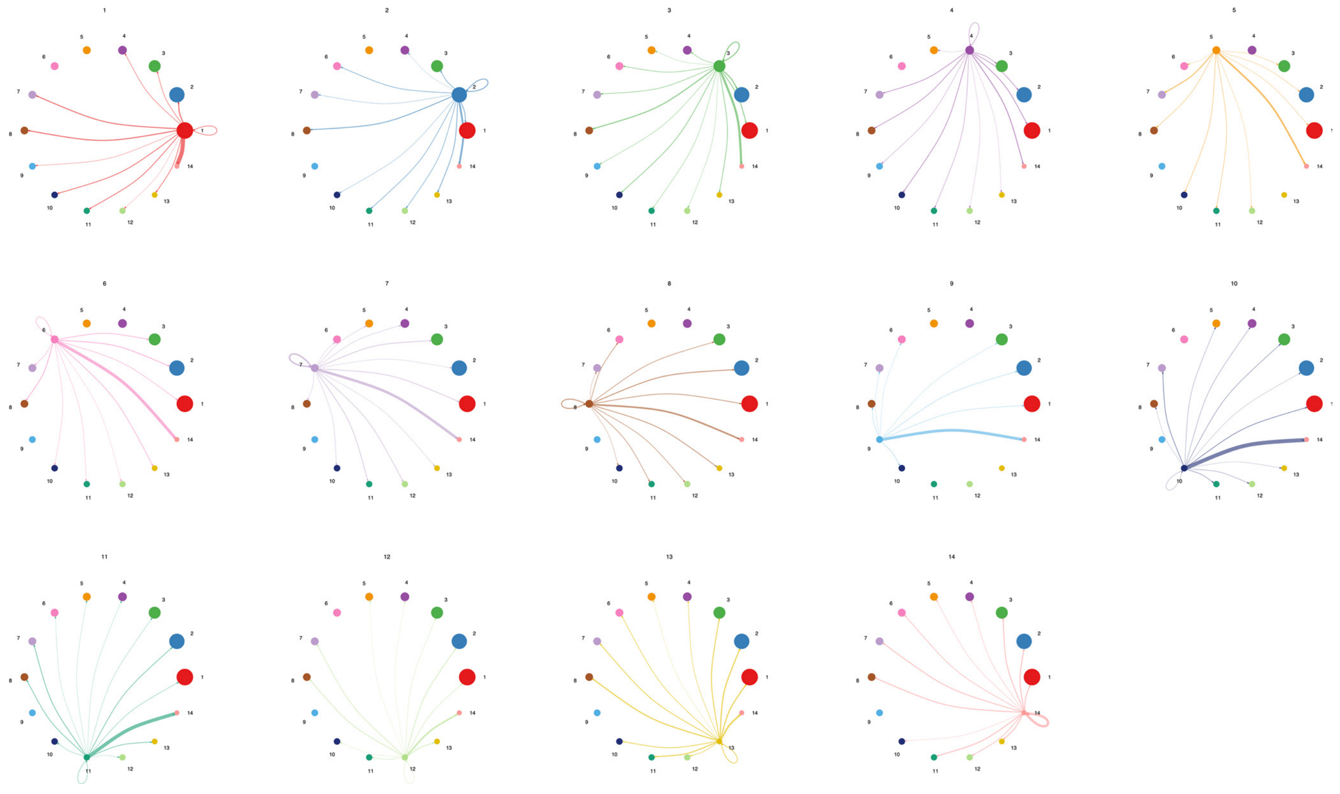


Figure S3 Cellular communication between functional subsets of cells.

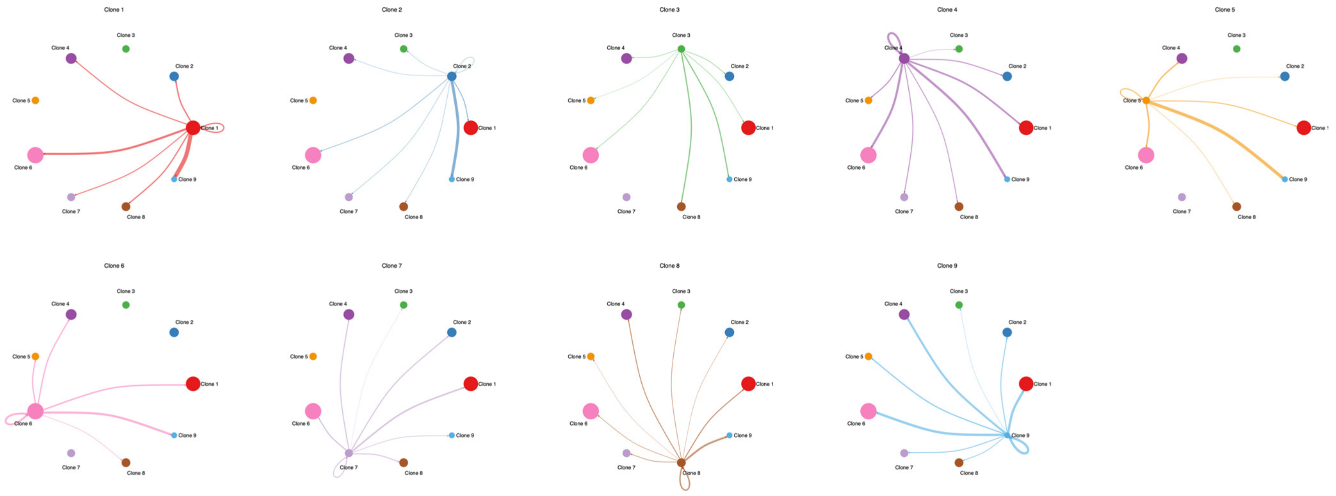
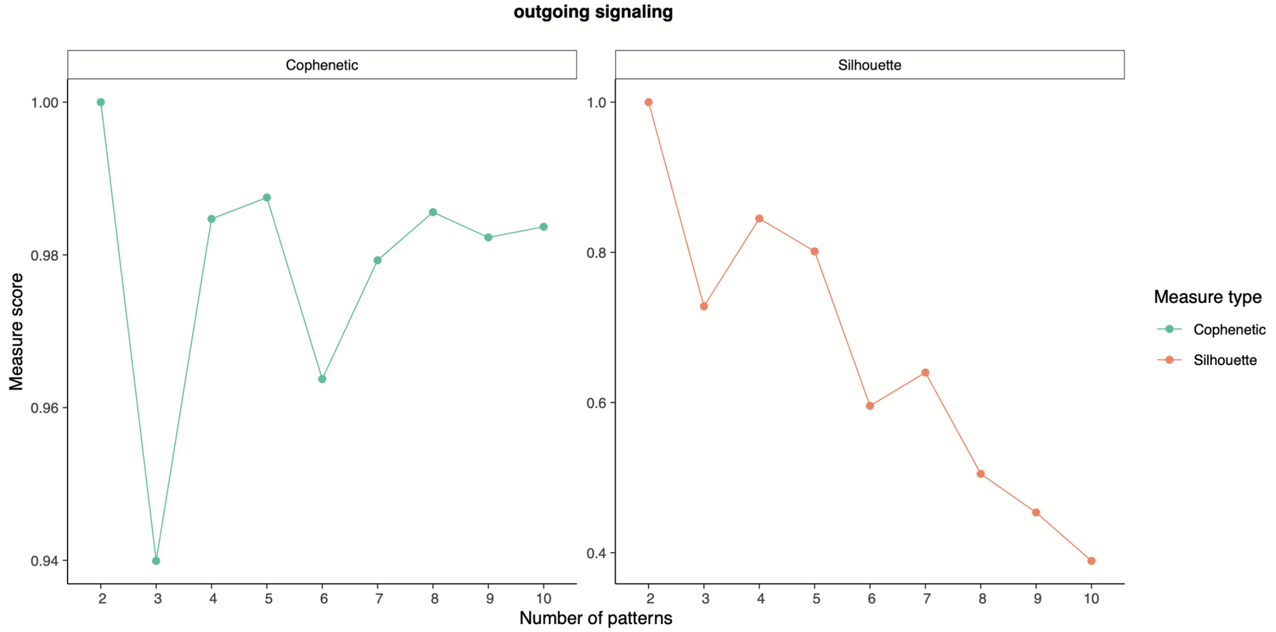


Figure S4 Cell communication between cell clones.

Subpopulation



Clone

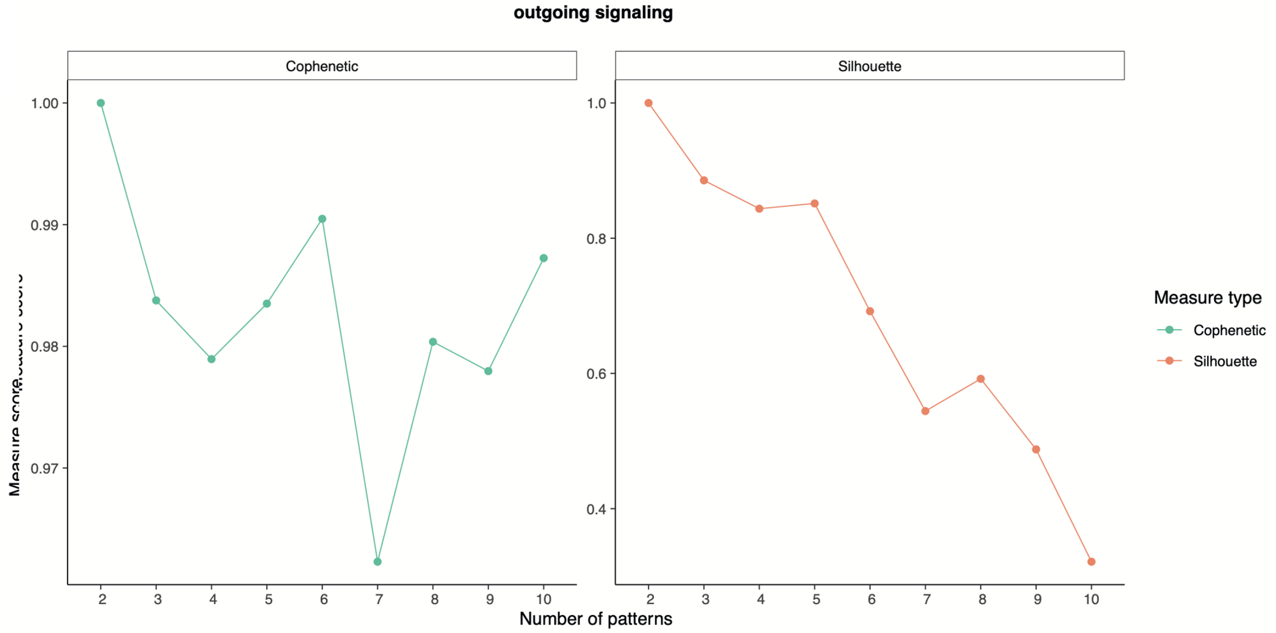


Figure S5 The function subset is determined with the outgoing pattern of the clone.

https://dx.doi.org/10.21037/tcr-2025-1019

Table S9 Key downstream pathway genes

Item	Gene
1	*ARHGEF15*
2	*BLK*
3	*CBL*
4	*CDK5*
5	*CRK*
6	*CRKL*
7	*EFNA1*
8	*EFNA2*
9	*EFNA3*
10	*EFNA5*
11	*EPHA1*
12	*EPHA2*
13	*EPHA3*
14	*EPHA4*
15	*EPHA5*
16	*EPHA6*
17	*EPHA7*
18	*EPHA8*
19	*FGR*
20	*FYN*
21	*HCK*
22	*LCK*
23	*LYN*
24	*NGEF*
25	*PIK3CG*
26	*PIK3R5*
27	*PIK3R6*
28	*PLCG1*
29	*RHOA*
30	*ROCK1*
31	*SRC*
32	*VAV2*
33	*VAV3*
34	*YES1*
35	*AFDN*
36	*CDC42*
37	*CDH1*
38	*CLDN1*
39	*CRK*
40	*CTNNA1*
41	*CTNNB1*
42	*F11R*
43	*FARP2*
44	*IQGAP1*
45	*ITGAV*
46	*ITGB3*
47	*NECTIN1*
48	*NECTIN2*
49	*NECTIN3*
50	*PDGFB*
51	*PDGFRB*
52	*PIK3CA*
53	*PIK3R1*
54	*PIP5K1C*
55	*PTK2*
56	*PTPRM*
57	*PVR*
58	*RAC1*
59	*RAP1A*
60	*RAP1B*
61	*RAPGEF1*
62	*SRC*
63	*TLN1*
64	*VAV2*
65	*CD99*
66	*APP*
67	*MPZ*

Table S9 (*continued*)