

Supplementary material

Inferring absolute cell proliferation and death rates from non-longitudinal single-cell transcriptomics

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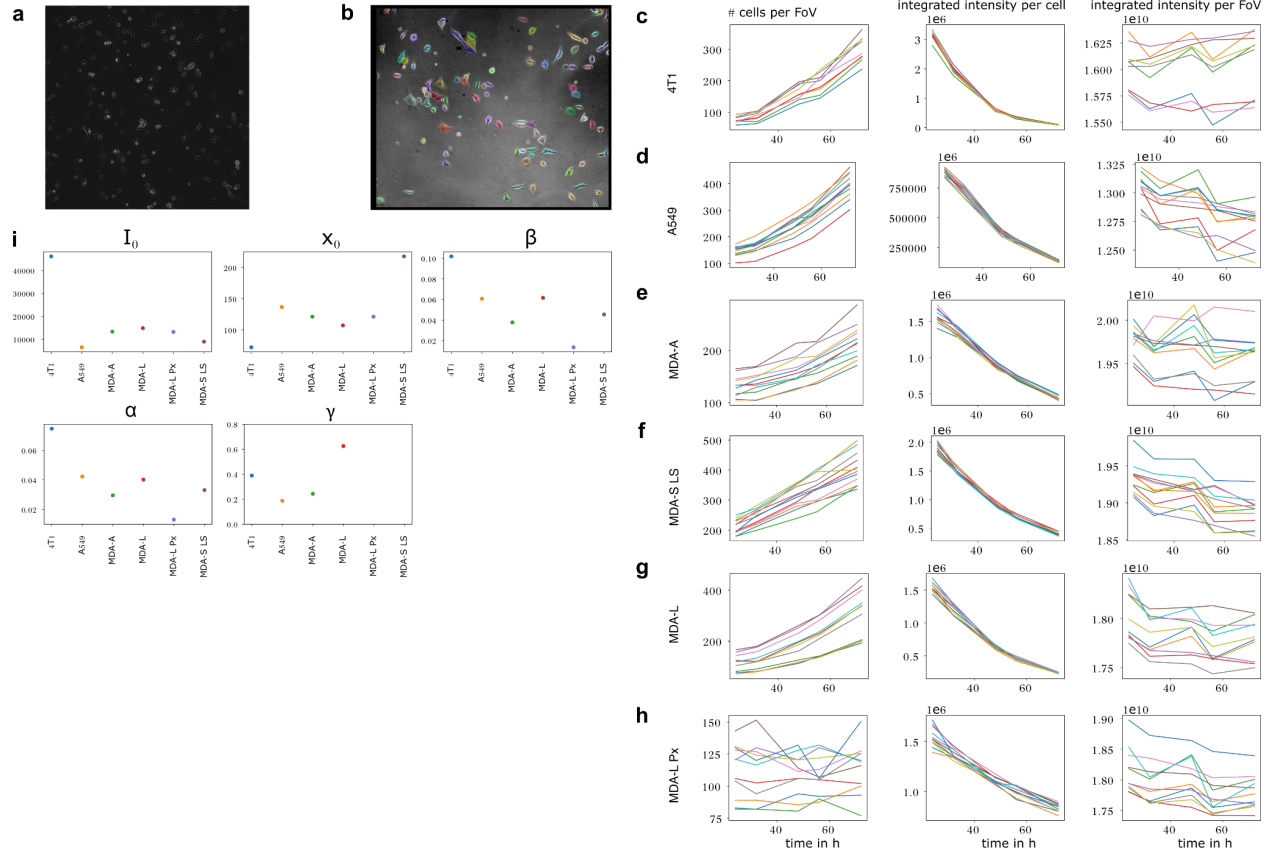


Figure S1 Proliferation and death rates in 6 cell cultures by longitudinal microscopy.

a. Representative brightfield image. **b.** Example of segmentation of the brightfield image by CellPose. Each segmented cell appears in a different color. **c-h.** Per well time dynamics of the number of cells per field of view (FoV), median CFSE intensity per segmented cell which are used as inputs of the model. The integrated image intensity per FoV stays roughly constant and is shown here as a validation of our model assumption that the total CFSE signal is conserved, except for signal loss through cell death.. These are used as an input to infer cell dynamics parameters - proliferation, death, and more (see panel i). **i.** Model parameters inferred from the longitudinal microscopy data of panels c-h. Parameters are defined in Equation 9 (Methods). I_0 : median CFSE intensity per cell at time $t=0h$. x_0 : number of cells per field of view at time $t=0h$. β : proliferation rate, unit: 1/h. α : death rate, unit: 1/h. γ : clearance rate of dead cells, unit: 1/h.

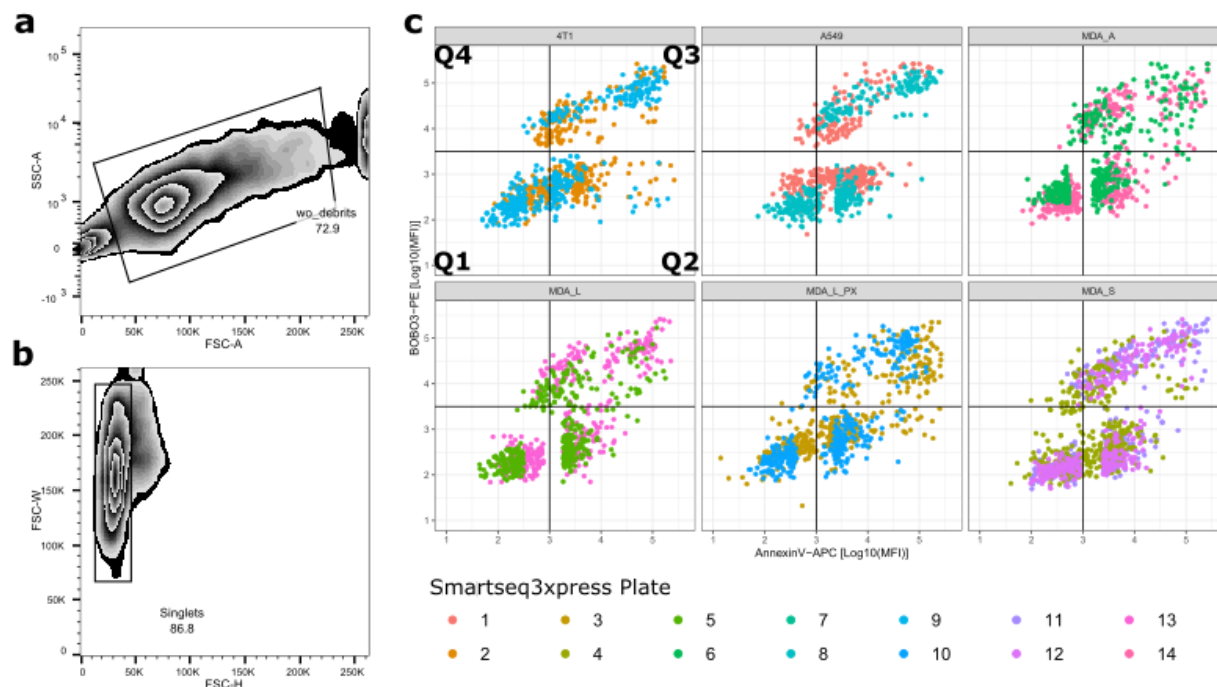


Figure S2 To define a transcriptional signature of cell death independently of the death pathway, we performed scRNAseq on sorted populations of live vs dying/dead cells. **a.** Cells were gated to remove small size debris and clumped cells. **b.** Following that, cells were gated to remove doublets. **c.** Subsequent gating defined live (Q1, AnnexinV-APC- BOBO3-), early apoptotic (Q2, AnnexinV-APC+ BOBO3-), late apoptotic (Q3, AnnexinV-APC+ BOBO3+) and necrotic (Q4, AnnexinV-APC- BOBO3+) cells for each cell line. Different plates contributed to all live-dead states. The high prevalence of dead/dying cells originates is due to us intentionally enriching them by FACS, not to low viability in the cell cultures. Panel: cell culture. Colors: 384-well Smartseq3xpress plate. PX = 1 μ M paclitaxel.

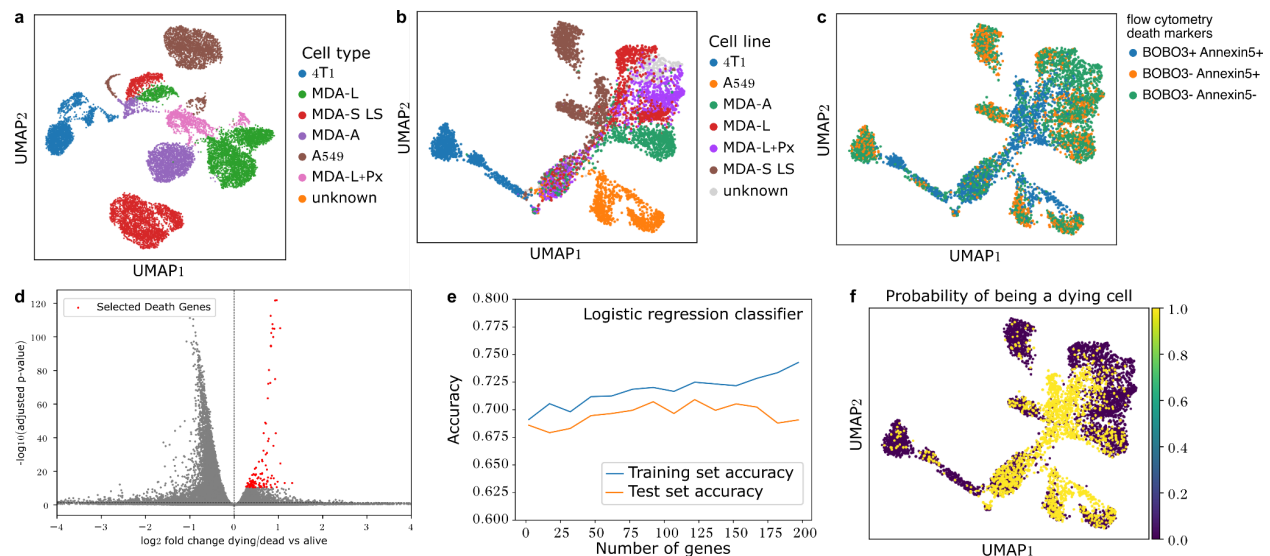


Figure S3 Expression of 122 genes discriminated and optimally classified live vs dead and dying cells across the 6 cell cultures. **a.** UMAP projection of single-cell transcriptomes from 3' end gene expression profile (10x Genomics) used to associate transcriptomes to proliferation and death rates. Single-cells cluster by cell lines and growth condition, as expected from a successful scRNAseq experiment. Unknown cell type: for a small fraction of cells, the multiplexing barcode could not be sequenced. These cells could thus not be assigned to their condition and were discarded. **b.** To identify generic transcriptional signatures of dying and dead cells, live and dying/dead cells were isolated by FACS (Fig. S2c) and their transcriptomes profiled by SmartSeq3xpress profiling. Unknown cell type: for a small fraction of cells, the well barcode could not be sequenced. These cells could thus not be assigned to their condition and were discarded. Axes: UMAP projection. Color: cell culture. **c.** Same as b., but colored by markers of apoptosis (Annexin5) and necrosis (BOBO3). **d.** Comparing expression in dying/dead cells vs live cells identified genes consistently up-regulated in dying/dead cells across cell cultures. P-value from t-test. **e.** From co-profiling of cell death markers and single-transcriptomes, a logistic regression model was trained to classify live vs dying/dead cells based on gene sets of increasing size. A set of 122 genes achieved highest accuracy on the test set. **f.** The probability of being a dead cell estimated by the logistic regression model overlaps with flow cytometry markers of dying dead cells (panel c).

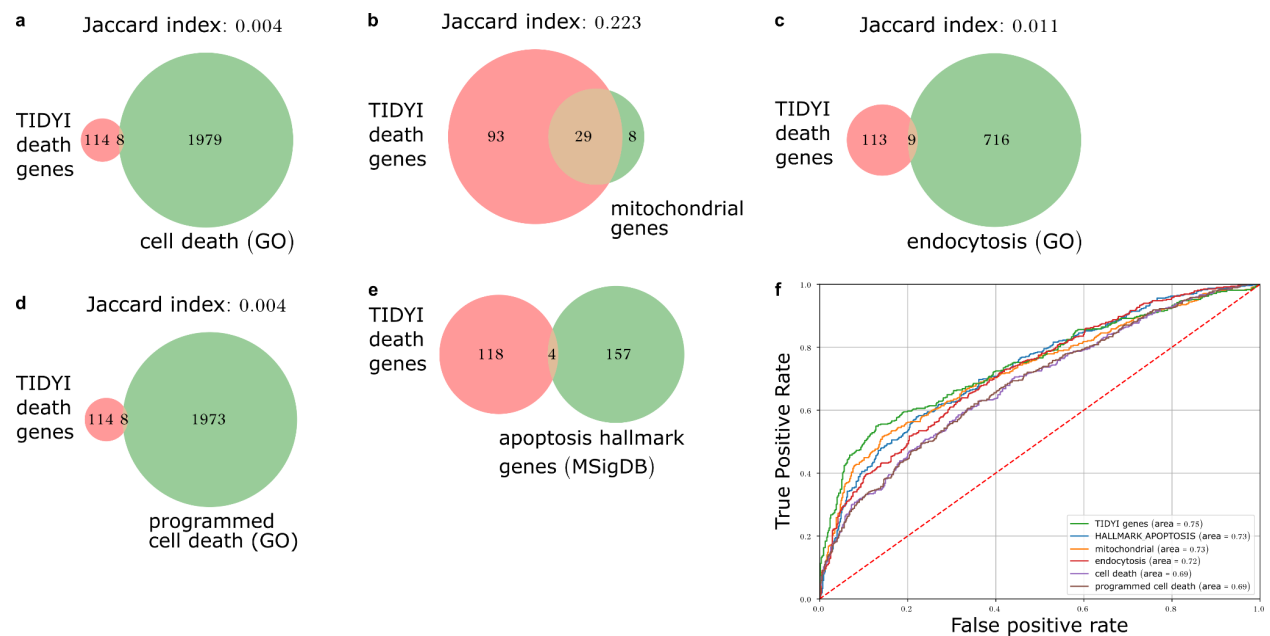


Figure S4 a-e. The 122 genes that discriminate and optimally classify live vs dead/dying cells across the 6 cell cultures (Fig S3) show low overlap with cell death genes, and overlap with previously identified markers of low-quality cells (mitochondrial genes). **f.** The 122 gene signature best classifies dead/dying cells vs live cells out of other established gene signatures.

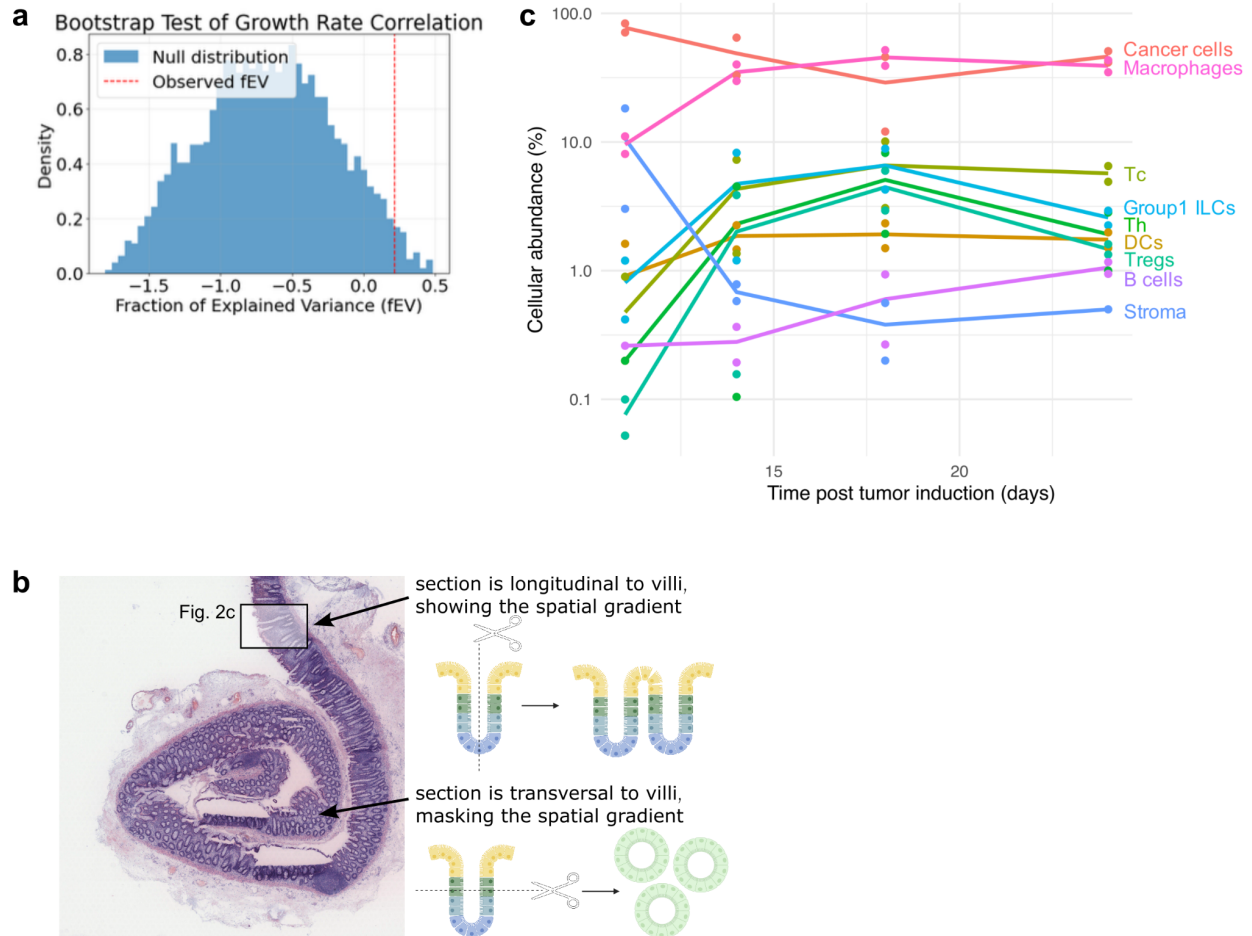


Figure S5 TIDYI recovers the known proliferation-death dynamics of homeostatic, expanding and shrinking tissues. **a.** We tested whether TIDYI predicted measured tumor growth rates beyond what is expected by chance using a bootstrapping approach. To do so, bootstrap testing was performed by randomly permuting the TIDYI growth rates relative to the BLI growth rates and recalculating the fraction of explained variance (fEV) for each shuffle. The observed fEV was then compared to this null distribution to assess its statistical significance. **b.** A region of the gut in which villi are sectioned longitudinally was selected to examine the spatial gradient of TIDYI proliferation and death signatures. There can be no spatial gradient in regions where villi were sectioned transversally. **c.** In the longitudinal tumor scRNAseq data of Gsell et al., stromal cells are lost relative to cancer cells over time. Immune cells have high prevalence (~50% of all cells). Cell typing and temporal dynamics: original study.

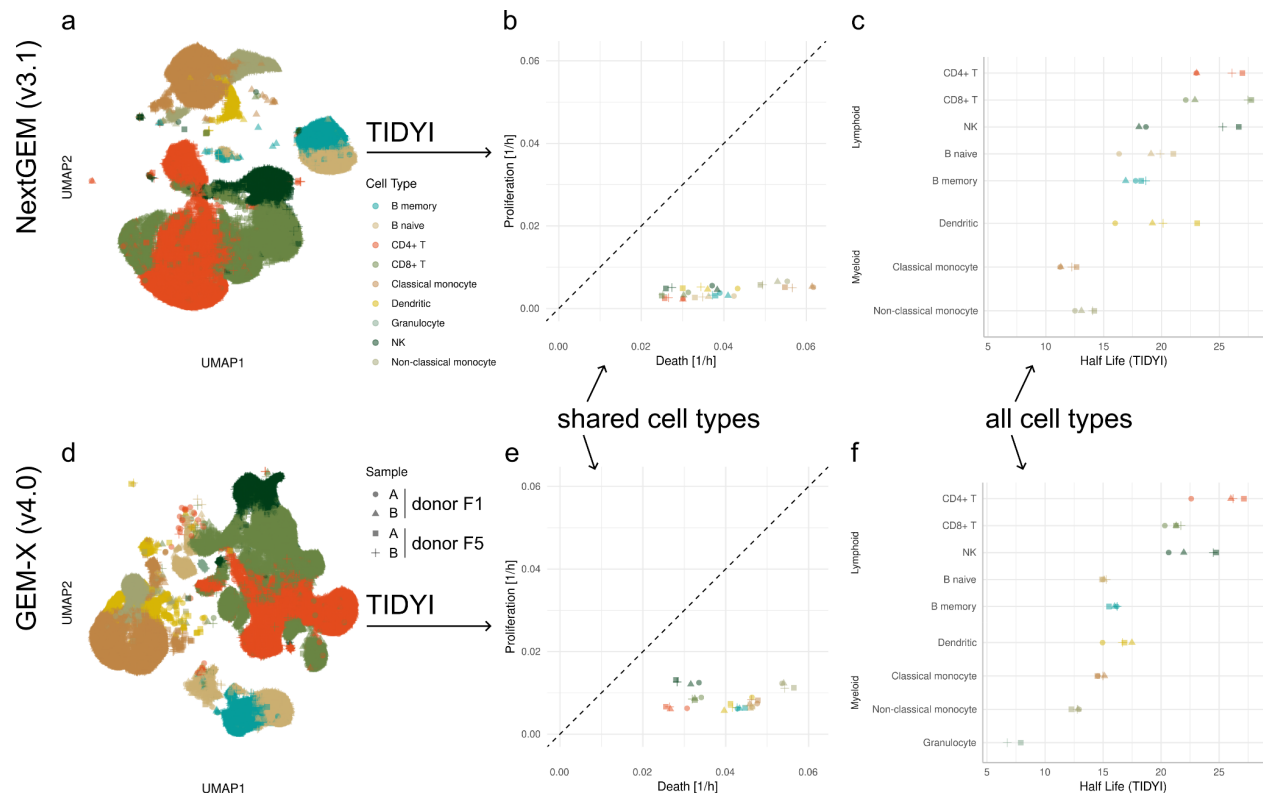


Figure S6 Performing TIDYI on human peripheral blood immune cells validates that immune cells proliferate little in the blood, that lymphoid cells are longer lived than myeloid cells, and that rate estimates are consistent across scRNAseq protocols and replicates. **a.** UMAP projection of the single-cell transcriptional profiles of 50,766 cells. Color: cell type. Shape: donor and technical replicate. **b.** Proliferation and death rates inferred by TIDYI suggest little proliferation among blood immune cells, consistent with their known genesis and proliferation in other compartments (bone marrow, peripheral infected tissue, lymph nodes, ...). Dots: cell types in different donors and replicates. **c.** TIDYI accurately estimates that myeloid cells are shorter lived than lymphoid cells. This is consistent with the role that lymphoid cells play in adaptive immune memory, thus requiring longer life spans than myeloid cells of the innate immune system. **d-f.** Same for 95,666 human peripheral blood immune cells. Data: Elz et al.¹.

Table S1 Top 200 genes discriminating between live vs dying/dead cells across 6 cell cultures. The first 122 genes optimized test set accuracy in classifying dead cells. Score: z-score. p-value: t-test comparing expression in dying/dead vs live cells. Adjusted p-value: false-discovery rate (Benjamini-Hochberg).

	Gene symbol	Score (z-score)	Log2 fold change	p-value	Adjusted p-value
0	MT-ND4L	24.94066	0.95959103	5.65E-127	1.53E-122
1	MT-CO3	24.88137	0.9254645	1.61E-126	2.17E-122
2	MT-CO1	23.8767	0.8245061	3.24E-117	2.91E-113
3	MT-ATP8	23.284239	0.8656687	6.35E-112	2.85E-108
4	MT-ND6	23.006527	1.0387713	2.05E-109	6.93E-106
5	MT-CO2	22.984577	0.8703126	3.46E-109	1.04E-105
6	MTCO1P12	22.941647	0.90795314	5.38E-109	1.45E-105
7	MT-CYB	22.670128	0.83794755	1.98E-106	4.45E-103
8	MT-RNR1	22.348156	0.8836431	6.18E-104	1.19E-100
9	MT-ND5	21.741798	0.83021146	1.35E-98	1.66E-95
10	MT-RNR2	21.689856	0.8299637	2.78E-98	3.26E-95
11	MTND2P28	21.672709	0.832038	3.37E-98	3.79E-95
12	MT-ND1	19.866695	0.78721845	1.20E-83	5.42E-81
13	MT-TS2	19.166939	0.9251042	4.32E-78	1.32E-75
14	MT-ND3	18.832218	0.8161499	8.43E-76	2.39E-73
15	MT-ATP6	18.76423	0.7696822	3.05E-75	8.31E-73
16	MT-ND2	17.546812	0.75996107	2.27E-66	3.55E-64
17	MT-TM	15.35279	0.70243263	1.42E-51	1.04E-49
18	MT-ND4	15.244308	0.7167931	5.05E-51	3.60E-49
19	MT-TS1	14.309895	0.94017553	4.18E-45	2.16E-43
20	MT-TP	14.293876	0.666166	3.69E-45	1.91E-43
21	MTCO2P12	13.708907	0.77989906	1.00E-41	4.27E-40
22	MTCO3P12	13.448419	0.76466995	2.68E-40	1.07E-38
23	MT-TY	12.943311	0.88646805	2.07E-37	7.25E-36
24	MTATP6P1	12.369338	0.66289693	1.71E-34	5.20E-33
25	MT-TF	12.122069	0.7427994	3.64E-33	1.05E-31
26	MT-TL1	11.927076	0.71267945	3.42E-32	9.36E-31
27	MT-TE	11.26495	0.6301697	5.85E-29	1.36E-27
28	MTND6P3	11.076671	0.6378556	4.70E-28	1.05E-26
29	MT-TH	11.011988	0.5590276	9.26E-28	2.03E-26
30	MTND6P4	10.810295	1.0442448	9.65E-27	2.00E-25

31	LAMB1	10.526579	0.7131328	1.58E-25	3.07E-24
32	ITGA3	10.217605	0.49482155	3.43E-24	6.24E-23
33	APP	10.060534	0.46614748	1.64E-23	2.91E-22
34	MTRNR2L8	9.947344	0.7396765	5.21E-23	8.99E-22
35	NOMO2	9.42386	0.6343406	7.84E-21	1.21E-19
36	MTND1P23	9.305844	0.6270748	2.24E-20	3.39E-19
37	MTRNR2L12	9.303804	0.59469354	2.26E-20	3.40E-19
38	ATP6AP2	9.2750635	0.43595862	3.01E-20	4.49E-19
39	MALAT1	9.236557	0.49411455	4.16E-20	6.17E-19
40	MYADM	9.210878	0.45116267	5.31E-20	7.84E-19
41	PDIA3	9.134356	0.4066095	1.09E-19	1.57E-18
42	ASPH	9.087481	0.47924653	1.59E-19	2.29E-18
43	ABCC3	9.034723	0.8525512	2.74E-19	3.88E-18
44	TCIRG1	8.777149	0.55019224	2.54E-18	3.42E-17
45	MTRNR2L1	8.751813	0.7634108	3.28E-18	4.36E-17
46	COL18A1	8.620276	0.83178854	1.03E-17	1.34E-16
47	FKBP10	8.611877	0.8948793	1.08E-17	1.39E-16
48	NCLN	8.585982	0.52809614	1.33E-17	1.71E-16
49	TGFBI	8.560648	0.59600204	1.64E-17	2.09E-16
50	GANAB	8.547338	0.34933186	1.85E-17	2.36E-16
51	SCARB1	8.412076	0.6764148	5.86E-17	7.27E-16
52	LAPTM4B	8.284524	0.42062613	1.64E-16	1.97E-15
53	NPIP5	8.254443	0.637717	2.19E-16	2.62E-15
54	MT-TN	8.212627	0.75102586	3.00E-16	3.56E-15
55	OS9	8.177175	0.38245997	4.00E-16	4.71E-15
56	CYBA	8.11758	0.3613018	6.46E-16	7.52E-15
57	MTCYBP18	8.0622835	0.74709266	1.06E-15	1.22E-14
58	PON2	8.06012	0.7561503	1.03E-15	1.19E-14
59	STT3B	8.058082	0.3722528	1.04E-15	1.20E-14
60	PCYOX1	8.049974	0.43203747	1.12E-15	1.29E-14
61	TMEM259	8.042963	0.47506782	1.18E-15	1.36E-14
62	SPP1	8.041185	0.9817146	1.22E-15	1.40E-14
63	CD81	8.006156	0.40931988	1.58E-15	1.79E-14
64	LENG8	7.875803	0.4394621	4.47E-15	4.94E-14
65	GLG1	7.819947	0.3960475	6.88E-15	7.49E-14
66	STRA6	7.8053575	1.3101159	8.35E-15	9.07E-14
67	MT-TL2	7.7987556	1.1414222	8.49E-15	9.21E-14
68	PRKCSH	7.776981	0.30870786	9.65E-15	1.04E-13
69	COL7A1	7.7704372	0.57351303	1.02E-14	1.10E-13

70	CD44	7.760179	0.29927182	1.10E-14	1.19E-13
71	MT-TV	7.7287717	0.45585826	1.37E-14	1.47E-13
72	MT-TD	7.726196	0.47536486	1.41E-14	1.51E-13
73	MT-TR	7.6781864	0.665416	2.10E-14	2.22E-13
74	AGRN	7.668081	0.49386352	2.24E-14	2.37E-13
75	PDIA4	7.6498723	0.36939606	2.56E-14	2.70E-13
76	COL6A2	7.639105	0.72567695	2.83E-14	2.96E-13
77	MTATP8P1	7.6362653	0.6694691	2.90E-14	3.04E-13
78	NUP210	7.6219625	0.9234732	3.24E-14	3.38E-13
79	SREBF1	7.6017346	0.6751768	3.75E-14	3.90E-13
80	TSPAN4	7.5230937	0.33681354	6.70E-14	6.87E-13
81	ACSL3	7.5162373	0.41336158	7.09E-14	7.25E-13
82	SLC2A1	7.4969044	0.377214	8.17E-14	8.32E-13
83	SLC38A10	7.450583	0.5574224	1.16E-13	1.17E-12
84	CA12	7.4269314	0.8226232	1.40E-13	1.40E-12
85	EBP	7.424861	0.37081903	1.40E-13	1.40E-12
86	MPDU1	7.4219723	0.32049125	1.43E-13	1.44E-12
87	CLSTN1	7.4065633	0.42617622	1.61E-13	1.61E-12
88	SPDYE2	7.3917265	0.66601056	1.82E-13	1.81E-12
89	PLPP2	7.373435	0.42702413	2.06E-13	2.04E-12
90	CRIM1	7.3727984	0.40225658	2.06E-13	2.04E-12
91	TMED7	7.348677	0.42884547	2.46E-13	2.42E-12
92	PLOD1	7.3374324	0.41133156	2.67E-13	2.62E-12
93	6-Mar	7.3277617	0.39597264	2.88E-13	2.81E-12
94	EMC10	7.3126154	0.5765065	3.27E-13	3.18E-12
95	MET	7.2953334	0.36855182	3.64E-13	3.53E-12
96	SPG7	7.292242	0.44407478	3.75E-13	3.63E-12
97	HSPG2	7.2915025	0.67540526	3.83E-13	3.70E-12
98	DCBLD2	7.287997	0.39023158	3.83E-13	3.70E-12
99	TSPAN3	7.2157974	0.37194735	6.47E-13	6.18E-12
100	GJA1	7.1967974	0.60162526	7.53E-13	7.17E-12
101	APMAP	7.165182	0.2984173	9.37E-13	8.87E-12
102	HSP90B1	7.1631985	0.28268912	9.54E-13	9.03E-12
103	TMEM245	7.1518197	0.35327798	1.03E-12	9.73E-12
104	PFAS	7.1477523	0.43256375	1.07E-12	1.01E-11
105	IGF2R	7.1220164	0.3735415	1.28E-12	1.19E-11
106	RPN2	7.1045446	0.2701013	1.45E-12	1.35E-11
107	VPS13C	7.1042624	0.5930632	1.46E-12	1.36E-11
108	RPN1	7.0929894	0.29219833	1.57E-12	1.46E-11

109	TMEM30A	7.0761943	0.36154273	1.77E-12	1.64E-11
110	AL390728.6	7.0689864	0.73511463	1.91E-12	1.77E-11
111	AC015813.1	7.062697	0.6184257	1.97E-12	1.82E-11
112	NEO1	7.0531073	0.68371034	2.13E-12	1.96E-11
113	SLC2A6	7.031217	0.58261555	2.45E-12	2.25E-11
114	LOXL2	7.0302763	0.3450516	2.45E-12	2.24E-11
115	COL5A2	7.0148234	0.9620949	2.81E-12	2.56E-11
116	CNTN1	7.003814	0.83903813	2.98E-12	2.72E-11
117	COL4A2	7.003591	0.4834653	2.97E-12	2.70E-11
118	GAA	6.99445	0.59573054	3.19E-12	2.89E-11
119	SDC1	6.9887333	0.44381607	3.28E-12	2.98E-11
120	NRCAM	6.965286	0.83912295	3.92E-12	3.53E-11
121	SNX14	6.964105	0.4222483	3.93E-12	3.54E-11
122	ADGRE5	6.963911	0.39028075	3.93E-12	3.54E-11
123	RDH11	6.9473915	0.299369	4.39E-12	3.93E-11
124	ZNF331	6.946303	0.5536565	4.51E-12	4.03E-11
125	FTX	6.94059	0.5810515	4.69E-12	4.19E-11
126	DST	6.9251714	0.33482784	5.13E-12	4.58E-11
127	TPP1	6.9209075	0.44217533	5.28E-12	4.71E-11
128	CD151	6.9087844	0.2850064	5.74E-12	5.10E-11
129	PLOD3	6.9066806	0.42770106	5.88E-12	5.22E-11
130	ADAM10	6.8867364	0.33553693	6.72E-12	5.95E-11
131	CCDC14	6.876796	0.48281178	7.23E-12	6.39E-11
132	HACD2	6.8622746	0.46557218	7.97E-12	7.02E-11
133	COL27A1	6.8594775	0.64095527	8.22E-12	7.23E-11
134	MT-TC	6.8525534	0.8579205	8.68E-12	7.60E-11
135	KDELR1	6.8379073	0.2837961	9.39E-12	8.20E-11
136	SYNGR2	6.831047	0.3589614	9.86E-12	8.60E-11
137	MT-TQ	6.8296747	0.65845674	1.00E-11	8.72E-11
138	GOLGA8B	6.811949	0.52658445	1.13E-11	9.77E-11
139	AC159540.2	6.7894893	0.7305338	1.32E-11	1.14E-10
140	SLC6A6	6.7756634	0.43850347	1.44E-11	1.24E-10
141	STEAP3	6.772553	0.42876396	1.48E-11	1.27E-10
142	LGALS3BP	6.7453837	0.2821858	1.77E-11	1.50E-10
143	PLOD2	6.7252493	0.41673213	2.03E-11	1.72E-10
144	HERC2P2	6.7093706	0.44912368	2.26E-11	1.90E-10
145	COCH	6.70466	1.0747436	2.41E-11	2.02E-10
146	ABHD2	6.703213	0.3707439	2.37E-11	1.99E-10
147	RTN3	6.690706	0.27206266	2.57E-11	2.16E-10

148	AHNAK2	6.6750507	0.40679723	2.84E-11	2.37E-10
149	GNS	6.67019	0.3644802	2.95E-11	2.46E-10
150	RNF149	6.6696258	0.41890666	2.95E-11	2.46E-10
151	STAG3L3	6.6641045	0.49372572	3.09E-11	2.57E-10
152	POR	6.652652	0.40281427	3.31E-11	2.75E-10
153	HAVCR1	6.6496415	1.23611	3.47E-11	2.88E-10
154	CXCL5	6.633603	0.87781686	3.77E-11	3.12E-10
155	MELTF	6.629326	0.563357	3.91E-11	3.23E-10
156	RRBP1	6.5920777	0.31717646	4.96E-11	4.06E-10
157	ABCC2	6.5910788	0.77014583	5.03E-11	4.12E-10
158	HKDC1	6.58556	0.6217197	5.24E-11	4.29E-10
159	DGCR2	6.568929	0.52207667	5.85E-11	4.76E-10
160	ASPM	6.5670395	0.5075888	5.87E-11	4.78E-10
161	SEMA4B	6.563051	0.54971886	6.06E-11	4.92E-10
162	P3H3	6.5558195	1.1140841	6.53E-11	5.30E-10
163	NOMO1	6.5383444	0.35878694	7.12E-11	5.75E-10
164	COL4A5	6.5358047	0.71881217	7.28E-11	5.88E-10
165	MTCO1P40	6.530147	0.6857234	7.57E-11	6.11E-10
166	ALDH1A1	6.5174813	0.8126325	8.08E-11	6.50E-10
167	C17orf62	6.51504	0.38556242	8.28E-11	6.65E-10
168	GALNT14	6.508517	0.6772806	8.67E-11	6.96E-10
169	CIT	6.4891295	0.48758036	9.87E-11	7.89E-10
170	ATP2A2	6.480929	0.2778898	1.03E-10	8.23E-10
171	LAMA5	6.4800997	0.5000577	1.04E-10	8.32E-10
172	LMF2	6.475717	0.42810002	1.08E-10	8.56E-10
173	CYP24A1	6.473982	0.68739307	1.09E-10	8.63E-10
174	PLBD2	6.4677167	0.41375807	1.13E-10	8.98E-10
175	NUCB1	6.466104	0.32559344	1.14E-10	9.05E-10
176	ABCC1	6.458512	0.4820879	1.20E-10	9.54E-10
177	ERBB2	6.45707	0.5388719	1.23E-10	9.73E-10
178	GTF3C1	6.4536853	0.43420154	1.24E-10	9.83E-10
179	PILRB	6.448906	0.8533556	1.31E-10	1.03E-09
180	SRPX	6.4419956	0.63123137	1.34E-10	1.05E-09
181	EPHB2	6.434918	0.44207788	1.40E-10	1.10E-09
182	AHNAK	6.421301	0.28040957	1.53E-10	1.20E-09
183	OSMR	6.409525	0.42888913	1.65E-10	1.29E-09
184	PROCR	6.408034	0.34780633	1.66E-10	1.30E-09
185	SLC27A2	6.407939	1.1675622	1.70E-10	1.33E-09
186	NPIP4	6.389238	0.5906413	1.90E-10	1.48E-09

187	MIR16-2	6.3848343	0.79084325	1.96E-10	1.52E-09
188	MMP7	6.378044	0.9912295	2.05E-10	1.59E-09
189	ADPGK	6.3742228	0.40500113	2.07E-10	1.61E-09
190	TFRC	6.372249	0.25689417	2.10E-10	1.63E-09
191	HACD3	6.3692036	0.27643642	2.14E-10	1.66E-09
192	ARHGAP11B	6.360773	0.54680663	2.28E-10	1.76E-09
193	ARL6IP1	6.358463	0.32091114	2.28E-10	1.76E-09
194	AKR1C2	6.3429327	0.7793359	2.52E-10	1.94E-09
195	FN1	6.3423433	0.42334434	2.54E-10	1.95E-09
196	CPD	6.333567	0.3209834	2.68E-10	2.06E-09
197	AKR1B10	6.3118224	0.78388387	3.07E-10	2.35E-09
198	ELOVL5	6.2931147	0.2809626	3.49E-10	2.66E-09
199	TMEM51	6.258672	0.6146429	4.38E-10	3.32E-09

Table S2: Software and versions

Software/package	version	Company	City	State	Country
Cellpose	2.2.2				
CellProfiler	4.2.1				
R	4.0.3				
Rstudio	1.3.1073				
Zen Blue	3.3	Zeiss	Oberkochen		Germany
Zen Blue	3.5	Zeiss	Oberkochen		Germany
Axiovision	4.8	Zeiss	Oberkochen		Germany
Excel	2016	Microsoft			
Omega	1.11	BMG Labteck	Ortenberg		Germany
Inkscape	1.0.2-2	Inkscape			
ggplot2	3.3.5				
tidyverse	1.3.1				
plotly	4.10.0				
ggpubr	0.4.0				
readxl	1.3.1				
readr	2.1.2				

Table S3:

Product	Reference	Supplier	City	State	Country
MycoXpert	MYX_B	Nordic Biolabs	Taby		Sweden
DMEM/HIGH with 4.0mM L-glut, with Sodium Pyruvate	SH30243.LS	Nordic Biolabs	Taby		Sweden
HyClone FBS, EU approved, Heat Inactivated, South American	SV30160.03HI	Nordic Biolabs	Taby		Sweden
Penicillin-Streptomycin Solution	SV30010	Nordic Biolabs	Taby		Sweden
MDA-MB-231	ATCC-HTB-26	LGC	Teddington		UK
4T1; Mammary Tumor; Mouse (Mus musculus)	ATCC-CRL-2539	LGC	Teddington		UK
CELLTRACE CFSE	C34554	thermoScientific	ThermoScientific	Waltham	MA
PBS 1X 0.0067 M PO4, without Ca, Mg, Phenol Red, 6x1000 ml	SH30256.LS	Nordic Biolabs	Taby		Sweden
TC flask with Filter cap 75cm2 X2	90076	Nordic Biolabs	Taby		Sweden
TC Microplate 6 well, flat bottom, 4/bag	92406	NordicBiolabs	Taby		Sweden
PACLITAXEL	Y0000698	MERK	Kenilworth	NJ	USA
Countess™ Cell Counting Chamber Slides	C10312	ThermoScientific	Waltham	MA	USA
Falcon® 5 mL Round Bottom Polystyrene Test Tube, with Cell Strainer Snap Cap, 25/Pack, 500/Case	352235	Fisher Scientific	Waltham	MA	USA
Annexin V APC Ready Flow Conjugate	R37176	thermoScientific	Waltham	MA	USA
BOBO™-3 Iodide (570/602), 1 mM solution in DMSO	B3586	thermoScientific	Waltham	MA	USA
Chromium Next GEM Single Cell 3' GEM, Library & Gel Bead Kit v3.1, 4 rxns	PN-1000128	10X Genomics	Pleasanton	CA	USA

Table S4:

[illegible]

1. Elz, A. E. *et al.* Evaluating the practical aspects and performance of commercial single-cell RNA sequencing technologies. Preprint at <https://doi.org/10.1101/2025.05.19.654974> (2025).