

# Appendix B

## Additional information to Chapter 3

This Appendix contains supplementary figures for Chapter 3.

### B.1 Supplementary Figures

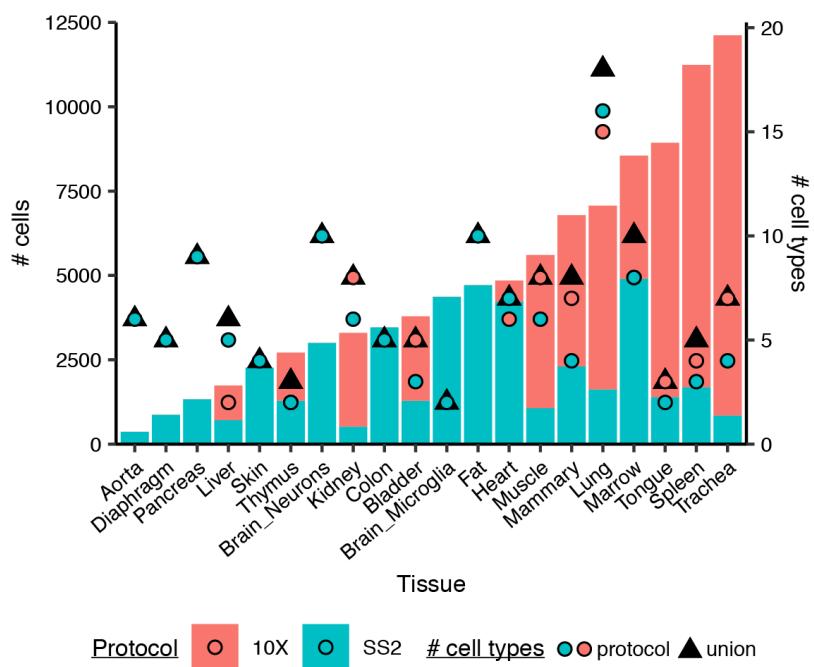


Fig. B.1: Cell numbers in the *Tabula Muris* dataset

Bars show number of cells (left y axis) collected from different tissues (x axis), split by scRNA-seq protocol (colour). Points show the number of cell types (right y axis) identified by protocol (coloured circles) or their union (triangle). 10X - Chromium (10X Genomics) protocol; SS2 - Smart-seq2 protocol.

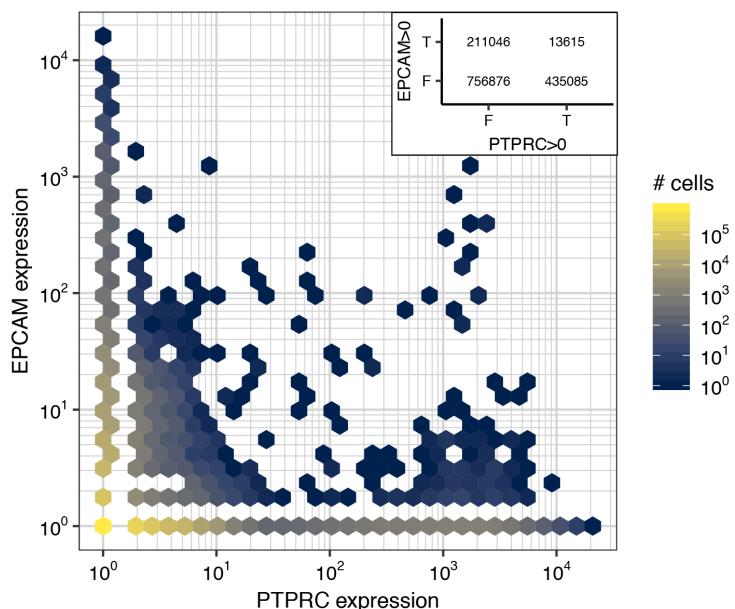
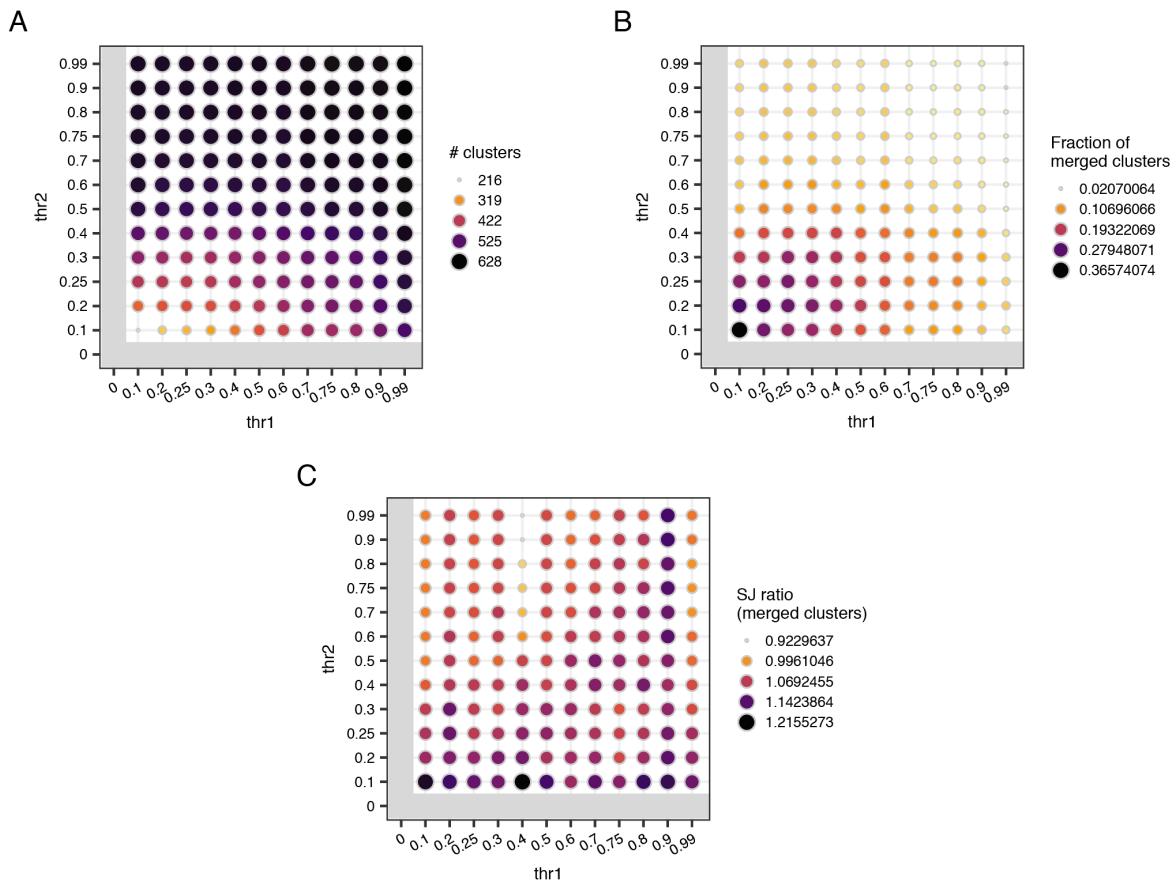
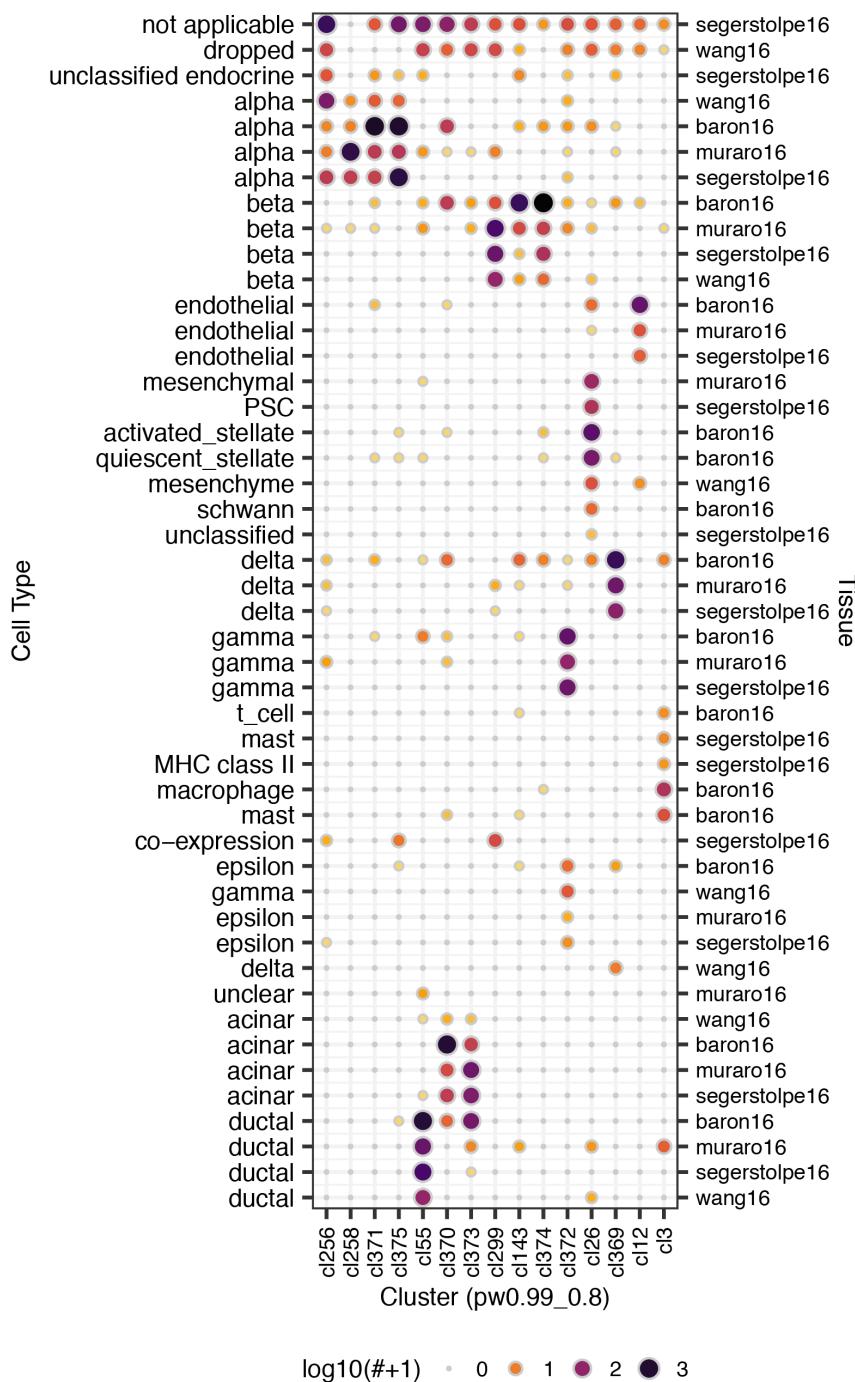


Fig. B.2: Expression of *PTPRC* and *EPCAM* in human data collection (Related to Figure 3.6)

2D-binned plot of single-cell expression of *PTPRC* (encoding for the CD45 receptor, an immune cell marker), and *EPCAM* (an epithelial cell marker). Inset table (top right) shows the number of cell expressing (T) or not (F) each of the genes. Cells expressing both genes are likely doublets or affected by ambient RNA in droplet-based experiments.

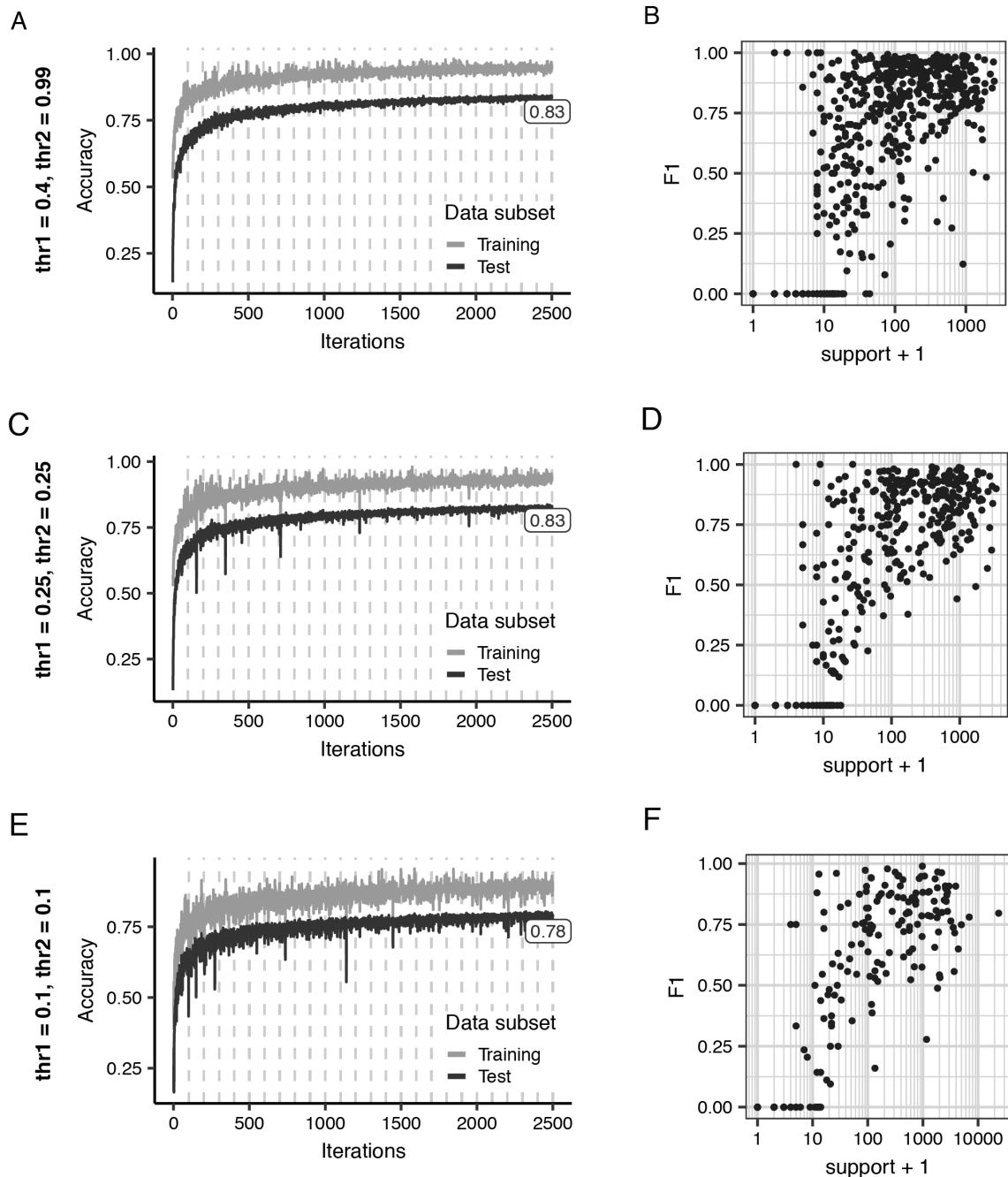


**Fig. B.3: *CellTypist* parameters grids with other statistics (Related to Figure 3.7)**  
 Parameter grids for *CellTypist* showing variation in (A) total number of clusters; (B) fraction of merged clusters; (C) SJ ratio calculated only for merged clusters.



**Fig. B.4: Grouping of annotated cell types and datasets in human pancreas data (Related to Figure 3.7)**

Number of cells of each cluster coming from a specific dataset (right y-axis), with a particular cell type annotation (left y-axis). Pancreas was used for this example due to the consistent cell type annotations used across datasets. *CellTypist* parameters:  $\text{thr1} = 0.99$ ;  $\text{thr2} = 0.8$ .



**Fig. B.5: Training statistics for other *CellTypist* models (Related to Figure 3.7)**  
 For each model trained ( $\text{thr1} = 0.4$  and  $\text{thr2} = 0.99$  - top;  $\text{thr1} = 0.25$  and  $\text{thr2} = 0.25$  - middle;  $\text{thr1} = 0.1$  and  $\text{thr2} = 0.1$  - bottom): (A, C, E) accuracy during model fitting for training and held-out test data; (B, D, F) F1-score for each cluster label (black dots) as a function of class size (in  $\log_{10}$  scale).

## B.2 Supplementary Tables

Table B.1: F1 scores and class sizes for *CellTypist* trained on the *Tabula Muris* with cell type labels. Cell type labels were obtained from the annotation accompanying the *Tabula Muris* gene expression data, described in the original publication.

Cell Type	F1 Score	Support (Test set)	Total Cells
Bergmann glial cell	1.00	3	30
brain pericyte	1.00	13	132
Brush cell of epithelium	1.00	4	45
proper of large intestine			
enteroendocrine cell	1.00	2	25
mesothelial cell	1.00	3	26
neuronal stem cell	1.00	4	36
pancreatic ductal cell	1.00	13	131
type II pneumocyte	1.00	18	183
microglial cell	1.00	433	4329
keratinocyte stem cell	1.00	137	1371
oligodendrocyte	1.00	119	1186
basal cell	0.99	167	1668
luminal epithelial cell	0.99	55	552
of mammary gland			
type B pancreatic cell	0.99	41	411
chondroblast	0.99	38	380
B cell	0.98	1237	12382
kidney tubule cell	0.98	218	2182
mesenchymal cell	0.98	184	1842
stromal cell	0.98	1261	12610
skeletal muscle satellite stem cell	0.98	44	442
neuron	0.98	20	196
oligodendrocyte precursor cell	0.97	20	202
mesenchymal stem cell of adipose	0.97	192	1924
basal cell of epidermis	0.97	652	6520
hematopoietic stem cell	0.97	267	2672
hepatocyte	0.97	141	1405
skeletal muscle satellite cell	0.97	90	895
pancreatic A cell	0.97	29	287
epithelial cell	0.97	102	1017
astrocyte of the cerebral cortex	0.96	40	403
Fraction A pre-pro B cell	0.96	24	240
endocardial cell	0.96	24	240
T cell	0.96	835	8346
keratinocyte	0.95	278	2777
epithelial cell of large intestine	0.95	179	1793
endothelial cell	0.95	692	6914
large intestine goblet cell	0.95	81	814

Table B.2: F1 scores and class sizes for *CellTypist* trained on the *Tabula Muris* with cell type labels. Cell type labels were obtained from the annotation accompanying the *Tabula Muris* gene expression data, described in the original publication. (continued)

Cell Type	F1 Score	Support (Test set)	Total Cells
fibroblast	0.95	248	2487
pancreatic D cell	0.95	9	91
pancreatic acinar cell	0.94	18	177
enterocyte of epithelium of large intestine	0.94	78	782
luminal cell of lactiferous duct	0.93	43	430
neutrophil	0.93	82	820
mesenchymal stem cell	0.93	163	1630
endothelial cell of hepatic sinusoid	0.92	20	196
epidermal cell	0.92	45	445
granulocyte	0.91	156	1559
monocyte	0.91	106	1056
neuroendocrine cell	0.90	54	543
Kupffer cell	0.89	5	51
fenestrated cell	0.88	41	414
cardiac muscle cell	0.87	22	223
smooth muscle cell	0.87	37	367
natural killer cell	0.85	117	1168
macrophage	0.85	194	1924
leukocyte	0.84	187	1878
bladder cell	0.84	146	1455
erythrocyte	0.81	21	208
ciliated cell	0.80	5	55
ciliated epithelial cell	0.80	2	20
pancreatic stellate cell	0.80	3	29
myeloid cell	0.79	53	527
pancreatic PP cell	0.78	11	107
kidney collecting duct cell	0.76	12	116
stem cell of epidermis	0.75	4	45
dendritic cell	0.71	43	438
unknown	0.67	63	625
Clara cell	0.67	2	18
hematopoietic cell	0.67	2	17
mast cell	0.44	2	22
basal cell of urothelium	0.40	36	365
basal cell of epithelium of trachea	0.12	4	36
epicardial adipocyte	0.00	9	93
lung neuroendocrine cell	0.00	0	2
type I pneumocyte	0.00	0	2

**Table B.3:** F1 scores and class sizes for *CellTypist* trained on the *Tabula Muris* with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3.

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl103	1.00	21	207	endothelial cell (93.7%)	Lung (100%)
cl124	1.00	8	82	neuron (100%)	Brain_Neurons (100%)
cl135	1.00	3	26	neuron (100%)	Brain_Neurons (100%)
cl138	1.00	6	57	neuron (98.2%)	Brain_Neurons (100%)
cl147	1.00	15	147	kidney collecting duct cell (57.1%)	Kidney (100%)
cl154	1.00	2	17	neuron (100%)	Brain_Neurons (100%)
cl166	1.00	5	50	type B pancreatic cell (100%)	Pancreas (100%)
cl175	1.00	10	96	Fraction A pre-pro B cell (65.6%)	Marrow (100%)
cl185	1.00	5	47	Brush cell of epithelium proper of large intestine (89.4%)	Colon (100%)
cl186	1.00	1	8	neuron (100%)	Brain_Neurons (100%)
cl189	1.00	46	462	hepatocyte (97.4%)	Liver (100%)
cl193	1.00	4	39	unknown (61.5%)	Aorta (100%)
cl194	1.00	1	14	enteroendocrine cell (100%)	Colon (100%)
cl20	1.00	12	123	pancreatic ductal cell (99.2%)	Pancreas (100%)
cl27	1.00	1	9	enteroendocrine cell (100%)	Colon (100%)
cl65	1.00	2	21	pancreatic stellate cell (90.5%)	Pancreas (100%)
cl73	1.00	2	21	leukocyte (100%)	Pancreas (100%)
cl89	1.00	1	13	astrocyte of the cerebral cortex (69.2%)	Brain_Neurons (69.2%)
cl161	0.99	96	959	keratinocyte (93.8%)	Tongue (100%)
cl150	0.99	83	833	keratinocyte stem cell (97.7%)	Skin (100%)
cl70	0.99	163	1631	basal cell (99.8%)	Mammary (100%)
cl157	0.99	68	682	luminal epithelial cell of mammary gland (57.8%)	Mammary (100%)
cl190	0.99	58	583	hepatocyte (100%)	Liver (100%)
cl143	0.99	54	544	kidney tubule cell (98%)	Kidney (100%)
cl171	0.99	54	539	keratinocyte stem cell (99.6%)	Skin (100%)
cl26	0.99	36	357	luminal cell of lactiferous duct (51%)	Mammary (100%)
cl81	0.99	72	715	endothelial cell (93.3%)	Lung (100%)
cl38	0.98	223	2227	fibroblast (99.3%)	Heart (100%)
cl100	0.98	105	1052	mesenchymal cell (97.1%)	Bladder (100%)
cl108	0.98	49	494	epithelial cell (54.5%)	Trachea (55.9%)
cl31	0.98	496	4961	stromal cell (97.4%)	Trachea (100%)
cl49	0.98	82	823	mesenchymal cell (98.4%)	Bladder (100%)
cl122	0.97	39	386	stromal cell (99.7%)	Lung (100%)
cl37	0.97	367	3665	stromal cell (98.4%)	Trachea (100%)
cl17	0.97	74	742	epithelial cell of large intestine (99.9%)	Colon (100%)
cl95	0.97	90	899	T cell (99.8%)	Thymus (100%)
cl6	0.97	227	2267	hematopoietic stem cell (73.7%)	Marrow (100%)
cl165	0.97	101	1008	kidney tubule cell (98.5%)	Kidney (100%)
cl47	0.97	116	1157	bladder cell (78%)	Bladder (100%)
cl1	0.97	454	4543	basal cell of epidermis (95%)	Tongue (100%)
cl54	0.97	180	1798	granulocyte (61.5%)	Marrow (100%)
cl136	0.97	63	631	T cell (100%)	Thymus (100%)
cl24	0.97	63	631	epithelial cell (92.4%)	Trachea (100%)
cl106	0.96	41	407	chondroblast (93.1%)	Muscle (99.3%)
cl180	0.96	39	392	kidney tubule cell (98.7%)	Kidney (100%)
cl141	0.96	128	1279	skeletal muscle satellite cell (67.9%)	Muscle (70%)
cl71	0.96	24	239	smooth muscle cell (98.7%)	Heart (100%)
cl32	0.96	24	238	mesenchymal stem cell (97.5%)	Diaphragm (100%)
cl85	0.96	82	822	natural killer cell (99.8%)	Lung (100%)
cl44	0.96	143	1434	mesenchymal stem cell (93.4%)	Muscle (100%)
cl176	0.96	24	242	enterocyte of epithelium of large intestine (97.9%)	Colon (100%)
cl181	0.96	23	229	astrocyte of the cerebral cortex (92.6%)	Brain_Neurons (100%)

Table B.4: F1 scores and class sizes for *CellTypist* trained on the *Tabula Muris* with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. (continued 1)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl76	0.95	23	232	endocardial cell (98.7%)	Heart (100%)
cl151	0.95	32	324	hepatocyte (99.7%)	Liver (100%)
cl126	0.95	22	223	keratinocyte (95.5%)	Tongue (100%)
cl39	0.95	159	1593	endothelial cell (72.8%)	Trachea (65.3%)
cl99	0.95	87	868	stromal cell (99.1%)	Lung (100%)
cl140	0.95	68	684	hematopoietic stem cell (64%)	Marrow (100%)
cl83	0.95	38	379	macrophage (53.6%)	Marrow (98.2%)
cl187	0.95	19	188	type II pneumocyte (97.3%)	Lung (100%)
cl159	0.94	17	174	oligodendrocyte precursor cell (99.4%)	Brain_Neurons (100%)
cl62	0.94	196	1955	endothelial cell (98.7%)	Heart (68%)
cl86	0.94	101	1012	basal cell of epidermis (95.6%)	Tongue (99.4%)
cl125	0.94	17	168	type B pancreatic cell (98.2%)	Pancreas (100%)
cl144	0.94	77	771	basal cell of epidermis (95.2%)	Tongue (100%)
cl64	0.94	150	1504	T cell (99.1%)	Mammary (100%)
cl48	0.94	68	678	stromal cell (99%)	Mammary (100%)
cl131	0.94	86	862	oligodendrocyte (96.6%)	Brain_Neurons (100%)
cl60	0.94	239	2391	T cell (99.3%)	Spleen (100%)
cl74	0.94	753	7534	B cell (98.6%)	Spleen (70.5%)
cl14	0.94	123	1232	B cell (60%)	Mammary (100%)
cl110	0.94	63	630	bladder cell (81.4%)	Bladder (99.4%)
cl18	0.94	97	965	leukocyte (97.3%)	Trachea (100%)
cl96	0.94	73	729	mesenchymal stem cell of adipose (55.4%)	Fat (55.7%)
cl55	0.94	132	1318	endothelial cell (98%)	Muscle (100%)
cl113	0.94	143	1434	keratinocyte (97.6%)	Tongue (99.7%)
cl132	0.94	23	226	epithelial cell of large intestine (83.2%)	Colon (100%)
cl43	0.93	120	1197	monocyte (69.2%)	Marrow (100%)
cl112	0.93	8	84	large intestine goblet cell (100%)	Colon (100%)
cl97	0.93	8	80	mesenchymal stem cell of adipose (100%)	Fat (100%)
cl173	0.93	22	220	epidermal cell (93.2%)	Skin (100%)
cl67	0.93	29	294	granulocyte (94.6%)	Fat (100%)
cl129	0.93	36	360	stromal cell (99.2%)	Lung (100%)
cl0	0.93	118	1182	T cell (87.9%)	Thymus (100%)
cl127	0.93	35	348	large intestine goblet cell (87.9%)	Colon (100%)
cl35	0.92	48	481	leukocyte (88.4%)	Heart (100%)
cl82	0.92	18	179	brain pericyte (58.1%)	Brain_Neurons (58.1%)
cl21	0.92	31	307	endothelial cell (94.8%)	Mammary (100%)
cl57	0.92	54	537	B cell (98.7%)	Muscle (100%)
cl11	0.91	11	115	ciliated cell (47%)	Lung (100%)
cl58	0.91	21	211	endothelial cell of hepatic sinusoid (85.8%)	Liver (100%)
cl121	0.90	41	413	epithelial cell of large intestine (99.8%)	Colon (100%)
cl42	0.90	20	204	neuroendocrine cell (95.1%)	Trachea (100%)
cl88	0.90	31	308	myeloid cell (99%)	Fat (100%)
cl52	0.90	54	538	endothelial cell (99.3%)	Fat (100%)
cl184	0.89	12	117	pancreatic acinar cell (97.4%)	Pancreas (100%)
cl34	0.89	33	327	macrophage (96.9%)	Muscle (100%)
cl130	0.89	18	176	large intestine goblet cell (96%)	Colon (100%)
cl72	0.89	94	938	mesenchymal stem cell of adipose (99.9%)	Fat (100%)
cl94	0.89	62	617	stromal cell (97.4%)	Lung (100%)
cl142	0.88	16	156	type B pancreatic cell (100%)	Pancreas (100%)
cl77	0.88	31	309	leukocyte (48.9%)	Lung (58.3%)
cl13	0.88	33	326	unknown (61%)	Muscle (100%)
cl145	0.88	38	384	basal cell of epidermis (80.7%)	Skin (100%)

**Table B.5:** F1 scores and class sizes for *CellTypist* trained on the *Tabula Muris* with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. (continued 2)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl45	0.88	55	545	stromal cell (94.3%)	Lung (100%)
cl102	0.87	17	170	stromal cell (87.6%)	Lung (97.1%)
cl153	0.87	14	137	pancreatic A cell (71.5%)	Pancreas (100%)
cl84	0.86	22	216	monocyte (81.9%)	Lung (100%)
cl15	0.86	24	239	macrophage (74.9%)	Kidney (100%)
cl51	0.86	123	1229	microglial cell (99.6%)	Brain_Microglia (100%)
cl172	0.86	18	177	large intestine goblet cell (52%)	Colon (100%)
cl87	0.86	29	294	dendritic cell (88.4%)	Lung (100%)
cl90	0.86	8	76	endothelial cell (100%)	Aorta (100%)
cl10	0.85	271	2706	B cell (98.1%)	Spleen (100%)
cl7	0.85	53	535	macrophage (63.6%)	Spleen (100%)
cl177	0.85	21	208	enterocyte of epithelium of large intestine (90.4%)	Colon (100%)
cl53	0.83	27	273	endothelial cell (96.3%)	Lung (100%)
cl183	0.83	13	128	large intestine goblet cell (98.4%)	Colon (100%)
cl29	0.83	170	1700	microglial cell (100%)	Brain_Microglia (100%)
cl162	0.83	24	237	enterocyte of epithelium of large intestine (98.7%)	Colon (100%)
cl115	0.83	22	219	mesenchymal stem cell of adipose (99.5%)	Fat (100%)
cl188	0.83	20	197	astrocyte of the cerebral cortex (87.3%)	Brain_Neurons (100%)
cl119	0.83	32	317	oligodendrocyte (99.7%)	Brain_Neurons (100%)
cl40	0.83	26	260	neuroendocrine cell (74.2%)	Trachea (100%)
cl107	0.82	9	94	epidermal cell (43.6%)	Skin (96.8%)
cl109	0.82	26	265	mesenchymal stem cell of adipose (100%)	Fat (100%)
cl12	0.81	143	1427	microglial cell (98.5%)	Brain_Microglia (100%)
cl152	0.81	15	155	pancreatic A cell (98.1%)	Pancreas (100%)
cl56	0.80	47	467	T cell (72.8%)	Fat (100%)
cl9	0.80	5	49	epithelial cell (95.9%)	Fat (100%)
cl69	0.80	11	113	neuroendocrine cell (90.3%)	Trachea (100%)
cl80	0.79	22	222	neutrophil (98.2%)	Fat (100%)
cl36	0.79	16	162	myeloid cell (90.1%)	Fat (100%)
cl149	0.79	19	186	epidermal cell (57.5%)	Skin (100%)
cl68	0.79	77	766	T cell (74.7%)	Marrow (60.8%)
cl191	0.78	13	131	epithelial cell of large intestine (59.5%)	Colon (100%)
cl63	0.77	31	315	T cell (91.1%)	Lung (100%)
cl2	0.77	16	156	Kupffer cell (32.7%)	Liver (100%)
cl158	0.77	25	255	epithelial cell of large intestine (76.1%)	Colon (100%)
cl197	0.76	10	97	unknown (58.8%)	Brain_Neurons (100%)
cl114	0.75	35	354	macrophage (99.4%)	Lung (100%)
cl28	0.75	9	94	B cell (69.1%)	Diaphragm (100%)
cl101	0.75	5	48	endothelial cell (93.8%)	Fat (91.7%)
cl111	0.75	5	53	oligodendrocyte (64.2%)	Brain_Neurons (100%)
cl4	0.71	31	313	cardiac muscle cell (62.9%)	Heart (100%)
cl5	0.70	21	210	fibroblast (66.2%)	Kidney (100%)
cl148	0.70	11	107	pancreatic D cell (57.9%)	Pancreas (100%)
cl30	0.69	36	362	T cell (96.4%)	Muscle (100%)
cl93	0.67	1	9	unknown (44.4%)	Aorta (100%)
cl41	0.62	19	187	macrophage (73.8%)	Lung (100%)
cl25	0.62	6	60	leukocyte (90%)	Bladder (100%)
cl8	0.59	11	106	unknown (67.9%)	Brain_Neurons (100%)
cl50	0.57	5	46	fibroblast (58.7%)	Aorta (100%)
cl33	0.55	8	78	endothelial cell (92.3%)	Diaphragm (100%)
cl19	0.50	1	14	leukocyte (78.6%)	Pancreas (100%)
cl79	0.50	3	26	smooth muscle cell (96.2%)	Fat (100%)
cl16	0.48	7	69	endothelial cell (85.5%)	Bladder (100%)

Table B.6: F1 scores and class sizes for *CellTypist* trained on the *Tabula Muris* with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. (continued 3)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl66	0.45	26	262	B cell (98.1%)	Lung (100%)
cl59	0.44	4	36	leukocyte (77.8%)	Kidney (100%)
cl23	0.22	7	67	epicardial adipocyte (47.8%)	Aorta (100%)
cl155	0.18	2	18	pancreatic acinar cell (100%)	Pancreas (100%)
cl104	0.00	0	5	mesenchymal stem cell of adipose (100%)	Fat (100%)
cl105	0.00	0	4	mesenchymal stem cell of adipose (100%)	Fat (100%)
cl116	0.00	0	5	endothelial cell (100%)	Fat (100%)
cl117	0.00	1	12	smooth muscle cell (100%)	Brain_Neurons (100%)
cl118	0.00	0	3	epithelial cell of large intestine (66.7%)	Colon (100%)
cl120	0.00	0	5	endothelial cell (100%)	Brain_Neurons (100%)
cl123	0.00	2	16	pancreatic PP cell (100%)	Pancreas (100%)
cl128	0.00	1	6	pancreatic PP cell (100%)	Pancreas (100%)
cl133	0.00	1	9	oligodendrocyte precursor cell (100%)	Brain_Neurons (100%)
cl134	0.00	0	4	epithelial cell of large intestine (100%)	Colon (100%)
cl137	0.00	1	14	pancreatic A cell (64.3%)	Pancreas (100%)
cl139	0.00	3	34	pancreatic A cell (64.7%)	Pancreas (100%)
cl146	0.00	1	9	T cell (88.9%)	Fat (100%)
cl156	0.00	3	26	pancreatic D cell (100%)	Pancreas (100%)
cl160	0.00	1	8	type B pancreatic cell (100%)	Pancreas (100%)
cl163	0.00	0	3	type B pancreatic cell (100%)	Pancreas (100%)
cl164	0.00	0	4	neuron (100%)	Brain_Neurons (100%)
cl167	0.00	0	3	pancreatic ductal cell (100%)	Pancreas (100%)
cl168	0.00	1	8	smooth muscle cell (37.5%)	Aorta (100%)
cl169	0.00	1	6	unknown (100%)	Brain_Neurons (100%)
cl170	0.00	0	4	pancreatic A cell (100%)	Pancreas (100%)
cl174	0.00	1	6	fibroblast (66.7%)	Aorta (100%)
cl178	0.00	0	3	epicardial adipocyte (100%)	Aorta (100%)
cl179	0.00	1	6	type B pancreatic cell (100%)	Pancreas (100%)
cl182	0.00	0	3	Brush cell of epithelium proper of large intestine (100%)	Colon (100%)
cl192	0.00	0	5	epithelial cell of large intestine (60%)	Colon (100%)
cl195	0.00	0	4	pancreatic acinar cell (100%)	Pancreas (100%)
cl196	0.00	5	50	pancreatic acinar cell (78%)	Pancreas (100%)
cl22	0.00	5	53	skeletal muscle satellite stem cell (90.6%)	Diaphragm (100%)
cl3	0.00	1	6	keratinocyte stem cell (100%)	Skin (100%)
cl46	0.00	1	11	epicardial adipocyte (54.5%)	Aorta (100%)
cl61	0.00	2	16	B cell (93.8%)	Diaphragm (100%)
cl75	0.00	1	10	hematopoietic cell (60%)	Aorta (60%)
cl78	0.00	2	20	hematopoietic cell (55%)	Aorta (55%)
cl91	0.00	0	3	endothelial cell (100%)	Aorta (100%)
cl92	0.00	7	70	endothelial cell (58.6%)	Aorta (100%)
cl98	0.00	0	3	macrophage (100%)	Diaphragm (100%)

Table B.7: Human scRNA-seq datasets collected and corresponding cell numbers

Dataset	Reference	# cells
baron16	(Baron et al., 2016)	8.569
bjorklund16	(Bjorklund et al., 2016)	648
gierahn17	(Gierahn et al., 2017)	3.694
guo18	(Guo et al., 2018)	12.053
habib17	(Habib et al., 2017)	14.963
hcaImmune18	HCA Data Portal	593.844
henry18	(Henry et al., 2018)	109.061
jaitin19	(Jaitin et al., 2019)	13.199
james20	<i>Unpublished</i>	32.228
lamanno16	(La Manno et al., 2016)	1.977
li19	(Li et al., 2019b)	1.886
masuda19	(Masuda et al., 2019)	6.144
menon18	(Menon et al., 2018)	9.846
miragaia18	(Miragaia et al., 2019)	1.168
muraro16	(Muraro et al., 2016)	2.126
nowakowski17	(Nowakowski et al., 2017)	4.261
popescu19	(Popescu et al., 2019)	113.063
segal19	(Segal et al., 2019)	1.475
segerstolpe16	(Segerstolpe et al., 2016)	3.363
smillie19	(Smillie et al., 2019)	110.110
sohni19	(Sohni et al., 2019)	34.729
takeda19	(Takeda et al., 2019)	33.257
vento18	(Vento-Tormo et al., 2018)	69.883
vieira19	(Braga et al., 2019)	26.013
wang16	(Wang et al., 2016)	635
young18	(Young et al., 2018)	44.526
zhang18	(Zhang et al., 2018)	5.989
zheng17	(Zheng et al., 2017)	163.234
<b>Total</b>		1.421.944

Table B.8: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it.

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl19	1.00	6	56	No annotation (100%)	Intestine (100%)
cl198	1.00	4	41	No annotation (100%)	Brain_Microglia (100%)
cl264	1.00	8	76	Endo (m) (96.1%)	Decidua (100%)
cl311	1.00	12	123	Smooth muscle (56.9%)	Lung Parenchyma (100%)
cl319	1.00	1	7	SCT (100%)	Placenta (100%)
cl362	1.00	2	21	No annotation (100%)	Brain_Microglia (100%)
cl67	1.00	33	326	Endo L (97.5%)	Decidua (100%)
cl307	0.99	392	3916	Type 2 (97.8%)	Lung Parenchyma (100%)
cl282	0.99	450	4496	Myoid cells (6.6%)	Testis (100%)
cl295	0.99	46	464	dS1 (35.3%)	Decidua (100%)
cl376	0.99	1039	10393	No annotation (100%)	Prostate (100%)
cl242	0.99	905	9047	dS1 (50.8%)	Decidua (100%)
cl34	0.99	71	710	Fibroblasts (99.7%)	Lung Parenchyma (100%)
cl179	0.99	1013	10132	dNK2 (49%)	Decidua (100%)
cl131	0.98	193	1932	Macrophages (97%)	Lung Parenchyma (100%)
cl451	0.98	976	9763	CD19+ B (96.4%)	Blood (100%)
cl83	0.98	310	3104	Leydig cells (18.8%)	Testis (100%)
cl12	0.98	30	302	endothelial (90.4%)	Pancreas (100%)
cl27	0.98	369	3685	Endothelial cells (8.8%)	Testis (100%)
cl266	0.98	55	547	Neutrophils (74.2%)	Lung Parenchyma (100%)
cl127	0.98	26	258	Macrophages (98.1%)	Lung Parenchyma (100%)
cl269	0.98	26	264	NK (87.1%)	Lung Parenchyma (100%)
cl55	0.98	180	1797	ductal (88.1%)	Pancreas (100%)
cl44	0.98	551	5513	dM1 (50.2%)	Decidua (100%)
cl286	0.98	173	1731	ffB1 (99.2%)	Placenta (100%)
cl97	0.98	188	1875	dP1 (54.7%)	Decidua (100%)
cl24	0.98	91	910	Macrophages (37.1%)	Testis (100%)
cl109	0.98	424	4240	No annotation (100%)	BoneMarrow (100%)
cl102	0.98	353	3529	ffB1 (0.1%)	Testis (99.8%)
cl122	0.98	128	1276	HB (98.2%)	Placenta (100%)
cl345	0.98	101	1012	MGE newborn neurons (29.5%)	Brain (100%)
cl64	0.97	78	783	Endo (m) (97.3%)	Decidua (100%)
cl494	0.97	314	3137	No annotation (100%)	BoneMarrow (100%)
cl133	0.97	79	791	Macrophages (97.1%)	Lung Parenchyma (100%)
cl35	0.97	89	885	dM3 (86.4%)	Placenta (100%)
cl284	0.97	53	533	Ciliated (99.6%)	Upper airway (100%)
cl369	0.97	89	889	delta (95.6%)	Pancreas (100%)
cl79	0.97	702	7018	NK (52.3%)	Liver (100%)
cl23	0.97	18	178	Neutrophils (52.8%)	Upper airway (100%)
cl442	0.97	894	8944	CD56+ NK (91.2%)	Blood (100%)
cl341	0.97	227	2269	Sperm (84.5%)	Testis (100%)
cl113	0.97	2447	24471	CD19+ B (0.3%)	Blood (100%)
cl252	0.97	228	2276	Macrophages (90%)	Lung Parenchyma (100%)
cl447	0.97	919	9192	Treg (0%)	Blood (100%)
cl192	0.97	155	1551	Neutrophils (93.5%)	Lung Parenchyma (100%)
cl523	0.97	985	9851	No annotation (100%)	BoneMarrow (100%)
cl338	0.97	15	145	EVT (82.8%)	Decidua (100%)
cl379	0.97	116	1159	Type 2 (97.7%)	Lung Parenchyma (100%)
cl281	0.97	99	994	dS3 (85.5%)	Decidua (100%)
cl517	0.96	595	5952	No annotation (100%)	BoneMarrow (100%)
cl75	0.96	162	1619	No annotation (100%)	BoneMarrow (100%)
cl118	0.96	89	887	Macrophages (98.9%)	Lung Parenchyma (100%)
cl327	0.96	266	2658	Differentiating Spermatogonia (11.6%)	Testis (100%)
cl378	0.96	419	4194	No annotation (100%)	Prostate (100%)
cl312	0.96	141	1413	Early Primary Spermatocytes (38.7%)	Testis (100%)
cl314	0.96	396	3959	No annotation (100%)	Prostate (100%)
cl321	0.96	76	759	dNK1 (31.4%)	Decidua (100%)

Table B.9: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 1)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl208	0.96	134	1335	dM1 (51%)	Decidua (99.7%)
cl69	0.96	1184	11840	CD19+ B (30.9%)	Blood (100%)
cl322	0.96	107	1070	Elongated Spermatids (66%)	Testis (100%)
cl570	0.96	70	699	OPC (86.6%)	Brain (100%)
cl326	0.96	365	3653	No annotation (100%)	Kidney (100%)
cl22	0.96	12	121	No annotation (100%)	Brain Microglia (100%)
cl455	0.95	1072	10721	CD8+/CD45RA+	Blood (100%)
				Naive Cytotoxic (0.9%)	
cl49	0.95	244	2441	Fibroblast (29.9%)	Liver (100%)
cl543	0.95	172	1722	No annotation (100%)	BoneMarrow (100%)
cl380	0.95	543	5433	No annotation (100%)	Prostate (100%)
cl7	0.95	102	1015	No annotation (100%)	Omentum Adipose Tissue (100%)
cl15	0.95	49	486	MG (70.2%)	Brain (100%)
cl11	0.95	57	572	Endothelium (65%)	Lung Parenchyma (56.3%)
cl606	0.95	623	6230	WNT2B+ Fos-lo 1 (27.4%)	Colon (100%)
cl413	0.95	1834	18344	CD8+/CD45RA+	Blood (100%)
				Naive Cytotoxic (0.1%)	
cl45	0.95	486	4862	Macrophages (70.2%)	Colon (100%)
cl308	0.95	66	656	Type 2 (98.6%)	Lung Parenchyma (100%)
cl40	0.95	267	2669	Kupffer Cell (19.8%)	Liver (100%)
cl440	0.95	931	9305	CD34+ (87.6%)	Blood (100%)
cl316	0.94	122	1216	Secretory (91.2%)	Upper airway (100%)
cl77	0.94	269	2694	No annotation (100%)	BoneMarrow (100%)
cl155	0.94	237	2373	pro-B cell (25%)	Liver (99.8%)
cl240	0.94	74	744	dNK2 (47.6%)	Decidua (100%)
cl2	0.94	461	4613	No annotation (100%)	Prostate (100%)
cl503	0.94	692	6923	No annotation (100%)	BoneMarrow (100%)
cl268	0.94	176	1760	dS1 (94%)	Decidua (100%)
cl243	0.94	81	808	dS1 (87.5%)	Decidua (100%)
cl63	0.94	41	406	Secretory (67.5%)	Lung Parenchyma (100%)
cl582	0.94	193	1933	Th cell (0.1%)	Kidney (100%)
cl261	0.94	108	1078	EVT (97%)	Placenta (100%)
cl206	0.94	44	439	ffB1 (98.9%)	Placenta (100%)
cl283	0.94	165	1650	dT CD8 (26.2%)	Decidua (88.3%)
cl403	0.94	357	3568	Megakaryocyte (45.3%)	Liver (100%)
cl68	0.94	207	2071	ILC precursor (39.3%)	Liver (100%)
cl492	0.93	343	3425	No annotation (100%)	BoneMarrow (100%)
cl370	0.93	124	1239	acinar (80%)	Pancreas (100%)
cl372	0.93	63	630	gamma (87.6%)	Pancreas (100%)
cl456	0.93	1151	11506	CD34+ (1.4%)	Blood (100%)
cl47	0.93	493	4926	Normal_cell (4%)	Kidney (100%)
cl377	0.93	432	4324	No annotation (100%)	Prostate (100%)
cl536	0.93	30	296	No annotation (100%)	BoneMarrow (100%)
cl547	0.93	60	595	No annotation (100%)	BoneMarrow (100%)
cl219	0.93	57	574	Endothelial cells (3.8%)	Testis (100%)
cl540	0.93	179	1785	No annotation (100%)	BoneMarrow (100%)
cl432	0.93	743	7430	No annotation (100%)	Prostate (100%)
cl375	0.93	207	2065	alpha (90.4%)	Pancreas (100%)
cl515	0.93	638	6377	No annotation (100%)	BoneMarrow (100%)
cl374	0.93	204	2040	beta (98.9%)	Pancreas (100%)
cl271	0.93	105	1047	No annotation (100%)	Omentum Adipose Tissue (100%)
cl371	0.93	134	1343	alpha (97.5%)	Pancreas (100%)
cl401	0.92	455	4553	No annotation (100%)	Prostate (100%)
cl506	0.92	914	9140	No annotation (100%)	BoneMarrow (100%)
cl504	0.92	1595	15946	No annotation (100%)	BoneMarrow (100%)
cl260	0.92	81	811	Basal (98.3%)	Upper airway (100%)
cl250	0.92	135	1353	No annotation (100%)	axLN (100%)

Table B.10: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 2)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl301	0.92	14	138	Secretary (87%)	Upper airway (100%)
cl542	0.92	175	1748	No annotation (100%)	BoneMarrow (100%)
cl490	0.92	1166	11658	No annotation (100%)	BoneMarrow (100%)
cl568	0.92	761	7609	TA 1 (37.4%)	Colon (100%)
cl458	0.92	1177	11771	CD56+ NK (47.2%)	Blood (100%)
cl474	0.92	92	920	Mast cell (49.1%)	Liver (100%)
cl48	0.92	18	177	Tcm (57.1%)	Skin (100%)
cl495	0.92	308	3084	No annotation (100%)	BoneMarrow (100%)
cl509	0.92	760	7595	No annotation (100%)	BoneMarrow (100%)
cl277	0.92	12	115	No annotation (100%)	Brain_Microglia (100%)
cl470	0.92	1345	13446	NK CD16+ (9.1%)	Blood (100%)
cl592	0.92	925	9250	No annotation (100%)	BoneMarrow (100%)
cl340	0.92	259	2593	Hepatocyte (40.9%)	Liver (100%)
cl335	0.92	57	566	Late primary Spermatocytes (41.3%)	Testis (100%)
cl255	0.92	114	1144	EVT (98.8%)	Placenta (100%)
cl70	0.91	381	3813	No annotation (100%)	BoneMarrow (100%)
cl59	0.91	36	356	END (66%)	Brain (100%)
cl233	0.91	407	4066	VCT (99.9%)	Placenta (100%)
cl511	0.91	573	5731	No annotation (100%)	BoneMarrow (100%)
cl464	0.91	610	6102	Mid Erythroid (25.5%)	Liver (100%)
cl323	0.91	107	1068	Spermatogonial Stem cell (0.7%)	Testis (100%)
cl554	0.91	498	4982	B cell IgA plasma (45.9%)	Colon (100%)
cl552	0.91	93	926	No annotation (100%)	BoneMarrow (100%)
cl258	0.91	75	747	alpha (99.9%)	Pancreas (100%)
cl457	0.91	2216	22163	PB Naive CD4 (0.1%)	Blood (100%)
cl25	0.91	95	951	No annotation (100%)	Omentum Adipose Tissue (100%)
cl38	0.91	32	319	Unknown1 (24.8%)	Brain (100%)
cl232	0.91	70	702	CD4 Thf (71.2%)	mLN (100%)
cl486	0.90	441	4414	No annotation (100%)	BoneMarrow (100%)
cl404	0.90	1304	13039	No annotation (100%)	Prostate (100%)
cl612	0.90	698	6977	Immature Enterocytes 1 (35.6%)	Colon (100%)
cl214	0.90	16	157	ILC2 (83.4%)	Tonsil (100%)
cl581	0.90	279	2792	Normal_cell (6.5%)	Kidney (100%)
cl488	0.90	389	3888	No annotation (100%)	BoneMarrow (100%)
cl293	0.90	42	424	Ciliated (99.8%)	Upper airway (100%)
cl115	0.90	277	2767	Kupffer Cell (26.7%)	Liver (100%)
cl373	0.90	63	632	acinar (59.3%)	Pancreas (100%)
cl429	0.90	567	5673	No annotation (100%)	Prostate (100%)
cl518	0.90	234	2344	No annotation (100%)	BoneMarrow (100%)
cl56	0.90	575	5748	Mid Erythroid (29.5%)	Liver (100%)
cl417	0.90	257	2570	No annotation (100%)	Prostate (100%)
cl491	0.90	366	3663	No annotation (100%)	BoneMarrow (100%)
cl505	0.90	1430	14301	No annotation (100%)	BoneMarrow (100%)
cl278	0.90	100	1000	VCT (97.7%)	Placenta (100%)
cl390	0.90	55	547	earlyRG (2.2%)	Brain (100%)
cl575	0.90	278	2780	Endothelium; Mixed_phenotype (<0.1%)	Kidney (100%)
cl279	0.90	85	849	VCT (93.1%)	Placenta (100%)
cl36	0.89	172	1717	Endothelial (25.6%)	Colon (100%)
cl210	0.89	104	1038	dNK3 (87.5%)	Decidua (100%)
cl444	0.89	2513	25130	CD8+/CD45RA+ Naive Cytotoxic (59%)	Blood (100%)
cl299	0.89	77	774	beta (89%)	Pancreas (100%)

Table B.11: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 3)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl538	0.89	204	2038	No annotation (100%)	BoneMarrow (100%)
cl430	0.89	680	6797	No annotation (100%)	Prostate (100%)
cl567	0.89	789	7894	TA 1 (75.4%)	Colon (100%)
cl498	0.89	276	2763	No annotation (100%)	BoneMarrow (100%)
cl569	0.89	490	4899	Plasma (94.8%)	Colon (100%)
cl247	0.89	4	37	No annotation (100%)	Omentum Adipose Tissue (100%)
cl259	0.89	15	154	EVT (100%)	Placenta (100%)
cl336	0.89	10	101	No annotation (100%)	Brain_Microglia (100%)
cl88	0.89	47	466	Endothelium (1.3%)	axLN (98.7%)
cl478	0.89	1857	18568	CD4+/CD45RA+/CD25-Naive T (48.1%)	Blood (100%)
cl57	0.89	157	1571	DCs (60.2%)	Lung Parenchyma (100%)
cl8	0.89	225	2246	dT CD8 (31.5%)	Decidua (100%)
cl512	0.88	679	6788	No annotation (100%)	BoneMarrow (100%)
cl100	0.88	17	169	Plasma (1.8%)	Omentum Adipose Tissue (98.2%)
cl267	0.88	13	126	No annotation (100%)	Brain_Microglia (100%)
cl433	0.88	821	8207	No annotation (100%)	Prostate (100%)
cl408	0.88	73	727	EVT (97.2%)	Placenta (100%)
cl1	0.88	724	7237	Renal_cell_carcinoma (3.4%)	Kidney (100%)
cl339	0.88	192	1917	Spermatogonial Stem cell (4.5%)	Testis (100%)
cl392	0.88	56	563	Newborn Excitatory Neuron - late born (1.2%)	Brain (100%)
cl317	0.88	123	1226	VCT (97.5%)	Placenta (100%)
cl280	0.88	9	92	No annotation (100%)	Brain_Microglia (100%)
cl382	0.88	8	83	Fibroblasts (77.1%)	Lung Parenchyma (100%)
cl391	0.87	115	1147	Newborn Excitatory Neuron - early born (42%)	Brain (100%)
cl134	0.87	946	9463	Early Erythroid (44.5%)	Liver (100%)
cl617	0.87	176	1764	CD69+ Mast (50.6%)	Colon (100%)
cl350	0.87	19	190	Unclassified (75.3%)	Brain (100%)
cl355	0.87	43	432	Ciliated (97.5%)	Upper airway (100%)
cl18	0.87	21	206	ILC3 (96.6%)	Tonsil (100%)
cl387	0.87	268	2680	Spermatogonial Stem cell (6.7%)	Testis (100%)
cl256	0.87	80	801	not applicable (65.9%)	Pancreas (99.6%)
cl74	0.87	605	6048	No annotation (100%)	Prostate (100%)
cl508	0.87	864	8640	No annotation (100%)	BoneMarrow (100%)
cl610	0.87	310	3098	CD4+ Memory (81.7%)	Colon (100%)
cl46	0.87	601	6013	CD14+ Monocyte (30%)	Blood (100%)
cl431	0.87	742	7415	No annotation (100%)	Prostate (100%)
cl613	0.87	273	2734	Follicular (74.8%)	Colon (100%)
cl4	0.86	27	272	Sertoli cells (5.9%)	Testis (100%)
cl309	0.86	33	325	No annotation (100%)	axLN (100%)
cl500	0.86	453	4529	No annotation (100%)	BoneMarrow (100%)
cl14	0.86	87	865	T cell (76.2%)	Lung Parenchyma (100%)
cl510	0.86	689	6892	No annotation (100%)	BoneMarrow (100%)
cl13	0.86	24	240	No annotation (100%)	hnLN (100%)
cl203	0.86	11	108	ffB2 (97.2%)	Placenta (100%)
cl37	0.86	8	79	NK (88.6%)	Tonsil (100%)
cl62	0.86	7	72	No annotation (100%)	Brain_Microglia (100%)
cl501	0.86	464	4637	No annotation (100%)	BoneMarrow (100%)
cl601	0.86	84	835	B cell IgA plasma (71.9%)	Colon (100%)
cl590	0.85	386	3857	B cell IgA plasma (70.7%)	Colon (100%)
cl343	0.85	97	968	NSC (13.4%)	Brain (100%)

Table B.12: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 4)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl516	0.85	1394	13939	No annotation (100%)	BoneMarrow (100%)
cl238	0.85	141	1411	B cell memory (40%)	mLN (100%)
cl595	0.85	637	6372	Plasma (97.3%)	Colon (100%)
cl611	0.85	168	1677	B cell IgA plasma (64.9%)	Colon (100%)
cl306	0.85	38	384	Myoid cells (5.5%)	Testis (100%)
cl475	0.84	146	1457	Mid Erythroid (24.6%)	Liver (100%)
cl101	0.84	221	2213	Plasma (85.6%)	Colon (100%)
cl497	0.84	278	2784	No annotation (100%)	BoneMarrow (100%)
cl51	0.84	834	8335	Kupffer Cell (27.8%)	Liver (100%)
cl438	0.84	314	3141	HSC_MPP (36%)	Liver (100%)
cl452	0.84	1198	11980	MO (0.6%)	Blood (100%)
cl183	0.84	49	494	Mast cell (86.2%)	Lung Parenchyma (86.6%)
cl534	0.84	951	9505	No annotation (100%)	BoneMarrow (100%)
cl514	0.84	938	9378	No annotation (100%)	BoneMarrow (100%)
cl93	0.84	528	5279	Myeloid (31.8%)	Blood (100%)
cl110	0.84	132	1318	No annotation (100%)	BoneMarrow (100%)
cl576	0.83	1353	13527	Th cell (3.7%)	Kidney (100%)
cl386	0.83	62	619	MGE Progenitors (22%)	Brain (100%)
cl43	0.83	7	66	No annotation (100%)	Intestine (100%)
cl439	0.83	1849	18491	Bcell (0%)	Blood (100%)
cl220	0.83	234	2342	Sperm (0.6%)	Testis (100%)
cl26	0.83	69	692	activated_stellate (40.5%)	Pancreas (100%)
cl507	0.83	892	8923	No annotation (100%)	BoneMarrow (100%)
cl275	0.83	16	161	No annotation (100%)	Prostate (100%)
cl50	0.83	32	316	No annotation (100%)	Omentum Adipose Tissue (100%)
cl332	0.83	94	937	GABA1 (50.6%)	Brain (100%)
cl428	0.83	42	421	No annotation (100%)	Prostate (100%)
cl615	0.83	252	2520	CD4+ CD25- T cells (31.3%)	Colon (100%)
cl520	0.83	214	2137	No annotation (100%)	BoneMarrow (100%)
cl270	0.83	84	842	No annotation (100%)	axLN (100%)
cl329	0.83	253	2534	Private (4.9%)	Kidney (100%)
cl493	0.82	329	3289	No annotation (100%)	BoneMarrow (100%)
cl30	0.82	9	93	ILC1 (100%)	Tonsil (100%)
cl276	0.82	35	349	No annotation (100%)	Brain_Microglia (100%)
cl304	0.82	361	3610	Sertoli cells (0.1%)	Testis (100%)
cl551	0.82	107	1070	No annotation (100%)	BoneMarrow (100%)
cl549	0.82	116	1156	No annotation (100%)	BoneMarrow (100%)
cl418	0.82	979	9790	Mid Erythroid (67.6%)	Liver (100%)
cl389	0.82	17	171	No annotation (100%)	Brain_Microglia (100%)
cl96	0.82	21	205	EVT (94.6%)	Placenta (98.5%)
cl246	0.82	71	714	Basal (99.4%)	Upper airway (100%)
cl3	0.82	13	125	macrophage (43.2%)	Pancreas (100%)
cl448	0.82	921	9207	CD14+ Monocyte (1.8%)	Blood (100%)
cl87	0.82	642	6419	Treg NL-like (0%)	BoneMarrow (100%)
cl465	0.82	292	2919	Mid Erythroid (71.9%)	Liver (100%)
cl229	0.82	35	347	No annotation (100%)	hnLN (100%)
cl71	0.82	1018	10179	CD8+ Cytotoxic T (49.7%)	Blood (100%)
cl524	0.81	15	148	No annotation (100%)	BoneMarrow (100%)
cl480	0.81	291	2914	CD4+ CD25high T cells (28.1%)	Blood (100%)
cl263	0.81	62	617	Basal (99.2%)	Upper airway (100%)
cl586	0.81	88	881	exPFC1 (55.2%)	Brain (100%)
cl477	0.81	155	1554	Early Erythroid (55.1%)	Liver (100%)
cl537	0.81	53	525	No annotation (100%)	BoneMarrow (100%)
cl143	0.81	62	620	beta (90.6%)	Pancreas (100%)
cl577	0.81	83	834	NK cell 1 (4.2%)	Kidney (100%)
cl178	0.81	40	401	No annotation (100%)	hnLN (100%)
cl502	0.80	571	5707	No annotation (100%)	BoneMarrow (100%)

Table B.13: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 5)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl571	0.80	459	4593	TA 1 (51.9%)	Colon (100%)
cl298	0.80	15	146	No annotation (100%)	Brain_Microglia (100%)
cl553	0.80	86	861	No annotation (100%)	BoneMarrow (100%)
cl359	0.80	31	309	Unclassified (66%)	Brain (100%)
cl360	0.80	458	4577	Sertoli cells (0%)	Testis (100%)
cl76	0.80	1487	14872	MO (3.5%)	Blood (100%)
cl80	0.80	61	614	No annotation (100%)	Omentum Adipose Tissue (100%)
cl296	0.80	57	565	Early Born Deep Layer/ subplate Excitatory Neuron V1 (25%)	Brain (100%)
cl460	0.80	487	4866	PB Naive CD4 (0.1%)	Blood (100%)
cl459	0.79	1360	13598	CD8+/CD45RA+ Naive Cytotoxic (58.9%)	Blood (100%)
cl272	0.79	58	579	No annotation (100%)	axLN (100%)
cl227	0.79	121	1205	No annotation (100%)	axLN (100%)
cl41	0.79	25	249	EVT (87.1%)	Decidua (100%)
cl358	0.79	494	4938	Sertoli cells (0.1%)	Testis (100%)
cl262	0.79	86	862	Basal (98.5%)	Upper airway (100%)
cl89	0.79	471	4714	CD8+ LP (58%)	Colon (100%)
cl160	0.79	166	1656	No annotation (100%)	Omentum Adipose Tissue (99.8%)
cl313	0.79	53	528	SCT (78.6%)	Placenta (100%)
cl449	0.78	1453	14529	CD4+/CD25 T Reg (49.5%)	Blood (100%)
cl626	0.78	117	1172	B cell IgA plasma (53.2%)	Colon (100%)
cl616	0.78	249	2494	CD8+ IELs (52.4%)	Colon (100%)
cl361	0.78	112	1124	exPFC1 (88.9%)	Brain (100%)
cl399	0.78	50	499	GABA2 (55.5%)	Brain (100%)
cl435	0.78	1197	11966	Kupffer Cell (67%)	Liver (100%)
cl254	0.77	19	190	No annotation (100%)	hnLN (100%)
cl422	0.77	412	4117	Late Erythroid (23.9%)	Liver (100%)
cl618	0.77	158	1583	Plasma (84.2%)	Colon (100%)
cl556	0.77	548	5477	Cycling TA (47.1%)	Colon (100%)
cl60	0.77	114	1137	No annotation (100%)	Omentum Adipose Tissue (100%)
cl402	0.77	497	4972	No annotation (100%)	Prostate (100%)
cl318	0.77	159	1591	VCT (97.4%)	Placenta (100%)
cl453	0.76	983	9833	CD4+/CD25 T Reg (35.3%)	Blood (100%)
cl548	0.76	1017	10174	No annotation (100%)	BoneMarrow (100%)
cl483	0.76	73	726	Sertoli cells (0.3%)	Testis (100%)
cl400	0.76	774	7742	Mid Erythroid (63.6%)	Liver (100%)
cl412	0.76	58	581	Kupffer Cell (32.7%)	Liver (100%)
cl388	0.76	59	590	exCA3 (62.5%)	Brain (100%)
cl367	0.76	121	1206	ASC1 (58%)	Brain (100%)
cl224	0.76	21	206	No annotation (100%)	hnLN (100%)
cl147	0.76	414	4144	Mid Erythroid (28.2%)	Liver (99.9%)
cl463	0.76	1431	14305	CD8+/CD45RA+ Naive Cytotoxic (1.1%)	Blood (100%)
cl128	0.75	611	6107	TA 2 (39%)	Colon (100%)
cl621	0.75	653	6529	CD4+ Activated Fos-lo (36.6%)	Colon (100%)
cl303	0.75	36	355	SCT (97.5%)	Placenta (100%)
cl31	0.75	51	514	No annotation (100%)	axLN (100%)
cl485	0.75	445	4453	No annotation (100%)	BoneMarrow (100%)
cl52	0.75	5	52	Fibroblasts (86.5%)	Upper airway (100%)
cl39	0.74	103	1034	No annotation (100%)	Omentum Adipose Tissue (100%)
cl473	0.74	124	1237	CD4 (46.6%)	Blood (100%)
cl58	0.74	179	1793	B cell memory (38.8%)	mLN (100%)
cl225	0.74	24	237	No annotation (100%)	hnLN (100%)
cl519	0.74	1064	10640	No annotation (100%)	BoneMarrow (100%)
cl132	0.74	23	229	No annotation (100%)	hnLN (100%)

Table B.14: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 6)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl496	0.74	281	2810	No annotation (100%)	BoneMarrow (100%)
cl285	0.73	129	1290	CD4 Thf (41.4%)	mLN (100%)
cl623	0.73	122	1224	TA 2 (31.9%)	Colon (100%)
cl434	0.73	867	8667	No annotation (100%)	Prostate (100%)
cl16	0.73	39	389	Endothelium (56.3%)	Lung Parenchyma (100%)
cl593	0.73	4	38	Best4+ Enterocytes (100%)	Colon (100%)
cl148	0.73	15	147	No annotation (100%)	hnLN (100%)
cl54	0.73	122	1217	ODC1 (93.1%)	Brain (100%)
cl513	0.72	659	6588	No annotation (100%)	BoneMarrow (100%)
cl441	0.72	759	7588	CD8+/CD45RA+	Blood (100%)
				Naive Cytotoxic (0.9%)	
cl248	0.72	27	267	No annotation (100%)	hnLN (100%)
cl173	0.72	13	127	No annotation (100%)	hnLN (100%)
cl454	0.72	1072	10715	CD8+/CD45RA+ Naive	Blood (100%)
				Cytotoxic (0.3%)	
cl598	0.72	22	219	Immature Goblet (77.6%)	Colon (100%)
cl409	0.72	1576	15761	CD4+/CD45RO+	Blood (100%)
				Memory (44.6%)	
cl315	0.72	46	461	exPFC1 (45.3%)	Brain (100%)
cl555	0.71	506	5061	Immature Goblet (28.8%)	Colon (100%)
cl212	0.71	27	267	DC1 (89.9%)	Decidua (100%)
cl416	0.71	19	192	No annotation (100%)	Prostate (100%)
cl0	0.70	23	231	Endo (f) (34.2%)	Placenta (100%)
cl337	0.70	79	789	exDG (87.6%)	Brain (100%)
cl174	0.70	79	785	No annotation (100%)	axLN (100%)
cl415	0.70	1267	12670	PB Naive CD4 (25.7%)	Blood (100%)
cl205	0.70	781	7807	Nephron_epithelium (6.6%)	Kidney (100%)
cl476	0.70	218	2183	CD8+ Cytotoxic T (83.3%)	Blood (100%)
cl385	0.69	152	1523	No annotation (100%)	Omentum Adipose Tissue (100%)
cl274	0.69	60	600	No annotation (100%)	axLN (100%)
cl427	0.68	149	1487	No annotation (100%)	axLN (100%)
cl53	0.68	481	4814	Granulocytes (2%)	Blood (100%)
cl137	0.68	28	275	No annotation (100%)	axLN (100%)
cl180	0.68	107	1066	No annotation (100%)	axLN (100%)
cl574	0.67	330	3304	Plasma (94.3%)	Colon (100%)
cl185	0.67	155	1554	B cell follicular (53%)	mLN (100%)
cl622	0.67	134	1338	Immature Enterocytes 2	Colon (100%)
				(52.9%)	
cl546	0.67	119	1191	No annotation (100%)	BoneMarrow (100%)
cl213	0.67	105	1051	No annotation (100%)	axLN (100%)
cl384	0.67	4	43	No annotation (100%)	Omentum Adipose Tissue (100%)
cl28	0.66	170	1703	No annotation (100%)	BoneMarrow (100%)
cl472	0.66	405	4046	CD8+ T cells (20%)	Blood (100%)
cl325	0.66	27	274	No annotation (100%)	Brain_Microglia (100%)
cl184	0.66	31	311	No annotation (100%)	axLN (100%)
cl152	0.66	20	203	Ciliated (100%)	Lung Parenchyma (100%)
cl423	0.66	35	345	No annotation (100%)	axLN (100%)
cl443	0.65	971	9705	Kupffer Cell (69.9%)	Liver (100%)
cl479	0.65	248	2480	Bcell (1.8%)	Blood (100%)
cl365	0.65	74	740	ODC1 (93.9%)	Brain (100%)
cl410	0.65	1714	17137	PB Naive CD4 (0.2%)	Blood (100%)
cl450	0.65	676	6759	CD4+ T Helper (43.9%)	Blood (100%)
cl624	0.65	108	1078	Immature Enterocytes 1	Colon (100%)
				(78.7%)	
cl218	0.65	54	544	No annotation (100%)	axLN (100%)
cl156	0.65	1652	16515	PB Naive CD4 (0.1%)	Blood (100%)
cl541	0.65	176	1756	No annotation (100%)	BoneMarrow (100%)
cl141	0.65	12	121	No annotation (100%)	Intestine (100%)

Table B.15: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 7)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl221	0.65	1297	12967	PB Naive CD4 (0.3%)	Blood (100%)
cl580	0.64	633	6331	NK cell (6.7%)	Kidney (100%)
cl215	0.64	22	217	No annotation (100%)	hnLN (100%)
cl414	0.64	88	883	Kupffer Cell (29.7%)	Liver (100%)
cl145	0.64	65	646	No annotation (100%)	hnLN (100%)
cl484	0.64	13	134	No annotation (100%)	hnLN (100%)
cl251	0.64	91	906	B cell memory (47.7%)	mLN (100%)
cl176	0.63	42	416	No annotation (100%)	hnLN (100%)
cl33	0.63	15	152	No annotation (100%)	Brain_Microglia (100%)
cl614	0.63	266	2655	CD4+ Memory (41.7%)	Colon (100%)
cl297	0.63	11	113	ILC3 (92%)	Tonsil (100%)
cl124	0.63	392	3915	Plasma (43.6%)	Colon (100%)
cl144	0.62	27	268	No annotation (100%)	hnLN (100%)
cl241	0.62	61	614	No annotation (100%)	axLN (100%)
cl187	0.62	42	418	No annotation (100%)	hnLN (100%)
cl172	0.62	100	1003	No annotation (100%)	axLN (100%)
cl175	0.62	75	748	No annotation (100%)	axLN (100%)
cl420	0.61	134	1337	No annotation (100%)	axLN (100%)
cl273	0.61	12	117	CD4 T central memory (81.2%)	mLN (100%)
cl346	0.60	7	72	Unknown4 (59.7%)	Brain (100%)
cl619	0.59	87	869	CD4+ Activated Fos-hi (48.4%)	Colon (100%)
cl591	0.59	328	3283	Plasma (48.4%)	Colon (100%)
cl529	0.58	39	389	No annotation (100%)	BoneMarrow (100%)
cl231	0.58	17	167	No annotation (100%)	hnLN (100%)
cl597	0.58	24	238	Enterocytes (41.6%)	Colon (100%)
cl550	0.58	113	1128	No annotation (100%)	BoneMarrow (100%)
cl265	0.57	26	262	CD4 T central memory (83.2%)	mLN (100%)
cl368	0.57	23	229	No annotation (100%)	Brain_Microglia (100%)
cl324	0.57	7	73	No annotation (100%)	Brain_Microglia (100%)
cl197	0.56	44	436	No annotation (100%)	hnLN (100%)
cl216	0.56	80	797	No annotation (100%)	axLN (100%)
cl190	0.56	29	289	No annotation (100%)	hnLN (100%)
cl73	0.55	374	3741	B cell IgA plasma (21.1%)	Colon (100%)
cl366	0.55	78	782	exPFC1 (61.8%)	Brain (100%)
cl106	0.55	35	347	CD4 T central memory (73.5%)	mLN (100%)
cl608	0.55	51	512	Macrophages (28.1%)	Colon (100%)
cl584	0.54	79	794	ASC1 (50.5%)	Brain (100%)
cl419	0.54	121	1208	No annotation (100%)	axLN (100%)
cl620	0.54	151	1509	Plasma (67.1%)	Colon (100%)
cl153	0.53	136	1355	No annotation (100%)	axLN (100%)
cl445	0.52	1945	19446	PB Naive CD4 (0.2%)	Blood (100%)
cl625	0.52	91	907	Enterocyte Progenitors (62.7%)	Colon (100%)
cl573	0.52	32	315	ODC1 (89.2%)	Brain (100%)
cl290	0.52	26	262	No annotation (100%)	Brain_Microglia (100%)
cl446	0.52	911	9111	PB Naive CD8 (0.3%)	Blood (100%)
cl162	0.50	14	144	No annotation (100%)	hnLN (100%)
cl200	0.50	3	27	DC1 (100%)	Decidua (100%)
cl226	0.50	28	277	No annotation (100%)	hnLN (100%)
cl302	0.50	86	856	VCT (62.4%)	Placenta (100%)
cl559	0.47	37	365	ODC1 (95.9%)	Brain (100%)
cl425	0.47	57	574	No annotation (100%)	axLN (100%)
cl522	0.47	19	193	No annotation (100%)	BoneMarrow (100%)
cl426	0.47	71	709	No annotation (100%)	axLN (100%)
cl10	0.46	9	95	No annotation (100%)	axLN (100%)
cl349	0.46	18	180	exCA3 (72.8%)	Brain (100%)
cl223	0.46	31	312	No annotation (100%)	hnLN (100%)
cl222	0.45	30	296	No annotation (100%)	hnLN (100%)
cl237	0.45	68	677	B cell memory (34.4%)	mLN (100%)

Table B.16: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 8)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl42	0.44	7	66	No annotation (100%)	Brain_Microglia (100%)
cl320	0.43	44	444	exDG (68.7%)	Brain (100%)
cl596	0.43	38	383	CD4+ Memory (35.5%)	Colon (100%)
cl189	0.43	14	143	No annotation (100%)	hnLN (100%)
cl217	0.42	18	176	No annotation (100%)	hnLN (100%)
cl126	0.40	4	40	Mast cell (92.5%)	Lung Parenchyma (100%)
cl20	0.40	21	208	B cell memory (38.5%)	mLN (100%)
cl253	0.38	21	205	No annotation (100%)	hnLN (100%)
cl85	0.38	20	198	No annotation (100%)	axLN (100%)
cl9	0.38	9	86	No annotation (100%)	hnLN (100%)
cl287	0.37	10	104	No annotation (100%)	Brain_Microglia (100%)
cl411	0.37	34	340	Mid Erythroid (46.8%)	Liver (100%)
cl353	0.37	21	205	exPFC1 (95.1%)	Brain (100%)
cl424	0.37	46	459	No annotation (100%)	axLN (100%)
cl169	0.36	19	194	No annotation (100%)	hnLN (100%)
cl609	0.36	85	848	Enterocyte Progenitors (28.8%)	Colon (100%)
cl364	0.35	14	139	No annotation (100%)	Brain_Microglia (100%)
cl351	0.33	20	201	exPFC1 (92%)	Brain (100%)
cl481	0.33	21	205	CD8+/CD45RA+	Blood (100%)
				Naive Cytotoxic (0.5%)	
cl594	0.32	43	425	TA 1 (38.1%)	Colon (100%)
cl146	0.32	45	453	No annotation (100%)	hnLN (100%)
cl357	0.32	23	234	exDG (71.8%)	Brain (100%)
cl348	0.32	16	158	ASC1 (19.6%)	Brain (100%)
cl310	0.29	6	58	CD4 T central memory (34.5%)	mLN (100%)
cl245	0.28	119	1186	No annotation (100%)	axLN (100%)
cl395	0.27	17	168	No annotation (100%)	Brain_Microglia (100%)
cl421	0.27	16	161	No annotation (100%)	axLN (100%)
cl129	0.27	12	116	No annotation (100%)	Intestine (100%)
cl234	0.25	14	140	No annotation (100%)	hnLN (100%)
cl354	0.25	21	208	exCA3 (65.9%)	Brain (100%)
cl5	0.25	7	71	Tcm (36.6%)	Skin (100%)
cl181	0.22	8	78	No annotation (100%)	Intestine (100%)
cl565	0.22	33	332	ODC1 (92.2%)	Brain (100%)
cl168	0.20	12	115	No annotation (100%)	Intestine (100%)
cl194	0.19	28	276	No annotation (100%)	hnLN (100%)
cl356	0.17	21	214	exPFC1 (94.9%)	Brain (100%)
cl347	0.15	12	123	exPFC1 (86.2%)	Brain (100%)
cl151	0.15	35	349	No annotation (100%)	hnLN (100%)
cl171	0.14	67	666	No annotation (100%)	axLN (100%)
cl149	0.13	138	1376	No annotation (100%)	axLN (100%)
cl186	0.12	14	138	No annotation (100%)	hnLN (100%)
cl230	0.11	101	1006	CD4 T central memory (42.7%)	mLN (100%)
cl383	0.11	18	179	No annotation (100%)	Omentum Adipose Tissue (100%)
cl352	0.10	20	202	exDG (81.2%)	Brain (100%)
cl135	0.09	4	43	B cell (9.3%)	Intestine (90.7%)
cl394	0.07	17	171	No annotation (100%)	Brain_Microglia (100%)
cl103	0.00	0	3	dS2 (100%)	Decidua (100%)
cl104	0.00	0	3	CD8 T cell (66.7%)	mLN (100%)
cl105	0.00	0	3	B cell follicular (66.7%)	mLN (100%)
cl107	0.00	0	4	CD4 T central memory (50%)	mLN (100%)
cl108	0.00	0	3	dS3 (100%)	Decidua (100%)
cl111	0.00	0	4	VCT (100%)	Placenta (100%)
cl112	0.00	0	3	No annotation (100%)	axLN (100%)
cl114	0.00	0	3	Neutrophils (100%)	Lung Parenchyma (100%)
cl116	0.00	0	4	VCT (100%)	Placenta (100%)
cl117	0.00	0	3	B cell memory (66.7%)	mLN (100%)
cl119	0.00	0	3	Endothelium (100%)	Lung Parenchyma (100%)

Table B.17: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 9)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl120	0.00	0	3	Endo (m) (100%)	Decidua (100%)
cl121	0.00	0	3	Type 2 (66.7%)	Lung Parenchyma (100%)
cl123	0.00	0	5	dNK p (60%)	Decidua (100%)
cl125	0.00	1	15	B cell (100%)	Lung Parenchyma (100%)
cl130	0.00	0	5	No annotation (100%)	axLN (100%)
cl136	0.00	7	75	Treg NL-like (41.3%)	mLN (100%)
cl138	0.00	7	73	No annotation (100%)	Intestine (100%)
cl139	0.00	0	3	EVT (100%)	Placenta (100%)
cl140	0.00	0	4	No annotation (100%)	Brain_Microglia (100%)
cl142	0.00	0	4	Macrophages (100%)	Lung Parenchyma (100%)
cl150	0.00	10	103	No annotation (100%)	Intestine (100%)
cl154	0.00	0	4	CD4 T central memory (75%)	mLN (100%)
cl157	0.00	0	5	ffB1 (100%)	Placenta (100%)
cl158	0.00	1	14	B cell (100%)	Lung Parenchyma (100%)
cl159	0.00	0	4	Endo L (100%)	Decidua (100%)
cl161	0.00	11	115	No annotation (100%)	Intestine (100%)
cl163	0.00	3	31	B cell memory (83.9%)	mLN (100%)
cl164	0.00	9	93	No annotation (100%)	Intestine (100%)
cl165	0.00	7	67	No annotation (100%)	Intestine (100%)
cl166	0.00	8	81	No annotation (100%)	Intestine (100%)
cl167	0.00	6	57	No annotation (100%)	Intestine (100%)
cl17	0.00	0	3	No annotation (100%)	Brain_Microglia (100%)
cl170	0.00	7	69	No annotation (100%)	Intestine (100%)
cl177	0.00	9	91	No annotation (100%)	Intestine (100%)
cl182	0.00	1	13	B cell memory (69.2%)	mLN (100%)
cl188	0.00	7	68	No annotation (100%)	Intestine (100%)
cl191	0.00	4	37	No annotation (100%)	Intestine (100%)
cl193	0.00	4	42	No annotation (100%)	Intestine (100%)
cl195	0.00	7	67	No annotation (100%)	Intestine (100%)
cl196	0.00	6	64	No annotation (100%)	Intestine (100%)
cl199	0.00	1	7	Secretory (100%)	Upper airway (100%)
cl201	0.00	1	9	Plasma (100%)	Decidua (100%)
cl202	0.00	7	68	No annotation (100%)	Intestine (100%)
cl204	0.00	8	82	No annotation (100%)	Intestine (100%)
cl207	0.00	5	53	No annotation (100%)	Intestine (100%)
cl209	0.00	1	10	B cell (100%)	Lung Parenchyma (100%)
cl21	0.00	2	22	No annotation (100%)	Intestine (100%)
cl211	0.00	0	4	No annotation (100%)	Brain_Microglia (100%)
cl228	0.00	11	114	No annotation (100%)	hnLN (100%)
cl235	0.00	1	9	B cell follicular (33.3%)	mLN (100%)
cl236	0.00	1	8	Type 1 (100%)	Lung Parenchyma (100%)
cl239	0.00	0	3	No annotation (100%)	Brain_Microglia (100%)
cl244	0.00	1	6	Granulocytes (100%)	Decidua (100%)
cl249	0.00	18	182	No annotation (100%)	axLN (100%)
cl257	0.00	1	15	VCT (100%)	Placenta (100%)
cl288	0.00	8	79	No annotation (100%)	Brain_Microglia (100%)
cl289	0.00	5	52	No annotation (100%)	Brain_Microglia (100%)
cl29	0.00	0	4	B cell follicular (75%)	mLN (100%)
cl291	0.00	1	7	dS1 (100%)	Decidua (100%)
cl292	0.00	2	24	No annotation (100%)	Brain_Microglia (100%)
cl294	0.00	1	14	No annotation (100%)	Brain_Microglia (100%)
cl300	0.00	26	259	Ciliated (97.7%)	Upper airway (100%)
cl305	0.00	1	6	No annotation (100%)	Omentum Adipose Tissue (100%)
cl32	0.00	0	3	Endo (m) (100%)	Placenta (100%)
cl328	0.00	12	121	No annotation (100%)	Brain_Microglia (100%)
cl330	0.00	8	78	No annotation (100%)	Brain_Microglia (100%)
cl331	0.00	11	109	No annotation (100%)	Brain_Microglia (100%)
cl333	0.00	11	107	No annotation (100%)	Brain_Microglia (100%)

Table B.18: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 10)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl334	0.00	12	119	CD4 Tfh (73.1%)	mLN (100%)
cl342	0.00	0	5	exCA3 (80%)	Brain (100%)
cl344	0.00	2	21	GABA2 (57.1%)	Brain (100%)
cl363	0.00	6	57	No annotation (100%)	Brain_Microglia (100%)
cl381	0.00	1	7	Ciliated (100%)	Lung_Parenchyma (100%)
cl393	0.00	3	35	No annotation (100%)	Brain_Microglia (100%)
cl396	0.00	2	22	No annotation (100%)	Brain_Microglia (100%)
cl397	0.00	4	41	No annotation (100%)	Brain_Microglia (100%)
cl398	0.00	4	43	No annotation (100%)	Brain_Microglia (100%)
cl405	0.00	3	26	Kupffer Cell (69.2%)	Liver (100%)
cl406	0.00	0	5	ILC precursor (100%)	Liver (100%)
cl407	0.00	1	8	Kupffer Cell (62.5%)	Liver (100%)
cl436	0.00	0	3	CD8+/CD45RA+	Blood (100%)
				Naive Cytotoxic (100%)	
cl437	0.00	0	3	CD4+/CD25 T Reg (100%)	Blood (100%)
cl461	0.00	0	3	CD4+/CD25 T Reg (100%)	Blood (100%)
cl462	0.00	2	20	CD4+/CD45RA+/CD25-	Blood (100%)
				Naive T (55%)	
cl466	0.00	0	3	CD4+/CD25 T Reg (100%)	Blood (100%)
cl467	0.00	0	4	CD56+ NK (50%)	Blood (100%)
cl468	0.00	1	7	No annotation (100%)	Blood (100%)
cl469	0.00	1	10	No annotation (100%)	Blood (100%)
cl471	0.00	2	24	No annotation (100%)	Blood (100%)
cl482	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl487	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl489	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl499	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl521	0.00	2	19	No annotation (100%)	BoneMarrow (100%)
cl525	0.00	13	129	No annotation (100%)	BoneMarrow (100%)
cl526	0.00	4	43	No annotation (100%)	BoneMarrow (100%)
cl527	0.00	3	29	No annotation (100%)	BoneMarrow (100%)
cl528	0.00	1	8	No annotation (100%)	BoneMarrow (100%)
cl530	0.00	0	5	No annotation (100%)	BoneMarrow (100%)
cl531	0.00	0	5	No annotation (100%)	BoneMarrow (100%)
cl532	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl533	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl535	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl539	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl544	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl545	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl557	0.00	3	29	No annotation (100%)	Brain_Microglia (100%)
cl558	0.00	13	131	No annotation (100%)	Brain_Microglia (100%)
cl560	0.00	12	118	No annotation (100%)	Brain_Microglia (100%)
cl561	0.00	10	101	No annotation (100%)	Brain_Microglia (100%)
cl562	0.00	4	39	No annotation (100%)	Brain_Microglia (100%)
cl563	0.00	3	30	No annotation (100%)	Brain_Microglia (100%)
cl564	0.00	3	28	No annotation (100%)	Brain_Microglia (100%)
cl566	0.00	0	3	No annotation (100%)	Brain_Microglia (100%)
cl572	0.00	13	133	No annotation (100%)	Brain_Microglia (100%)
cl578	0.00	1	12	Endothelium; Ascending_vasa_recta; VCAM1- (8.3%)	Kidney (100%)
cl579	0.00	15	154	No annotation (100%)	hnLN (100%)
cl583	0.00	0	3	dS2 (100%)	Decidua (100%)
cl585	0.00	0	3	No annotation (100%)	BoneMarrow (100%)
cl587	0.00	1	12	ODC1 (100%)	Brain (100%)
cl588	0.00	2	19	ODC1 (94.7%)	Brain (100%)
cl589	0.00	9	88	ASC1 (48.9%)	Brain (100%)
cl599	0.00	10	101	Immature Goblet (81.2%)	Colon (100%)

Table B.19: F1 scores and class sizes for *CellTypist* trained on the human collection with integrated cluster labels. Labels are derived from the *CellTypist* pipeline, as described in Chapter 3. "Major Cell Type" refers to the most represented cell type, not counting cell without annotation, unless none have it. (continued 11)

Cluster	F1 Score	Test Support	Total Cells	Major Cell Type	Major Tissue
cl6	0.00	3	34	T cell (41.2%)	Upper airway (100%)
cl600	0.00	2	21	TA 2 (85.7%)	Colon (100%)
cl602	0.00	2	20	Immature Enterocytes 1 (35%)	Colon (100%)
cl603	0.00	1	8	Cycling TA (50%)	Colon (100%)
cl604	0.00	0	4	Enterocytes (100%)	Colon (100%)
cl605	0.00	0	3	Immature Goblet (100%)	Colon (100%)
cl607	0.00	0	3	Macrophages (66.7%)	Colon (100%)
cl61	0.00	4	39	No annotation (100%)	Intestine (100%)
cl65	0.00	0	3	Basal (100%)	Upper airway (100%)
cl66	0.00	0	4	No annotation (100%)	Intestine (100%)
cl72	0.00	2	23	B cell (87%)	Upper airway (100%)
cl78	0.00	0	3	dM2 (100%)	Decidua (100%)
cl81	0.00	1	6	dM2 (83.3%)	Decidua (100%)
cl82	0.00	0	3	dT CD4 (33.3%)	Decidua (100%)
cl84	0.00	0	3	Neutrophils (100%)	Lung Parenchyma (100%)
cl86	0.00	0	3	Basal (100%)	Upper airway (100%)
cl90	0.00	0	3	dM2 (100%)	Decidua (100%)
cl91	0.00	0	3	dM2 (66.7%)	Decidua (100%)
cl92	0.00	0	3	VCT (100%)	Decidua (100%)
cl94	0.00	0	3	CD4 Tfh (66.7%)	mLN (100%)
cl95	0.00	0	3	dNK1 (100%)	Decidua (100%)
cl98	0.00	0	5	dM3 (60%)	Placenta (100%)
cl99	0.00	0	3	CD4 Tfh (33.3%)	mLN (100%)

Table B.20: Top genes in the largest merged clusters of each *CellTypist* model

Model	Cluster	Top Genes
thr1 = 0.99, thr2 = 0.8	cl87	S100A4, FOS, KLRB1, DUSP1, NFKBIA, KLF6, LTB, CXCR4, ANXA1, SRGN
	cl147	HBG2, EEF1A1, RNASE1, HMOX1, RPL39, AL138963.3, AC026803.1, H3F3A, EGFL7, FP671120.4
	cl102	C7, DCN, DLK1, IGF2, COL3A1, COL1A1, HSPA1A, TSHZ2, HSPA1B, MMP2
	cl155	IGLL1, VPREB1, HIST1H4C, HMGB2, H3F3A, PTTG1, IL7R, CD24, SMC4, HMGA1
	cl160	MT-RNR2, MT-TT, MT-TG, SNORA31, MT-RNR1, MTCO1P40, MT-TK, EEF1A1P5, MT2A, Y_RNA
thr1 = 0.4, thr2 = 0.99	cl263	RPL10P9, RPS3A, DONSON, RPL9, RPS10, AL031280.1, SELENOM, RPS26, DPY30, RPL7
	cl530	PPBP, MT-RNR1, GNG11, HIST1H2AC, MIR1244-2, NCOA4, GPX1, PF4, OAZ1, CAVIN2
	cl215	GLRX, REXO2, CPVL, GYPB, HIST1H4C, FAM178B, HEMGN, RGS16, TUBA3C, GIHCG
	cl234	GNLY, CD52, NKG7, GZMH, CD3D, CD3G, IL32, TRGC2, TRAC, TRBC1
	cl233	IGLC2, IGLC3, HLA-DRA, CD74, AL365357.1, CD52, MIR1244-2, MTATP6P1, HLA-DQB1, AC005912.1
thr1 = 0.25, thr2 = 0.25	cl114	FN1, TPT1, MARCO, RPL10, SARAF, EEF1A1, PS3A, TIMP3, RPS29, AL365357.1
	cl72	CCL3L1, AL450405.1, RPL41, KLRF1, IGHA1, DUSP4, GZMK, CCL4L1, TYROBP, CCN1
	cl102	MTND1P23, RPS26, JUNB, AL450405.1, MTCO1P12, RPS4Y1, ACTB, C20orf204, LTB, MIR1244-2
	cl10	PLP1, LINC01116, SELE, HMOX1, IGFBP5, CXCL12, MTRNR2L8, TFPI2, HBG1, APOE
	cl23	AL450405.1, HLA-DRA, AC027290.2, RPL26, CD74, RPL39, H3F3A, RPS26, LINC01781, HLA-DRB6
thr1 = 0.1, thr2 = 0.1	cl10	AMH, DHRS2, ADAMDEC1, SELE, CRHBP, AL450405.1, INS, POSTN, TMEM88, GZMK
	cl1	FAM178B, PNMT, GAL, CCL3L1, SFTPB, GCG, RAB38, KLF1, HLA-DRB6, CCL5
	cl2	WFDC1, PHGR1, IGFBP3, PAGE4, Bambi, MARCO, IGSF6, SERPINB3, FRZB, HAPLN1
	cl20	MTND1P23, AL450405.1, NHSL2, ZNF90, JUNB, CPA5, MTCO1P12, AL513365.1, RPL9P9, RP11-138A9.2
	cl57	AL365226.1, MTRNR2L12, XAGE2, ANAPC4, AC068134.2, IL24, RETREG1, C3, CSF1R, EMX1