Table S1. General sample information across scRNA-seq replicates, Related to Figure 1.

Sample	Age	Raw reads	Clean reads (1)	Cell # (after filtering)	UMI number distribution of single cells						Mito% (2)	Ribo% (3)	Correlation coefficient (4)	
					Mean	5%	25%	Median	75%	95%				
Human-D1-T1	40y	124.9M	57.8M	808	7218	1771	2983	5114	10341	18365	5.39%	3.91%	0.9967	0.9165
Human-D1-T2		72.1M	34.2M	777	6184	1721	2795	4614	8396	15099	6.06%	3.66%		
Human-D2-T1	45y	81.3M	37.4M	420	6305	1908	2863	4914	9041	14037	0.33%	2.55%	0.9982	
Human-D2-T2		107.0M	43.8M	549	6036	2063	3072	5234	8200	13290	0.30%	2.53%		
Mouse-D1	4m	70.1M	37.3M	591	8472	1663	3717	7259	11975	19647	1.48%	1.83%	0.9655	
Mouse-D2	4m	179.5M	78.0M	1002	9308	1669	3436	7466	13484	23744	1.00%	2.28%		

Note: **(1):** The clean reads were determined by having valid barcode, UMI and linker (W1 sequence) sequences, and the mRNA region of the read was uniquely mapped to the reference genome.

(2): Mito% stands for the ratio of total UMI count of mitochondria genes versus total UMI counts of all genes.

(3): Ribo% stands for the ratio of total UMI count of ribosomal protein genes versus total UMI counts of all genes.

(4): Pearson correlation coefficient between the average gene expression profiles of biological/technical replicates.

Table S2. Detected gene numbers across scRNA-seq studies of human developmental systems, Related to Figure 1.

scRNA-seq sample / Publication	Accession Number	scRNA-seq method	Cell cluster name (1)	Cell number	Gene number distribution of single cells (2)						Gene number per cluster by bootstrap 1000 cells (3)	Gene number per sample by bootstrap 1000 cells (4)
					Mean	5%	25%	Median	75%	95%		
Human adult testicular cells / Guo et al, Cell Research, 2018	GSE112013	10X Genomics scRNA-seq	SSCs	294	4528	2524	3572	4447	5254	6539	16186	15783
			Diff. Sg	320	3971	2129	3005	4023	4817	6162	14697	
			Early Sc	560	3324	2259	2794	3149	3584	5191	14420	
			Late Sc	319	4041	1892	2866	3854	5298	6330	14391	
			RS	509	4074	1915	2964	4067	5101	6371	14746	
			ES	876	3470	1569	2355	3334	4364	6002	14904	
			Sperm-1	920	1843	1035	1358	1733	2248	2998	12535	
			Sperm-2	1025	1320	858	1034	1211	1481	2122	11576	
			PMC	338	2422	1350	1970	2385	2909	3540	13506	13951
			Macrophage	341	1815	1204	1543	1797	2039	2414	12442	
			Endothelia	353	2495	1450	1843	2229	2802	4646	13322	
			Sertoli	28	2465	1282	1947	2252	3194	3656	11522	
			Leydig	607	1747	1270	1473	1685	1955	2464	12809	
Human adult bone marrow hematopoietic cells / Pellin et al, Nature Communication, 2019	GSE117498	InDrop	HSC	1282	883	533	743	854	988	1304	11206	11703
			MPP	215	980	646	841	965	1080	1330	12322	
			MLP	123	1377	929	1122	1250	1435	2357	14348	
			PreB/NK	592	987	491	760	919	1166	1678	12238	
			MEP	1211	922	593	701	825	1048	1632	11096	
			CMP	1576	1068	478	834	996	1255	1808	11433	
			GMP	1012	1432	650	974	1326	1814	2553	12176	
			CD34+CD164+	6343	1057	510	723	966	1305	1891	11195	
			CD34-CD164high	4434	941	243	434	790	1284	2146	10505	
			CD34lowCD164high	4266	1683	693	1270	1712	2079	2663	11679	
			CD34NegCD164low	358	655	128	360	539	801	1568	10347	
Human embryonic midbrain / Le Manno et al, Cell, 2016	GSE76381	Fluidigm C1 System and protocols from Islam et al., 2014	hDA0	47	1665	908	1211	1493	2036	2853	11333	14173
			hDA1	38	2348	1056	1666	2006	2829	4438	11566	
			hDA2	37	1887	1027	1370	1689	2213	3573	10816	
			hEndo	77	2428	1273	1866	2276	2841	3923	12917	
			hGaba	59	1952	1098	1572	1809	2334	3012	12551	
			hMgl	19	2025	1113	1460	1828	2334	3323	10092	
			hNProg	100	1714	945	1257	1661	2099	2824	12433	
			hNbGaba	22	2100	928	1399	1950	2440	4683	10626	
			hNbM	91	1922	975	1218	1806	2376	3328	12392	
			hNbML1	52	2133	1018	1457	2110	2629	3466	11651	
			hNbML5	47	1864	972	1236	1790	2272	3352	11428	
			hOMTN	106	2515	1339	1928	2494	3091	3712	13133	
			hOPC	29	2221	1215	1668	2277	2759	3028	11184	
			hPeric	191	2211	1097	1671	2188	2685	3502	13773	
			hProgBP	120	2035	1115	1540	1919	2426	3328	12658	
			hProgFPL	54	2685	1544	2200	2694	3212	3752	11984	
			hProgFPM	82	2025	1255	1621	1960	2361	3038	12163	
			hProgM	67	2259	1083	1639	2256	2903	3531	12329	
			hRN	40	1833	850	1306	1703	2183	3235	10760	
			hRgl1	39	2375	1358	1844	2189	2955	3518	11771	
			hRgl2a	210	2550	1375	1990	2549	3086	3791	13750	
			hRgl2b	77	1983	1259	1544	1880	2416	2931	12753	
			hRgl2c	26	2326	1226	1686	2350	2847	3614	11028	
			hRgl3	51	2616	1301	2124	2559	3142	4067	12463	
			hSert	14	2762	1315	1850	2457	3330	4793	9943	
Human developing cortex / Nowakowski et al, Science, 2017	https://cells.ucsc.edu/?ds=cortex-dev#	Fluidigm C1 Auto-prep System	Astrocyte	46	2568	1262	2012	2449	3260	4162	12499	14652
			Choroid	14	2514	1482	2049	2498	3005	3665	9211	
			EN-PFC	242	2306	1193	1621	2220	2830	3771	13967	
			EN-V	424	2360	1214	1808	2311	2837	3601	14567	
			Endothelial	30	2477	1375	1730	2483	3028	3775	11533	
			Glyc	77	2395	1016	1498	2155	3207	4403	13569	
			IN-CTX-CGE	301	2198	1049	1581	2142	2736	3470	14321	
			IN-CTX-MGE	287	2196	1120	1606	1995	2615	3808	14083	
			IN-STR	83	2307	1212	1735	2175	3002	3596	12948	
			IPC-div	87	2426	1226	1792	2304	2891	3930	13212	
			IPC-nEN	183	2244	1237	1641	2177	2738	3692	13691	
			MGE-IPC	146	2526	1195	1661	2319	3165	4292	15867	
			MGE-RG	114	2270	1065	1627	2183	2877	3866	14134	
			MGE-div	57	2259	1229	1520	2040	2797	4057	12809	
			Microglia	77	2110	1081	1540	1856	2501	4066	13200	
			Mural	19	2057	961	1495	2099	2724	2900	9538	

			OPC	37	2440	1332	1719	2119	2913	4432	11730	
			RG-div	257	2380	1115	1694	2208	2926	3946	14161	
			RG-early	53	2603	1128	1958	2655	3045	4201	12343	
			U	191	3609	1823	2652	3618	4516	5498	14691	
			nEN-early	507	2404	1221	1804	2330	2891	3772	14792	
			nEN-late	321	2207	1121	1683	2055	2639	3795	14522	
			nIN	314	2125	1089	1482	1906	2647	3638	13820	
			oRG	65	2372	1002	1556	2200	2847	4332	12822	
			tRG	100	2304	1257	1745	2274	2685	3739	13177	
			vRG	97	2113	1207	1556	1891	2472	3737	14057	
Human embryonic kidney, week 16 / Hochane et al, PLoS Biology, 2019	GSM3143601	10X Genomics scRNA-seq	CnT	80	2175	1237	1684	2015	2510	3713	12354	13356
			DTLH	67	2425	1182	1656	2010	2830	4970	12566	
			End	223	1736	953	1186	1524	2186	3224	12291	
			ErPrT	338	1926	1130	1552	1854	2182	3065	12608	
			ICa	653	1476	943	1110	1317	1643	2630	12213	
			ICb	677	1237	944	1057	1172	1344	1747	11411	
			IPC	177	1836	1070	1429	1771	2140	2965	12439	
			Leu	65	1457	791	1005	1300	1740	2812	10443	
			Mes	37	1278	893	1118	1232	1419	1777	9170	
			NPCa	522	1251	974	1094	1207	1343	1674	11473	
			NPCb	296	1550	1027	1268	1456	1722	2452	12127	
			NPCc	596	1521	1034	1256	1467	1690	2225	12003	
			NPCd	280	2178	1358	1747	2104	2515	3277	12936	
			PTA	459	2424	1165	2018	2381	2860	3576	13109	
			Pod	430	1590	1136	1259	1414	1786	2722	11734	
			Prolif	85	1021	745	856	961	1107	1581	9074	
			RVCSBa	367	1915	1245	1559	1828	2142	3045	12693	
			RVCSBb	312	1688	1056	1314	1552	1898	2802	12431	
			SSBm/d	151	2374	1393	1607	1826	2755	4957	12987	
			SSBpod	257	1789	1238	1516	1741	1968	2486	11938	
			SSBpr	213	2415	1425	1825	2171	2814	4365	13350	
			UBCD	317	2305	1282	1719	1985	2725	4213	13183	

Note: **(1):** The cell cluster names were extracted from the original publication.

(2): The gene counts only considered protein-coding genes, thus some numbers may be slightly different from the original publication.

(3): The number represents the number of detected genes of a corresponding cell cluster. Gene expression in a single cell was defined as >0 UMI/TPM count. Gene expression in a cell cluster was defined as having expression in at least 5 cells from a random sampling (with replacement) of 1000 cells. Then the presented number of genes indicates the average detected gene number through bootstrap sampling (with replacement) of 1000 cells for 100 times. Such a strategy allows an overall fair comparison of gene numbers across studies which have different total cell numbers.

(4): Same as determining the expressed gene number of a cell cluster in (3), but instead work with the mixture of all single cells from a tissue/sample type.

Colormap: The colormap represents the relative gene number abundance in each column across all cell clusters/samples.

Gene number: Because of random sampling and/or averaging, the gene numbers in this table were rounded to the nearest integer in case necessary.

Table S3. Human gene names across gene clusters defined by germ cell expression pattern, Related to Figure 1 and 2. The gene name lists correspond to the human gene clusters defined by germ cell expression pattern in Figure 2D-E.

Table S4. Mouse gene names across gene clusters defined by germ cell expression pattern, Related to Figure S2 and STAR Methods. The gene name lists correspond to the mouse gene clusters defined by germ cell expression pattern in Figure S2C-D.

Table S5. Gene lists of bidirectional gene pairs and all upstream-confounded genes, Related to Figure 3 and STAR Methods.

Table S6. Human gene names across gene groups defined by germ cell expression levels, Related to Figure 5 and STAR Methods. The gene name lists correspond to the gene groups defined by germ cell expression levels as shown in Figure 5B.

Table S7. Gene Ontology (GO) terms analysis of the unexpressed genes (sheet 1) and highly-expressed genes (sheet 2) during human spermatogenesis, Related to Figure 7. The GO term analysis was done by GOrilla (Eden et al., 2009). 'FDR q-value' is the corrected p-values for multiple testing using the Benjamini and Hochberg method (Benjamini and Hochberg). Enrichment (N, B, n, b) is defined as 'Enrichment = (b/n) / (B/N)'. N, total number of genes; B, total number of genes associated with a specific GO term; n, number of genes in the input list; b, number of genes in the intersection. The highlighted GO terms were displayed in Figure 7A.