

Cell, Volume 174

Supplemental Information

A Single-Cell Transcriptome Atlas of the Aging *Drosophila* Brain

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Table S1 – Sequencing Metrics Summary of the Fly Brain (DGRP-551 and w1118) 10x Genomics scRNA-seq Data, related to Figure 1.

A.

Genotype	Age	Rep.	Sequencer	Estimated	Median	Mean	Number of Reads	Valid	Reads Mapped	Reads Mapped	Reads Mapped	Reads	Sequencing Saturation (%)	Fraction	Total Genes Detected	Median UMI	Expected number of cells to recover	
				Number of	Genes per	Reads per		Barcodes	Confidently to	Confidently to	Confidently to	Mapped		Reads in		Counts per		
				Cells	Cell	Cell		(%)	Confidently to Transcriptome (%)	Exonic Regions	Intronic	Intergenic		Antisense to		Cells (%)		Cell
										(%)	Regions (%)	Regions (%)		Gene (%)				
DGRP-551	0	1	NextSeq500/ HiSeq4000	1661	1525	57795	95998867	97.6	72.6	76.0	3.7	0.6	2.8	73.4	63.2	10955	4566	5000
DGRP-551	0	2	HiSeq4000	2744	1433	81585	223870057	98.1	72.7	76.4	3.9	0.6	2.4	80.8	59.1	11431	4308	5000
DGRP-551	1	1	HiSeq4000	8239	1255	26290	216610062	97.5	79.1	83.7	7.8	0.8	2.9	72.2	70.3	11720	2943	10000
DGRP-551*	1	2	HiSeq4000	6054	1,098	17857	108112065	98.2	79.2	84.7	7.2	0.8	2.9	67.7	72.1	11236	2419	5000
DGRP-551	3	1	HiSeq4000	1166	1225	48821	56925656	90.6	69.4	72.5	5.6	0.6	2.1	67.0	39.6	10281	2774	2200
DGRP-551	3	2	HiSeq4000	1991	1132	22786	45368835	98.2	80.9	85.2	5.7	0.6	2.5	66.4	61.0	10373	2626	5000
DGRP-551	6	1	HiSeq4000	1244	1035	238428	296605663	94.2	74.8	78.3	5.6	0.8	2.2	95.2	53.2	10066	2222	10000
DGRP-551	6	2	HiSeq4000	2015	1119	20985	42284828	98.2	79.8	84.4	6.3	0.7	3.0	69.1	68.9	10429	2452	5000
DGRP-551	9	1	HiSeq4000	1215	753	54862	66657345	94.9	73.1	76.3	4.4	0.7	1.9	68.3	20.8	10066	1596	2200
DGRP-551*	9	2	HiSeq4000	5331	978	19354	103177317	98.3	76.6	81.9	7.8	0.8	2.9	74.5	67.9	10,964	1884	5000
DGRP-551	15	1	NextSeq500/ HiSeq4000	3158	758	61643	194670374	97.9	71.2	74.6	6.3	0.8	2.5	91.4	61.0	10471	1573	5000
DGRP-551*	15	2	HiSeq4000	7945	842	12848	102084892	98.2	77.4	82.8	8.2	0.9	3.0	72.4	72.6	11286	1510	5000
DGRP-551	30	1	NextSeq500/ HiSeq4000	1418	631	56670	80358284	97.4	73.2	76.7	4.2	0.6	2.8	88.0	47.5	10043	1135	5000
DGRP-551	30	2	HiSeq4000	4328	922	52245	226118957	98.0	73.1	77.2	6.9	0.8	2.5	90.4	69.1	11133	1725	5000
DGRP-551	50	1	HiSeq4000	3098	810	47936	148507145	97.7	73.4	77.2	4.8	0.6	2.5	86.2	50.3	10969	1545	5000

* Short dissociation protocol

B.

Genotype	Age	Rep.	Sequencer	Estimated	Median	Mean	Number of Reads	Valid	Reads Mapped	Reads Mapped	Reads Mapped	Reads Mapped	Reads	Sequencing Saturation (%)	Fraction Reads in Cells (%)	Total Genes Detected	Median UMI Counts per Cell	Expected number of cells to recover
				Number of	Genes per	Reads per		Barcodes	Confidently to	Confidently to	Confidently to	Confidently to	Mapped					
				Cells	Cell	Cell		(%)	Transcriptome (%)	Exonic Regions	Intronic	Intergenic	Antisense to					
										(%)	Regions (%)	Regions (%)	Gene (%)					
w1118	0	1	NextSeq500/ HiSeq4000	5271	1082	42203	222453410	97.9	74.4	78.0	5.8	0.6	2.3	84.6	71.4	11051	3003	5000
w1118	0	2	HiSeq4000	2846	1515	40695	115820138	90.7	75.7	83.6	6.6	0.7	5.7	72.9	73.4	10864	3976	5000
w1118	1	1	HiSeq4000	2805	1180	60252	169007559	97.0	78.6	82.2	5.6	0.7	2.3	76.3	42.1	10995	2874	10000
w1118	3	1	HiSeq4000	1576	1113	67394	106213697	96.0	72.8	76.5	5.5	0.8	2.0	63.2	24.5	10361	2663	2500
w1118	3	2	HiSeq4000	2517	1068	31625	79600766	98.3	81.0	85.9	5.5	0.7	2.6	76.2	56.9	10492	2297	5000
w1118	3	3	HiSeq4000	2164	1141	68288	147776972	98.3	81.0	85.9	5.3	0.8	2.5	86.0	54.8	10449	2592	5000
w1118	6	1	HiSeq4000	1906	800	144181	274809678	95.1	76.4	79.7	4.8	0.8	2.1	90.2	33.8	10562	1735	10000
w1118	6	2	HiSeq4000	1794	1028	34441	61788760	95.4	73.3	76.9	6.5	0.8	2.3	54.8	29.6	10328	2187	2500
w1118	6	3	HiSeq4000	3092	1062	46310	143193161	98.3	80.0	85.1	6.2	0.8	2.7	85.7	62.2	10511	2255	5000
w1118	9	1	HiSeq4000	1151	870	89081	102532256	96.6	72.4	76.8	6.9	1.0	2.2	86.2	33.3	9845	1733	1250
w1118	9	2	HiSeq4000	1091	2039	42219	86084665	98.3	80.2	85.4	5.9	0.8	2.8	81.6	58.0	10492	2325	5000
w1118	9	3	HiSeq4000	1033	2361	39415	93059943	98.3	80.2	85.3	5.8	0.8	2.8	81.7	56.6	10433	2181	5000
w1118	14	1	NextSeq500/ HiSeq4000	1298	781	76666	99513713	97.5	69.1	72.5	5.5	0.7	2.6	92.1	63.9	9683	1714	5000
w1118	29	1	HiSeq4000	1131	374	145046	164047375	94.7	74.4	77.8	4.1	0.8	2.4	94.9	37.7	9660	714	10000