

Supplemental tables for

Transcriptional and mutational signatures of the *Drosophila* ageing germline

Evan Witt, Christopher B Langer, Nicolas Svetec, Li Zhao*

Laboratory of Evolutionary Genetics and Genomics, The Rockefeller University, New York, NY 10065, USA

*Correspondence to: lzhao@rockefeller.edu

Replicate	Number of cells	Average UMIs detected per cell	ScRNA-seq number of mapped reads	gDNA number of mapped reads	gDNA coverage
Old1	10558	10659.74	410919834	100179710	104.553
Old2	14289	4241.488	140702200	41647804	43.4658
Old3	4014	6692.628	142874684	53553546	55.8913
Young1	4000	9958.403	138231341	102792328	107.279
Young2	10000	13011.76	276598073	101604985	106.04
Young3	9489	13014.51	327810578	41436733	43.2455

Supplemental table 1: Summary statistics of each replicate and corresponding gDNA file.

Gene	Fbgn name	P value	Log ₂ fold change	Bonferroni-adjusted P	Cell type	Enriched in age
RplI215	FBgn0003277	4.12E-09	0.3973355	6.33E-05	gsc, early spermatogonia	Young
RplI18	FBgn0003275	8.75E-71	0.61734681	1.34E-66	early spermatids	Young
RplI18	FBgn0003275	3.71E-107	0.4150375	5.70E-103	early spermatocytes	Young
RplI18	FBgn0003275	5.65E-29	0.82130144	8.67E-25	gsc, early spermatogonia	Young
RplI18	FBgn0003275	2.57E-12	0.76464915	3.95E-08	late spermatids	Young
RplI18	FBgn0003275	2.56E-179	0.4866866	3.94E-175	late spermatocytes	Young
RplI18	FBgn0003275	3.36E-114	0.44202857	5.15E-110	late spermatogonia	Young
RplI15	FBgn0004855	3.79E-33	0.80140188	5.83E-29	gsc, early spermatogonia	Young
Rpb8	FBgn0037121	1.68E-41	1.0299795	2.58E-37	gsc, early spermatogonia	Young
Rpb8	FBgn0037121	2.79E-140	0.49454147	4.29E-136	late spermatogonia	Young
Rpb5	FBgn0033571	3.75E-22	0.675871	5.76E-18	gsc, early spermatogonia	Young
Mes4	FBgn0034726	3.21E-08	0.27180462	0.00049248	gsc, early spermatogonia	Young
DNApol-iota	FBgn0037554	9.08E-08	0.25715784	0.00139522	gsc, early spermatogonia	Young
Tctp	FBgn0037874	1.82E-16	-0.254537	2.80E-12	late spermatogonia	Old

RpS3	FBgn0002622	1.11E-07	-0.2738453	0.00171142	early spermatocytes	Old
RpS3	FBgn0002622	1.02E-33	-0.400618	1.56E-29	late spermatogonia	Old
Rad23	FBgn0026777	6.71E-09	-0.2740551	0.000103	early spermatocytes	Old
Rad23	FBgn0026777	1.30E-06	-0.3137124	0.02001701	gsc, early spermatogonia	Old
Pop2	FBgn0036239	3.95E-17	-0.4439238	6.07E-13	early spermatids	Old
Polr2I	FBgn0004855	4.11E-37	-0.9381206	6.31E-33	gsc, early spermatogonia	Old
Polr2I	FBgn0004855	4.64E-41	-0.2622246	7.12E-37	late spermatogonia	Old
Polr2H	FBgn0037121	3.63E-15	-0.3432375	5.58E-11	early spermatocytes	Old
Polr2H	FBgn0037121	1.04E-46	-1.27946	1.60E-42	gsc, early spermatogonia	Old
Polr2H	FBgn0037121	5.90E-33	-0.3419196	9.06E-29	late spermatocytes	Old
Polr2H	FBgn0037121	1.55E-88	-0.5176787	2.37E-84	late spermatogonia	Old
Polr2F	FBgn0003275	8.72E-30	-0.5970404	1.34E-25	early spermatocytes	Old
Polr2F	FBgn0003275	5.58E-51	-1.3372644	8.56E-47	gsc, early spermatogonia	Old
Polr2F	FBgn0003275	9.39E-29	-1.2519184	1.44E-24	late spermatids	Old
Polr2F	FBgn0003275	8.57E-121	-0.9244289	1.32E-116	late spermatocytes	Old
Polr2F	FBgn0003275	1.55E-130	-0.6554289	2.38E-126	late spermatogonia	Old
Polr2F	FBgn0003275	0	-1.2930938	0	early spermatids	Old
Polr2E	FBgn0033571	1.67E-34	-0.9207733	2.56E-30	gsc, early spermatogonia	Old
Polr2A	FBgn0003277	1.46E-19	-0.6032016	2.24E-15	gsc, early spermatogonia	Old
PolD3	FBgn0283467	1.63E-13	-0.3674564	2.51E-09	gsc, early spermatogonia	Old
CycG	FBgn0039858	4.03E-46	-0.4248538	6.20E-42	early spermatids	Old
CG32756	FBgn0052756	3.52E-08	-0.3531289	0.00054089	gsc, early spermatogonia	Old
Caf1-55	FBgn0263979	2.79E-10	-0.4207472	4.29E-06	gsc, early spermatogonia	Old
14-3-3epsilon	FBgn0020238	2.41E-07	-0.2607687	0.00370001	early spermatocytes	Old
14-3-3epsilon	FBgn0020238	2.29E-10	-0.5121799	3.51E-06	gsc, early spermatogonia	Old
14-3-3epsilon	FBgn0020238	1.76E-27	-0.3352841	2.71E-23	late spermatogonia	Old

Supplemental Table 2: Table of differentially expressed genome maintenance genes. These were calculated by splitting the main Seurat object into each cell type and setting the Idents to “age”. Raw P values are from a two-sided Wilcoxon test.

Gene	P value	Log ₂ fold change	Bonferroni-adjusted P	Enriched in fly age	Cell type	Gene class
dmel-testis-AG-merged.15917	3.38E-49	0.29428559	5.33E-45	Young	Early spermatids	segregating
dmel-testis-AG-mergedplus.2408	5.55E-20	0.29227805	8.75E-16	Young	Early spermatocytes	segregating
dmel-testis-AG-mergedminus.14760	3.92E-09	0.3235566	6.18E-05	Young	Late spermatogonia	segregating
dmel-testis-AG-merged.15917	1.70E-16	0.26208888	2.67E-12	Old	Late spermatids	segregating
dmel-testis-AG-mergedplus.3086	6.28E-195	1.28564792	9.90E-191	Old	Early spermatids	fixed
dmel-testis-AG-merged.15917	1.17E-40	0.33935426	1.84E-36	Old	Early spermatids	fixed
CG43760	8.56E-87	0.5905714	1.35E-82	Young	Early spermatids	fixed
CG43750	3.19E-46	0.25678987	5.02E-42	Young	Early spermatids	fixed
CG43449	3.44E-41	0.2949748	5.42E-37	Young	Early spermatids	fixed
CG44174	2.47E-149	1.19382429	3.89E-145	Old	Early spermatocytes	fixed
CG44227	2.61E-27	0.29089427	4.12E-23	Old	Early spermatocytes	fixed
CG43760	1.16E-10	0.26595429	1.83E-06	Young	Early spermatocytes	fixed
CG43750	8.31E-154	0.93040937	1.31E-149	Old	Cyst cells	fixed
CG43449	3.10E-91	0.74957663	4.89E-87	Old	Cyst cells	fixed
CG43760	5.47E-47	0.96654881	8.62E-43	Old	Late spermatocytes	fixed
CG43750	1.01E-24	0.94625088	1.59E-20	Old	Epithelial cells	fixed
CG43760	1.27E-08	0.4154728	0.00019959	Old	Epithelial cells	fixed
CG43760	5.91E-70	1.07260707	9.31E-66	Old	Hub cells	fixed
CG43750	1.78E-25	0.44217757	2.81E-21	Old	Hub cells	fixed
CG43760	1.26E-48	0.99877606	1.98E-44	Old	Late spermatogonia	fixed
dmel-testis-AG-merged.2415	4.16E-17	0.44607375	6.55E-13	Old	Late spermatogonia	fixed
CG43760	5.80E-42	1.28883889	9.15E-38	Old	Late spermatids	fixed
CG44329	1.08E-15	0.29891384	1.71E-11	Old	Late spermatids	fixed
CG43760	6.07E-27	1.9003241	9.56E-23	Young	Late spermatids	fixed
dmel-testis-AG-merged.7007	1.94E-11	0.91881875	3.06E-07	Young	GSC, Early spermatogonia	fixed

Supplemental Table 3: Differentially expressed *de novo* genes. Unannotated *de novo* transcripts contain the string “dmel-testis-AG-merged” and correspond to entries in our custom reference gtf file using *de novo* transcripts published in our previous work (Witt et al., 2019). Raw P values are from a two-sided Wilcoxon test.

Name	P value	Log ₂ fold change	Bonferroni-adjusted P	Enriched in fly age	Cell type
DM412	4.45E-17	0.28765355	7.02E-13	Old	Early spermatids
Jockey2	5.23E-28	0.40396657	8.25E-24	Old	Early spermatocytes
Jockey2	2.63E-37	0.60405864	4.15E-33	Young	Early spermatocytes
BS2	4.30E-20	1.04723415	6.78E-16	Young	Early spermatocytes
DMRT1B	1.61E-79	0.50192081	2.53E-75	Old	Cyst cells
DOC	1.37E-62	0.26769752	2.16E-58	Old	Cyst cells

Jockey2	9.17E-62	0.26235339	1.45E-57	Old	Cyst cells
TAHRE	3.06E-61	0.28940335	4.82E-57	Old	Cyst cells
DMRT1B	4.01E-53	0.2895345	6.32E-49	Old	Cyst cells
HETA	2.91E-52	0.34062078	4.59E-48	Old	Cyst cells
TRANSIB2	2.63E-36	0.87271865	4.14E-32	Old	Late spermatocytes
DOC	3.39E-33	0.7125252	5.34E-29	Old	Late spermatocytes
DMRT1B	2.44E-24	0.54239771	3.84E-20	Old	Late spermatocytes
Jockey2	5.76E-11	0.29940896	9.07E-07	Old	Late spermatocytes
DM412	1.74E-07	0.29024674	0.00273574	Old	Late spermatocytes
TAHRE	2.69E-09	0.37897876	4.24E-05	Old	Epithelial cells
DOC	6.17E-32	0.53975512	9.73E-28	Old	Hub cells
Jockey2	1.91E-16	0.28563862	3.00E-12	Old	Hub cells
Jockey2	5.22E-08	1.12125594	0.00082305	Young	Late spermatogonia
DOC	3.03E-07	1.88372443	0.00477686	Young	Late spermatogonia
BS2	7.18E-19	0.3484718	1.13E-14	Old	Late spermatids
DMRT1B	4.46E-16	0.39895427	7.02E-12	Old	Late spermatids
DOC	1.33E-13	0.42069063	2.09E-09	Old	Late spermatids
DM412	1.53E-11	0.29732294	2.41E-07	Old	Late spermatids
Jockey2	3.01E-10	0.56404339	4.74E-06	Old	GSC, Early spermatogonia

Supplemental Table 4: Table of differentially expressed transposable elements. Raw P values are from a two-sided Wilcoxon test.