

--- Supplementary Material ---

Fifty generations of amitosis: tracing asymmetric allele segregation in polyploid cells with single-cell DNA sequencing

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Running title: Investigating amitosis via single-cell DNA sequencing

Keywords: Amitosis, single-cell DNA sequencing, developmental variation, copy number variation, somatic mutations, somatic assortment, polyploidy

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Supplementary Figures

Supplementary Figure S1

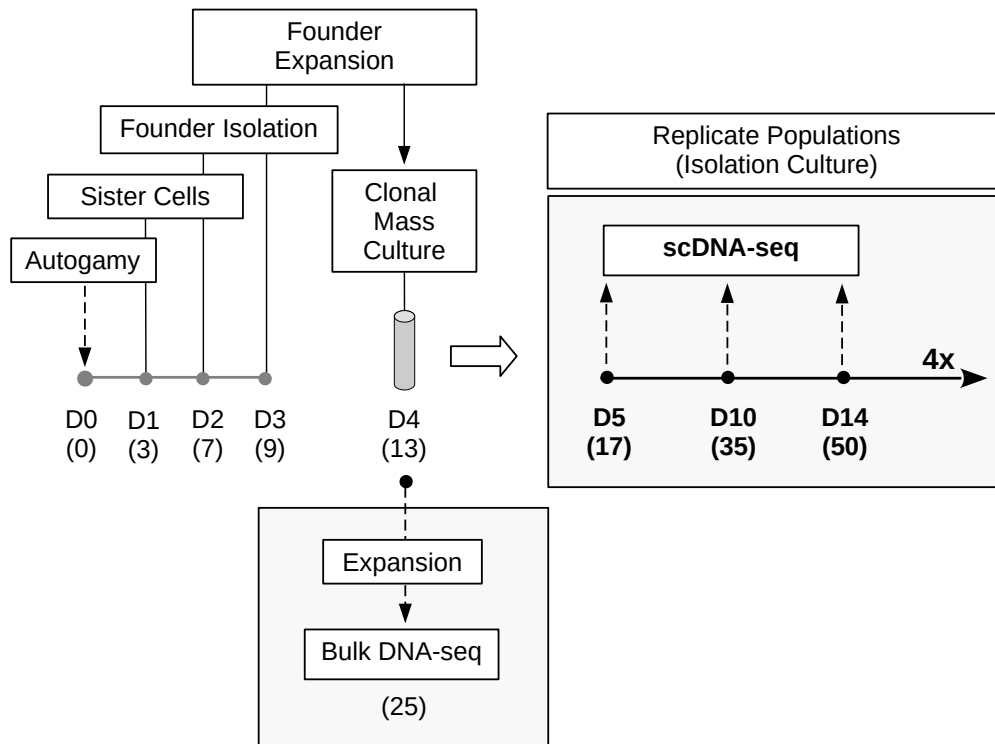


Figure S1. Experimental setup. Schematic drawing depicting the experimental setup for the time-course scDNA-seq experiment. The clonal age (divisions since last autogamy, div.) is indicated in parentheses below each day of propagation (D1 to D14). D0 → D1, post-autogamous cell isolation. D1 → D2, isolation of clonal founder (caryonide) at ~3 div. D2 → D3 → D4, expansion of clonal founder to small mass culture used to set up a series of experiments. The clonal mass culture was further expanded for bulk DNA-seq of macronuclear DNA. Clonal age is rounded to the nearest unit. For the scDNA-seq time course, the clonal age reported is the mean clonal age of the four replicate populations. The cumulative clonal age was calculated based on the divisions accrued at the time of isolation (D4 → D5), and the average (across replicates and time points) of three cell count recordings taken between D5 and D14 (D5, D6 and D10; 3.73 div./24h).

Supplementary Figure S2

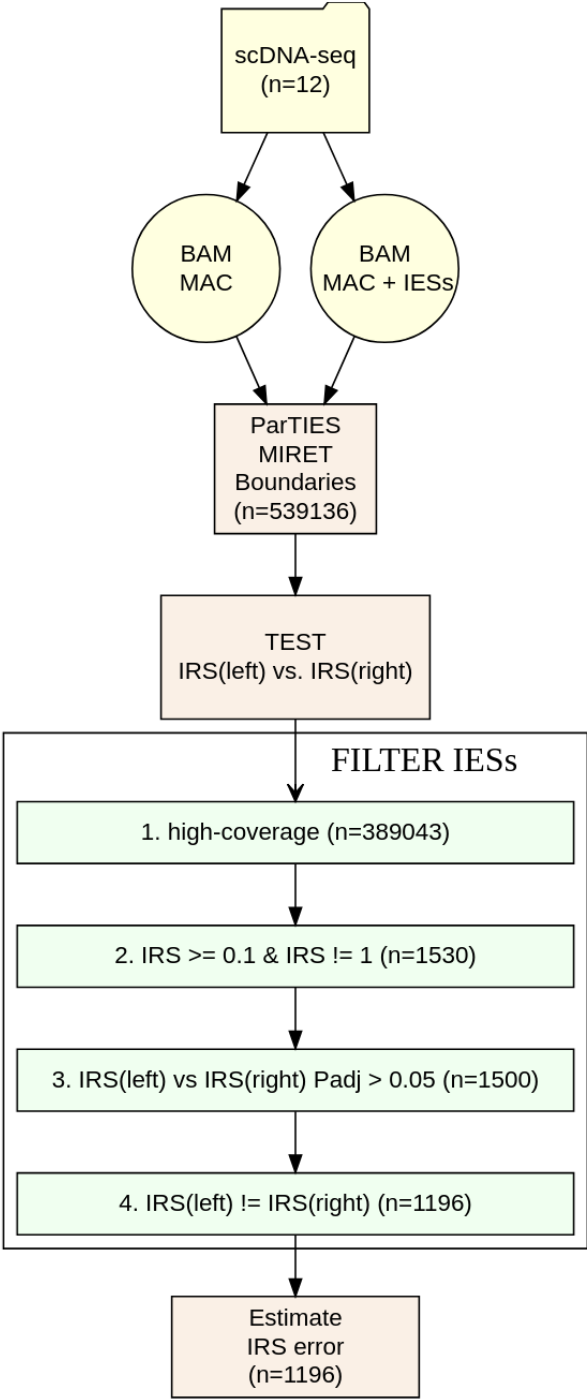


Figure S2. Quantification of the measurement error of IES Retention Scores. The diagram summarizes the bioinformatic pipeline used to estimate the random error of IES Retention Scores from scDNA-seq samples (n=12). The number of IESs passing each filtering step is indicated in parenthesis.

Supplementary Figure S3

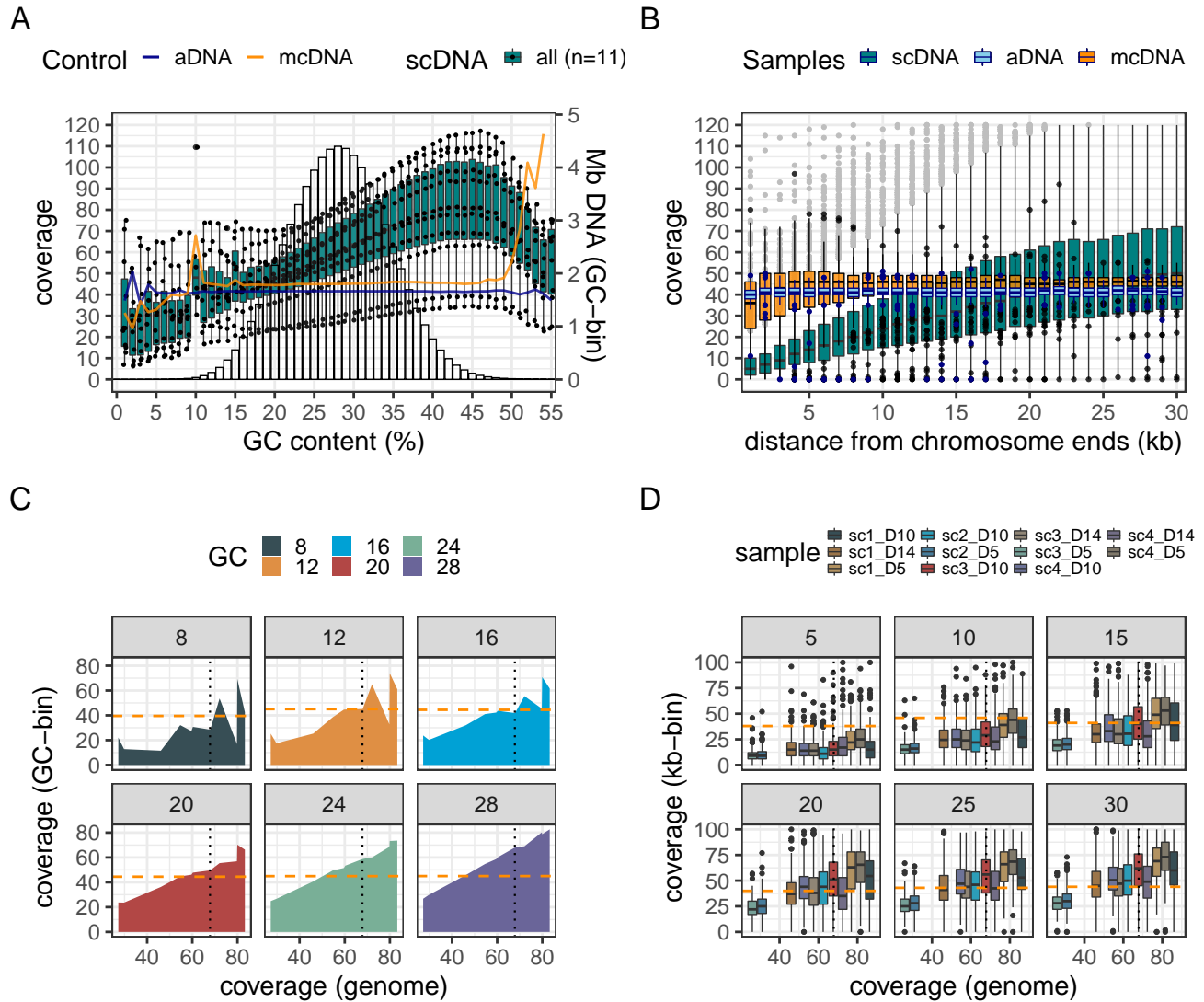


Figure S3. Genome representation biases from unnormalized coverage data. **A)** *Positive GC* Change in GC-bin coverage with GC content (1% bins). Bar chart in the background shows the amount of DNA for each GC bin (Megabases, Mb, secondary axis). **B)** *Terminal Bias.* Change in distance-bin coverage with distance (kilobases, kb) from chromosome termini (1kb bins). **C)** Change in GC-bin coverage with genome coverage for the lower half of the GC content spectrum (GC bin in % is shown above each facet). **D)** Change in distance-bin coverage with genome coverage (distance bin in kb is shown above each facet) up to 30kb from scaffold ends. Horizontal yellow dashed lines mark the coverage in the reference mcDNA-seq. Vertical black dotted lines mark the 1.5x genome coverage increase (~68) relative to mcDNA-seq (~45). scDNA, single-cell DNA sequencing ($n=11$). mcDNA, mass culture DNA sequencing ($n=1$). aDNA, artificial DNA sequencing ($n=1$). Genome coverage, average number of per-base mapped reads computed on the whole genome. GC-bin coverage, average number of per-base mapped reads computed within GC content bins. Distance-bin coverage, average number of per-base mapped reads computed within distance bins.

Supplementary Figure S4

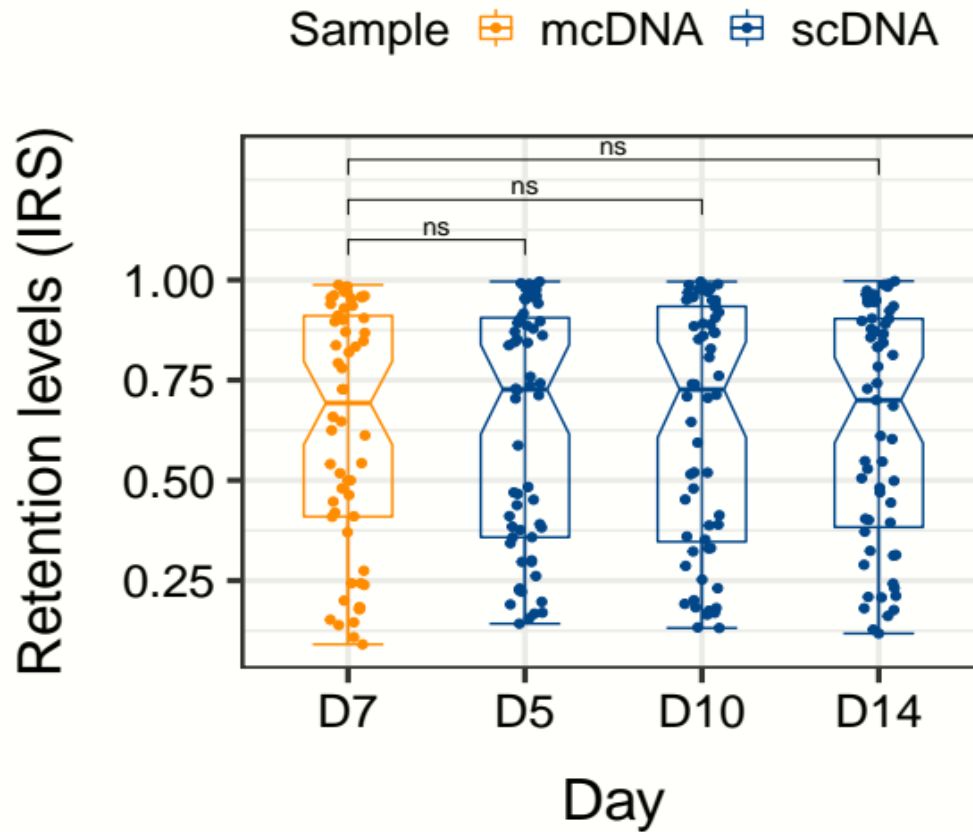


Figure S4. Comparison of empirical IES retention levels between bulk DNA-seq from mass culture and DNA-seq from single cells. A set of highly covered (>20 reads) somatic across scDNA samples ($n=75$, "Track Set") was selected for comparison. scDNA samples were collected in quadruplicates on each day (D5, D10, D14). IES retention levels (IRS) for scDNA samples were averaged out across replicates. IESs with IRS = 1 were excluded. IES sample size after filtering: D7 ($n=58$); D5 ($n=60$); D10 ($n=60$); D14 ($n=59$). IRS distributions were compared with a Wilcoxon rank sum test. mcDNA was used as reference for comparison. Significance levels for pairwise comparisons are shown above each plot (ns: $P_{adj} > 0.05$). IRS, IES retention score / retention level. IES, Internal Eliminated Sequences. Somatic IESs, IESs from macronuclear DNA with IRS ≥ 0.1 . mcDNA, bulk DNA-seq from mass culture. scDNA, DNA-seq from single-cell whole-genome amplification products (MDA reactions). MDA, Multiple, Displacement Amplification.

Supplementary Figure S5

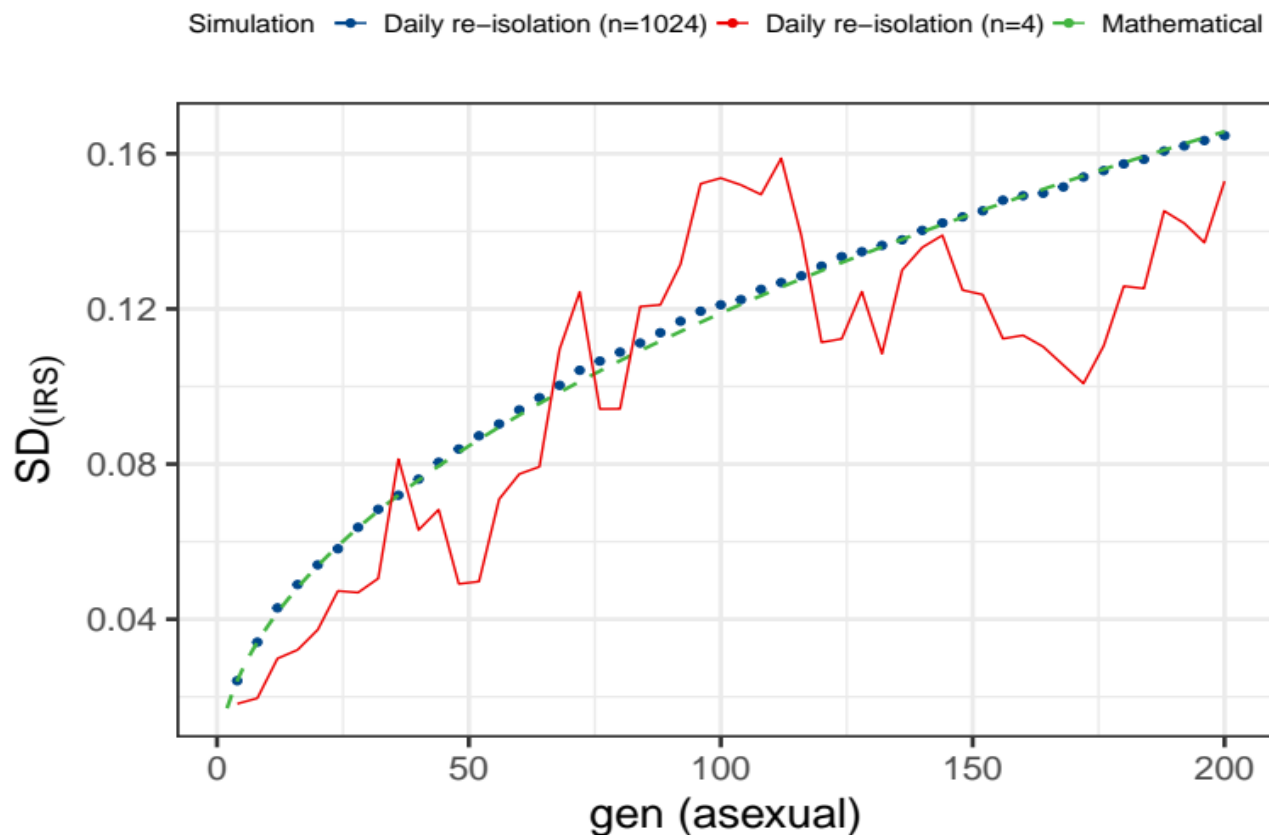


Figure S5. Validation of mathematical modeling through bioinformatic simulation of somatic assortment. Change in standard deviation (SD) of IES retention levels (IRS) across asexual generations as predicted by bioinformatic and mathematical simulations of somatic assortment. All predictions are based on the *haploid model*. See Methods for details on the simulations.

Supplementary Figure S6

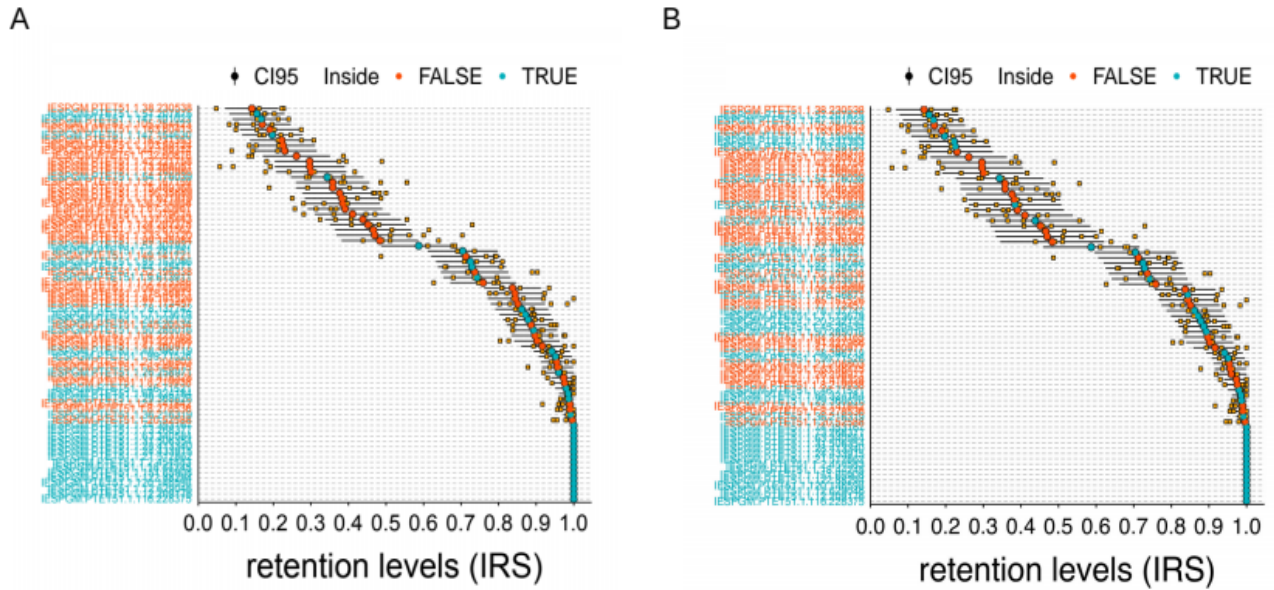


Figure S6. Observed and theoretical variation of IES retention levels after ~35 amitotic divisions. A) Haploid model. The empirical distribution of IES retention levels is compared to the theoretical distribution predicted by the haploid model (random assortment of haploid whole-genome subunits). **B) Chromosomal model.** The empirical distribution of IES retention levels is compared to the theoretical distribution predicted by the chromosomal model (random assortment of chromosomes).

Supplementary Figure S7

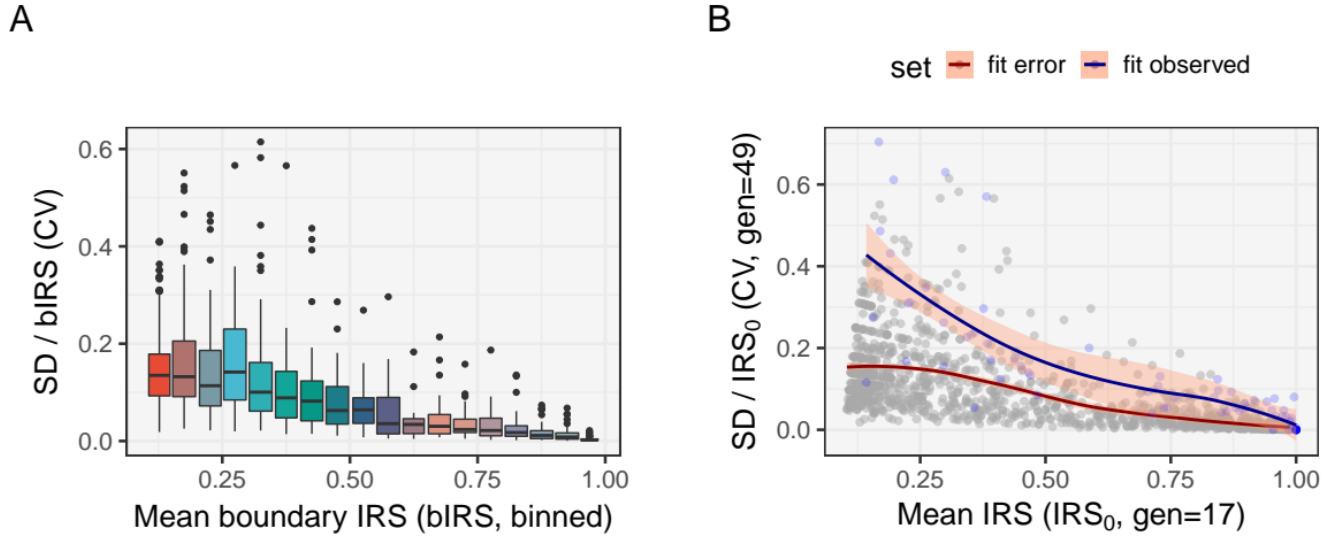


Figure S7. Random error distribution for IRS measurements. A) Relative error of IRS measurements (binned, size = 0.05) across IRS values. For each IES, the coefficient of variation of the boundary scores ($SD_{bIRS} / bIRS$) is plotted against the mean boundary score ($bIRS$). $N = 1,196$ (11 scDNA samples). SD_{bIRS} values were computed across left and right boundary scores (see Methods for details). Summary statistics for the relative random error distribution are: 1st Qu. = 0.0196562, Median = 0.0656980, Mean = 0.0937853, 3rd Qu. = 0.1355395. **B) Observed relative variation of IRSs 14 days post self-fertilization (blue circles).** For each IES, the coefficient of variation of the IRSs measured on day 14 (SD_{IRS} / IRS_0 , gen = 49) is plotted against the mean IRSs measured on day 5 (IRS_0 , gen = 17). $N = 75$ (D5, $n = 4$; D14, $n = 3$). The distribution of IRS errors (as in A) is shown for comparison (gray circles, not binned). Local polynomial regression is shown in red and blue lines for the error and the empirical distribution, respectively. Summary statistics for the absolute random error distribution are: 1st Qu. = 0.0099702, Median = 0.0189858, Mean = 0.0266522, 3rd Qu. = 0.0354437.

Supplementary Tables

Supplementary Table S1

Table S1. Genome coverage statistics for individual samples. Total pairs (M), number of read pairs (millions). **Mapped pairs (M)**, number of mapped read pairs (millions). **Mapping rate (%)**, percentage of mapped reads. **COV**, average number of per-base mapped reads. **COV 20 (%)**, proportion of bases in the genome covered by at least 20 reads (percentage). **Scaffold COV**, number of per-base mapped reads averaged across scaffolds (average scaffold coverage weighted on scaffold size). **Scaffold COV 20 (%)**, proportion of bases in a scaffold covered by at least 20 reads averaged across scaffolds (percentage). **aDNA**, artificially-generated DNA sequencing. **mcDNA**, mass culture DNA sequencing. **scDNA**, single-cell DNA sequencing.

Sample	Total pairs (M)	Mapped pairs (M)	Mapping rate (%)	COV	COV20 (%)	Scaffold COV	Scaffold COV20 (%)
aDNA	10.00	10.00	100.00	41.57	99.02	41.43	90.68
mcDNA	13.56	10.92	80.28	45.23	95.89	31.39	53.97
sc1_D5	20.77	19.35	92.92	79.78	92.92	39.10	44.81
sc1_D10	20.74	20.25	97.16	83.28	91.09	39.26	40.33
sc1_D14	12.13	11.21	92.11	46.06	87.66	24.11	37.04
sc2_D5	7.69	7.23	93.76	29.77	74.66	15.04	27.54
sc2_D10	15.12	14.69	96.59	60.25	88.15	30.36	37.18
sc2_D14*	9.72	0.44	4.75	1.77	1.34	0.00	0.71
sc3_D5	7.87	6.62	83.90	27.23	71.48	13.76	25.51
sc3_D10	17.28	16.62	95.29	67.94	90.61	37.49	40.29
sc3_D14	15.27	14.71	94.96	59.62	88.99	34.35	38.48
sc4_D5	20.79	19.41	93.10	79.94	94.16	39.25	46.45
sc4_D10	14.04	13.27	94.11	54.67	90.49	25.47	38.34
sc4_D14	18.35	17.77	96.14	72.09	89.00	44.75	39.84

Supplementary Table S2

Table S2. Genome coverage statistics (aggregates). **Total pairs (M)**, total number of read pairs (millions). **Mapped pairs (M)**, total number of mapped read pairs (millions). **Mapping rate**, fraction of reads mapped to the reference genome. **Coverage**, average number of per-base mapped reads. **Average scaffold coverage**, number of per-base mapped reads averaged across scaffolds (Coverage = average scaffold coverage weighted on scaffold size). **Coverage 20 (%)**, proportion of bases in the genome covered with at least 20 reads (expressed in percentage). **Average scaffold coverage 20 (%)**, proportion of bases in a scaffold covered with at least 20 reads averaged out across scaffolds (expressed in percentage). **aDNA**, artificially-generated DNA sequencing. **mcDNA**, mass culture DNA sequencing. **scDNA**, single-cell DNA sequencing. with a mean number of number of mapped reads comparable to the mcDNA sample ($5 \times 10^6 < n^\circ \text{ of mapped reads} < 15 \times 10^6$, $n=6$). **scDNA_2x**, scDNA samples with approximately twice as many mapped reads compared to the mcDNA sample ($n^\circ \text{ of mapped reads} > 19 \times 10^6$, $n=4$).

Sample	Total pairs (M)	Mapped pairs (M)	Mapping rate	Genome		Scaffolds	
				Coverage (reads)	Coverage 20 (%)	Average coverage (reads)	Average coverage 20 (%)
aDNA	9.99	9.99	1.00	41.57	99.02	41.43	90.68
mcDNA	13.56	10.92	0.80	45.23	95.89	31.39	53.97
scDNA 1x	12.02 ± 3.47	11.29 ± 3.62	0.93 ± 0.05	46.27 ± 14.69	83.57 ± 8.26	23.85 ± 8.18	34.01 ± 5.87
scDNA 2x	20.77 ± 0.027	19.67 ± 0.51	0.94 ± 0.024	81.00 ± 1.97	92.72 ± 1.54	39.20 ± 0.089	43.86 ± 3.17

Supplementary Table S3.

Table S3. **Selected set of 75 highly covered IES loci tracked in this study (“track set”).** **COV**, average coverage at each IES locus (averaged across all 11 scDNA samples). **mc**, mass culture sample. **sc**, single-cell sample. **D**, day of recording.

		D5				D10				D14			
IES_ID	COV	mc_D7	sc1_D5	sc2_D5	sc3_D5	sc4_D5	sc1_D10	sc2_D10	sc3_D10	sc4_D10	sc1_D14	sc3_D14	sc4_D14
IESPGM.PTET51.1.103.59124	43.00	0.0909	0.2708	0.2667	0.1786	0.1864	0.1356	0.2222	0.2143	0.1538	0.1053	0.2400	0.1395
IESPGM.PTET51.1.104.223165	46.60	0.9583	0.9455	0.9200	0.8519	0.8696	0.9091	0.9737	0.9767	0.9388	0.8462	0.9189	0.8049
IESPGM.PTET51.1.105.264423	74.80	0.2745	0.1028	0.1707	0.2759	0.1308	0.0824	0.1463	0.1964	0.1017	0.1548	0.2680	0.1071
IESPGM.PTET51.1.109.145698	53.20	0.8704	0.8507	0.7600	0.8846	0.8523	0.9344	0.8571	0.8095	0.8077	0.8036	0.7857	0.9091
IESPGM.PTET51.1.112.223386	55.90	0.7800	0.7708	0.7667	0.7576	0.7391	0.7465	0.6271	0.8000	0.7872	0.8043	0.6852	0.7377
IESPGM.PTET51.1.11.418328	44.80	0.9296	0.9400	1.0000	1.0000	0.9524	0.9750	1.0000	0.9302	1.0000	0.9259	0.9818	0.9831
IESPGM.PTET51.1.11.621919	41.80	0.3704	0.4528	0.1538	0.3810	0.5417	0.2500	0.3902	0.4865	0.4237	0.4545	0.7442	0.3171
IESPGM.PTET51.1.116.228375	62.60	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.118.231353	78.20	0.1837	0.2074	0.2439	0.2500	0.1875	0.2153	0.2747	0.2118	0.3077	0.2400	0.1695	0.2254
IESPGM.PTET51.1.120.146598	72.20	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.12.209176	56.10	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.12.260986	32.40	0.2000	0.1714	0.3125	0.2857	0.4318	0.3095	0.1786	0.2414	0.4167	0.6087	0.2500	0.3250
IESPGM.PTET51.1.122.88294	58.10	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.124.141842	70.50	0.9111	0.9722	1.0000	1.0000	0.9881	0.9593	0.9167	0.9706	0.9846	0.9600	1.0000	0.9891
IESPGM.PTET51.1.124.202375	50.00	0.5405	0.4634	0.3750	0.5000	0.4684	0.4583	0.7297	0.4082	0.4808	0.6250	0.4889	0.5263

IESPGM.PTET51.1.12.629046	89.80	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.132.167159	31.00	0.4091	0.5882	0.3750	0.2273	0.2414	0.4857	0.5556	0.3889	0.3793	0.4762	0.4483	0.4857
IESPGM.PTET51.1.133.30120	53.20	0.6122	0.6071	0.3600	0.3636	0.5484	0.7031	0.6000	0.5614	0.5116	0.6829	0.5714	0.5778
IESPGM.PTET51.1.136.214958	93.90	0.4800	0.3040	0.4314	0.3721	0.4307	0.3348	0.2800	0.3967	0.3971	0.3030	0.2388	0.4000
IESPGM.PTET51.1.137.35443	56.50	0.4634	0.4167	0.3478	0.5000	0.4881	0.3651	0.3243	0.4068	0.5556	0.5625	0.4103	0.4711
IESPGM.PTET51.1.1.379624	67.60	0.5000	0.4227	0.3750	0.3939	0.4512	0.4706	0.4464	0.3607	0.2807	0.4138	0.3452	0.4444
IESPGM.PTET51.1.138.161562	58.50	0.5179	0.5890	0.3448	0.3548	0.5769	0.4615	0.5152	0.6140	0.4694	0.4524	0.5733	0.4706
IESPGM.PTET51.1.144.125471	51.30	0.6471	0.6974	0.7037	0.8400	0.6739	0.8060	0.6604	0.6567	0.7308	0.6190	0.7750	0.7917
IESPGM.PTET51.1.144.159374	105.00	0.2432	0.2484	0.1964	0.2857	0.1895	0.1447	0.0889	0.2339	0.2111	0.1304	0.2212	0.2718
IESPGM.PTET51.1.147.101023	48.90	0.1458	0.1667	0.2400	0.1364	0.1270	0.2128	0.1579	0.2407	0.1562	0.1818	0.3659	0.1461
IESPGM.PTET51.1.147.154630	93.20	0.1818	0.2364	0.1351	0.1842	0.2324	0.2195	0.1752	0.2462	0.1628	0.3125	0.0761	0.1538
IESPGM.PTET51.1.149.141721	38.20	0.6250	0.7692	0.6800	0.6667	0.7333	0.7907	0.4865	0.7931	0.7667	0.6129	0.5714	0.6250
IESPGM.PTET51.1.151.65908	43.50	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.15.489368	53.90	0.2432	0.3788	0.3667	0.2963	0.3902	0.4023	0.4426	0.1887	0.2909	0.2619	0.4103	0.2647
IESPGM.PTET51.1.156.35689	45.80	0.4468	0.4706	0.2778	0.4000	0.3571	0.4667	0.5000	0.4828	0.4688	0.4800	0.4565	0.2759
IESPGM.PTET51.1.163.60413	87.80	0.1389	0.1635	0.1429	0.2500	0.2051	0.2743	0.1561	0.1000	0.2025	0.3333	0.1735	0.2203
IESPGM.PTET51.1.178.46871	64.10	0.8475	0.8814	0.9211	0.7317	0.8396	0.8222	0.9221	0.7927	0.7761	0.8810	0.7966	0.6735
IESPGM.PTET51.1.18.44245	52.20	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.20.232132	69.50	0.8367	0.9059	0.8235	0.8810	0.9036	0.9149	0.8971	0.8247	0.8444	0.8393	0.7971	0.8929
IESPGM.PTET51.1.20.52588	52.40	0.9688	0.9841	1.0000	1.0000	1.0000	0.9455	0.9792	0.9556	1.0000	0.8529	0.9811	1.0000
IESPGM.PTET51.1.21.206803	48.40	0.9800	0.9123	0.9722	0.9333	1.0000	0.9524	1.0000	0.9400	0.9811	1.0000	1.0000	1.0000

IESPGM.PTET51.1.21.512862	75.60	0.9877	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	0.9912	1.0000
IESPGM.PTET51.1.2.287251	66.60	0.7925	0.6300	0.6786	0.7692	0.7391	0.7355	0.6923	0.7051	0.6901	0.6364	0.6607	0.7600
IESPGM.PTET51.1.24.433915	44.40	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.2.454583	87.80	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.26.258971	92.40	0.9841	1.0000	0.8929	0.9778	0.9681	0.9739	0.9194	0.9579	0.9750	0.9778	0.9365	0.9167
IESPGM.PTET51.1.28.413340	40.90	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.29.368626	68.80	0.9615	1.0000	0.9630	1.0000	0.9836	0.9778	0.9899	0.9818	0.9643	1.0000	1.0000	0.9651
IESPGM.PTET51.1.31.506354	35.20	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.32.60876	68.70	0.2391	0.2644	0.3333	0.2703	0.1772	0.3864	0.1333	0.1429	0.2609	0.1154	0.2967	0.2155
IESPGM.PTET51.1.36.216319	75.40	1.0000	1.0000	1.0000	0.9737	0.9929	1.0000	1.0000	1.0000	0.9833	1.0000	0.9880	0.9818
IESPGM.PTET51.1.38.230538	67.20	0.1778	0.1522	0.1136	0.1395	0.1647	0.1618	0.0476	0.2273	0.2222	0.1321	0.1094	0.1414
IESPGM.PTET51.1.42.221758	47.20	0.5429	0.2529	0.3913	0.2083	0.3333	0.4889	0.1818	0.3750	0.3939	0.4250	0.3409	0.3500
IESPGM.PTET51.1.45.20534	51.20	0.9048	0.8776	0.8621	0.9032	0.9032	0.9535	0.8378	0.9474	0.9388	0.8723	0.8750	0.9457
IESPGM.PTET51.1.46.71521	75.90	0.9556	0.9391	1.0000	1.0000	0.9794	0.9865	1.0000	0.9872	0.9839	0.9500	1.0000	0.9416
IESPGM.PTET51.1.47.260977	50.00	0.9400	0.8871	0.8710	0.9706	0.9362	0.9756	1.0000	0.8929	0.9333	0.8750	1.0000	0.9762
IESPGM.PTET51.1.48.396719	77.70	0.9600	0.8889	0.9623	0.9762	0.9386	0.9314	0.9344	0.9688	0.9167	0.8481	0.9589	0.9619
IESPGM.PTET51.1.50.285016	83.20	0.8961	0.8468	0.8788	0.9643	0.8819	0.8376	0.9125	0.8962	0.9178	0.8596	0.8977	0.9510
IESPGM.PTET51.1.52.195338	46.20	0.8333	0.7297	0.6129	0.7778	0.8243	0.7174	0.8889	0.9032	0.7188	0.7778	0.8571	0.8036
IESPGM.PTET51.1.54.176039	90.50	0.5000	0.3500	0.3191	0.3333	0.3707	0.3871	0.3511	0.2951	0.2879	0.3485	0.2371	0.3868
IESPGM.PTET51.1.57.207875	54.40	0.1087	0.1250	0.2381	0.1071	0.1538	0.2020	0.1429	0.1778	0.1765	0.0870	0.1667	0.1000
IESPGM.PTET51.1.57.307937	58.20	0.6585	0.5955	0.4167	0.6818	0.6543	0.6774	0.6835	0.6111	0.6111	0.6486	0.5769	0.4189

IESPGM.PTET51.1.63.340584	61.80	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.63.46475	62.00	0.9355	0.9487	0.9375	1.0000	0.9412	0.9524	0.8780	0.9643	0.9362	0.8511	0.9870	0.9655
IESPGM.PTET51.1.67.20967	59.40	0.4103	0.3218	0.4565	0.3333	0.4512	0.3529	0.2571	0.3671	0.3137	0.3750	0.5079	0.4500
IESPGM.PTET51.1.68.324184	63.30	1.0000	0.9412	1.0000	1.0000	1.0000	0.9802	1.0000	0.9825	0.9865	1.0000	1.0000	1.0000
IESPGM.PTET51.1.71.73679	70.70	0.9697	0.8919	0.8333	0.8667	0.8919	0.8889	0.8594	0.8955	0.8947	0.9625	0.8116	0.9375
IESPGM.PTET51.1.73.268051	53.80	0.1522	0.3600	0.3750	0.2143	0.2375	0.1915	0.0923	0.1912	0.0571	0.3784	0.2344	0.2553
IESPGM.PTET51.1.73.268377	66.00	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.74.353167	105.00	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
IESPGM.PTET51.1.77.172457	61.20	0.9000	0.8990	0.8261	0.8462	0.8333	0.8023	0.9394	0.8302	0.9831	0.9054	0.8333	0.8750
IESPGM.PTET51.1.78.137742	63.90	0.9091	0.8133	0.9048	0.9130	0.8154	0.8909	0.8491	0.8875	0.8444	0.9333	0.8587	0.8784
IESPGM.PTET51.1.8.219938	100.00	1.0000	0.9802	1.0000	0.9512	0.9708	1.0000	0.9916	0.9892	0.9421	1.0000	1.0000	0.9194
IESPGM.PTET51.1.8.278536	59.70	0.9535	0.9620	1.0000	1.0000	1.0000	1.0000	0.9846	0.9556	0.9661	0.9556	0.9661	0.9118
IESPGM.PTET51.1.85.151526	58.20	0.7273	0.8481	0.8400	0.8182	0.8732	0.8660	0.9194	0.8387	1.0000	0.9189	0.9310	0.7843
IESPGM.PTET51.1.85.153086	64.30	0.8194	0.7333	0.7692	0.6250	0.7711	0.8101	0.7833	0.7083	0.7414	0.8667	0.7432	0.8876
IESPGM.PTET51.1.91.227966	62.50	0.8679	0.9394	1.0000	0.7600	0.9091	0.9104	0.9020	0.8267	0.8039	0.8226	0.8548	0.9194
IESPGM.PTET51.1.9.613911	97.50	0.7273	0.7099	0.8696	0.6744	0.7153	0.7957	0.7356	0.7478	0.6790	0.7093	0.6567	0.7341
IESPGM.PTET51.1.99.145984	47.60	0.4194	0.4098	0.4483	0.5000	0.5758	0.4386	0.4906	0.5106	0.6400	0.5000	0.5098	0.5758
IESPGM.PTET51.1.99.71526	112.00	0.9565	0.9514	0.9608	0.9118	0.9808	0.9548	0.9487	0.9655	0.9278	0.9870	0.8992	0.9620

Supplementary Table S4

Table S4. Empirical and theoretical estimates of IES retention levels across asexual divisions.

Empirical, observed variation in IES retention levels (IRS). Haploid, calculations based on the haploid whole-genome subunits model. Chromosomal, calculations based on the chromosomal model. Median standard deviation of IRS values is shown within brackets. Mean retention levels at Day 5 were taken as starting retention levels (IRS_0). Data are relative to 75 highly covered IES loci (> 20 mapped reads). IRS, IES Retention Scores. Day, 5, 10 and 14, ~17, ~35 and ~49 divisions after self-fertilization respectively. SD_{IRS} , observed and predicted standard deviation of retention levels.

Mean SD_{IRS} (<i>median</i>)	Time Point		
	Day 5	Day 10	Day 14
Empirical	0.0449 (0.0392)	0.0449 (0.0401)	0.0507 (0.0461)
Haploid	n/a	0.0296 (0.0356)	0.0394 (0.0474)
Chromosomal	n/a	0.0394 (0.0506)	0.0559 (0.0673)

Supplementary Table S5

Table S5. Predictions of somatic assortment-generated variability in allele frequency distribution across 250 divisions according to this study and Preer 1976. Predictions with the *haploid model* are for an initial number of 430 subunits and a total number of 860. Predictions with the *chromosomal model* are for an initial number of 430 subunits and a total number of 43). The standard deviation of the allele frequency is reported as fraction of the starting number of segregating subunits as in Preer 1976 (rather than fraction of the ploidy level as reported by SENES.py (this study)). The discrepancy between SENES.py and Preer's predictions for the *chromosomal model* is due to our assumption that the tendency toward chromosomal loss will affect both alleles and thus the relative fraction of IES+ copies (retention level) would remain symmetrical. To drop this assumption and reproduce Preer's predictions exactly, SENES.py should be ran with the --nullisomics flag on.

GEN	<i>Haploid model</i>		<i>Chromosomal Model</i>	
	SD (SENES.py) ^a	SD (Preer 1976) ^b	SD (SENES.py) ^c	SD (Preer 1976) ^d
50	0.16934	0.17000	0.23960	0.24000
100	0.23776	0.24000	0.33576	0.34000
150	0.28911	0.29000	0.40283	0.42000
200	0.33146	0.33000	0.45346	0.48000
250	0.36795	0.37000	0.49376	0.54000

^a Simulation with -m haploid -k 860 -i 0.5 -g 250

^b Data from Table 5

^c Simulation with -m chromosomal -c 43 -k 860 -i 0.5 -g 250

^d Data from Table 3