Rahman, et al. SUPPLEMENTARY MATERIALS SUPPLEMENTAL FIGURES AND TABLES LEGENDS

Figure S1. Detailed flowchart of the TIDAL program.

After the split, transposon insertions are detected through the steps on the left, while depletions are detected through the steps on the right. Complete parameter details are described in the Methods section.

Figure S2. Comparison of the overall transposon distributions and genomic architecture between the current Release6/dm6 build and the previous Release5/dm3 build, and functional annotations of TE InDels in cell line genomes.

(**A**) The percentage content of RepeatMasker masked sequences per 50kb window is shown above the banding patterns for each chromosome of the *D. melanogaster* genome. Many of the regions previously absent in the diagrams for Release5/dm3 were not assembled as contiguous portions of the main chromosome arms. (**B**) Proportions of the functional annotations for TE InDels in the various cell line genomes. This panel relates to Fig. 2.

Figure S3. Genomic PCR validation of TIDAL predictions for *D. melanogaster* S2c1 cells (Part 1) and ISO1 sub-strains (Part 2).

Part 1: (**A**) Transposon insertions validation tests for S2c1 cells predictions. Top, schematic of primers designed to flank the TE insertion by pairing to unique genomic sequence. Middle, gels of 15 sites tested by PCR with genomic DNA from S2c1 cells, and ISO1-BL and RAL-362 flies. Bottom, table listing the loci with TE insertions tested in the PCR assays above. (**B**) Transposons depletions validation tests for S2c1 cells predictions. Top, schematic of primers designed to flank the TE depletion by pairing to unique genomic sequence. Middle, gels of 10 sites tested by PCR with genomic DNA from S2c1 cells, and ISO1-BL and RAL-362 flies. Bottom, table listing the TE depletion by pairing to unique genomic sequence. Middle, gels of 10 sites tested by PCR with genomic DNA from S2c1 cells, and ISO1-BL and RAL-362 flies. Bottom, table listing the loci with TE depletions tested in the PCR assays above. Asterisks mark judgement calls for validations based on the absence of the reference genome allele for TE Insertions and

presence of a smaller band in the TE Depletions as an indication that the PCR result was supportive of the TIDAL prediction. **Part 2:** (**C**) Transposon insertions validation tests for ISO1-BL predictions. Top, schematic of primers designed to flank the TE insertion by pairing to unique genomic sequence. Middle, gels of 12 sites tested by PCR with genomic DNA from RAL-362, ISO1-UC, and ISO1-BL flies. Bottom, table listing the loci with TE insertions tested in the PCR assays above. (**D**) Transposons depletions validation tests for ISO1-BL predictions. Top, schematic of primers designed to flank the TE depletion by pairing to unique genomic sequence (left) and a PCR that uses one reverse primer base-pairing to the TE sequence present in the reference genome sequence (right). The reverse primer against the TE is more prone to generating a TE amplicon artifact. Middle, gels of 12 sites tested by PCR with genomic DNA from RAL-362, ISO1-UC, and ISO1-BL flies. Left gels are PCRs from primers that both flank the TE, while the right gels are PCRs with one reverse primer against TE sequence, which tends to fail more frequently with primer dimers. Bottom, table listing the loci with TE depletions tested in the PCR assays above.

Figure S4. Additional analyses of TLs in Canton-S sub-strains.

(A) Euler diagrams showing the overlap of TE InDels between sub-strains from 5 different labs, with all TE InDels in the top diagrams, whereas below are only the TE InDels with CR≥3.0. (B) Similar Euler diagrams as in (A) except that the CanS-JC substrain replaces the CanS-SH sub-strain. These diagrams are to illustrate the notably stronger overlap in TE insertions between the CanS-JC and the CanS-TP sub-strains, which are two lines maintained independently but both originating from the same single lab source. (C) Proportions of all of the InDels by TE family between the CanS substrains. (D) Proportions of InDels with CR≥3.0 by TE family between the CanS substrains, which is generally similar to the proportions of all TE InDels in (C). (E) Proportions of the genomic functional annotations immediately near the sites of TE InDels. (F) Scatterplot comparing sequencing depth to numbers of TE InDels detected amongst CanS sub-strain libraries (various combinations of independent sequencing runs). Trend lines show linear relationship between sequencing depth and server

processing time, and logarithmic relationship between depth and numbers of TE InDels detected by TIDAL.

Figure S5. Additional analyses of TLs in ISO1 sub-strains.

(A) Euler diagrams comparing the overlap of TE InDels between -BL and -CL substrain of ISO1, (B) between –BL and –AS sub-strains, and (C) between different tissues of the ISO1–AS fly line. Abbreviations: BL, Bloomington; CL, Charles Langley lab; AS, Alan Spradling lab; HEm12, Haploid Embryo samples 1&2; Ova, Ovaries; LSg123, Larval Salivary gland samples 1,2,3; Emb123, Embryos sample 1,2,3. The ISO1-BL library is from adult females from the Bloomington Drosophila Stock Center, the ISO1-CL libraries (whole flies and haploid embryos) are from the Langley lab, and the ISO1-AS libraries (ovaries, embryos, and larval salivary glands) are from the Spradling lab. (D) Proportions of InDels by TE family between ISO1 sub-strains. (E) Comparison of the InDels proportions by TE family predicted by TIDAL from different combinations of sequencing runs of the ISO1-BL libraries. Greater sequencing depth generally uncovers the rarer TE InDels in the genomic library. (F) Scatterplot comparing sequencing depth to numbers of TE InDels detected amongst ISO1 sub-strains. Trend lines show linear relationship between sequencing depth and server processing time, and logarithmic relationship between depth and numbers of TE InDels detected by TIDAL. (G) Scatterplot comparing sequencing depth to numbers of TE InDels detected amongst various combinations of independent sequencing runs of the ISO1-BL library. (H) Calculations of transposition rates in the ISO1-BL sub-strain for each TE per genomic copy and per generation, assuming that ~450 generations (~15 years between the sequencing of ISO1-BL and the original reference genome isolate, and an average 12 day life cycle).

Figure S6. Additional benchmarking results comparing TIDAL with LnB, CnT, and TEMP programs for TE insertion predictions in DGRP fly strains.

(A) For DGRP strains that are only analyzed by TEMP and TIDAL, there is much greater overlap in TE depletion predictions between the two programs (red bars) compared to the TE insertion predictions. (B) Table comparing the general design,

distinctions, and limitations of our TIDAL program compared to the other three programs with common outputs for DGRP strains. A diagram of chromosome 4's high density of transposons, from Figure S2, is shown as a reminder for how false positives can be spotted in other programs. (**C**) Euler diagrams of the overlap in TE insertions predicted by all four programs for RAL-109 and RAL-391 strains, with diagrams on the left showing all TE insertions and the diagrams on the right that lack obvious false positives such as Chr4 and Chr#Het predictions, these are frequently repetitive genomic loci that for some reason have not been masked by RepeatMasker. Note the removal of these false positives largely only reduce the predictions unique to TEMP and CnT programs.

Figure S7. Comparison of genomic PCR validation tests between TIDAL, LnB, CnT and TEMP programs for transposon insertions predictions for the RAL-765 strains. (A) Transposon insertions only predicted by TIDAL. Top, gels of 12 sites tested by PCR with genomic DNA from RAL-765, RAL-362, RAL-517, and ISO1-BL flies. Bottom, table listing the loci with TE insertions tested in the PCR assays above. The same format of panel A extends to panels B, C, and D. (B) Transposon insertions predicted by LnB which also mostly overlap with TIDAL calls. (C) Transposon insertions only predicted by the TEMP program. (D) Transposon insertions only predicted by the CnT program. Asterisks mark judgement calls for validations based on the absence of the reference genome allele for TE Insertions and presence of a smaller band in the TE Depletions as an indication that the PCR result was supportive of the TIDAL prediction.

Figure S8. Detailed profiles of transposon depletion landscapes in DGRP and DGN fly strains and pools of flies. (A) 45 DGRP Fly strains. (B) 46 DGN Fly strains. (C) 32 Pools of flies. The top panels show the total counts of transposon insertions, the middle panels show the proportions of each transposon class, and the bottom panels show the proportions of the transposon species with \geq 20 insertions (the rest are grouped together at the top). The dashed lines and labels in the bottom panels mark notable transposon species.

Figure S9. Detailed profiles of transposon insertion landscapes in DGRP and DGN fly strains and pools of flies, referring to the abridged profiles in Fig. 5. (A) 45 DGRP Fly strains. (B) 46 DGN Fly strains. (C) 32 Pools of flies. The top panels show the total counts of transposon insertions, the middle panels show the proportions of each transposon class, and the bottom panels show the proportions of the transposon species with \geq 20 insertions (the rest are grouped together at the top). The dashed lines and labels in the bottom panels mark notable transposon species.

Table S1. Details and accession numbers for Illumina libraries of *D. melanogaster* cell lines and fly strains analyzed in this study and incorporated into the TIDAL-Fly database. There are 5 tabs in this worksheet. (A) *D. melanogaster* cell lines. (B) DGRP fly strains. (C) DGN fly strains. (D) Key for the demographics of DGN fly strains. (E) Pools of flies.

Table S2. Oligonucleotides used in this study.

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See Methods Text for details of program parameters and equations.

Rahman et al. Figure S2.





Site. No.	T.E.	Locus	Nearest Gene	Coverage Ratio	Size w/o insertion	Size with insertion	PCR evidence
1	1731	chrX:325934-326139	CG3777 +,CG32816 -	4.5	349	4998	yes
2	1731	chr2L:87055-87258	net -	4	404	5053	yes
3	opus	chr2R:2675584-2675743	not near genes	3.4	332	8891	yes
4	17.6	chr3L:516184-516383	klar -	5.1	349	7788	yes
5	3S18	chr3R:6430955-6431163	gpp +	5.6	293	6126	yes
6	blood	chrX:141518-141720	CR45473 -	5.6	379	7790	yes
7	roo	chrX:6005755-6005959	CR44498 +	5	381	9473	yes*
8	297	chrX:1082310-1082488	CR44779 +,CG3655 -	3.7	373	7368	yes
9	roo	chr3R:23470563-23470775	CG4374 -	4	367	9459	yes*
10	Stalker2	chr2L:312233-312444	Plc21C +	5.9	411	8661	no
11	HMS-Beagle	chr2R:544728-544940	CG40378 +	4.9	353	6882	yes*
12	Juan	chr3L:552782-552981	hipk +	3.3	344	4580	no
13	1360	chr3R:7492347-7492543	alpha-Est10 -	4.7	374	4480	no
14	297	chr2L:522270-522480	ush +	4.9	386	7381	no
15	roo	chr3L:957937-958157	Glut1 +	7.6	296	9388	no

Sito no	TE	Locus	Notrost Cono	Coverage	Size with	Size without	PCR
Sile. 110.	1.6.	Locus	Nearest Gene	Natio	uepienon	depietion	evidence
1	jockey	chr3R:24072059-24072628	4EHP -	4.5	150	341	yes
2	roo	chr2L:7343256-7350536	Wnt6 +	4.6	5757	7480	yes
3	pogo	chrX:3842276-3842647	ec +	5.8	355	541	yes
4	Tirant	chrX:6562758-6571399	CG34417 +	5.2	1240	8802	yes
5	roo	chr2R:21753020-21753663	not near genes	5.2	405	833	yes
6	opus	chr3L:15423693-15426700	not near genes	4.6	2642	3160	yes
7	Tirant	chr3L:3061219-3069958	CG32486 -	4.6	1350	8912	yes*
8	Stalker4	chr3L:7886449-7889129	CG32365 +	4.3	1107	2873	no
9	NOF	chr3L:7985303-7987783	nmo +	4.2	620	2650	no
10	Doc	chr3R:24927069-24932010	not near genes	5.7	395	5120	no

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0.00		i touroot			0120 11/0	0.20 11111	1 010
No.	Locus	gene	T.E.	C.R.	insertion	insertion	validation
1	chr2R:19768184-19768307	not near genes	copia	4.5	295bp	5.1kb	yes
2	chr3L:4390337-4390468	slow	roo	4.5	330bp	9kb	yes
3	chr2R:8528862-8528983	mtt	I-element	4.4	273bp	7.8kb	yes
4	chr3R:29777197-29777247	kay	F-element	17.9	414bp	5kb	yes
5	chr2L:1068653-1068778	S	FB	4.2	517bp	2kb	yes
6	chrX:6542904-6543018	CG34417	I-element	4.3	501bp	7.9 kb	yes
7	chrX:19018636-19018748	CG43759	copia	4.7	469bp	5.6kb	yes
8	chr3R:5066592-5066727	not near genes	Tirant	4.4	515bp	9kb	yes
9	chrX:10556247-10556301	spri	Doc	5.7	363bp	5.3kb	yes
10	chr2L:5999659-5999785	lid	hobo	5.6	479bp	3.5kb	yes
11	chr2R:22786248-22786444	CG42260	hobo	5.3	523bp	3.5 kb	yes
12	chr2L:9485261-9485390	not near genes	hobo	4.2	514bp	3.5kb	no

Site					size with	size without	PCR vali	dation
No.	Locus	Nearest gene	T.E.	C.R.	depletion	depletion	Flank TE	Gene-T.E.
1	chr3L:2927813-2927871	shab+	Tirant	3.5	393bp	8.5kb	Yes	yes
2	chrX:11633392-11633445	Ptp10D+	297	2.9	497bp	7.3kb	Yes	No
3	chr2R:7608382-7608431	CG1358-	I-element	2.6	509bp	5.4kb	No	No
4	chr2R:8398189-8398240	CG2121-	Doc	3	502bp	5.0kb	Yes*	No
5	chr3R:31279353-31279405	not near genes	diver	2.5	436bp	6.4kb	Yes	yes
6	chrX:6335185-6335241	not near genes	Tirant	4.6	380bp	2.7kb	Yes	yes
7	chr3R:5045818-5045876	CR43635-	HMS-Beagle	4.4	448bp	7.3kb	No	yes*
8	chr3R:31691509-31691562	not near genes	Doc	4.3	449bp	5.0kb	Yes	yes*
9	chr3R:16756294-16756346	bxd-	diver	3.6	436 bp	6.4kb	Yes	yes*
10	chr2L:17951924-17951978	CR44398-	hobo	3.5	381bp	1.7kb	Yes	yes*
11	chr2L:12861671-12861728	not near genes	hobo	3.5	458bp	1.7kb	Yes	yes*
12	chr3L:8481746-8481802	CG43163-	roo	3.3	487bp	9.4kb	No	No

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Rahman et al. Figure S5.



(Cridland et al, **Thornton**)



В Program TIDAL-Fly TEMP CnT LnB Citation (Rahman et al, this study) (Zhuang et al, 2014) (Cridland et al, 2013) (Linheiro and Bergman, 2012) Bowtie1 aligner for split reads Bowtie2 aligner for reference BWA aligner, full tracking of BWA aligner, full tracking of BLAT aligner for split reads, genome reads, and BLAT to matched paired ends, natched paired ends, first stage identifies discordant Pipeline comparison to reference enforce TE insertion read calls reconstruction of candidate reads, second stage selects only unambigous reads on both summary Only single-end split reads supporting reads across strains InDels, use of BlastN for processed for discordant and computes a population alidation sides of TE insertion. mappings on both sides of requency. InDel Optimization of split short-read Versatility in application being approaches to balance applied to both Drosophila and Identifies specific Target Site sensitivity with specificity. human genomes. Strain-Duplication sequences. First Outputs and analyses focused Strain-specific TE landscapes specific DGRP InDels genomic split-read pipeline applied to on population genetics studies Distinctions in user-accessible outputs that ocations can be extracted. both 454-Roche and Illumina for Drosophila datasets from DGRP fly include rich genomic annotations for Dm6/Rel6 aenomes. genome release. Many program-specific Excludes any TE InDels in 100% Several program-specific redictions, some in Pioneering pipeline sacrificed maior heterochromatin, given predictions in Drosophila, som neterochromatic regions, that high mapping ambiguity. ensitivity by promoting strong in heterochromatic regions, nave potential to be artifacts. Cannot automatically specificity of BLAT algorithm. that have potential to be Outputs only available for Limitations determine Target Site Only detects TE insertions, no artifacts. Libraries with ibraries meeting read depth Duplication sequences apacity to detect TE multiple read lengths can trip utoff. TE Depletion data at Chr. 4 💵 Currently only optimized for depletions. up program. broad population level, not Drosophila melanogaste strain level. enomes.





Site. No.	T.E.	Locus	Coverage Ratio	Size w/o insertion	Size with insertion	PCR evidence
1	HMS-Beagle	chr2L8133670::-8133752	2.4	275	7575	yes
2	hobo	chr2L:19834994-19835061	4.7	354	3354	yes
3	BS	chr2L:12227998-12228146	5.3	274	5374	yes
4	pogo	chr2R:12581030-12581105	5	333	2533	no
5	mdg1	chr2R:7621371-7621430	4	328	7628	no
6	roo	chr3L:4481564-4481640	4.1	337	9337	yes
7	1360	chr3L:18394377-18394445	4.2	360	4760	yes
8	1360	chr3R:4885334-4885399	1.7	354	4754	yes
9	jockey	chr3R:20125023-20125087	2.4	360	5360	no
10	roo	chr3R:11089486-11089562	5.4	359	9359	no
11	hobo	chrX:7785488-7785556	3.3	342	3342	no
12	roo	chrX:15391856-15391929	4.1	341	9341	yes



Site. No.	T.E.	Locus	Coverage Ratio	Size w/o insertion	Size with insertion	PCR evidence
1	P-element	chr2L:267478-267547	4.4	314	3214	yes
2	opus	chr2L:1167146-1167232	2.6	386	8386	yes
3	Burdock	chr2L:20800099-20800248	5.8	329	6729	yes
4	3S18	chr2R:9380884-9380961	2.4	365	6465	yes
5	412	chr2R:9442941-9443015	3.9	331	7931	yes
6	blood	chr2R:11578561-11578638	5.6	372	5672	yes
7	hobo	chr3L:934796-934851	8.3	364	3364	yes
8	hobo	chr3L:22566716-22566793	4.3	367	3367	yes
9	Burdock	chr3R:18968019-18968094	3.8	375	6775	no
10	412	chr3R:30626323-30626403	5.2	379	7979	yes
11	blood	chrX:6487781-6487856	4.3	375	5675	yes
12	pogo	chrX:21399401-21399469	3.6	381	2581	yes

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Site No.	Leeve	Amuliaan Siza	PCR
Site. NO.	Locus	Amplicon Size	evidence
1	chr2L:9850436-9850443	383	yes
2	chr2L:1558495-1558995	482	no
3	chr2R:5334166-5334666	494	yes
4	chr2R:2095477-2095485	405	no
5	chr3L:9571935-9572435	482	yes
6	chr3L:5056174-5056674	499	no
7	chr3R:5035704-5035739	296	no
8	chr3R:1211275-1211285	398	no
9	chrX:294866-294869	395	yes
10	chrX:5410656-5411156	488	no
11	chrY:203747-204247	487	no
12	chrY:1565254-1565753	645	no



Site. No.	Locus	Amplicon Size*	PCR evidence
1	chrX:4334105-4334327	376	yes
2	chrX:14001033-14007159	6092	yes
3	chr3R:7696150-7703338	7171	no
4	chr3R:14021702-14023463	1734	yes
5	chr3L:4361048-4361901	844	no
6	chr3L:17180645-17180660	394	no
7	chr2R:6948454-6948972	493	no
8	chr2R:13064762-13064861	357	yes
9	chr2L:1809645-1810122	447	yes
10	chr2L:9783398-9783415	394	no
11	chr4:180927-183823	2892	yes
12	chr4:999517-1001425	2008	no

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Table S1A. Drosophila Cell Lines in the TIDAL-Fly v1 database

				modENCODE			Min Library	Library Size	Read 1				
Number	Official name	Tissue origin	Origin genotype	Name	Library ID*	SRR Accesion	Length	(M)	length	Read 2 length	Latest Ref	Other accessions	3
1	S2_C1	Embryo	Oregon R	n/a	S2c1	SRR1983913	150	33.8	150	na	This Study		
2	S2R+	Embryo	Oregon R	modENCODE_5492	S2R+	SRR497719	100	7.7	100	100	Lee et al. Genome Bio 2014	SRR497722	2x75
3	S1	Embryo	Oregon R	modENCODE_5491	S1	SRR497713	75	31.8	75	75	Lee et al. Genome Bio 2014		
4	S3	Embryo	Oregon R	modENCODE_5493	S3	SRR497721	100	11.4	100	100	Lee et al. Genome Bio 2014		
5	Sg4	Embryo	Oregon R	modENCODE_5494	Sg4	SRR497720	100	20.5	5 100	100	Lee et al. Genome Bio 2014		
6	W2	Wing disc	Oregon R	modENCODE_5495	W2	SRR497730	75	30.5	5 75	75	Lee et al. Genome Bio 2014		
7	CME W1 CI.8+	L3 wing disc	Oregon R	modENCODE_5480	CI.8	SRR497726	75	18.8	75	75	Lee et al. Genome Bio 2014		
8	CME L1	L3 leg disc	Oregon R	modENCODE_5489	L1	SRR497712	100	46.9	100	100	Lee et al. Genome Bio 2014		
9	OSS_C	Ovary	?	n/a	OSS_C	SRR1185816	150	33.7	150	na	Sytnikova et al. Genome Res 2014		
10	OSS_E	Ovary	?	n/a	OSS_E	SRR1185793	150	26.6	5 150	na	Sytnikova et al. Genome Res 2014		
11	OSC_C	Ovary	?	n/a	OSC_C	SRR609664	100	65.7	100	na	Sienski et al. Cell 2013		
12	OSC_E	Ovary	?	n/a	OSC_C	SRR1185771	150	24.6	5 150	na	Sytnikova et al. Genome Res 2014		
13	ML-DmD16-c3	L3 wing disc	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5482	D16-c3	SRR497710	100	36.6	5 100	100	Lee et al. Genome Bio 2014	SRR497715	2x75
14	ML-DmD17-c3	L3 haltere disc	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5483	D17-c3	SRR497725	100	43.4	100	100	Lee et al. Genome Bio 2014		
15	ML-DmD20-c2	L3 antennal disc	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5484	D20-c2	SRR497724	75	26.7	75	75	Lee et al. Genome Bio 2014		
16	ML-DmD20-c5	L3 antennal disc	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5490	D20-c5	SRR497723	100	12.5	5 100	100	Lee et al. Genome Bio 2014	SRR497718	2x75
17	ML-DmD4-c1	L3 mixed discs	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5486	D4-c1	SRR497716	75	36.5	5 75	75	Lee et al. Genome Bio 2014		
18	ML-DmD8	L3 wing disc	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5487	D8	SRR497729	75	29.4	75	75	Lee et al. Genome Bio 2014		
19	ML-DmD9	L3 wing disc	y ¹ v ¹ f ¹ mal ^{F1}	modENCODE_5488	D9	SRR497711	100	30.2	100	100	Lee et al. Genome Bio 2014	SRR497714	2x75
20	1182-4H	Embryo	mh	modENCODE_5479	1182-4H	SRR497717	100	21.1	100	100	Lee et al. Genome Bio 2014		
21	Mbn2	L3 hemocytes	l(2)mbn	modENCODE_5496	Mbn2	SRR497728	75	18.3	75	75	Lee et al. Genome Bio 2014		

Table S1B. Drosophila Lab Strains in the TIDAL-Fly v1 database

						Min Read	PE Reads	Read	Read	
Number	Stock ID*	Stock Location	Genome Type	Library ID*	SRA Accession	Length	(M)	Length 1	Length 2	Data Group
1	Oregon R	Terry Orr-Weaver	OregonR adult mix male female	OreR-TO1	SRR1538752	125	8.6	125	125	ModEncode
2	Oregon R	Terry Orr-Weaver	OregonR adult mix male female	OreR-TO2	SRR1538753	85	36.1	85	85	ModEncode
3	Oregon R	Sarah Elgin	OregonR adult mix male female	OreR-SE	SRR1538754	125	27.7	125	125	ModEncode
4	Oregon R	Peter Cherbas	OregonR adult mix male female	OreR-PB1	SRR1538751	85	38	125	85	ModEncode
5	Oregon R	Peter Cherbas	OregonR adult mix male female	OreR-PB2	SRR1538755	125	9.9	125	125	ModEncode
6	Oregon R	modENCODE_5497_Brent Graveley	OregonR adult virgin female	OreR-BG	SRR497727	75	19.9	75	75	ModEncode
7	Oregon-R	Dworkin lab	OregonR adult mix male female	OreR-Dw1	SRR1104304, SRR1104305	75	16.7,18	75	75	Dworkin Lab, Genetics paper
8	DarkFly	Fuse lab	OregonR-S mix	OreR-Dark	DRR001446	48	44.5	48	48	Izutsu Fuse PlosONE paper
g	Samarkand	Dworkin lab	Samarkand adult mix	Samar-Dw1	SRR1104160, SRR1104161	75	12.9	75	75	Dworkin Lab, Genetics paper
10	Canton-S substrain JC	Brembs lab, Julien Colomb from Tomas Preat	20 adult females	CanS-JC	ERR744541, ERR744542, ERR744543, ERR744544	100	8.8, 8.7, 8.7, 8.7	100	100	Brembs Lab, F1000 paper and this study
11	Canton-S substrain BS	Brembs lab, Bruno Swinderen from Ralf Greenspan	20 adult females	CanS-BS	ERR744549, ERR744550, ERR744551, ERR744552	100	7.1, 7.1, 7.2, 7.2	100	100	Brembs Lab, F1000 paper and this study
12	Canton-S substrain HS	Brembs lab, Henrike Scholz from Ulrike Herberlein	20 adult females	CanS-HS	ERR744545, ERR744546, ERR744547, ERR744548	100	10.3, 10.2, 10.3, 10.2	100	100	Brembs Lab, F1000 paper and this study
13	Canton-S substrain TP	Brembs lab, Tim Tully lab, Brandeis	20 adult females	CanS-TP	ERR744537, ERR744538, ERR744539, ERR744540	100	9.4, 9.4, 9.5, 9.6	100	100	Brembs Lab, F1000 paper and this study
14	Canton-S substrain	Brembs lab, Troy Zars from Martin Heisenberg	20 adult females	CanS-TZ	ERR744533, ERR744534, ERR744535, ERR744536	100	10.2, 10.1, 10.0, 10.0	100	100	Brembs Lab, F1000 paper and this study
15	CanS-SH	Stowers Institute, Scott Hawley lab	Adult mix, iso-2,3,X	CanS-SH	SRR2044310	150	25.5	150	150	Public deposit
16	w[1118]	Stowers Institute, Scott Hawley lab	Adult mix, iso-2,3,X	w_1118	SRR2044312	150	27.2	150	150	Public deposit
17	ISO1 - BL	Bergman lab, ISO1 from Bloomington	10 adult males	ISO1-BL	ERR701706, ERR701707, ERR701708, ERR701709, ERR701710, ERR701711	100	15, 14.9, 14.9, 15.1, 14.8, 15.0	100	100	Gutzwiller et al, ArXiv
18	ISO1-CL1	Langley lab ISO1, mixed adults	mixed adult	ISO1-CL1	SRR350908	75	21.8	100	100	Langley et al (Begun), Genetics 2012
19	ISO1-CL-HEm3	Langley lab ISO1, haploid embryos	haploid embryos	ISO1-CL-HEm3	SRR306608	100	16.4	100	100	Langley et al (Begun), Genetics 2012
20	ISO1-CL-HEm12	Langley lab ISO1, haploid embryos	haploid embryos	ISO1-CL-HEm12	SRR097732, SRR306607	75	24.2, 19.7	75	75	Langley et al (Begun), Genetics 2012
21	ISO1-AS-Ova	Spradling lab ISO1, Ovaries	females	ISO1-AS-Ova	SRR1519054	100	71.5	100	100	Yarosh and Spradline, GenesDev 2014
22	ISO1-AS-Emb123	Spradling lab, ISO1 embryos	0-18hr embryos	ISO1-AS-Emb123	SRR1516224	100	81.8, 69.1, 50.5	100	100	Yarosh and Spradline, GenesDev 2014
23	ISO1-AS-LSg123	Spradling lab ISO1, L3 Salivary gland	L3 instar	ISO1-AS-LSg123	SRR1516221, SRR1516223, SRR1516225	100	62.9, 88.4, 68.6	100	100	Yarosh and Spradline, GenesDev 2014
24	OreR-AS-FC	Spradling lab OreR, stg10-14 follicle cells	females	OreR-AS-FC	SKK1519051	100	43.1	100	100	Yarosh and Spradline, GenesDev 2014

Table S1C. Drosophila Lab Strains in the TIDAL-Fly v1 database

-Fly v1 database Genomes previously examined in McKay et al, Nature 2012, and Huang et al, Genome Res, 2014

PHASE 1: First Set of Libraries Analyzed for the paper. The remaining libraries in Phase 2 below are also listed in the TIDAL-Fly database

	Oto alla ID*		SRA	Liberry IDt		Min Read	Deedlarsth 4	Read	Data Gauna	Reads	Raw Read Length:Read Number	Freeze	E	Bloomingto n Stock Synonym	NCBI SRA	Reads R	lapped leads	Mapped Coverage	Strains
Library	1 DGRP 362	Bloomington-25187 inbred line.	mix of SRX006288	RAI -362	SRR Accession SRR846985	Length 125	Read Length 1 merged, use min lengt	Length 2 h 125.0	Data Group	(IVI) 56.3	45bp:18900352, 75bp:19241828, 1		Blor	25187 RAI -362	SRX006288 and	70.4	70.371.466	39.4	- 1
	2 DGRP 517	Bloomington-25197 inbred line,	mix of SRX024363	RAL-517	SRR933579	75	merged, use min lengt	h 75.0	DGRP-F1	59.8	45bp:75005702, 75bp:44531158	DGRIF1 F	Blo	25197 RAL-517	SRX024363 and	115.8	115,773,424	37	2
	3 DGRP_765	Bloomington-25204 inbred line,	mix of SRX006169	RAL-765	SRR933595	75	75.0	75.0	DGRP-F1	19.9	75bp:39893442	DGRIF1 E	Blo	25204 RAL-765	SRX006169 and	38.1	38,107,800	16.3	3
	4 DGRP_109	Bloomington-28140 inbred line,	mix of SRX020746	RAL-109_75b	SRR835219	75	merged, use min lengt	h 125.0	DGRP-F1	44.8	75bp:28899572, 125bp:60695744	DGREF1 E	Blo	28140 RAL-109	SRX020746 and	78.6	78,598,946	48.7	4
	5 DGRP_109	Bloomington-28140 inbred line,	mix of SRX020746	RAL-109_125b	SRR835219	125	merged, use min lengt	h 125.0	DGRP-F1	44.8	75bp:28899572, 125bp:60695744	DGRIF1 E	Blo	28140 RAL-109	SRX020746 and	78.6	78,598,946	48.7	4
	6 DGRP_229	Bloomington-29653 inbred line,	mix of SRX021052	RAL-229_75b	SRR835221	75	merged, use min lengt	h 125.0	DGRP-F1	49.6	75bp:27785294, 125bp:71504164	DGRIF1 E	Blo	29653 RAL-229	SRX021052	83.9	83,937,442	52.7	5
	7 DGRP_229	Bloomington-29653 inbred line,	mix of SRX021052	RAL-229_125b	SRR835221	125	merged, use min lengt	h 125.0	DGRP-F1	49.6	75bp:27785294, 125bp:71504164	DGRIF1 E	Blo	29653 RAL-229	SRX021052	83.9	83,937,442	52.7	5
	8 DGRP_301	Bloomington-25175 inbred line,	mix of SRX005978	RAL-301_75b	SRR835223	75	merged, use min lengt	h 125.0	DGRP-F2	73.6	45bp:13099368, 64bp:10588312, 7	75DGRFF2 E	Blo	25175 RAL-301	SRX155995 and	133.5	133,504,636	71.7	6
	9 DGRP_301	Bloomington-25175 inbred line,	mix of SRX005978	RAL-301_125b	SRR835223	125	merged, use min lengt	h 125.0	DGRP-F2	73.6	45bp:13099368, 64bp:10588312, 7	/SDGRF2 E	Blo	25175 RAL-301	SRX155995 and	133.5	133,504,636	/1./	6
1	0 DGRP_303	Bloomington-25176 Inbred line,	mix of SRX005986	RAL-303_1000	SRR835228	100	merged, use min lengt	n 100.0	DGRP-F2	161.6	45bp:79536584, 64bp:4167822, 10	JUDGRIFZ E	Blo	25176 RAL-303	SRX155978 and	287.4	287,358,990	148	7
1	1 DGRP_303	Bloomington 25177 inbred line,	mix of SRX005966	RAL-303_1250	SRR033220	125	merged, use min lengt	h 100.0	DGRP-F2	142.6	450p:79536584, 640p:4167822, 10 46bp:26081102, 64bp:7071260, 76	DOGRIFZ E	Blo	25176 RAL-303	SRX155976 and SRX156000 and	207.4	267,356,990	140	
1	2 DGRP_304	Bloomington-25177 Inbred line,	mix of SRX005988	RAL-304_730	SRR835236	100	merged, use min lengt	h 100.0	DGRP-F2	142.0	45bp:25081192, 64bp:7071260, 75		BIO	25177 RAL-304	SRX156009 and	252.1	252,108,056	133.0	5
1	4 DGRP 304	Bloomington-25177 inbred line,	mix of SRX005988	RAL-304_1000	SRR835236	125	merged, use min lengt	h 100.0	DGRP-F2	142.0	45bp:25081192_64bp:7071260_75	STDGRIF2 F	Blo	25177 RAL-304	SRX156009 and	252.1	252,100,050	133.6	c 8
1	5 DGRP 306	Bloomington-37525 inbred line.	mix of SRX006140	RAL-306 75b	SRR835242	75	merged, use min lengt	h 125.0	DGRP-F2	63.2	45bp:29368112, 64bp:8510324, 75	DGRIF2 F	Blor	37525 RAL-306	SRX156007 and	100.4	100.446.332	50.7	9
1	6 DGRP_306	Bloomington-37525 inbred line,	mix of SRX006140	RAL-306_125b	SRR835242	125	merged, use min lengt	h 125.0	DGRP-F2	63.2	45bp:29368112, 64bp:8510324, 75	5tDGRFF2 E	Blo	37525 RAL-306	SRX156007 and	100.4	100,446,332	50.7	g
1	7 DGRP_307	Bloomington-25179 inbred line,	mix of SRX006186	RAL-307_75b	SRR835247	75	merged, use min lengt	h 75.0	DGRP-F2	144.8	36bp:9641364, 45bp:17304248, 75	5tDGRFF2 E	Blo	25179 RAL-307	SRX156012 and	252.2	252,236,309	142.1	10
1	8 DGRP_307	Bloomington-25179 inbred line,	mix of SRX006186	RAL-307_100b	SRR835247	100	merged, use min lengt	h 100.0	DGRP-F2	144.8	36bp:9641364, 45bp:17304248, 75	5LDGRFF2 E	Blo	25179 RAL-307	SRX156012 and	252.2	252,236,309	142.1	10
1	9 DGRP_307	Bloomington-25179 inbred line,	mix of SRX006186	RAL-307_125b	SRR835247	125	merged, use min lengt	h 125.0	DGRP-F2	144.8	36bp:9641364, 45bp:17304248, 75	5tDGRFF2 E	Blo	25179 RAL-307	SRX156012 and	252.2	252,236,309	142.1	10
2	0 DGRP_315	Bloomington-25181 inbred line,	mix of SRX006143	RAL-315_75b	SRR835252	75	merged, use min lengt	h 125.0	DGRP-F2	63.1	45bp:48481060, 75bp:20407822, 8	BEDGREF2 E	Blo	25181 RAL-315	SRX156010 and	114.4	114,404,766	51	11
2	1 DGRP_315	Bloomington-25181 inbred line,	mix of SRX006143	RAL-315_125b	SRR835252	125	merged, use min lengt	h 125.0	DGRP-F2	63.1	45bp:48481060, 75bp:20407822, 8	BEDGRIF2 E	Blo	25181 RAL-315	SRX156010 and	114.4	114,404,766	51	11
2	DGRP_340	Bloomington-28174 inbred line,	mix of SRX156030	RAL-340_100b	SRR835939	100	merged, use min lengt	h 100.0	DGRP-F2	103.7	75bp:41788984, 100bp:165697712		Blo	28174 RAL-340	SRX156030	130.2	130,158,488	73.8	12
2	3 DGRP_371	Bloomington-28183 inbred line,	mix of SRX021257	RAL-371_75b	SRR835326	75	merged, use min lengt	h 125.0	DGRP-F1 + F2	42.6	75bp:30869276, 125bp:27187181	DGREF1 + F2 E	Blo	28183 RAL-371	SRX021257 and	78.6	78,638,404	42.5	13
2	4 DGRP_371	Bloomington-28183 inbred line,	mix of SRX021257	RAL-371_125b	SRR835326	125	merged, use min lengt	h 125.0	DGRP-F1 + F2	42.6	75bp:30869276, 125bp:27187181	DGRFF1 + F2 E	Blo	28183 RAL-371	SRX021257 and	78.6	78,638,404	42.5	13
2	5 DGRP_373	Bloomington-28184 inbred line,	mix of SRX023425	RAL-373_95b	SRR835329	95	merged, use min lengt	h 125.0	DGRP-F1	42.8	95bp:40216244, 125bp:45373906	DGRIF1 E	Blo	28184 RAL-373	SRX023425 and	76.7	76,690,462	48.3	14
2	6 DGRP_373	Bloomington-28184 inbred line,	mix of SRX023425	RAL-373_125b	SRR835329	125	merged, use min lengt	h 125.0	DGRP-F1	42.8	95bp:40216244, 125bp:45373906	DGRIF1 E	Blo	28184 RAL-373	SRX023425 and	76.7	76,690,462	48.3	14
2	7 DGRP_409	Bloomington-28278 inbred line,	mix of SRX021243	RAL-409_95b	SRR835331	95	merged, use min lengt	h 125.0	DGRP-F1	38.7	95bp:33305170, 125bp:44122246	DGRIF1 E	Blo	28278 RAL-409	SRX021243 and	55.1	55,099,676	35.7	15
2	8 DGRP_409	Bloomington-28278 inbred line,	mix of SRX021243	RAL-409_125b	SRR835331	125	merged, use min lengt	h 125.0	DGRP-F1	38.7	95bp:33305170, 125bp:44122246	DGRIF1 E	Blo	28278 RAL-409	SRX021243 and	55.1	55,099,676	35.7	15
2	9 DGRP_584	Bloomington-28212 inbred line,	mix of SRX155987	RAL-584_95b	SRR835942	95	merged, use min lengt	h 125.0	DGRP-F2	70	95bp:93885100, 125bp:46038390	DGRFP2 E	Blo	28212 RAL-584	SRX155987 and	79.7	79,663,962	49.4	16
3	0 DGRP_584	Bloomington-28212 Inbred line,	mix of SRX155987	RAL-584_1250	SRR835942	125	merged, use min lengt	n 125.0	DGRP-F2	/(95bp:93885100, 125bp:46038390	DGRF2 E	Blo	28212 RAL-584	SRX155987 and	79.7	79,663,962	49.4	16
3	DGRP_746	Bloomington 28224 Inbred line,	mix of SRX156019	RAL-746_950	SERESSSS	95	merged, use min lengt	n 125.0	DGRP-F2	43.7	950p.36957084, 1250p.50455402	DGRIF2 E	Blo	20224 RAL-740	SRX156019 and SRX156010 and	57.4	57,410,828	30.3	1/
3	2 DGRP_748	Bloomington-28234 inbred line,	mix of SRX130019	RAL-746_1250	SRR835341	125	merged, use min lengt	h 125.0	DGRP-F2	43.7	a5bp:32022146_125bp:53800816	DGRIFZ E	BIO	28224 RAL-746	SRX130019 and	50.3	59 280 892	38.4	1/
3	4 DGRP 801	Bloomington-28234 inbred line,	mix of SRX021391	RAL-801_335	SRR835341	125	merged, use min lengt	h 125.0	DGRP-F1	43.4	95bp:32922146, 125bp:53899816	DGRIFI E	Blo	28234 RAL-801	SRX021391 and	59.3	59 280 892	38.4	10
3	5 DGRP 802	Bloomington-28235 inbred line,	mix of SRX025318	RAL-802 95b	SRR835343	95	merged, use min lengt	h 125.0	DGRP-F1	47.1	95bp:27114342, 125bp:67142296	DGRIE1 F	Blor	28235 RAI -802	SRX025318 and	78.6	78,579,930	52.4	10
3	6 DGRP 802	Bloomington-28235 inbred line.	mix of SRX025318	RAL-802 125b	SRR835343	125	merged, use min lengt	h 125.0	DGRP-F1	47.1	95bp:27114342, 125bp:67142296	DGRIF1 F	Blor	28235 RAL-802	SRX025318 and	78.6	78.579.930	52.4	19
3	7 DGRP_808	Bloomington-28238 inbred line,	mix of SRX021402	RAL-808 75b	SRR835345	75	merged, use min lengt	h 125.0	DGRP-F1	53.8	75bp:44482188, 125bp:63083538	DGRIF1 E	Blo	28238 RAL-808	SRX021402 and	83.0	82,954,992	49.3	20
3	8 DGRP_808	Bloomington-28238 inbred line,	mix of SRX021402	RAL-808_125b	SRR835345	125	merged, use min lengt	h 125.0	DGRP-F1	53.8	75bp:44482188, 125bp:63083538	DGRIF1 E	Blo	28238 RAL-808	SRX021402 and	83.0	82,954,992	49.3	20
-	DGRP_821	Bloomington-28243 inbred line,	mix of SRX155991	RAL-821_100b	SRR835347	100	merged, use min lengt	h 100.0	DGPP-F2	108.2	100bp:132570414, 125bp:83747778	DGRI ^{F2}	Blo	28243 RAL-821	SRX155990 and	179.3	179,277,520	112	21
	DGRP_821	Bloomington-28243 inbred line,	mix of SRX155991	RAL-821_125b	SRR835347	100	merged, use min lengt	h 100.0	DCPP F2	108.2	100bp:132570414, 125bp:83747778	DORI F2		28243 RAL-821	SRX155990 and	179.3	179,277,520	112	21
4	. DGRP_853	Bloomington-28250 inbred line,	mix of SRX021491	RAL-853_110b	SRR835349	125	merged, use min lengt	h 125.0	DGRP-F2	55.3	110bp:42021476, 125bp:68611046	DGR E		28250 RAL-853	SRX021491 and	69.8	69,801,922	48.9	21
4	DGRP 853	Bloomington-28250 inbred line	mix of SRX021491	RAL-853 125b	SRR835349	110	merced use min lengt	h 125.0	DGRP-FZ	55.3	110bp:42021476_125bp:68611046	DGRI E	BIO	28250 RAL-853	SRX021491 and	69.8	69 801 922	48.9	22
4	2	Discourse and a second second second		DAL 000_05	00000400000	125	5,o minisingi		DGRP-F2			DGRI E	Blo	00001 011 000	000/450000		77.055.51	.5.5	22
4	3 DGRP_900	Dicomington-28261 Inbred line,	mix of SRX156023	RAL-900_95b	SKK846989	95	mergea, use min lengt	n 125.0	DGRP-F2	47.6	9500130160598, 12500165136580	DGRIF2 E	BIO	28261 KAL-900	SRX156023	77.4	77 255 542	52.3	23
4	4 DGRP_900	Bloomington-28190 inbred line,	mix of SRX156012	RAL-900_125b	SPR83/662	125	mergeu, use min iengt	125.0	DGRP-F2	47.6	330p:30100396, 1250p:65136580		BIO	20201 KAL-900	SRX 100023	11.4 E7.6	57 502 490	52.3	23
4	6 DGRP 223	Bloomington-28155 inbred line,	mix of SRX155004	RAL-302	SRR83/527	125	12	5 105	DGRP-F2	30.5	1255p.73012234	DGRIF2 E	BIC	28155 RAL-302	SRX15500/	57.0	57 181 804	41.1	24
4	7 DGRP 850	Bloomington-28249 inbred line,	mix of SRX155993	RAL-850	SRR835061	125	12	5 125	DGRP-F2	34 8	125bp:69699750	DGRIE2	Blo	28249 RAI -850	SRX155993	61.0	60,987,804	43.6	25
4	8 DGRP_913	Bloomington-28265 inbred line.	mix of SRX156024	RAL-913	SRR835077	125	12	5 125	DGRP-F2	34.6	125bp:69250292	DGRIF2 F	Blo	28265 RAL-913	SRX156024	61.2	61,221,716	43.7	20
4	9 DGRP_843	Bloomington-28247 inbred line,	mix of SRX156036	RAL-843	SRR835059	125	12	5 125	DGRP-F2	34.3	125bp:68658714	DGRFF2 E	Blo	28247 RAL-843	SRX156036	59.2	59,174,050	42.3	28
5	0 DGRP_361	Bloomington-28180 inbred line,	mix of SRX155984	RAL-361	SRR834553	125	12	5 125	DGRP-F2	34.1	125bp:68254340	DGRIF2 E	Blo	28180 RAL-361	SRX155984	56.9	56,897,940	40.6	29
5	1 DGRP_189	Bloomington-28152 inbred line,	mix of SRX155979	RAL-189	SRR834523	125	12	5 125	DGRP-F2	31.6	125bp:63289120	DGRIF2 E	Blo	28152 RAL-189	SRX155979	52.9	52,919,862	37.8	30
5	2 DGRP_849	Bloomington-28248 inbred line,	mix of SRX156035	RAL-849	SRR835060	125	125	5 125	DGRP-F2	30.8	125bp:61687178	DGRFF2 E	Blo	28248 RAL-849	SRX156035	55.8	55,797,340	39.9	31
5	3 DGRP_142	Bloomington-28144 inbred line,	mix of SRX020759	RAL-142	SRR834551	100	110	110	DGRP-F1	20.6	110bp:41167794	DGRI F1 E	Blo	28144 RAL-142	SRX020759	31.4	31,409,058	19.7	32
5	4 DGRP_822	Bloomington-28244 inbred line,	mix of SRX021476	RAL-822	SRR835055	100	110	110	DGRP-F1	20.5	110bp:41079524	DGRIF1 E	Blo	28244 RAL-822	SRX021476	28.1	28,098,026	17.7	33
5	5 DGRP_75	Bloomington-28132 inbred line,	mix of SRX021384	RAL-75	SKR835087	100	11(110	DGRP-F1	19.1	110bp:38161744	DGRIF1 E	Blo	28132 RAL-75	SRX021384	29.5	29,460,700	18.5	34
5	6 DGRP_395	Bioomington-28194 inbred line,	mix of SRX156015	RAL-395	SKK834521	100	10'	101	DGRP-F2	43.6	1010p:8/233368	DGR#F2 E	Blo	28194 RAL-395	SRX156015	81.5	81,549,134	47.1	35
5	DCRP_819	Bloomington-28242 Inbred line,	mix of SRX156006	RAL-819	SKK833054	100	100	100	DGRP-F2	/5.4	1000p:150745358	DGRIF2 E	Blo	28242 KAL-819	SRX156006	127.8	127,803,094	73	36
5	0 DGRP_5/	Bloomington-28052 Inbred line,	mix of SRX021296	RAL-07	SRR933381	100	100	100		32.5	1000p:64900990 100bp:61689820		BIO	29032 KAL-57 281/3 RAL 429	SPX021296	57.0	52 620 402	32.6	37
5	DGRP_130	Bloomington-25182 inbred line,	mix of SRX006145	RAL-324 100	SRR835256	100	100 merced use min lengt	- 100 h 100	DGRP-F1	127 3	45bp:79789940 100bp:174874844		Blo	25182 RAL-130	SRX006144 and	233.0	233 891 168	30.1	38
6	1 DGRP 360	Bloomington-25186 inbred line,	mix of SRX155999	RAL-360 125	SRR835260	100	merged, use min lengt	h 125	DGRP-F2	87 3	36bp:59319927, 125bp:55959646	DGRIE2	BIO	25186 RAL-360	SRX155999 and	233.9	85,563,461	38.2	39
		Bloomington-25194 inbred line,	mix of SRX006156	RAL-437_125	SRR835333	125	merged, use min lengt	h 125		46.9	45bp:43208064, 125bp:50502476	F1		25194 RAL-437	SRX006156 and	83.9	83,861,754	40.4	40
6	DGRP 774	Bloomington-25205 inbred line	mix of SRX006170	RAL-774 125	SRR835338	125	meraed, use min lenat	h 125	UGRP-F1	38.2	45bp:42434168, 125bp:33991884	DGRI E	BIO	25205 RAL-774	SRX006170 and	68.9	68.894.652	30	41
6	3 4 DGRP_391A	Bloomington-25191 inbred line,	mix of SRX006152	RAL-391_75b	SRR018294	125 75	merged, use min lengt	h 75	DGRP-F1 DGRP-F1 + F2	9.5	45bp:40955170, 75bp:18124720, 9	DGRE E	Blo Blo	25191 RAL-391	SRX023452,SR	95.3	95,313,294	38	42
6	5 DGRP_391B	Bloomington-25191 inbred line,	mix of SRX023452	RAL-391_95b	SRR060098	95	merged, use min lengt	h 95	DGRP-F1 + F2	19	45bp:40955170, 75bp:18124720, 9	DGRIF1 + F2 E	Blo	25191 RAL-391	SRX023452,SR	95.3	95,313,294	38	44
6	6 DGRP_380	Bloomington-25190 inbred line,	mix of SRX006300	RAL-380	SRR018591, SR	75	merged, use min lengt	h 75	DGRP-F1 + F2	10.2, 10.3	45bp:505064, 74bp:20092700, 75b	DGRIF1 + F2 E	Blo	25190 RAL-380	SRX006303,SR	69.2	69,152,136	29.5	45
6	7 DGRP_176	Bloomington-28149 inbred line,	mix of SRX020762, S	RRAL-176	SRR048925, SR	75	7	5 75	DGRP-F1	19.7, 20.3	75bp:79996860	DGRIF1 E	Blo	28149 RAL-176	SRX020762, SR	73.7	73,734,058	31.6	46

69 DGRP_358	Bloomington-25185	inbred line, mix of SRX006282, S	R RAL-358	SRR018574, SR	75.0) merged, use min length	n 75.0 DGRP-F1	6.8, 14	.1 45bp:18011532, 75bp:2773	39857 DGRIF1	Blo	25185	RAL-358	SRX006283 and	42.5	42,499,891	15.2	47
70 DGRP_399	Bloomington-25192	inbred line, mix of SRX006153	RAL-399	SRR933575	75.0	merged, use min length	75.0 DGRP-F1	27	.8 45bp:41011932, 75bp:1466	5138 DGRI F1	Blo	25192	RAL-399	SRX006154 and	51.6	51,632,558	15.5	48
71 DGRP_313	Bloomington-25180	inbred line, mix of SRX006277	RAL-313	SRR018519	75.0	single end only	75.0 DGRP-F1 + F2	1	4 36bp:9477876, 45bp:18165	5034, 75t DGRI F1 + F2	Blo	25180	RAL-313	SRX006277, SRX	39.1	39,060,649	11.7	49
72 DGRP_375	Bloomington-25188	inbred line, mix of SRX006148	RAL-375	SRR933572	75.0	merged, use min length	75.0 DGRP-F1	51	.8 45bp:52106222, 75bp:5141	3814 DGRI F1	Blo	25188	RAL-375	SRX006150,SRX	99.3	99,258,956	33.8	50
73 DGRP_555	Bloomington-25198	inbred line, mix of SRX006159	RAL-555	SRR933580	75	5 75	75 DGRP-F1	25	1 75bp:50103810	DGRFF1	Blo	25198	RAL-555	SRX006159	44.9	44,883,398	19.2	51
74 DGRP_705	Bloomington-25744	inbred line, mix of SRX006162	RAL-705	SRR933585	75	5 75	5 75 DGRP-F1	23	.5 75bp:47006608	DGRI F1	Blo	25744	RAL-705	SRX006162	38.9	38,920,070	16.7	52
75 DGRP_707	Bloomington-25200	inbred line, mix of SRX006163	RAL-707	SRR933586	75	5 75	5 75 DGRP-F1	23	.3 75bp:46657404	DGRI F1	Blo	25200	RAL-707	SRX006163	41.6	41,568,952	17.8	53
76 DGRP_712	Bloomington-25201	inbred line, mix of SRX006164	RAL-712	SRR933587	75	5 75	5 75 DGRP-F1	22	.3 75bp:44687868	DGRI F1	Blo	25201	RAL-712	SRX006164	37.9	37,949,898	16.3	54
77 DGRP_714	Bloomington-25745	inbred line, mix of SRX006166	RAL-714	SRR933588	75.0	75.0	75.0 DGRP-F1	2	1 75bp:42090922	DGRI F1	Blo	25745	RAL-714	SRX006166 and	40.0	39,955,902	17.1	55
78 DGRP_732	Bloomington-25203	inbred line, mix of SRX006167	RAL-732	SRR933591	75	5 75	75 DGRP-F1	21	.1 75bp:42170344	DGRI ^{F1}	Blo	25203	RAL-732	SRX006167	38.1	38,082,012	16.3	56
79 DGRP_379	Bloomington-25189	inbred line, mix of SRX006293	RAL-379	SRR018583, SR	75.0	single end only	75.0 DGRP-F1	6.1, 12	.445bp:19006960, 75bp:1849	6338 DGRI F1	Blo	25189	RAL-379	SRX006293 and	34.0	34,014,707	11.4	57
80 DGRP_340	Bloomington-28174	inbred line, mix of SRX156030	RAL-340_75b	SRR835939	75	merged, use min length	100.0 DGRP-F2	103	.7 75bp:41788984, 100bp:165	697712 DGRI F2	Blo	28174	RAL-340	SRX156030	130.2	130,158,488	73.8	12 This

PHASE 2: Additional DGRP Illumina-sequenced libaries compatible for TIDAL analysis loaded into TIDAL-Fly database but not part of analysis in paper.

Library Stock ID*	Stock Location	Genome Type SRA Accession	Library ID*	SRA Accession	Min Read	Read Length 1	Read Length 2	Data Group	Reads (M) Raw Read Length:Read Number	F	reeze	Bloomington Stock	Synonym	NCBI SRA	Reads	Mapped Reads	Mapped Coverage	Strains
1 DGRP_365	Bloomington-25445	inbred line, mix of SRX006290, SI	RRAL-365	SRR018580, SRR	75	75.0	75.0	DGRP-F1	10.1 45bp:18394996, 75bp:32783196	DGRIF	1 B	25445	RAL-365	SRX006291,5	SR) 42.9	42,859,487	15.6	58
3 DGRP_852	Bloomington-25209	inbred line, mix of SRX006304, SI	R RAL-852	SRR018600	75	75.0	75.0	DGRP-F1	11.7 45bp:41788724, 75bp:59375261	DGRFF	1 B	o 25209	RAL-852	SRX006304 a	and 90.6	90,552,271	32.2	59
7 DGRP_730	Bloomington-25202	inbred line, mix of SRX006308	RAL-730	SRR933590	75	75	75	DGRP-F1	38 75bp:38019145	DGRFF	1 B	o 25202	RAL-730	SRX006308	30.9	30,891,608	13.2	60
8 DGRP_738	Bloomington-28223	inbred line, mix of SRX021383	RAL-738	SRR933593	75	75	75	DGRP-F1	37.9 75bp:75804508	DGRF	1 B	o 28223	RAL-738	SRX021383	63.1	63,119,910	27.1	61
9 DGRP_737	Bloomington-28222	inbred line, mix of SRX023451	RAL-737	SRR933592	75	75	75	DGRP-F1	37.4 75bp:74740132	DGRFF	⁻ 1 B	o 28222	RAL-737	SRX023451	58.5	58,531,732	25.1	62
10 DGRP_757	Bloomington-28226	inbred line, mix of SRX021385	RAL-757	SRR933594	75	75	75	DGRP-F1	37.2 75bp:74326240	DGRF	1 B	o 28226	RAL-757	SRX021385	66.2	66,207,766	28.4	63
11 DGRP_727	Bloomington-28221	inbred line, mix of SRX021382	RAL-727	SRR933589	75	75	75	DGRP-F1	36.9 75bp:73781476	DGRIF	1 B	o 28221	RAL-727	SRX021382	64.2	64,202,850	27.5	64
12 DGRP_897	Bloomington-28260	inbred line, mix of SRX023457	RAL-897	SRR933601	75	75	75	DGRP-F1	35.4 75bp:70892788	DGRIF	1 B	o 28260	RAL-897	SRX023457	63.0	63,033,690	27	65
13 DGRP_332	Bloomington-28171	inbred line, mix of SRX021095	RAL-332	SRR933569	75	75	/5	DGRP-F1	32.8 /5bp:65583082	DGRF	1 B	0 28171	RAL-332	SRX021095	60.0	59,985,078	25.7	66
14 DGRP_181	Bioomington-28151	Inbred line, mix of SRX020912	RAL-181	SRR933563	75	/5	75	DGRP-F1	32 750p:64093862	DGRIF	1 B	0 28151	RAL-181	SRX020912	57.6	57,566,276	24.7	67
15 DGRP_325	Bioomington-28170	inbred line, mix of SRX021793	RAL-325	SKK933568	75	/5	75	DGRP-F1	31.5 /500:3145/046	DGRIF	-1 B	0 28170	RAL-325	SRX021793	26.3	26,299,389	11.3	68
17 DGRP_361	Bloomington-28146	inbred line, mix of SRX021112	RAL-301 RAL-153	SRR933573	75	75	75	DGRP-F1	21.2 / 500:54335852 26.8 / 75bp:26821499	DCRIF	1 B	0 20100	RAL-301 PAL-153	SRX021112	40.7	46,706,404	20.9	59
18 DGPP 352	Bloomington-28177	inbred line, mix of SRX021314	RAL-153	SPR83/516	75	75	75	DGRP-F1	20.6 750p.2002 1499	DGRIF	1 B	0 28140	RAL-155 PAL-352	SRX021314	21.0	36 302 672	9.3	70
19 DGRP 882	Bloomington-28255	inbred line, mix of SRX021496	RAL-882	SRR835067	75	75	75	DGRP-F1	22.0 75bp:44302300	DGRIF	1 B	28255	RAL-882	SRX021496	40.6	40 585 544	17.0	72
20 DGRP 879	Bloomington-28254	inbred line, mix of SRX021494	RAL-879	SRR835066	75	75	75	DGRP-F1	21.7 75bp:43485194	DGRIF	1 B	28254	RAL-879	SRX021494	30.5	30,475,860	13.1	73
21 DGRP 805	Bloomington-28237	inbred line, mix of SRX021400	RAL-805	SRR835095	75	75	75	DGRP-F1	21.6 75bp:43182102	DGRIF	1 B	28237	RAL-805	SRX021400	37.7	37,672,090	16.1	74
22 DGRP 356	Bloomington-28178	inbred line, mix of SRX023833	RAL-356	SRR834537	75	75	75	DGRP-F1	21.5 75bp:42903612	DGREE	1 B	28178	RAL-356	SRX023833	36.1	36,113,766	15.5	75
23 DGRP_884	Bloomington-28256	inbred line, mix of SRX021498	RAL-884	SRR835068	75	75	75	DGRP-F1	21.3 75bp:42658114	DGRIF	-1 B	0 28256	RAL-884	SRX021498	32.6	32,585,778	14	76
24 DGRP_890	Bloomington-28257	inbred line, mix of SRX021499	RAL-890	SRR835071	75	75	75	DGRP-F1	21.0 75bp:41954706	DGRIF	1 B	28257	RAL-890	SRX021499	37.1	37,101,876	15.9	77
25 DGRP_861	Bloomington-28253	inbred line, mix of SRX021493	RAL-861	SRR835065	75	75	75	DGRP-F1	20.6 75bp:41295320	DGRFF	1 B	28253	RAL-861	SRX021493	29.5	29,478,054	12.6	78
26 DGRP_83	Bloomington-28134	inbred line, mix of SRX023456	RAL-83	SRR835058	75	75	75	DGRP-F1	20.5 75bp:41070470	DGRIF	1 B	o 28134	RAL-83	SRX023456	38.0	37,982,090	16.3	79
27 DGRP_491	Bloomington-28202	inbred line, mix of SRX021268	RAL-491	SRR835035	75	75	75	DGRP-F1	20.5 75bp:40944392	DGRFF	1 B	0 28202	RAL-491	SRX021268	35.3	35,336,140	15.1	80
28 DGRP_761	Bloomington-28227	inbred line, mix of SRX021386	RAL-761	SRR835088	75	75	75	DGRP-F1	20.4 75bp:40867250	DGRF	1 B	o 28227	RAL-761	SRX021386	35.6	35,577,354	15.2	81
29 DGRP_149	Bloomington-28145	inbred line, mix of SRX020760	RAL-149	SRR834550	75	75	75	DGRP-F1	20.3 75bp:40637646	DGRF	1 B	o 28145	RAL-149	SRX020760	33.9	33,914,600	14.5	82
30 DGRP_535	Bloomington-28208	inbred line, mix of <u>SRX021293</u>	RAL-535	SRR835046	75	75	75	DGRP-F1	20.1 75bp:40234802	DGRFF	⁻ 1 B	0 28208	RAL-535	SRX021293	35.4	35,362,252	15.2	83
31 DGRP_776	Bloomington-28229	inbred line, mix of SRX021387	RAL-776	SRR835089	75	75	75	DGRP-F1	19.9 75bp:39890986	DGRIF	⁻¹ B	o 28229	RAL-776	SRX021387	36.4	36,432,512	15.6	84
32 DGRP_787	Bloomington-28231	inbred line, mix of SRX021388	RAL-787	SRR835091	75	75	75	DGRP-F1	19.9 75bp:39795416	DGRFF	1 B	o 28231	RAL-787	SRX021388	35.9	35,896,250	15.4	85
33 DGRP_136	Bloomington-28142	inbred line, mix of SRX020753	RAL-136	SRR834542	75	75	75	DGRP-F1	19.5 75bp:38970964	DGRFF	1 B	o 28142	RAL-136	SRX020753	33.9	33,947,560	14.5	86
34 DGRP_318	Bioomington-28168	Inbred line, mix of SRX021082	RAL-318	SRR834507	75	/5	75	DGRP-F1	19.5 750p:39068236	DGRIF	-1 B	0 28168	RAL-318	SRX021082	35.4	35,366,996	15.2	87
35 DGRP_804	Bioomington-28236	inbred line, mix of SRX021399	RAL-804	SKK835094	75	/5	75	DGRP-F1	19.5 / 50p:38910810	DGRIF	-1 B	0 28236	RAL-804	SRX021399	34.5	34,482,650	14.8	88
36 DGRP_612	Dioomington-26240	inbred line, mix of SRX021419	RAL-012	SKR635052	75	75	75	DGRP-F1	19.4 750p.38719004	DGRIF	-1 B	0 26240	RAL-012	SRX021419	37.5	37,540,214	16.1	89
37 DGRP_796	Bloomington-28206	inbred line, mix of SRX021390	RAL-790	SPR835041	75	75	75	DGRP-F1	19.3 750p:38085002	DCRIF	1 D	28206	RAL-790 RAL-500	SRX021390 SRX021273	34.7	35,615,726	14.9	90
39 DGRP 818	Bloomington-28241	inbred line, mix of SRX021275	RAL-818	SRR835053	75	75	75	DGRP-F1	18.8 75bp:37531016	DGRIF	1 B	20200	RAL-818	SRX021275	34.2	34 210 842	14.7	91
40 DGRP 859	Bloomington-25210	inbred line, mix of SRX006176	RAL-859	SRR933600	75	75	75	DGRP-F1	18.5 75bp:36919488	DGRIE	1 B	0 25210	RAL-859	SRX006176	34.0	33 950 076	14.7	92
41 DGRP 810	Bloomington-28239	inbred line, mix of SRX021418	RAL-810	SRR835051	75	75	75	DGRP-F1	18.5 75bp:36972402	DGRIF	1 B	28239	RAL-810	SRX021418	36.1	36.075.996	15.5	94
42 DGRP 783	Bloomington-28230	inbred line, mix of SRX023455	RAL-783	SRR835090	75	75	75	DGRP-F1	18.3 75bp:36692434	DGRIF	1 B	28230	RAL-783	SRX023455	31.4	31,444,902	13.5	95
43 DGRP_45	Bloomington-28128	inbred line, mix of SRX021261	RAL-45	SRR835032	75	75	75	DGRP-F1	18.2 75bp:36472946	DGRFF	1 B	o 28128	RAL-45	SRX021261	33.0	32,984,934	14.1	96
44 DGRP_59	Bloomington-28129	inbred line, mix of SRX021327	RAL-59	SRR835081	75	75	75	DGRP-F1	18.2 75bp:36484216	DGRFF	1 B	o 28129	RAL-59	SRX021327	34.9	34,871,104	14.9	97
45 DGRP_280	Bloomington-28164	inbred line, mix of SRX021058	RAL-280	SRR834534	75	75	75	DGRP-F1	17.8 75bp:35581218	DGRFF	1 B	o 28164	RAL-280	SRX021058	33.0	32,968,684	14.1	98
46 DGRP_595	Bloomington-28215	inbred line, mix of SRX021328	RAL-595	SRR835101	75	75	75	DGRP-F1	17.8 75bp:35536106	DGRFF	1 B	0 28215	RAL-595	SRX021328	29.2	29,176,032	12.5	99
47 DGRP_93	Bloomington-28137	inbred line, mix of SRX021504	RAL-93	SRR835080	75	75	75	DGRP-F1	17.6 75bp:35127632	DGRFF	⁻ 1 B	o 28137	RAL-93	SRX021504	33.9	33,871,000	14.5	100
48 DGRP_195	Bloomington-28153	inbred line, mix of SRX021039	RAL-195	SRR834524	75	75	75	DGRP-F1	17.6 75bp:35114464	DGRF	1 B	o 28153	RAL-195	SRX021039	33.4	33,435,584	14.3	101
49 DGRP_287	Bloomington-28165	inbred line, mix of <u>SRX021059</u>	RAL-287	SRR834535	75	75	75	DGRP-F1	17.6 75bp:35285772	DGRFF	⁻ 1 B	o 28165	RAL-287	SRX021059	22.8	22,778,884	9.8	102
50 DGRP_101	Bloomington-28138	inbred line, mix of SRX020747	RAL-101	SRR834536	75	75	75	DGRP-F1	17.4 75bp:34790704	DGRIF	1 B	o 28138	RAL-101	SRX020747	28.6	28,625,600	12.3	103
51 DGRP_256	Bloomington-28162	Inbred line, mix of SRX021055	RAL-256	SRR834533	75	75	75	DGRP-F1	17.4 75bp:34717354	DGRFF	1 B	0 28162	RAL-256	SKX021055	32.6	32,570,608	14	104
52 DGRP_239	DIUUININGTON-28161	inbred line, mix of SRX021054	RAL-239	OKK834532	75	/5	/5	DGRP-F1	17.2/500:34456900 17.1/76bp:34326883	DGRF	B	28161	RAL-239	SRX021054	33.0	32,977,516	14.1	105
53 DGKP_642	BioUnington 28276	inbred line, mix of SRX021331	RAL-042	SRR033082	/5	/5	/5	DORD F1	17.1750p:34223882	DGRIF	B	28216	NAL-042	SRAU21331	32.7	32,078,408	14	106
54 DGRP_65	Bloomington-28166	inbred line, mix of SRX021490	RAL-00	SRR834504	75	/5	/5	DORP-FI	17.1750p:34270000	DCB	1 B	28166	RAL-00	SRX021490	32.8	30 967 802	14.1	107
56 DGRP 563	Bloomington-28211	inbred line mix of SRX023836	RAL-563	SRR835049	75	75	75	DGRP-F1	17.075bp:33949618	DGRIF	- B	20100	RAL-563	SRX023836	31.0	32 699 510	13.3	108
57 DGRP 69	Bloomington-28130	inbred line, mix of SRX023000	RAL-505	SPP033583	75	75	75	DGRP-F1	16.9 75bp:33850154	DGRIF	1 B	20211	RAL-505	SPX023449	31.3	31 330 920	13.4	110
58 DGRP 161	Bloomington-28148	inbred line, mix of SRX020761	RAL-161	SRR834548	75	75	75	DGRP-F1	16.8 75bp:33569140	DGRIF	1 B	28148	RAL-05	SRX020761	31.9	31,889,608	13.4	111
59 DGRP 721	Bloomington-28220	inbred line, mix of SRX021381	RAL-721	SRR835099	75	75	75	DGRP-F1	16.8 75bp:33513644	DGRIF	1 B	28220	RAL-721	SRX021381	29.3	29.343.228	12.6	112
60 DGRP_310	Bloomington-28276	inbred line, mix of SRX021080	RAL-310	SRR834505	75	75	75	DGRP-F1	16.8 75bp:33591214,	DGRIF	1 B	0 28276	RAL-310	SRX021080	29.3	29,276,428	12.5	113
61 DGRP_73	Bloomington-28131	inbred line, mix of SRX023450	RAL-73	SRR835100	75	75	75	DGRP-F1	16.6 75bp:33134294	DGRIF	1 B	o 28131	RAL-73	SRX023450	31.7	31,685,126	13.6	114
62 DGRP_91	Bloomington-28136	inbred line, mix of SRX021503	RAL-91	SRR835078	75	75	75	DGRP-F1	16.6 75bp:33211530	DGRIF	1 B	0 28136	RAL-91	SRX021503	31.5	31,458,484	13.5	115
63 DGRP_367	Bloomington-28181	inbred line, mix of SRX021103	RAL-367	SRR834544	75	75	75	DGRP-F1	16.4 75bp:32780338	DGRFF	1 B	0 28181	RAL-367	SRX021103	30.6	30,576,784	13.1	116
64 DGRP_336	Bloomington-28172	inbred line, mix of SRX021096	RAL-336	SRR933570	75	75	75	DGRP-F2	16.3 75bp:32559800	DGRIF	2 B	o 28172	RAL-336	SRX021096	26.5	26,524,196	11.4	117
65 DGRP_646	Bloomington-28217	inbred line, mix of SRX021332	RAL-646	SRR835083	75	75	75	DGRP-F1	16.2 75bp:32350764	DGRIF	1 B	o 28217	RAL-646	SRX021332	28.7	28,739,440	12.3	118
66 DGRP_88	Bloomington-28135	inbred line, mix of SRX021495	RAL-88	SRR835070	75	75	75	DGRP-F1	16.0 75bp:32012994	DGRIF	1 B	o 28135	RAL-88	SRX021495	30.9	30,899,746	13.2	119
67 DGRP_105	Bloomington-28139	inbred line, mix of SRX020745	RAL-105	SRR834538	75	75	75	DGRP-F1	15.9 75bp:31797740	DGRFF	1 B	o 28139	RAL-105	SRX020745	30.8	30,788,030	13.2	120
68 DGRP_716	Bloomington-28219	inbred line, mix of SRX021380	RAL-716	SRR835085	75	75	75	DGRP-F1	15.8 75bp:31572156	DGRIF	1 B	o 28219	RAL-716	SRX021380	29.2	29,244,674	12.5	121
69 DGRP_217	Bloomington-28154	inbred line, mix of SRX021041	RAL-217	SRR834525	75	75	75	DGRP-F1	15.7 75bp:31354632	DGRFF	1 B	o 28154	RAL-217	SRX021041	29.9	29,857,218	12.8	122
70 DGRP_158	Bloomington-28147	inbred line, mix of SRX021009	RAL-158	SRR834549	75	75	75	DGRP-F1	15.5 75bp:31050122	DGRFF	1 B	o 28147	RAL-158	SRX021009	27.6	27,629,766	11.8	123
71 DGRP_227	Bloomington-28156	Inbred line, mix of SRX021042	RAL-227	SRR834528	75	75	75	DGRP-F1	15.5 75bp:30993282	DGRFF	1 B	0 28156	RAL-227	SKX021042	27.8	27,790,122	11.9	124
72 DGRP_233	BIOOMINGTON-28159	Inbrea line, mix of SRX021061	KAL-233	SKR834530	75	75	75	DGRP-F1	14.9 /5bp:29/95450	DGRFF	1 B	o 28159	KAL-233	5KX021061	28.4	28,358,088	12.2	125

73 DGRP_338	Bloomington-28173	inbred line, mix of	f SRX021097	RAL-338	SRR834513	75	75	75 DGRP-F1	14.5 75bp:28907664	DGRI F1	Blo	28173 RAL-33	8 SRX021097	26.0	25,964,076	11.1	126
74 DGRP_228	Bloomington-28157	inbred line, mix of	f SRX021043	RAL-228	SRR834529	75	75	75 DGRP-F1	14.4 75bp:28874696	DGRI F1	Blo	28157 RAL-22	8 SRX021043	27.3	27,339,700	11.7	127
75 DGRP 350	Bloomington-28176	inbred line, mix of	f SRX021100	RAL-350	SRR834515	75	75	75 DGRP-F1	14.0 75bp:27970002	DGRIF1	Blo	28176 RAL-35	0 SRX021100	25.4	25.355.594	10.9	128
76 DGRP_317	Bloomington-28167	inbred line, mix of	f SRX021081	RAL-317	SRR834506	75	75	75 DGRP-F1	13.6 75bp:27246088	DGRIF1	Blo	28167 RAL-31	7 SRX021081	23.3	23,252,944	10	129
77 DGRP_129	Bloomington-28141	inbred line, mix of	f SRX020748	RAL-129	SRR834540	75	75	75 DGRP-F1	13.4 75bp:26898800	DGRI F1	Blo	28141 RAL-12	9 SRX020748	25.8	25,797,252	11.1	130
78 DGRP 26	Bloomington-28123	inbred line, mix of	f SRX021056	RAL-26	SRR933566	75 merged.	use min lenath	75.0 DGRP-F1	18.4 44bp:4452211. 75bp:	32432947 DGRIF1	Blo	28123 RAL-26	SRX021056	35.6	35.642.606	14.5	131
79 DGRP 208	Bloomington-25174	inbred line, mix of	f SRX005977	RAI -208	SRR933564	75 merged.	use min length	75.0 DGRP-E1 + E2	36.3 45bp:11112096.64bp	8693462, 75t DGRIE1 + F2	Blo	25174 RAL-20	8 SRX005977	69.8	69.801.276	27.5	132
80 DGRP 237	Bloomington-28160	inbred line mix of	f SRX023423	RAL-237	SRR933565	75 merged	use min length	75.0 DGRP-E1	29.1.44bp:15879498_75bp	34500267 DCPIE1	Blo	28160 RAL-23	7 SRX023423 an	45.0	44 995 628	16.7	133
86 DORE 28	Bloomington 20124	inbrod line, mix of	f CDV021792	DAL 20	CDD022567	75 morgod,	use min length	76.0 DORD F4	26.1 11bp:16010100; 76bp	26422488 DODIE1	Die	20100 TULE 20	SBV021782 on	20.1	20.007.962	14.1	100
81 DOIN _20	Disomington-20124	inbred line, mix of	6 CDX024704	DAL 44	CDD000570	75 merged,	use min length	75.0 DORP F1	20.4 44bp:13405030,75bp	24428422 DORIT	DIU	20124 RAL-20	CDV021703 an	35.1	35,037,003	42.4	134
82 DGRF_41	Bioomington=28120	inbred line, mix of	0DX000101	RAL-41	00000000	75 mergeu,	use minnengin	75.0 DGRP-F1	24.4 440p.14055721, 750p	0.24430432 DGRFT	DIO	20120 RAL-4	<u>3KA021791</u> all	30.1	30,082,007	13.1	135
83 DGRP_639	Bioomington-25199	inbred line, mix of	SRX006161	RAL-639	SRR933582	75	75.0	75.0 DGRP-F1	21.1 75bp:42120400	DGRIFI	Blo	25199 RAL-63	9 <u>SRX006161</u> an	39.0	39,017,668	16.7	136
84 DGRP_799	Bloomington-25207	inbred line, mix of	t <u>SRX006173</u>	RAL-799	SRR933597	75	75.0	75.0 DGRP-F1	20.7 75bp:41386962	DGRIF1	Blo	25207 RAL-79	9 <u>SRX006172</u> an	38.9	38,942,298	16.7	137
85 DGRP_386	Bloomington-28192	inbred line, mix of	f <u>SRX021798</u>	RAL-386	SRR933574	75 merged,	use min length	75.0 DGRP-F1	20.5 44bp:11122819, 75bp	:20778304 DGRFF1	Blo	28192 RAL-38	6 <u>SRX021798</u> an	. 29.6	29,626,175	10.8	138
86 DGRP_820	Bloomington-25208	inbred line, mix of	f SRX006174	RAL-820	SRR933598	75	75.0	75.0 DGRP-F1	18.8 75bp:37666476	DGRI F1	Blo	25208 RAL-82	0 <u>SRX006174</u> an	33.9	33,910,170	14.5	139
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PHASE 3: Remain	ning DGRP illun	nina-sequenc	ed libaries	s compatib	le for TIDAL and	alysis to be loa	aea into TIDA	L-Fly database.									
87 DGRP_359	Bloomington-28179	inbred line, mix of	f <u>SRX023424</u>	RAL-359	SRR834546	95	95.0	95.0 DGRP-F1	18.6 95bp:37271884	DGRI F1	Blo	28179 RAL-35	9 <u>SRX023424</u>	37.3	37,271,884	20.2	
88 DGRP_589	Bloomington-28213	inbred line, mix of	f <u>SRX023837</u>	RAL-589	SRR060821	75	75.0	75.0 DGRP-F1	16.5 75bp:32998374	DGRI F1	Blo	28213 RAL-58	9 <u>SRX023837</u>	190.1	190,072,852	104.4	
89 DGRP_40	Bloomington-29651	inbred line, mix of	f <u>SRX021235</u>	RAL-40	SRR835025	95	95	95 DGRP-F1	34.5 95bp:69063428	DGRIF1	Blo	29651 RAL-40	SRX021235	61.3	61,345,170	33.3	
90 DGRP_321	Bloomington-29655	inbred line, mix of	f SRX021094	RAL-321	SRR834511	95	95	95 DGRP-F1	33.7 95bp:67314152	DGRIF1	Blo	29655 RAL-32	1 <u>SRX021094</u>	61.7	61,687,556	33.5	
91 DGRP_443	Bloomington-28199	inbred line, mix of	f <u>SRX021260</u>	RAL-443	SRR835031	95	95	95 DGRP-F1	28.8 95bp:57567568	DGRI F1	Blo	28199 RAL-44	3 <u>SRX021260</u>	52.5	52,492,412	28.5	
92 DGRP_38	Bloomington-28125	inbred line, mix of	f SRX025317	RAL-38	SRR834541	95	95	95 DGRP-F1	28.1 95bp:56154204	DGRI F1	Blo	28125 RAL-38	SRX025317	51.6	51,612,838	28	
93 DGRP_320	Bloomington-29654	inbred line, mix of	f SRX021063	RAL-320	SRR834510	95	95	95 DGRP-F1	25.9 95bp:51875680	DGRI F1	Blo	29654 RAL-32	0 <u>SRX021063</u>	44.5	44,510,214	24.2	
94 DGRP_406	Bloomington-29657	inbred line, mix of	f SRX021254	RAL-406	SRR835024	95	95	95 DGRP-F1	25.9 95bp:51821248	DGRI F1	Blo	29657 RAL-40	6 <u>SRX021254</u>	46.0	46,001,604	25	
95 DGRP_392	Bloomington-28194	inbred line, mix of	f SRX021157	RAL-392	SRR834520	95	95	95 DGRP-F1	25.6 95bp:51156860	DGRI F1	Blo	28194 RAL-39	2 SRX021157	42.8	42,803,392	23.2	
96 DGRP_405	Bloomington-29656	inbred line, mix of	f SRX021242	RAL-405	SRR835023	95	95	95 DGRP-F1	25.0 95bp:50080536	DGRI F1	Blo	29656 RAL-40	5 SRX021242	42.2	42,196,622	22.9	
97 DGRP_461	Bloomington-28200	inbred line, mix of	f SRX021262	RAL-461	SRR835033	95	95	95 DGRP-F1	24.7 95bp:49324528	DGRI F1	Blo	28200 RAL-46	1 <u>SRX021262</u>	40.4	40,407,678	21.9	
98 DGRP_177	Bloomington-28150	inbred line, mix of	f SRX021026	RAL-177	SRR834547	95	95	95 DGRP-F1	24.6 95bp:49114764	DGRIF1	Blo	28150 RAL-17	7 SRX021026	45.3	45,259,994	24.6	
99 DGRP_837	Bloomington-28246	inbred line, mix of	f SRX021479	RAL-837	SRR933599	95	95	95 DGRP-F1	23.2 95bp:46411538	DGRI F1	Blo	28246 RAL-83	7 SRX021479	38.0	38,040,748	20.7	
100 DGRP_892	Bloomington-28258	inbred line, mix of	f SRX023838	RAL-892	SRR835072	95	95	95 DGRP-F1	22.9 95bp:45702226	DGRI F1	Blo	28258 RAL-89	2 SRX023838	37.8	37,797,872	20.5	
101 DGRP_439	Bloomington-29658	inbred line, mix of	f SRX021244	RAL-439	SRR835028	95	95	95 DGRP-F1	22.4 95bp:44762436	DGRI F1	Blo	29658 RAL-43	9 SRX021244	37.5	37,522,394	20.4	
102 DGRP_492	Bloomington-28203	inbred line, mix of	f SRX021270	RAL-492	SRR835036	95	95	95 DGRP-F1	22.3 95bp:44580310	DGRI F1	Blo	28203 RAL-49	2 SRX021270	40.7	40,704,078	22.1	
103 DGRP_502	Bloomington-28204	inbred line, mix of	f <u>SRX021271</u>	RAL-502	SRR835038	95	95	95 DGRP-F1	22.2 95bp:44336646	DGRIF1	Blo	28204 RAL-50	2 SRX021271	40.0	39,968,920	21.7	
104 DGRP_370	Bloomington-28182	inbred line, mix of	f SRX021104	RAL-370	SRR834539	95	95	95 DGRP-F1	21.9 95bp:43793604	DGRIF1	Blo	28182 RAL-37	0 SRX021104	38.4	38,408,446	20.9	
105 DGRP_377	Bloomington-28186	inbred line, mix of	f SRX023834	RAL-377	SRR834543	95	95	95 DGRP-F1	21.9 95bp:43796182	DGRIF1	Blo	28186 RAL-37	7 SRX023834	40.2	40,225,994	21.8	
106 DGRP_426	Bloomington-28196	inbred line, mix of	f SRX021245	RAL-426	SRR835026	95	95	95 DGRP-F1	21.9 95bp:43746634	DGRI F1	Blo	28196 RAL-42	6 SRX021245	38.9	38,928,098	21.1	
107 DGRP_887	Bloomington-28279	inbred line, mix of	f SRX021527	RAL-887	SRR835069	95	95	95 DGRP-F1	21.8 95bp:43595728	DGRI F1	Blo	28279 RAL-88	7 SRX021527	35.9	35,939,248	19.5	
108 DGRP_440	Bloomington-28197	inbred line, mix of	f SRX021246	RAL-440	SRR835029	95	95	95 DGRP-F1	21.6 95bp:43161850	DGRI F1	Blo	28197 RAL-44	0 SRX021246	31.7	31,659,420	17.2	
109 DGRP_513	Bloomington-29659	inbred line, mix of	f SRX021282	RAL-513	SRR835042	95	95	95 DGRP-F1	21.3 95bp:42640722	DGRI F1	Blo	29659 RAL-51	3 SRX021282	36.0	36,025,830	19.6	
110 DGRP_508	Bloomington-28205	inbred line, mix of	f SRX021272	RAL-508	SRR835040	95	95	95 DGRP-F1	21.2 95bp:42338556	DGRIF1	Blo	28205 RAL-50	8 SRX021272	39.1	39,078,690	21.2	
111 DGRP_441	Bloomington-28198	inbred line, mix of	f SRX023835	RAL-441	SRR835030	95	95	95 DGRP-F1	21.1 95bp:42278010	DGRIF1	Blo	28198 RAL-44	1 SRX023835	34.4	34,448,902	18.7	
112 DGRP_531	Bloomington-28207	inbred line, mix of	f SRX021290	RAL-531	SRR835045	95	95	95 DGRP-F1	20.8 95bp:41560152	DGRIF1	Blo	28207 RAL-53	1 SRX021290	32.9	32,916,204	17.9	
113 DGRP_383	Bloomington-28190	inbred line, mix of	f SRX021113	RAL-383	SRR834554	95	95	95 DGRP-F1	19.9 95bp:39897030	DGRI F1	Blo	28190 RAL-38	3 SRX021113	35.1	35,149,446	19.1	
114 DGRP_235	Bloomington-28275	inbred line, mix of	f SRX021053	RAL-235	SRR834531	95	95	95 DGRP-F1	19.1 95bp:38296004	DGRIF1	Blo	28275 RAL-23	5 SRX021053	33.8	33,829,434	18.4	
115 DGRP_42	Bloomington-28127	inbred line, mix of	f SRX021255	RAL-42	SRR835027	95	95	95 DGRP-F1	18.6 95bp:37186556	DGRI F1	Blo	28127 RAL-42	SRX021255	37.2	37,186,556	20.2	
116 DGRP_21	Bloomington-28122	inbred line, mix of	f SRX021040	RAL-21	SRR834526	95	95	95 DGRP-F1	18.5 95bp:37046984	DGRI F1	Blo	28122 RAL-21	SRX021040	29.2	29,159,002	15.8	
117 DGRP_907	Bloomington-28262	inbred line, mix of	f SRX021500	RAL-907	SRR835074	95	95	95 DGRP-F1	18.2 95bp:36385056	DGRIF1	Blo	28262 RAL-90	7 SRX021500	32.3	32,273,788	17.5	
118 DGRP_790	Bloomington-28232	inbred line, mix of	f SRX021389	RAL-790	SRR835092	95	95	95 DGRP-F1	17.8 95bp:35620658	DGRIF1	Blo	28232 RAL-79	0 SRX021389	31.3	31,287,054	17	
119 DGRP_894	Bloomington-28259	inbred line, mix of	f SRX021528	RAL-894	SRR835073	95	95	95 DGRP-F1	17.6 95bp:35128536	DGRI F1	Blo	28259 RAL-89	4 SRX021528	30.9	30,860,088	16.8	
120 DGRP_832	Bloomington-28245	inbred line, mix of	f SRX021477	RAL-832	SRR835057	95	95	95 DGRP-F1	16.9 95bp:33770198	DGRI F1	Blo	28245 RAL-83	2 SRX021477	26.0	26,008,378	14.1	
121 DGRP_908	Bloomington-28263	inbred line, mix of	f SRX021501	RAL-908	SRR835075	95	95	95 DGRP-F1	16.8 95bp:39111536	DGRIF1	Blo	28263 RAL-90	8 SRX021501	36.7	36,702,788	19.9	
122 DGRP_911	Bloomington-28264	inbred line, mix of	f SRX021502	RAL-911	SRR835076	95	95	95 DGRP-F1	16.8 95bp:33571736	DGRI F1	Blo	28264 RAL-91	1 SRX021502	26.3	26,331,524	14.3	
123 DGRP_703	Bloomington-28218	inbred line, mix of	f SRX021508	RAL-703	SRR835084	95	95	95 DGRP-F1	16.5 95bp:32953564	DGRI F1	Blo	28218 RAL-70	3 SRX021508	26.3	26,272,930	14.3	
124 DGRP_385	Bloomington-28191	inbred line, mix of	f SRX159098	RAL-385	SRR834518	95	95	95 DGRP-F2	14.2 95bp:28408672	DGRIF2	Blo	28191 RAL-38	5 SRX159098	21.0	20,956,926	11.4	
125 DGRP_374	Bloomington-28185	inbred line, mix of	f SRX023427	RAL-374	SRR835103	95	95	95 DGRP-F1	13.9 95bp:27645755	DGRI F1	Blo	28185 RAL-37	4 SRX023427	24.7	24,704,590	13.4	

Table S1D. Drosophila Genome Nexus Strains in the TIDAL-Fly v1 database

Genomes previously examined in Lack et al (Pool lab), Genetics 2015

PHASE	E 1: First S	Set of	f Libraries	Analyzed for	or the paper.	The remaining	libraries in P	hase 2 bel	ow are a	lso liste	d in the T	IDAL-Fly da	atabase

							Min Read		Read	Read				
	Stock ID*	Stock Location	Genome Type	SRA Accession	Library ID*	SRA Accession	Length	Reads (M)	Length 1	Length 2	Data Group	Focal Genome Repr	Coverage**	Mean Depth**
1	CK1	Langley lab	haploid_embryo	SRX058145	CK1_1-HE	SRR189038	75	35.0	76	76	DPGP2	X,2L,2R,3L,3R	110,870,215	39.4
2	CK2	Langley lab	haploid_embryo	SRX058146	CK2_1-HE	SRR189040	145	20.6	146	146	DPGP2	X,2L,2R,3L,3R	111,567,582	44.7
3	CO13N	Pool Lab	haploid_embryo	SRX058151	CO13N_1-HE	SRR189045	145	18.1	146	146	DPGP2	X,2L,2R,3L,3R	111,264,202	39.8
4	CO15N	Pool Lab	haploid_embryo	SRX058153	CO15N_1-HE	SRR189047	75	38.2	76	76	DPGP2	X,2L,2R,3L,3R	111,058,052	44.2
5	CO4N	Pool Lab	haploid_embryo	SRX058156	CO4N_1-HE	SRR189050	75	32.8	76	76	DPGP2	X,2L,2R,3L,3R	111,025,671	37.7
6	EA119	Pool Lab	haploid_embryo	SRX791698	EA119_1-HE	SRR1686794	100	16.6	100	100	AGES	X,2L,2R,3L,3R	110,802,511	23.9
7	EA49	Pool Lab	haploid_embryo	SRX791713	EA49_1-HE	SRR1686797	100	13.0	100	100	AGES	X,2L,2R,3L,3R	110,446,851	18.2
8	EA87	Pool Lab	haploid_embryo	SRX791850	EA87_1-HE	SRR1686966	100	27.6	100	100	AGES	X,2L,2R,3L,3R	111,259,464	38.9
9	EB148	Langley lab	haploid_embryo	SRX791858	EB148_1-HE	SRR1686971	100	19.1	100	100	AGES	X,2L,2R,3L,3R	110,799,356	27.4
10	EB18	Langley lab	haploid_embryo	SRX792309	EB18_1-HE	SRR1687447	100	16.5	100	100	AGES	X,2L,2R,3L,3R	110,159,072	22.7
11	EB25	Langley lab	haploid_embryo	SRX792329	EB25_1-HE	SRR1687462	100	15.6	100	100	AGES	X,2L,2R,3L,3R	103,098,821	19.4
12	EF39	Pool lab	haploid_embryo	SRX792510	EF39_1-HE	SRR1687668	100	17.7	100	100	AGES	X,2L,2R,3L,3R	110,937,745	24.9
13	EF65	Pool lab	haploid_embryo	SRX792606	EF65_1-HE	SRR1687770	100	12.2	100	100	AGES	X,2L,2R,3L,3R	107,539,051	17.1
14	EF78	Pool lab	haploid_embryo	SRX792639	EF78_1-HE	SRR1687793	100	16.8	100	100	AGES	X,2L,2R,3L,3R	110,871,321	23.8
15	EG40N	Pool lab	inbred_line	SRX792675	EG40N	SRR1687832	100	10.8	100	100	AGES	X,2R	25,659,426	14.3
16	EG69N	Pool lab	inbred_line	SRX793022	EG69N	SRR1688188	100	10.2	100	100	AGES	X,2L,2R,3R	73,335,770	13.6
17	EG73N	Pool lab	inbred_line	SRX793046	EG73N	SRR1688222	100	10.3	100	100	AGES	X,2L,2R,3L,3R	105,554,844	13.8
18	FR180	Pool Lab	haploid_embryo	SRX058184	FR180_2-HE	SRR189090	145	19.1	146	146	DPGP2	X,2L,2R,3L,3R	112,084,373	42.3
19	FR207	Pool Lab	haploid_embryo	SRX058185	FR207_2-HE	SRR189091	145	18.1	146	146	DPGP2	X,2L,2R,3L,3R	112,168,144	38.9
20	FR229	Pool Lab	haploid_embryo	SRX058187	FR229_2-HE	SRR189093	145	19.1	146	146	DPGP2	X,2L,2R,3L,3R	112,159,960	40.6
21	GA129	Pool lab	haploid_embryo	SRX058193	GA129_1-HE	SRR189101	75	41.4	76	76	DPGP2	X,2L,2R,3L,3R	111,099,834	47.9
22	GA130	Pool lab	haploid_embryo	SRX058194	GA130_1-HE	SRR189102	75	43.4	76	76	DPGP2	X,2L,2R,3L,3R	111,771,726	47.6
23	GA141	Pool lab	haploid_embryo	SRX058196	GA141_1-HE	SRR189105	75	40.7	76	76	DPGP2	X,2L,2R,3L,3R	111,146,499	45.1
24	GU10	Langley lab	haploid_embryo	SRX058205	GU10_1-HE	SRR189114	75	33.2	76	76	DPGP2	X,2L,2R,3L,3R	110,887,105	38.9
25	GU2	Langley lab	haploid_embryo	SRX058207	GU2_1-HE	SRR189117	75	33.0	76	76	DPGP2	X,2L,2R,3L,3R	110,886,266	38.4
26	GU6	Langley lab	haploid_embryo	SRX058209	GU6_1-HE	SRR189120	75	33.0	76	76	DPGP2	X,2L,2R,3L,3R	110,933,340	38.1
27	KN133N	Langley lab	haploid_embryo	SRX058256	KN133N_1-HE	SRR189242	75	30.1	76	76	DPGP2	X,2L,2R,3L,3R	111,123,747	35.0
28	KN20N	Langley lab	haploid_embryo	SRX058253	KN20N_1-HE	SRR189239	75	32.0	76	76	DPGP2	X,2L,2R,3L,3R	110,974,588	37.6
29	KN35	Langley lab	haploid_embryo	SRX058258	KN35_1-HE	SRR189245	75	30.2	76	76	DPGP2	X,2L,2R,3L,3R	111,066,184	34.3
30	KR39	Langley lab	haploid_embryo	SRX058267	KR39_1-HE	SRR189254	75	30.2	76	76	DPGP2	X,2L,2R,3L,3R	111,101,981	34.7
31	KR42	Langley lab	haploid_embryo	SRX058268	KR42_1-HE	SRR189255	75	28.5	76	76	DPGP2	X,2L,2R,3L,3R	110,823,311	32.9
32	KR4N	Langley lab	haploid_embryo	SRX058269	KR4N_1-HE	SRR189256	75	29.5	76	76	DPGP2	X,2L,2R,3L,3R	111,045,036	29.6
33	KT1	Langley lab	haploid_embryo	SRX058273	KT1_1-HE	SRR189260	75	25.5	76	76	DPGP2	X,2L,2R,3L,3R	111,229,668	37.6
34	KT6	Langley lab	haploid_embryo	SRX058274	KT6_1-HE	SRR189262	75	27.6	76	76	DPGP2	X,2L,2R,3L,3R	111,074,001	29.6
35	NG10N	Langley lab	haploid_embryo	SRX058275	NG10N_1-HE	SRR189263	75	33.5	76	76	DPGP2	X,2L,2R,3L,3R	111,001,728	38.9
36	NG3N	Pool lab	haploid_embryo	SRX058378	NG3N_1-HE	SRR189414	75	32.3	76	76	DPGP2	X,2L,2R,3L,3R	111,022,313	36.4
37	NG6N	Pool lab	haploid_embryo	SRX058278	NG6N_1-HE	SRR189266	75	33.9	76	76	DPGP2	X,2L,2R,3L,3R	111,483,632	38.4
38	RC1	Langley lab	haploid_embryo	SRX058281	RC1_1-HE	SRR189269	75	26.2	76	76	DPGP2	X,2L,2R,3L,3R	110,659,330	30.3
39	RC5	Langley lab	haploid_embryo	SRX058282	RC5_1-HE	SRR189270	75	29.6	76	76	DPGP2	X,2L,2R,3L,3R	110,723,230	24.9
40	RG33	Pool lab	haploid_embryo	SRX058353	RG33_1-HE	SRR189389	145	37.0	146	146	DPGP2	X,2L,2R,3L,3R	111,689,097	69.8
41	RG4N	Pool lab	haploid_embryo	SRX058362	RG4N_1-HE	SRR306629	145	24.9	146	146	DPGP2	X,2L,2R,3L,3R	111,396,200	54.2
42	RG6N	Langley lab	haploid_embryo	SRX058368	RG6N_1-HE	SRR306624	145	22.0	146	146	DPGP2	X,2L,2R,3L,3R	111,216,270	47.7
43	SB10	Pool lab	haploid_embryo	SRX799453	SB10_1-HE	SRR1696817	100	23.7	100	100	AGES	X,2L,2R,3L,3R	111,238,977	34.2

44	SB16	Pool lab	haploid_embryo	SRX799458	SB16_1-HE	SRR1696818	100	24.1	100	100	AGES	X,2L,2R,3L,3R	111,438,387	32.4
45	SB31	Pool lab	haploid_embryo	SRX799471	SB31_1-HE	SRR1696822	100	21.4	100	100	AGES	X,2L,2R,3L,3R	110,110,096	30.2
46	SF332	Langley lab	haploid_embryo	SRX799661	SF332_1-HE	SRR1696987	100	13.7	100	100	AGES	X,2L,2R,3L,3R	110,582,475	19.9
47	SF428	Langley lab	haploid_embryo	SRX799663	SF428_1-HE	SRR1696988	100	12.6	100	100	AGES	X,2L,2R,3L,3R	110,495,354	16.5
48	SF447	Pool lab	haploid_embryo	SRX799664	SF447_1-HE	SRR1696989	100	15.3	100	100	AGES	X,2L,2R,3L,3R	110,719,070	20.7
49	SP188	Langley lab	haploid_embryo	SRX058287	SP188_1-HE	SRR306632	145	18.4	146	146	DPGP2	X,2L,2R,3L,3R	111,309,908	38.6
50	SP221	Pool lab	haploid_embryo	SRX058288	SP221_1-HE	SRR189277	145	18.9	146	146	DPGP2	X,2L,2R,3L,3R	111,199,509	40.7
51	SP80	Langley lab	haploid_embryo	SRX058292	SP80_1-HE	RR189281	145	18.3	146	146	DPGP2	X,2L,2R,3L,3R	111,128,089	41.6
52	TZ10	Langley lab	haploid_embryo	SRX058283	TZ10_1-HE	SRR189272	75	23.4	76	76	DPGP2	X,2L,2R,3L,3R	110,737,417	26.9
53	TZ14	Langley lab	haploid_embryo	SRX058284	TZ14_1-HE	SRR189273	75	31.7	76	76	DPGP2	X,2L,2R,3L,3R	111,045,117	35.3
54	TZ8	Langley lab	haploid_embryo	SRX058285	TZ8_1-HE	SRR189274	75	31.2	76	76	DPGP2	X,2L,2R,3L,3R	110,920,135	35.9
55	UG19	Pool lab	haploid_embryo	SRX058376	UG19_1-HE	SRR189412	75	33.9	76	76	DPGP2	X,2L,2R,3L,3R	110,998,446	37.2
56	UG28N	Pool lab	haploid_embryo	SRX058277	UG28N_1-HE	SRR189265	75	33.1	76	76	DPGP2	X,2L,2R,3L,3R	110,922,524	38.8
57	UG5N	Pool lab	haploid_embryo	SRX058379	UG5N_1-HE	SRR189415	75	32.1	76	76	DPGP2	X,2L,2R,3L,3R	111,110,172	34.2
58	UK120	Langley lab	haploid_embryo	SRX799667	UK120_1-HE	SRR1696992	100	15.6	100	100	AGES	X,2L,2R,3L,3R	108,541,523	23.2
59	UK2	Langley lab	haploid_embryo	SRX799668	UK2_1-HE	SRR1696993	100	18.3	100	100	AGES	X,2L,2R,3L,3R	111,035,774	25.2
60	UK57	Langley lab	haploid_embryo	SRX799669	UK57_1-HE	SRR1696994	100	20.7	100	100	AGES	X,2L,2R,3L,3R	110,904,117	29.9
61	ZI191	Langley/Pool Lab	haploid_embryo	SRR202128	ZI191-HE	SRR202128	145	23.3	146	146	DPGP3	X,2L,2R,3L,3R	110,845,648	49.2
62	ZI216N	Langley/Pool Lab	haploid_embryo	SRR203328	ZI216N-HE	SRR203328	145	20.4	146	146	DPGP3	X,2L,2R,3L,3R	111,176,278	44.2
63	ZI220	Langley/Pool Lab	haploid_embryo	SRR203067	ZI220-HE	SRR203067	145	23.2	146	146	DPGP3	X,2L,2R,3L,3R	111,180,528	51.3
64	ZI227	Langley/Pool Lab	haploid_embryo	SRR202126	ZI227-HE	SRR202126	145	25.7	146	146	DPGP3	X,2L,2R,3L,3R	111,269,290	54.7
65	ZI254N	Langley/Pool Lab	haploid_embryo	SRR203335	ZI254N-HE	SRR203335	145	18.1	146	146	DPGP3	X,2L,2R,3L,3R	111,099,774	41.2
66	ZI273N	Langley/Pool Lab	haploid_embryo	SRR210786	ZI273N-HE	SRR210786	145	21.1	146	146	DPGP3	X,2L,2R,3L,3R	111,341,925	43.2
67	ZS11	Langley lab	haploid_embryo	SRX058372	ZS11_1-HE	SRR189408	75	32.4	76	76	DPGP2	X,2L,2R,3L,3R	110,736,467	37.7
68	ZS37	Langley lab	haploid_embryo	SRX058373	ZS37_1-HE	SRR189409	75	36.0	76	76	DPGP2	X,2L,2R,3L,3R	110,877,107	41.2
69	ZS5	Langley lab	haploid_embryo	SRX058374	ZS5_1-HE	SRR900425	75	33.4	76	76	DPGP2	X,2L,2R,3L,3R	110,504,765	38.2
70	ZS56	Langley lab	haploid_embryo	SRX058375	ZS56_1-HE	SRR189411	75	30.7	76	76	DPGP2	X,2L,2R,3L,3R	110,737,628	36.0

	Populatio	Country	Locality	Date	Collector(s)	Latitude (I	Longitude	Elevation	Х	2	3	Comments
1	СК	Congo	Kisangani	8/2010	J. Kennis	0.51	25.19	400	2	2	2	
2	CO	Cameroon	Oku	4/2004	J. Pool	6.25	10.43	2169	10	10	10	3 additional chromosome 3 extractions exist, but derive from s
3	EA	Ethiopia	Gambella	12/2011	R. Corbett-Detig	8.25	34.59	525	4	4	4	
4	EB	Ethiopia	Bonga	12/2011	R. Corbett-Detig	7.26	36.25	1725	5	5	5	
5	ED	Ethiopia	Dodola	12/2008	J. Pool	6.98	39.18	2492	6	7	6	
6	EF	Ethiopia	Fiche	12/2011	R. Corbett-Detig	9.81	38.63	3070	5	5	5	
7	EG	Egypt	Cairo	1/2011	J. Atallah	30.10	31.32	25	3	2	2	contains heterozygous intervals (masked in consensus seque
8	EM	Ethiopia	Masha	12/2011	R. Corbett-Detig	7.74	35.48	2260	3	3	3	
9	ER	Ethiopia	Debre Birha	12/2011	R. Corbett-Detig	9.68	39.53	2840	5	5	5	
10	EZ	Ethiopia	Ziway	12/2008	J. Pool	7.93	38.72	1642	5	4	5	
11	FR	France	Lyon	7/2010	J. Pool	45.77	4.86	175	9	9	9	
12	GA	Gabon	Franceville	3/2002	B. Ballard & S. Charlat	-1.65	13.60	332	10	9	10	GA191 is missing chromosome 2 data due to heterozygosity
13	GU	Guinea	Dondé	6/2005	B. B. Sow	10.70	-12.25	801	5	5	7	
14	KM	Kenya	Malindi	7/2002	B. Ballard	-1.43	40.03	78	4	3	1	contains heterozygous intervals (masked in consensus seque
15	KN	Kenya	Nyahururu	1/2009	J. Pool	0.04	36.36	2303	6	5	6	
16	ко	Kenya	Molo	1/2009	J. Pool	-0.25	35.73	2506	4	0	4	
17	KR	Kenya	Marigat	1/2009	J. Pool	0.47	35.98	1062	6	4	6	
18	KT	Kenya	Thika	1/2009	J. Pool	-1.04	37.08	1531	2	2	2	
19	NG	Nigeria	Maiduguri	9/2004	D. Gwary & B. Sastawa	11.85	13.16	295	6	6	6	
20	RAL	United State	Raleigh NC	2003	T. Mackay	35.76	-78.66	91	205	205	205	(sample sizes before heterozygosity and IBD masking)
21	RC	Rwanda	Cyangugu	12/2008	J. Pool	-2.29	28.55	1602	2	2	2	
22	RG	Rwanda	Gikongoro	12/2008	J. Pool	-2.49	28.92	1927	27	27	27	
23	SB	South Africa	Barkly East	12/2011	J. Pool	-30.97	27.59	1800	5	5	5	
24	SD	South Africa	Dullstroom	12/2011	J. Pool	-25.42	30.10	2000	5	4	5	SD82 is missing chromosome 2 data due to heterozygosity
25	SE	South Africa	Port Edward	12/2011	J. Pool	-31.06	30.22	50	3	3	3	
26	SF	South Africa	Fouriesburg	12/2011	J. Pool	-28.60	28.05	1800	5	4	5	SF7 is missing chromosome 2 data due to heterozygosity
27	SP	South Africa	Phalaborwa	7/2010	R. Corbett-Detig	-23.94	31.14	350	7	7	7	
28	TZ	Tanzania	Uyole	12/2009	L. Nsemwa	-8.89	33.44	1800	3	3	3	
29	UG	Uganda	Namulonge	4/2005	J. Ogwang	0.53	32.60	1134	4	4	6	
30	UK	Uganda	Kisoro	1/2012	R. Corbett-Detig	-1.28	29.69	1925	5	4	5	UK120 is missing chromosome 2 data due to heterozygosity
31	UM	Uganda	Masindi	7/2010	J. Pool	1.68	31.72	1170	3	3	3	
32	ZI	Zambia	Siavonga	7/2010	R. Corbett-Detig	-16.54	28.72	530	196	197	197	ZI382 is missing chromosome X due to heterozygosity
33	ZK	Zimbabwe	Lake Kariba	5/1994	T. Mutangadura	-16.52	28.80	619	3	0	2	contains heterozygous intervals (masked in consensus seque
34	ZL	Zambia	Livingstone	7/2010	R. Corbett-Detig	-17.86	25.86	900	1	1	1	
35	ZO	Zambia	Solwezi	7/2010	R. Corbett-Detig	-12.18	26.40	1380	2	2	2	
36	ZS	Zimbabwe	Sengwa	9/1990	R. Ramey	-18.16	28.22	865	4	4	4	

Table S1E. Key for Two-letter code for the demography of the Drosophila Genome Nexus Strains in the TIDAL-Fly v1 database

Table S1F.Pools of flies analyzed in the TIDAL-Fly v1 database

							Min Read		Read	Read	
	Fly Pool ID	Fly Pool Location	Genome Type	SRA Accession	Library ID*	SRA Accession	Length	Reads (M)	Length 1	Length 2	Reference
1		Australia Cairos	Pool	SRR1177951	nool-ALI-CI	SRR1177951	75	26M	75	0	Reinhardt et al. 2014
2		Australia, Cardwell	Pool	SRR1177952	pool-AU-CR	SRR1177952	75	36M	75	0	Reinhardt et al. 2014
		Australia, Miller's Orchard	Pool	SRR1177953	pool-AU-MO	SRR1177953	75	24M	75	0	Reinhardt et al. 2014
4		Australia, Sorell	Pool	SRR1177955	pool-AU-SO	SRR1177955	75	38M	75	0	Reinhardt et al. 2014
F	FU-PO1	Furope Portugal	Pool	SRR188217	pool-FU-PO1	SRR188217	75	19.5M	75	75	Kofler et al. 2012
F	FIL-PO2	Europe Portugal	Pool	SRR189066	pool-EU-PO2	SRR189066	73	60.9M	74	74	Kofler et al. 2012
7	NA-SC	North America Eutawville SC	50-100 pooled individuals	SRX661835	pool-NA-SC	SRR1525696	100	82M	100	100	Rendand et al. 2012
، ۶		North America, Habira, GA	50-100 pooled individuals	SRX661834	pool-NA-GA	SRR1525695	100	97M	100	100	Bergland et al. 2014
		North America, 90 of the DGRP fly stra	Pool	SRX661836	pool-NA-NC	SRR1525697	90	42M	90	90	Bergland et al. 2014
10		North America, Job of the Dorth hy stra	50-100 pooled individuals	SRX661837	pool-NA-RA1	SRR1525768	100	181M	100	100	Bergland et al. 2014
11	ΝΔ-ΡΔ2	North America Linvilla PA fall 2009	50-100 pooled individuals	SRX661838	pool-NA-PA2	SRR1525769	100	73.7M	100	100	Bergland et al. 2014
12		North America Linvilla, PA, spring 2010	50-100 pooled individuals	SRX661839	pool-NA-PA3	SRR1525770	100	35M	100	100	Bergland et al. 2014
12		North America Linvilla, PA, fall 2010	50-100 pooled individuals	SRX661840	pool-NA-PA4	SRR1525771	100	70M	100	100	Bergland et al. 2014
1/		North America Linvilla, PA, fail 2010	50-100 pooled individuals	SRX661841	pool-NA-PA5	SRR1525772	90	78.1M	90	90	Bergland et al. 2014
16		North America Linvilla, PA, fall 2011 (n	50-100 pooled individuals	SRX661842	pool-NA-PA6	SRR1525773	100	73.2M	100	100	Bergland et al. 2014
16		North America Linvilla, PA, fall 2011 (p	50-100 pooled individuals	SPX6618/3		SPR1525774	90	82.1M	90	00	Bergland et al. 2014
17		North America Bowdoinham ME	50-100 pooled individuals	SRX001043	pool-NA-FA7	SRR1525698	100	95M	100	100	Bergland et al.,2014
11		North America Bowdoinham, ME	50-100 pooled individuals	SRX001044	pool-NA-ME2	SPR1525600 SPR2006283	100	32M 32M	100	100	Bergland et al.,2014
10		North America Homestead, El	50-100 pooled individuals	SRX001043	pool-NA-MLZ	SRR1525685	100	64M	100	100	Bergland et al.,2014
20		North America Homostood, FL	50-100 pooled individuals	SRA001032		SRR1525604	100	04IVI,	100	100	Bergland et al.,2014
20		Austria, lightest females	Pool 100 fomalos	SKA001033	pool ELLALLE1	5RR 1525094	100	41.0IVI 96.1	100	100	Dergianu et al.,2014
2		Austria, lightest females	Pool, 100 females	ERX149309		ERR 17 3223	100	00.1	100	100	Bastide et al., 2013
22		Austria, lightest females	Pool, 100 females	ERA 149370		ERR 173220	100	95.0	100	100	Dastide et al., 2013
		Austria, darkest females	Pool, 100 females	ERA 14937 1	pool-EU-AU-DF1	ERR173227	100	34.5	100	100	Dastide et al., 2013
24		Austria, darkest females	Pool, 100 females	ERX149372	pool-EU-AU-DF2	ERR173228	150	39.7	150	85	Bastide et al., 2013
25	EU-AU-DF3		Pool, 100 ternales	ERA 149373	pool-EU-AU-DF3	ERR 173229	100	95.0	100	100	Dastide et al., 2013
20		Austria/Vienna reference	Pool, 100-150 females	ERA 149374		ERR 173230	100	41.0	100	100	Dastide et al., 2013
21		Austria/Vienna reference	Pool, 100-150 females	ERA 149373	pool-EU-AU2	ERR 173231	150	30.3	100	00	Bastide et al., 2013
20		Austria/Vienna reference	Pool, 100-150 females	ERA 149370	pool-EU-AU3	ERR 173232	100	30.910	100	100	Dastide et al., 2013
28		Austria/Vienna reference	Pool, 100-150 females	ERA 149377	pool-EU-AU4	ERR 173233	100	40.7	100	00	Dastide et al., 2013
30	JEU-AU5	Austria/Vienna reference	Pool, 100-150 females	ERX149378	pool-EU-AU5	ERR173234	100	41.7	100	100	Bastide et al., 2013
3		Austria/Vienna reference	Pool, 100-150 females	ERX149379		ERR173235	100	41.9	100	100	Bastide et al., 2013
32		Austria/Vienna reference	Pool, 100-150 ternales	ERA 149300	pool-EU-AU7	ERR 17 3230	100	40.8	100	100	Dastide et al., 2013
30		Austria/Vienna reference	Pool, 100-150 females	ERA 149301		ERR173237	100	40.2	100	100	Dastide et al., 2013
34	EU-AU9	Austria/Vienna reference	Pool, 100-150 females	ERX149382	pool-EU-AU9	ERR173238	100	40.61/1	100	100	Bastide et al., 2013
35		Austria/Vienna reference	Pool, 100-150 females	ERX149383	pool-EU-AU10	ERR173239	150	40.910	150	80	Bastide et al., 2013
30		Austria/Vienna reference	Pool, 100-150 females	ERA 149304	POOLED-AUTT	ERR173240	100	40	100	100	Dastide et al., 2013
3/		Austria/Vienna reference	Pool, 100-150 remaies	ERA149385		ERR 1/3241	150	40.1	150	80	Dastide et al., 2013
38		Italy, lightest females	Pool, 100 females	ERA149386		ERR1/3242	90	14.6	90	90	Dastide et al., 2013
39		Italy, lightest females	Pool, 100 temales	ERA 14938/		ERR 1/ 3243	90	10.0	90	90	Dastide et al., 2013
40		Italy, lightest females	Pool, 100 females	ERA149388	pool EU-II-LF3	ERR 1/3244	90	100.0	90	90	Dastide et al., 2013
41		Italy, lightest females	Pool, 100 temales	ERA149389		ERR 1/ 3243	100	138.8	100	100	Dastide et al., 2013
42		Italy, lightest temales	Pool, 100 females	ERX149390	pool-EU-II-LF5	EKK173246	100	131.7	100	100	Bastide et al., 2013
43		Italy, darkest females	Poul, 100 females	ERX149391		ERR1/324/	92	11.1	92	92	Dastide et al., 2013
44	HEU-II-DF2	Italy, darkest females	Poul, 100 females	ERX149392	PUOI-EU-IT-DF2	ERR1/3248	92	10.3	92	92	Dastide et al., 2013
45		Italy, darkest females	Pool, 100 females	ERX149393	pool-EU-II-DF3	EKK173249	92	9.5	92	92	Bastide et al., 2013
46		Italy, uarkest remaies	Pool, 100 temales	ERA149394	POOLED-IT-DF4	ERR 1/3200	100	138.4	100	100	Dastide et al., 2013
47		Italy, uarkest remaies		ERA149395	PUOI-EU-IT-DF5	ERR 1/3201	100	138.4	100	100	Dastide et al., 2013
48			Poul, 100-150 females	ERX149396		ERR1/3202	94	21.6	94	94	Dastide et al., 2013
49			Pool, 100-150 females	ERX149397		ERR1/3203	94	17.4	94	94	Dastide et al., 2013
50			Pool 100-150 females	ERA 149398		ERR 1/3234	94	10.0	94	94	Dastide et al., 2013
51				ERA149399		ERR 1/ 3200	150	13211	150	150	Dastide et al., 2013
52		italy, reference	FUUL TUU-TOU TEMAIES	EKA149400	1001-EU-115	ERR1/3200	150	153IVI	150	150	Dastide et al., 2013

Iries	PE_Tdot_common_C* linker	AATGATACGGCGACCACCGAGATCTACACTCTTTCCCTACACGACGCTCTTCCGATC*T
A libra ion	Barcoded linker PE_tdot_CAGCACTA	/5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGcagcactaATCTCGTATGCCGTCTTCTGCTTG
gDN/ struct	Barcode linker PE_tdot_AGAGATGC	/5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGagagatgcATCTCGTATGCCGTCTTCTGCTTG
os for cons	Barcode linker PE_tdot_TCACGTGT	/5Phos/GATCGGAAGAGCGGTTCAGCAGGAATGCCGAGACCGtcacgtgtATCTCGTATGCCGTCTTCTGCTTG
olig	PE-POSTPCR_1	AATGATACGGCGACCACCGAGA
0	PE-POSTPCR_2	CAAGCAGAAGACGGCATACGAG

Table S2 Primer Lists

PRIMER SEQUENCE FOR S2c1 INSERTS

Sr. no.	SV#	t Chr	Chr_coord_	Chr_coord_	TE	Forward Prmer Sequence	Forward primer Length	Reverse Primer Sequence	Reverse Primer length	Length w/c L	ength with TE
1	. :	14 chr2L	312233	312444	Stalker2	ACTGGCAAGACCTCGATTGTC	21	1 CGGATTGTCCGACGTATTAGA	2	1 411	8661
2		5 chr2L	87055	87258	1731	GGTGCCGCACAATTCGCAGGC	21	1 GCTCCGGTCAGAAGATTTTAC	2	2 404	5053
3	6	21 chr2R	544728	544940	HMS-Beag	€ ATGGGGAACACAGTCAAAATG	21	1 CATATTATTCAAAGATTGGAT	2	1 353	6882
4	6	30 chr2R	2675584	2675743	opus	GAAGAATGAGACGGGCTACCG	21	1 CTGTAATTGTGTACACAGTCA	2	1 332	8891
5	11	.23 chr3L	516184	516383	17.6	AGTCCTCCCAACCGAGATGG	20) GATTGAATTTCAGTTGGCCGG	2	1 349	7788
e	11	.31 chr3L	552782	552981	Juan	TTTATAATAATGTTGCTGGAC	21	1 GGCATTTCTATAGCCCAACCC	2	1 344	4580
7	17	'43 chr3R	6430955	6431163	3S18	ATTGAGGCTTTTATTAATCAG	21	1 GTTCCTATATGCTTGTGATGA	2	1 293	6126
8	17	'62 chr3R	7492347	7492543	1360	AATACAAGATATTGATACATC	21	1 CGAAAGTTCATACAAATGTATA	2	2 374	4480
9	24	06 chrX	141518	141720	blood	TTAATGAAGCCGTTGGGCTAGG	22	2 CTGTGGTGAATTTGCAGCCTT	2	1 379	7790
10	24	13 chrX	325934	326139	1731	TTTTACACTAAGAGTACCGGC	21	1 CGACCTAATAGTGCGGAAGCT	2	1 349	4998
11	24	27 chrX	1082310	1082488	297	AGATAAGACGCCTATTAAGTG	21	1 CATTGTATGTTGCATCTGTAG	2	1 373	7368
12		32 chr2L	522270	522480	297	ATTTCGAATACGTATCGAATG	21	1 CATTTCCCTGGCAACTTTGCA	2	1 386	7381
13	210	65 chr3R	2.3E+07	2.3E+07	roo	ATCGCTTTTTCCAATAAATTGCAT	23	3 CAGAGACAGCGATTTCAAAT	2	1 367	9459
14	25.	31 chrX	6005755	6005959	roo	ACCTTCACGCAGTCCAGCTTCG	22	2 GCACCTGGCAGGGGATTTTAATT	2.	3 381	9473
15	110	62 chr3L	957937	958157	roo	TATACAACCACGAGTTCTTGGAAG	24	4 ACAACATAAATAATTGCAGAGGC	2:	3 296	9388

PRIMER SEQUENCE FOR S2c1 DEPLETION

Sr. No. (Chr_cc Chr_3p	Chr_coord_Chr_coord_repName	Forward Primer Sequence	Forward Primer Length Reverse Primer Sequence	Reverse PrimerLength	Length witl L	ength withTE depletic
1	chr2L	7350447 7350536 roo	CTCGCGGTGAGTCAACCCCAG	21 GAGAATTTCGGTGGTTACGCCC	22	2 7480	5757
2	chrX	6571315 6571399 Tirant	CCATATTTAGACAATTATTC	20 CAGTCCCACAAGTGCGAGCGG	2	3 8802	1240
3	chr2R	21753581 21753663 roo	GAACACTTTAAGCCCAGTTTG	21 GAACTTCAACAATATCCGAT	20	833	405
4	chr3L	3069878 3069958 Tirant	GACTCCTATGACGCAATACAG	21 CATTCTGTATACAAACAAATC	22	2 8912	1350
5	chr3L	7889043 7889129 Stalker4	TATGCCTATAATCAATAAATC	21 CTTCATGTTGCTACATAAATCAT	2	3 2873	1107
6	chr3L	7987706 7987783 NOF	TCCCGAATAGCACCGAATTTC	21 CAATTAATGTGTGAATCTCAAG	22	2 2650	620
7	chr3L	15426613 15426700 opus	TTTTGGTCGAGTTCTGTTCTG	21 GAAGTCTTTATAAGTCAAGAA	2	l 3160	2642
8	chr3R	24072571 24072628 jockey	CATTTCTTTGCGCCTGCCATG	21 GACAGCACTTGGATGATCCA	20	341	150
9	chrX	3842569 3842647 pogo	GATCCTTGTCCCGGATAAGTC	21 GATTTTCCCGTTCTGGAGTAA	2	1 541	355
10	chr3R	24931935 24932010 Doc	TGCAGAATTGTACAAGAGATG	21 CAGATATGTACAATTCCGGACA	22	2 5120	395

Table S2 Primer Lists

Tuble SE	· · · · · ·															
	TIDAL	_only_TEIn:	s_sites													
						RAL-										Predicted
Site		Chr_coord	Chr_coord		Coverage	765_Inserts_Annotat										Amplicon
Number	Chr	_5p	_3p	TE	_Ratio	ed.Insert_Code	Space	FW primer name	FW primer sequence	Fw Length	Tm	RV primer name	RV primer sequence	Rv Length	Tm	Size
1	chr2L	8133670	8133752	HMS-Beag	2.4	chr2L_17_8130001	82	Telns_TID_1_Fw	GATCAAGTCGAACGAACAATT	21	56.8	Telns_TID_1_Rv	CGCATGCATATAGGCGGATGC	21	67.7	275
2	chr2L	19834994	19835061	hobo	4.7	chr2L_20_19830001	67	Telns_TID_2_Fw	TAAATATTTATCATTGTGAGCTG	23	51.9	Telns_TID_2_Rv	AGTTTTATGGCATTTATGTCG	21	54.6	354
3	chr2L	12227998	12228146	BS	5.3	chr2L_10_12225001	148	Telns_TID_3_Fw	CCAGCTGGCACAAATGAATG	20	62.6	Telns_TID_3_Rv	CGTTTTAAGCCCACATTGCTG	21	62.7	274
4	chr2R	12581030	12581105	pogo	5	chr2R_14_12580001	75	Telns_TID_4_Fw	ATTGAAAGAAAAATAGTCATGC	22	53.1	Telns_TID_4_Rv	CCACTAAGCGATGACGAACGCG	22	69.1	333
5	chr2R	7621371	7621430	mdg1	4	chr2R_10_7620001	<u>59</u>	Telns_TID_5_Fw	ATGTCAAGAATCTGAAGTTACG	22	53.8	Telns_TID_5_Rv	CGTTTGTTTATGGTCCAAATGC	22	61.4	328
6	chr3L	4481564	4481640	roo	4.1	chr3L_14_4480001	76	Telns_TID_6_Fw	GAGTGCAGACCCTACTATTAG	21	51	Telns_TID_6_Rv	CACGTTCTTATGTGTATAATTA	22	47.8	337
7	chr3L	18394377	18394445	1360	4.2	chr3L_11_18390001	<mark>68</mark>	Telns_TID_7_Fw	TCAAACTATGTGTTTTAAGAGTAT	24	50	Telns_TID_7_Rv	CAGGGTGGATTCGCTATCAGG	21	64	360
8	chr3R	4885334	4885399	1360	1.7	chr3R_13_4885001	65	Telns_TID_8_Fw	ATTTATGCCAGTCATGGGCC	20	62	Telns_TID_8_Rv	CGAGCAAGAATGTACCTCAAGT	22	58.5	354
9	chr3R	20125023	20125087	jockey	2.4	chr3R_12_20125001	64	Telns_TID_9_Fw	AATTGACTTGCCACGATGTGC	21	63.3	Telns_TID_9_Rv	CCGAGTGCAATGGGAGTGGGC	21	71.3	360
10	chr3R	11089486	11089562	roo	5.4	chr3R_15_11085001	<mark>76</mark>	Telns_TID_10_Fw	TTTGAACACAATTTGGAAGTG	21	56.2	Telns_TID_10_Rv	CAGTCCGCCCAAGAAACCAAA	21	66.5	359
11	chrX	7785488	7785556	hobo	3.3	chrX_10_7785001	68	Telns_TID_11_Fw	AAGTTTTATGACCTCCATATG	21	51.1	Telns_TID_11_Rv	CATTAATTTCGCCAGCACAGC	21	62.9	342
12	chrX	15391856	15391929	roo	4.1	chrX 13 15390001	73	Teins TID 12 Fw	TATATATTTCGGTAAAACCCTG	22	53.3	Teins TID 12 Rv	CTTTGCATGATAACATTAAGT	21	49.9	341

Table S2 Primer Lists TIDAL and LnB shared sites

						Tidal													Predicted
Site		Chr_coord Chr	_coord		Coverage	Insert													Amplicon
Number	Chr	_5p	_3p	TE	_Ratio	Code	LnB765	TIDAL CnT	TEMP	Space	FW primer name	FW primer sequence	Fw Length	Tm	RV primer name	RV primer sequence	Rv Length	Tm	Size
1	chr2L	267478	267547 F	P-element	4.4	chr2L_18	chr2L_26	5 chr2L_265	chr2L_265	69	TeIns_LnB_1_Fw	ACATACACAGAGACAGGAAAGC	22	56.1	TeIns_LnB_1_Rv	CGAATTTATGGAATTCAGCATT	22	58.2	314
2	chr2L	1167146 1	167232 0	opus	2.6	chr2L_21	chr2L_116	5 chr2L_116 chr2L	_1	86	TeIns_LnB_2_Fw	GTCCACTATAACGTTACCCAAC	22	55.3	TeIns_LnB_2_Rv	CAAGAGACCATTGCGCAGGT	20	63.6	386
3	chr2L	20800099 208	800248 E	Burdock	5.8	chr2L_22		3lchr2L_2080	chr2L_208	149	TeIns_LnB_3_Fw	CCTCCTGTCCCTACCAACTGG	21	63.1	Telns_LnB_3_Rv	GACCTCTCCTGTCTCTTATTT	21	51.8	329
4	chr2R	9380884 93	380961	3518	2.4	chr2R_16	chr2R_93	8 chr2R_938 chr2R	_9 chr2R_938	77	TeIns_LnB_4_Fw	GGGGAGAAAATGGGAGAAAGC	21	63.3	TeIns_LnB_4_Rv	CCAAGTCGAAAATGTTGCTTC	21	59.7	365
5	chr2R	9442941 94	443015 4	412	3.9	chr2R_13	chr2R_94	4 chr2R_944 chr2R	_9	74	Telns_LnB_5_Fw	TGTCAAGAATCTGAAGTTACG	21	53.1	Teins_LnB_5_Rv	GATTCGTTTGTTTATGGTCCA	21	57.5	331
6	chr2R	11578561 115	578638 b	blood	5.6	chr2R_14	chr2R_11	5 chr2R_115 chr2R	_1 chr2R_115	77	Telns_LnB_6_Fw	CATTTTTGAGTGCAGACCCTAC	22	58.8	Telns_LnB_6_Rv	TGTCAAGTGTATATTGCTTCT	21	50.1	372
7	chr3L	934796	934851	nobo	8.3	chr3L_15	chr3L_930	0chr3L_9300		55	TeIns_LnB_7_Fw	ATACGGAATTCAAACTATGTG	21	52	TeIns_LnB_7_Rv	TGGATTCGCTATCAGGATGTG	21	61	364
8	chr3L	22566716 225	566793	nobo	4.3	chr3L_32	chr3L_22	6 chr3L_225		77	Telns_LnB_8_Fw	TTGCACTGCTATTTGCAGAAG	21	59.3	Teins_LnB_8_Rv	CAATCGTCTCCATTTTGTATG	21	55.7	367
9	chr3R	18968019 189	968094 E	Burdock	3.8	chr3R_19	chr3R_18	9 chr3R_189	chr3R_189	6 75	Telns_LnB_9_Fw	AGAGTGTTATCTATGGGAGAG	21	50.2	Telns_LnB_9_Rv	GTCCATTTGTTTGTCCGCTCAC	22	63.9	375
10	chr3R	30626323 306	626403 4	412	5.2	chr3R_22	chr3R_30	6 chr3R_306	chr3R_306	80	Telns_LnB_10_Fw	GAAATCCAAATGCCCGTTTCATG	23	66.5	TeIns_LnB_10_Rv	CTAGATTAGTGGCCATATTAAAG	23	52.3	379
11	chrX	6487781 64	487856 b	blood	4.3	chrX_18_	6 chrX_648	5 chrX_6485 chrX_	64	75	Telns_LnB_11_Fw	TTTCATTCAAAATGCTTATGC	21	55.6	Teins_LnB_11_Rv	CATGTAATGCGTGCATACATG	21	58.5	375
12	chrX	21399401 213	399469 p	oogo	3.6	chrX_12_	2 chrX_213	9 chrX_2139	chrX_2139	68	Telns_LnB_12_Fw	CGTGGAGGTAAGTGAAATTTC	21	56.4	Telns_LnB_12_Rv	CGATGCTGCAACAAAACAAAT	21	61	321

Table S2 Primer Lists

CnT Only sites

Site														Predicted
Number	Insert_code	Chr	Start	Stop	Space	FW primer name	FW primer sequence	Fw Length	Tm	RV primer name	RV primer sequence	Rv Length	Tm	Amplicon Size
1	chrX_4330001	chrX	4334105	4334327	222	Telns_CnT_1_Fw	CTAGGCTACTCCTAAAAGATATC	23	50.8	Telns_CnT_1_Rv	ACGAGGCTAAAATAAAGGCCC	21	60.8	376
2	chrX_14000001	chrX	14001033	14007159	6126	Telns_CnT_2_Fw	AACAAGAGAGAATGCTATAGTCG	23	54.8	Telns_CnT_2_Rv	GATGAATTTTCGCAATTCACA	21	58.6	6092
3	chr3R_7695001	chr3R	7696150	7703338	<mark>7188</mark>	Telns_CnT_3_Fw	CCACACTTATATTA ATTGGCA	22	53.1	Telns_CnT_3_Rv	GATCTCTCGCCGCTGTCACTG	21	65.8	7171
4	chr3R_14020001	chr3R	14021702	14023463	1761	Telns_CnT_4_Fw	CAGTTTGTCAAGAAACTGTTTAC	23	53.6	Telns_CnT_4_Rv	CAGTTTGTCAAGAAACTGTTT	21	52.2	1734
5	chr3L_4360001	chr3L	4361048	4361901	<mark>853</mark>	Telns_CnT_5_Fw	AGCTCAAAGAAGCTGGGGTCG	21	65.2	Telns_CnT_5_Rv	CCATGAAATGAAACAATGATTAA	23	56.7	844
6	chr3L_17180001	chr3L	17180645	17180660	15	Telns_CnT_6_Fw	ACGATTTTGCCGCTCACGC	19	66.8	Telns_CnT_6_Rv	GCCGAAATTTGTAGTTAAAAT	21	52.2	394
7	chr2R_6945001	chr2R	6948454	6948972	<mark>518</mark>	Telns_CnT_7_Fw	TCTAAAGTCGTGTTCCCTGAC	21	56.9	Telns_CnT_7_Rv	CGTAAATTAAATTGGTTGAGGA	22	56	493
8	chr2R_13060001	chr2R	13064762	13064861	<mark>99</mark>	Telns_CnT_8_Fw	TATATTTATGCCAGTCATGGG	21	55.2	Telns_CnT_8_Rv	CGAGCAAGAATGTACCTCAAGT	22	58.5	357
9	chr2L_1805001	chr2L	1809645	1810122	477	Telns_CnT_9_Fw	TTCAGGATTAGTTTGTCTAACAA	23	53.6	Telns_CnT_9_Rv	ATTCCGAGAAATTTATTCCGA	21	57.7	447
10	chr2L_9780001	chr2L	9783398	9783415	17	Telns_CnT_10_Fw	ATACGGGGTGCTGGTAAACTCC	22	63.4	Telns_CnT_10_Rv	CGTCTTTGTCAACGAATCAATTG	23	61.7	394
11	chr4_180001	chr4	180927	183823	2896	Telns_CnT_11_Fw	CTTTCTTATACGCATACATTG	21	50.6	Telns_CnT_11_Rv	CGGCCATACACATTGGTCTTG	21	63.5	2892
12	chr4_1000001	chr4	999517	1001425	1908	Telns_CnT_12_Fw	GTTCGTATTTACACTAGCTAAGG	23	52.4	Telns_CnT_12_Rv	GTTACTCAGCAAAACGTAGTG	21	52.9	2008

Table S2 Primer Lists

TEMP Only Sites

		-													
															Predicted
Site															Amplicon
Number	Chr	Start	Stop	rounder	InsertCode	Space	FW primer name	FW primer sequence	Fw Length	Tm	RV primer name	RV primer sequence	Rv Length	Tm	Size
1	chr2L	9850436	9850443	9850001	chr2L_9850001	7	Telns_TEM_1_Fw	GGTTGTCGTTGTCCTTCCTG	20	60.5	Telns_TEM_1_Rv	GGTTCAGGTCAGGCAGGCAG	20	62	383
2	chr2L	1558495	1558995	1555001	chr2L_1555001	500	Telns_TEM_2_Fw	CAGACAAAAGTAATGTGAAAC	21	50	Telns_TEM_2_Rv	CAACCATTAATTGCTATATCA	21	50.7	482
3	chr2R	5334166	5334666	5330001	chr2R_5330001	500	Telns_TEM_3_Fw	CCGTGTAGGCTTACAAGCAATAG	23	60.2	Telns_TEM_3_Rv	CTTGTGGTGCAAAGTCAAATG	21	59.2	494
4	chr2R	2095477	2095485	2095001	chr2R_2095001	8	Telns_TEM_4_Fw	GTCGACTATGTATGGAGGCTGCG	23	65.2	Telns_TEM_4_Rv	CTTACAATTAGATTTAATGCTTT	23	50	405
5	chr3L	9571935	9572435	9570001	chr3L_9570001	500	Telns_TEM_5_Fw	TCCGCAAATGTAAGGTATAGTG	22	57	Telns_TEM_5_Rv	GTTTCGATGGATACGAAAACA	21	57.6	482
6	chr3L	5056174	5056674	5055001	chr3L_5055001	500	Telns_TEM_6_Fw	CAATCCGCACTCAGACACTCAC	22	63.2	Telns_TEM_6_Rv	GGCTCTAATCGTTTAGTTATAAA	25	52.1	499
7	chr3R	5035704	5035739	5035001	chr3R_5035001	35	Telns_TEM_7_Fw	TGAATTTTACATTAAAGGCGG	21	57	Telns_TEM_7_Rv	AATCCGAACCCGAATCGGAA	20	65.8	296
8	chr3R	1211275	1211285	1210001	chr3R_1210001	10	Telns_TEM_8_Fw	TAGAACTATAGATCTAGCTAAGGG	24	50.8	Telns_TEM_8_Rv	GTGATTGCCTTAGTTTTGTTT	21	53.8	398
9	chrX	294866	294869	290001	chrX_290001	3	Telns_TEM_9_Fw	ATTGTATGCATAATTTACCACTT	23	52.6	Telns_TEM_9_Rv	CGCATTCAGCTTCGGGTCGAC	21	61.8	395
10	chrX	5410656	5411156	5410001	chrX_5410001	500	Telns_TEM_10_Fw	GTTAATAGTAATTAGCACATTGCA	24	53.5	Telns_TEM_10_Rv	GAATCTCCGATATCATCAACGA	22	59	488
11	chrY	203747	204247	200001	chrY_200001	500	Telns_TEM_11_Fw	CGTATCAGACAATCTAGTAGCAG	23	53.8	Telns_TEM_11_Rv	GGACAACACCATTTCATAAT	20	52.3	487
12	chrY	1565254	1565753	1565001	chrY_1565001	<mark>499</mark>	Telns_TEM_12_Fw	TCATCAAATCGGAGACACTCC	21	60.1	Telns_TEM_12_Rv	ATGAATTTGTTCTATTTGAACTC	23	52.2	645

Primers for TE InDels In the ISO1-BL Line

TE Insertions

Site		Chr_coor	Chr_coor		Coverage			Fw				Rv		Amplicon
Number	Chr	d_5p	d_3p	TE	_Ratio	FW primer name	FW primer sequence	Length	Tm	RV primer name	RV primer sequence	Length	Tm	Size
1	chr2R	2E+07	19768307	copia	4.5	ISO1_BL_FI1	TGCCTAGAATTTGCTATGCCGC	22	65.5	ISO1_BL_RI1	GTTTAAGTAAGGATCGATTTTAG	23	51.5	295bp
2	chr3L	4390337	4390468	roo	4.5	ISO1_BL_FI2	GTTGGACAAAGGAATCGGTAATG	23	61.8	ISO1_BL_RI2	GCATTCTGTACTGTTCCCAGCA	22	62.5	330bp
3	chr2R	8528862	8528983	I-element	4.4	ISO1_BL_FI3	CCATCAAAACGCACATATTGC	21	61.3	ISO1_BL_RI3	TTTCCGCTTTCCCACTTTC	19	60.1	273bp
4	chr3R	3E+07	29777247	F-element	17.9	ISO1_BL_FI4	TGGCGCTACGCTAATGAAATC	21	62.4	ISO1_BL_RI4	GCGGTCCTGATAAACGTATTT	21	58.2	414bp
5	chr2L	1068653	1068778	FB	4.2	ISO1_BL_FI5	CTGATAAGCGGCAGCATAAGCAG	23	65.3	ISO1_BL_RI5	GAGCCAAGCTTAGGCTGCAATT	22	64.1	517bp
6	chrX	6542904	6543018	I-element	4.3	ISO1_BL_FI6	TTGAAGTTGGCCATTTACGGG	21	64.1	ISO1_BL_RI6	GGACGCCAATGGAGCTTATTG	21	63.9	501bp
7	chrX	1.9E+07	19018748	copia	4.7	ISO1_BL_FI7	AAGATTTAGAGACACTCCACC	21	52.6	ISO1_BL_RI7	GCTTAAGGCCGCCGAACAA	19	65.6	469bp
8	chr3R	5066592	5066727	Tirant	4.4	ISO1_BL_FI8	TTATTACCACAGCTAAGAGTC	21	49.1	ISO1_BL_RI8	GATATGCTAATTCGGCGCG	19	61.6	515bp
9	chrX	1.1E+07	10556301	Doc	5.7	ISO1_BL_FI9	AGCCAAGATCTGTCATTTGTC	21	56.8	ISO1_BL_RI9	CAAACGACACAGCGAAGCGTA	21	64.6	363bp
10	chr2L	5999659	5999785	hobo	5.6	ISO1_BL_FI10	GTCGAAGTGCCGGAAACGT	19	63.5	ISO1_BL_RI10	CAAATTCTTAAAGCCAAGGCTT	22	59	479bp
11	chr2R	2.3E+07	22786444	hobo	5.3	ISO1_BL_FI11	AAGAATTTCTTTTCCCAAGCTC	22	58.1	ISO1_BL_RI11	GGTATACTTACCTTTTATGCAG	22	50.6	523bp
12	chr2L	9485261	9485390	hobo	4.2	ISO1 BL FI12	GAGTGTCGCAGAGTCCGTCTG	21	63.6	ISO1 BL RI12	CTAGTAGAATGATTTTGGGGGCAA	23	59.5	514bp

TE Depletions

														Predicted						Predicted
Site		Chr coor	Chr coor		Coverage			Fw				Rv		Amplicon				Rv		Amplicon
Number	Chr	d_5p	d_3p	TE	_Ratio	FW primer name	FW primer sequence	Length	Tm	RV primer name	RV primer sequence	Length	Tm	Size	R١	primer name	RV primer sequence	Length	Tm	Size
	l chrX	6335185	6335241	Tirant	4.6	ISO1_BL_FD1	GCTGATTTACGAATCACTTGAAG	23	3 58.1	ISO1_BL_RD1	GGCTAGCTGGGGGACAATGTTG	21	64	380bp	IS	D1_BL_RD1.1	CGTCATTGTATCGCGCTTATA	21	58.8	2757b.p.
	2 chr3R	5045818	5045876	HMS-Beagle	4.4	ISO1_BL_FD2	GGTTACACAAGAGCGTGCAGC	21	63.2	ISO1_BL_RD2	CTAAGTCCCTAGCAATCAAGTGA	23	57.7	448bp	IS	D1_BL_RD2.1	GCCACTTATTATAAATGTCA	22	50	7393
	3 chr3R	3.2E+07	31691562	Doc	4.3	ISO1_BL_FD3	AAGAGCGACTGAATAACGAAG	21	56.4	ISO1_BL_RD3	CCAGAACAATATGGAATAATT	21	51.1	449bp	IS	D1_BL_RD3.1	GTCCATATCTGCTGCCACGC	20	64	5068
	4 chr3R	1.7E+07	16756346	diver	3.6	ISO1_BL_FD4	CAATCAAACAGCGCGGCAC	19	64.1	ISO1_BL_RD4	CTGAACTGTATTCTTTCTTTCGC	23	57.4	436 bp	IS	D1_BL_RD4.1	GGCCACCTCGGAGTGGCTC	19	65	6493
	5 chr2L	1.3E+07	12861728	hobo	3.5	ISO1_BL_FD5	ATTTATCTTATCCTGTTATCCCA	24	4 53.9	ISO1_BL_RD5	CGACGCAAAACACCGTATTGA	21	64.1	458bp	IS	D1_BL_RD5.1	TACTCCAGAATGTGCGTGGAG	21	61.2	. 1720
(5 chr2L	1.8E+07	17951978	hobo	3.5	ISO1_BL_FD6	TAGAGCTAAGCCAGCCAGGAC	21	61	ISO1_BL_RD6	CACTCGAGTATTTTGTGTTGCC	22	59.7	381bp	IS	D1_BL_RD6.1	AACTGTTACGAGATGATACAG	21	50	1785
	7 chr3L	2927813	2927871	Tirant	3.5	ISO1_BL_FD7	GTCAGAGATAAAGAAGAAACTAA	23	3 50.5	ISO1_BL_RD7	GACTCGAGTAGCCACTCTCTG	21	55.9	393bp	IS	D1_BL_RD7.1	TGTTGTTTTGGTGGTGTATACAA	23	57.9	8527
:	8 chrX	1.2E+07	11633445	297	2.9	ISO1_BL_FD8B	AACACAGATCAGTGTGTGAGT	21	1 52.8	ISO1_BL_RD8B	TCTCCTCAATCCAATTTGCAT	21	59.5	430bp	IS	D1_BL_RD8.1	CAGAATGGAAATAAATTTGTT	21	51.4	7371
	ehr3L	8481746	8481802	roo	3.3	ISO1_BL_FD9B	AGTAGCTGTGGATCTGTGGC	20) 57.9	ISO1_BL_RD9B	ATTTACTTAGGCCTCTGCGTA	21	56	408bp	IS	D1_BL_RD9.1	TTGCGTTCTGCATCTGTCAGA	21	63.1	9454
10) chr2R	7608382	7608431	I-element	2.6	ISO1_BL_FD10B	ATTCAAGCGTATTGTTTATTG	21	52.4	ISO1_BL_RD10B	CATAACAAGCCAGCAATTAGTT	22	56.3	317bp	IS	D1_BL_RD10.1	TGATCGAAATGGTGTTAAAGTCG	23	61.2	5489
1	l chr2R	8398189	8398240	Doc	3	ISO1_BL_FD11B	TCGGAGACGGTGGATAGGTAG	21	61.4	ISO1_BL_RD11B	GTAGGTGCACTTGGAGCACC	20	57.2	399bp	IS	D1_BL_RD11.1	GAGGCACGAACTGCTGGCT	19	65	5061
11	2 chr3R	3.1E+07	31279405	diver	2.5	ISO1_BL_FD12B	AGAGATCCAAATTCAAATATG	21	51.1	ISO1_BL_RD12B	ATCACGTCTGATCGCTATGAC	21	57.8	301bp	IS	D1_BL_RD12.1	CTTGGCTAAAACCCACACAC	20	58.1	6402