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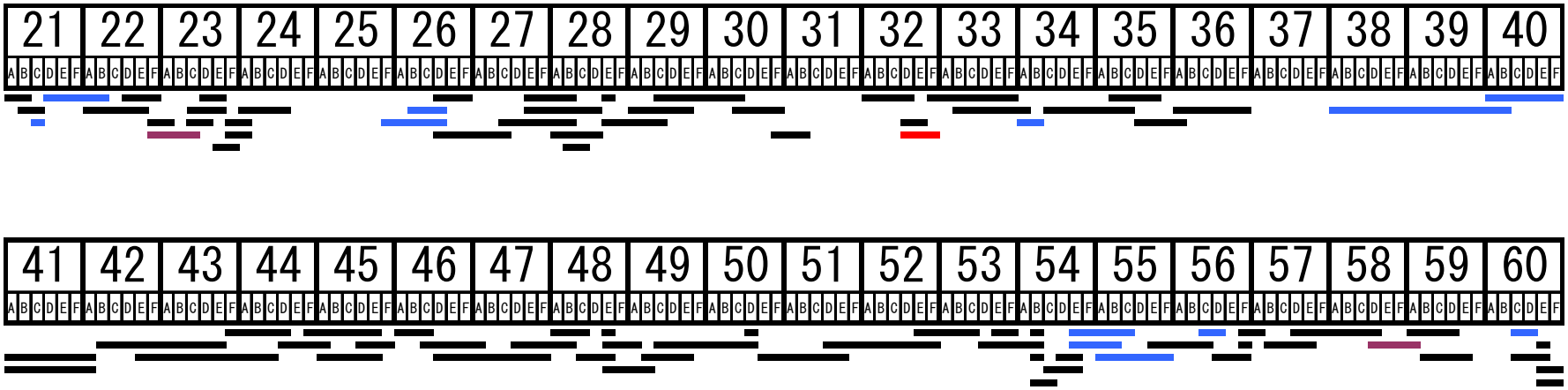

Deficiency mapping of recessive lethal mutations in *In(2LR)SM1* and *In(2LR)Pm*.

Blue bar, lethal over *In(2LR)Pm*

Red bar, lethal over *In(2LR)SM1*

Purple bar, lethal over both *In(2LR)Pm* and *In(2LR)SM1*

According to a Poisson distribution, the number of deficiencies which uncover multiple recessive lethal mutations is expected to be less than 1.14.

No inversion breakpoints are accompanied with recessive lethal mutations.

Figure S1.

Table S1. Numbers of flies from the cross of *In(2LR)SM1/In(2LR)Pm* females an

DGRC No.	*In(2LR)SM1/Df*	*In(2LR)Pm/Df*	Control
107147	13	18	22
108717	16	40	0
108848	52	0	48
106828	96	0	135
106871	370	434	395
130344	69	60	61
130323	63	62	61
108889	0	0	97
108890	160	153	142
130332	55	55	70
107967	76	104	81
130336	33	45	30
108811	47	56	31
108815	62	86	84
108178	28	54	62
108906	74	0	89
108730	76	0	98
108739	47	62	65
108756	81	67	79
106706	44	47	55
107969	24	19	23
106823	20	8	125
130347	27	35	39
107968	41	31	51
108892	366	359	22
108894	88	93	81
130359	60	91	111
107489	61	44	74
108797	33	62	45
130358	114	128	119
130342	34	38	33
130343	54	45	39
108471	0	118	107
106825	73	90	106
106992	25	24	26
130337	122	0	125
106874	30	45	109
107112	46	45	44

106710	42	46	48
106898	39	35	50
108893	69	0	137
107971	109	0	123
108913	171	148	146
108912	70	68	100
106723	81	58	65
107012	105	83	154
108896	114	122	106
108897	98	92	89
107115	194	214	193
107976	114	91	102
130334	133	133	137
106719	46	74	170
106718	73	97	126
108904	50	52	54
108895	129	159	169
106704	80	69	0
130345	91	115	116
107972	68	77	80
130346	91	51	85
108477	71	70	66
108915	240	294	269
108903	80	110	118
108816	81	94	93
108784	75	82	86
107077	93	79	16
107079	215	230	249
130355	79	72	79
108769	169	175	184
130352	161	208	147
108308	114	152	138
108360	65	75	84
130353	153	147	152
130328	84	84	109
130329	224	0	223
106815	97	0	61
106715	80	0	80
108916	63	76	84
130330	64	0	79

130322	119	114	130
108907	117	135	132
108849	124	128	114
107052	142	157	174
108117	82	99	116
108898	0	0	0
107262	100	82	157
130348	208	198	1
107424	171	0	198
130356	172	151	142
107354	157	104	204
106881	143	168	149
107973	58	41	133

Note: Control flies are *In(2LR)Pm/Bal* or *In(2LR)SM1/Bal* . Because *In(2LR)SM1/Bal* is let
derived (majority of the cases), the numbers of *In(2LR)Pm/Bal* flies are shown. Because *In*
if *Bal* is *In(2LR)Pm*, the numbers of *In(2LR)SM1/Bal* flies are shown. When *Bal* is *In(2LR)*
In(2LR)SM1/Gla flies are shown. The numbers of *Gla/In(2LR)Pm* flies are 57, 123, and 99
#108889, and #106701, respectively. If numbers of control flies are close to zero, it means
have a common recessive lethal mutation(s): DGRC #106704 and #130348. Exceptional fli
phenotype were produced by unknown reasons (e.g., spontaneous mutations, nondisjunctio
DGRC #106709 has a suppressor-of-*Curly* on the Y chromosome (our unpublished observa
#108898: The offsprings die by the end of the pupal stage.

d tester males

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thal if *Bal* is *Curly-*
(2LR)Pm/Bal is lethal
Gla, the numbers of
for DGRC #130323,
Bal and *In(2LR)Pm*
es with unusual
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tion). DGRC

Table S2. Calculation for expected number of recessive lethal mutations

Balancer	Inversion	Period (*t*)	Relative length (*L*)	*vtL*	Σ*vtL*	Σ*vtL* x 0.844
In(2LR)Pm	21C8-D1;60D1.2	2011-1929	236/240	12.6	12.6	10.6
	22D1.2;33F5-34A1	1953-1921	70/240	1.5		
In(2LR)SM1	42A2.3;58A4-B1	1953-1921	94/240	2.0	12.0	10.2
	22A3-B1;60B-C	2011-1953	229/240	8.6		

Note: *v* represents the mutation rate, 0.156. Σ*vtL* is the expected number of recessive lethal mutations on *In(2LR)Pm* and *In(2LR)SM1*. Because we examined 84.4% of the second-chromosome using the deficiencies, the expected number of recessive lethal mutations detected on the balancers is Σ*vtL* x 0.844.

Table S3. A list for the second-chromosome Kyoto Deficiency kit compiled in Decem

DGRC No.	Genotype
107147	Df(2L)net-PMF/SM6a
108717	Df(2L)BSC4, w[+mC], net[1] cn[1]/SM5
108848	Df(2L)BSC16, net[1] cn[1]/SM6a
106828	Df(2L)ast2/SM1
106871	Df(2L)dp-79b, dp[DA] cn[1]/In(2LR)bw[V1], b[1] bw[V1]
130344	Df(2L)BSC37/CyO
130323	Df(2L)dpp[d14]/In(2LR)Gla, wg[Gla-1]
108889	Df(2L)C144, dpp[d-ho] ed[1]/In(2LR)Gla, wg[Gla-1] Bc[1] Egfr[E1]
108890	Df(2L)JS32, dpp[d-ho]/CyO, P{ry+t7.2=sevRas1.V12}FK1
130332	Df(2L)BSC28/SM6a, bw[k1]
107967	Df(2L)S2590/CyO, P{ry[+t7.2]=sevRas1.V12}FK1
130336	Df(2L)BSC31, net[1] cn[1]/CyO, b[81f2] rk[81f2]
108811	Df(2L)tim-02/CyO
108815	y[1] w[*]; Df(2L)drm-P2, P{w[+mC]=lacW}Pdsw[k10101]/SM6b
108178	Df(2L)ed1/CyO; P{ry[+t7.2]=ftz/lacC}1
108909	Df(2L)sc19-8/SM6b; Dp(2;1)B19, y[1], ed[1] dp[o2] cl[1]
107243	Df(2L)sc19-4/In(2L)Cy[L]t[R] In(2R)Cy, Cy[1] amos[Roi-1] cn[2] sp[2] (or[*]); Dp(2;1)B19, y[1] ac[1] sc[1] pn[1] ed[1] dp[o2] cl[1]
108918	Df(2L)cl-h3/SM6b
108906	In(1)w[m4]; Df(2L)E110/CyO
108730	Df(2L)BSC5, w[+mC]/SM6a
108739	Df(2L)BSC6, dp[ov1] cn[1]/SM6a
108756	w[1118]; Df(2L)BSC7/CyO
106706	Df(2L)J-H/SM5
107969	Df(2L)XE-3801/CyO, P{ry[+t7.2]=sevRas1.V12}FK1
106823	Df(2L)spd, al[1] dp[ov1]/CyO
130347	Df(2L)BSC41, dp[ov1] cn[1]/CyO
107968	Df(2L)XE-2750/CyO, P{ry[+t7.2]=sevRas1.V12}FK1
108892	y[1] w[67c23]; Df(2L)Trf-C6R31/CyO
108894	In(1)w[m4h], y[1]; Df(2L)TE29Aa-11, dp[*]/CyO
130359	Df(2L)BSC53, dp[ov1] cn[1]/T(1;2)OR64/SM6a
107489	Df(2L)N22-14/CyO
108797	Df(2L)BSC17/SM6a
106703	Df(2L)Mdh, cn[1]/Dp(2;2)Mdh3, cn[1]
130358	Df(2L)BSC50/SM6a
106709	Df(2L)J39/In(2L)Cy; Dp(2;Y)cb50, Dp(1;Y)B[S]Yy[+]/C(1)RM
130342	Df(2L)BSC32/SM6a, bw[k1]
130343	Df(2L)BSC36/SM6a, bw[k1]
108471	Df(2L)FCK-20, dp[ov1] bw[1]/CyO, P{ry[+t7.2]=sevRas1.V12}FK1
106825	Df(2L)Prl, Prl[1] nub[Prl]/CyO
106992	Df(2L)prd1.7, b[1] Adh[n2] pr[1] cn[1] sca[1]/CyO, P{ry[+t*]=elav-lacZ.H}YH2
130337	Df(2L)BSC30/SM6a, bw[k1]
106874	Df(2L)b87e25/CyO
107112	Df(2L)TE35BC-24, b[1] pr[1] pk[1] cn[1] sp[1]/CyO
106710	Df(2L)r10, cn[1]/CyO
106898	Df(2L)H20, b[1] pr[1] cn[1] sca[1]/CyO
108900	Df(2L)TW137, cn[1] bw[1]/CyO, Dp(2;2)M(2)m[+]
106903	Df(2L)TW50, cn[1]/CyO, Dp(2;2)M(2)m[+]
108893	Df(2L)TW161, cn[1] bw[1]/CyO
107971	Df(2L)C'/CyO
108913	In(2R)bw[VDe2L]Cy[R]/In(2LR)Gla, wg[Gla-1]

108912	Df(2R)M41A4/SM5
106701	Df(2R)nap9/In(2LR)Gla, Dp(2;2)BG, wg[Gla-1]
106723	Df(2R)ST1, Adh[n5] pr[1] cn[*]/CyO
107012	Df(2R)cn9/CyO, amos[Roi-1] sp[*]
108896	w[118]; Df(2R)H3C1/CyO
108897	w[118]; Df(2R)H3E1/CyO
107115	w[1]; Df(2R)Np5, In(2LR)w45-32n, cn[1]/CyO
107976	w[1]; Df(2R)w45-30n, cn[1]/CyO
130334	Df(2R)BSC29, cn[1] bw[1] sp[1]/CyO
106719	w[1118]; Df(2R)B5, px[1] sp[1]/CyO, Adh[nB]
106718	Df(2R)X1, Mef2[X1]/CyO, Adh[nB]
108904	Df(2R)stan1, P{ry+t7.2=neoFRT}42D cn[1] sp[1]/CyO
108895	Df(2R)en-A/CyO
106704	Df(2R)en30/SM5; Dp(1;Y)B[S]
130345	Df(2R)BSC39, cn[1] bw[1]/SM6a, bw[k1]
107972	Df(2R)CB21/CyO; ry[506]
130346	Df(2R)BSC40/SM6a
108477	Df(2R)BSC3, w[+mC] unch[k15501] cn[1] bw[1] sp[1]/SM6a, bw[k1]
108915	Df(2R)vg-C/CyO, P{ry[+t7.2]=sevRas1.V12}FK1
108903	Df(2R)CX1, b[1] pr[1]/SM1
108816	Df(2R)BSC18/SM6a
108784	Df(2R)BSC11/SM6a
107077	w[a] N[fa-g]; Df(2R)Jp1/CyO
107079	w[a] N[fa-g]; Df(2R)Jp8, w[+]/CyO
130355	Df(2R)BSC49/SM6a
108769	y[1]; Df(2R)P803-Delta15, cn[1]/SM1; sv[spa-pol]
130352	Df(2R)BSC44/SM6a
108308	y[1] w[67c23]; Df(2R)k10408, P{w[+mC]=lacW}BEST:GM02553[k10408]/CyO
108360	Df(2R)robl-c/CyO, y[+]
130353	Df(2R)BSC45/SM6a
130328	y[1] w[67c23]; Df(2R)14H10Y-53/SM6a
130329	y[1] w[67c23]; Df(2R)14H10W-35/SM6a
106815	Df(2R)Pcl7B/CyO
106715	Df(2R)PC4/CyO
108916	y[1] w[*]/Dp(1;Y)y[+]; Df(2R)P34/CyO
130330	Df(2R)BSC26/CyO
130322	Df(2R)BSC22/SM6a
108907	Df(2R)017/SM1
108849	Df(2R)BSC19, cn[1] bw[1]/SM6a
107052	Df(2R)AA21, c[1] px[1] sp[1]/SM1
108117	Df(2R)Egfr5, b[1] pr[1] cn[1] sca[1]/CyO, P{ry[+t7.2]=sevRas1.V12}FK1
108898	Dp(1;Y)y[+]/y[1]; Df(2R)X58-12/SM5
107262	w[*]; Df(2R)59AD/SM1
130348	Df(2R)vir130/CyO
106716	Df(2R)or-BR6, cn[1] bw[1] sp[1]/In(2LR)lt[G16L]bw[V32gR], bw[V32g]
107424	Df(2R)Px2/SM5
130356	w[*]; Df(2R)ED4071, P{w[+mW.ScerFRT.hs3]=3'.RS5+3.3'}ED4071/CyO
107354	Df(2R)M60E/In(2LR)bw[V32g], bw[V32g]
106881	Df(2R)ES1, b[1] pr[1] cn[1] wx[wxt]/SM1
107973	Df(2R)Kr10, b[1] pr[1] Bl[1] c[1]/CyO

Note: DGRC #108893, #107012, #107077, #108308, #108849, #107052 and #108117: The use of strains fron
#36570, #3368, #3518, #5574, #6609, #3467 and #5246) were alternated because a dominant visible marker o
exhibits poor expression in the Kyoto strains. DGRC #108909, #107243, #108918, #106703, #106709, #1089(
#106701 and #106716: Not included in the present results because the haploinsufficiency regions have to be c
duplication. DGRC #108918: Not included in the present results because insufficient offspring were obtained,
trials of the cross. DGRC #130343: *SM6a, bw[k1]* was replaced with *CyO, P{ry[+t7.2]=sevRas1.V12}FK1*. D
The use of DGRC #103256 was alternated because #106898 was not available at the time.

Deficiency region
021A01;021B08
021B07;021C03
021C03;021C08
021D01;022B03
022A02;022E01
022D01;022F02
022F01;023A02
022F04;023C03
023C03;023D02
023C05;023E02
023D02;023E3
023E05;023F05
023F02;024A01
023F03;024A02
024A02;024D04
024C02;025C08
025A05;025E05
025D02;026B05
025F03;026D11
026B01;026D02
026D03;026F07
026D10;027C01
027C05;028B04
027E02;028D01
027E1;028B3
028A04;028D09
028B05;028C09
028E01
028E04;029C01
029A02;29E01
029C01;030C09
030C03;030F01
030D;031F
030F05;31B01
031C;032E5
032A01;032D01
032D01;032E01
032D01;032F3
032F01;033F02
033B03;034A02
034A03;034B09
034C01;035C01
035B04;035E2
035D01;036A07
036A08;036F01
036C02;037B10
036E04;038A07
038A06;040B01
040A01;h35
041→h42;42A03

041→h44;42A02
042A01;042F01
042B03;043E18
042E;044C1
043F;044D08
044D01;045A01
044F12;045E03
045A06;045E03
045D03;045F06
046A1;046C12
046C2;047A01
046D07;047F16
047D07;048B02
048A03;048C08
048C05;048E01
048E;049A
048E01;048E10
048E12;049B06
049B02;049E02
049C01;050D05
050D01;050D07
050E06;051E04
051D03;052F09
052E1;53C01
053D09;54B10
053E;053F11
054B01;54B10
054B16
054B17;054C04
054C08;54E07
054D01;054E07
054E05;055B07
054E08;055C01
055A1;055F2
055E06;056C01
056C04;056D10
056D07;056F12
056F05;056F15
056F12-;057A04
057B19;057E06
057D02;058D01
058D01;059A01
059A01;059D04
059B;059E01
059D05;060B08
060C06;060D09
060C08;60E08
060E06;060E11
060E06;060F02
060E10;060F05

ɪ Bloomington (BL
n the balancer
)0, #106903,
ɔmplemented by a
despite several
)GRC #106898: