Supplementary Data for

Buffering and proteolysis are induced by segmental monosomy in

Drosophila melanogaster

Lina E. Lundberg[1], Margarida L. A. Figueiredo[1], Per Stenberg[1,2] & Jan Larsson[1]

[1]Department of Molecular Biology, Umeå University, SE-90187 Umeå, Sweden

[2]Computational Life Science Cluster (CLiC), Umeå University, Sweden.

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Supplementary Figure S1, Supplementary Tables S1-S4

LEGENDS SUPPLEMENTARY DATA

Supplementary Table S1. List of fly crosses.

Supplementary Table S2. Spearman correlation matrix of buffering effects versus gene features. Spearman Rank correlation was used to determine the correlation between median buffering effect (median expression ratio of all replicates in $\log_2$ scale) of each gene uncovered by a *Df* and 16 different gene criteria. Correlation coefficients marked in red are significant at $p<0.05$. (For definitions of criteria, see Materials and Methods).

Supplementary Figure S1. Expression ratios are approximately normally distributed. The distribution of expression ratios for genes present in haploid versus diploid condition with a normal distribution curve superimposed.

Supplementary Table S3. List of top 100 diploid genes up-regulated as a response to segmental aneuploidy. Genes marked with an "x" belong to one of the four significantly enriched GO-terms (as detected using the Functional Annotation Chart in NIH DAVID, GOterm levels 5).

Supplementary Table S4. List of qPCR primer sequences used in this study.

List of crosses

Females	Males	Comment
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Crosses for six wild type replicates
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(3R)ED10953/TM6c	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(2L)ED4559/SM6a	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(2L)ED748/SM6a	No *Df*, see Material and Methods[*]
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(2R)ED1770/SM6a	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(2R)ED1612/SM6a	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(2L)ED3/ SM6a	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(3R)ED5071/TM6C	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(3R)ED7665/TM6C	
$w^{1118}_{iso}; 2_{iso}; 3_{iso}$	Df(3R)ED10946/TM6C	No *Df*, see Material and Methods[*]
Df(3R)ED5071/TM6C	Df(2L)ED4559/SM6a	
Df(3R)ED5071/TM6C	Df(3R)ED10953/TM6c	
Df(3R)ED5071/TM6C	Df(2R)ED1770/SM6a	
Df(3R)ED5071/TM6C	Df(2R)ED1612/SM6a	
Df(3R)ED5071/TM6C	Df(2L)ED3/SM6a	
Df(3R)ED5071/TM6C	Df(3R)ED7665/TM6C	Lethal combination
Df(3R)ED5071/TM6C	Df(3R)ED10946/TM6C	Treated as *Df(3R)ED5071/+*
Df(3R)ED7665/TM6C	Df(2L)ED4559/SM6a	
Df(3R)ED7665/TM6C	Df(3R)ED10953/TM6c	
Df(3R)ED7665/TM6C	Df(2R)ED1770/SM6a	
Df(3R)ED7665/TM6C	Df(2R)ED1612/SM6a	
Df(3R)ED7665/TM6C	Df(2L)ED3/SM6a	
Df(3R)ED7665/TM6C	Df(3R)ED10946/TM6C	Treated as *Df(3R)ED7665/+*
Df(3R)ED10946/TM6C	Df(2L)ED4559/SM6a	Treated as *Df(2L)ED4559/+*
Df(3R)ED10946/TM6C	Df(3R)ED10953/TM6c	Treated as *Df(3R)ED10953/+*
Df(3R)ED10946/TM6C	Df(2R)ED1770/SM6a	Treated as *Df(2R)ED1770/+*
Df(3R)ED10946/TM6C	Df(2R)ED1612/SM6a	Treated as *Df(2R)ED1612/+*
Df(3R)ED10946/TM6C	Df(2L)ED3/SM6a	Treated as *Df(2L)ED3/+*
Df(3R)ED10953/TM6c	Df(2L)ED4559/SM6a	
Df(3R)ED10953/TM6c	Df(2L)ED748/SM6a	Treated as *Df(3R)ED10953/+*
Df(3R)ED10953/TM6c	Df(2R)ED1770/SM6a	Lethal combination
Df(3R)ED10953/TM6c	Df(2R)ED1612/SM6a	
Df(3R)ED10953/TM6c	Df(2L)ED3/SM6a	
Df(2L)ED4559/SM6a	Df(2L)ED748/SM6a	Treated as *Df(2L)ED4559/+*
Df(2L)ED4559/SM6a	Df(2R)ED1770/SM6a	
Df(2L)ED4559/SM6a	Df(2R)ED1612/SM6a	
Df(2L)ED4559/SM6a	Df(2L)ED3/SM6a	
Df(2L)ED748/SM6a	Df(2R)ED1770/SM6a	Treated as *Df(2R)ED1770/+*
Df(2L)ED748/SM6a	Df(2R)ED1612/SM6a	Treated as *Df(2R)ED1612/+*
Df(2L)ED748/SM6a	Df(2L)ED3/SM6a	Treated as *Df(2L)ED3/+*
Df(2R)ED1770/SM6a	Df(2R)ED1612/SM6a	
Df(2R)ED1770/SM6a	Df(2L)ED3/SM6a	
Df(2R)ED1612/SM6a	Df(2L)ED3/SM6a	

[*]: Not included in the analysis

Supplementary Table 2

	Df-Wt	3' UTR length	CDS length	Gene Length (bp)	Intron length	5' UTR length	Median WT expression	FlyAtlas expression pattern (12 tissue types)	Normalized 3'UTR length	Standard deviation FlyAtlas expression pattern	Normalized CDS length	Distance to expressed 5' neighbouring gene	Normalized Intron length	Normalized 5'UTR length	Buffering level of neighbouring gene	Standard deviation 6 WT	Distance to 5' neighbouring gene
Df-Wt	1,000	0,308	0,259	0,249	0,176	0,132	-0,127	-0,121	0,111	0,108	-0,100	0,098	0,097	-0,094	0,068	0,025	0,023
3' UTR length	0,308	1,000	0,234	0,512	0,476	0,530	0,056	-0,061	0,618	0,172	-0,614	0,089	0,381	0,060	0,105	0,101	-0,059
CDS length	0,259	0,234	1,000	0,661	0,420	0,303	-0,139	-0,043	-0,329	0,067	0,037	0,108	0,203	-0,276	0,028	0,085	0,040
Gene Length (bp)	0,249	0,512	0,661	1,000	0,803	0,582	0,014	-0,112	-0,202	0,196	-0,539	0,083	0,655	-0,191	0,104	0,155	-0,022
Intron length	0,176	0,476	0,420	0,803	1,000	0,593	0,066	-0,160	-0,237	0,251	-0,792	0,143	0,955	-0,159	0,088	0,146	0,043
5' UTR length	0,132	0,530	0,303	0,582	0,593	1,000	0,128	0,076	0,063	0,099	-0,605	0,017	0,528	0,549	0,080	0,017	-0,043
Median WT expression	-0,127	0,056	-0,139	0,014	0,066	0,128	1,000	0,425	0,105	0,007	-0,138	-0,053	0,088	0,205	0,092	-0,113	-0,009
FlyAtlas expression pattern	-0,121	-0,061	-0,043	-0,112	-0,160	0,076	0,425	1,000	0,077	-0,671	0,117	-0,232	-0,188	0,304	-0,039	-0,474	-0,154
Normalized 3'UTR length	0,111	0,618	-0,329	-0,202	-0,237	0,063	0,105	0,077	1,000	0,014	-0,154	-0,040	-0,226	0,349	0,004	-0,039	-0,058
Standard deviation FlyAtlas expression pattern	0,108	0,172	0,067	0,196	0,251	0,099	0,007	-0,671	0,014	1,000	-0,209	0,273	0,266	-0,135	0,098	0,532	0,187
Normalized CDS length	-0,100	-0,614	0,037	-0,539	-0,792	-0,605	-0,138	0,117	-0,154	-0,209	1,000	-0,097	-0,844	-0,096	-0,130	-0,102	-0,008
Distance to expressed 5' neighbouring gene	0,098	0,089	0,108	0,083	0,143	0,017	-0,053	-0,232	-0,040	0,273	-0,097	1,000	0,134	-0,114	0,041	0,202	0,708
Normalized Intron length	0,097	0,381	0,203	0,655	0,955	0,528	0,088	-0,188	-0,226	0,266	-0,844	0,134	1,000	-0,114	0,089	0,131	0,051
Normalized 5'UTR length	-0,094	0,060	-0,276	-0,191	-0,159	0,549	0,205	0,304	0,349	-0,135	-0,096	-0,114	-0,114	1,000	-0,035	-0,180	-0,045
Buffering level of neighbouring gene	0,068	0,105	0,028	0,104	0,088	0,080	0,092	-0,039	0,004	0,098	-0,130	0,041	0,089	-0,035	1,000	0,096	-0,016
Standard deviation 6 WT replicates	0,025	0,101	0,085	0,155	0,146	0,017	-0,113	-0,474	-0,039	0,532	-0,102	0,202	0,131	-0,180	0,096	1,000	0,166
Distance to 5' neighbouring gene	0,023	-0,059	0,040	-0,022	0,043	-0,043	-0,009	-0,154	-0,058	0,187	-0,008	0,708	0,051	-0,045	-0,016	0,166	1,000

Supplementary Figure S1
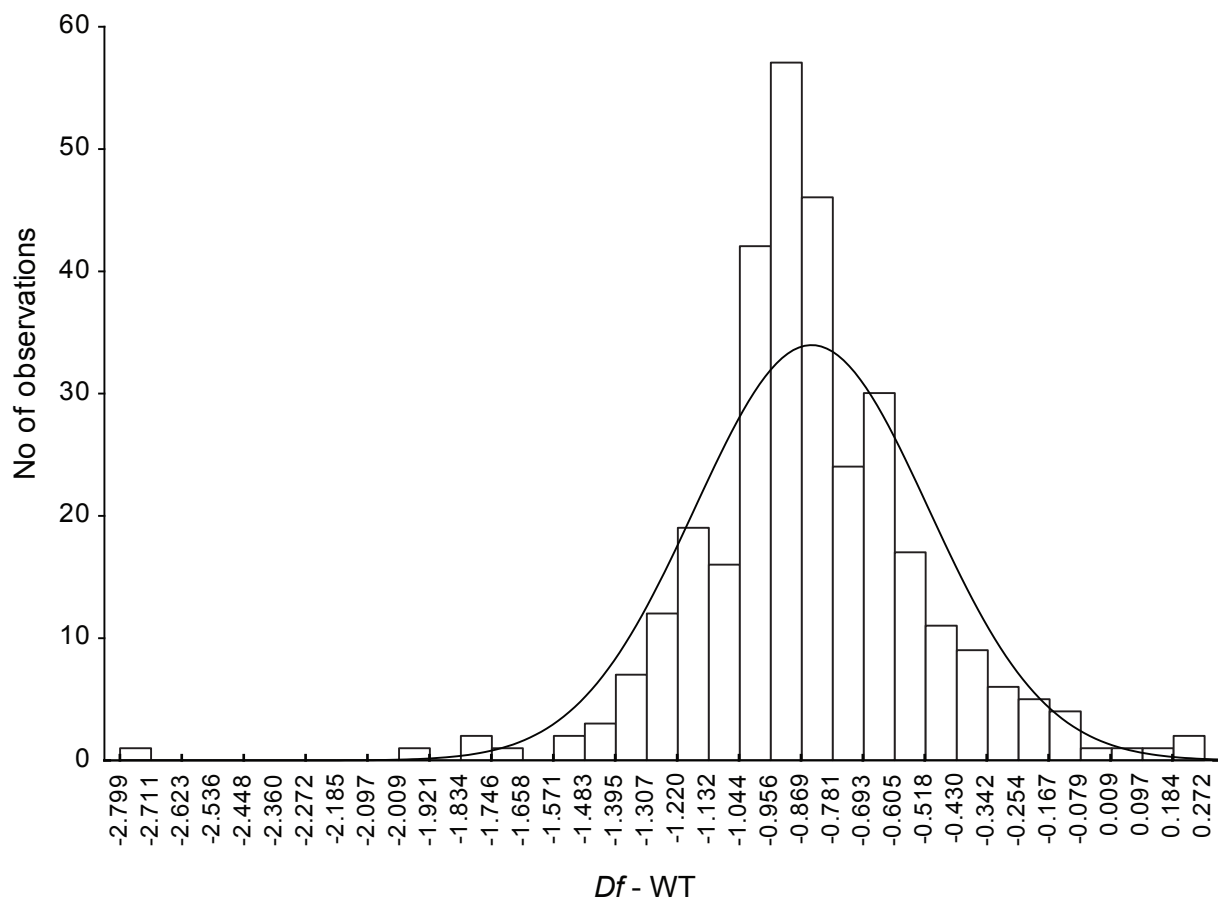
Supplementary Table S3

Probset ID	Number datasets with Df-wt >1.0	Fold Change (mean of 38 datasets)	SD	Gene Symbol	chromosome	Proteolysis	Serine-type peptidase activity	Serine-type endopeptidase activity	endopeptidase activity
1624543_s_at	32	1,947	1,042	---	chr2RHet				
1640407_at	27	1,245	0,567	CG9897	chr2R	x	x	x	x
1628963_at	25	1,240	0,576	CG4716	chr2R				
1623884_at	23	1,221	0,821	CG16775	chr3L				
1633631_at	27	1,176	0,516	CG9682	chr3R				
1633214_at	20	1,151	0,844	CG4835	chr3L				
1629050_at	21	1,135	0,576	CG10477	chr3L	x	x	x	x
1624285_at	21	1,087	0,598	CG3088	chr3L	x	x	x	x
1629098_at	23	1,085	0,588	CG7631	chr2L	x			x
1634158_at	24	1,076	0,569	Npc2f	chr3R				
1639729_s_at	20	1,071	0,989	---	chr2L				
1625141_at	17	0,981	1,102	CG14715	chr3R				
1635446_at	19	0,980	0,502	CG15043	chrX				
1624137_at	21	0,979	0,842	CG11911	chr2L	x	x	x	x
1640884_at	20	0,979	0,504	CG15784	chrX				
1627895_at	20	0,963	0,367	CG18404	chr3R				
1630822_at	21	0,934	0,915	CG13078	chr2L				
1632964_at	20	0,930	0,673	pirk	chr2R				
1627144_at	18	0,905	0,264	CG10560	chr3R				
1625538_at	17	0,895	1,201	Jon66Ci	chr3L	x	x	x	x
1633002_at	16	0,893	0,364	CG2196	chr3R				
1635086_at	18	0,891	0,459	CG4666	chrX				
1630667_at	11	0,874	0,265	CG34043	chr2L	x	x	x	x
1625058_at	19	0,874	0,446	yellow-d	chr2R				
1633675_at	18	0,866	0,567	CG30008	chr2R				
1624805_at	14	0,851	0,835	CG31041	chr3R				
1639641_at	16	0,851	0,743	CG8560	chr3L	x			
1627489_a_at	15	0,851	0,401	CG10433	chr2R				
1632453_at	18	0,843	0,569	eloF	chr3R				
1629046_a_at	19	0,838	0,545	CG4716	chr2R				
1639268_at	15	0,834	0,567	CG13324	chr2R				
1633425_at	12	0,828	0,347	Smvt	chr3R				
1636183_at	16	0,826	0,951	CG32198	chr3L				
1634871_s_at	12	0,826	0,361	---	chr3L				
1641234_at	15	0,824	0,554	CG16997	chr2L	x	x	x	x
1638182_at	12	0,822	0,463	CG5999	chr3R				
1636885_at	17	0,817	0,580	CG17560	chr3R				
1636798_at	16	0,816	0,545	CG13482	chr3L				
1635498_at	12	0,812	0,405	CG9259	chr2L				
1634240_at	17	0,808	0,509	CG5107	chr3R				
1632072_at	8	0,803	0,229	CG34134	chr2L				
1636420_at	14	0,803	0,472	CG16826	chr2L				
1633642_at	12	0,799	0,480	---	chrX				
1627463_at	12	0,796	0,575	Damm	chr2R	x			x
1635267_s_at	17	0,791	0,428	Tsp66E	chr3L				
1631224_at	13	0,786	0,396	Est-6	chr3L				
1636470_at	13	0,784	0,483	CG34026	chrX				
1629969_at	10	0,781	0,519	CG11426	chr3L				
1641711_at	10	0,768	0,323	CG13360	chrX				
1636293_at	11	0,743	0,817	CG2217	chr3R				
1632874_at	5	0,728	0,280	CG6602	chr3L				
1623363_at	12	0,726	0,544	CG6432	chr3R				
1636501_at	7	0,726	0,319	Muc11A	chrX				
1626832_at	11	0,723	0,394	CG31343	chr3R	x			
1630363_at	14	0,723	0,538	CG10469	chr3L	x	x	x	x
1631446_at	9	0,718	0,466	Cht9	chr2R				
1635846_a_at	15	0,711	0,588	orb	chr3R				
1625374_at	8	0,705	0,470	CG9466	chr2L				
1630419_a_at	12	0,694	0,684	CG7300	chr2L				
1640221_at	9	0,690	0,381	CG10479	chr3L				
1631529_at	8	0,687	0,361	Ser12	chr2L	x	x	x	x
1627259_a_at	13	0,685	0,482	ovo	chrX				
1632584_at	9	0,676	0,607	CG3344	chr3L	x	x		
1630669_at	14	0,673	0,838	CG7299	chr2L				
1639953_at	16	0,668	0,811	osk	chr3R				
1633344_at	9	0,658	0,338	Cpr92F	chr3R				
1640249_at	7	0,656	0,437	CG33173	chrX				
1625648_at	12	0,656	0,637	CG3868	chr3L				
1635525_at	9	0,654	0,439	CG9672	chrX	x	x	x	x
1633613_at	10	0,653	0,532	CG2765	chr2R				
1624596_at	8	0,652	0,436	CG31463	chr3R				
1640355_at	11	0,648	0,593	CG5246	chr3R	x	x	x	x
1638661_at	13	0,644	0,661	yip7	chr3L	x	x	x	x
1638774_at	7	0,642	0,405	CG16904	chr3R				
1625400_at	9	0,635	0,506	Cpr47Ea	chr2R				
1624069_at	3	0,633	0,347	CG7296	chr2L				
1631472_at	10	0,632	0,563	Cht4	chr3L				
1629446_at	7	0,629	0,393	CG1136	chr3L				
1629007_at	6	0,629	0,359	CG8952	chrX	x	x	x	x
1639394_at	8	0,627	0,413	m1	chr3R				
1624558_at	16	0,624	1,214	dro3	chr3L				
1627122_at	11	0,619	0,462	CG32767	chrX				
1634449_at	8	0,616	0,434	CG9459	chr3R				
1625257_s_at	8	0,614	0,402	CG31523	chr3R				
1638903_at	4	0,611	0,373	CG5724	chr3R				
1625436_at	12	0,606	0,742	Uro	chr2L				
1635815_at	3	0,606	0,353	zetaTry	chr2R	x	x	x	x
1626524_at	6	0,606	0,442	CG16996	chr2L	x	x	x	x
1626309_at	6	0,604	0,409	Muc68D	chr3L				
1631369_at	9	0,603	0,573	CG7567	chr3R				
1623165_at	9	0,602	0,513	thetaTry	chr2R	x	x	x	x
1625266_at	6	0,599	0,408	Ag5r	chrX				
1626414_at	2	0,593	0,233	Jheh1	chr2R				
1633009_a_at	14	0,591	1,029	CG6640	chr3L				
1625948_at	12	0,590	0,576	CG17633	chr2L	x			
1625218_at	9	0,584	0,457	CG11399	chr3L				
1626044_at	6	0,584	0,401	---	chr2L				
1635968_at	3	0,583	0,343	CG3604	chr2L				
1625195_s_at	12	0,579	1,135	shn	chr2R				
1636488_at	0	0,578	0,207	CG4468	chr3R				

	Sense	Antisense
CG9897	5'-AGTGCCGTGCAATTGGACAG-3'	5'-AACCTGCGAGCTACTCAACACC-3'
CG7631	5'-GGAATGGACAGCTATCCGAG-3'	5'-AGGCACAAATCGAATACAAGAC-3'
CG11911	5'-TTGCTCTGTTGCAGGGAAG-3'	5'-ACCACCCAAATTTTGAACTACG-3'
CG3088	5'-CACTGTCACCGTAAACTGG-3'	5'-TGGACAGAGCAACATCTGG-3'
CG10477	5'-GGACCCATAGTAGATGGTCAC-3'	5'-AACCAGTTTCCCTACCAGG-3'
CG8560	5'-GTATACTTCGTTCCGGTCGC-3'	5'-TACCTGACCCTCCACTCCTATG-3'
CG5384	5'-CCAAAAAACTGGTCGATAAACG-3'	5'-AAATGGCACATACAGGCAG-3'
Rpl32	5'-CGATGTTGGGCATCAGATAC-3'	5'-CCCAAGATCGTGAAGAAGC-3'