SUPPLEMENTARY METHODS

Drosophila embryo chromatin preparation

For chromatin preparation from *Drosophila* embryos, 0-24hr-old embryos were collected from population cages, dechorionated in 50% bleach for 90 seconds, washed with running water and transferred into Falcon tubes, 1.5g dry embryos/50ml PBS-0.1% Tween-20 (PBST). Let embryos settle for 5 minutes and removed supernatant. Embryos were first cross-linked with 10ml of 1.8% Formaldehyde in PBST, 30ml n-Heptane, for 15 minutes, shaking vigorously at RT. Pelleted embryos 1 minute at 500g, RT; removed supernatant and washed twice with PBST; resuspended embryos in 10ml PBST and homogenized with 10 strokes from a tight-fitting pestle to release the nuclei; centrifuged 1 minute, 400g, and collected supernatant into a new tube; centrifuged 10 minutes, 1100g, and discarded supernatant. Cross-linked nuclei with 10ml of 3% Formaldehyde in PBST, at RT, 30 minutes. Washed the Chromatin 5 times with PBST.

GO term analysis

GO Term analysis was performed on the FuncAssociate software (S1), using the web interface. The following lists of proteins were used as input to calculate GO term enrichments: 1) all the proteins identified in both TAS purifications from both cell lines (and that were not present in the negative control or “common contaminants” list, and that were identified through more than 1 peptide); 2) all the proteins identified associated with TAS-R (same filters); 3) proteins associated exclusively with TAS-R (same filters); 4) all the proteins associated with TAS-L (same filters); and 5) proteins associated exclusively with TAS-L (same filters, except for the “1 peptide” filter, because the number of exclusive TAS-L factors was too low to analyze GO term enrichment otherwise).

Capture probe design

Oligo selection is done with the help of the Exiqon oligo tools found at http://www.exiqon.com/oligo-tools. Oligos are selected on the basis of their Tm (usually higher than 78C), the lowest possible self-annealing propensity, and the least homology to non-target regions in the genome, as determined by BLAST. No thresholds for self-hybridization and BLAST complementarity have been determined. Rather, for the locus of interest, we look for the region within this locus where these parameters are most favorable. This was done empirically. LNA-C bases were not included in the design of capture probes for several reasons: the difficulty in solubilizing the lyophilized reagent; the limitation of the synthesizer to hold 9 reagent bottles, making it possible to do the synthesis in one step when we exclude one of the LNA bases; the active search for regions in the target with a predominance of G over C (on one or the other strand), so that the self-annealing energies would be reduced; and the empirical evidence that capture probes with LNA-G work better than capture probes with LNA-C (when using the exact same target, with complementary capture probes targeting one or the other strand). The capture probe spacer is similar, but not identical to the design previously reported (11). The original protocol used a custom-made 108-atom spacer; for this work, we used commercially available phosphoramidite spacer-18 monomers (4 units), plus the DesthiobiotinTEG phosphoramidite (Glen Research), bringing the total spacer length close to 100 atoms (comparable with the 108 atom length previously reported). We tested possible probe designs for their ability to enrich before arriving at the design described above. After showing that this design worked for TAS-R, we designed three other probes for this same region with similar success in enrichment. Each of these TAS-R probes hybridized to sequences that clustered with the TAS-R region in a manner similar to the arrangement of clustered sequences that hybridize to the probe presented in the Results. The TAS-L oligo was the only one tested for the TAS-L region.

A detailed capture probe synthesis protocol can be found at http://tiny.cc/h9356

SUPPLEMENTARY TABLES

Table S1: Total peptides identified in PICh experiments

		Kc						S3					
		Scrambled		TAS-L		TAS-R		Scrambled		TAS-L		TAS-R	
		peptides		peptides		peptides		peptides		peptides		peptides	
Flybase ID	**Name**	**total**	**unique**	**total**	**unique**	**total**	**unique**	**total**	**unique**	**total**	**unique**	**total**	**unique**
Proteins identified in the Scramble purifications													
FBgn0003732	**Top2**	7	5	25	19	99	54	29	26	56	26	132	59
FBgn0051611	**Histone H4**	14	8	41	13	35	10	17	8	28	9	32	9
FBgn0027580	**CG1516**	19	12	0	0	1	1	9	7	3	3	7	7
FBgn0010173	**RpA-70**	13	9	13	6	47	22	9	7	13	6	41	20
FBgn0061209	**Histone H2B**	6	4	28	8	27	8	14	8	21	8	23	7
FBgn0000556	**Ef1α48D**	7	3	28	12	37	12	10	5	28	13	36	13
FBgn0002183	**dre4**	7	5	22	13	48	29	9	9	36	17	49	26
FBgn0000047	**Act88F**	4	3	8	6	20	6	10	8	7	4	20	14
FBgn0001197	**Histone H2Av**	5	2	9	2	12	2	5	2	8	2	11	3
FBgn0034962	**Histone H1**	3	3	19	10	15	9	4	4	11	6	9	9
FBgn0034961	**Histone H3**	1	1	8	3	15	5	5	4	17	5	15	4
FBgn0014965	**gypsy\gag**	0	0	0	0	0	0	6	5	17	6	17	6
FBgn0002525	**Lam**	2	2	6	5	23	12	3	3	4	3	22	13
FBgn0003022	**Ote**	1	1	4	4	12	12	4	3	10	8	12	6
FBgn0033998	**row**	2	2	5	5	20	15	2	2	4	3	15	8
FBgn0001219	**Hsc70-4**	3	2	23	15	33	17	1	1	11	6	12	6
FBgn0032244	**RfC3**	0	0	1	1	5	5	4	4	3	3	2	2
FBgn0004913	**Gnf1**	0	0	3	3	19	15	3	3	9	8	29	17
FBgn0032050	**CG13096**	3	3	5	3	10	6	0	0	3	2	3	3
FBgn0001226	**Hsp27**	0	0	0	0	0	0	2	2	3	3	6	5
FBgn0001220	**Hsc70-5**	2	2	3	2	3	2	0	0	0	0	0	0
FBgn0003459	**stwl**	1	1	1	1	2	1	1	1	2	1	3	2
FBgn0010278	**Ssrp**	1	1	18	12	29	17	1	1	11	7	26	14
FBgn0033879	**CG6543**	1	1	2	2	2	2	1	1	1	1	1	1
FBgn0003607	**Su(var)205**	1	1	35	18	22	13	1	1	19	12	6	6
FBgn0259937	**Nop60B**	2	2	1	1	1	1	0	0	0	0	0	0
FBgn0010438	**mtSSB**	2	2	1	1	3	3	0	0	0	0	3	3
FBgn0037137	**Nopp140**	2	1	1	1	3	2	0	0	0	0	0	0
FBgn0020496	**CtBP**	0	0	12	8	12	8	2	2	0	0	3	1
FBgn0024271	**ZAM\gag**	2	2	3	1	6	4	0	0	2	2	0	0

FBgn0040266	**Transpac\gag**	0	0	0	0	0	0	2	2	8	7	4	4
FBgn0000043	**Act42A**	1	1	2	2	1	1	0	0	2	1	4	4
FBgn0001091	**Gapdh1**	0	0	0	0	0	0	1	1	0	0	0	0
FBgn0004907	**14-3-3ζ**	0	0	2	2	2	2	1	1	0	0	0	0
FBgn0013275	**Hsp70Aa**	0	0	0	0	1	1	1	1	0	0	0	0
FBgn0026761	**Trap1**	0	0	1	1	2	1	1	1	0	0	0	0
FBgn0004867	**RpS2**	1	1	1	1	1	1	0	0	0	0	0	0
FBgn0004924	**Top1**	1	1	0	0	3	2	0	0	0	0	2	2
FBgn0004237	**Hrb87F**	0	0	1	1	0	0	1	1	2	1	2	1
FBgn0050122	**CG30122**	0	0	0	0	1	1	1	1	0	0	3	2
FBgn0004795	**retn**	1	1	0	0	1	1	0	0	0	0	3	1
FBgn0013269	**FK506-bp1**	0	0	4	4	4	4	1	1	9	7	3	3
FBgn0040284	**SF2**	0	0	0	0	2	2	1	1	0	0	1	1
FBgn0003062	**Fib**	1	1	3	3	5	5	0	0	2	2	2	2
FBgn0034528	**CG11180**	1	1	0	0	0	0	0	0	0	0	0	0
FBgn0011764	**Dsp1**	1	1	1	1	3	1	0	0	2	1	1	1
FBgn0035674	**CG13295**	1	1	0	0	0	0	0	0	0	0	0	0
FBgn0260985	**RfC4**	0	0	2	2	4	4	1	1	1	1	5	4
FBgn0030362	**Regucalcin**	0	0	0	0	0	0	1	1	1	1	4	4
FBgn0010417	**Taf6**	1	1	0	0	0	0	0	0	0	0	0	0
FBgn0040345	**CG3708**	1	1	0	0	0	0	0	0	0	0	0	0
FBgn0010328	**woc**	1	1	0	0	14	8	0	0	4	3	10	8
FBgn0027889	**ball**	0	0	1	1	8	7	1	1	2	2	0	0
FBgn0030871	**CG8142**	0	0	0	0	2	2	1	1	0	0	2	2
Proteins identified as non-specific in Rees et al (2011)													
FBgn0010397	**LamC**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0027783	**SMC2**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0035630	**CG10576**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0011661	**Moe**	0	0	2	2	0	0	0	0	0	0	2	2
FBgn0033636	**tou**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0010217	**ATPsyn-β**	0	0	2	2	1	1	0	0	0	0	0	0
FBgn0015391	**glu**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0039857	**RpL6**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0015245	**Hsp60**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0260789	**mxc**	0	0	0	0	3	3	0	0	0	0	0	0
FBgn0032620	**CG12288**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0001233	**Hsp83**	0	0	2	2	0	0	0	0	0	0	0	0
FBgn0024939	**RpL8**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0010551	**l(2)03709**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0086897	**sqd**	0	0	0	0	1	1	0	0	0	0	0	0

FBgn0003360	**sesB**	0	0	6	6	10	9	0	0	0	0	0	0
FBgn0002780	**mod**	0	0	2	2	4	4	0	0	5	5	3	3
FBgn0017545	**RpS3A**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0035213	**CG2199**	0	0	2	1	4	2	0	0	3	1	1	1
FBgn0000559	**Ef2b**	0	0	4	3	2	2	0	0	0	0	0	0
FBgn0003885	**αTub84D**	0	0	6	4	8	3	0	0	1	1	0	0
FBgn0003276	**RpII140**	0	0	1	1	3	3	0	0	0	0	3	3
FBgn0003888	**βTub60D**	0	0	3	3	7	7	0	0	0	0	0	0
FBgn0011211	**blw**	0	0	3	3	2	2	0	0	0	0	0	0
FBgn0037027	**CG3680**	0	0	2	2	1	1	0	0	0	0	0	0
FBgn0004551	**Ca-P60A**	0	0	1	1	3	3	0	0	0	0	0	0
FBgn0086133	**kdn**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0024332	**Mcm3**	0	0	2	2	0	0	0	0	0	0	0	0
FBgn0027948	**msps**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0003031	**pAbp**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0036548	**l(3)72Ab**	0	0	0	0	0	0	0	0	1	1	0	0
FBgn0040283	**SMC1**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0086254	**CG6084**	0	0	2	2	4	4	0	0	0	0	0	0
FBgn0004363	**porin**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0021765	**scu**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0031728	**Hsp60C**	0	0	1	1	2	2	0	0	0	0	0	0
FBgn0020235	**ATPsyn-γ**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0038608	**WRNexo**	0	0	2	2	4	3	0	0	2	2	1	1
FBgn0038609	**Nup43**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0039713	**RpS8**	0	0	0	0	3	3	0	0	0	0	0	0
FBgn0002924	**ncd**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0011604	**Iswi**	0	0	3	2	17	15	0	0	2	2	11	8
FBgn0026577	**CG8677**	0	0	0	0	1	1	0	0	1	1	0	0
FBgn0260817	**gkt**	0	0	0	0	2	1	0	0	0	0	0	0
FBgn0001942	**eIF-4a**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0003887	**βTub56D**	0	0	2	1	3	2	0	0	1	1	0	0
FBgn0015615	**Cap**	0	0	0	0	5	5	0	0	0	0	2	1
FBgn0004922	**RpS6**	0	0	1	1	2	2	0	0	0	0	0	0
FBgn0030054	**Caf1-180**	0	0	2	1	2	2	0	0	0	0	0	0
FBgn0039877	**CG2118**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0085261	**SA**	0	0	3	3	4	4	0	0	0	0	0	0
FBgn0086902	**kis**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0002441	**l(3)mbt**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0003567	**su(Hw)**	0	0	0	0	3	3	0	0	0	0	3	3
FBgn0040268	**Top3α**	0	0	1	1	3	3	0	0	3	3	4	4
FBgn0003261	**Rm62**	0	0	0	0	4	4	0	0	0	0	0	0

FBgn0004587	**B52**	0	0	0	0	0	0	0	0	1	1	2	1
FBgn0010774	**Aly**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0005630	**lola**	0	0	1	1	0	0	0	0	1	1	0	0
FBgn0260991	**Incenp**	0	0	28	13	20	9	0	0	11	5	1	1
FBgn0037810	**sle**	0	0	32	15	22	15	0	0	10	8	2	2
FBgn0003277	**RpII215**	0	0	0	0	6	6	0	0	0	0	2	2
FBgn0015929	**dpa**	0	0	2	2	1	1	0	0	0	0	0	0
FBgn0030301	**HP5**	0	0	4	3	0	0	0	0	1	1	1	1
FBgn0260012	**pds5**	0	0	1	1	1	1	0	0	2	2	0	0
FBgn0002542	**lds**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0029704	**CG2982**	0	0	0	0	3	3	0	0	0	0	0	0
FBgn0011785	**BRWD3**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0000541	**E(bx)**	0	0	0	0	4	4	0	0	1	1	3	3
FBgn0026575	**hang**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0014026	**RpL7A**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0023509	**mip130**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0012036	**Aldh**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0003278	**RpI135**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0025815	**Mcm6**	0	0	2	2	0	0	0	0	0	0	0	0
FBgn0017577	**Mcm5**	0	0	5	5	3	3	0	0	0	0	0	0
FBgn0004227	**nonA**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0250754	**CG42232**	0	0	0	0	0	0	0	0	0	0	3	3
FBgn0011272	**RpL13**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0043456	**CG4747**	0	0	3	3	17	11	0	0	2	1	11	7
FBgn0015268	**Nap1**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0037082	**CG5664**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0000212	**brm**	0	0	0	0	3	3	0	0	0	0	1	1
FBgn0259113	**DNApol-α180**	0	0	0	0	5	5	0	0	0	0	0	0
FBgn0025716	**Bap55**	0	0	0	0	5	4	0	0	0	0	0	0
FBgn0040237	**bor**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0036478	**CTPsyn**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0002906	**mus309**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0036486	**Msh6**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0036213	**RpL10Ab**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0033062	**Ars2**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0019644	**ATPsyn-b**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0013756	**Mtor**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0031759	**lid**	0	0	0	0	4	4	0	0	0	0	2	2
FBgn0004378	**Klp61F**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0005655	**mus209**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0010100	**Acon**	0	0	0	0	1	1	0	0	0	0	0	0

FBgn0032906	**RPA2**	0	0	0	0	6	6	0	0	1	1	2	2
FBgn0027338	**Kap-α3**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0040075	**rept**	0	0	1	1	5	5	0	0	2	2	1	1
Proteins not identified in negative controls													
FBgn0001149	**GstD1**	0	0	0	0	0	0	0	0	1	1	0	0
FBgn0037811	**CG12592**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0034390	**CG15093**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0020270	**mre11**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0024804	**Dbp80**	0	0	0	0	0	0	0	0	1	1	0	0
FBgn0030269	**CG18292**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0002872	**mu2**	0	0	2	2	0	0	0	0	0	0	0	0
FBgn0015024	**Cklα**	0	0	0	0	0	0	0	0	1	1	0	0
FBgn0023181	**Orc4**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0015270	**Orc2**	0	0	2	2	0	0	0	0	0	0	0	0
FBgn0032988	**Tif-IA**	0	0	1	1	0	0	0	0	1	1	0	0
FBgn0053523	**CG33523**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0005654	**lat**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0030853	**CG5703**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0026257	**cav**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0003600	**Su(var)3-9**	0	0	4	4	0	0	0	0	0	0	0	0
FBgn0035689	**CG7376**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0026573	**CG8290**	0	0	8	6	0	0	0	0	0	0	0	0
FBgn0037621	**CG9797**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0037633	**CG9839**	0	0	1	1	0	0	0	0	0	0	0	0
FBgn0033951	**CG10139**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0026196	**Nop5**	0	0	1	1	0	0	0	0	0	0	1	1
FBgn0004838	**Hrb27C**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0261403	**sxc**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0086441	**Acn**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0015657	**DnaJ-1**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0003082	**phr**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0027334	**l(1)G0004**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0250830	**CG12547**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0040465	**Dip3**	0	0	10	5	1	1	0	0	0	0	0	0
FBgn0033526	**Caf1-105**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0033609	**fbl6**	0	0	0	0	0	0	0	0	2	2	1	1
FBgn0038964	**Nop56**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0030268	**Klp10A**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0038035	**lig3**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0038827	**Fancd2**	0	0	0	0	1	1	0	0	0	0	0	0

FBgn0033934	**CG17385**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0023537	**CG17896**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0010342	**Map60**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0033107	**koi**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0004399	**psq**	0	0	0	0	0	0	0	0	2	2	1	1
FBgn0250753	**exba**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0034962	**MAN1**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0001133	**grau**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0015737	**Hmu**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0011327	**Uch-L3**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0010422	**TfIIS**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0030418	**CG4004**	0	0	4	1	1	1	0	0	0	0	0	0
FBgn0001986	**l(2)35Df**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0004926	**eIF-2β**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0015546	**spel1**	0	0	1	1	0	0	0	0	0	0	1	1
FBgn0016687	**Nurf-38**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0020633	**Mcm7**	0	0	2	2	1	1	0	0	0	0	0	0
FBgn0000566	**Eip55E**	0	0	3	3	1	1	0	0	0	0	0	0
FBgn0011016	**SsRβ**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0011236	**ken**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0015790	**Rab11**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0039125	**CG5857**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0005696	**DNApol-α73**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0016693	**Past1**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0020412	**JIL-1**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0020443	**Elf**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0024227	**ial**	0	0	5	5	1	1	0	0	1	1	0	0
FBgn0030093	**dalao**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0015805	**Rpd3**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0014861	**Mcm2**	0	0	3	2	1	1	0	0	0	0	0	0
FBgn0025457	**Bub3**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0260962	**pic**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0039697	**CG7834**	0	0	1	1	1	1	0	0	0	0	0	0
FBgn0026373	**RpII33**	0	0	1	1	0	0	0	0	0	0	1	1
FBgn0001179	**hay**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0033897	**Rcd1**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0011704	**RnrS**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0031769	**CG9135**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0037669	**CG9740**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0003687	**Tbp**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0004925	**eIF-2α**	0	0	2	2	1	1	0	0	0	0	0	0

FBgn0010416	**TH1**	0	0	0	0	1	1	0	0	0	0	0	0
FBgn0040265	**Transpac\pol**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0011715	**Snr1**	0	0	0	0	2	1	0	0	0	0	0	0
FBgn0022772	**Orc1**	0	0	0	0	2	1	0	0	0	0	0	0
FBgn0033571	**Rpb5**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0000054	**Adf1**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0086855	**CG17078**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0040066	**wds**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0051363	**Jupiter**	0	0	1	1	2	2	0	0	0	0	0	0
FBgn0034961	**CG3163**	0	0	12	7	2	2	0	0	2	1	0	0
FBgn0045852	**ham**	0	0	1	1	2	1	0	0	0	0	0	0
FBgn0064122	**CG33691**	0	0	3	1	2	1	0	0	1	1	0	0
FBgn0003507	**srp**	0	0	1	1	2	1	0	0	0	0	0	0
FBgn0022720	**zf30C**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0029798	**CG4078**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0011823	**Pen**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0004106	**cdc2**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0011703	**RnrL**	0	0	1	1	2	1	0	0	0	0	0	0
FBgn0039019	**HP1c**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0030082	**HP1b**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0031977	**baf**	0	0	1	1	1	1	0	0	1	1	1	1
FBgn0003013	**osa**	0	0	0	0	2	2	0	0	0	0	0	0
FBgn0003612	**Su(var)2-10**	0	0	3	2	2	2	0	0	0	0	0	0
FBgn0000289	**cg**	0	0	0	0	2	2	0	0	1	1	0	0
FBgn0022764	**Sin3A**	0	0	0	0	1	1	0	0	0	0	1	1
FBgn0037719	**bocksbeutel**	0	0	0	0	2	2	0	0	1	1	0	0
FBgn0026401	**Nipped-B**	0	0	0	0	3	3	0	0	0	0	0	0
FBgn0022349	**CG1910**	0	0	1	1	1	1	0	0	2	1	2	1
FBgn0010247	**Parp**	0	0	0	0	1	1	0	0	0	0	2	2
FBgn0032105	**borr**	0	0	10	6	3	3	0	0	0	0	0	0
FBgn0001224	**Hsp23**	0	0	0	0	0	0	0	0	1	1	3	3
FBgn0026533	**Dek**	0	0	0	0	1	1	0	0	1	1	2	1
FBgn0000283	**Cp190**	0	0	0	0	0	0	0	0	0	0	3	3
FBgn0011606	**Klp3A**	0	0	0	0	1	1	0	0	0	0	2	2
FBgn0015602	**BEAF-32**	0	0	0	0	4	3	0	0	0	0	0	0
FBgn0035370	**CG1240**	0	0	1	1	2	2	0	0	1	1	2	2
FBgn0034878	**pita**	0	0	0	0	2	1	0	0	0	0	2	1
FBgn0015610	**Caf1**	0	0	2	2	2	2	0	0	1	1	2	1
FBgn0027381	**Idefix\gag**	0	0	3	3	4	4	0	0	2	2	0	0
FBgn0044324	**Chro**	0	0	0	0	2	2	0	0	0	0	3	2
FBgn0037659	**Kdm2**	0	0	0	0	2	2	0	0	0	0	3	2

FBgn0002783	**mor**	0	0	0	0	5	4	0	0	0	0	0	0
FBgn0001994	**crp**	0	0	0	0	5	3	0	0	0	0	0	0
FBgn0039743	**CG7946**	0	0	0	0	0	0	0	0	1	1	5	4
FBgn0015623	**Cpr**	0	0	0	0	1	1	0	0	0	0	5	4
FBgn0031057	**Ubqn**	0	0	0	0	6	5	0	0	0	0	0	0
FBgn0039338	**XNP**	0	0	14	11	6	6	0	0	3	3	0	0
FBgn0015664	**Dref**	0	0	1	1	4	4	0	0	0	0	2	1
FBgn0259785	**pzg**	0	0	0	0	4	4	0	0	0	0	2	2
FBgn0033039	**gp210**	0	0	1	1	4	4	0	0	0	0	2	2
FBgn0028700	**RfC38**	0	0	0	0	5	5	0	0	1	1	2	2
FBgn0000412	**D1**	0	0	0	0	4	3	0	0	3	2	3	3
FBgn0020309	**crol**	0	0	5	2	7	4	0	0	1	1	1	1
FBgn0034657	**LBR**	0	0	3	2	6	3	0	0	0	0	2	2
FBgn0013591	**Mi-2**	0	0	0	0	5	4	0	0	3	3	3	3
FBgn0030854	**CG8289**	0	0	7	4	7	6	0	0	10	6	1	1
FBgn0020255	**ran**	0	0	4	3	6	6	0	0	1	1	4	4
FBgn0013263	**Trl**	0	0	9	3	9	3	0	0	3	2	2	1
FBgn0026170	**smt3**	0	0	17	5	11	4	0	0	5	1	1	1
FBgn0040078	**pont**	0	0	0	0	6	5	0	0	0	0	7	5
FBgn0038016	**MBD-R2**	0	0	0	0	0	0	0	0	0	0	1	1
FBgn0002638	**Bj1**	0	0	18	9	14	10	0	0	5	3	9	7
FBgn0004584	**Rrp1**	0	0	7	7	13	13	0	0	7	6	14	9

Table S2: GO Term enrichment for TAS-L and TAS-R purifications

TAS-R, TAS-L proteins (aggregate)							
Rank	**N**	**X**	**LOD**	**P**	**P-adj**	**GO Attribute**	
1	49	1698	1.273	2.60E-28	<0.001	GO:0005634	nucleus
2	50	2641	1.07	1.60E-20	<0.001	GO:0043231	intracellular membrane-bounded organelle
3	50	2644	1.07	1.70E-20	<0.001	GO:0043227	membrane-bounded organelle
4	52	3171	1.044	6.90E-19	<0.001	GO:0043229	intracellular organelle
5	52	3173	1.044	7.10E-19	<0.001	GO:0043226	organelle
6	55	4069	1.028	1.10E-16	<0.001	GO:0044424	intracellular part
7	56	4485	1.016	1.50E-15	<0.001	GO:0005622	intracellular
8	29	936	0.98	1.80E-15	<0.001	GO:0003677	DNA binding
9	11	60	1.691	1.90E-14	<0.001	GO:0003682	chromatin binding
10	26	828	0.956	7.00E-14	<0.001	GO:0006350	transcription
11	34	1567	0.859	8.60E-14	<0.001	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
12	18	339	1.135	2.20E-13	<0.001	GO:0005694	chromosome
13	17	290	1.174	2.30E-13	<0.001	GO:0044427	chromosomal part
14	24	739	0.954	4.40E-13	<0.001	GO:0045449	regulation of transcription
15	19	437	1.049	1.50E-12	<0.001	GO:0051276	chromosome organization and biogenesis
16	24	808	0.911	3.00E-12	<0.001	GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
17	24	833	0.896	5.80E-12	<0.001	GO:0010468	regulation of gene expression
18	21	621	0.947	9.20E-12	<0.001	GO:0006355	regulation of transcription, DNA-dependent
19	22	705	0.917	1.20E-11	<0.001	GO:0006351	transcription, DNA-dependent
20	22	707	0.915	1.30E-11	<0.001	GO:0032774	RNA biosynthetic process
21	25	1006	0.833	4.50E-11	<0.001	GO:0019222	regulation of metabolic process
22	21	678	0.905	4.80E-11	<0.001	GO:0051252	regulation of RNA metabolic process
23	56	5573	0.846	8.20E-11	<0.001	GO:0005488	binding

24	24	961	0.827	1.20E-10	<0.001	GO:0031323	regulation of cellular metabolic process
25	34	2014	0.728	1.20E-10	<0.001	GO:0003676	nucleic acid binding
26	32	1783	0.738	1.30E-10	<0.001	GO:0044446	intracellular organelle part
27	32	1786	0.738	1.40E-10	<0.001	GO:0044422	organelle part
28	35	2161	0.717	1.70E-10	<0.001	GO:0043283	biopolymer metabolic process
29	57	5942	0.852	2.70E-10	<0.001	GO:0005623	cell
30	57	5942	0.852	2.70E-10	<0.001	GO:0044464	cell part
31	23	947	0.805	5.80E-10	<0.001	GO:0043228	non-membrane-bounded organelle
32	23	947	0.805	5.80E-10	<0.001	GO:0043232	intracellular non-membrane-bounded organelle
33	35	2255	0.694	5.80E-10	<0.001	GO:0016043	cellular component organization and biogenesis
34	28	1496	0.72	1.50E-09	<0.001	GO:0050794	regulation of cellular process
35	25	1193	0.75	1.70E-09	<0.001	GO:0006996	organelle organization and biogenesis
36	12	217	1.111	2.30E-09	<0.001	GO:0006259	DNA metabolic process
37	19	673	0.845	2.40E-09	<0.001	GO:0044428	nuclear part
38	14	330	1	2.80E-09	<0.001	GO:0006325	establishment and/or maintenance of chromatin architecture
39	19	683	0.838	3.10E-09	<0.001	GO:0030528	transcription regulator activity
40	11	177	1.159	3.40E-09	<0.001	GO:0000785	chromatin
41	9	103	1.309	5.10E-09	<0.001	GO:0006260	DNA replication
42	14	363	0.956	9.60E-09	<0.001	GO:0031981	nuclear lumen
43	23	1097	0.733	1.00E-08	<0.001	GO:0016070	RNA metabolic process
44	28	1637	0.674	1.20E-08	<0.001	GO:0050789	regulation of biological process
45	12	272	1.006	2.90E-08	<0.001	GO:0005654	nucleoplasm
46	28	1732	0.645	4.10E-08	<0.001	GO:0010467	gene expression
47	11	257	0.986	1.60E-07	<0.001	GO:0044451	nucleoplasm part
48	7	75	1.332	1.80E-07	0.001	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
49	7	75	1.332	1.80E-07	0.001	GO:0045941	positive regulation of transcription
50	8	115	1.197	2.30E-07	0.001	GO:0009893	positive regulation of metabolic process
51	8	115	1.197	2.30E-07	0.001	GO:0031325	positive regulation of cellular metabolic process
52	28	1911	0.593	3.50E-07	0.001	GO:0065007	biological regulation
53	6	61	1.354	1.10E-06	0.001	GO:0006261	DNA-dependent DNA replication

54	14	535	0.775	1.20E-06	0.001	GO:0031974	membrane-enclosed lumen
55	14	535	0.775	1.20E-06	0.001	GO:0043233	organelle lumen
56	5	34	1.55	1.20E-06	0.001	GO:0016585	chromatin remodeling complex
57	4	15	1.865	1.20E-06	0.001	GO:0006270	DNA replication initiation
58	43	4273	0.532	1.30E-06	0.001	GO:0044238	primary metabolic process
59	5	35	1.535	1.40E-06	0.001	GO:0030261	chromosome condensation
60	10	260	0.931	1.60E-06	0.001	GO:0003702	RNA polymerase II transcription factor activity
61	8	157	1.052	2.50E-06	0.001	GO:0016568	chromatin modification
62	5	40	1.469	2.70E-06	0.001	GO:0008094	DNA-dependent ATPase activity
63	8	165	1.029	3.60E-06	0.003	GO:0006323	DNA packaging
64	11	379	0.806	7.20E-06	0.005	GO:0000278	mitotic cell cycle
65	6	87	1.186	8.70E-06	0.005	GO:0016251	general RNA polymerase II transcription factor activity
66	3	8	2.069	9.20E-06	0.005	GO:0035060	brahma complex
67	5	53	1.333	1.10E-05	0.005	GO:0045893	positive regulation of transcription, DNA-dependent
68	5	53	1.333	1.10E-05	0.005	GO:0051254	positive regulation of RNA metabolic process
69	37	3588	0.476	1.10E-05	0.005	GO:0043170	macromolecule metabolic process
70	22	1510	0.545	1.30E-05	0.005	GO:0043234	protein complex
71	4	27	1.554	1.40E-05	0.006	GO:0003678	DNA helicase activity
72	9	264	0.871	1.50E-05	0.006	GO:0006333	chromatin assembly or disassembly
73	7	154	0.996	2.30E-05	0.009	GO:0006357	regulation of transcription from RNA polymerase II promoter
74	41	4369	0.457	2.60E-05	0.009	GO:0044237	cellular metabolic process
75	23	1704	0.512	2.60E-05	0.01	GO:0005515	protein binding
76	7	158	0.984	2.70E-05	0.012	GO:0007067	mitosis
77	7	159	0.981	2.90E-05	0.012	GO:0000087	M phase of mitotic cell cycle
78	10	361	0.78	2.90E-05	0.012	GO:0048699	generation of neurons
79	8	221	0.894	3.00E-05	0.012	GO:0048522	positive regulation of cellular process
80	5	66	1.229	3.30E-05	0.03	GO:0005700	polytene chromosome
81	8	225	0.886	3.50E-05	0.031	GO:0006366	transcription from RNA polymerase II promoter
82	10	377	0.76	4.30E-05	0.033	GO:0022008	neurogenesis
83	8	238	0.861	5.20E-05	0.036	GO:0048518	positive regulation of biological process

84	6	123	1.026	6.30E-05	0.044	GO:0006338	chromatin remodeling
85	6	129	1.004	8.20E-05	0.048	GO:0016358	dendrite development
86	6	129	1.004	8.20E-05	0.048	GO:0048813	dendrite morphogenesis

TAS-R proteins

Rank	N	X	LOD	P	P-adj	GO Attribute	
1	45	1698	1.265	5.60E-26	<0.001	GO:0005634	nucleus
2	46	2641	1.065	6.60E-19	<0.001	GO:0043231	intracellular membrane-bounded organelle
3	46	2644	1.064	6.90E-19	<0.001	GO:0043227	membrane-bounded organelle
4	48	3171	1.046	1.40E-17	<0.001	GO:0043229	intracellular organelle
5	48	3173	1.045	1.50E-17	<0.001	GO:0043226	organelle
6	51	4069	1.043	8.90E-16	<0.001	GO:0044424	intracellular part
7	28	936	1.017	1.30E-15	<0.001	GO:0003677	DNA binding
8	51	4485	0.975	8.30E-14	<0.001	GO:0005622	intracellular
9	10	60	1.676	3.80E-13	<0.001	GO:0003682	chromatin binding
10	31	1567	0.849	1.60E-12	<0.001	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
11	23	828	0.926	5.50E-12	<0.001	GO:0006350	transcription
12	16	339	1.111	9.00E-12	<0.001	GO:0005694	chromosome
13	15	290	1.146	1.20E-11	<0.001	GO:0044427	chromosomal part
14	53	5573	0.939	2.70E-11	<0.001	GO:0005488	binding
15	17	437	1.029	3.80E-11	<0.001	GO:0051276	chromosome organization and biogenesis
16	21	739	0.917	4.10E-11	<0.001	GO:0045449	regulation of transcription
17	32	2014	0.747	2.10E-10	<0.001	GO:0003676	nucleic acid binding
18	21	808	0.874	2.20E-10	<0.001	GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
19	21	833	0.86	3.80E-10	<0.001	GO:0010468	regulation of gene expression
20	33	2255	0.715	8.20E-10	<0.001	GO:0016043	cellular component organization and biogenesis
21	18	621	0.9	1.10E-09	<0.001	GO:0006355	regulation of transcription, DNA-dependent
22	19	705	0.874	1.10E-09	<0.001	GO:0006351	transcription, DNA-dependent

23	19	707	0.872	1.20E-09	<0.001	GO:0032774	RNA biosynthetic process
24	32	2161	0.709	1.40E-09	<0.001	GO:0043283	biopolymer metabolic process
25	29	1783	0.723	1.60E-09	<0.001	GO:0044446	intracellular organelle part
26	29	1786	0.722	1.70E-09	<0.001	GO:0044422	organelle part
27	22	1006	0.8	1.90E-09	<0.001	GO:0019222	regulation of metabolic process
28	52	5942	0.812	4.00E-09	<0.001	GO:0005623	cell
29	52	5942	0.812	4.00E-09	<0.001	GO:0044464	cell part
30	18	678	0.858	4.40E-09	<0.001	GO:0051252	regulation of RNA metabolic process
31	21	961	0.791	5.20E-09	<0.001	GO:0031323	regulation of cellular metabolic process
32	23	1193	0.748	8.10E-09	<0.001	GO:0006996	organelle organization and biogenesis
33	12	272	1.049	1.10E-08	<0.001	GO:0005654	nucleoplasm
34	10	177	1.151	2.00E-08	<0.001	GO:0000785	chromatin
35	20	947	0.766	2.40E-08	<0.001	GO:0043228	non-membrane-bounded organelle
36	20	947	0.766	2.40E-08	<0.001	GO:0043232	intracellular non-membrane-bounded organelle
37	25	1496	0.696	2.50E-08	<0.001	GO:0050794	regulation of cellular process
38	17	673	0.826	2.80E-08	<0.001	GO:0044428	nuclear part
39	13	363	0.959	3.00E-08	<0.001	GO:0031981	nuclear lumen
40	17	683	0.819	3.50E-08	<0.001	GO:0030528	transcription regulator activity
41	8	103	1.289	5.10E-08	<0.001	GO:0006260	DNA replication
42	11	257	1.029	6.60E-08	<0.001	GO:0044451	nucleoplasm part
43	12	330	0.96	9.30E-08	<0.001	GO:0006325	establishment and/or maintenance of chromatin architecture
44	7	75	1.372	1.00E-07	<0.001	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
45	7	75	1.372	1.00E-07	<0.001	GO:0045941	positive regulation of transcription
46	8	115	1.237	1.20E-07	<0.001	GO:0009893	positive regulation of metabolic process
47	8	115	1.237	1.20E-07	<0.001	GO:0031325	positive regulation of cellular metabolic process
48	10	217	1.056	1.40E-07	<0.001	GO:0006259	DNA metabolic process
49	25	1637	0.65	1.50E-07	<0.001	GO:0050789	regulation of biological process
50	20	1097	0.694	2.80E-07	<0.001	GO:0016070	RNA metabolic process
51	25	1732	0.62	4.60E-07	<0.001	GO:0010467	gene expression
52	5	34	1.588	7.70E-07	0.002	GO:0016585	chromatin remodeling complex

53	5	40	1.507	1.80E-06	0.002	GO:0008094	DNA-dependent ATPase activity
54	40	4273	0.543	2.10E-06	0.002	GO:0044238	primary metabolic process
55	13	535	0.779	2.60E-06	0.002	GO:0031974	membrane-enclosed lumen
56	13	535	0.779	2.60E-06	0.002	GO:0043233	organelle lumen
57	25	1911	0.569	3.00E-06	0.003	GO:0065007	biological regulation
58	23	1704	0.568	5.50E-06	0.009	GO:0005515	protein binding
59	9	260	0.919	6.70E-06	0.01	GO:0003702	RNA polymerase II transcription factor activity
60	3	8	2.106	7.20E-06	0.01	GO:0035060	brahma complex
61	5	53	1.371	7.40E-06	0.01	GO:0045893	positive regulation of transcription, DNA-dependent
62	5	53	1.371	7.40E-06	0.01	GO:0051254	positive regulation of RNA metabolic process
63	4	27	1.592	1.00E-05	0.012	GO:0003678	DNA helicase activity
64	7	154	1.035	1.40E-05	0.017	GO:0006357	regulation of transcription from RNA polymerase II promoter
65	10	361	0.822	1.40E-05	0.02	GO:0048699	generation of neurons
66	5	61	1.305	1.50E-05	0.02	GO:0006261	DNA-dependent DNA replication
67	8	221	0.935	1.70E-05	0.022	GO:0048522	positive regulation of cellular process
68	8	225	0.927	1.90E-05	0.023	GO:0006366	transcription from RNA polymerase II promoter
69	10	377	0.802	2.00E-05	0.023	GO:0022008	neurogenesis
70	10	379	0.8	2.10E-05	0.023	GO:0000278	mitotic cell cycle
71	5	66	1.268	2.20E-05	0.023	GO:0005700	polytene chromosome
72	34	3588	0.472	2.80E-05	0.033	GO:0043170	macromolecule metabolic process
73	8	238	0.901	2.80E-05	0.034	GO:0048518	positive regulation of biological process
74	4	35	1.464	3.00E-05	0.034	GO:0030261	chromosome condensation
75	38	4369	0.463	4.20E-05	0.04	GO:0044237	cellular metabolic process
76	49	6671	0.527	4.80E-05	0.04	GO:0009987	cellular process
77	6	129	1.043	5.10E-05	0.042	GO:0016358	dendrite development
78	6	129	1.043	5.10E-05	0.042	GO:0048813	dendrite morphogenesis
79	3	15	1.75	5.70E-05	0.043	GO:0006270	DNA replication initiation
80	19	1449	0.523	7.60E-05	0.049	GO:0048731	system development

TAS-R-only proteins

Rank	N	X	LOD	P	P-adj	GO Attribute	
1	21	1698	1.442	2.60E-14	<0.001	GO:0005634	nucleus
2	22	2641	1.333	1.10E-11	<0.001	GO:0043231	intracellular membrane-bounded organelle
3	22	2644	1.332	1.10E-11	<0.001	GO:0043227	membrane-bounded organelle
4	22	3171	1.225	5.10E-10	<0.001	GO:0043229	intracellular organelle
5	22	3173	1.225	5.20E-10	<0.001	GO:0043226	organelle
6	12	828	1.079	4.30E-08	<0.001	GO:0006350	transcription
7	22	4069	1.066	9.10E-08	<0.001	GO:0044424	intracellular part
8	11	705	1.087	9.30E-08	<0.001	GO:0006351	transcription, DNA-dependent
9	11	707	1.085	9.60E-08	<0.001	GO:0032774	RNA biosynthetic process
10	11	739	1.064	1.50E-07	<0.001	GO:0045449	regulation of transcription
11	12	936	1.02	1.70E-07	<0.001	GO:0003677	DNA binding
12	10	621	1.077	3.30E-07	<0.001	GO:0006355	regulation of transcription, DNA-dependent
13	11	808	1.022	3.70E-07	<0.001	GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
14	11	833	1.008	5.10E-07	<0.001	GO:0010468	regulation of gene expression
15	3	8	2.508	5.20E-07	<0.001	GO:0035060	brahma complex
16	22	4485	0.998	6.60E-07	<0.001	GO:0005622	intracellular
17	10	678	1.036	7.50E-07	<0.001	GO:0051252	regulation of RNA metabolic process
18	4	34	1.892	8.00E-07	<0.001	GO:0016585	chromatin remodeling complex
19	14	1567	0.902	8.10E-07	<0.001	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
20	11	961	0.94	2.10E-06	<0.001	GO:0031323	regulation of cellular metabolic process
21	8	437	1.093	2.70E-06	<0.001	GO:0051276	chromosome organization and biogenesis
22	11	1006	0.918	3.30E-06	0.001	GO:0019222	regulation of metabolic process
23	14	1783	0.836	4.00E-06	0.003	GO:0044446	intracellular organelle part
24	14	1786	0.835	4.10E-06	0.003	GO:0044422	organelle part
25	5	115	1.437	4.30E-06	0.004	GO:0009893	positive regulation of metabolic process
26	5	115	1.437	4.30E-06	0.004	GO:0031325	positive regulation of cellular metabolic process
27	7	339	1.129	5.80E-06	0.005	GO:0005694	chromosome

28	9	673	0.968	7.10E-06	0.005	GO:0044428	nuclear part
29	11	1097	0.876	7.80E-06	0.005	GO:0016070	RNA metabolic process
30	4	60	1.623	8.10E-06	0.005	GO:0003682	chromatin binding
31	7	363	1.098	9.10E-06	0.005	GO:0031981	nuclear lumen
32	6	257	1.169	1.50E-05	0.008	GO:0044451	nucleoplasm part
33	10	947	0.878	1.50E-05	0.008	GO:0043228	non-membrane-bounded organelle
34	10	947	0.878	1.50E-05	0.008	GO:0043232	intracellular non-membrane-bounded organelle
35	4	75	1.52	2.00E-05	0.011	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
36	4	75	1.52	2.00E-05	0.011	GO:0045941	positive regulation of transcription
37	6	272	1.143	2.10E-05	0.013	GO:0005654	nucleoplasm
38	12	1496	0.791	2.50E-05	0.015	GO:0050794	regulation of cellular process
39	2	4	2.685	2.80E-05	0.023	GO:0000791	euchromatin
40	6	290	1.114	3.00E-05	0.023	GO:0044427	chromosomal part
41	5	177	1.241	3.50E-05	0.024	GO:0000785	chromatin
42	14	2161	0.734	4.00E-05	0.024	GO:0043283	biopolymer metabolic process
43	22	5573	0.829	4.90E-05	0.033	GO:0005488	binding
44	12	1637	0.745	6.20E-05	0.034	GO:0050789	regulation of biological process
45	6	330	1.055	6.20E-05	0.034	GO:0006325	establishment and/or maintenance of chromatin architecture
46	14	2255	0.711	6.50E-05	0.035	GO:0016043	cellular component organization and biogenesis
47	13	2014	0.704	9.80E-05	0.049	GO:0003676	nucleic acid binding
48	5	221	1.141	0.0001	0.049	GO:0048522	positive regulation of cellular process

TAS-L proteins

Rank	N	X	LOD	P	P-adj	GO Attribute	
1	28	1698	1.158	1.80E-15	<0.001	GO:0005634	nucleus
2	28	2641	0.919	1.50E-10	<0.001	GO:0043231	intracellular membrane-bounded organelle
3	28	2644	0.919	1.60E-10	<0.001	GO:0043227	membrane-bounded organelle
4	30	3171	0.925	2.50E-10	<0.001	GO:0043229	intracellular organelle

5	30	3173	0.924	2.50E-10	<0.001	GO:0043226	organelle
6	33	4069	0.971	4.00E-10	<0.001	GO:0044424	intracellular part
7	34	4485	0.989	8.10E-10	<0.001	GO:0005622	intracellular
8	7	60	1.688	1.00E-09	<0.001	GO:0003682	chromatin binding
9	11	290	1.204	2.10E-09	<0.001	GO:0044427	chromosomal part
10	17	936	0.946	2.70E-09	<0.001	GO:0003677	DNA binding
11	11	339	1.132	1.10E-08	<0.001	GO:0005694	chromosome
12	20	1567	0.824	2.60E-08	<0.001	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
13	9	217	1.222	3.60E-08	<0.001	GO:0006259	DNA metabolic process
14	7	103	1.431	4.80E-08	<0.001	GO:0006260	DNA replication
15	5	35	1.773	1.10E-07	0.001	GO:0030261	chromosome condensation
16	11	437	1.015	1.50E-07	0.001	GO:0051276	chromosome organization and biogenesis
17	14	828	0.867	2.80E-07	0.001	GO:0006350	transcription
18	21	2014	0.738	3.30E-07	0.001	GO:0003676	nucleic acid binding
19	13	739	0.873	5.40E-07	0.001	GO:0045449	regulation of transcription
20	35	5942	0.863	5.80E-07	0.001	GO:0005623	cell
21	35	5942	0.863	5.80E-07	0.001	GO:0044464	cell part
22	34	5573	0.82	5.90E-07	0.001	GO:0005488	binding
23	21	2161	0.7	1.10E-06	0.001	GO:0043283	biopolymer metabolic process
24	7	165	1.213	1.20E-06	0.001	GO:0006323	DNA packaging
25	13	808	0.831	1.50E-06	0.001	GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process
26	12	683	0.86	1.70E-06	0.001	GO:0030528	transcription regulator activity
27	13	833	0.816	2.10E-06	0.001	GO:0010468	regulation of gene expression
28	21	2255	0.677	2.30E-06	0.001	GO:0016043	cellular component organization and biogenesis
29	14	1006	0.774	2.90E-06	0.001	GO:0019222	regulation of metabolic process
30	15	1193	0.738	4.00E-06	0.001	GO:0006996	organelle organization and biogenesis
31	11	621	0.852	4.70E-06	0.001	GO:0006355	regulation of transcription, DNA-dependent
32	18	1783	0.67	6.50E-06	0.001	GO:0044446	intracellular organelle part
33	18	1786	0.669	6.70E-06	0.001	GO:0044422	organelle part
34	13	947	0.755	8.60E-06	0.001	GO:0043228	non-membrane-bounded organelle

35	13	947	0.755	8.60E-06	0.001	GO:0043232	intracellular non-membrane-bounded organelle
36	4	40	1.595	9.80E-06	0.001	GO:0008094	DNA-dependent ATPase activity
37	13	961	0.748	1.00E-05	0.001	GO:0031323	regulation of cellular metabolic process
38	11	678	0.811	1.10E-05	0.001	GO:0051252	regulation of RNA metabolic process
39	8	330	0.966	1.30E-05	0.006	GO:0006325	establishment and/or maintenance of chromatin architecture
40	16	1496	0.671	1.40E-05	0.006	GO:0050794	regulation of cellular process
41	4	44	1.55	1.40E-05	0.007	GO:0016569	covalent chromatin modification
42	4	44	1.55	1.40E-05	0.007	GO:0016570	histone modification
43	11	705	0.792	1.60E-05	0.008	GO:0006351	transcription, DNA-dependent
44	11	707	0.791	1.60E-05	0.008	GO:0032774	RNA biosynthetic process
45	3	15	1.94	1.60E-05	0.008	GO:0006270	DNA replication initiation
46	6	177	1.103	2.70E-05	0.013	GO:0000785	chromatin
47	3	20	1.794	4.00E-05	0.04	GO:0007076	mitotic chromosome condensation
48	16	1637	0.625	4.30E-05	0.04	GO:0050789	regulation of biological process
49	4	61	1.397	5.30E-05	0.041	GO:0006261	DNA-dependent DNA replication
50	27	4273	0.567	5.50E-05	0.042	GO:0044238	primary metabolic process
51	10	673	0.759	6.40E-05	0.043	GO:0044428	nuclear part

TAS-L-only proteins *

Rank	N	X	LOD	P	P-adj	GO Attribute	
1	3	7	2.786	9.60E-08	<0.001	GO:0000808	origin recognition complex
2	3	7	2.786	9.60E-08	<0.001	GO:0005664	nuclear origin of replication recognition complex
3	6	217	1.475	4.60E-07	<0.001	GO:0006259	DNA metabolic process
4	4	47	1.939	5.80E-07	<0.001	GO:0044454	nuclear chromosome part
5	4	51	1.901	8.10E-07	<0.001	GO:0000228	nuclear chromosome
6	3	15	2.342	1.20E-06	<0.001	GO:0006270	DNA replication initiation
7	10	1698	0.905	3.70E-05	0.009	GO:0005634	nucleus
8	12	2641	0.879	4.40E-05	0.011	GO:0043231	intracellular membrane-bounded organelle

9	12	2644	0.879	4.40E-05	0.013	GO:0043227	membrane-bounded organelle
10	5	290	1.233	4.90E-05	0.015	GO:0044427	chromosomal part
11	3	61	1.67	9.40E-05	0.034	GO:0006261	DNA-dependent DNA replication
12	5	339	1.163	0.0001	0.035	GO:0005694	chromosome
13	2	12	2.243	0.00014	0.05	GO:0000723	telomere maintenance
14	2	12	2.243	0.00014	0.05	GO:0032200	telomere organization and biogenesis

***** Includes proteins for which 1 peptide only was detected, because there wasn't a sufficient number of factors with more peptides for term enrichment analysis.

GO analysis performed with the FuncAssociate software (S1).

Table legend	
Rank	Position in the attribute list ranked by significance of association with query
N	Number of genes in query with this attribute
X	Number of genes overall with this attribute
LOD	The logarithm (base 10) of the odds ratio; positive and negative values indicate over- and underrepresentation, respectively
P	Single hypothesis one-sided P-value of the association between attribute and query (based on Fisher's Exact Test)
P-adj	Adjusted P-value: fraction (as a %) of 1000 null-hypothesis simulations having attributes with this single-hypothesis P value or smaller

<u>Table S3</u>: Proteins common to TAS-L/R in S3, Kc, embryos

			Kc				S3				Embryo *
			TAS-L		TAS-R		TAS-L		TAS-R		TAS-R
			peptides		peptides		peptides		peptides		peptides
Flybase ID	**CG#**	**Name**	**total**	**unique**	**total**	**unique**	**total**	**unique**	**total**	**unique**	**total**
FBgn0037810	CG12819	**sle**	32	15	22	15	10	8	2	2	0
FBgn0002638	CG10480	**Bj1**	18	9	14	10	5	3	9	7	4
FBgn0004584	CG3178	**Rrp1**	7	7	13	13	7	6	14	9	8
FBgn0260991	CG12165	**Incenp**	28	13	20	9	11	5	1	1	0
FBgn0043456	CG4747		3	3	17	11	2	1	11	7	0
FBgn0011604	CG8625	**Iswi**	3	2	17	15	2	2	11	8	2
FBgn0026170	CG4494	**smt3**	17	5	11	4	5	1	1	1	0
FBgn0030854	CG8289		7	4	7	6	10	6	1	1	3
FBgn0013263	CG33261	**Trl**	9	3	9	3	3	2	2	1	0
FBgn0002780	CG2050	**mod**	2	2	4	4	5	5	3	3	4
FBgn0020255	CG1404	**ran**	4	3	6	6	1	1	4	4	0
FBgn0040268	CG10123	**Top3α**	1	1	3	3	3	3	4	4	0
FBgn0020309	CG14938	**crol**	5	2	7	4	1	1	1	1	0
FBgn0035213	CG2199		2	1	4	2	3	1	1	1	0
FBgn0038608	CG7670	**WRNexo**	2	2	4	3	2	2	1	1	0
FBgn0040075	CG9750	**rept**	1	1	5	5	2	2	1	1	3
FBgn0015610	CG4236	**Caf1**	2	2	2	2	1	1	2	1	3
FBgn0035370	CG1240		1	1	2	2	1	1	2	2	0
FBgn0031977	CG7380	**baf**	1	1	1	1	1	1	1	1	0
FBgn0022349	CG1910		1	1	1	1	1	1	1	1	0

***** PICh experiment performed on chromatin from 0-24hr old embryos; red background: factors identified as non-specific in Rees et al, 2011; yellow background: no enrichment seen by Western blot.

Table S4: TAS-L proteins, ranked by confidence score

rank	detectable peptides/ 1000 [a]	detectability score [b]	Normalized Gene Expression Score [c]		Expression level [d]		Confidence score [e]	Flybase ID	Name	Kc				S3			
										TAS_L		TAS_R		TAS_L		TAS_R	
										peptides		peptides		peptides		peptides	
			Kc	S3	Kc	S3				total	unique	total	unique	total	unique	total	unique
1	17.54	3.29	0.89	1.22	726	1072	3.92	FBgn0039338	**XNP**	14	11	6	6	3	3	0	0
2	14.16	2.65	1.17	1.35	951	1181	3.58	FBgn0004584	**Rrp1**	7	7	13	13	7	6	14	9
3	14.37	2.69	0.19	0.14	155	119	3.50	FBgn0040465	**Dip3**	10	5	1	1	0	0	0	0
4	20.83	3.90	0.94	1.09	764	956	3.46	FBgn0030854	**CG8289**	7	4	7	6	10	6	1	1
5	25.59	4.79	2.85	1.55	2327	1356	3.29	FBgn0002638	**Bj1**	18	9	14	10	5	3	9	7
6	15.67	2.94	0.84	0.87	687	767	2.64	FBgn0032105	**borr**	10	6	3	3	0	0	0	0
7	9.12	1.71	0.50	0.74	407	647	2.58	FBgn0024227	**ial**	5	5	1	1	1	1	0	0
8	12.03	2.25	3.40	4.41	2774	3868	1.95	FBgn0013263	**Trl**	9	3	9	3	3	2	2	1
9	20.85	3.90	0.53	0.82	435	717	1.75	FBgn0026573	**CG8290**	8	6	0	0	0	0	0	0
10	19.02	3.56	5.10	5.03	4158	4413	1.62	FBgn0034961	**CG3163**	12	7	2	2	2	1	0	0
11	33.33	6.24	9.65	6.72	7873	5894	1.52	FBgn0026170	**smt3**	17	5	11	4	5	1	1	1
12	9.36	1.75	4.45	3.59	3629	3149	1.04	FBgn0020309	**crol**	5	2	7	4	1	1	1	1
13	17.70	3.31	0.29	1.49	239	1305	0.95	FBgn0030418	**CG4004**	4	1	1	1	0	0	0	0
14	12.94	2.42	0.34	0.37	277	323	0.72	FBgn0015270	**Orc2**	2	2	0	0	0	0	0	0
15	28.47	5.33	1.87	0.92	1525	806	0.59	FBgn0064122	**CG33691**	3	1	2	1	1	1	0	0
16	11.27	2.11	2.81	3.09	2294	2710	0.59	FBgn0000412	**D1**	0	0	4	3	3	2	3	3
17	19.16	3.59	1.44	2.00	1171	1754	0.57	FBgn0013591	**Mi-2**	0	0	5	4	3	3	3	3
18	16.28	3.05	2.49	2.63	2029	2302	0.54	FBgn0015610	**Caf1**	2	2	2	2	1	1	2	1
19	25.94	4.86	5.10	5.03	4158	4413	0.50	FBgn0027381	**GAG**	3	3	4	4	2	2	0	0
20	25.93	4.86	1.08	1.20	885	1050	0.50	FBgn0014861	**Mcm2**	3	2	1	1	0	0	0	0
21	4.10	0.77	3.23	3.40	2634	2981	0.49	FBgn0035370	**CG1240**	1	1	2	2	1	1	2	2
22	19.53	3.66	0.67	0.56	549	489	0.47	FBgn0002872	**mu2**	2	2	0	0	0	0	0	0
23	12.22	2.29	1.46	2.61	1189	2289	0.46	FBgn0004399	**psq**	0	0	0	0	2	2	1	1
24	21.88	4.10	2.15	2.66	1755	2332	0.46	FBgn0003612	**Su(var)2-10**	3	2	2	2	0	0	0	0
25	32.39	6.07	0.87	1.00	710	877	0.43	FBgn0034657	**LBR**	3	2	6	3	0	0	2	2

26	20.83	3.90	0.51	1.06	413	929	0.43	FBgn0033609	**fbl6**	0	0	0	0	2	2	1	1
27	17.32	3.24	7.55	5.47	6159	4797	0.41	FBgn0003600	**Su(var)3-9**	4	4	0	0	0	0	0	0
28	27.78	5.20	10.00	6.31	8160	5529	0.37	FBgn0020255	**ran**	4	3	6	6	1	1	4	4
29	22.49	4.21	1.85	6.03	1513	5287	0.37	FBgn0022349	**CG1910**	1	1	1	1	2	1	2	1
30	14.66	2.75	3.19	3.00	2605	2629	0.34	FBgn0004925	**eIF-2α**	2	2	1	1	0	0	0	0
31	27.78	5.20	1.04	1.22	847	1071	0.32	FBgn0020633	**Mcm7**	2	2	1	1	0	0	0	0
32	31.10	5.82	1.45	1.64	1185	1441	0.27	FBgn0032988	**Tif-IA**	1	1	0	0	1	1	0	0
33	25.45	4.77	5.37	8.18	4380	7170	0.26	FBgn0000566	**Eip55E**	3	3	1	1	0	0	0	0
34	20.05	3.75	0.83	0.50	674	440	0.23	FBgn0037719	**bocksbeutel**	0	0	2	2	1	1	0	0
35	21.05	3.94	0.55	1.10	452	966	0.21	FBgn0039743	**CG7946**	0	0	0	0	1	1	5	4
36	44.44	8.32	2.62	1.70	2135	1487	0.19	FBgn0031977	**baf**	1	1	1	1	1	1	1	1
37	24.37	4.56	1.99	0.03	1624	29	0.18	FBgn0045852	**ham**	1	1	2	1	0	0	0	0
38	18.47	3.46	2.30	2.68	1880	2353	0.17	FBgn0011703	**RnrL**	1	1	2	1	0	0	0	0
39	13.45	2.52	2.00	5.44	1630	4769	0.16	FBgn0026533	**Dek**	0	0	1	1	1	1	2	1
40	26.80	5.02	1.16	1.31	950	1148	0.16	FBgn0015664	**Dref**	1	1	4	4	0	0	2	1
41	33.71	6.31	0.49	0.46	398	400	0.15	FBgn0028700	**RfC38**	0	0	5	5	1	1	2	2
42	26.65	4.99	1.66	2.09	1351	1834	0.15	FBgn0033039	**gp210**	1	1	4	4	0	0	2	2
43	9.49	1.78	3.47	6.94	2829	6083	0.14	FBgn0003507	**srp**	1	1	2	1	0	0	0	0
44	15.76	2.95	5.07	4.22	4139	3701	0.13	FBgn0000289	**cg**	0	0	2	2	1	1	0	0
45	53.76	10.07	1.49	9.26	1217	8122	0.06	FBgn0001224	**Hsp23**	0	0	0	0	1	1	3	3
46	43.27	8.10	9.64	5.89	7866	5163	0.06	FBgn0051363	**Jupiter**	1	1	2	2	0	0	0	0

a. Detectable Peptides calculated using the Peptide detectability predictor at http://darwin.informatics.indiana.edu/applications/PeptideDetectabilityPredictor/ (Tang et al, 2006). The values presented are for the number of peptides with a detectability >0.6; **b**. the Detectability Score is the number of detectable peptides/1000 normalized to a scale of 0-10, where 10 is the value found for the protein with the highest detectable peptides/1000 (Hsp23, 53.76); **c.** the Normalized Gene Expression Score is the relative gene expression, on a scale of 0-10, where 10 is the value of the highest expressing gene in the respective cell line (Kc: ran, 8160; S3: cpr, 8796); **d.**

expression data obtained from the modENCODE database (Celniker et al, 2009); **e.** the Confidence Score is the value resulting from the division of the number of peptides detected in both cell lines by the sum of the Detectability Score and the average of the Normalized Gene Expression Scores from the 2 cell lines; **Red font**: expression levels not available; attributed average expression level of all factors detected.

Table S5: TAS-R proteins, ranked by confidence score

rank	detectable peptides/ 1000 [a]	detectability score [b]	Normalized Gene Expression Score [c]		Expression level [d]		Confidence score [e]	Flybase ID	Name	Kc				S3			
										TAS_L		TAS_R		TAS_L		TAS_R	
										peptides		peptides		peptides		peptides	
			Kc	S3	Kc	S3				total	unique	total	unique	total	unique	total	unique
1	14.16	2.65	1.17	1.35	951	1181	6.91	FBgn0004584	**Rrp1**	7	7	13	13	7	6	14	9
2	25.59	4.79	2.85	1.55	2327	1356	3.29	FBgn0002638	**Bj1**	18	9	14	10	5	3	9	7
3	32.89	6.16	0.79	1.13	641	991	1.83	FBgn0040078	**pont**	0	0	6	5	0	0	7	5
4	12.03	2.25	3.40	4.41	2774	3868	1.79	FBgn0013263	**Trl**	9	3	9	3	3	2	2	1
5	8.78	1.65	0.61	0.71	498	626	1.73	FBgn0034878	**pita**	0	0	2	1	0	0	2	1
6	20.83	3.90	0.94	1.09	764	956	1.63	FBgn0030854	**CG8289**	7	4	7	6	10	6	1	1
7	19.16	3.59	1.44	2.00	1171	1754	1.51	FBgn0013591	**Mi-2**	0	0	5	4	3	3	3	3
8	9.36	1.75	4.45	3.59	3629	3149	1.39	FBgn0020309	**crol**	5	2	7	4	1	1	1	1
9	11.27	2.11	2.81	3.09	2294	2710	1.38	FBgn0000412	**D1**	0	0	4	3	3	2	3	3
10	17.54	3.29	0.89	1.22	726	1072	1.38	FBgn0039338	**XNP**	14	11	6	6	3	3	0	0
11	32.39	6.07	0.87	1.00	710	877	1.14	FBgn0034657	**LBR**	3	2	6	3	0	0	2	2
12	20.08	3.76	0.92	2.17	753	1906	1.13	FBgn0259785	**pzg**	0	0	4	4	0	0	2	2
13	21.05	3.94	0.55	1.10	452	966	1.05	FBgn0039743	**CG7946**	0	0	0	0	1	1	5	4
14	16.54	3.10	0.95	2.41	778	2115	1.05	FBgn0002783	**mor**	0	0	5	4	0	0	0	0
15	33.71	6.31	0.49	0.46	398	400	1.03	FBgn0028700	**RfC38**	0	0	5	5	1	1	2	2
16	22.30	4.18	0.71	0.88	581	769	1.01	FBgn0037659	**Kdm2**	0	0	2	2	0	0	3	2
17	4.10	0.77	3.23	3.40	2634	2981	0.98	FBgn0035370	**CG1240**	1	1	2	2	1	1	2	2
18	26.80	5.02	1.16	1.31	950	1148	0.96	FBgn0015664	**Dref**	1	1	4	4	0	0	2	1
19	16.20	3.03	1.74	2.87	1421	2515	0.94	FBgn0044324	**Chro**	0	0	2	2	0	0	3	2
20	8.44	1.58	0.67	0.53	547	465	0.92	FBgn0039019	**HP1c**	0	0	2	2	0	0	0	0
21	26.65	4.99	1.66	2.09	1351	1834	0.87	FBgn0033039	**gp210**	1	1	4	4	0	0	2	2
22	33.33	6.24	9.65	6.72	7873	5894	0.83	FBgn0026170	**smt3**	17	5	11	4	5	1	1	1
23	26.94	5.05	0.73	1.31	599	1150	0.82	FBgn0001994	**crp**	0	0	5	3	0	0	0	0
24	15.67	2.94	0.84	0.87	687	767	0.79	FBgn0032105	**borr**	10	6	3	3	0	0	0	0
25	27.42	5.14	2.39	2.70	1953	2369	0.78	FBgn0031057	**Ubqn**	0	0	6	5	0	0	0	0

26	27.78	5.20	10.00	6.31	8160	5529	0.75	FBgn0020255	**ran**	4	3	6	6	1	1	4	4
27	18.98	3.55	0.43	0.79	347	696	0.72	FBgn0011606	**Klp3A**	0	0	1	1	0	0	2	2
28	24.73	4.63	0.88	1.00	717	873	0.72	FBgn0015602	**BEAF-32**	0	0	4	3	0	0	0	0
29	16.28	3.05	2.49	2.63	2029	2302	0.71	FBgn0015610	**Caf1**	2	2	2	2	1	1	2	1
30	18.25	3.42	1.09	2.36	892	2070	0.58	FBgn0000283	**Cp190**	0	0	0	0	0	0	3	3
31	25.04	4.69	2.18	10.03	1782	8796	0.56	FBgn0015623	**Cpr**	0	0	1	1	0	0	5	4
32	21.13	3.96	1.64	1.43	1336	1254	0.55	FBgn0010247	**Parp**	0	0	1	1	0	0	2	2
33	15.27	2.86	0.82	0.97	667	851	0.53	FBgn0000054	**Adf1**	0	0	2	2	0	0	0	0
34	10.68	2.00	1.60	2.36	1305	2066	0.50	FBgn0003013	**osa**	0	0	2	2	0	0	0	0
35	13.45	2.52	2.00	5.44	1630	4769	0.48	FBgn0026533	**Dek**	0	0	1	1	1	1	2	1
36	19.48	3.65	0.56	0.68	459	600	0.47	FBgn0022772	**Orc1**	0	0	2	1	0	0	0	0
37	16.67	3.12	1.22	1.16	992	1019	0.46	FBgn0030082	**HP1b**	0	0	1	1	0	0	1	1
38	19.05	3.57	0.56	0.93	459	813	0.46	FBgn0033571	**CG11979**	0	0	2	2	0	0	0	0
39	20.05	3.75	0.83	0.50	674	440	0.45	FBgn0037719	**bocksbeutel**	0	0	2	2	1	1	0	0
40	23.11	4.33	3.15	1.93	2571	1692	0.44	FBgn0026401	**Nipped-B**	0	0	3	3	0	0	0	0
41	9.12	1.71	0.50	0.74	407	647	0.43	FBgn0024227	**ial**	5	5	1	1	1	1	0	0
42	21.31	3.99	0.89	0.99	723	864	0.41	FBgn0086855	**CG17078**	0	0	1	1	0	0	1	1
43	25.94	4.86	5.10	5.03	4158	4413	0.40	FBgn0027381	**GAG**	3	3	4	4	2	2	0	0
44	22.49	4.21	1.85	6.03	1513	5287	0.37	FBgn0022349	**CG1910**	1	1	1	1	2	1	2	1
45	24.37	4.56	1.99	0.03	1624	29	0.36	FBgn0045852	**ham**	1	1	2	1	0	0	0	0
46	14.37	2.69	0.19	0.14	155	119	0.35	FBgn0040465	**Dip3**	10	5	1	1	0	0	0	0
47	24.93	4.67	0.99	1.18	810	1037	0.35	FBgn0040066	**wds**	0	0	1	1	0	0	1	1
48	23.17	4.34	0.91	1.93	743	1690	0.35	FBgn0022720	**zf30C**	0	0	2	2	0	0	0	0
49	27.03	5.06	0.66	0.76	535	662	0.35	FBgn0011715	**Snr1**	0	0	2	1	0	0	0	0
50	18.47	3.46	2.30	2.68	1880	2353	0.34	FBgn0011703	**RnrL**	1	1	2	1	0	0	0	0
51	29.44	5.51	0.54	0.66	437	583	0.33	FBgn0029798	**CG4078**	0	0	2	2	0	0	0	0
52	20.37	3.81	1.57	3.78	1284	3312	0.31	FBgn0022764	**Sin3A**	0	0	1	1	0	0	1	1
53	21.88	4.10	2.15	2.66	1755	2332	0.31	FBgn0003612	**Su(var)2-10**	3	2	2	2	0	0	0	0
54	28.47	5.33	1.87	0.92	1525	806	0.30	FBgn0064122	**CG33691**	3	1	2	1	1	1	0	0
55	30.30	5.67	0.77	1.67	632	1461	0.29	FBgn0004106	**cdc2**	0	0	2	2	0	0	0	0
56	9.49	1.78	3.47	6.94	2829	6083	0.29	FBgn0003507	**srp**	1	1	2	1	0	0	0	0
57	15.76	2.95	5.07	4.22	4139	3701	0.26	FBgn0000289	**cg**	0	0	2	2	1	1	0	0
58	17.70	3.31	0.29	1.49	239	1305	0.24	FBgn0030418	**CG4004**	4	1	1	1	0	0	0	0
59	19.02	3.56	5.10	5.03	4158	4413	0.23	FBgn0034961	**CG3163**	12	7	2	2	2	1	0	0
60	12.22	2.29	1.46	2.61	1189	2289	0.23	FBgn0004399	**psq**	0	0	0	0	2	2	1	1

61	20.83	3.90	0.51	1.06	413	929	0.21	FBgn0033609	**fbl6**	0	0	0	0	2	2	1	1
62	53.76	10.07	1.49	9.26	1217	8122	0.19	FBgn0001224	**Hsp23**	0	0	0	0	1	1	3	3
63	44.44	8.32	2.62	1.70	2135	1487	0.19	FBgn0031977	**baf**	1	1	1	1	1	1	1	1
64	30.65	5.74	7.54	4.23	6154	3707	0.17	FBgn0011823	**Pen**	0	0	2	2	0	0	0	0
65	14.66	2.75	3.19	3.00	2605	2629	0.17	FBgn0004925	**eIF-2α**	2	2	1	1	0	0	0	0
66	25.93	4.86	1.08	1.20	885	1050	0.17	FBgn0014861	**Mcm2**	3	2	1	1	0	0	0	0
67	27.78	5.20	1.04	1.22	847	1071	0.16	FBgn0020633	**Mcm7**	2	2	1	1	0	0	0	0
68	43.27	8.10	9.64	5.89	7866	5163	0.13	FBgn0051363	**Jupiter**	1	1	2	2	0	0	0	0
69	25.45	4.77	5.37	8.18	4380	7170	0.09	FBgn0000566	**Eip55E**	3	3	1	1	0	0	0	0

a. Detectable Peptides calculated using the Peptide detectability predictor at http://darwin.informatics.indiana.edu/applications/PeptideDetectabilityPredictor/ (Tang et al, 2006). The values presented are for the number of peptides with a detectability >0.6; **b**. the Detectability Score is the number of detectable peptides/1000 normalized to a scale of 0-10, where 10 is the value found for the protein with the highest detectable peptides/1000 (Hsp23, 53.76); **c.** the Normalized Gene Expression Score is the relative gene expression, on a scale of 0-10, where 10 is the value of the highest expressing gene in the respective cell line (Kc: ran, 8160; S3: cpr, 8796); **d.** expression data obtained from the modENCODE database (Celniker et al, 2009); **e.** the Confidence Score is the value resulting from the division of the number of peptides detected in both cell lines by the sum of the Detectability Score and the average of the Normalized Gene Expression Scores from the 2 cell lines; **Red font**: expression levels not available; attributed average expression level of all factors detected.

Table S6: Eye color phenotypes.

Gene	**Allele**	**Eye color M26; C62**[a]	**Eye color +; C62**[b]	**Interpretation**
+[c]	+	+ red	+ orange	Negative control
"	*Df(3R)BSC497*	+ red Ubx red	+ brown Ubx dark orange	Negative
"	*Df(3R)BSC739*	+ orange Ubx orange	+ brown Ubx orange	Mutant not on III
woc	*Df(3R)D605*	+ orange Ubx orange	+ orange Ubx orange	Mutant not on III
mod	*07570*	+ bright red Ubx red	+ red Ubx brown	Su(TPE)[e]
"	*Df(3R)04661*	+ bright red Ubx red	+ red Ubx dark orange	Su(TPE)[e]
WRNexo	*Df(3R)Cha7*	+ dark orange Ubx red	+ dark orange Ubx red	Mutant, but too weak to map.
sle	*057*	+ red Ubx red	+ ND[d] Ubx ND	Negative
brm	*2*	+ orange Ubx red	+ orange Ubx red	Mutant on III
SMC1	*exc46*	+ red Ubx red	+ ND Ubx ND	Negative
su(Hw)	*3*	+ red Ubx red	+ ND Ubx ND	Negative
rept	*6945*	+ red Ubx red	+ ND Ubx ND	Negative
CG2199	*Df(3L)Ar14-8*	+ red Ubx red	+ ND Ubx ND	Negative
"	*Df(3L)BSC289*	+ red Ubx red	+ ND Ubx ND	Negative
Snr1	*01319*	+ red Ubx red	+ ND Ubx ND	Negative
osa	*00090*	+ red Ubx red	+ ND Ubx ND	Negative
mor	*Df(3R)Po4*	+ dark red Ubx red	+ orange Ubx dark orange	Mutant, but too weak to map.
CAF1	*Df(3R)BSC471*	+ red Ubx red	+ red Ubx dark red	Negative
borr	*Df(2L)TE30Cb*	+ red Cy red	+ ND Ubx ND	Negative
Bj1	*Df(3L)XAS96*	+ red Ubx red	+ orange Ubx brown	Negative
XNP	*1*	+ red Ubx red	+ ND Ubx ND	Negative
"	*UY3132*	+ dark orange Ubx dark orange	+ ND Ubx ND	Mutant not on III
CG1240	*Df(3L)BSC119*	+ red Ubx red	+ ND Ubx ND	Negative

crol	*04418*	+ orange Cy dark orange	+ ND Ubx ND	Mutant not on II
"	*Df(2L)BSC243*	+ red Cy red	+ ND Ubx ND	Negative
Trl	*Df(3L)fz-M21*	+ brown Ubx red	+ ND Ubx ND	Mutant on III; False positive[f]
"	*Df(3L)XG3*	+ red Ubx w5	+ ND Ubx ND	Negative

[a] *y w*^{67c23}*; Df(2L)M26; P{w*$^{+}$*}39C-62* females were crossed to *y w*^{67c23}*;* mutant*/SM1, Cy* or *y w*^{67c23}*;* mutant*/TM6, Ubx*. F$_1$ males were aged for three days, then examined for eye color. Males without the balancer constitute the test for suppressors of the Su(TPE) activity of M26 on the C62 telomeric insert. Males with the balancer act as a sibling control.

[b] *y w*^{67c23}*; P{w*$^{+}$*}39C-62* females were crossed to *y w*^{67c23}*;* mutant*/SM1, Cy* or *y w*^{67c23}*;* mutant*/TM6, Ubx*. F$_1$ males were aged for three days, then examined for eye color. Males without the balancer constitute the test for suppressors of the Su(TPE) activity of M26 on the C62 telomeric insert. Males with the balancer act as a sibling control.

[c] Oregon R was a negative control.

[d] ND indicates not done.

[e] Mutant is a dominant suppressor of TPE at C62, in 3R TAS, but not at 11-5, in 2LTAS. *Df(3R)04661* removes part of 3R TAS. Deficiencies for 3R TAS are known to be dominant suppressors of TPE at the 3R telomere (Laurenti et al, 1995). The apparent enhancement of the suppression caused by M26 is likely due to a combination of suppression due to M26 with suppression due to the *mod* mutant.

[f] The *Df(3L)fz-M21* chromosome carries a suppressor of the M26 suppressor, but the *Df(3L)XG3* chromosome does not. The simplest explanation is that the observed effect is due to a genetic factor at an unrelated site.

Chromosome 3R TAS repeat unit

GTGAGGTCCGATCGGGTTGTCAAGAAGGCACGAACAGCCTCAGCAGCTAAGTGAGGTCCGATTGGGTTGTCAAGAAT
AGTGTGTTAGAGGGAGATGACAATGTAGTGAACGCCAGTGTGTATAGATATTAGAGAATATGTAGAAGAAGGGAAAT
GTAAGAAGATTCCTTCAGGTGAGGTCCGATCGGGTTGTCAAGAAGGCACGAACAACCTCTGCAGCTGCGTGAGGTCC
GATCGGGTTGTCAAGAATAGTGTGTTAGAGGGAGATGAAAATTCTGTCGAGCGCTGCGGCAGAGGCACGAACAACCT
CTGCAGCTGCGTGAGGTCCGATCGGGTTGTCAAGAATAGTGTGTTAGAGGGAGATGAAAATGTAGTGAACGCCAGTG
TGTATAGATATTAGAGAATATGTTGAAGAAGGGAAATGTAAGAAGATCCCTTCAGTCAAGTTTGACTGGTCGTGTTG
ATCGGTACTTGCTGCGCCGCCGCACCAAATAATAAACTGAATAAAGGAAATGGATGAGACACTAACTTATTAATAAT
ATATTAATTAACAATATTAATAATCGTTTTGTTCTTGCCGGTGTATAAAAGAAATTATATTTTTAAAACATTATCCT
TCTGGAAATCTTTTTTCAATTTTTATCGAATATAATCTTACAAAAGCAACTAACAAAAATTAATCTAAAAAATTTTC
GTATATTAAATTAAGTGACGATTAATACGAAAACTTACAAACAAATTATTGAAGTATTTGTTAGTTCGAAATTATAC
TAAAAATGTTTATACATCTTAAAAAGATATTTGATTATTATTATATTATTATATTTTTTGCATAAAAAATATACATT
TTTAATGTTCTCTGTTTTTGGTGTAAAAGCATTGCAAAAATATAACGACGCGTACACATATGTCGCAGCGTGACTGT
TCGCATTCTAGGAATTCCTTCTGTTATTTAACATTCTTATAAAATAGTAATATTGCGG

Chromosome 2L TAS repeat unit

ATCGACAATGCACGACAGAGGAAGCAGAACAGATATTTAGATTGCCTCTCATTTTCTCTCCCATATTATA
GGGAGAAATATGATCGCGTATGCGAGAGTAGTGCCAACATATTGTGCTCTTTGATTTTTTGGCAACCCAA
AATGGTGGCGGATGAACGAGATGATAATATATTCAAGTTGCCGCTAATCAGAAATAAATTCATTGCAACG
TTAAATACAGCACAATATATGATCGCGTATGCGAGAGTAGTGCCAACATATTGTGCTAATGAGTGCCTCT
CGTTCTCTGTCTTATATTACCGCAAACCCAAAAAGACAATACACGACAGAGAGAGAGAGCAGCGGAGATA
TTTAGATTGCCTATTAAATATGATCGCGTATGCGAGAGTAGTGCCAACATATTGTGCTCTCTATATAATG
ACTGCCTCTCATTCTGTCTTATTTTACCGCAAACCCAA

Figure S1: DNA sequence of a TAS-R repeat unit from Chromosome *3*R and a TAS-L repeat unit from Chromosomes *2*L and *3*L. Capture probe hybridization sequences are highlighted in yellow and single mismatch in red.

SUPPLEMENTARY REFERENCES

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