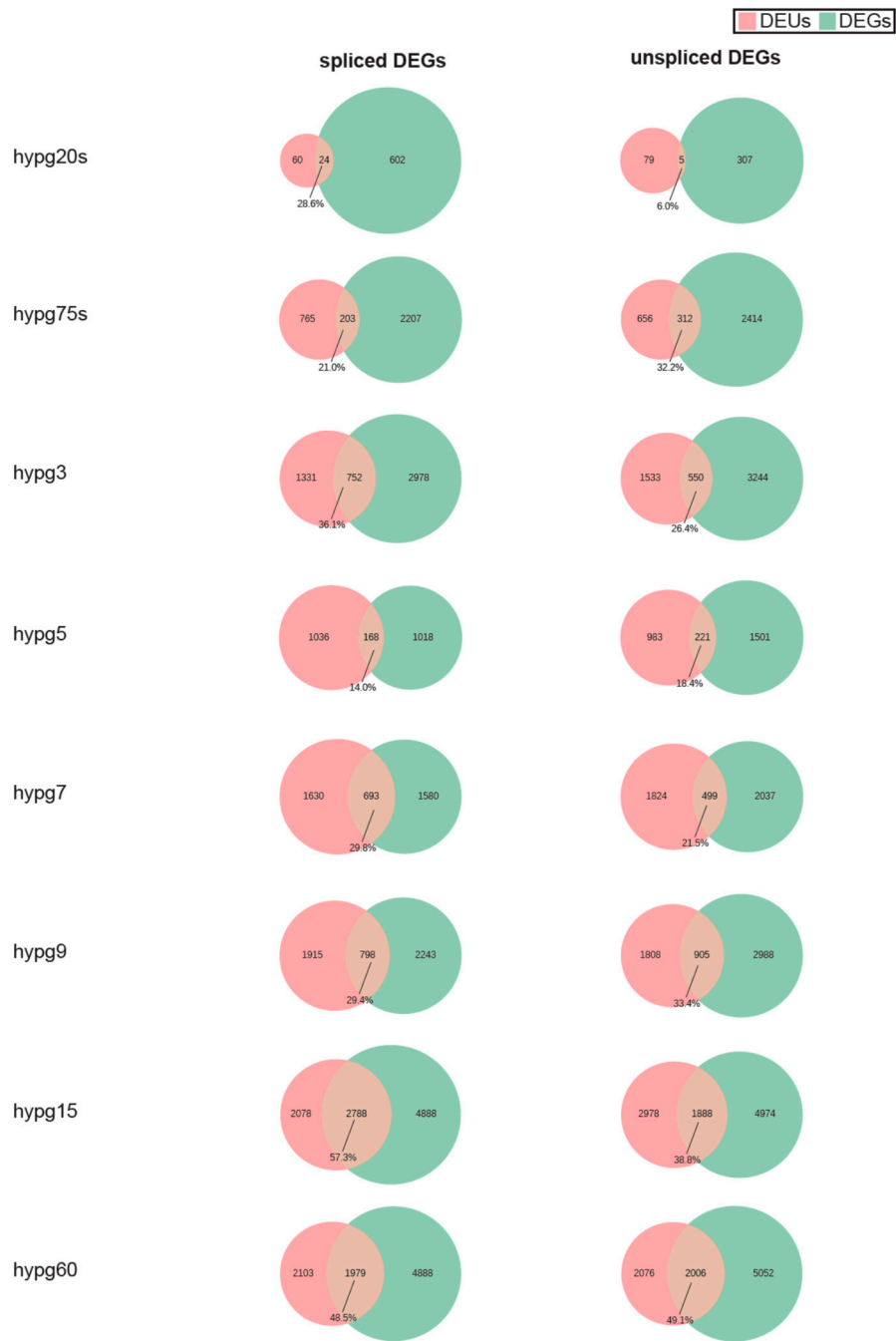
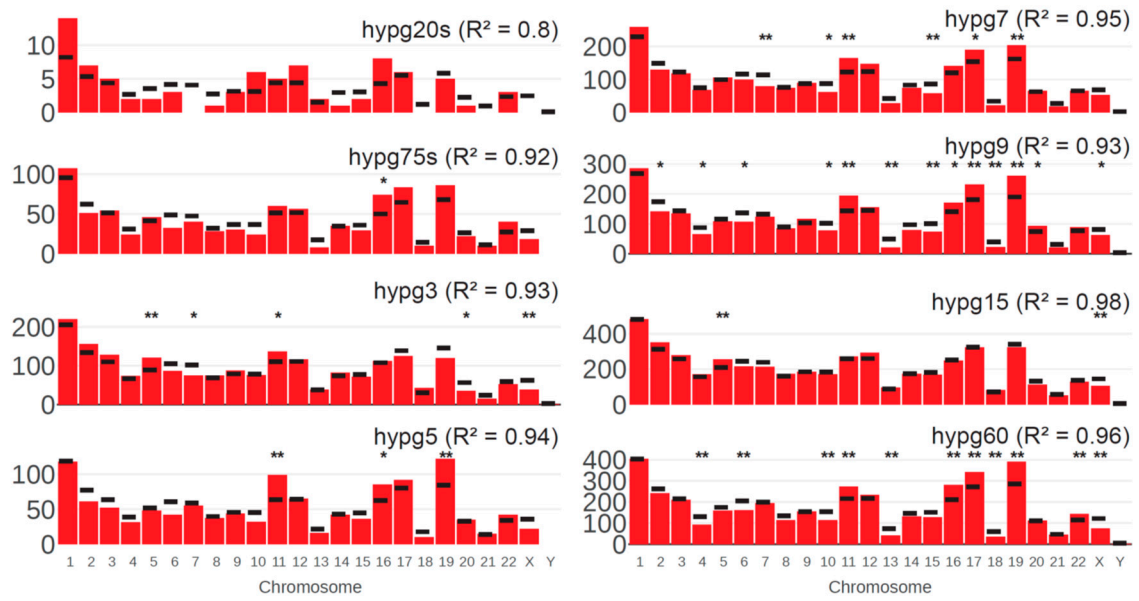


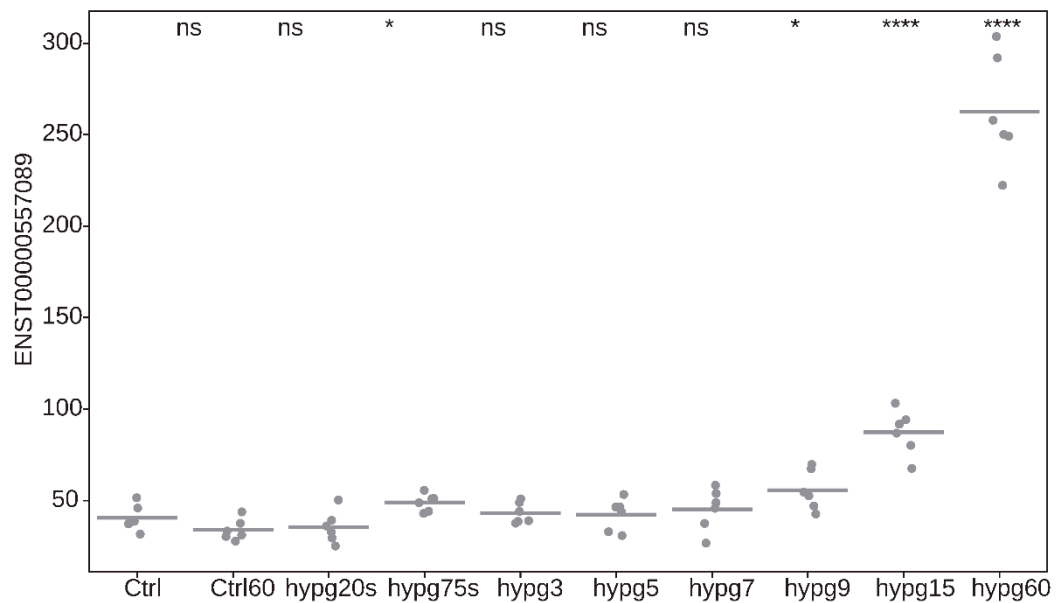
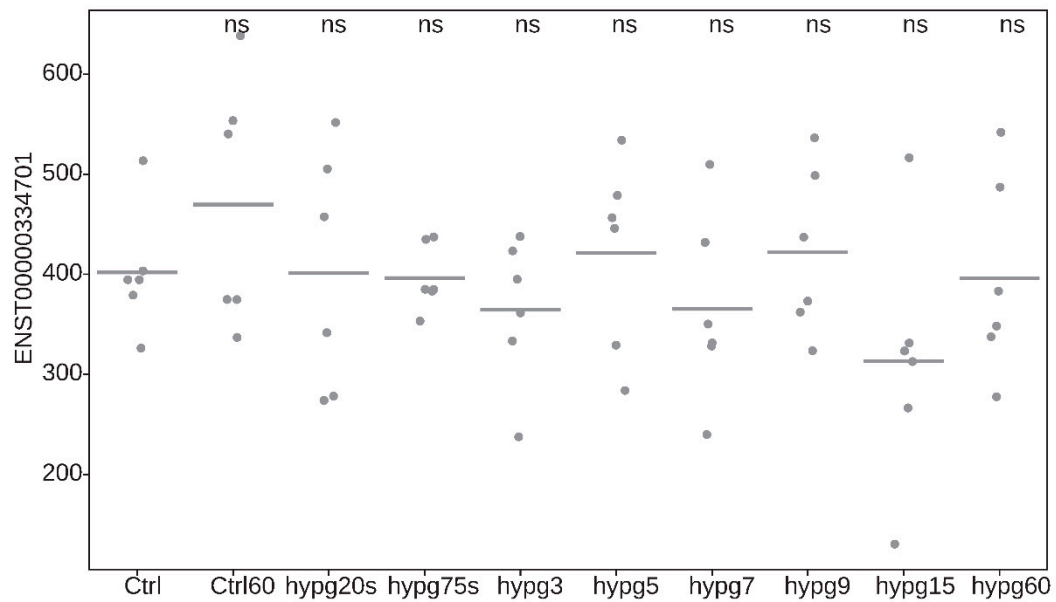
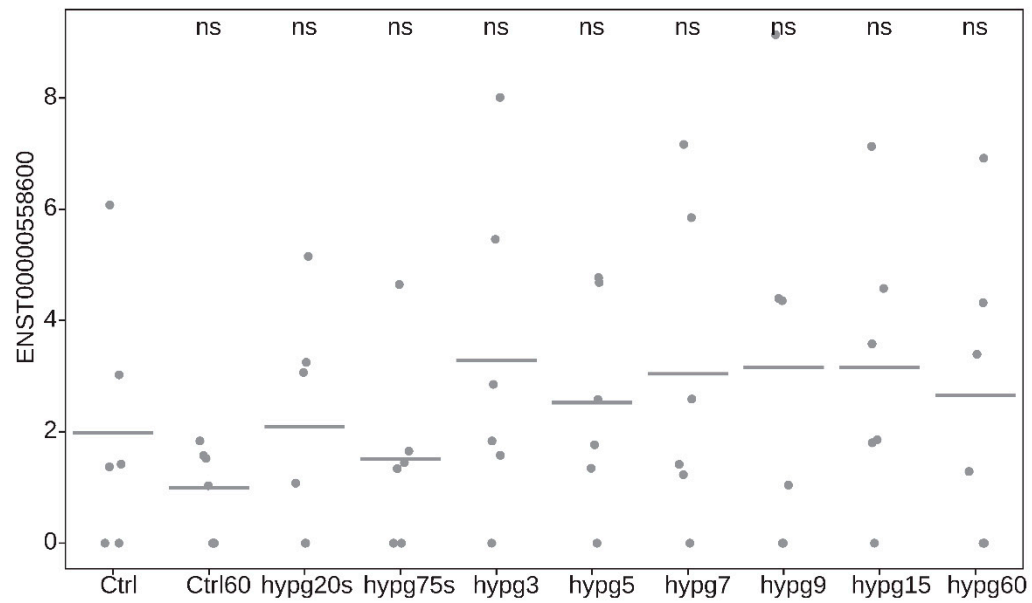
Supplementary Figure S1. Validation of 3d models from Figure 2. (a-b) The average location of chromosomes for all models was compared to each other. It is known from previous studies that chr16-chr22 behave very similar in altered gravity studies. It was controlled if they behave similarly when comparing the angular distance (as seen from the center of the nucleus) (a) and the Euclidean distance (length of the shortest connection between two point) (b) of chromosomes to each other. This is displayed as a clustering dendrogram and as a heatmap that indicates if two chromosomes have similar distances to other chromosomes (indicated in yellow, indicating proximity) or if they behave very differently (in blue, indicating remoteness). (c) The average radial distance of different parts of chromosomes 18 and 19. It is known from external studies that chr18 tends to localize more at the lamina of the nucleus and chr19 more in the center. It was controlled if the 3d models indicate such a predicted behavior.

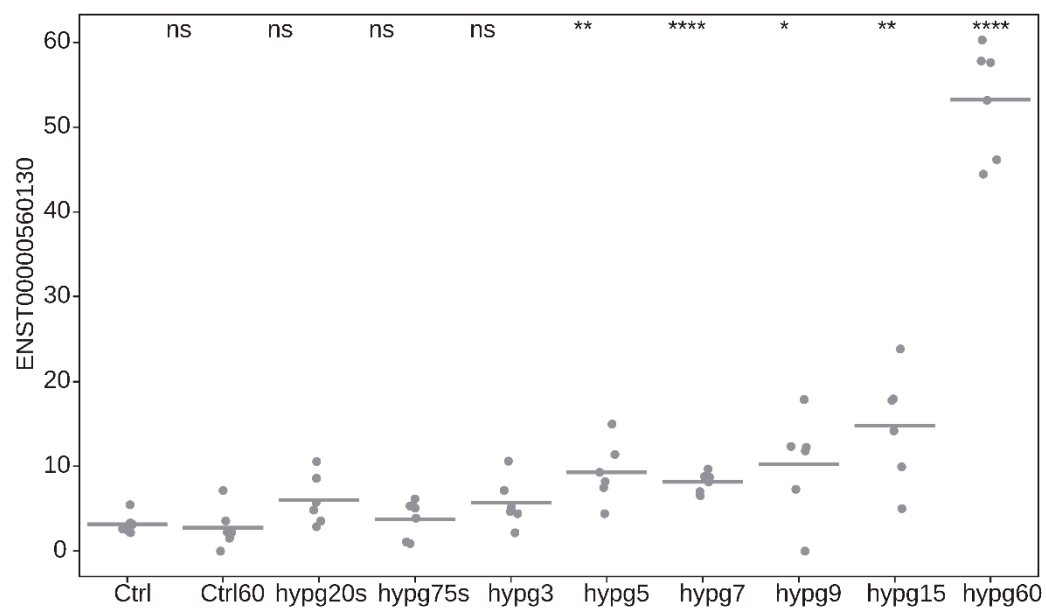
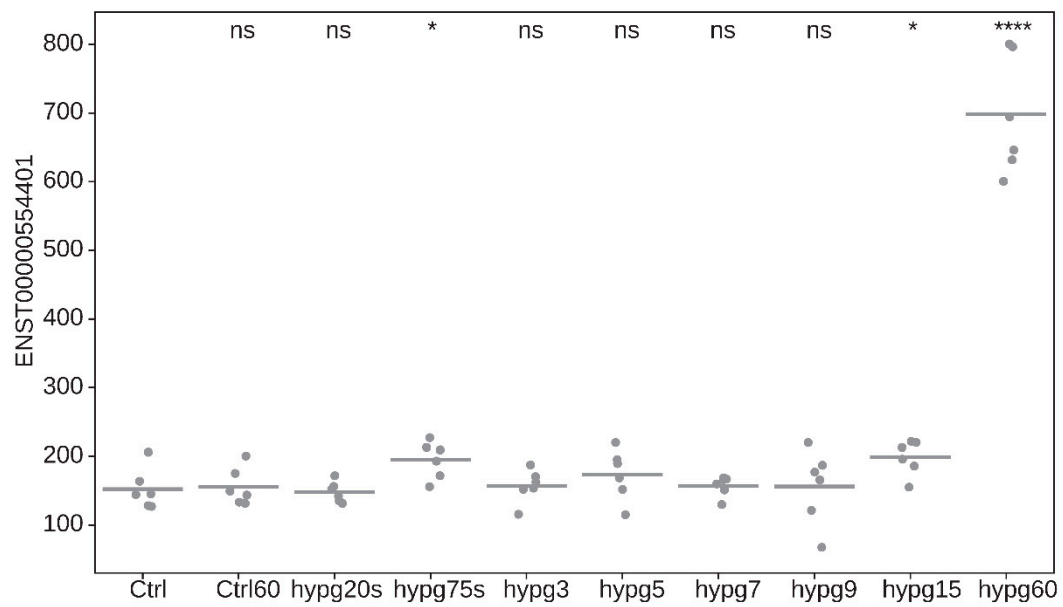
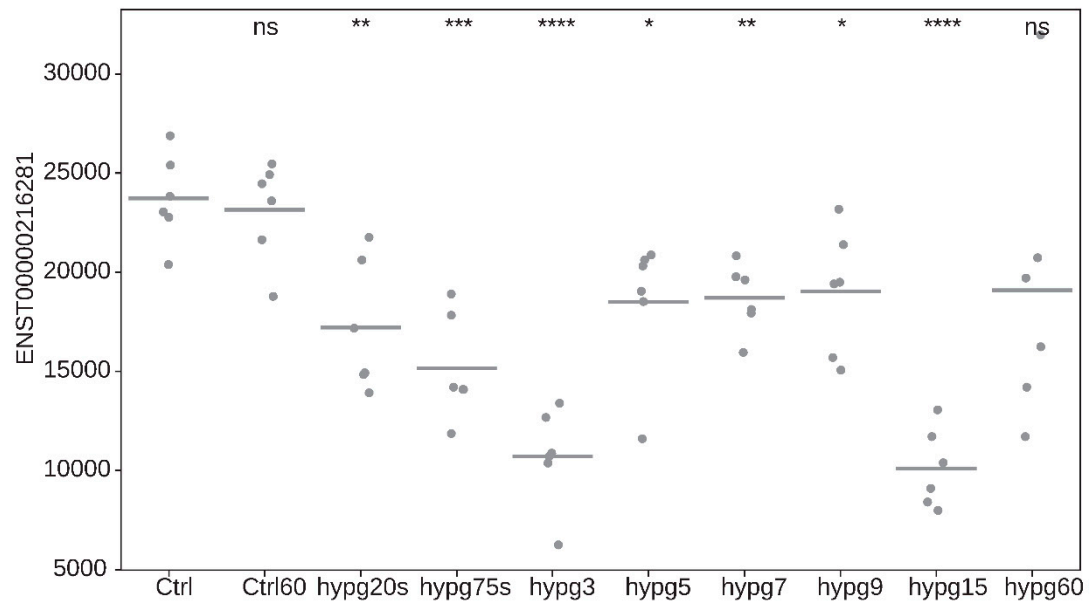


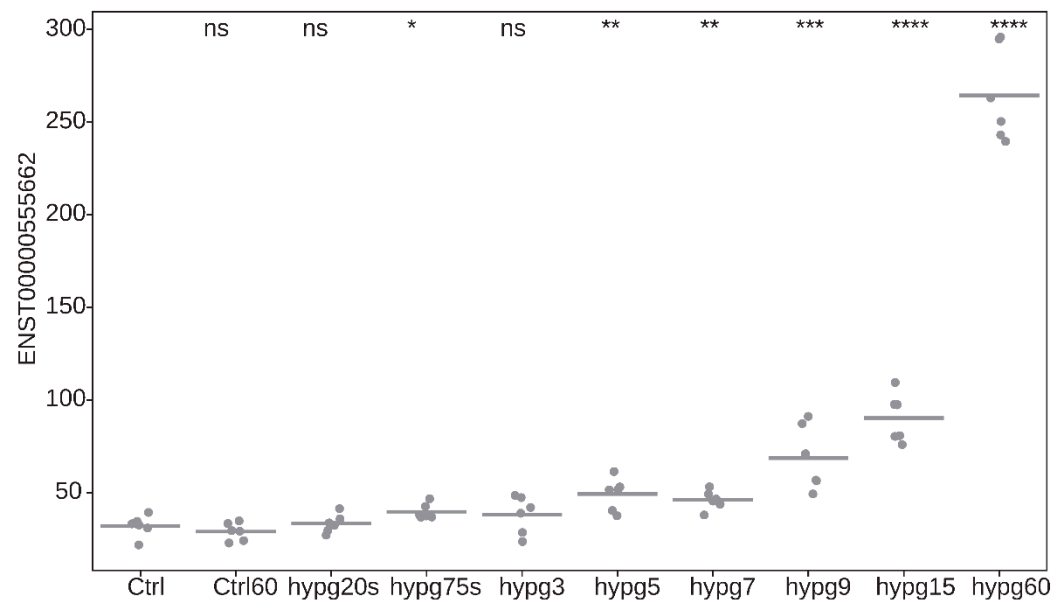
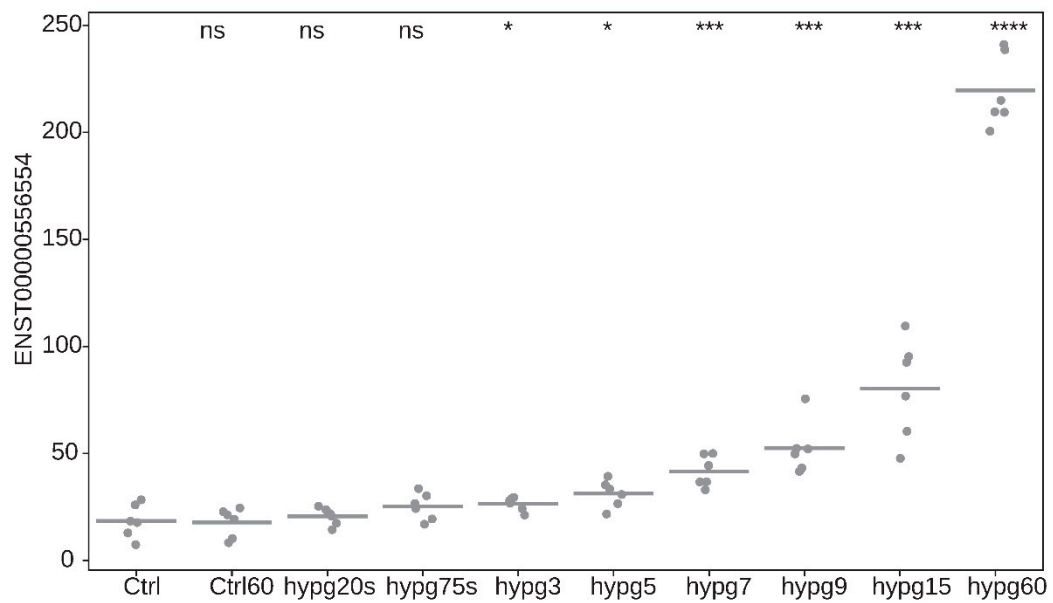
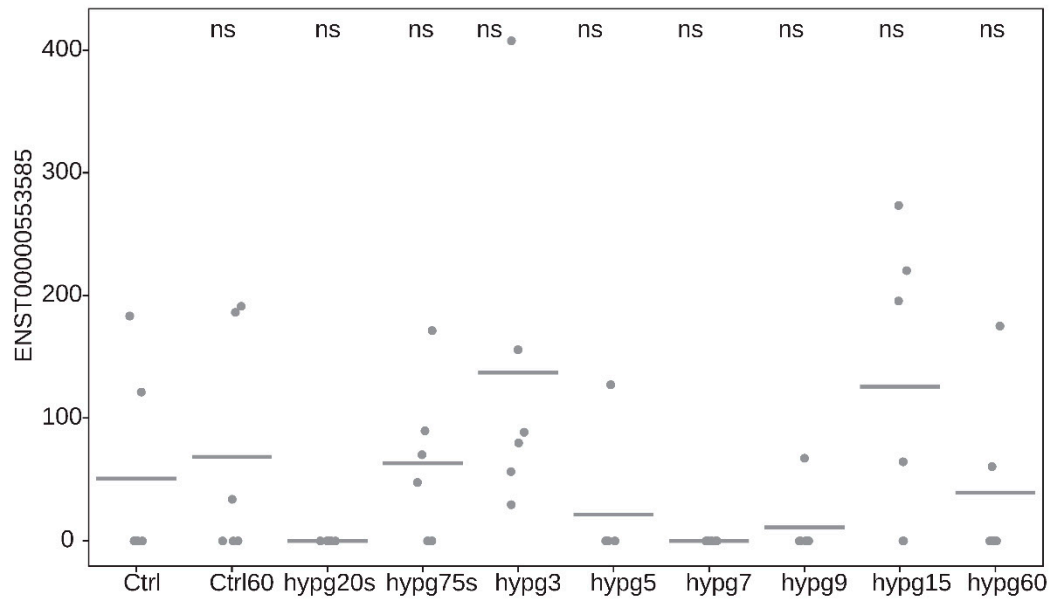
Supplementary Figure S2. Overlap between genes with differential exon usage (DEU, red) with genes that are differentially expressed (DEG, green). Fraction of overlapping DEU compared to all DEU is indicated in percent. Additional to Figure 9d.

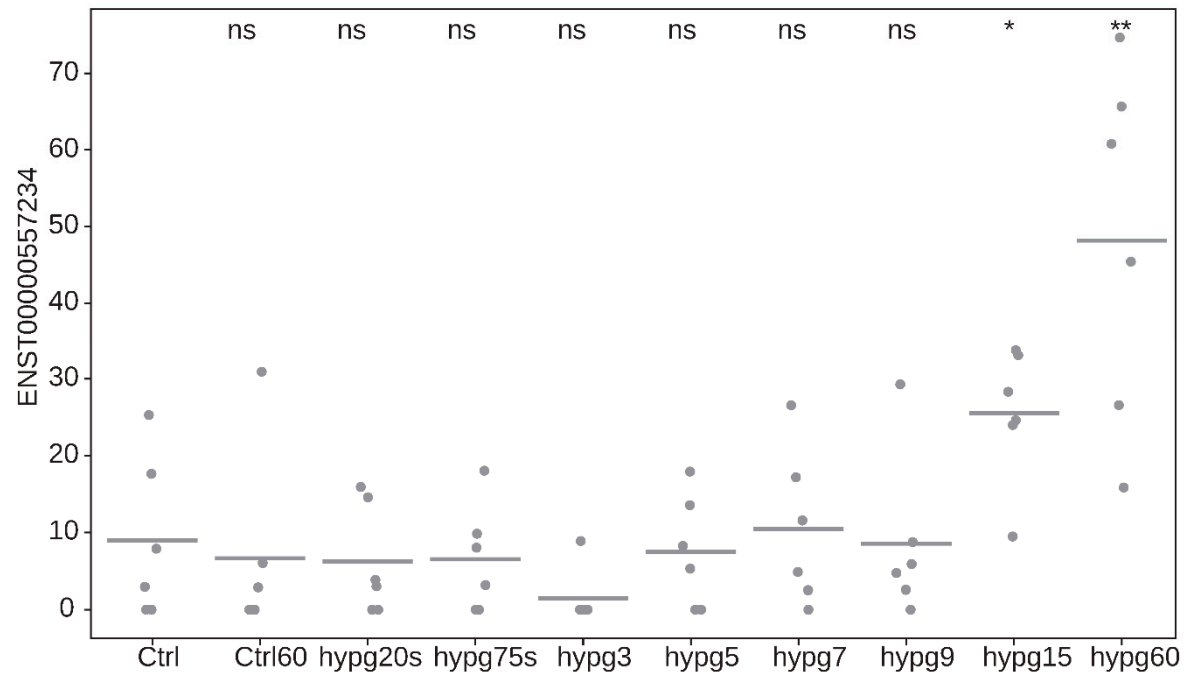


Supplementary Figure S3. Distribution of DEU genes along chromosomes. Genes from Figure 9, methodology as in Figure 7. Significant deviations from expectation are indicated by */** for a p-value below 0.05/0.01, based on a Fisher's exact test.









Supplementary Figure S4. Counts of all samples for each transcript of HSP90AA1, from Figure 10. Significant deviations from expectation are indicated by */**/***/**** for a p-value below 0.05/0.01/0.001/0.0001, based on a t test.

	Treatment	Effect time	up	down	total	SG - coding	P-Bodies	SG - Protein	SG - coding	P-Bodies	SG - Protein
Exp. Set 2	hypp20s	20s	962	753	1715	**		**	**		
	hypp75s	75s	2096	1830	3926	**		**	**		**
	hypp3	3min	3001	3442	6443	**	**	**	**	**	**
	hypp5	5min	896	535	1431	**		**	**		**
	hypp7	7min	1021	1018	2039	**	**	**	**	**	**
	hypp9	9min	1470	1164	2634	**		**	**	**	**
	hypp15	15min	4191	4537	8728	**	**	**	**	**	**
	hypp60	60min	3704	3295	6999	**		**	**	**	**
	Ctrl60-Ctrl	(60min)	4	7	11						
	hypp20s	20s	373	253	626	**		**	**	**	**
Exp. Set 2 spliced	hypp75s	75s	657	1753	2410	**		**	**	**	**
	hypp3	3min	963	2767	3730	**		**	**	**	**
	hypp5	5min	243	943	1186	**	**	**	**	**	**
	hypp7	7min	290	1983	2273	**	**	**	**	**	**
	hypp9	9min	500	2541	3041	**	**	**	**	**	**
	hypp15	15min	1323	6393	7676	**	**	**	**	**	**
	hypp60	60min	1855	5012	6867	**	**	**	**	**	**
	Ctrl60-Ctrl	(60min)	8	7	15						
	hypp20s	20s	252	60	312	**	**	**	**	**	**
	hypp75s	75s	2440	286	2726	**	**	**	**	**	**
Exp. Set 2 unspliced	hypp3	3min	3028	766	3794	**	**	**	**	**	**
	hypp5	5min	1629	93	1722	**	**	**	**	**	**
	hypp7	7min	2314	222	2536	**	**	**	**	**	**
	hypp9	9min	3599	294	3893	**	**	**	**	**	**
	hypp15	15min	5382	1580	6962	**	**	**	**	**	**
	hypp60	60min	3911	1147	7058	**	**	**	**	**	**
	Ctrl60-Ctrl	(60min)	0	0	0						
	hypp3	3min	2464	2593	5057	**	**	**	**	**	**
	hypp15	15min	1844	3230	5074	**	**	**	**	**	**
	instant	5min	8043	7030	15073	**	**	**	**	**	**
Exp. Set 1	wait1min	5min+1min	7906	7020	14926	**	**	**	**	**	**
	wait15min	5min+15min	8100	7130	15230	**	**	**	**	**	**
	wait15min-instant	5min+15min	15	56	71						
	heat	42°C	1279	3719	4998	**	**	**	**	**	**
	GSE138290	2mM H2O2	1023	46	1069	**	**	**	**	**	**
	GSE145453	anti CD3/CD28 antibodies	1081	663	1744	**	**	**	**	**	**
	GSE145453	+ 100ng/ml chemokines CXCL12 & CCL19	981	506	1487	**	**	**	**	**	**
	GSE85201	activation with 50 mM PMA + 1µM Ionomycin	405	379	784	**	**	**	**	**	**
	GSE174380	100IU/ml Interferon IFNβ	246	391	637	**	**	**	**	**	**
	GSE174380	100IU/ml Interferon IFNβ	359	98	457	**	**	**	**	**	**
External GEO reference data sets	GSE174380	100IU/ml Interferon IFNβ	347	204	551	**	**	**	**	**	**
	GSE93594	20ng/ml phorbol ester PMA	5840	5779	11619	**	**	**	**	**	**
	GSE166630	pEF-GFP transfection with Lipofectamine LTX	68	88	156	**	**	**	**	**	**
	GSE134401	NOTCH inhibition with DAPT	571	397	968	**	**	**	**	**	**
	GSE134401	NOTCH inhibition with RIN1	17	29	46	**	**	**	**	**	**
	GSE134401	NOTCH inhibition with siRBP1	796	644	1440	**	**	**	**	**	**
	GSE120612	10µM topoisomerase II inhibitor etoposide	5090	4656	9746	**	**	**	**	**	**
	GSE160349	2µM NOTCH inhibitor Chidamide	5802	4785	10587	**	**	**	**	**	**
	GSE182659	1µM CDK4/6 inhibitor Palbociclib	2512	2476	4988	**	**	**	**	**	**
	GSE139621	30 nM splicing modulator H388800	7173	6674	13847	**	**	**	**	**	**
	GSE139621	30 nM splicing modulator H388800	4878	5054	9932	**	**	**	**	**	**
	GSE139621	10µM Ubiquitin-spec. prot. 7 inhibitor P5091	6356	5606	11962	**	**	**	**	**	**
	GSE97435	1µM NOTCH inhibitor GSI	347	351	698	**	**	**	**	**	**
	GSE97435	500nM BRD4 histone acetylase inhibitor JQ1	4291	5145	9436	**	**	**	**	**	**

Supplementary Table S1. Extension to Table 1. For all analyzed data sets, the significantly upregulated and downregulated genes were compared to the RNA composition of stress granules and P bodies, and the protein composition of stress granules. If significantly more (**/*: FDR-adjusted P value < 0.01/0.05) or less (-**/-*: FDR-adjusted P value < 0.01/0.05) differential genes were also contained in the stress granules / P bodies data set, this was indicated. This analysis was separately performed for upregulated and for downregulated genes.