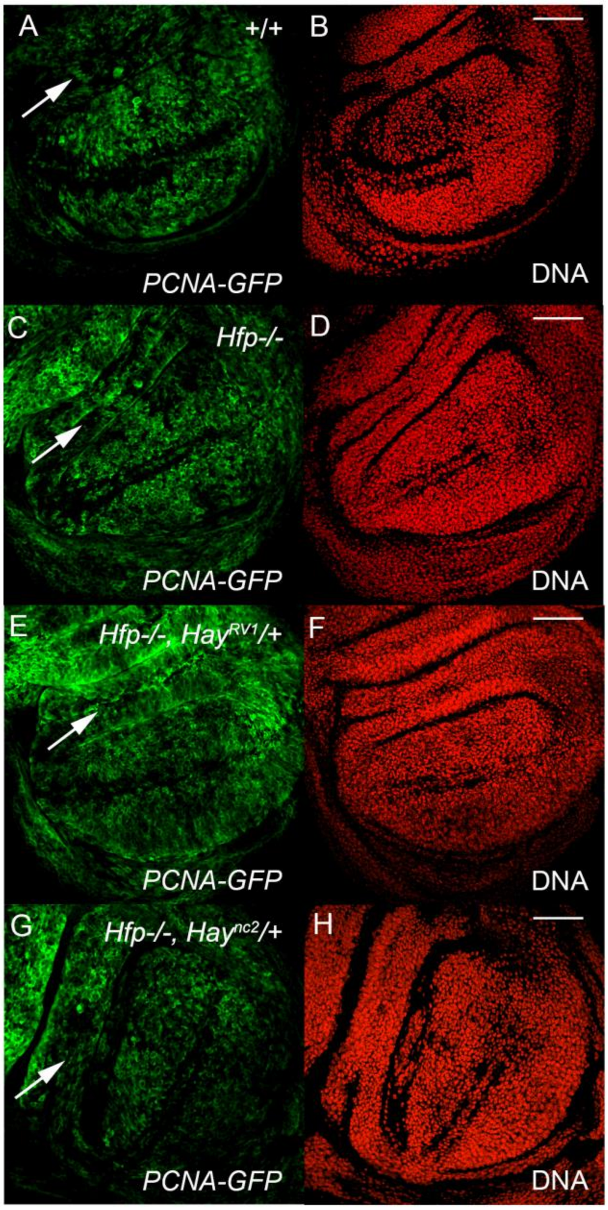
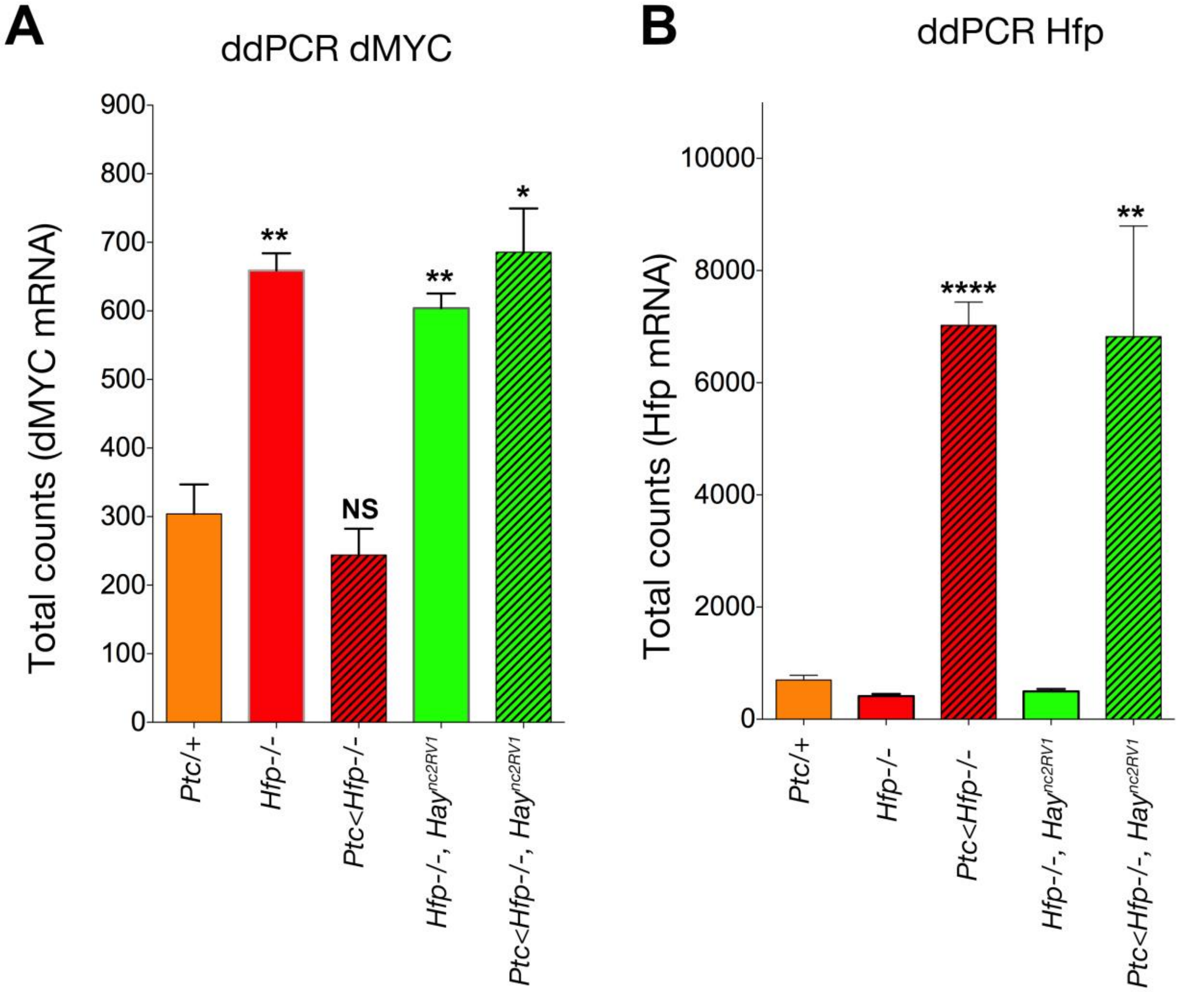
Supplementary Figure 1 - PCNA-GFP activity in pouch and hinge of the 3rd instar wing imaginal disc for the genotypes marked. The wing pouch surrounds the hinge, which is marked with a white arrow. PCNA-GFP is shown in green and DNA in red. All scale bars represent 50um.



Supplementary Figure 2 - ddPCR to measure **A** - *dMYC* and **B** - *Hfp* mRNA abundance for the genotypes marked. Statistical tests were performed with Graphpad Prism 6 using unpaired 2-tailed t-test with 95% confidence interval. Error bars represent SEM and according to the Graphpad classification of significance points * is significant (p=0.01 to 0.05), ** is very significant p=0.001 to 0.01, *** extremely significant (p=0.0001 to 0.001) and **** extremely significant (p<0.0001). See supplementary Table 7 for mean, SEM and biological replicates.



Supplementary Table 1 - Quantification of larval area (from Figure 1). Mean pixel area (± SEM) for each genotype.

Genotype	**larval area pixels**	**SEM**	**n**
w1118	101665	1100	9
Hfp -/ -	125928	2870	10
Hfp -/ -, Hay^{nc2RV1}*/ +*	157333	5068	11
Hfp -/ -, Hay^{nc2RV3}*/ +*	157912	3233	6
Hfp -/ -, Hay^{nc2RV7}*/ +*	161613	3472	7
Hfp -/ -, Hay^{nc2}*/ +*	103516	4206	7

Supplementary Table 2 - Quantification of mitoses in the wing pouch and hinge region (from Figure 1).

Genotype	**PH3**	**SEM**	**n**
w1118	140.7	7.0	13
Hfp -/ -	175.0	9.6	14
Hay^{nc2RV1}*/ +*	129.8	2.9	9
Hfp -/ -, Hay^{nc2RV1}*/ +*	212.9	8.9	15
Hay^{nc2}*/ +*	141.4	6.4	11
Hfp -/ -, Hay^{nc2}*/ +*	114.1	3.8	8
Hay^{nc2RV7}*/ +*	120.7	5.6	7
Hfp -/ -, Hay^{nc2RV7}*/ +*	226.1	15.9	8
Hay^{pBac}*/ +*	130.2	4.7	9
Hfp -/ -, Hay^{pBac}*/ +*	115.5	4.3	6

Supplementary Table 3 - Quantification of *dMYC-lacZ* activity (from Figure 2).

Genotype	B-gal total	SEM	n	B-gal ZNC	SEM	n
w1118	888.3	86.74	6	108.8	30.52	5
Hfp-/-	1462	61.74	6	216.0	23.16	4
Hfp-/-, Hay^{nc2RV1}/ +	1794	70.69	7	213.4	12.75	7
Hfp-/-, Hay^{nc2}/ +	969.4	67.57	6	78.35	18.31	4

Supplementary Table 4 - ddPCR for *MYC* and *Hfp* mRNA abundance in wing imaginal discs, normalised to tubulin. n= biological replicates for each technical triplicate (from Figure 2).

Genotype	ddMYC	SEM	n	ddHfp	SEM	n
w1118	51.7	1.1	4	49.6	7.7	4
Hfp-/-	96.5	6.5	3	21.2	1.5	4
Hay^{nc2RV1}/ +	52.4	5.2	3	45.5	7.4	3
Hfp-/-, Hay^{nc2RV1}/ +	99.0	12.8	4	15.5	1.6	3
Hay^{nc2}/ +	30.1	0.9	4	38.1	3.2	3
Hfp-/-, Hay^{nc2}/ +	57.1	3.6	3	21.2	1.5	3
Hay^{pBac}/ +	43.3	2.4	3	54.0	2.6	3
Hfp-/-, Hay^{pBac}/ +	57.8	4.0	3	24.8	0.6	3

Supplementary Table 5 - Quantification of PCNA-GFP activity in pouch and hinge (from Figure 3). The relative intensity of GFP (mean pixel intensity ± SEM) is shown for each genotype.

Genotype	PCNA	SEM	n
w1118	695.2	85.44	5
Hfp-/-	1175	111.0	5
Hfp-/-, Hay^{nc2RV1}/ +	1634	69.12	10
Hfp-/-, Hay^{nc2}/ +	713.5	78.63	6

Supplementary Table 6 - Quantification of S phase using BrdU (from Figure 3). Number of BrdU positive cells (± SEM) for each genotype.

Genotype	BrdU	SEM	n
w1118	340.44	18.550	10
Hfp-/-	459.62	19.840	10
Hfp-/-, Hay^{nc2RV1}/ +	553.27	25.430	10
Hfp-/-, Hay^{nc2}/ +	341.73	26.300	8

Supplementary Table 7 - ddPCR to measure *dMYC* and *Hfp* mRNA abundance for the genotypes marked. n= biological replicates for each technical triplicate.

Genotype	ddMYC	SEM	n	ddHfp	SEM	n
Ptc-Gal4/ +	304	43	6	698	84	3
Hfp-/-	659	25	3	411	41	3
Ptc-Gal4/ +, Hfp-/-	244	38	3	7025	415	3
Hfp-/-, Hay^{nc2RV1}/ +	604	21	3	498	40	3
Ptc-Gal4/ +, Hfp-/-, Hay^{nc2RV1}/ +	686	64	3	6822	1973	3

Supplementary Table 8 - Quantification of larval area (from Figure 4). Mean pixel area (± SEM) for each genotype.

Genotype	larval area	SEM	n
Arm/ +	100533	1423	6
w1118	101665	1100	9
Hfp EP	125928	2870	10
Arm <Hfp EP	113450	4907	6
Hfp EP, Hay RV1	157333	5068	11
Arm <Hfp EP, Hay RV1	134980	3969	6
dm P0/ +	88149	2792	9
dm P0/ +; Hfp-/-	89277	10052	10
dm P0/ +; Hay RV1	103398	4325	8
dm P0/ +; Hfp-/-, Hay RV1	106722	2652	9

Supplementary Table 9 - ddPCR to measure *dMYC* for the genotypes marked (from Figure 4). n= biological replicates.

Genotype	ddMYC	SEM	n
+/ +	51.70	1.13	4
Hfp-/ -	96.53	6.50	3
Hay^{nc2RV1}/ +	52.40	5.17	3
Hfp-/ -, *Hay*^{nc2RV1}/ +	99.03	12.76	4
dm^{P0}/ +	18.88	3.02	4
dm^{P0}/ +; *Hfp*-/ -	44.41	9.00	4
dm^{P0}/ +; *Hay*^{nc2RV1}/ +	23.42	7.65	4
dm^{P0}/ +; *Hfp*-/ -, *Hay*^{nc2RV1}/ +	42.11	12.0	4

Supplementary Table 10 - Quantification of mitoses in the wing pouch and hinge region following the *dMYC* rescue (from Figure 4).

Genotype	**PH3**	**SEM**	**n**
+/ +	140.7	7.0	13
dm-/ +	142.4	4.8	6
Hfp-/ -	175.0	9.6	14
dm-/ +; *Hfp*-/ -	138.0	6.2	8
Hay^{nc2RV1}/ +	129.8	2.9	9
dm-/ +; *Hay*^{nc2RV1}/ +	121.8	10.1	9
Hfp-/ -, *Hay*^{nc2RV1}/ +	212.9	8.9	15
dm-/ +; *Hfp*-/ -, *Hay*^{nc2RV1}/ +	128.2	9.0	16
Hay^{nc2}/ +	141.4	6.4	11
dm-/ +; *Hay*^{nc2}/ +	138.8	7.3	7
Hfp-/ -, *Hay*^{nc2}/ +	114.1	3.8	8
dm-/ +; *Hfp*-/ -, *Hay*^{nc2}/ +	125.8	5.4	6

Supplementary Table 11 - ChIP for Ser 5 RNA Pol II followed by qPCR with amplicons proximal to the *dMYC* TSS for genotypes as marked (from Figure 5). n= biological replicates for each technical triplicate.

Genotype	**Amplicon**	% Ser5	SEM	n
w1118	*MYC1*	0.368	0.07	4
Hfp-/-		0.393	0.11	3
$Hay^{nc2RV1}/+$		0.230	0.04	4
Hfp-/-, $Hay^{nc2RV1}/+$		0.330	0.04	3
$Hay^{nc2}/+$		0.218	0.03	3
Hfp-/-, $Hay^{nc2}/+$		0.313	0.03	3
Mock IP		0.077	0.02	5
w1118	*MYC2*	4.890	0.29	6
Hfp-/-		3.018	0.44	5
$Hay^{nc2RV1}/+$		0.658	0.12	3
Hfp-/-, $Hay^{nc2RV1}/+$		1.462	0.05	3
$Hay^{nc2}/+$		1.147	0.05	3
Hfp-/-, $Hay^{nc2}/+$		0.749	0.05	3
Mock IP		0.063	0.01	6
w1118	*MYC3*	0.808	0.04	4
Hfp-/-		1.147	0.17	4
$Hay^{nc2RV1}/+$		0.310	0.05	4
Hfp-/-, $Hay^{nc2RV1}/+$		0.642	0.11	3
$Hay^{nc2}/+$		0.322	0.04	3
Hfp-/-, $Hay^{nc2}/+$		0.478	0.02	3
Mock IP		0.065	0.02	6
w1118	*MYC4*	1.109	0.07	3
Hfp-/-		0.930	0.16	4
$Hay^{nc2RV1}/+$		0.305	0.08	4
Hfp-/-, $Hay^{nc2RV1}/+$		0.519	0.07	3
$Hay^{nc2}/+$		0.273	0.04	3
Hfp-/-, $Hay^{nc2}/+$		0.389	0.01	3

Mock IP		0.065	0.01	6

Supplementary Table 12 - ChIP for Total RNA Pol II followed by qPCR with amplicons proximal to the dMYC TSS for genotypes as marked (from Figure 5). n= biological replicates for each technical triplicate.

Genotype	**Amplicon**	% Pol II	SEM	n
w1118	*MYC1*	0.213	0.052	3
Hfp-/-		0.189	0.013	3
$Hay^{nc2RV1}/+$		0.123	0.008	3
Hfp-/-, $Hay^{nc2RV1}/+$		0.188	0.032	4
$Hay^{nc2}/+$		0.522	0.040	3
Hfp-/-, $Hay^{nc2}/+$		0.182	0.048	5
w1118	*MYC2*	1.000	NA	3
Hfp-/-		0.678	0.058	3
$Hay^{nc2RV1}/+$		0.427	0.008	3
Hfp-/-, $Hay^{nc2RV1}/+$		0.322	0.006	4
$Hay^{nc2}/+$		0.912	0.034	3
Hfp-/-, $Hay^{nc2}/+$		0.793	0.100	5
w1118	*MYC3*	0.325	0.029	3
Hfp-/-		0.202	0.025	3
$Hay^{nc2RV1}/+$		0.109	0.015	3
Hfp-/-, $Hay^{nc2RV1}/+$		0.097	0.008	4
$Hay^{nc2}/+$		0.290	0.045	3
Hfp-/-, $Hay^{nc2}/+$		0.195	0.029	5
w1118	*MYC4*	0.283	0.053	3
Hfp-/-		0.191	0.044	3
$Hay^{nc2RV1}/+$		0.084	0.012	3
Hfp-/-, $Hay^{nc2RV1}/+$		0.084	0.012	4
$Hay^{nc2}/+$		0.213	0.012	3
Hfp-/-, $Hay^{nc2}/+$		0.160	0.030	5