Supplementary Table 1. Modifiers of *hop*$^{Tum\text{-}l}$ tumorigenesity

Modifier of *Tum-l*	Allele tested	Tumor Index	Protein product/function	Category
E(tum-l)				
Tp(3;Y)ry506-85C	--	1.89±0.16	--	--
unchained	*unch[k15501]*	1.74±0.19	Unknown	--
TBP-associated factor 1	*Taf1[1]*	1.63±0.06	TAFII-230 TBP-binding	Transcription
Df(2R)H3C1	--	1.58+0.09	--	--
Cdc27	*Cdc27[L7123]*	1.45±0.05	Cell cycle	Cell cycle
abnormal wing discs	*awd[j2A4]*	1.42±0.06	nm23-H1; Nucleoside-diphosphate kinase	Metabolism
Ets at 97D	*Ets97D[tne-4]*	1.39±0.12	Winged-helix DNA binding domains	Transcription
spindle E	*spn-E[1]*	1.38±0.08	DEAD-box helicase; RNAi component	Chromatin modification
HEM-protein	*Hem[03335]*	1.34±0.09	Receptor binding; Cell shape	Cytoskeleton
Toll	*Tl[r4]*	1.33±0.04	Cytokine receptor	Signaling
sallimus	*sls[1]*	1.31±0.08	Myosin-light-chain kinase activity	Cytoskeleton
Krüppel	*Kr[1]*	1.29±0.16	Zinc finger, transcription repressor	Transcription
plume	*plume[k00308]*	1.28±0.11	Unknown	--
rhino	*rhi[02086]*	1.24±0.12	Chromodomain; chromatin-binding	Chromatin modification
Suppressor of variegation 2-5	*Su(var)205[5]*	1.18±0.06	Heterochromatin Protein 1 (HP1)	Chromatin modification
Rpd3	*Rpd3[04556]*	1.17±0.08	HDAC	Chromatin modification
bellwether	*blw[1]*	1.07±0.06	Mitochon. ATP synthase	Metabolism
knirps	*kni[6]*	0.98±0.07	Transcription factor	Transcription
Suppressor of variegation 3-4	*Su(var)3-4[1]*	0.94±0.04	Unknown	Chromatin modification
moira	*mor[1]*	0.93±0.06	Chromatin binding; brahma complex	Chromatin modification
hairy	*h[08247]*	0.91±0.07	HLH transcriptional repressor	Transcription
labial	*lab[4]*	0.91±0.06	Homeodomain, transcription	Transcription
polo	*polo[01673]*	0.89±0.05	Kinase, cell devison	Cell cycle
Deformed	*Dfd[6]*	0.88±0.05	Homeodomain, transcription	Transcription
Enhancer of bithorax	*E(bx)[ry122]*	0.87±0.21	NURF complex	Chromatin modification
Vacuolar H+-ATPase 55kD B subunit	*Vha55[j2E9]*	0.85±0.13	H^+-ATPase	Metabolism
gooseberry	*gsb[01155]*	0.84±0.06	Homeodomain, transcription	Transcription
Protein tyrosine phosphatase 69D	*Ptp69D[1]*	0.84±0.04	Tyrosine phosphatase	Signaling
Suppressor of variegation 3-9	*Su(var)3-9[1]*	0.83±0.03	Histone H3-K9 methyltransferase	Chromatin modification
domino	*dom[k08108]*	0.82±0.03	SNF2-related ATPase	Chromatin modification
piwi	*piwi[06843]*	0.82±0.04	RNAi component	Chromatin modification
Suppressor of variegation 2-10	*Su(var)2-10[03697]*	0.80±0.04	PIAS; nuclear lamina component	Signaling/Chromatin modification
Su(Tum-l)				
even skipped	*eve[3]*	0.08±0.02	Homeodomain	Transcription
baboon	*babo[32]*	0.02±0.01	Activin Type I receptor	Signaling
Serrate	*Ser[VX82]*	0.01±0.00	Notch ligand	Signaling
Df(3L)Exel6111	--	0.00±0.00	--	--
lethal with a checkpoint kinase	*lack[KG07014]*	0.00±0.00	Smurf, HECT Ubiquitin ligase	Signaling

hop$^{Tum\text{-}l}$*/FM7* females were mated to *mutant/Balancer* males. Mutant alleles used for testing are listed in column 2. Tumor indices were calculated from *hop*$^{Tum\text{-}l}$/+; *mutant*/+ F1 progeny flies. "—" indicates functions or candidate genes are unknown.