

NuRD complex subunit	Genotype crossed to <i>y w; ush^{VX22}, MSN-C/CyO y+ or y w; MSN-C</i>	genetic background (selected based on <i>MSN-C</i> , <i>y</i> and/or <i>Tb</i> phenotypic markers)	number of <i>MSN</i> larvae tested	number of <i>MSN</i> larvae with $\geq 10x$ <i>Im</i> *	% larvae w/ $\geq 10x$ <i>Im</i> *	Estimated penetrance
	<i>w¹¹¹⁸</i>	<i>y w; ush^{VX22}, MSN-C/+</i>	32	3	9.4	9.4
	<i>y; ush^{r24}/CyO y+ #</i>	<i>y w; ush^{VX22}, MSN-C/ush^{r24}</i>	14	14	100.0	100.0
dMTA-1like	<i>w¹¹¹⁸; MTA1-like^{d09140}/TM6B, Tb¹ +</i>	<i>w¹¹¹⁸/yw; MSN-C/+; MTA1-like^{d09140}/+</i>	28	2	7.1	7.1
		<i>w¹¹¹⁸/yw; ush^{VX22}, MSN-C/+; MTA1-like^{d09140}/+</i>	48	25	52.1	52.1
	<i>y¹ w*; MTA1-like^{Mi01790} **</i>	<i>y w; MSN-C/+; MTA1-like^{Mi01790}/+</i>	31	1	3.2	3.2
		<i>y w; ush^{VX22}, MSN-C/+; MTA1-like^{Mi01790}/+</i>	38	28	73.7	73.7
dp66	<i>w¹¹¹⁸; simj^{BG00403}/TM6B, Tb¹ +</i>	<i>w¹¹¹⁸/yw; MSN-C/+; simj^{BG00403}/+</i>	26	0	0.0	0.0
		<i>w¹¹¹⁸/y w; ush^{VX22}, MSN-C/+; simj^{BG00403}/+</i>	39	17	43.6	43.6
	<i>simj⁰¹⁸¹⁴ ry⁵⁰⁶ **</i>	<i>y w/+; MSN-C/+; simj⁰¹⁸¹⁴ ry⁵⁰⁶/+</i>	40	2	5.0	5.0
		<i>y w/+; ush^{VX22}, MSN-C/+; simj⁰¹⁸¹⁴ ry⁵⁰⁶/+</i>	61	31	50.8	50.8
dRpd3	<i>y¹ w*; HDAC1¹²⁻³⁷/TM6B, Tb¹ *</i>	<i>y w; MSN-C/+; HDAC1¹²⁻³⁷ /+</i>	30	15	50.0	50.0
		<i>y w; ush^{VX22}, MSN-C/+; HDAC1¹²⁻³⁷ /+</i>	42	35	83.3	83.3
	<i>HDAC1⁰⁴⁵⁵⁶ ry⁵⁰⁶/TM3, ry^{RK} Sb¹ Ser¹ ++</i>	<i>y w/+; MSN-C/+; HDAC1⁰⁴⁵⁵⁶ ry⁵⁰⁶ /+ AND y w/+; MSN-C/+; TM3, ry^{RK} Sb¹ Ser¹ /+</i>	27	2	7.4	14.8
		<i>y w/+; ush^{VX22}, MSN-C/+; HDAC1⁰⁴⁵⁵⁶ ry⁵⁰⁶ /+ AND y w/+; ush^{VX22}, MSN-C/+; TM3, ry^{RK} Sb¹ Ser¹ /+</i>	53	17	32.1	64.2
dMi-2	<i>Mi-2⁴ red¹ e⁴/TM6B, Sb¹ Tb¹ ca¹ +</i>	<i>y w/+; MSN-C/+; Mi-2⁴ red¹ e⁴/+</i>	NT	NT	NT	NT
		<i>y w/+; ush^{VX22}, MSN-C/+; Mi-2⁴ red¹ e⁴/+</i>	45	16	35.6	35.6
	<i>y¹ w¹¹¹⁸; Mi-2^{L1243}/TM3, Ser¹ ++</i>	<i>y w; MSN-C/+; Mi-2^{L1243}/+ AND y w; MSN-C/+; TM3, Ser¹/+</i>	NT	NT	NT	NT
		<i>y w; ush^{VX22}, MSN-C/+; Mi-2^{L1243}/+ AND y w; ush^{VX22}, MSN-C/+; TM3, Ser¹/+</i>	51	8	15.7	31.4

*Estimated number of lamellocytes (*Im*)

#To identify animals with the *ush^{r24}/ush^{VX22}, MSN* genotype, larvae with yellow mouth hooks were selected.

+The *Tb* balancer chromosome is easily distinguished from the *MTA-1* like chromosome.

**Homozygous viable

++Heterozygous, which assumes only 50% of the animals that carry the *ush; MSN-mCherry* chromosome are double heterozygotes and thus, the estimated penetrance may be twice the value of the % larvae with increased lamellocyte differentiation.

NT: not tested