

+ cot-1 cys-4 NM213t + + 21 22	16 24 5 7 7 6 1 1	67 (67%) IV	NM213t C102t K7
+ D306 + tryp-4 + pan-1 1.8 1.8	52 58 2 0 0 2 0 0	114 (72%) IV	Y2198 D306 5531
+ NM359 + cot-1 + cys-4 16 16	40 17 7 7 9 5 0 0	85 (85%) IV	C102t NM359 K7
+ tryp-4 pan-1 P1898 + + 17 19	- 31 7 - - 8 1 -	47 (69%) IV	P1898 Y2198 5531
+ M111 + aspt + lys-1 3.1 2.1	49 42 2 1 1 1 0 0	96 (96%) V	44303t M111 33933
+ + val-1 lys-1 NM221 + 7.4 8.4	37 43 4 3 2 6 0 0	95 (95%) V	33933 NM221 45201
+ thi-3 me-7 C-L2B + + 27 7.3	59 22 26 7 7 2 0 0	123 (67%) VII	C-L2B 18558 4894
+ for P1163 me-7 + + 5.8 3.2	107 36 2 7 5 0 0 0	157 (56%) VII	4894 C24 P1163
+ + arg-10 me-7 P1163 + 18 12	55 60 15 12 9 9 1 1	162 (82%) VII	4894 P1163 B368

Loci designated by isolation number are mutants listed in Table 1; the symbol morph or col has been omitted. Crosses are arranged in order of linkage groups, and numerically by isolation number of morphological mutant within each linkage group. In the body of the table numbers at left within each pair represent the class having the + allele of the left-most marker (or A).

* Scoring uncertain for al-2 among morph classes, enclosed in parentheses.