

Restriction polymorphism maps of *Neurospora crassa*: 2000 update

Mary Anne Nelson¹ and David D. Perkins² - ¹Department of Biology, University of New Mexico, Albuquerque, NM 87131; ²Department of Biological Sciences, Stanford University, Stanford, CA 94305-5020

Restriction fragment length polymorphisms (RFLPs) can be used to determine the approximate map location of any cloned piece of DNA. To establish an RFLP mapping system for *N. crassa*, R.L. Metzenberg and coworkers crossed strains with multiple sequence differences, an Oak Ridge laboratory strain (designated "O") and a Mauriceville-1c wild-collected strain (designated "M"; Metzenberg *et al.* 1984 *Neurospora* Newsl. 31:35-39; *ibid.* 1985 *Proc. Natl. Acad. Sci. U.S.A.* 82:2067-2071; Metzenberg and Grotelueschen 1995 *Fungal Genet. Newsl.* 42:82-90). Progeny from two separate crosses have been widely distributed and used for mapping. For the first cross, 38 progeny from 18 ordered asci were analyzed. Because nonsister spores from the same half of the ascus were selected, first-division segregation can be distinguished from second-division. For the second cross 18 random ascospore progeny were analyzed. The first cross is preferred for RFLP mapping, for several reasons: resolution is better because more loci have been scored; distance from the centromere can be estimated regardless of which linkage group is involved; double crossovers within intervals can be recognized, as can putative gene conversions or scoring errors. However, updated maps for both crosses are presented here.

Most loci are identified in the new compendium (Perkins, Radford and Sachs 2000 *The Neurospora Compendium: Chromosomal Loci*. Academic Press) and in the recent update to the *N. crassa* genetic maps (Perkins 2000 *Fungal Genet. Newsl.* 47). The previous version of the RFLP map contains details on the methods employed to list the loci in map order (Nelson *et al.* 1998 *Fungal Genet. Newsl.* 45:44-54). In scoring, "M" or "O" indicate segregants that are like the Mauriceville parent or the Oak Ridge-derived parent, respectively. A dash (-) indicates that the scoring was not done or was equivocal. (O) in Isolate 1 and (M) in Isolate 6 of the second cross indicate parental rather than progeny strains. (These isolates are O and M by definition.)

Newly mapped loci included in the first cross are *aob-1* (am alpha binding protein; H. Chen, J.W. Crabb and J.A. Kinsey); *amt* (amidinotransferase; C. Hillyer); *asd-1* (ascus development), *asd-3*, *sdv-1* (sexual development), *sdv-2*, *sdv-3*, *sdv-4*, *sdv-5*, *sdv-6*, *sdv-7*, *sdv-8*, *sdv-9*, *sdv-11*, *sdv-12*, *sdv-13* and *sdv-14* (M.A. Nelson); *Asm-1* (Ascospore maturation; R. Aramayo); *cox-4* (cytochrome oxidase) and *cox-6* (M. Sachs); *cpc-3* (cross pathway control; E. Sartlegger); *fr* (frost; T. Sone); *mip-1* (MIP1-like DNA polymerase; H. Bertrand); *ndp64* (NADH dehydrogenase; A.M.P. Melo, M. Duarte and A. Videira); *nop-1* (new opsin-1; D.O. Natvig); *pex2* (peroxisome assembly factor; K. Howe); *poi-1* (plenty of it) and *poi-2* (H. Kim); *scp* (serine carboxypeptidase; E. Kato); *Tel-IVR* (telomere; R. Schechtman); *tim17* (translocase of mitochondrial inner membrane; W. Tan and F. Nargang); *tnr* (tetrahydroxynaphthalene reductase; P. Dolan); *un-18* (unknown-18; encodes the second largest subunit of RNA polymerase I; K. Onai, S. Katagiri, M. Akiyama, H. Nakashima); *ypt-1* (ypt-like-1; K. Heintz); *zip-1* (bZip; H. Platero). In the second cross, newly-mapped loci include *alc-1* (allantoicase; G.A. Marzluf); *cyt-5* (cytochrome; B. Chen and S. Mohr); *gna-1* (guanine nucleotide-binding protein α subunit), *gna-2*, *gna-3* and *gna-4* (guanine nucleotide-binding protein β subunit; K. Borkovich); *gpd-1* (glyceraldehyde-3-phosphate dehydrogenase; M. Sahni and J.A. Kinsey); *mlh-1* (mutL homolog), *msh-1* (mutS homolog) and *msh-2* (C. Ishii).

Several loci whose identities were previously kept confidential have been converted from five-digit numbers to informative names. Markers in the first cross beginning with AP#- or R##, where # is a number, are RAPD markers (Williams *et al.* 1991, pp. 431-439, in *More Gene Manipulations in Fungi*, J.W. Bennett and L. Lasure, Editors, Academic Press). In those cases where the RFLP patterns of the RAPD markers were identical to those of cloned genes, the RAPDs have been removed; these redundant RAPDs can be found in earlier versions of the RFLP maps (Nelson *et al.* 1998 *Fungal Genet. Newsl.* 45:44-54).

The nomenclature of the following genes was changed (with previous names in parentheses): *cmt* (*ccg-12*), *cox-8* (*COXVIII*), *gpd-1* (*ccg-7*), *grp78* (*hsp-2*), *hH3* (histone H3), *hH4-1* (histone H4), *hsp70* (*hsp-1*), *hsp80* (*hsp-1*), *hil* (*vac-5*), *matA/a* (*A/a*), *pzl-1* (*ppz-1*) and *sod-2* (MnSOD). The *ssr* entries are simple sequence repeats that were previously called Ncr (I. de la Serna and B. Tyler). Clones designated 00003, 00006, 00008, 00032 and 00036 are random fragments of the *Neurospora* genome that contain polymorphisms.

There was a discrepancy between the 1998 placement of *con-8* (and therefore *phr*, with an identical RFLP profile) on the left arm of LG I (Nelson *et al.* 1998 *Fungal Genet. Newsl.* 45:44-54) and conventional genetic mapping, which suggested that these genes are located on the right arm (Shimura *et al.* 1999 *Fungal Genet. Biol.* 28:12-20). The *con-8* gene was probably incorrectly placed in the 1998 RFLP map, so it has been moved to the right arm of LG I.

Attempts have been made to streamline this version of the RFLP maps. Entries that have identical (or probably identical)

RFLP patterns, except for one or two lanes that were not scored, have been pooled into a single consensus line. As a result, each line is separated from its neighbors by one or more crossovers. Also, in the previous versions of the RFLP map, gene conversions or probable errors in mapping were listed on separate lines. These gene conversions or scoring errors could be identified as either (1) an apparent 4-strand double exchange (NPD) in an interval containing few or no single exchanges or (2) an apparent double crossover consisting of coincident single crossovers in flanking regions when there are few or no single crossovers in either region. Finally, the positions of gaps in the RFLP maps have been indicated, both to highlight the need to fill those gaps and to present a more accurate picture of distance relationships. While this streamlined version of the RFLP maps no doubt contains errors, it is hoped and anticipated that the errors in this shortened version will be less problematic than the errors caused by gene conversions or scoring errors.

An on-line RFLP mapping program for the first cross was developed to facilitate placement of new loci; this program is available through the *Neurospora* Genome Project HomePage (<http://www.unm.edu/~ngp/>). Updated versions of the RFLP map will also be available through the *Neurospora* Genome Project HomePage.

Acknowledgements

The authors thank Robert L. Metzenberg and Alan Radford for consultations, and numerous researchers (cited above) for sharing RFLP data. This work was supported by the National Science Foundation Grant MCB-9874488 to M.A.N.

LG II	A	B	C	D	E	E	E	F	G	H	I	J	K	L	M	N	N	O	O	P	Q	Q	R	R
	1	4	6	7	1	3	5	7	1	3	1	4	5	7	6	8	1	4	1	4	1	4	2	4
<i>Tet-III</i>	M	M	O	M	O	O	M	O	O	M	O	O	M	O	O	M	O	M	M	O	O	M	O	M
<i>hsp70</i>	M	M	O	M	O	O	M	O	M	O	M	O	M	O	M	O	M	O	M	O	M	O	M	O
(GAP)	-	-	O	O	-	O	M	O	O	M	O	O	M	O	M	O	M	O	M	O	O	M	O	M
00008	O	M	O	O	M	O	O	O	O	M	O	O	M	O	M	O	O	M	O	O	O	M	O	M
pSK2-1A	O	M	O	O	M	O	O	O	O	M	O	O	M	O	M	O	O	M	O	M	O	M	O	M
3:9A	M	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>Fsr-52, vph-1</i>	M	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>Fsr-32</i>	M	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>Cen-III, arg-5, alp-2, 25:1D, G8:11H</i>	M	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>cya-4, Fsr-55</i>	M	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
AP3.2, AP8u.4	M	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>pma-1, 12:11C</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>cit-1, nuo78, preg</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>ssr-5</i>	O	M	O	O	-	O	M	-	O	O	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>ssr-2</i>	O	M	O	O	-	O	M	-	O	O	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>hH3, hH4-1</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
X18:9A	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
11:F3, 21:D3	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>gpd-1</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>vma-2, DB0001</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>Fsr-3, ypt-1</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
X24:A11	O	O	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>eas = ccg-2 = bli-7</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>bli-4, Fsr-34</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
<i>Fsr-17, 8:4GL</i>	O	M	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M
AP32c.2, R32.2	O	-	O	O	M	O	O	O	O	M	M	M	M	M	M	M	M	M	M	O	O	M	O	M

LG II (continued)

leu-6
Tel-II/R

A	A	B	B	C	C	D	D	E	E	E	E	F	F	G	G	H	H	I	I	J	J	K	K	L	L	M	M	N	N	O	O	P	P	Q	Q	R	R
1	4	6	7	1	4	5	7	1	3	5	7	1	3	1	4	5	7	6	8	1	4	1	4	1	4	5	8	2	3	2	4	1	4	2	4	1	4
O	M	O	M	O	M	O	M	O	M	O	M	O	M	O	M	O	M	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	O	
O	M	M	O	M	O	M	M	O	M	O	M	O	M	O	M	M	O	O	M	O	M	O	M	M	O	M	M	O	M	O	O	M	O	M	O	M	

)
)
)

LG III

LG III	A	A	B	B	C	C	D	D	E	E	E	E	F	F	G	G	H	H	I	I	J	J	K	K	L	L	M	M	N	N	O	O	P	P	Q	Q	R	R
	1	4	6	7	1	4	5	7	1	3	5	7	1	3	1	4	5	7	6	8	1	4	1	4	1	4	5	8	2	3	2	4	1	4	2	4	1	4
<i>con-1</i>	O	M	-	O	M	M	M	M	O	M	M	M	M	M	-	M	M	M	O	O	M	O	M	O	M	O	O	O	M	M	O	O	O	O	O	M		
AP31a.4, R15.4	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	-	M	M	O	M	O	M	O	O	O	O	M	M	O	O	O	M			
<i>Cen-III, crp-2</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	O	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
<i>thi-4, pSK7-81C</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	O	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
<i>pro-1, ser-1</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	M	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
<i>ace-2</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	M	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
LZE4, LZE5, RRK	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	M	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
<i>cox-4, cyt-8</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	O	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
X14:1F	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	O	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
<i>aab-1, con-7, mip-1, G22:1H</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	O	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
<i>ad-2, trp-1, DB002</i>	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	M	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
32:2G	O	O	O	O	M	M	M	M	O	M	M	M	M	M	M	M	M	O	M	M	M	O	M	O	M	O	O	M	M	O	O	O	O	M				
AP32a.2	O	O	M	M	O	M	M	M	O	M	M	M	M	M	M	M	M	O	M	M	M	O	M	O	M	O	M	M	M	O	-	O	O	M				
LZC1	O	O	O	O	O	O	M	O	O	M	M	M	O	M	M	M	O	O	M	M	M	O	O	O	O	M	M	-	M	O	O	M	O	M				
(GAP)																																						
00032	M	O	O	O	O	M	O	M	-	M	O	M	M	O	M	O	O	O	M	O	M	O	O	O	O	O	M	O	O	M	M	O	M	O	M			
<i>Fsr-45</i>	M	O	M	O	O	O	O	M	O	M	M	M	M	O	M	M	O	O	M	O	M	O	M	O	O	O	M	O	O	M	M	O	M	O	M			
<i>cat-3</i>	M	O	M	O	O	O	O	M	O	-	O	M	M	M	M	M	O	-	M	-	M	-	M	M	M	-	M	-	M	O	M	-	O	M	O			
<i>ssr-6</i>	M	O	M	O	O	M	O	M	O	M	O	M	M	M	M	M	O	O	M	O	M	O	M	O	M	M	-	M	O	O	M	M	O	O	M			
AP81.1	M	O	M	O	O	M	O	M	O	M	O	M	M	O	M	M	O	O	M	O	M	O	M	O	O	O	M	O	O	M	M	O	M	O	M			
AP121.4	M	O	M	O	O	M	O	M	O	M	O	M	M	O	M	M	O	O	M	O	M	O	M	O	O	O	M	O	O	M	M	O	M	O	M			
<i>Tel-III</i>	M	O	M	O	O	M	O	M	O	M	O	M	M	-	M	O	O	O	M	O	M	O	M	O	O	O	M	O	O	M	M	O	M	O	M			

LG IV	A	A	B	B	C	C	D	D	E	E	E	E	F	F	G	G	H	H	I	I	J	J	K	K	L	L	M	M	N	N	O	O	P	P	Q	Q	R	R		
	1	4	6	7	1	4	5	7	1	3	5	7	1	3	1	4	5	7	6	8	1	4	1	4	1	4	5	8	2	3	2	4	1	4	2	4	1	4		
<i>Tel-IVL</i>	O	M	O	O	M	O	O	M	O	M	O	M	O	M	O	O	O	O	M	M	O	M	O	M	O	M	O	M	O	O	O	O	M	M	O	M	O	M		
AP32a.5, R29.5	O	M	O	O	M	O	O	M	O	M	O	M	O	M	O	-	O	O	M	M	O	M	O	M	O	M	O	M	O	M	-	O	M	M	O	M	O	M		
SPIAE	O	M	O	O	M	O	O	M	O	M	O	M	O	M	O	M	O	O	M	M	O	M	M	O	M	O	M	O	M	O	O	O	O	M	M	O	M	O	M	
(GAP)																																								
<i>sdv-1, sdv-2, sdv-3, 4:3A</i>	M	O	O	O	M	O	O	M	O	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	O	O	O	O	M	M	M	M	M	M		
<i>Cen-IV, aod-1, X17:10G</i>	M	M	O	O	M	O	O	M	O	O	M	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	O	O	O	O	O	M	M	M	M	M		
<i>Fsr-63</i>	M	M	O	M	O	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	-	O	O	M	O	M	M	M	M	M		
<i>pyr-1, snz-1, 27:1F</i>	M	M	O	M	O	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	O	O	O	M	O	M	O	M	M	M		
<i>pho-5, tom20</i>	M	M	O	M	O	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	O	O	O	M	O	M	O	M	M	M		
NP4E6, R230.1, AP37c.1	M	M	O	M	O	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	O	O	O	M	O	M	O	M	M	M		
<i>sdv-11, sdv-12, 20:11A</i>	M	O	O	M	O	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	O	O	O	M	O	M	O	M	M	M		
G13:C8, X25:D7	M	O	O	M	O	M	O	-	O	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	M	O	O	O	M	O	M	O	M	M		
<i>trp-4, G6:C9, G6:E12, X4:E10, X10:A4, X17:C11</i>	M	O	O	M	O	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	M	M	O	M	M	O	M	O	M	O	M	O	M	O	M	O	M	M		
<i>Fsr-62</i>	M	O	N	O	M	O	O	M	O	O	M	O	O	O	M	O	O	M	O	O	M	O	M	M	O	M	M	M	O	O	M	O	M	O	M	O	M	M		
<i>bli-3, Fsr-51, G3:4D</i>	M	O	O	M	O	O	O	M	O	O	M	O	O	O	M	O	M	O	O	M	O	M	M	O	M	M	M	O	O	O	M	O	M	O	M	O	M	M		
<i>Fsr-13, vma-8</i>	M	O	O	M	O	O	O	M	O	O	M	O	O	O	M	O	O	M	O	O	M	M	O	M	M	O	M	O	O	O	M	O	M	O	M	O	M	M		
<i>crp-3</i>	M	O	O	M	O	O	O	M	O	O	M	O	O	O	M	O	O	M	O	M	O	M	M	O	M	M	M	O	O	O	M	O	M	O	M	O	M	M		
<i>sdv-7, sdv-8, sdv-9, 12:2E</i>	M	O	O	O	M	O	O	O	M	O	O	O	O	O	M	O	O	M	O	M	O	M	M	O	M	M	M	O	O	O	M	O	M	O	M	O	M	M		
<i>cre-1</i>	M	O	O	O	M	O	O	O	M	O	O	O	O	O	M	O	O	-	M	O	O	O	M	M	O	M	O	M	O	O	M	O	M	O	M	O	M	M		
<i>nuo29.9</i>	M	O	M	M	O	O	O	M	O	O	O	M	O	O	M	O	O	M	O	O	O	O	M	M	O	M	O	M	O	O	M	O	M	O	M	O	M	M		
<i>ndp64, nuo21</i>	N	O	M	M	O	O	M	O	M	O	O	M	O	M	O	O	O	M	O	O	O	O	M	O	M	O	M	O	M	O	M	O	M	O	M	M	O	M	O	
<i>Fsr-4</i>	M	O	M	O	M	O	M	N	O	M	O	O	M	O	M	O	O	O	O	O	O	O	O	M	O	M	O	M	O	-	M	O	O	M	M	M	O	M	O	
<i>Tel-IVR</i>	M	O	O	M	O	M	O	M	O	M	O	O	M	O	O	M	O	O	M	O	O	O	M	O	M	O	M	O	M	O	M	O	M	O	M	M	M	O	M	O

LG	V	A	A	B	B	C	C	D	D	E	E	E	E	F	F	G	G	H	H	I	I	J	J	K	K	L	L	M	M	N	N	O	O	P	P	Q	Q	R	R
		1	4	6	7	1	4	5	7	1	3	5	7	1	3	1	4	5	7	6	8	1	4	1	4	1	4	5	8	2	3	2	4	1	4	2	4	1	4
AP8w.4		O	M	O	M	O	M	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	M	M	M	M	O	O	O	M	M	O	M	M	M	M	M	
rDNA, X15:4E		O	M	O	M	O	M	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	M	M	M	M	O	O	O	M	M	O	M	M	M	M	O	
AP5c.3, AP13.3		O	M	O	O	O	M	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	M	M	M	M	O	O	O	M	M	O	M	M	M	M	O	
con-2		O	M	O	O	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	M	M	M	M	O	O	O	M	M	O	M	M	M	O		
AP4a.6		O	M	O	O	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	M	M	O	O	O	O	O	M	M	M	M	M	M	O		
Cen-V, ccg-8, Fsr-9, Fsr-16, lys-1, pSK21d		M	M	O	O	O	O	O	O	O	M	M	M	M	M	O	M	O	M	O	N	M	M	M	O	O	M	M	O	O	M	M	M	M	M	M	O		
AP36c.2, R64.2		M	M	O	O	O	O	O	O	O	M	M	M	M	M	O	M	O	M	O	M	O	M	O	O	O	M	M	O	O	M	M	M	M	M	M	O		
ccg-1 = grg-1, AP12g.1		M	O	O	O	O	O	O	O	O	M	M	M	M	M	O	M	O	M	O	M	O	M	O	O	O	M	M	O	M	M	M	M	M	O	M	O		
ilv-2		-	O	-	-	-	O	O	-	-	-	-	-	-	-	-	M	O	M	-	M	O	-	O	-	O	-	M	O	-	O	-	-	M	M	M	O		
X11:D2		M	O	O	O	O	O	O	M	O	M	M	M	O	M	O	M	O	M	O	O	M	O	O	O	O	M	M	O	M	O	M	M	M	M	M	O		
AP8w.7		M	O	O	O	O	O	M	O	M	O	M	M	M	M	O	M	O	M	O	O	M	O	O	O	O	M	M	O	M	O	M	M	M	O	M	O		
cpc-3, cyh-2, mcb, nuo24, poi-1, rca-1, sod-2, tom40, vma-1, vma-3, 14:10G, G16:11H, X23:C8		M	O	O	O	O	O	O	O	O	M	M	M	O	M	O	M	O	M	O	O	M	O	O	O	O	M	M	O	M	O	M	M	O	M	M	O		
leu-5, mfa		M	O	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	O	M	O	M	O	O	M	M	O	M	O	M	M	O	M	M	O		
al-3, Asm-1, ccg-6, 18:10A, 23:1A		M	M	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	O	M	O	M	O	O	M	M	O	M	O	M	M	O	M	M	O		
ini		M	M	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	O	M	O	O	O	M	M	O	M	O	M	M	O	M	M	O		
cit-2		M	M	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	-	M	O	M	M	O	M	M	M	O	M	O	M	M	O	M	M	O		
cox-6, cya-2		M	M	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	O	M	O	O	O	M	M	O	M	O	M	M	O	M	M	O		
cmd, hsp80		M	M	O	O	O	M	O	M	O	M	M	M	O	M	O	M	O	M	O	M	O	M	O	O	O	M	M	O	M	O	M	M	O	M	M	O		
tom70		-	M	-	O	M	O	-	M	O	M	M	M	O	M	O	M	M	M	O	M	O	M	O	O	O	M	M	M	M	-	M	M	O	M	M	O		
AP34b.3, R42.3		O	M	O	O	O	M	O	O	O	M	M	M	M	M	O	M	O	M	O	M	O	M	O	O	O	M	M	M	M	O	M	O	M	O	M	O		
Fsr-20		O	M	O	O	M	O	O	M	O	M	M	M	M	M	M	M	M	M	O	M	O	M	M	O	O	M	M	M	M	-	O	M	M	O	M	O		
crp-4, sdv-6, 8:9A		O	M	O	O	O	M	O	M	O	M	M	M	M	M	M	M	M	M	O	M	O	M	M	O	O	M	M	M	M	O	M	M	O	M	M	O		
clone 129		O	M	O	M	O	O	O	M	O	M	M	M	M	M	M	M	M	M	O	M	O	M	M	O	O	M	M	M	M	O	M	M	O	M	M	O		
AP35a.2, R47.2		O	M	O	M	O	O	O	M	O	M	M	M	M	M	M	M	M	M	O	M	O	M	M	O	O	M	M	M	M	O	M	M	O	M	M	O		

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
LG VI	1	4	6	7	1	3	5	7	6	8	1	4	1	4	5	8	2	3
Tel-VIL	M	O	M	O	M	O	M	O	M	O	M	O	M	O	O	O	O	O
cax	M	O	M	O	M	O	M	O	M	O	M	O	-	O	O	O	M	O
tfd'	O	M	M	-	O	M	O	M	O	M	O	O	O	O	O	O	O	O
Ap8d.5	M	M	-	M	O	M	O	M	O	M	O	M	O	O	O	M	-	O
R249.1	M	O	O	-	O	-	-	M	M	O	O	M	-	O	M	M	O	M
gdh-1, tom22, X25:7C	M	O	O	O	M	O	O	M	O	M	O	O	O	O	M	M	O	M
AP3b.1	M	O	M	M	O	O	M	M	O	O	O	O	O	O	M	M	O	M
nuc19.3	M	-	M	O	M	M	O	O	O	-	O	M	O	O	O	M	M	M
AP8g.3	O	M	M	O	M	O	O	O	O	O	M	M	O	O	M	M	O	O
tim17	O	M	M	O	M	O	O	M	O	O	M	M	O	O	M	M	O	O
asd-1, asd-3, 12:7B	O	M	M	O	O	M	O	O	O	O	O	M	O	O	O	M	O	O
cmt, G9:12G	O	M	M	O	O	M	O	O	O	O	O	M	O	O	M	M	O	O
AP31a.7, R15.7	O	M	M	M	O	O	M	O	O	O	O	M	O	O	O	M	O	O
Cen-VI, Bml, Fsr-50, hspp-1, nuc30.4,	M	M	M	M	O	M	M	O	O	O	O	M	O	O	O	M	O	M
pan-2, G2:3A, G7:5F, G8:1C, G8:6D,																		
G12:10C, X5:9H, X7:8E, X13:5A,																		
X13:5H, X16:12D, X24:8E, pHL200																		
con-11	M	O	-	M	M	M	O	O	M	O	O	O	O	O	O	M	O	O
AP9b.3	M	O	M	M	M	O	M	O	M	O	O	O	O	O	M	M	O	O
Tel-VIR, nuc21.3c, DA122	M	O	O	M	O	O	M	O	M	O	O	O	O	O	M	O	O	O

Second Cross

LG I

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>cyl-21, msh-1</i>	(O)	O	M	O	O	(M)	M	M	O	M	O	O	O	O	O	O	O	O	M	M
<i>mus-40, pzl-1</i>	(O)	O	M	O	M	(M)	M	M	O	M	O	O	O	O	O	O	O	O	M	M
<i>Fsr-12</i>	(O)	O	M	M	M	(M)	M	O	O	M	M	O	O	O	O	O	M	O	-	-
<i>krev-1, mus-38, nil-2</i>	(O)	O	M	M	M	(M)	M	O	O	M	M	O	O	O	O	O	O	O	M	O
<i>matA/a, arg-3, chs-4, leu-4, rgb-1, tef-1, G3:F4</i>	(O)	M	M	M	M	(M)	O	O	O	M	M	O	O	O	O	O	O	O	O	O
<i>Fsr-33</i>	(O)	M	M	M	M	(M)	O	O	O	M	M	O	O	O	O	O	O	O	M	O
<i>al-2, arg-6, cr-1, Fsr-1, met-6, un-7, 26:4H</i>	(O)	M	M	M	M	(M)	O	O	O	O	M	M	O	O	O	O	O	O	O	O
<i>31:2B</i>	(O)	M	M	M	M	(M)	O	O	O	O	M	O	M	O	O	O	O	O	O	O
<i>20:5G</i>	(O)	M	M	M	M	(M)	O	O	O	O	M	M	M	-	O	-	O	-	-	O
<i>Fsr-18, nic-1</i>	(O)	M	M	M	M	(M)	O	O	O	O	M	O	M	O	O	O	O	O	O	O
<i>con-8, phr</i>	(O)	O	M	M	M	(M)	M	O	O	M	O	M	O	O	O	O	O	O	O	O

LG II

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>cys-3</i>	(O)	O	M	M	O	(M)	O	M	O	M	O	O	O	O	O	M	O	O	M	O
<i>00008</i>	(O)	O	M	M	O	(M)	O	M	O	O	O	O	O	O	M	O	O	M	O	O
<i>Fsr-32, Fsr-52</i>	(O)	O	O	M	O	(M)	O	M	O	O	O	O	O	O	O	O	O	O	O	O
<i>Fsr-54</i>	(O)	O	O	M	M	(M)	O	M	O	O	O	O	M	O	O	M	O	O	M	O
<i>hbs</i>	(O)	O	O	M	M	(M)	O	M	O	O	O	O	M	O	O	M	O	M	M	O
<i>con-6</i>	(O)	O	O	M	O	(M)	O	M	O	O	O	O	M	O	O	M	O	O	M	M
<i>Fsr-55</i>	(O)	O	O	M	M	(M)	M	M	O	O	O	O	M	O	O	M	O	O	M	M
<i>alc-1, arg-12, gpd-1, nik-2</i>	(O)	O	O	M	M	(M)	M	M	O	O	O	O	M	O	O	M	O	O	M	M
<i>Fsr-21, Fsr-34</i>	(O)	O	O	M	M	(M)	M	M	O	O	M	M	M	O	O	M	M	O	M	M
<i>trp-3</i>	(O)	O	O	M	M	(M)	M	O	O	O	M	M	M	O	O	M	O	O	M	M
<i>G5:H2</i>	(O)	O	O	M	M	(M)	M	O	O	O	M	M	M	M	O	O	O	O	M	M
<i>Fsr-17, leu-6</i>	(O)	O	O	M	M	(M)	M	O	O	O	M	M	M	M	O	O	M	O	M	O

LG III

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>cyt-22</i>	(O)	M	O	M	M	(M)	O	O	M	M	O	M	M	M	O	M	O	M	M	M
<i>con-1</i>	(O)	O	O	M	M	(M)	O	O	M	M	O	O	M	M	O	M	O	O	O	M
<i>cyt-8</i>	(O)	O	O	M	M	(M)	O	O	M	M	O	O	M	M	O	M	O	O	O	M
<i>DA25</i>	(O)	M	O	M	M	(M)	O	O	M	M	O	O	M	M	O	M	O	O	O	M
<i>con-7, gnb-1, trp-1, LZE4</i>	(O)	M	O	M	M	(M)	O	O	M	M	O	O	M	M	O	M	O	M	O	M
<i>gna-1</i>	(O)	M	O	M	O	(M)	O	O	M	M	O	O	M	M	O	O	O	M	O	M
<i>ro-2</i>	(O)	O	O	M	O	(M)	O	O	M	M	O	O	M	M	O	O	O	O	O	M
<i>Fsr-45</i>	(O)	O	O	M	O	(M)	O	O	M	M	O	O	M	O	O	M	O	O	O	M

LG IV

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>Tel-IVL</i>	(O)	O	M	M	M	(M)	O	M	M	M	O	O	O	O	O	O	O	O	O	M
<i>SPIAE</i>	(O)	O	M	M	M	(M)	O	M	M	M	O	O	O	O	O	O	M	O	O	O
<i>Fsr-62, Fsr-63, mlh-1, mtr, mus-8, pph-1, 4:E12, 5:3B, 5:4H, 22:G3, 23:B5, G16:C5, X12:B4</i>	(O)	M	M	M	O	(M)	M	M	M	M	M	O	O	O	O	O	O	O	O	O
<i>cyt-5, X5:H4</i>	(O)	M	M	M	O	(M)	M	M	M	O	M	O	O	O	O	O	O	O	O	O
<i>arg-14, YAC 6H3</i>	(O)	M	M	M	O	(M)	M	M	M	M	M	O	M	O	O	O	O	O	O	O
<i>X15:A10</i>	(O)	-	-	O	O	(M)	M	M	M	M	M	M	M	O	O	O	O	O	O	O
<i>G17:B4, G17:G6</i>	(O)	M	O	M	O	(M)	M	M	M	M	M	O	O	O	O	O	O	O	O	O
<i>Fsr-51</i>	(O)	M	M	M	O	(M)	M	M	M	M	O	O	O	O	O	O	O	O	O	O
<i>chs-5</i>	(O)	M	M	M	O	(M)	M	M	M	M	O	M	O	O	O	O	O	O	O	O
<i>con-5, con-9, con-10, col-1, 7:A1, G25:D4</i>	(O)	M	M	M	M	(M)	M	M	M	M	O	O	O	O	O	O	O	O	O	O
<i>met-5</i>	(O)	M	M	M	M	(M)	M	M	M	M	O	O	O	O	O	O	O	O	O	O
<i>ras-1</i>	(O)	M	M	M	M	(M)	M	M	M	M	O	O	O	O	O	O	O	O	O	O
<i>nit-3</i>	(O)	M	M	M	M	(M)	M	M	M	M	O	O	O	O	O	O	O	M	O	O
<i>chs-2, Fsr-4</i>	(O)	M	M	M	M	(M)	M	M	M	M	O	O	O	M	O	O	O	M	M	O
<i>gna-3, uvs-2</i>	(O)	O	M	M	M	(M)	M	M	O	O	O	O	M	M	M	O	M	M	M	M

LG V

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>rDNA, mus-18</i>	(O)	M	O	O	O	(M)	O	M	M	O	O	O	M	O	M	O	M	O	M	M
<i>X22:H1</i>	(O)	M	O	O	O	(M)	O	M	O	O	O	O	M	O	M	O	M	O	M	M
<i>con-2</i>	(O)	M	O	O	O	(M)	O	M	M	O	O	O	M	O	M	O	M	M	M	M
<i>con-4a</i>	(O)	M	O	O	O	(M)	O	M	M	M	M	M	M	O	M	O	M	M	M	M
<i>Fsr-9, Fsr-16</i>	(O)	M	O	O	O	(M)	O	M	M	M	M	M	M	O	M	O	M	M	M	M
<i>chs-1</i>	(O)	O	O	O	O	(M)	O	M	M	M	M	M	M	O	M	O	M	M	M	M
<i>am</i>	(O)	O	O	O	O	(M)	M	M	M	M	M	M	M	M	M	M	M	M	M	M
<i>chs-3</i>	(O)	O	O	O	O	(M)	M	O	M	M	M	M	M	M	M	M	O	M	M	M
<i>gna-2, inl, ppt-1, 3:B5, G15:B8, G23:3H</i>	(O)	O	O	O	O	(M)	M	M	M	M	M	M	M	M	O	M	O	M	M	M
<i>ro-4, 16:2C</i>	(O)	O	O	O	O	(M)	M	O	M	M	M	M	M	M	O	M	O	M	M	M
<i>Fsr-20</i>	(O)	O	O	O	O	(M)	M	O	M	M	M	M	M	M	O	M	M	M	M	M

LG VI

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>cmt</i>	(O)	M	O	M	O	(M)	M	M	O	O	M	M	M	M	M	O	M	M	M	M
<i>Bml, con-3, G8:C8</i>	(O)	M	M	M	O	(M)	M	M	O	O	M	M	M	M	M	O	M	M	M	M
<i>Fsr-50</i>	(O)	M	M	M	O	(M)	M	M	O	O	M	M	M	M	M	O	O	M	M	M
<i>00006</i>	(O)	O	M	M	M	(M)	M	M	O	O	M	O	M	M	M	O	M	M	M	M
<i>trp-2, con11</i>	(O)	M	M	M	M	(M)	M	O	O	O	M	O	M	M	M	M	M	O	M	M

LG VII

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
<i>00003</i>	(O)	M	M	O	O	(M)	O	M	-	M	O	M	M	O	O	O	O	-	O	M
<i>lacc</i>	(O)	M	M	M	O	(M)	O	M	O	M	O	M	M	O	O	O	O	M	O	O
<i>G10:F1</i>	(O)	M	M	M	O	(M)	O	M	O	M	M	M	M	O	O	O	O	M	O	O
<i>msh-2, un-10</i>	(O)	M	M	M	O	(M)	O	M	O	M	O	O	M	O	O	O	O	M	O	O
<i>cox-8</i>	(O)	M	M	M	O	(M)	O	O	O	O	M	O	M	O	O	O	O	M	O	O