

chromosome	marker#	Cosmid name	SNP location on cosmid	Map position		Position in % of chromosomal size		Primers		Polymorphism		Previously identified	Restriction enzyme	Digestion results (bp)			
				bp	cM	if size in bp	if size in cM	Forward	Reverse	Wormbase 106 name	type			N2	CB4856		
I	1	F56C11	22274	168807	-18.2603	1.12	1.17	atcgaatccctctgctacc	60	aggtgctcccaactctttag	66	pkP1050	TTT(G)/TAA	Y	Dra I	95, 475	570
	2	C54G6	1258	992188	-17.2825	6.58	3.20	cgctggttaatgatctg	56	gaactctcagtcactctg	62	pkP1101	GAATC(A)/A	Y	Eco RI	104, 278	382
	3	Y71G12A	10851	1884415	-11.9590	12.47	14.24	accgaataaataaaggcgag	64	tttgctttatcagatctg	60	pkP1103	GAATC(A)/C	Y	Rsa I	85, 231	316
	4	W43B4	26138	26138	-6.1004	18.69	18.69	ccaccactctg	60	ccaccactctg	60	pkP1052	TTT(G)/TAA	Y	Dra I	174, 334	
	5	Y47G6A	69880	3502476	-3.5488	23.23	31.68	ttgttccagcaaacctag	58	atcgacacgagggatgttg	58	snp Y47G6A.8	TTT(T)/AAA	N	Dra I	98, 200, 252	25, 98, 200, 227
	6	T03A1	28270	4338254	-1.4887	28.77	35.96	actacggcaatgatcaacct	60	cagaaatgactgaatcaacc	58	snp T03A1.3[?]	GTC(A)/GAC	Y	Sac I	525	252, 273
	7	F5Y29	43691	4845518	-0.5162	32.13	32.13	actgagcagctgtagg	60	ttcttctctgacacaaac	60	pkP1059	CCG(A)/A	Y	Sma I	262, 294	
	8	C34G6	15466	5893622	0.4597	39.08	40.00	atgacagggctgaaabaag	58	ggaccctcactctcttagc	60	snp C34G6.3	TTT(C)/GAA	Y	Taq I	127, 258	42, 127, 216
	9	K04F10	19618	6359867	0.9366	42.17	40.99	atctctctccagccacttacc	66	ctaaactgtaagcaaacacc	66	pkP1057	CATT(A)/ITG	Y	Nde I	595	294, 301
	10	D2030	16772	7598963	1.2576	50.33	43.52	gggtctatggctcttccaagt	68	cgactcactctttattcaacc	64	pkP1116	AAC(G)/AAT	Y	Acc I	113, 224	337
	11	F59D12	7894123	7894123	-0.0182	52.35	52.35	ttctgctctgctgacaaac	60	aaattctgacagcaaac	60	snp F59D12.3	TTT(G)/TAA	N	Dra I	211, 229	337
	12	VF39H2L	3079	8653640	2.9456	57.39	45.16	ttccgtcccaatttatccg	60	catcggaagcttctctaac	60	pkP1059	TTTA(G)/AIA	Y	Dra I	641	219, 422
	13	C36F7	23997	9569914	3.7959	63.46	46.92	tatgaaagtctccacactg	64	ccgaataataagcttaaacg	62	pkP1122	TTT(A)/GAT	Y	Nsi I	388	154, 234
	14	ZC247	14561	10259909	4.7801	68.03	48.96	ccactgcttccgtttcaacg	60	ttccactgctttccaaacg	58	snp ZC247.2	GGATC(C)/T	Y	Bam HI	233, 238	571
	15	W02B9	8155	11085291	6.0193	73.51	57.77	ttatcccaaatgactgacg	60	aaattctgacagcaaac	60	snp W02B9.2	TTT(G)/TAA	N	Dra I	84, 158, 250	158, 434
	16	ZK1151	1902	11760182	7.5226	77.98	54.65	cgacctctgttaagctg	60	agaactctgctgactctc	60	pkP1068	[A/G]G/C	Y	Hae III	682	212, 470
	17	T07D10	11635	12614280	13.8659	83.65	67.81	cttggctggaggaataaag	66	tttgcctgattgactctg	60	pkP1070	GAT(C)/TCC	Y	Mbo I or Sau 3A1	62, 305	62, 96, 209
	18	M01E5	454	13280531	17.4648	88.06	75.27	ccagtaattggaatgagagc	60	ttgaaagccctggttaagt	60	snp M01E5.1	GTCA(T)/CT	N	Eco RI	129, 383	512
	19	C37A5	17439	14162948	22.9127	93.92	86.57	ctcaagcaagagactgagc	60	ctcaagcaagagactgagc	60	pkP1071	GAATC(T)/Y	Eco RI	241, 286	527	
	20	ZK909	10916	14958660	28.9192	99.19	99.03	cacaagtggttgaaagctac	66	caacaagtggttgaaagctac	66	pkP1072	AAC(G)/CTT	Y	Hind III	451	215, 236
II	1	T01D1	14052	176721	-17.3780	1.16	1.36	aagagggcttctctgcaac	60	accatacaccagcattctac	58	pkP2101	TTT(T)/AAA	Y	Dra I	217, 402	619
	2	Y57G7A	4213	1270097	-15.4084	8.31	4.90	tttgcagttccgactgaactg	62	ttttgctgaaagccctttagg	60	pkP2125	TTT(A)/GAA	Y	Dra I	143, 299	442
	3	F58E1	13123	1683953	-14.9140	11.28	5.79	ttccagctgtgactgctgac	62	aaatgacacagcactgttg	56	pkP2136	[C/T]C/TAG	Y	Xba I	336	58, 278
	4	R26A7	8269	2750474	-10.0273	18.03	18.03	cgagtttgaactctgagag	60	ttactcttccgctgtctgic	60	pkP2114	TTT(G)/TAA	Y	Alu I	274	333
	5	F18A12	7765	3403575	-5.9476	22.02	21.91	agaagttgctgactgctg	60	taaaagactctctccggag	60	snp F18A12.2	[A/G]G/C	Y	Alu I	69, 114, 319	183, 319
	6	F56D3	5769	4147051	-5.4083	27.14	22.88	ggcaactatgagggatgctg	60	atctacactcactctgtag	60	snp F56D3.3	GGT(A)/TAC	N	Kpn I	104, 145	249
	7	C33F10	6689	4800868	-3.5209	31.42	26.27	ttgtgttcataactgtctcg	60	aaatgctgaagtaagtagg	58	snp C33F10.1	CAT(T)/AAG	Y	Nde I	576	274, 302
	8	F10A1	18148	5761743	-0.8662	37.71	30.86	tttccagaccactgcaact	60	ctcactcactctctcagc	60	pkP2115	AGT(A)/CT	Y	Eco RI	408	122, 250
	9	K03H9	16942	6427387	-0.3160	42.07	32.03	atctggagaacctggttagt	66	ctctcactcaataaagaag	60	pkP2106	CAT(T)/T	Y	Nsi III	252, 638	890
	10	F32A5	35775	7257517	0.4409	47.50	33.39	atitactgaaacacactcg	58	atitactgaaacacactcg	58	snp F32A5.2	G/C)TCA	N	Dde I	380	180, 200
	11	T05C12	27580	8195651	0.7867	53.64	34.01	gtttgcccactctctcattga	64	tgaaattggaagtaagtagg	62	pkP2151	GT(T)/ATC	Y	Mbo I or Sau 3A1	381	99, 82
	12	R48E8	10717	1104838	0.8759	54.17	34.47	ctcactcactctctcagc	62	ctcactcactctctcagc	62	pkP2151	TTT(G)/TAA	Y	Dde I	49, 53, 240, 260	49, 62, 249, 313
	13	Y51B9A	7381	9401070	1.2287	61.53	34.81	ctaggaggtcccactactg	66	tgatcagaatcactctg	60	pkP2109	GAATC(C)/T	Y	Eco RI	37, 326	656
	14	E04D5	3557	10414073	2.4889	68.16	37.07	ttgcaaaaagaagttctcag	60	tttctcttccgtctcactcg	62	snp E04D5.1[?]	GTC(A)/CT	Y	Apa I	13, 155, 262	13, 417
	15	F37H8	7718	11180865	3.2851	73.18	39.08	ttcactgactttttccaac	60	ttcactgactttttccaac	60	pkP2110	TTT(G)/TAA	Y	Taq I	16, 112, 573	16, 112, 573, 379
	16	Y44E5	3808	11752128	4.0335	76.92	52.08	tttccctgctgctgcaagc	60	tttccctgctgctgcaagc	60	pkP2111	TTT(G)/G	N	Mse I	127, 249	619
	17	Y38E10A	6924	12630666	10.8343	82.67	52.08	aggaaataagcctgcaagc	60	tttccctgctgctgcaagc	60	snp Y38E10A.4[?]	T(T)/AA(T)TA	N	Pac I	741	342, 399
	18	F15D4	2813	13235559	15.8706	86.62	61.13	tttccactttctccag	54	tcaaaaaccagcaactg	56	pkP2116	TTT(T)/AAA	Y	Nde I	517	119, 398
	19	Y38G8B	11219	1398014	13.6552	72.86	51.50	aaatgctgaagtaagtagg	60	aaatgctgaagtaagtagg	60	snp Y38G8B.1	TTT(G)/TAA	N	Sac I	359	122, 250
	20	Y54E2A	20317	14758293	29.1025	96.59	84.92	aatgaagttcgctctcag	60	ttttccgaagttgtgtctc	58	snp Y54E2.1	[A/G]TGCAT	Y	Cla I	179, 277	456
III	1	K10F12	2024	360894	-27.0345	2.62	0.74	atcactctgctgacgagag	60	aaataccagactgctctg	60	snp K10F12.5	G(G)A)TTC	Y	Eco RI	642	305, 337
	2	K02F3	17776	840469	-25.8751	6.10	3.10	ggatcacatgatctgctgac	66	ggatctggtgattctgggaac	66	pkP3045	TTT(T)/AAA	Y	Mse I	23, 31, 110, 170	23, 31, 50, 60, 170
	3	B05Z4	10276	1893290	-18.0248	13.74	19.13	ataaagatcaaacnccctg	60	aaactagctttccgctctg	60	snp B05Z4.4	CTG(T)/AIG	Y	Dde I	400	152, 248
	4	Z03W9	23593	2459943	-9.1335	17.84	28.13	gaaacagacactctactc	62	aaagactctctcagcaactg	60	snp Z03W9.3	TTC(A)/G	Y	Mse I	366	130, 366
	5	H06J04	15629	3068098	-9.1335	22.26	26.88	ttatcacaagcttcttagg	60	aaacactctgctgctgac	60	snp H06J04.2	[C/G]TITAG	Y	Dde I	236, 270	505
	6	ZK1058	25918	3923438	-4.3164	28.47	47.12	ccaactctgcaactgatag	66	aattcctgctgcaactgat	56	pkP3096	GAAT(T)/GIC	Y	Eco RI	208, 258	466
	7	F25F2	15611	4517529	-3.2032	32.78	49.39	ttgttcaaacatctcggag	58	ttggagatgacactgaaac	58	snp F25F2.1	CTG(A)/C	Y	Dde I	488	189, 299
	8	H03A5	90345	5431252	4.9079	39.40	49.40	cgagcattggaatgaggaag	60	gaagcagctgctgctgctg	60	pkP3047	TTT(G)/TAA	Y	Mse I	164, 274	274
	9	C28H8	43335	5925983	-1.4086	42.99	53.05	aaagatgctctctacc	58	ttttcttctgcaactgatg	58	snp C28H8.2	GAT(T)/C	Y	Rsa I	37, 160	37, 58, 102
	10	R13F6	12315	6847169	-0.9176	49.68	54.06	cttcaaaactcggaggaag	60	actgaacactctgctgctg	62	pkP3100	G(A)TAC	Y	Rsa I	244, 277	521
	11	F56C9	13335	7320107	-0.7451	53.11	54.41	aaatgaaatgactgaggaag	58	taactgactctctactctc	60	snp F56C9.1	T(T)/A(T)AA	Y	Nde I	33, 275	125, 150
	12	Z06K4	29814	3998164	4.8552	58.03	53.03	ttcttccctctctctctg	60	ttcttccctctctctctg	60	snp Z06K4.4	G(A)GCTG	Y	Hin DIII	130, 250, 245	130, 250
	13	F10E9	39795	8318553	-0.3121	60.35	55.29	agcagtaagaattctcagc	60	ccccctgctgattatatac	60	pkP3049	GAT(T)/A(T)C	Y	Acc I	254, 600	854
	14	G40H1	186	9308858	0.3746	67.54	56.69	aattcagcaaacacactgac	58	aaaaagtctgcaatgatcg	58	pkP3107	[C/T]TTAA	Y	Dra I	62, 108	54, 54, 62
	15	M04D8	10485	1027496	1.4094	72.75	58.81	ttcagagcactcttttccag	60	aatctcgtggtatctgaa	58	snp M04D8.2	TTT(A)/GAA	Y	Dra I	58, 78, 217, 297	78, 217, 355
	16	Y38G8B	11219	1398014	13.6552	72.86	51.50	aaatgctgaagtaagtagg	60	aaatgctgaagtaagtagg	60	snp Y38G8B.1	TTT(G)/TAA	Y	Xba I	31, 212, 342	31, 212, 342
	17	T28D6	5473	11341120	6.8849	82.28	73.66	tttctgtagcaagctctc	60	aattcctgactctctctg	60	pkP3060	TTT(AA)(A)/A	Y	Dra I	501	218, 283
	18	Y5788A	23310	12301725	14.9161	89.25	86.38	aaacagatctgcaagcag	60	agcttaaacgcaactgatg	60	pkP3075	A(G)GCTG	Y	Hin DIII	16, 315	16, 56, 252
	19	Y1182A	247164	1273584	18.4889	92.43	93.67	aactcaagctctcagcagc	62	ctcacaactctctcagcagc	62	pkP3113	[A/G]GCTG	Y	Nsi III	32, 47, 195	32, 242
	20	Z38F4B	13308	13308	-0.8962	95.91	93.67	ttcactcactctctcagc	62	tttctcactcactctctcagc	60	snp Z38F4B.10	TTT(C)/TAT	N	Nsi I	221, 301	221, 301
IV	1	Y38C1AA	4951	151889	-27.2932	0.87	0.67	agagtaagagatgactcag	60	acttgactttaccagcaac	60	snp Y38C1A.2	TTT(C)TAA	Y	Xba I	515	74, 441
	2	C07B3	1388	1381409	-19.9736	7.90	17.01										

Column title		Additional information (if applicable)
chromosome		
marker#		One marker per segment (as defined by the SNP website: <a href="http://genome.wustl.edu/projects/celegans/index.php?snp=1">http://genome.wustl.edu/projects/celegans/index.php?snp=1</a> ) was selected
Cosmid name		
SNP location on cosmid		
Map position	bp	Position in bp is position of SNP on cosmid (relative to start of cosmid) + starting position of cosmid relative to chromosome
	cM	Interpolated position of cosmid on which SNP is mapped in cM. Obtained from Wormbase release 106 ( <a href="http://www.wormbase.org">http://www.wormbase.org</a> )
Position in % of chromosomal size	if size in bp if size in cM	Both relative to total size of chromosome in bp or cM according to Wormbase release 106
Primers	Forward	
	Tm	Primer melting temperature calculated by $2^{\circ}\text{C} \times (\#A + \#T) + 4^{\circ}\text{C} \times (\#C + \#G)$
	Reverse	
Polymorphism	Tm	Primer melting temperature calculated by $2^{\circ}\text{C} \times (\#A + \#T) + 4^{\circ}\text{C} \times (\#C + \#G)$
	name	names by which SNPs can be found in Wormbase. SNPs with a [?] are the likely/possible identities of the SNPs according to the authors; these could not be recovered in Wormbase.
	type	Shows the kind of polymorphism between brackets in the following order: [N2/CB4856].
Restriction enzyme		Restriction enzyme which has been used for detection. In some cases other restriction enzymes can be used as well, see <a href="http://rebase.neb.com/rebase/rebase.html">http://rebase.neb.com/rebase/rebase.html</a> for more details on restriction enzymes
Digestion results (bp)	N2	expected pattern for the N2-allele after digestion.
	CB4856	expected pattern for the CB4856-allele after digestion.