Single Nucleotide Polymorphisms in Wild Isolates of *Caenorhabditis elegans* ' Romke Koch, HGAM van Luenen, M. van der Horst, KL Thijssen and Ronald HA Plasterk. *Genome Research* 10:1690-1696 2000; rkoch@niob.knaw.nl

chromosome	map pos	cosmid	pos cosm	intron/exon	allele	WT seq	SNP seq	primer fw	primer rev	snipSNP	enzyme	WT digest	SNP digest		AB 1	AB 4	CB4555	CB4856	CB4857	DH424	KR314	RC301	RW7000	TR403	N2
I	-27.11	F56C11	32180	intergenic	1001	tttacgGttatct	tttacgAttatct	ctaaacaacaaacgattcg	cagaaattcaggttccaac	FALSE					-	+	-	+	+	-	+	+	-	-	-
I	-27.11	F56C11	32146	intergenic	1002	ataaaaTctgcaatt	ataaaaCctgcaatt	ctaaacaacaaacgattcg	cagaaattcaggttccaac	FALSE					-	+	-	-	+	-	+	+	-	-	-
I	-19.67	F53G12	19270	intergenic	1003	ttgtagCactgat	ttgtagTactgat	acatcattccacatattatc	atatcctcatccttctacc	TRUE	Rsa I	528, 266	323, 266, 205		-	+	-	+	+	-	+	+	-	-	-
I	-24.16	Y65B4BL	9872		1006	ttttttTaagtttt	ttttttAaagttt	tttgttctcggatctcacg	agaaattgaggagaacctc	TRUE	Dra I	311	262,50		-	+	-	+	+	-	+	+	-	-	-
I	-12.5	Y71G12A	5408		1015	gagagatatttct	gagagaGAtatttct	gacaatgaccaataagacg	gatccatgaaattattccg	FALSE					-	?	-	-	+	-	+	-	-	-	-
I	-12.5	Y71G12A	5470		1016	attactTgaacac	attactGgaacac	gacaatgaccaataagacg	gatccatgaaattattccg	TRUE	BsrI	440,125	364,125,76		-	+	-	+	+	-	+	-	-	-	-
I	-10.31	F12B6	8025	intron	1017	acccctCcttacaa	acccctActtacaa	atctatcaaagaacgatgg	aggattgatatgaggttac	FALSE					-	+	-	+	+	-	+	-	-	-	-
I	-10.31	F12B6	7913/7914	intron	1018	taacccACagtacc	taacccGTagtacc	atctatcaaagaacgatgg	aggattgatatgaggttac	FALSE					-	+	-	-	+	-	-	-	-	-	-
I	-10.31	F12B6	7715	exon 3	1019	ttacaaaaaaaa	ttacaaCaaaaaa	atctatcaaagaacgatgg	aggattgatatgaggttac	FALSE					-	+	-	-	+	-	-	-	-	-	-
I	-10.31	F12B6	7419	intron	1020	tacagtGctccta	tacagtActccta	cctaccatactccaccatg	gagccataccatgacgtg	TRUE	Sca I	475, 228, 75	475, 131, 97, 75		-	+	-	-	+	-	+	-	-	-	-
I	-7.4	K07A3	24012/24015		1021/22	atattgCatCcaaagt	atattgTatGcaaag	ttcacgccaagaagttcac	ccaaccacgtacttgttca	TRUE	SfaNI	171,161	337		+	+	-	+	+	-	+	-	-	-	-
I	-6.65	F32B5	21401	intergenic	1023	attttaGatagaa	attttaTatagaa	atttgtgtggttcgaggtgc	ggcaattgggaagttccg	FALSE					?	-	-	-	+	-	+	-	-	-	-
I	-6.65	F32B5	21656	intergenic	1024	aattggTtcgcaa	aattggCtcgcaa	atttgtgtggttcgaggtgc	ggcaattgggaagttccg	FALSE		890,80	830,80,50		?	-	-	-	+	-	+	-	-	-	-
I	-3.22	T12F5	1397	exon 5	1026	cagtgtCcaatacg	cagtgtAcaatacg	caatcacaatgctcaaggg	cgaggatcacaaggctatc	TRUE	Rsa I	721	396, 325		-	-	-	-	+	-	-	-	-	-	-
I	4.54	F45H11	4652	intergenic	1029	ataaatCtagtca	ataaatTtagtca	agaacgaacgagacaaacc	ggtttgttctcgaagactg	TRUE	Mae I	539, 187, 147	686, 187		-	+	-	-	+	-	-	-	-	-	-
I	19.26	Y40B1B	137	exon	1030	atgtgcTactttt	atgtgcCactttt	ctcggaataatgtcatccta	tcctcctcgttatcgtact	FALSE					+	-	-	+	-	-	+	-	-	-	-
I	18.64	T04D3	5116	intergenic	1031	cgaaacAgtctaa	cgaaacGgtctaa	ggtcacatagatttgactac	cagtggtcgtaaatgttcg	FALSE					+	-	-	+	-	-	-	-	-	-	-
I	18.75	W08E3	5279	intergenic	1032	gatcTtcccat	gatcCtcccat	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5313	intergenic	1033	tgttcaGaatctg	tgttcaAaatctg	ggaatgccagctatgccag	gctcccttcacaagaccac	TRUE	AlwN I	770, 300	1154		+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5388	intergenic	1034	aacccaGaattct	aacccaAaattct	ggaatgccagctatgccag	gctcccttcacaagaccac	TRUE	EcoR I	605, 410, 140	605, 549		+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5423	intergenic	1035	ttttttTattgta	tttttattgta	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5433	intergenic	1036	gtaaaaCacttaaaagt	gtaaaaacttaaaag	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5435-5437	intergenic	1037	aaaacaCTTaaaagt	aaaacaaaaagt	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5441	intergenic	1038	cttaaaAgtcgtc	cttaaagtcgtc	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5444	intergenic	1039	aaaagtCgtcagg	aaaagtTgtcagg	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5509	intergenic	1040	gttgatCggacgt	gttgatTggacgt	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5706	exon	1041	ccaatcGtgcgaa	ccaatcAtgcgaa	ggaatgccagctatgccag	gctcccttcacaagaccac	TRUE	Nla III	985, 70, 50, 20	540, 445, 70, 50, 20		+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5718	intron	1042	agtcctTtgattt	agtcctGtgattt	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5844	intron	1043	gcaaaaAttctatg	gcaaaattctatg	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5869	intron	1044	caattgAaaaaaa	caattgGaaaaaa	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5877	intron	1045	aaaaaaAgttagc	aaaaaagttagc	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	-	-	-	-	-	-	-	-
I	18.75	W08E3	5904	intron	1046	gcaaaataaata	gcaaaaAtaaata	ggaatgccagctatgccag	gctcccttcacaagaccac	FALSE					+	-	-	+	-	-	-	-	-	-	-
I	18.75	W08E3	5966	intron	1047	cgacgcAagagcc	cgacgcGagagcc	ggaatgccagctatgccag	gctcccttcacaagaccac	TRUE	BstU I	436, 404, 238, 74	436, 238, 225, 180, 74		+	-	-	+	-	-	-	-	-	-	-
I	22.56	F47G4	6184	exon 6	1048	taggtaTccgcca	taggtaCccgcca	ctaactgactcactgatc	cagtagcacacaatactac	TRUE	Kpn I	623	375, 248		+	-	-	-	-	-	-	-	-	-	-
II	-15.4	W08F4	33109	intergenic	2003	agatttTttaaaa	agatttCttaaaa	cagacttccaccgtaccat	gagacgaaacgatttacga	TRUE	Dra I	429, 319	748		-	+	-	-	+	-	-	-	-	-	-
II	-13.36	W09B6	7008	intron	2010	aatctgAgaaaat	aatctgGgaaaat	taatttctagcaccagtgac	cccaaatttccacctgtaa	TRUE	Dde I	480, 248	728		-	+	-	+	+	-	+	-	-	-	-
II	-11.82	ZC204	4516	exon 1	2014	agccggTgtcttc	agccggGgtcttc	gtacctaccgtcattgatac	ctttcagtggacagaatcc	TRUE	Nci I	760,270	550, 270, 210		-	+	-	+	+	-	+	-	-	-	-
II	-11.82	ZC204	4549	exon 1	2015	aaaaaaAtgcatt	aaaaaaGtgcatt	gtacctaccgtcattgatac	ctttcagtggacagaatcc	TRUE	Nsi I	800, 240	1040		-	+	-	+	+	-	+	-	-	-	-
II	-11.82	ZC204	4980/4982	intergenic	2016	aaatcgGaGagaatac	aaatcgAaAagaata	gtacctaccgtcattgatac	ctttcagtggacagaatcc	TRUE	Taq I	600, 300, 60, 50, 25, 15	375, 300, 225, 60, 50, 25, 15		-	+	-	-	+	-	+	-	-	-	-
II	-11.82	ZC204	5062	intergenic	2018	ttggtcCgctgaaa	ttggtcAgctgaaa	gtacctaccgtcattgatac	ctttcagtggacagaatcc	TRUE	Pvu II	1040	750, 290		-	+	-	-	+	-	+	-	-	-	-
II	-8.94	D2062	29086	intergenic	2021	tttggaTccagct	tttggaCccagct	ctatggtgcatcgaagtgtc	gtcagcacgttcttaacct	TRUE	BamH I,	435, 308	743		-	+	-	-	+	-	+	-	-	-	-
II	-8.62	T05A8	28559	intergenic	2022	cacgatCaccctt	cacgatGaccctt	cgatggattatgtggtgag	caggttggtcatcatttca	TRUE					+	+	-	+	+	-	+	-	-	-	-
II	-8.62	T05A8	28596	intergenic	2023	cgcgagGtcccgca	cgcgagAtcccgca	cgatggattatgtggtgag	caggttggtcatcatttca	TRUE					?	+	-	?	+	-	+	-	-	-	-
II	-8.62	T05A8	28827/28829	intergenic	2025	gatgaaCcCgacgag	gatgaaGcTgacgag	cgatggattatgtggtgag	caggttggtcatcatttca	TRUE	Alu I	295, 222, 203, 149	295, 222, 149, 110, 93		-	+	-	?	+	-	+	-	-	-	-
II	-8.62	T05A8	28934	intergenic	2026	tagagcTttggcg	tagagcCttggcg	cgatggattatgtggtgag	caggttggtcatcatttca	TRUE	Sty I	769	460, 310		-	+	-	+	+	-	+			-	-
II	-5.8	F19B10	12159	intron	2043	ggtttcaGggcctg	ggtttcaTggcctg	ctacttctctacaagtctac	cttggaacagtctctcaac	TRUE	Dra II	380, 225	640		+	+	-	-	+	-	+	-	-	-	-
II	-3.95	C01F1	33091	intergenic	2051	aaatcgGcgctaa	aaatcgAcgctaa	gcgtatttttccatcgatc	cagcatccagactggtttg	TRUE	Hae II	457, 217	674		+	+	-	+	+	-	+	-	-	-	-
II	-1.11	C18A3	8661	intron	2053	gaaatcGatcgat	gaaatcAatcgat	catgtggacgacgtgtactc	caatgtgcagtcgtctact	TRUE	Pvu I	443, 336	779		-	+	-	-	+	-	+	-	-	-	-
II	-0.39	K10B2	5930	exon 9	2056	aatattCgaaatc	aatattTgaaatc	ccttgtactcgggaacacg	gaatcagtcaaacgctgcc	TRUE	Sfu I	335, 333	668		-	+	-	-	+	-	+	-	-	-	-
II	2.57	ZK666	20260/20261	intron	2069/70	ctggggTCtagatc	ctggggCAtagatc	tcaaccttcatacgtgtcgc	ggaatgactgataaaggtc	TRUE	Xba I	530, 248	778		-	+	-	+	+	-	+	-	-	-	-
II	2.57	ZK666	20315	intron	2071	aagatcTttcagg	aagatcAttcagg	tcaaccttcatacgtgtcgc	ggaatgactgataaaggtc	TRUE	Bgl II	760	460, 300		-	+	-	+	+	-	+	-	-	-	-
III	-28.9	cTel54x	1009	intergenic	3001	gttcttCttcaatt	gttcttTttcaatt	gagcttcttggcttgtttcc	ttgtcaagttcagctccac	FALSE					+	+	-	?	+	-	+	?	-	-	-
III	-26.36	T17H7	15745	intergenic	3002	caatatAttctgt	caatatTttctgt	ctacttatagtcttcctgtc	gcaaccccaccttcaatga	TRUE	Ssp I	910	582, 328		+	+	-	+	+	-	+	-	-	-	-
III	-26.36	T17H7	16138	intergenic	3003	ttaaatGttccat	ttaaatTttccat	tgactcgatattcgcttctg	acatacgtcattgctttgg	FALSE					+	+	-	-	+	-	+	-	-	-	-
III	-26.36	T17H7	16248	intergenic	3004	cttaaaCgattat	cttaaaTgattat	tgactcgatattcgcttctg	acatacgtcattgctttgg	FALSE					+	+	-	+	+	-	+	-	-	-	-
III	-26.26	F42G9	14368	intergenic	3005	cattttTggagaa	cattttGggagaa	gatgacatttatgaaggtcc	tgacccaaccttactctcc	FALSE					+	+	+	-	+	-	+	+	-	-	-
III	-26.26	F42G9	14513	intergenic	3006	cggaaaCgttcaa	cggaaaTgttcaa	gatgacatttatgaaggtcc	tgacccaaccttactctcc	FALSE					+	+	+	-	+	-	+	+	-	-	-
III	-15.52	H04J21	12264	intergenic	3013	atttggCgagctt	atttggTgagctt	atattcatgcgaactttcta	tgagagtgggctacacag	FALSE					-	+	-	+	+	-	+	+	-	-	-
III	-15.52	H04J21	12349	intergenic	3014	agttcgTcaaact	agttcgGcaaact	atattcatgcgaactttcta	tgagagtgggctacacag	FALSE					-	+	-	+	+	-	+	+	-	-	-
III	-15.52	H04J21	12446	intergenic	3015	ttaaagGttactt	ttaaagAttactt	atattcatgcgaactttcta	tgagagtgggctacacag	FALSE					-	+	-	+	+	-	+	+	-	-	-
III	-15.52	H04J21	12524	intergenic	3016	aataaaAaaatat	aataaaTaaatat	atattcatgcgaactttcta	tgagagtgggctacacag	FALSE					-	+	-	-	+	-	-	+	-	-	-
III	-15	W04B5	23843		3017	ttttTacctta	ttttacctta	ggagcagaagattcataga	aagctgatggctgtagaac	FALSE					-	+	-	+	+	?	-	-	-	-	-
III	-7.48	F59A2	12490	intron	3019	attctcGaaaaat	attctcAaaaaat	ggctggataatgaaaccgg	taaaaatctctttgtttcg	FALSE					-	+	-	+	+	-	+	-	-	-	-
III	-7.48	F59A2	12840	intron	3020	ttggtaTttttttg	ttggtaCtttttg	tatttccagcagctgtgag	gcgaatttatcgattttcg	TRUE	Rsa I	481	341, 140		-	+	-	-	+	-	-	-	-	-	-
III	-6.62	M01F1	26492	intron	3021	ggcctGaaaccg	ggcctAaaaccg	agatatggtgcccagtacg	atgaagaggagctacgtg	FALSE					-	+	-	+	+	-	-	-	-	-	-
III	-6.62	M01F1	26645	intron	3022	ttttttAaattta	ttttttTaattta	agatatggtgcccagtacg	atgaagaggagctacgtg	FALSE					-	+	-	-	+	-	-	-	-	-	-
III	-5.01	C14B1	1795	exon 2	3023	ggttgaCgccacc	ggttgaTgccacc	cttcattgtagatgatagac	gatcacaaagtaatgacta	TRUE	Hind II	410, 315	725		-	+	-	-	+	-	-	-	-	-	-
III	-3.85	H38K22	4076	intergenic	3024	ttccatCtgaaaa	ttccatTtgaaaa	gtgaagagaatgcaaggac	tcaactttggcgcatacgc	FALSE					-	+	-	-	+	-	-	-	-	-	-
III	-0.76	R151	22061	exon 7	3025	tagaggAcaagat	tagaggGcaagat	tcgtacttctttgcctcag	ttattatacaccaacctag	FALSE					-	-	-	-	+	-	-	-	-	-	-
III	-0.74	B0361	15143	intron	3026	acctaaTaaataa	acctaaGaaataa	gtatttcttacccgagagtc	cagttcacctggaatctca	TRUE	Dde I	683	366, 317		-	+	-	-	+	-	-	-	-	-	-
III	-0.38	C50C3	26986	exon 8	3027	ctcaacCtcaatc	ctcaacTtcaatc	gctcttcttggtacattccc	cacgtcttctgagtatttc	FALSE					-	+	-	+	+	-	+	-	-	-	-
III	-0.38	C50C3	27035/27036/27037	exon 8	3028	tgtgggCAGctcatc	tgtgggctcatc	gctcttcttggtacattccc	cacgtcttctgagtatttc	TRUE	Alu I	339, 195, 120, 71	463, 120, 71		-	+	-	-	+	-	-	-	-	-	-
III	0.12	R107	13786	intergenic	3029	gcagttTttgtaa	gcagttCttgtaa	ctgaagaagcggcaaagta	gacaccgcatttgagaaac	FALSE					-	+	-	+	+	-	+	-	-	-	-
III	0.12	R107	24525	exon 3	3030	ccacagAggcatt	ccacagGggcatt	gagcatcaatagtgaacgc	agaggaactcatcatcatc	FALSE					-	+	-	+	+	-	+	-	-	-	-
III	0.21	ZK512	20159	intergenic	3031	gccatcAacactc	gccatcCacactc	ctttgcttcttccgtttcg	tgatctcagaaaagccagt	FALSE					-	+	-	+	+	-	-	-	-	-	-
III	0.21	ZK512	20266	intergenic	3032	tataagCccaggt	tataagTccaggt	ctttgcttcttccgtttcg	tgatctcagaaaagccagt	FALSE					-	+	-	+	+	-	-	-	-	-	-
III	0.21	ZK512	20369	intergenic	3033	cttcaaCtaactg	cttcaaAtaactg	ctttgcttcttccgtttcg	tgatctcagaaaagccagt	FALSE					-	+	-	-	+	-	-	-	-	-	-
III	0.32	ZC84	222-230		3034	tgcacgAAACTAAATaa	tgcacgaaactaa	cctctctttgcgtgtcatcc	gaaaccggaaattcattgc	FALSE					-	+	-	-	-	-	-	-	-	-	-
III	0.92	T05G5	34938	exon	3035	tccaaaCggacct	tccaaaAggacct	cgtaaactaccaaactcgg	ggtctactacaactataca	TRUE	Dra II=Eco0109I	782	450, 330		-	+	-	+	+	-	-	-	-	-	-
III	0.92	T05G5	35048	intron	3036	ttttttTaattta	ttttttAaattta	cgtaaactaccaaactcgg	ggtctactacaactataca	TRUE	Dra I, Apo I	782	443, 339		-	+	-	-	+	-	-	-	-	-	-
III	1.08	ZK632	10856	intergenic	3037	gatcagAactata	gatcagGactata	tgcgtagttattgacagtgc	acccataaatctgtctccc	FALSE					-	+	-	+	+	-	+	-	-	-	-
III	2.45	C38H2	6596	intergenic	3038	atacctTaaaata	atacctCaaaata	tgtgtgacaagttcaagtgc	aacagtttgagacgagaac	FALSE					-	+	-	-	+	-	-	-	-	-	-
III	15.29	Y75B8A	250677	intron	3039	tgaaaaGttccga	tgaaaaTttccga	aaccatggattggagagg	tcagttccgcgaattagc	FALSE					?	+	-	-	+	-	+	-	-	-	-
III	21.69	F53A2	25442 -25446	intergenic	3043	acaggaCTGATctgaga	acaggactgaga	tttggaggaccatcagagg	tggctcaccttctttctcc	TRUE	Sau3A	300, 100		400	+	+	-	-	+	-	-	-	-	-	-
III	23	T25C8	568	intergenic	3044	tagtgtGaacgcg	tagtgtAaacgcg	agagttgttcgtcgagtaga	agtagcagccagcaacaa	FALSE					+	+	-	+	+	-	+	-	-	-	-
IV	-10.53	R05C11	38297	intron	4005	tgtcttTaaatgg	tgtcttCaaatgg	ctagaaaaccacacattcta	ggattccgaagagtcattc	TRUE	Dra I	388, 321	709		+	-	-	-	-	-	-	-	-	-	-
IV	2.7	H32C10	13460	intron	4010	ttttaattgtttt	ttttaaAttgtttt	ccaaggagaaatgaatgag	cctttccggatttccacaa	TRUE	Dra I	513, 169	377, 169, 139		+	-	+	-	-	+	-	-	-	+	-
IV	24.53	C35D6	20076	intergenic	4024	aaaaatGttaaat	aaaaatAttaaat	gatttaggactagactcagc	gactaacatcatgccatt	TRUE	Ssp I	723	377, 346		-	-	-	+	-	-	+	-	+	-	-
V	-19.17	T01G6	14195/14196	intron	5002	ggtctaCAatgtat	ggtctaTCatgtat	ctggaatatcggtcacttcc	gttattcactcgcgtgttg	TRUE	Acc I	401, 286		685	+	-	-	-	-	-	-	-	-	-	-
V	-19.17	T01G6	14210/14214	intron	5004/5	atcatgCattCtata	atcatgTattTtatat	ctggaatatcggtcacttcc	gttattcactcgcgtgttg	TRUE	snp4 =Nsi I + snp5 = Bsm I	385, 300	685		+	-	-	-	-	-	-	-	-	-	-
V	-19.17	T01G6	14280	exon	5006	aataacTgcagcat	aataacCgcagcat	ctggaatatcggtcacttcc	gttattcactcgcgtgttg	TRUE	PstI	320, 370		690	+	-	-	-	-	-	-	-	-	-	-
V		ZK384	975		5034	cccgaaTgtgtcg	cccgaaCgtgtcg	gaatgaaacaccatcatttc	gaaaaatgtgacatcagca	TRUE	Afl III	374, 266	640		+	+	-	-	+	-	+	-	-	-	-
V	24.99	F19B2	29526	intron	5041	ccatggAaaccat	ccatggTaaccat	ttcagatgaaataagctgag	cataataccgttcgagtcc	TRUE	BstEII	827	620, 210		+	+	-	+	+	-	+	-	-	-	-
V	-19.17	M02H5	10960-10964	intron	5049/50	aaattgtTgtaAattgcc	aaattgtAgtaCattc	actccaaactgcaaaatgc	gcaccagtgggattttgt	TRUE	RsaI	400, 287, 200, 65	300, 287, 200, 100, 65		+	-	-	-	-	-	-	-	-	-	-
X	-3.03	C03B1	38853-38856	intron	6008	caaacgtatataTATAgat	caaacgtatataCCg	cgtagagacgcaaaatagg	gctcaatttcacgcgtcca	TRUE	Acc I	682	425, 257		-	-	-	+	+	-	-	-	-	-	-
X	-2.76	C25B8	5416	intergenic	6015	gcagttCtagaaa	gcagttGtagaaa	gtatctgagatagggtacg	cagaaaacctgttagacat	TRUE	Xba I	432, 243	675		-	-	-	-	+	-	-	-	-	-	-
X	-2.63	R03E9	33736	intergenic	6017	ttgactAcagttg	ttgactGcagttg	gaaaaacaggccccagtaa	caaacatgttttgaccgct	TRUE	Pst I	626	348, 278		+	+	-	-	+	-	+	-	-	-	-
X	-2.36	F41C6	10186	intergenic	6020	ttaaaaTtttttt	ttaaaaCtttttt	gtttggtcgctggagttttg	catcaaagaggcaacaag	TRUE	Fsi I	588, 192	780		+	+	-	-	+	-	+	-	-	-	-
X	-1.56	C44E12	944		6021	tgtaaaCttaatt	tgtaaaAttaatt	agaacagcggacagagatc	tgtcacgttacttgcaatc	TRUE	Asn I	359, 261	359, 184, 77		+	+	-	+	+	-	+	-	-	-	-
X	0.04	R04E5	20642	intron	6028	aacttaTccctat	aacttaGccctat	gtaatcagttactgtacact	ctacatcaatgtcaacacc	TRUE	Dde I	733	412, 312		+	+	-	+	+	-	+	+	-	-	-
X	2.17	F11A1	24535	intergenic	6037	atgtttTtaatag	atgtttCtaatag	cctcatctcatctttacttg	caagatgacttgccgattc	TRUE	Mse I	296, 240, 79	536, 79		+	+	-	+	+	-	+	+	-	-	-
X	2.17	F11A1	26014	intergenic	6038	aactgaCatccgc	aactgaTatccgc	cgtccgtatcgttttcctc	ccatttgaacttctaggtc	TRUE	EcoR V	725	374, 351		+	+	-	+	+	-	+	+	-	-	-
X	4.54	C35C5	26375	intergenic	6058	attcaaCatgcat	attcaaTatgcat	ccatttcttggtgtgtccg	cttagatctatagagatcg	TRUE	Nsp I	641, 130, 63	771, 63		+	-	-	+	+	-	-	-	-	+	-
X	4.54	C35C5	26673	intergenic	6060	aaaaagTtgtcga	aaaaagCtgtcga	ccatttcttggtgtgtccg	cttagatctatagagatcg	TRUE	Alu I	365, 273, 41	273, 258, 107		-	-	-	-	+	-	-	-	-	-	-
X	4.54	C35C5	31295	intergenic	6061	ggaaagTtaaatc	ggaaagCtaaatc	gaacaacatcataatgtgccct	cagctcgagtttatactgc	TRUE	Alu I	511, 125, 114	278, 233, 125, 114		-	-	-	-	+	-	-	-	-	-	-
X	5.5	T04F8	15879	exon	6065	gcagaaTcaacga	gcagaaCcaacga	cacaagacgtcctacaagt	catttgttcaatcctaccg	TRUE	Hinf I	290, 274, 144	434, 274		-	-	-	-	+	-	-	-	-	-	-
X	21.33	C33A11	1933	intron	6087	gttaacGgcctct	gttaacAgcctct	gttttcactggcactactcc	cggatatcgacctgaaaga	TRUE	Hae III	381, 308	689		+	-	-	+	-	-	-	+	-	-	-
X	23.79	F01G12	14985	exon	6093	aagaccGttaact	aagaccAttaact	tagatatcgtggaacccc	cctgggaatccgttttctc	TRUE	Hind II	331,206	537		+	+	-	+	+	-	+	-	-	-	-
X	23.79	F01G12	18932	intron	6096	atacagAacaaat	atacagTacaaat	gattgaacatagctcacag	tttcgatcgttttggacgc	TRUE	Rsa I	282, 105	158, 129, 105		+	+	-	+	+	-	+	+	-	-	-

SNPs were found by random shotgun sequencing of wild strains of *C. elegans* . SNPs were subsequently amplified by PCR and presence of the SNP in several natural isolates was tested by digestion with restriction enzymes or by sequencing.