

Supplementary Tables and Figure

Keightley *et al. Genome Res.*

Supplementary Table 1. Details of the 174 mutations detected by comparison of MAQ-3 alignments. Context sequences refer to M126, with the mutant base at position 6.

<i>Chrom.</i>	<i>Location</i>	<i>Ref.</i>	<i>M126</i>	<i>M138</i>	<i>M158</i>	<i>Depth</i>	<i>Context</i>	<i>Confirmed?</i>
4	775331	T	T	C	T	9	gatacctcacac	y
4	1094899	C	T	C	C	8	ttatattcatg	
2L	8517	G	G	G	A	8	aaagtgaccaa	
2L	112458	T	A	T	T	7	gcataaatata	y
2L	2057210	C	C	T	C	8	cattttccatca	y
2L	2445378	T	T	C	T	5	tttcttcttct	
2L	3185700	G	T	G	G	9	tgttttttctg	y
2L	4924824	T	C	T	T	7	tttttcttttag	
2L	5554400	G	A	G	G	8	ccaagagcttc	
2L	6170048	C	A	C	C	8	gcatcaagtga	y
2L	7687850	A	C	A	A	5	ctccacgagcc	
2L	8088659	G	G	A	G	6	tttctgcttag	
2L	8361979	T	G	T	T	8	gaatagaagta	
2L	8559489	C	C	C	T	10	caggccaaaca	y
2L	9133036	C	C	T	C	9	aaacacagagc	
2L	9222854	G	G	A	G	11	tagcgggtgaca	
2L	9915354	G	G	A	G	6	tgtctgcogca	
2L	11320192	G	G	C	G	5	cagtagcgaaa	
2L	12763434	T	T	C	T	6	acctttgctcc	
2L	12866765	C	G	C	C	6	cggatggcatt	y
2L	13550984	G	A	G	G	5	aacaaaaaaaa	y
2L	14330311	A	A	G	A	11	tgcacatcatt	y
2L	14395467	C	T	C	C	7	ttaaataaatc	
2L	14512005	A	A	A	G	8	cgttgacagtg	
2L	15089614	C	C	C	T	5	gaacgcaacct	
2L	16083946	C	C	C	T	6	cgttacctcag	
2L	16271868	G	G	A	G	5	agaatggggaa	
2L	16762345	A	C	A	A	7	taatgcttcga	
2L	17676976	G	A	G	G	5	agctaacgaaa	
2L	18156416	C	T	C	C	6	ctggattggtc	
2L	18719727	T	A	A	T	7	atataaatcaa	
2L	18810337	G	G	G	C	6	cactcgatgct	
2L	19112661	C	T	C	C	5	taaactctagt	y
2L	19135126	C	C	C	T	7	gttccccctcc	
2L	19847654	T	T	G	T	8	ctcattcggac	
2L	19856108	C	C	A	C	7	gcaacaaaat	
2L	20491038	T	T	T	C	5	ggttttgtggt	y
2L	20850063	G	A	G	G	5	ggaagaccgct	
2R	1945573	T	A	T	T	9	ctactatcttc	
2R	3224751	G	A	G	G	6	ttgatagggtg	
2R	4086957	G	G	C	G	12	ctcaagcccta	
2R	4839518	G	G	G	A	9	tgaagggagct	
2R	5050317	G	G	G	T	11	cattagaaatt	
2R	5098046	A	A	G	A	8	acacaaatgag	
2R	5159930	G	G	G	A	7	gccaaagtcga	
2R	5710424	C	C	G	C	6	atgaacaagta	
2R	6025632	G	A	G	G	7	caatgaacagt	
2R	6317864	G	G	T	G	10	taacggacaaa	
2R	7296839	G	G	A	G	6	gatggggaactt	y
2R	7649930	T	T	T	C	7	cttaatagaaa	
2R	9193724	T	C	T	T	7	aacgacaaaaa	
2R	10529551	T	T	A	T	7	gcagtttactc	
2R	11705889	A	A	A	T	6	gaataagccgc	
2R	12705718	C	T	C	C	8	taccgtagttt	
2R	12795492	A	A	A	G	9	ttcagattcac	
2R	13404236	C	C	C	T	8	atcatcccatt	
2R	13617204	A	A	A	G	5	ctgtcaaaaagt	y
2R	13648416	T	T	T	C	5	actcataaatg	
2R	13831195	C	T	C	T	10	tgcagtggtgga	

Supplementary Table 1 (continued)

<i>Chrom.</i>	<i>Location</i>	<i>Ref.</i>	<i>M126</i>	<i>M138</i>	<i>M158</i>	<i>Depth</i>	<i>Context</i>	<i>Confirmed?</i>
2R	13996330	T	T	G	T	6	aaaattgaact	y
2R	14696991	C	T	C	C	7	ctccttcgccc	
2R	14945925	T	G	T	T	5	gctccgcgggg	
2R	15517092	G	G	G	T	8	ttagtggaat	y
2R	15994558	T	T	C	T	6	cgtcgttgac	
2R	16424044	A	A	A	T	5	gtttgacaact	
2R	16868361	A	A	A	G	7	cacagatcata	
2R	17662262	G	G	T	G	5	aaaatgatgct	
2R	18123686	G	G	G	A	8	agagggctcac	y
2R	18615227	G	A	G	G	7	gtagcaattat	
2R	20306157	C	T	C	C	10	gtagttccgtg	y
2R	20331360	C	C	T	C	5	ccggcctgcat	y
2R	20795977	G	G	T	G	7	ctaagtgtatg	
3L	225604	T	T	A	T	5	aactgttaaaa	
3L	512524	C	C	C	A	5	agcaccgctgc	
3L	912754	T	T	T	A	6	tgctctcaacg	y
3L	3092030	C	C	C	T	11	catgtcgatgg	
3L	3209259	A	A	T	A	6	tagctaaaact	y
3L	4123037	A	G	A	A	9	acgatgagaag	
3L	5098081	A	A	A	C	7	agcacaaaaat	y
3L	5416411	T	T	C	C	5	cataatgtact	
3L	5705461	C	C	C	G	11	tggctcaaagg	
3L	5911754	G	G	G	T	7	tttacgtgccg	
3L	6106767	G	G	G	T	5	aataagtgaca	
3L	6478611	T	T	T	G	8	atcagtacacg	
3L	6534853	C	C	G	C	9	acacacacgca	
3L	7056502	C	T	C	C	9	taccatataacc	
3L	8068689	A	C	A	A	8	gaaaaccccag	
3L	8220579	C	G	C	C	10	gcatgggcttg	
3L	10314128	A	A	G	A	5	ccactagagga	y
3L	10318987	T	T	T	C	6	ttccttgtttc	
3L	11363513	A	A	C	A	8	aagttaaagaa	
3L	13078885	T	T	C	T	7	attccttgccg	
3L	13682287	C	C	T	C	7	gtggctctgggc	
3L	14278286	C	C	T	C	9	gttggcgatta	
3L	14478499	A	A	C	A	7	ttaaaatcatt	y
3L	14649202	G	G	T	G	9	cttttggaactc	
3L	14900626	G	G	G	T	5	ctgcgggcaca	y
3L	14905747	T	T	T	C	8	atttattgaat	
3L	14967781	T	T	T	G	6	aatatattggga	
3L	15541786	T	T	T	G	14	agcaatttaac	
3L	15910722	A	A	A	G	6	cctcgaaattc	
3L	16169205	G	A	G	G	5	gcaggagggtg	
3L	16353192	G	G	C	G	15	acttagacgtg	
3L	16784642	C	C	C	T	7	ttatacttata	
3L	16851478	C	T	C	C	6	tgcgatccgca	
3L	17882597	A	A	T	A	8	tttcgaaaagt	y
3L	18310228	C	C	T	C	6	gtccacggatc	
3L	19332561	A	T	A	A	8	agtagttatat	
3L	19626860	C	C	A	C	5	gaatcctgtat	
3L	22182346	T	T	T	G	8	cagagtacaga	
3L	22741983	T	T	A	T	9	cagtttacaaa	
3L	22742032	T	T	C	T	12	ttatttgtccg	
3L	22958765	C	T	C	C	5	ctgtatgctct	y
3L	22971050	A	A	A	G	5	atattaaatat	
3R	467108	G	A	G	G	9	gcgggagcgtt	
3R	1729794	T	T	T	C	9	attttttatat	
3R	2588353	C	C	C	A	5	ttttgcaactg	
3R	2870267	G	G	G	A	6	aatatgcaata	
3R	3125497	T	T	T	G	11	ggtatttatcc	

Supplementary Table 1 (continued)

<i>Chrom.</i>	<i>Location</i>	<i>Ref.</i>	<i>M126</i>	<i>M138</i>	<i>M158</i>	<i>Depth</i>	<i>Context</i>	<i>Confirmed?</i>
3R	4508271	T	T	A	T	5	tttagtgtgat	y
3R	5454267	C	A	C	C	5	agaaaaatcat	
3R	5864554	G	G	G	T	6	ctcgggataat	y
3R	6645578	T	G	T	T	6	gcaatgtaacc	
3R	7261155	G	G	G	T	5	cgctggggcac	
3R	7598055	C	C	A	C	5	acacacacaca	
3R	7755729	A	C	A	A	5	tggcacgaggt	
3R	7829629	G	G	G	A	8	taggcgtgtca	
3R	7905375	C	C	C	G	8	tcctccttctc	
3R	8395911	A	A	G	A	7	aatcaaatcct	
3R	11831986	T	G	T	T	5	atcttgaattt	
3R	12049751	T	T	A	T	8	agaaattatat	
3R	12369335	T	T	T	A	5	aaatctcgagg	
3R	12383937	G	C	G	G	9	aaacgccttct	
3R	12708708	T	C	T	T	6	aatctcgtttg	
3R	13177303	G	A	G	G	6	aaaccaaagt	
3R	13217990	T	A	T	T	12	ttagcatcaat	
3R	13665434	C	C	T	C	9	catgtcacgtc	y
3R	15206045	A	A	A	C	9	cttaaagaagt	
3R	15870127	C	C	T	C	6	aattaccgcga	
3R	16394875	C	T	C	C	11	acatatgagtt	
3R	17548107	C	T	C	C	7	ctgcctagcaa	
3R	17877795	T	T	C	T	13	acgtgtatttg	
3R	18008132	C	G	C	C	5	acgacgtaatg	
3R	18407567	A	G	A	A	10	gtgcagcgatg	y
3R	19459560	G	G	G	A	8	ccgatgcagcg	
3R	20480280	G	G	C	G	9	cgtctgtctga	y
3R	20740863	C	C	C	T	5	aaaaacttcgg	
3R	21630987	C	C	G	C	7	tttcacctttt	
3R	22196194	A	A	A	T	11	agcaaaagcttt	y
3R	22497356	C	G	C	C	5	aacgagggtcta	y
3R	23356720	C	C	C	G	7	gagcgcaacaa	
3R	24453598	A	A	A	G	10	ttaacaatttta	y
3R	26234389	A	T	A	A	9	aggaatggacc	y
3R	26842608	G	G	T	G	5	acagagagagc	
3R	27545050	C	C	A	C	7	ctaatacgcata	
3R	27545069	C	C	A	C	6	ttccccaaaat	y
X	2072387	G	G	G	C	8	ttccagcaggc	
X	2762835	C	T	C	C	6	cagggttaaaag	
X	4345553	G	G	G	T	5	aatttgcatgg	y
X	7484518	A	A	G	A	8	aatcgactact	
X	7840500	C	C	A	C	6	ttcttctgttt	
X	8145968	A	A	T	A	7	gtatcaagctt	
X	11668883	A	T	A	A	5	cacaatcttac	y
X	11668884	G	C	G	G	6	acaatcttact	y
X	12557644	G	T	G	G	5	gggcttcttct	
X	13445269	G	G	G	T	6	ccaaagggttg	
X	16839161	C	A	C	C	6	acgatagcttt	
X	17801352	T	C	T	T	7	gcgtaccgata	
X	18206889	G	A	G	G	9	gtcgaacggaa	
X	19358470	A	A	A	G	5	aaaccaaaccg	
X	19750998	G	G	C	G	9	ctttagcaaca	
X	20669767	T	T	T	G	8	aaaattttaaga	
X	20669802	C	C	C	G	7	ctaatacttttt	y
X	21383234	T	T	A	T	6	tcgtatogtct	

Supplementary Table 2. Counts of bases preceding (a) and following (b) sites at which a mutation was detected in MAQ-3 alignments. Expected numbers of bases, calculated on the basis of genomic dinucleotide content, are shown in parenthesis.

(a)

Wild type	Preceding base				χ^2 3df	P
	A	T	G	C		
A/T	31 (31.49)	25 (22.46)	14 (16.25)	19 (18.81)	0.60	0.90
G/C	21 (23.68)	37 (27.76)	14 (17.14)	13 (16.41)	4.7	0.20

(b)

Wild type	Following base				χ^2 3df	P
	A	T	G	C		
A/T	40 (31.49)	26 (25.65)	11 (16.04)	12 (15.82)	4.8	0.19
G/C	25 (23.98)	24 (23.36)	21 (17.14)	15 (20.53)	2.4	0.49

Supplementary Table 3. Numbers of candidate indel mutations called, numbers of sites, and mutation rate tabulated against minimum read depth from Novoalign alignments.

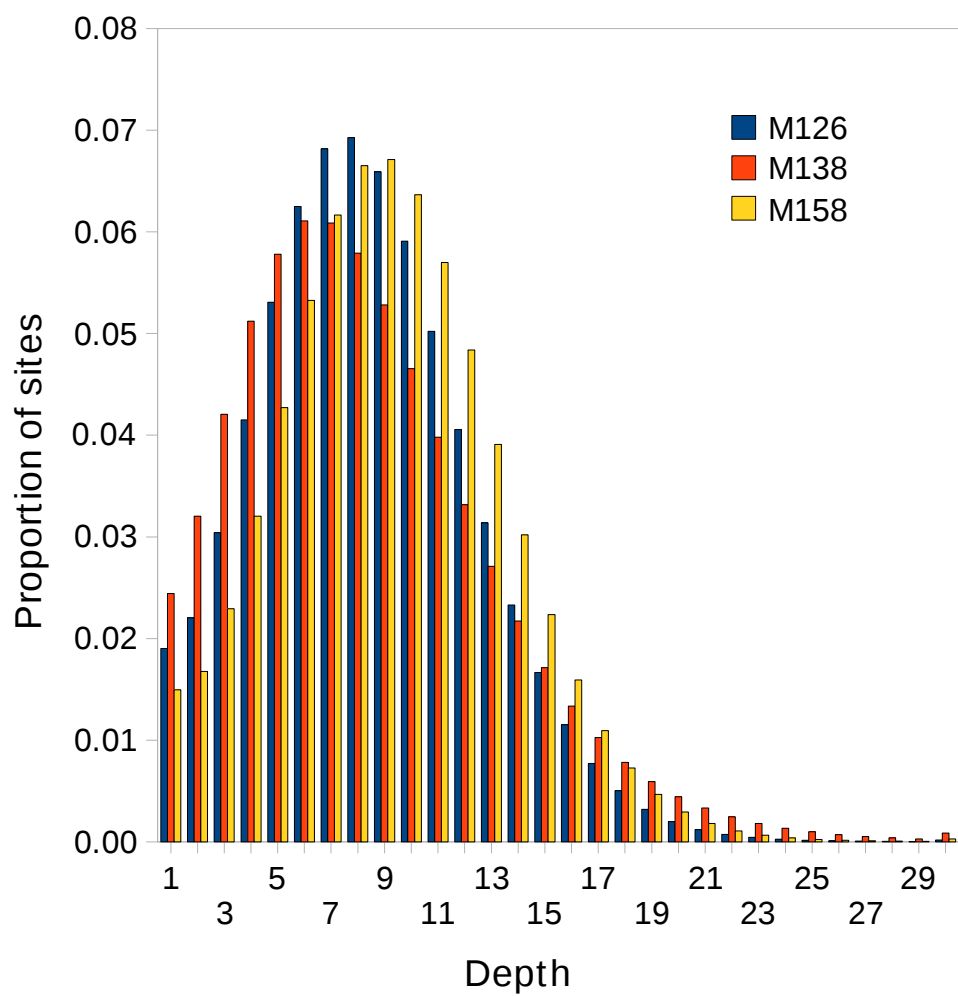
<i>Depth</i>	<i>No. indels called</i>	<i>No. sites</i>	<i>Mutation rate x 10⁻⁹</i>
2	1003	1211163	1053.60
3	303	1836039	209.96
4	118	2702387	55.55
5	43	3780800	14.47
6	29	5010572	7.36
7	16	6281464	3.24
8	8	7440803	1.37
9	6	8374538	0.91
10	6	8954527	0.85
11	4	9144603	0.56
12	5	8957353	0.71
13	2	8428806	0.30
14	2	7634188	0.33
15	1	6682747	0.19
16	0	5670651	0.00
17	0	4660939	0.00
18	0	3728305	0.00
19	1	2911044	0.44
>=20	0	8144634	0.00
Total >=8	35	90733138	

Supplementary Table 4. Candidate indel mutations called by Novoalign at read depth ≥ 8 .

<i>Depth</i>	<i>Chrom.</i>	<i>Location</i>	<i>MA line</i>	<i>Indel</i>	<i>Upstream context</i>	<i>Downstream context</i>	<i>Confirmed</i>
8	2L	5569655	M126	+GGATA	ATGGATGGGTAATAA	CTATAACTATTTTAG	No
8	2L	8846479	M126	-T	AGTTATTCTAATTTT	TAATTATAAGTTTTT	No
8	2L	13740070	M126	-G	CTAAAGCTGTTCAA	GCTTATTCAAATATA	No
8	3R	13039252	M126	+A	TATCTTGAAACAAAG	AAGGTTAGGTATTAG	No
8	X	15358987	M126	-CT	TAGTTAAAAGTTTGT	CTAAAAGTTTTTATT	No
8	X	20355521	M138	+C	ATGGGAAAACAAGAA	AACAAATCGTGAGAA	No
8	2R	17877344	M158	+T	AAATCATGTGTTATT	AATTGTCTTTATATT	No
8	X	11415304	M158	-T	ATGCACATTTTTTTT	TCCTATTTATTTAAA	Yes
9	3L	8947586	M126	-CAC	AAGTTATCGATATAC	CACAATACCACAAAC	Yes
9	3L	12283471	M126	-C	AATGAAATGAATTTT	CTCCTCTGCTTTCAA	No
9	3L	15257181	M126	+T	AATTTAATAACCTTT	CAATATAATATACTA	No
9	X	4479983	M126	-AA	AGTTTTAGTTTATT	AATTTTTTTTTTCAA	No
9	X	19985101	M126	-T	GTTGTAGCATGTACC	TGCTGTAAACAATACA	No
9	3L	21278	M138	-T	CTACCAATACTTTTA	TAAAAAAGTTCAATA	No
10	2L	14631954	M126	-ATCG	GTTTAGGGGTGATCG	ATCGTTGTTTGCCCC	Yes
10	3L	11134770	M126	+CAAAA	AAAAAGTTTTAAAAA	TATCCAACAAACTAA	No data
10	3L	16481100	M126	+G	ACAGTGATATTTTTA	AAAATATTTTTTAATT	No
10	3L	17537346	M126	+A	ATTTTTTTTTTAATAT	TTTTTCCAGACAAA	No
10	X	8706734	M126	+TTGTA	TTTTAAAAATATATA	CTTCTCGGCAACTTC	No
10	3R	1750359	M138	-T	GGCACAGAAATCAAT	TTGATGCTCCGCCAC	No
11	2R	15151631	M126	-G	AAGCCAAAGCTGCAG	GCAGACGTCGTCCAG	No
11	3R	7483420	M126	-TA	TGCGAACGGGCAGCA	TAAATCGCTGGGTAA	Yes
11	2R	13898306	M158	-G	GCGGGAATATGGGGG	GCGCGTCAGCTAACA	Yes
11	2R	14147261	M158	+C	CAAAGCTCCAGCATC	AGAGTATATGCTCGA	No
12	2L	12575955	M126	+T	ATTTTAATTGATTTT	AAAAATAAATATACA	No
12	2R	6468287	M126	-GT	TACCAATAGGATAGT	GTATGGCCAAAACCTC	Yes
12	2R	14242602	M126	-A	ATAAATAATAAAAAA	ACCAAGCACACCAAC	No data
12	3L	18596265	M126	+A	ATTAAGCCATTCAAA	TAAGTATATATTTTA	No
12	2L	18132958	M138	+T	AATATTATTCTTAAT	CTCACCATTCTGCAT	No data
13	2L	14518243	M126	-T	TTATTATAGATAAGA	TATAATCATATCAAA	No data
13	2L	15180866	M126	+A	TTAATATAATCCAAT	TATATTACAACCTTG	No
14	3R	26175815	M138	+A	ACTGGCCACACACAC	ACACACATGACGTCT	No
14	4	924821	M138	-GG	ATAACAACGCGGTA	GGTGTATTTAGCTGC	No data
15	3L	13103866	M158	+G	CAGCAGTATTGCAAG	ATATCGGGGAAAAAA	Yes
19	2R	16922821	M126	-ATT	TAAATATAAGTTTTT	ATTTTAGGCTTTTCT	No

The final column indicates whether the mutation was confirmed by Sanger sequencing of PCR products. Insertions are located between the upstream and downstream context sequences. Deletions delete the start of the downstream sequence.

Supplementary Figure 1.



Proportion of sites plotted against read depth (the number of reads at a site) for MAQ-3 alignments of each of the 3 MA lines. The proportion of sites at read depth 0 was 31-32%.