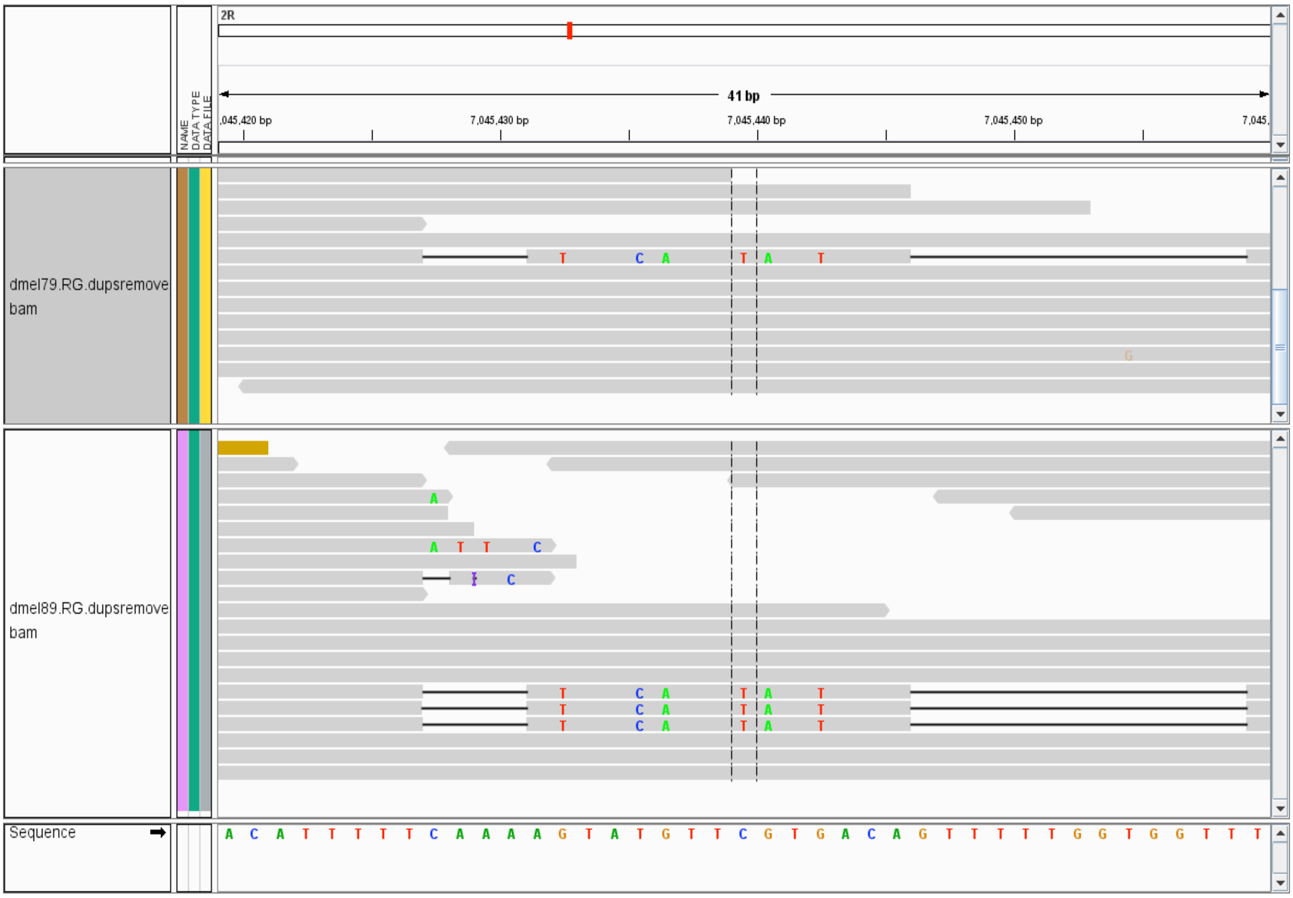

Figure S1 Screenshot from the IGV showing a typical example of a read mapping error. The reference sequence is shown at the bottom, indicated by "Sequence →". Reads are indicated as horizontal grey bars, and only bases that differ from the reference are shown. Two individuals separated by a double horizontal line have a candidate C→T mutation at the focal site delimited by the vertical dotted lines. However, each of the reads containing the non-reference base (T) also has five SNPs and two deletions (shown as solid horizontal lines) in perfect association, i.e., none of these variants are present in the reads containing the reference base (C) at the focal site.

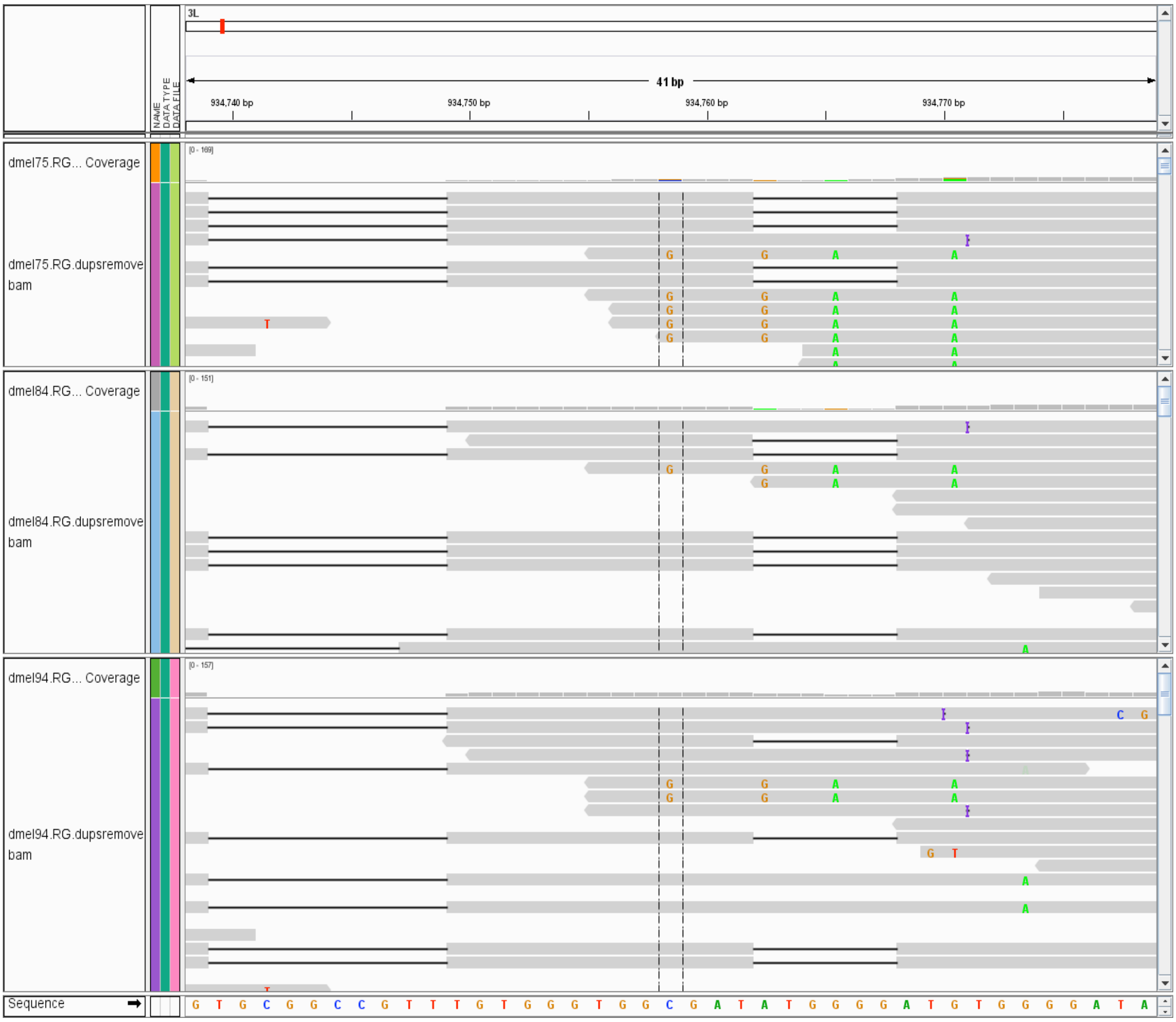

Figure S2 Screenshot from the IGV showing a second example of a read mapping error caused by mismapping of a paralogous region.

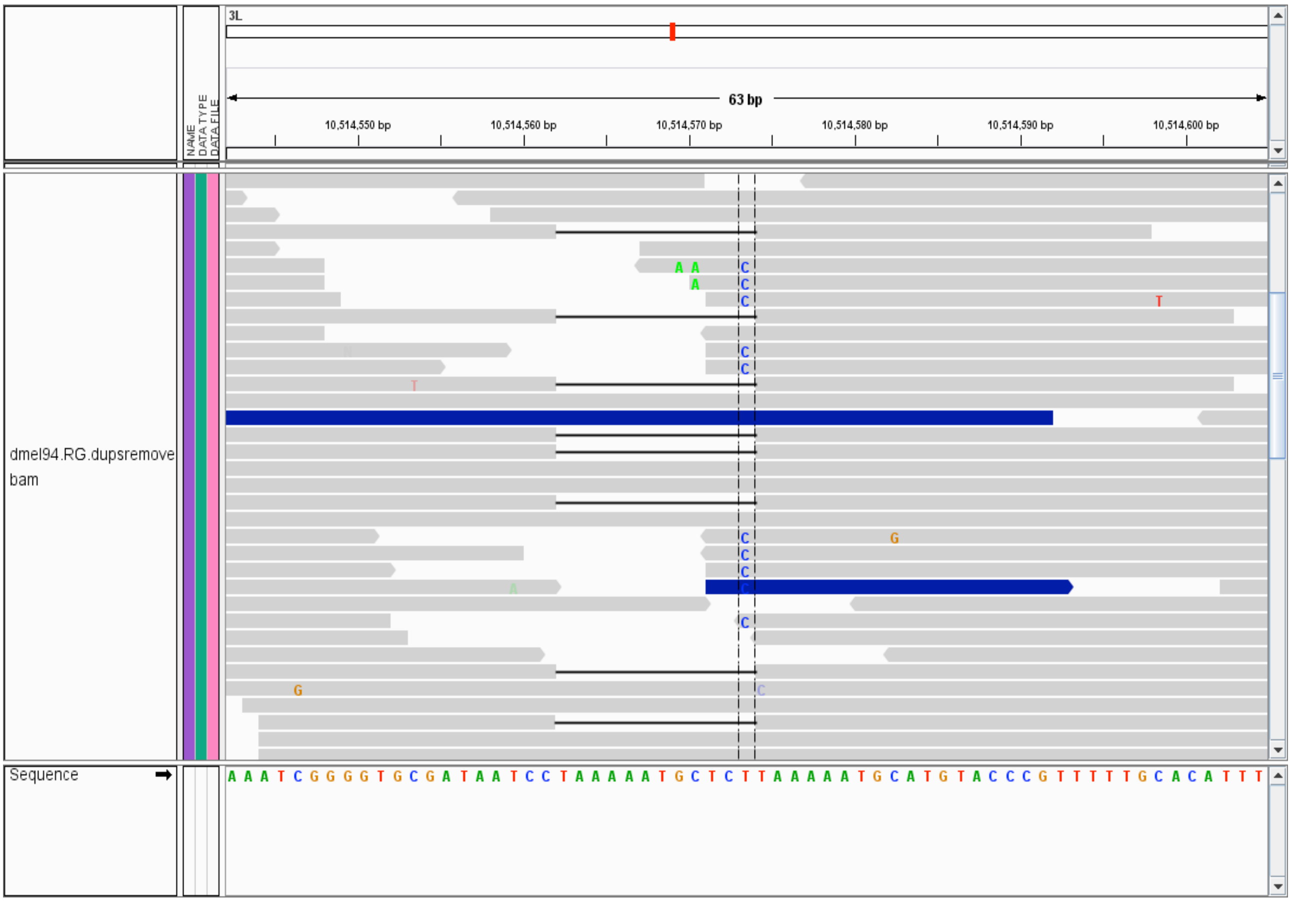

Figure S3 Screenshot from the IGV. The T→C candidate mutation can be resolving by moving bases leftwards to the opposite end of the deletion (in other words, reads have a deletion, not a SNP).

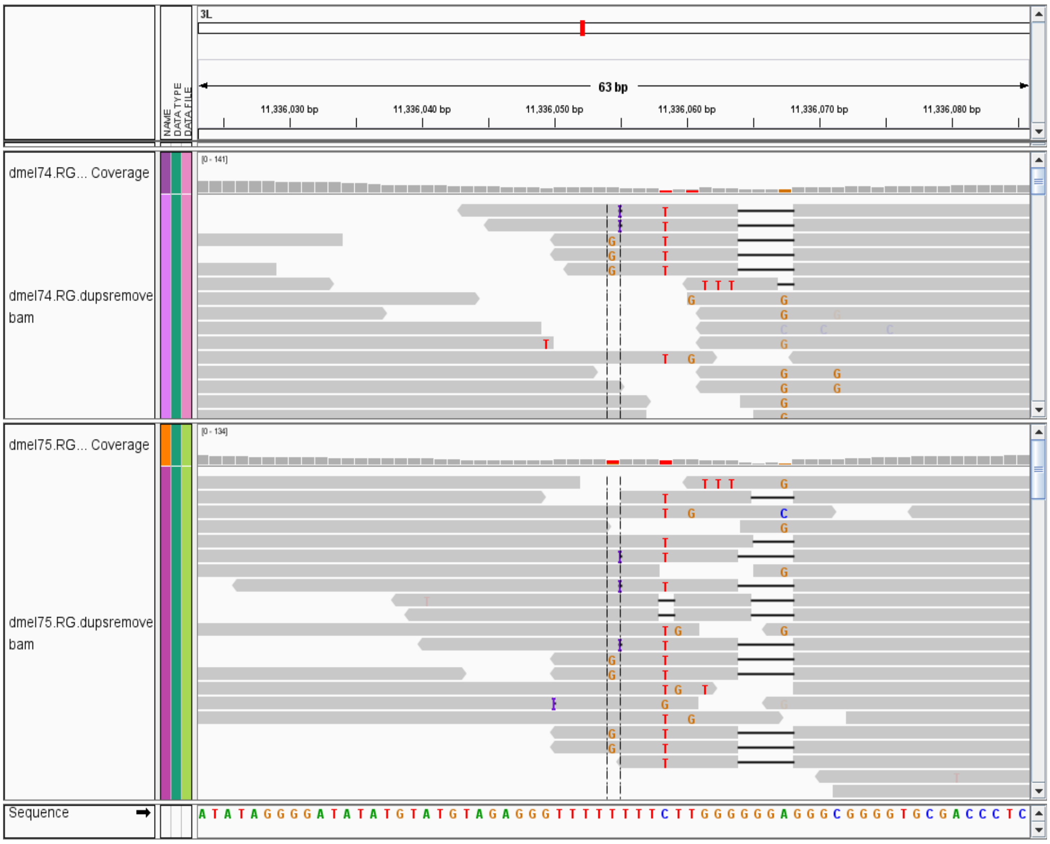

Figure S4 Screenshot from the IGV showing a candidate mutation associated with a misaligned polymorphic insertion. The T→G candidate mutation can be resolved by supposing that reads carrying the G allele have instead a TTTG insertion (shown as the vertical purple symbol), which is also present in reads of other individuals (including one parent) in addition to the two individuals shown.

Table S1 Numbers of heterozygous autosomal sites for read depth = 1..100 used to generate tables for the generation of synthetic mutations.

Depth	*Number*	*Depth*	*Number*
1	67	51	37606
2	90	52	37274
3	144	53	37501
4	182	54	64132
5	221	55	61228
6	321	56	31575
7	364	57	30263
8	487	58	29175
9	640	59	28289
10	778	60	27340
11	932	61	26041
12	1166	62	25037
13	1417	63	24209
14	1693	64	22691
15	2146	65	21498
16	2595	66	20759
17	3215	67	19868
18	7763	68	18728
19	9181	69	17907
20	6743	70	17107
21	7832	71	17203
22	9109	72	26887
23	10470	73	24931
24	11838	74	12298
25	13371	75	11724
26	14501	76	11197
27	16514	77	10459
28	18264	78	9884
29	19674	79	9350
30	21659	80	8883
31	23412	81	8353
32	25267	82	7700
33	26751	83	7377
34	28608	84	6966
35	31354	85	6520
36	62748	86	6140
37	62572	87	5764
38	36518	88	5310
39	37233	89	5520
40	38072	90	8159
41	38707	91	7616
42	39027	92	3793
43	39513	93	3653
44	40063	94	3329
45	39959	95	3175
46	39501	96	3005
47	39850	97	2804
48	39107	98	2621
49	38679	99	2517
50	38274	100	2360