SNPid	Location	map	cmCount	mCount	nmCount	wSNP%	cSNP%	ncSNP%	cmScore	nmScore	Ref	MPB	Pm(A)	Pm(C)	Pm(G)	Pm(T)	Pnm(A)	Pnm(C)	Pnm(G)	Pnm(T)
0	27	27	4	0	7	68.07%	63.63%	0.00%	2.43	5.22	C	G	0	0	0	0	0.09	0.09	99.7	0.09
1	8803	54	0	0	96	99.70%	100.00%	0.00%	0	78.65	G	C	0	0	0	0	0.09	99.7	0.09	0.09
2	41055	54	55	4	39	46.21%	41.48%	67.33%	39	33.7	C	A	59.07	28.66	6.13	6.13	99.68	0.11	0.09	0.09
3	47058	54	2	4	87	98.26%	97.75%	44.62%	0.98	67.75	A	G	42.37	7.82	34.15	15.64	0.09	0.1	99.69	0.1
4	49087	54	0	1	53	99.64%	100.00%	64.82%	0	44.33	C	T	32.8	23.6	0.09	43.49	0.15	0.09	0.09	99.64
5	68860	54	0	0	73	99.44%	100.00%	0.00%	0	58.5	T	C	0	0	0	0	0.18	99.44	0.26	0.1
6	69058	54	0	1	85	98.61%	100.00%	93.31%	0	69.51	A	G	4.7	1.53	65.68	28.07	0.1	0.11	98.61	1.16
7	69611	54	0	1	37	99.67%	100.00%	50.00%	0	31.6	A	G	25	25	25	25	0.09	0.09	99.67	0.12
8	69628	54	0	0	35	99.68%	100.00%	0.00%	0	24.76	T	C	0	0	0	0	0.11	99.68	0.09	0.09
9	70014	54	0	1	86	99.54%	100.00%	5.19%	0	74.83	C	T	70.35	28	0.09	1.53	0.12	0.09	0.22	99.54
10	70285	54	0	1	85	99.46%	100.00%	94.06%	0	70.89	T	C	0.09	93.87	0.09	5.92	0.09	99.46	0.33	0.09
11	70619	54	0	1	68	99.70%	100.00%	6.64%	0	53.17	G	A	5.9	0.09	82.88	11.11	99.7	0.09	0.09	0.09
12	71153	54	0	8	63	99.70%	100.00%	77.46%	0	51.16	T	G	0.28	1	76.46	22.24	0.09	0.09	99.7	0.09
13	71803	54	0	2	32	99.70%	100.00%	69.53%	0	26.75	G	A	59.8	13.89	26.2	0.09	99.7	0.09	0.09	0.09
14	71948	54	0	0	41	99.58%	100.00%	0.00%	0	27.84	C	T	0	0	0	0	0.09	0.1	0.21	99.58
15	73159	54	0	1	70	99.68%	100.00%	92.64%	0	58.8	G	A	92.45	0.09	7.34	0.09	99.68	0.09	0.09	0.12
16	74526	54	0	2	56	97.92%	100.00%	72.49%	0	50.04	C	A	41.08	15.58	10.06	33.27	97.92	0.09	1.87	0.09
17	74809	54	0	1	34	99.69%	100.00%	50.00%	0	29.24	T	C	25	25	25	25	0.1	99.69	0.09	0.09
18	74822	54	0	0	26	99.70%	100.00%	0.00%	0	24.46	T	G	0	0	0	0	0.09	0.09	99.7	0.09
19	75024	54	0	1	67	98.21%	100.00%	70.05%	0	57.97	C	T	3.77	28.09	2.41	65.71	0.09	0.09	1.58	98.21
20	75216	54	0	0	85	98.78%	100.00%	0.00%	0	70.68	G	A	0	0	0	0	98.78	1.01	0.09	0.09
21	75846	54	0	1	51	99.70%	100.00%	50.00%	0	42.37	T	C	0.09	49.75	0.39	49.75	0.09	99.7	0.09	0.09
22	76199	54	0	3	29	99.55%	100.00%	18.51%	0	20.24	G	A	10.39	5.59	45.76	38.23	99.55	0.22	0.11	0.09
23	76399	48	0	0	23	99.63%	100.00%	0.00%	0	14.1	T	C	0	0	0	0	0.16	99.63	0.09	0.09
24	76810	54	0	0	80	99.05%	100.00%	0.00%	0	63.97	C	T	0	0	0	0	0.19	0.09	0.65	99.05
25	78408	54	0	0	51	99.62%	100.00%	0.00%	0	43.28	T	C	0	0	0	0	0.17	99.62	0.09	0.09
26	79439	54	0	4	71	98.40%	100.00%	87.64%	0	56.9	G	A	73.47	1.02	10.35	15.13	98.4	1.38	0.1	0.11
27	80214	54	0	3	93	99.68%	100.00%	38.16%	0	78.77	G	A	22.36	39.27	36.23	2.13	99.68	0.09	0.09	0.11
28	80865	54	1	0	87	98.51%	98.86%	0.00%	0.87	72.17	C	T	0	0	0	0	0.09	0.09	0.09	99.7
29	84150	54	0	4	52	99.70%	100.00%	88.29%	0	33.66	T	G	0.09	1.26	87.09	11.54	0.09	0.09	99.7	0.09

SNPs Table: With each alignment, a SNP result table can be generated for each reference sequenced. This identifies locations with a level of mismatches that is higher than some threshold value. Where: Location=location of the SNP on the reference sequence, map=sequence complexity, cmCount=the number of crisp bases that match the reference, mCount=the number of non-crisp bases that match the reference, nmCount=the number of non-match bases that cover this location, cSNP%=nmCount/(cmCount+nmCount), wSNP% is cSNP% after adjusting for reads and base weights, ncSNP%[L] = average($P_{snpBase}$[L]) / (average($P_{snpBase}$[L]) + average($P_{refBase}$[L])), cmScore=the sum of the weight of the reads that cover this location with a crisp base, nmScore=the sum of the weight of the reads that cover this location with non-matched bases, Ref=Reference base, MPB=Most probably base, Pm(nucleotide)=the average probability of each nucleotide that cover this location with a non-crisp base, Pnm(nucleotide)= the average probability of each nucleotide that covers this location with a non-match base. We can see that SNPs ids 0 and 2 are heterozygous SNPs since they have about equal values for cmCount and nmCount which results in both cSNP% and wSNP% being about 50%. All other SNPs are homozygous with cSNP% and wSNP% near 100%. When wSNP% is higher than cSNP% it indicates that the mismatch bases and their reads at these SNPs have higher weight. Higher weight reads are less likely to have sequencing errors which allows them to align more accurately. As an example, the SNP with an id = 12 is a homozygous SNP with 63 mismatches and zero crisp matches which gives a cSNP% value of 100%. It also has 8 non crisp matches with ncSNP% value of 77.46%, which is the result of an average probability to the reference base (T) of 22.24% and 76.46% for the SNP base (G).