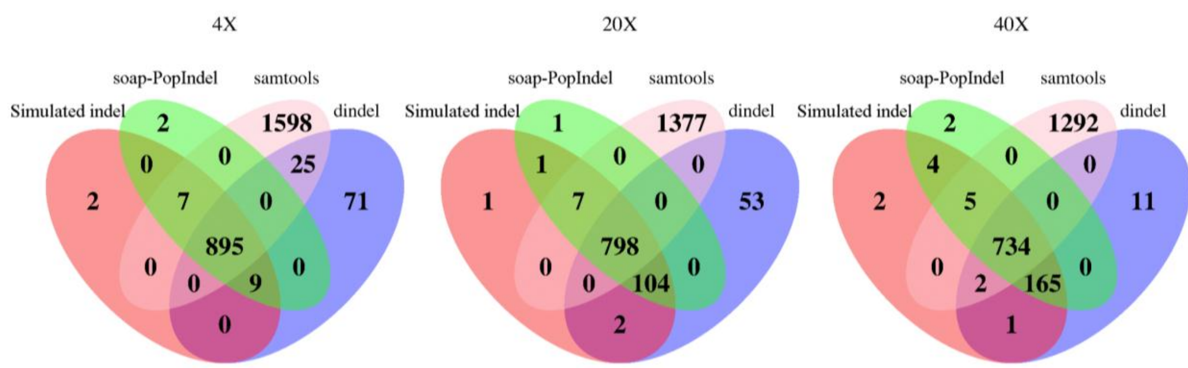
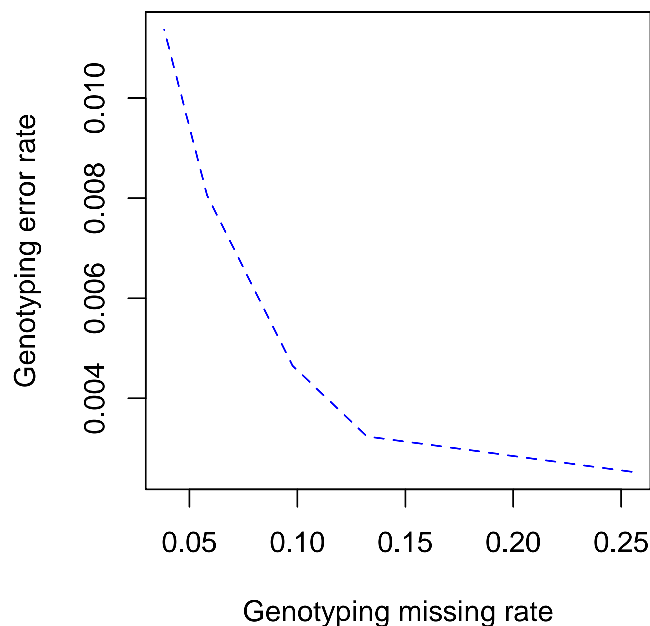
Supplementary Material

SUPPLEMENTARY FIGURES AND TABLES

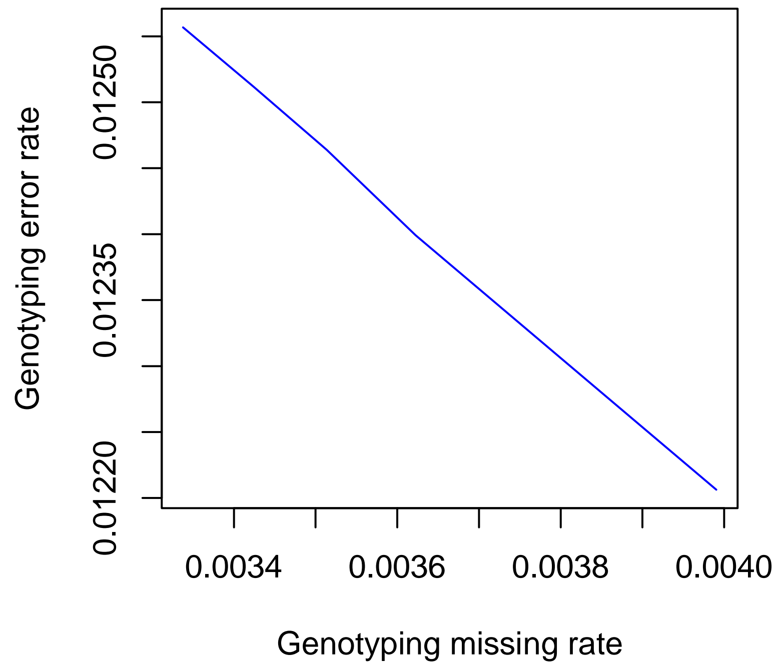
Supplementary Figure S1: SOAP-popIndel workflow



Supplementary Figure S2: Venn diagram illustrating overlaps between indel sites called by different algorithms with true indels on simulated data at different levels of coverage. Panel A: 4x average coverage; Panel B: 20x average coverage; panel C: 40x average coverage.



Supplementary Figure S3: Genotyping accuracy and missing rates on triploid 40X simulation data.



Supplementary Figure S4: Genotyping accuracy and missing rates on tri-allelic diploid 40X simulated data.

Method	Depth	Time(sec)	Memory(GB)
SAMtools	4X	18816	0.2
	20X	98168	0.22
	40X	138810	0.24
Dindel	4X	120176	0.1
	20X	501957	0.12
	40X	1451184	1
SOAP-popIndel	4X	3456	2
	20X	4149	2.5
	40X	5078	4
PiCall	4X	356594	0.14
	20X	550223	0.18
	40X	579355	0.22

Supplementary Table S1. Running time on simulation data.

Frequency	Genotyping error rate	Genotyping missing rate
5%	0.22%	0.16%
10%	0.34%	0.13%
20%	0.42%	0.16%
50%	1.45%	0.17%
80%	0.17%	0.16%
90%	1.33%	0.12%
95%	0.10%	0.12%

Supplementary Table S2. Error rate and missing rate by indel allele frequency for simulated diploid 40X data.

Inferred genotype	Simulated genotype			
	AAA	AAB	ABB	BBB
AAA	0.31	8.8e-4	1.1e-6	0
AAB	1.8e-4	0.16	3.6e-3	3.3e-6
ABB	5.5e-7	1.8e-3	0.15	1.9e-4
BBB	0	3.9e-6	5.7e-4	0.32
Missing	2.6e-4	2.3e-2	3.4e-2	1.6-e3

Supplementary Table S3. Triploid genotyping summary, showing the percentage of total indel genotypes categorized by simulated and inferred genotype. The cells in the table sum to 1.

Tri-allelic diploid	False negative rate	False positive rate
40X	3.18%	0.34%

Supplementary Table S4. False negative rate and false positive rate for detecting indels on tri-allelic diploid simulated data.

SUPPLEMENTARY METHODS

Pre-filtering of putative indel sites

For the medium or high depth data (including the analysis of real data), we first filtered putative indels sites with average depth lower than 4. We then filtered sites for which more than 66% of putative heterozygous indel sites (i.e. those which had greater than one aligned reference and one aligned indel read) were more consistent with genotyping error than genuine genetic variation. To achieve this we compared the probability that each putative heterozygous allele count was generated from an error model represented by the binomial distribution $B(n, 0.1)$ with 10% error rate, to the probability that it was generated by a genuine heterozygous model with no error $B(n, 0.5)$.

Sequenom validation

Indel genotyping assays were performed via iPLEX MassARRAY system (Sequenom Inc.,San Diego). Both PCR and MassEXTEND primers for each mutations were *in silico* designed by MassARRAY Assay design 4.0 software. Multiplex PCR were carried out by GeneAmp PCR System 9700 Dual 384-Well Sample Block Module (Applied Biosystems), followed by dephosphorylation, single base extention reaction and desalting. MassARRAY Nanodispenser RS1000 (Sequenom) was used to automatically spot reactions to 384 SpectroCHIP, which was further placed into the MALDI-TOF mass spectrometer (Sequenom). All genotype calls by MassARRAY Typer 4.0 (Sequenom) were manually confirmed by examining the spectra for each assay and sample. Peaks for two alleles were checked against the background of each well and a mutation call was confirmed if the peak is unique to that allele.