

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 02:14:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548968.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1548968 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548968.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 02:14:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548968.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,031,825
Mapped reads	6,022,286 / 85.64%
Unmapped reads	1,009,539 / 14.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	284,407 / 4.04%
Duplication rate	2.64%
Clipped reads	526,505 / 7.49%

2.2. ACGT Content

Number/percentage of A's	66,972,022 / 28.15%
Number/percentage of C's	51,378,824 / 21.6%
Number/percentage of T's	68,045,564 / 28.6%
Number/percentage of G's	51,499,254 / 21.65%
Number/percentage of N's	318 / 0%
GC Percentage	43.24%

2.3. Coverage

Mean	0.0769
Standard Deviation	0.8612

2.4. Mapping Quality

Mean Mapping Quality	35.57
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2.5. Mismatches and indels

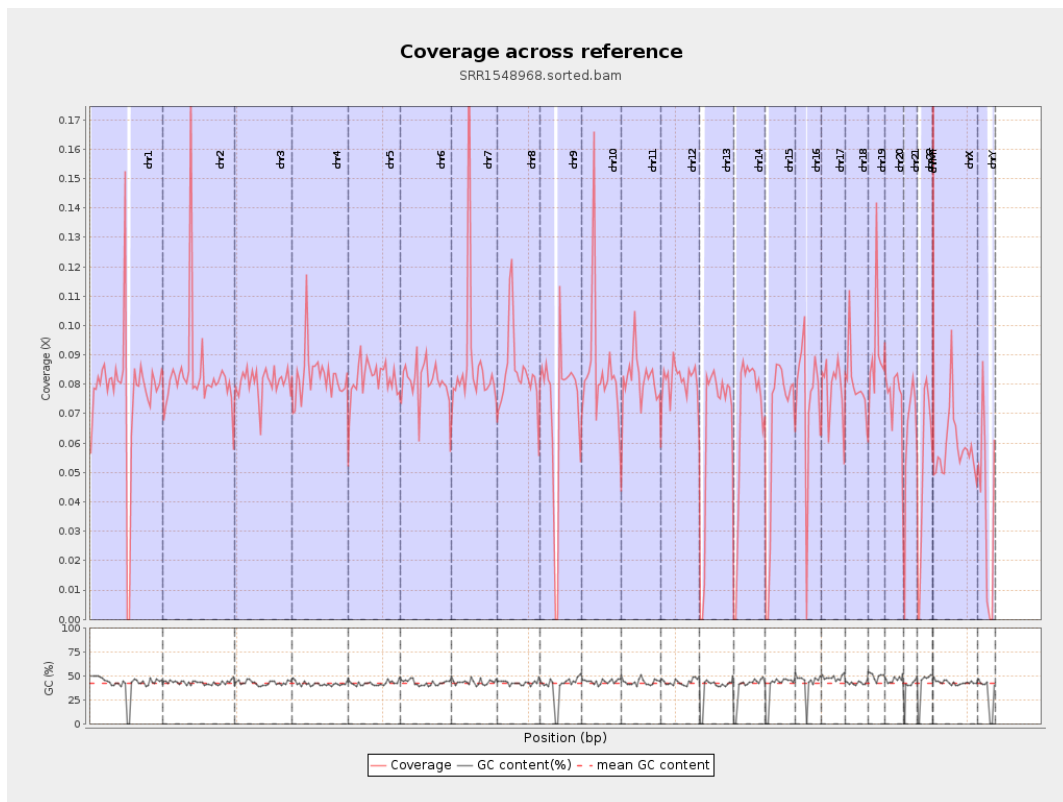
General error rate	0.33%
Mismatches	769,051
Insertions	8,286
Mapped reads with at least one insertion	0.14%
Deletions	17,218
Mapped reads with at least one deletion	0.29%
Homopolymer indels	37.92%

2.6. Chromosome stats

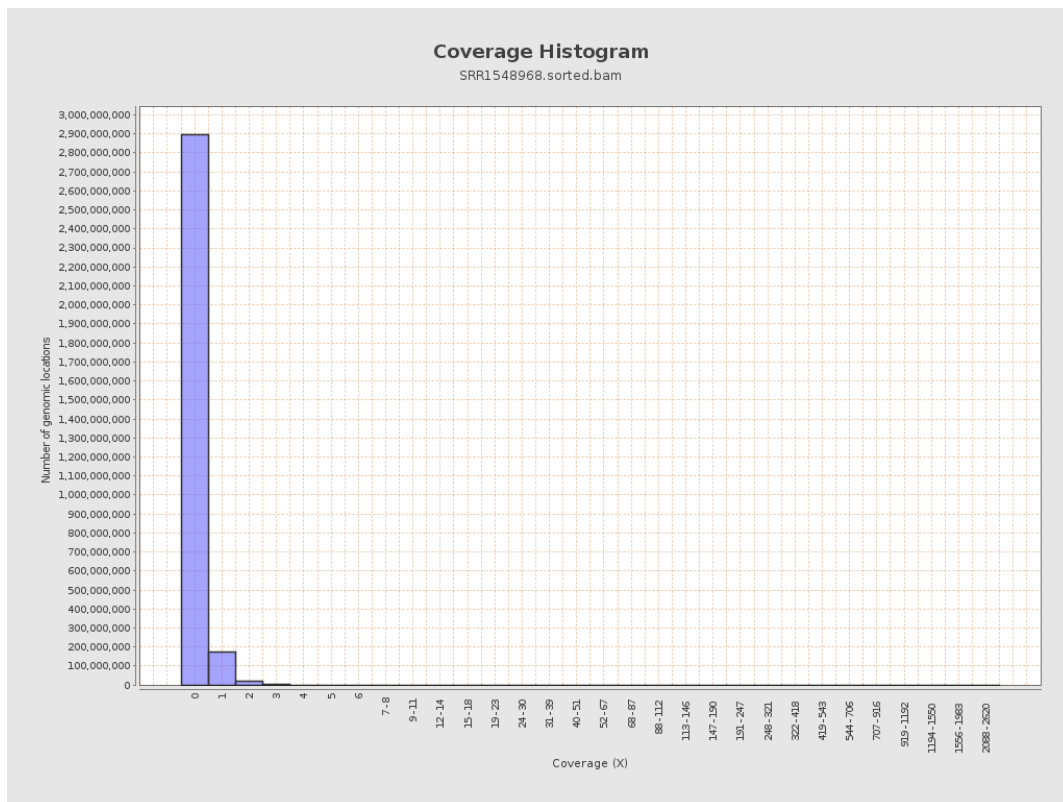
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19180567	0.077	1.6031
chr2	243199373	20296552	0.0835	0.8711
chr3	198022430	15960529	0.0806	0.3323
chr4	191154276	15831453	0.0828	0.3838
chr5	180915260	14800473	0.0818	0.3552
chr6	171115067	13849772	0.0809	0.3666
chr7	159138663	13874452	0.0872	1.3792
chr8	146364022	12291127	0.084	1.3893

chr9	141213431	10189341	0.0722	0.9018
chr10	135534747	11442349	0.0844	0.7136
chr11	135006516	11031756	0.0817	0.5944
chr12	133851895	10927527	0.0816	0.3778
chr13	115169878	7545329	0.0655	0.2875
chr14	107349540	7345854	0.0684	0.5071
chr15	102531392	6606856	0.0644	0.3019
chr16	90354753	6702599	0.0742	0.4527
chr17	81195210	6447739	0.0794	0.3715
chr18	78077248	6312958	0.0809	1.7303
chr19	59128983	5425402	0.0918	1.6392
chr20	63025520	4781911	0.0759	0.3596
chr21	48129895	3010977	0.0626	0.4695
chr22	51304566	2670446	0.0521	0.3966
chrMT	16571	6534	0.3943	0.7136
chrX	155270560	9109930	0.0587	0.4709
chrY	59373566	2275517	0.0383	0.3797

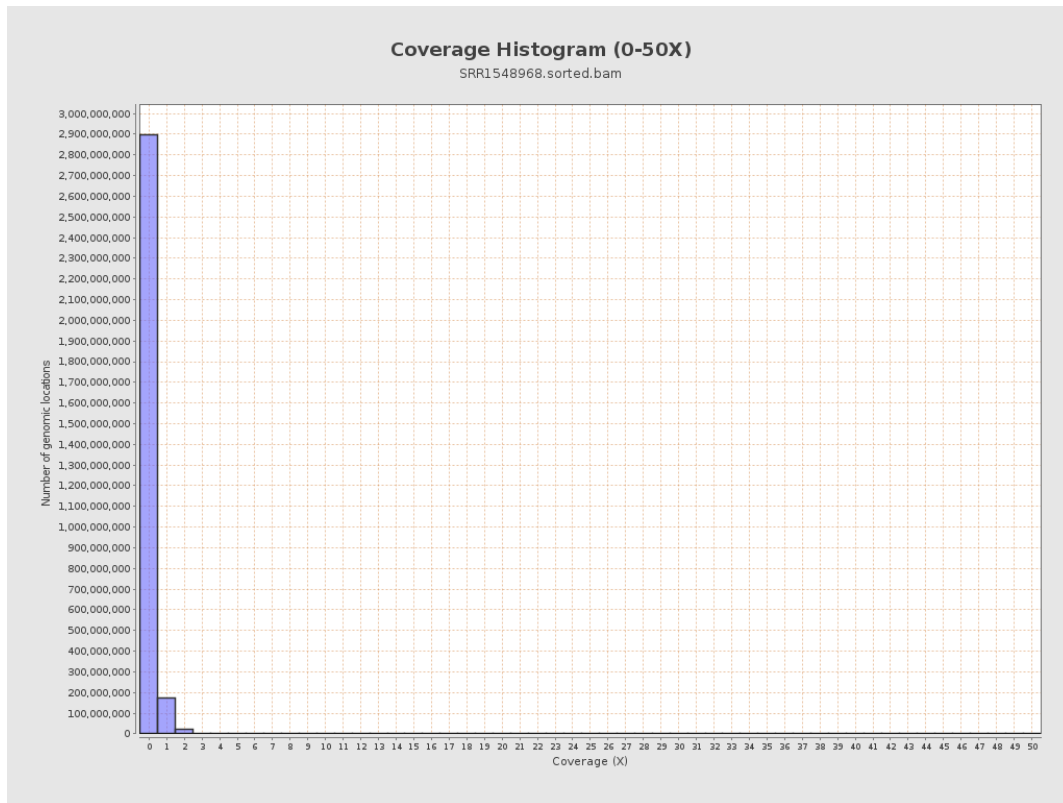
3. Results : Coverage across reference



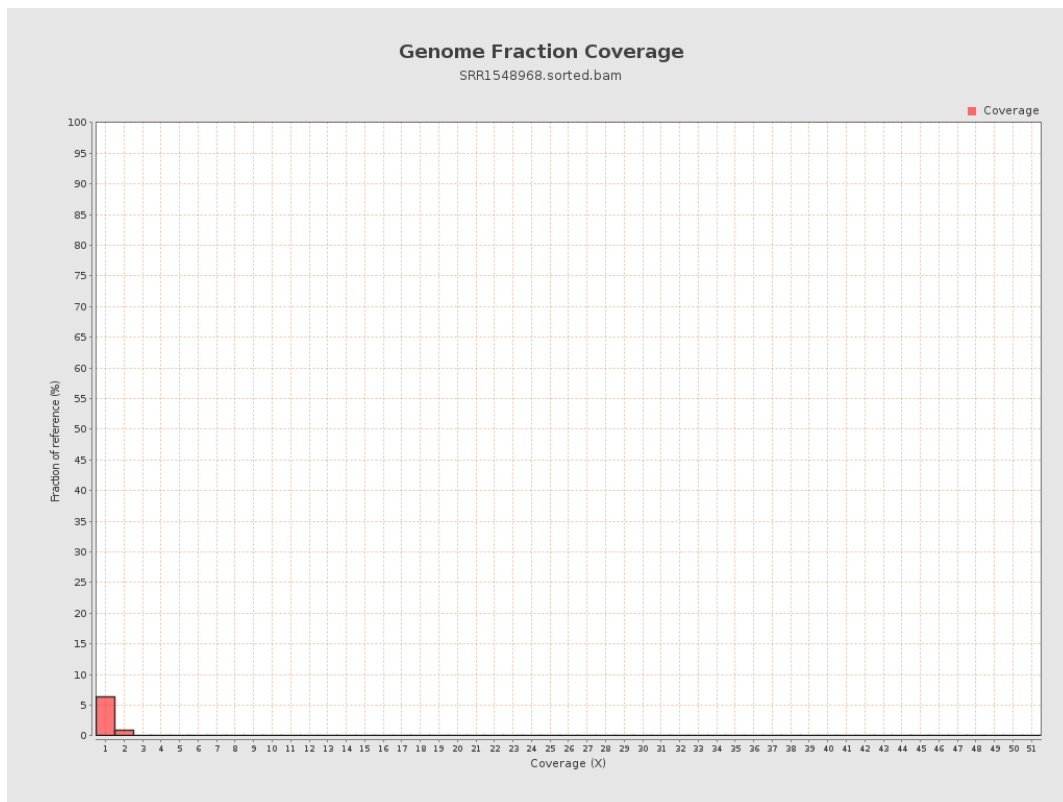
4. Results : Coverage Histogram



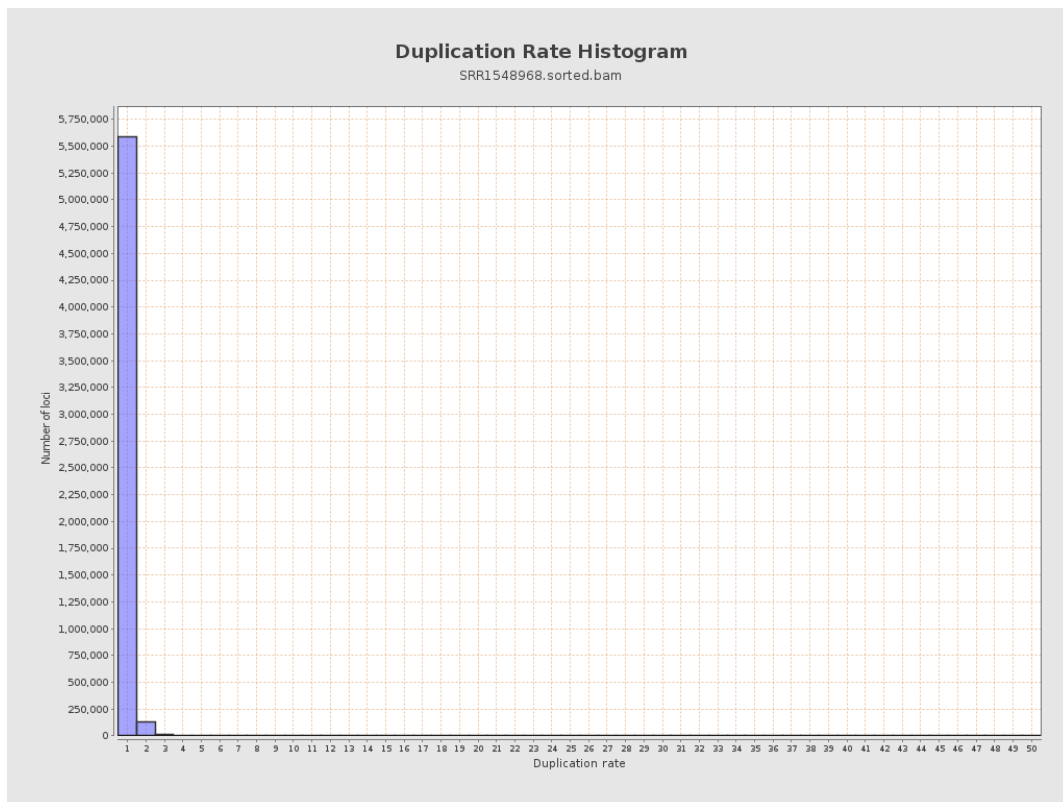
5. Results : Coverage Histogram (0-50X)



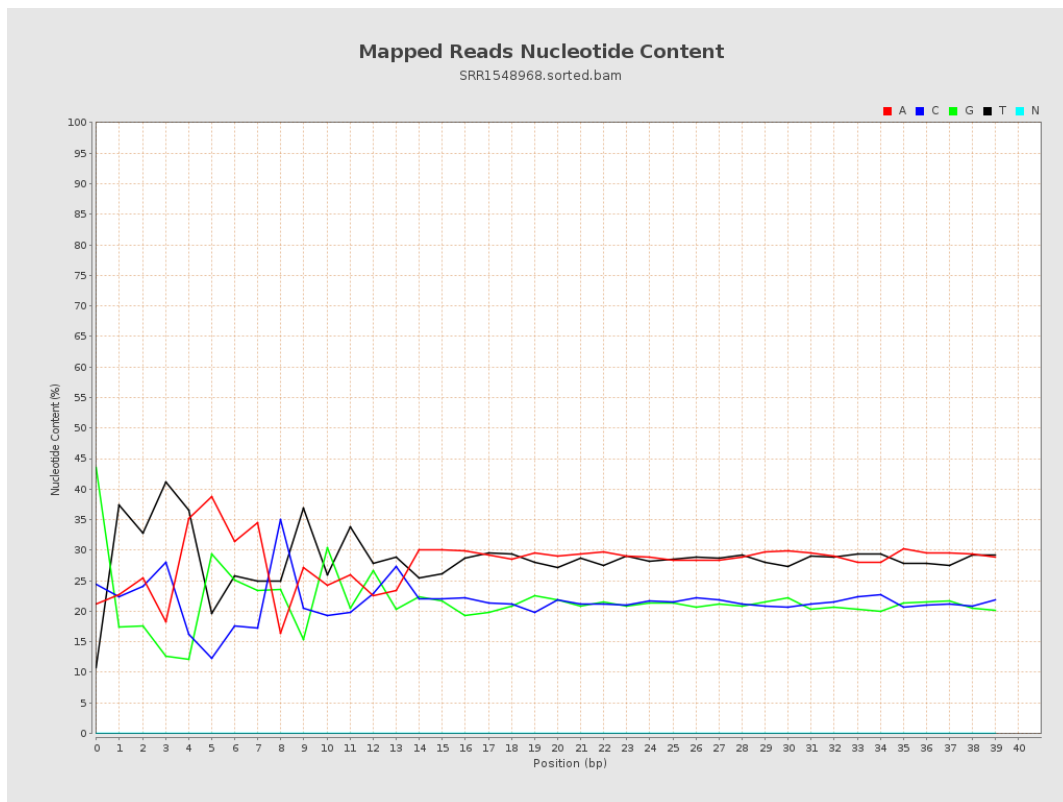
6. Results : Genome Fraction Coverage



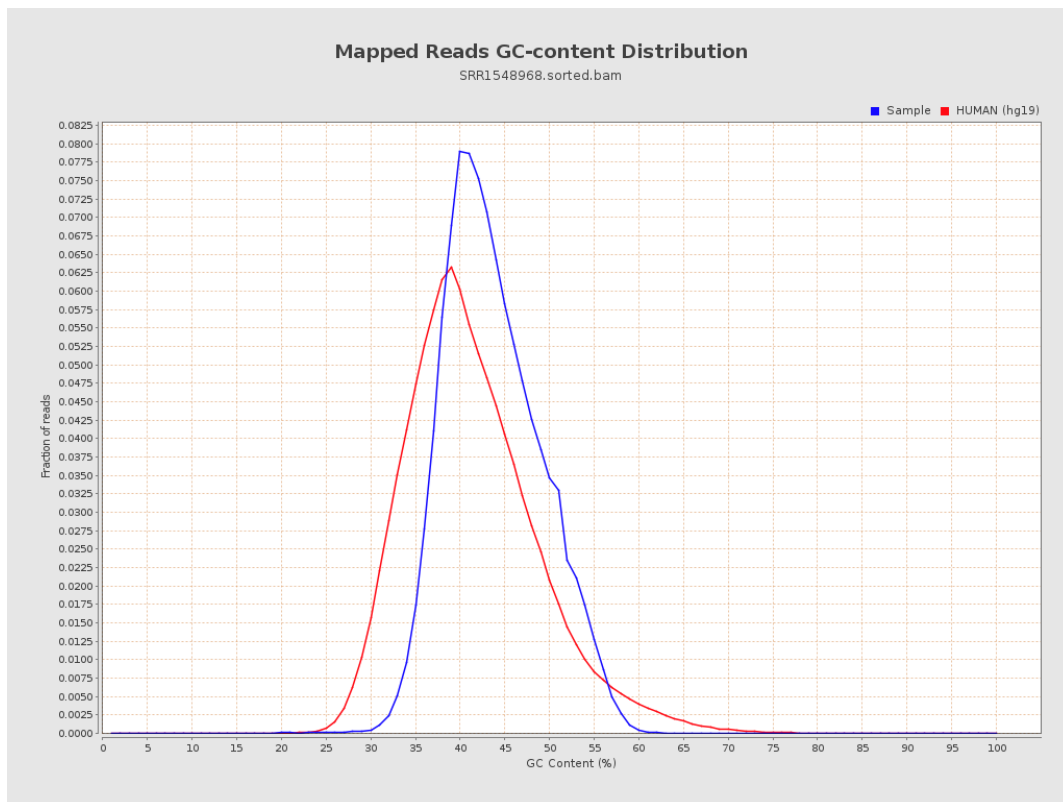
7. Results : Duplication Rate Histogram



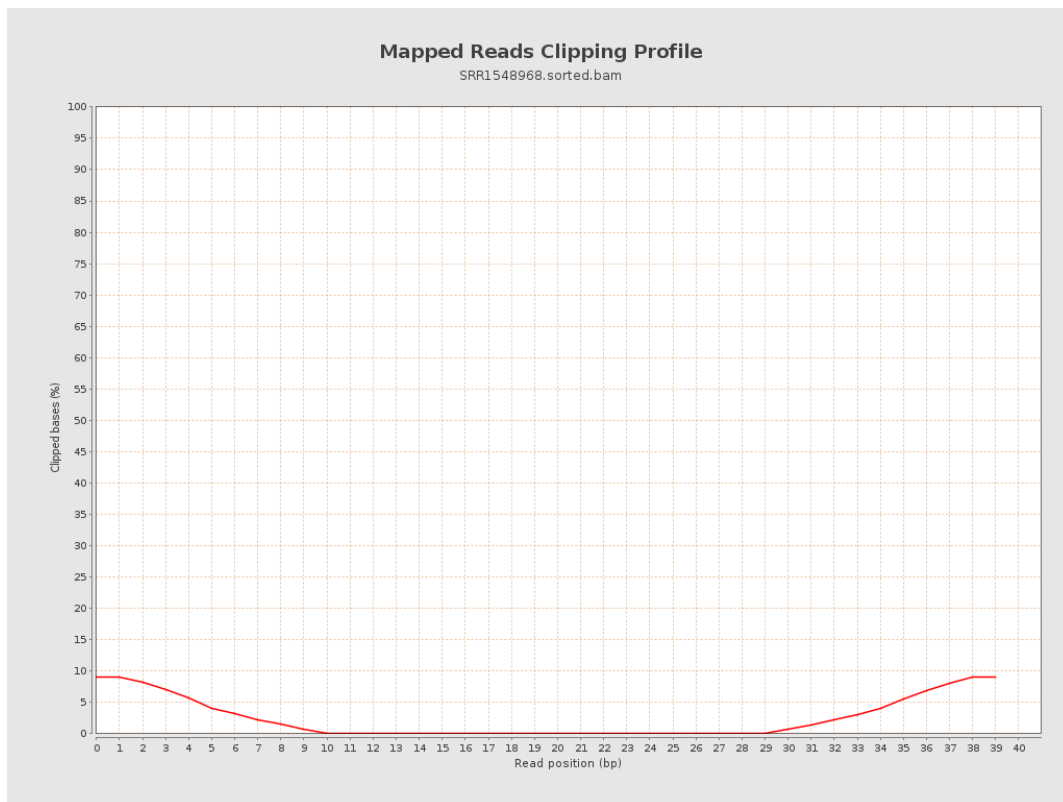
8. Results : Mapped Reads Nucleotide Content



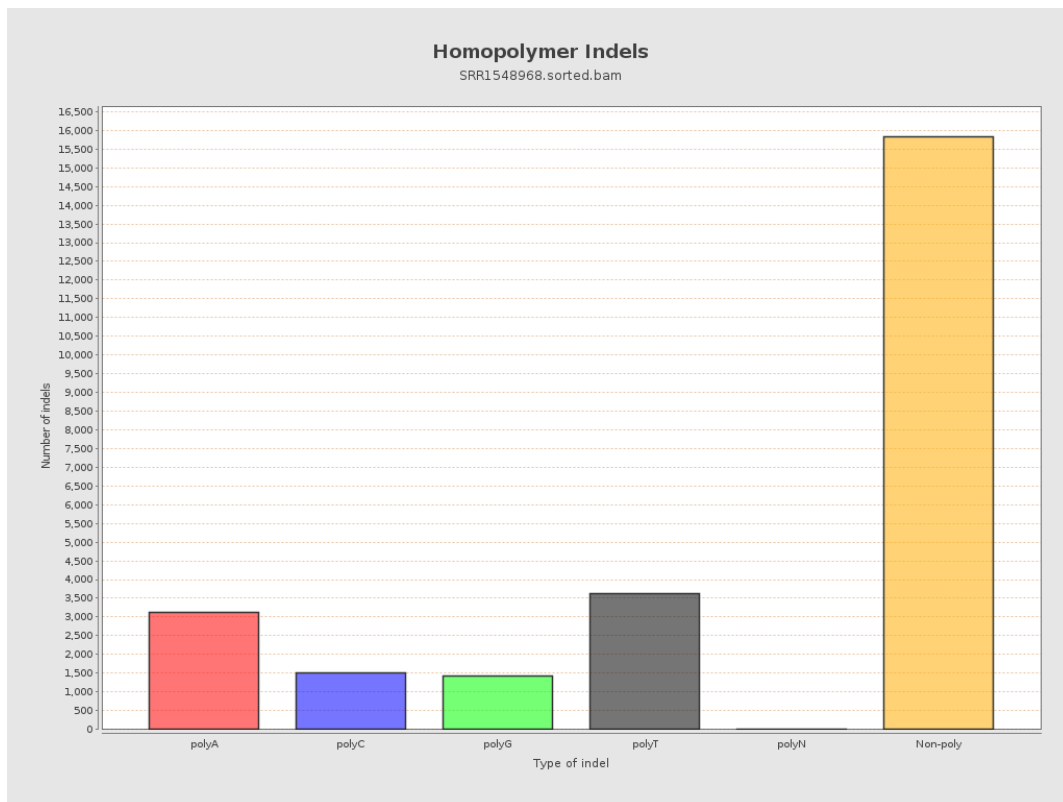
9. Results : Mapped Reads GC-content Distribution



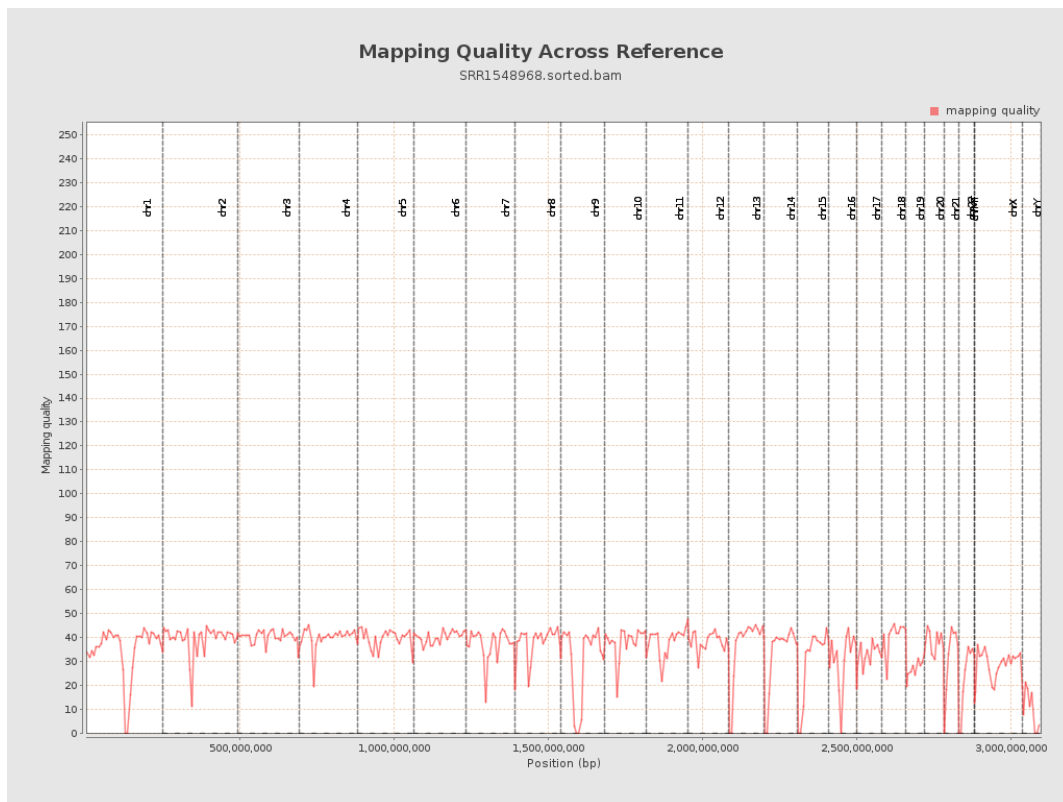
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

