

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:24:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548932.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_SRR1548932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548932.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:24:57 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,105,994
Mapped reads	8,809,236 / 87.17%
Unmapped reads	1,296,758 / 12.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	367,213 / 3.63%
Duplication rate	3.11%
Clipped reads	646,763 / 6.4%

2.2. ACGT Content

Number/percentage of A's	101,874,768 / 29.21%
Number/percentage of C's	72,191,552 / 20.7%
Number/percentage of T's	102,503,352 / 29.39%
Number/percentage of G's	72,202,842 / 20.7%
Number/percentage of N's	3,122 / 0%
GC Percentage	41.4%

2.3. Coverage

Mean	0.1127
Standard Deviation	1.2846

2.4. Mapping Quality

Mean Mapping Quality	42.09
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2.5. Mismatches and indels

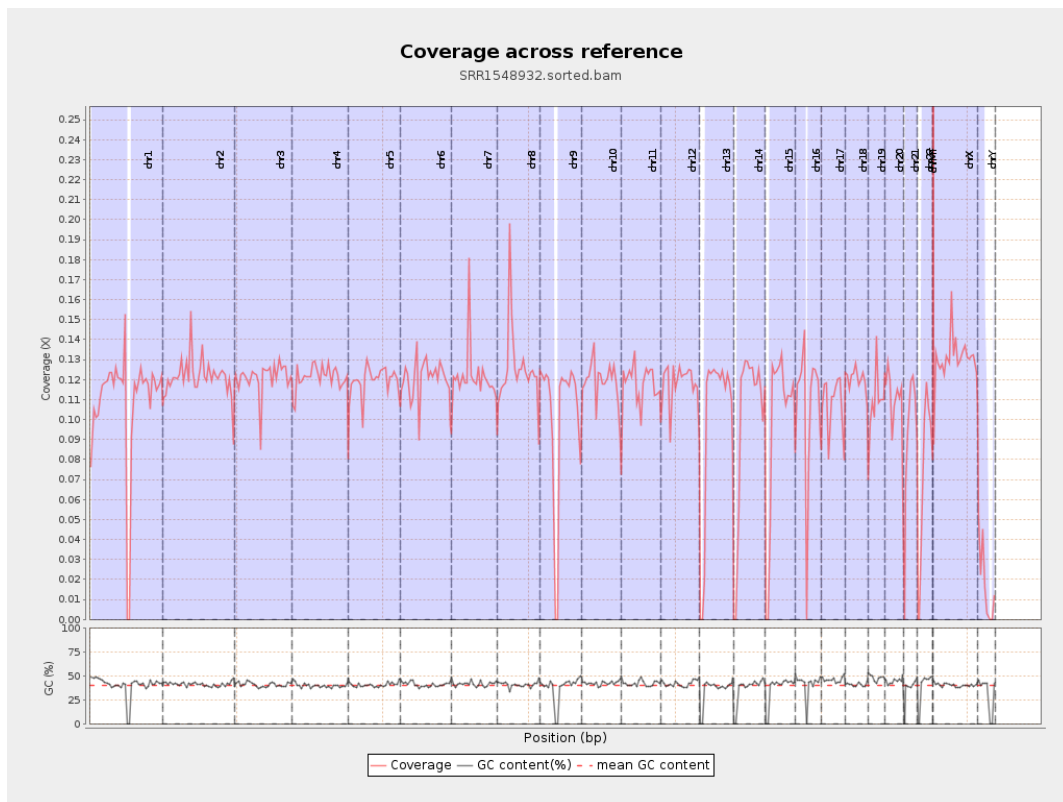
General error rate	0.27%
Mismatches	941,339
Insertions	11,036
Mapped reads with at least one insertion	0.13%
Deletions	29,065
Mapped reads with at least one deletion	0.33%
Homopolymer indels	41.13%

2.6. Chromosome stats

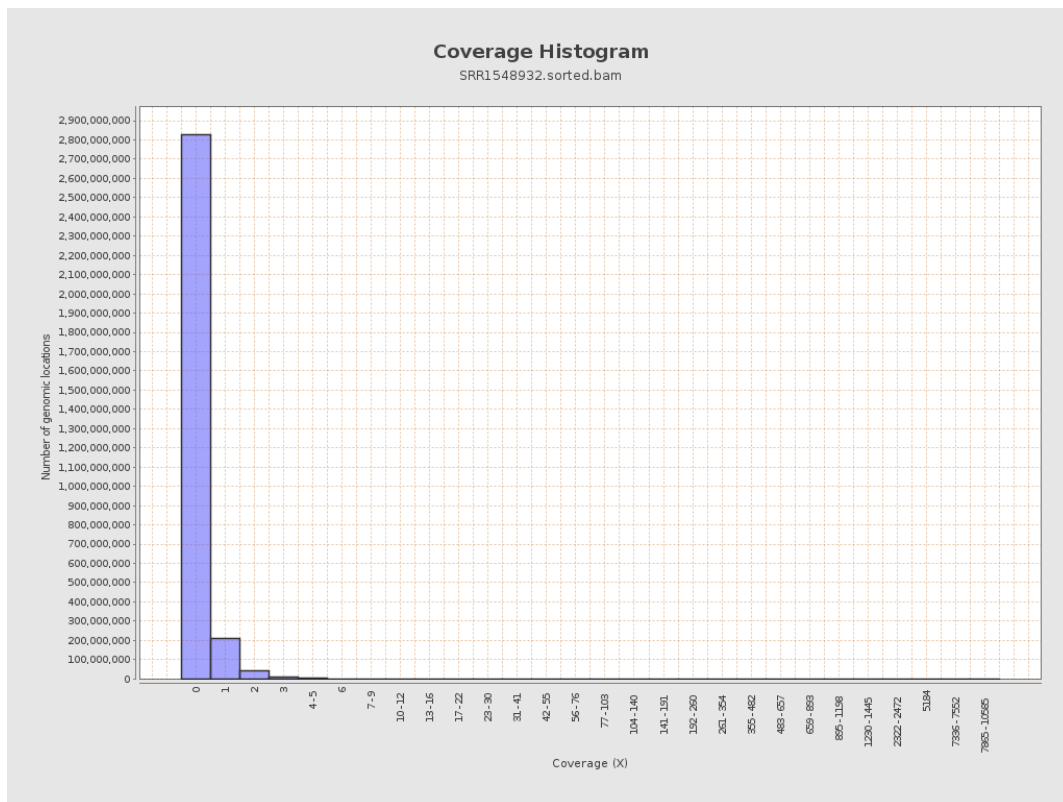
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	27119406	0.1088	1.1698
chr2	243199373	29547612	0.1215	0.6237
chr3	198022430	23975233	0.1211	0.4335
chr4	191154276	23174474	0.1212	0.4468
chr5	180915260	21510209	0.1189	0.4368
chr6	171115067	20643768	0.1206	0.4968
chr7	159138663	19316936	0.1214	0.9474
chr8	146364022	18372846	0.1255	5.1386

chr9	141213431	14359008	0.1017	0.6163
chr10	135534747	16175938	0.1193	0.5601
chr11	135006516	15875073	0.1176	0.7087
chr12	133851895	15847149	0.1184	0.4441
chr13	115169878	11537322	0.1002	0.3905
chr14	107349540	10835760	0.1009	0.4847
chr15	102531392	9949960	0.097	0.3872
chr16	90354753	9459473	0.1047	0.4476
chr17	81195210	8833146	0.1088	0.4417
chr18	78077248	9397282	0.1204	1.0571
chr19	59128983	6483766	0.1097	1.049
chr20	63025520	6974608	0.1107	0.4328
chr21	48129895	4426099	0.092	0.4257
chr22	51304566	3745615	0.073	0.4013
chrMT	16571	13286	0.8018	1.1691
chrX	155270560	20210754	0.1302	0.544
chrY	59373566	1030003	0.0173	0.2201

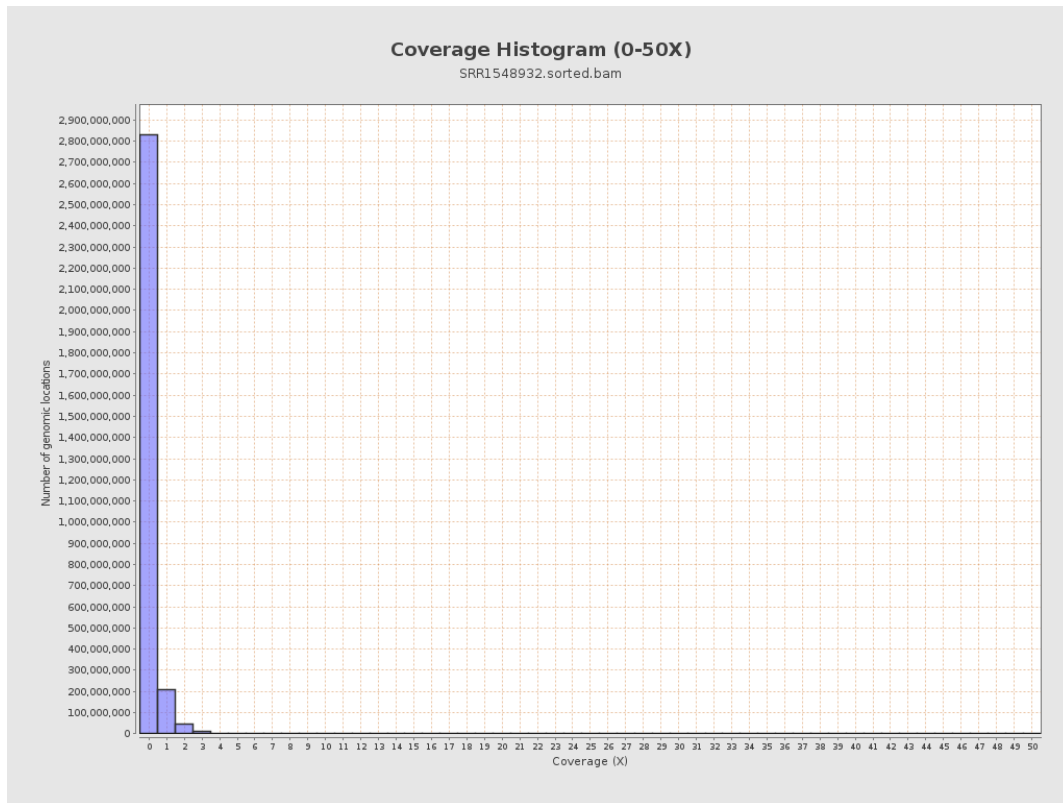
3. Results : Coverage across reference



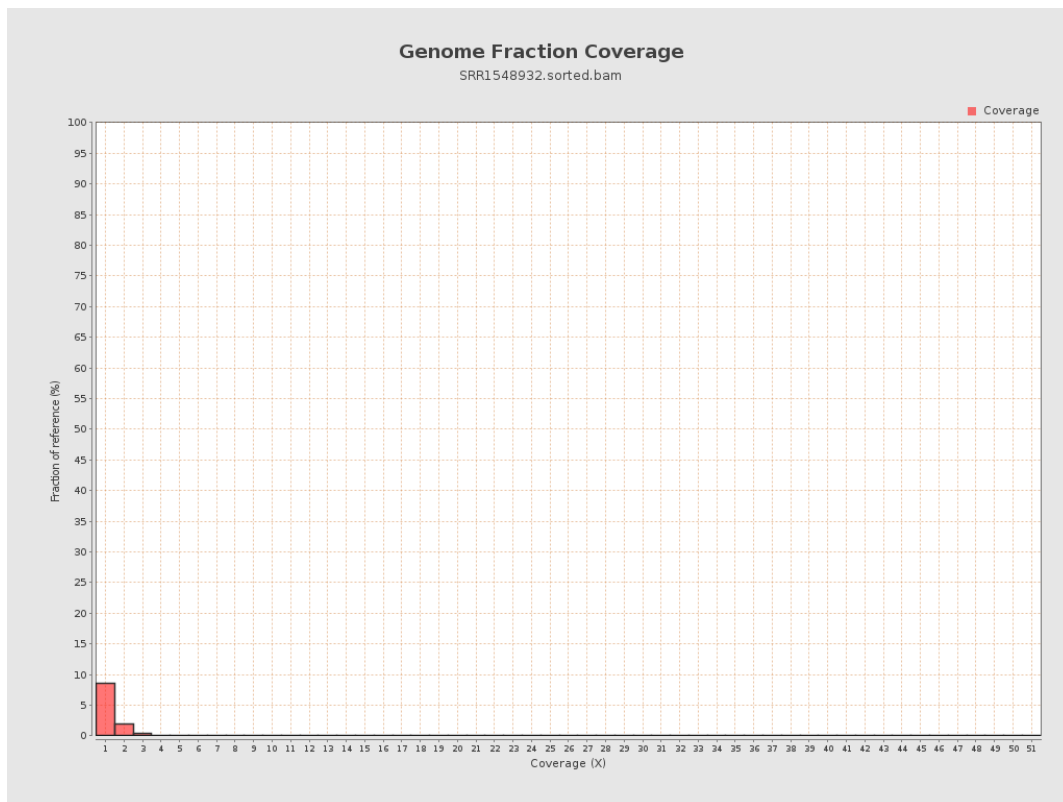
4. Results : Coverage Histogram



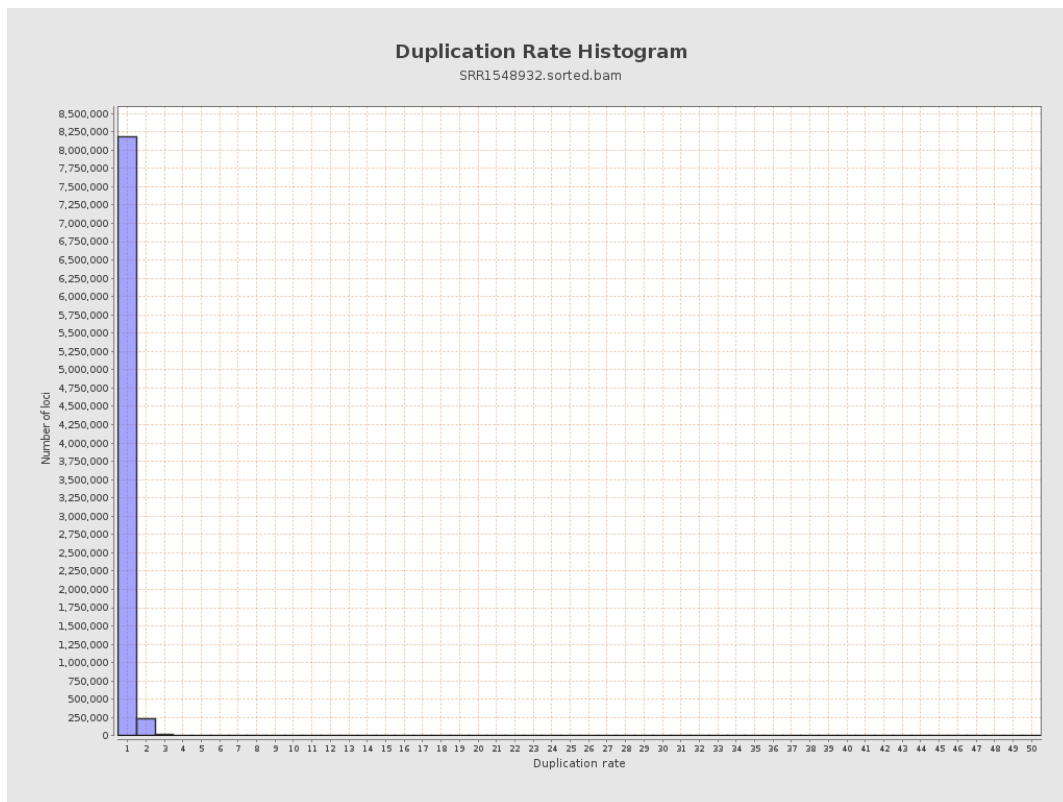
5. Results : Coverage Histogram (0-50X)



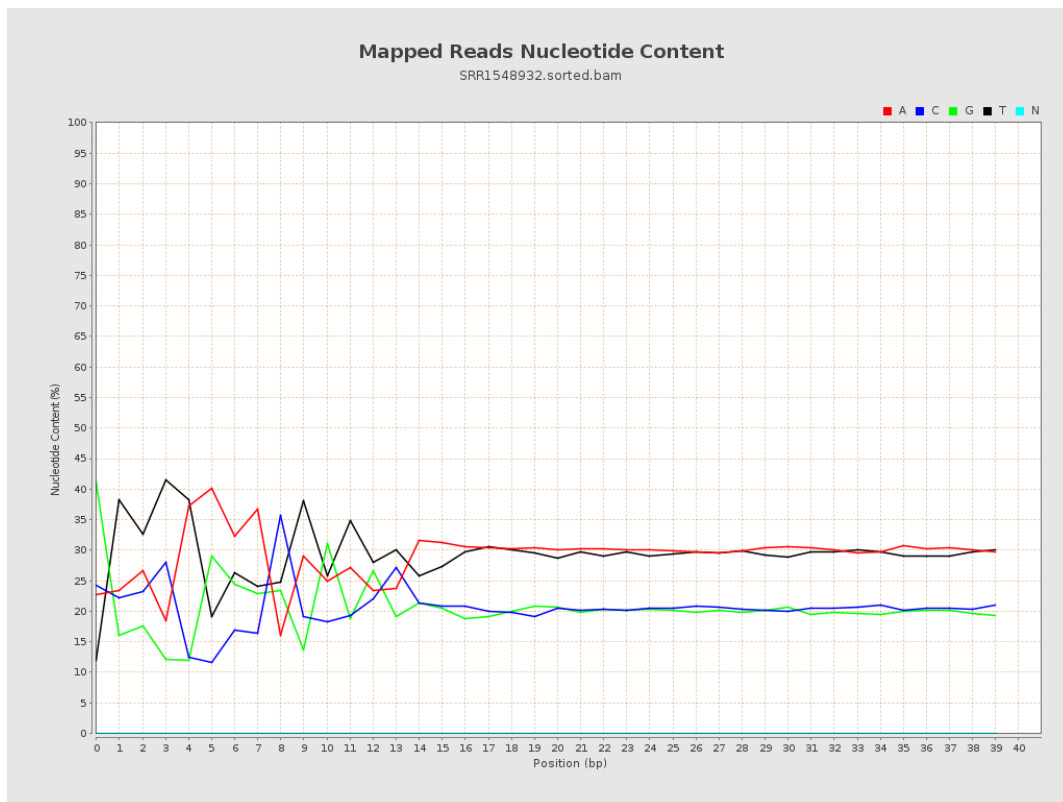
6. Results : Genome Fraction Coverage



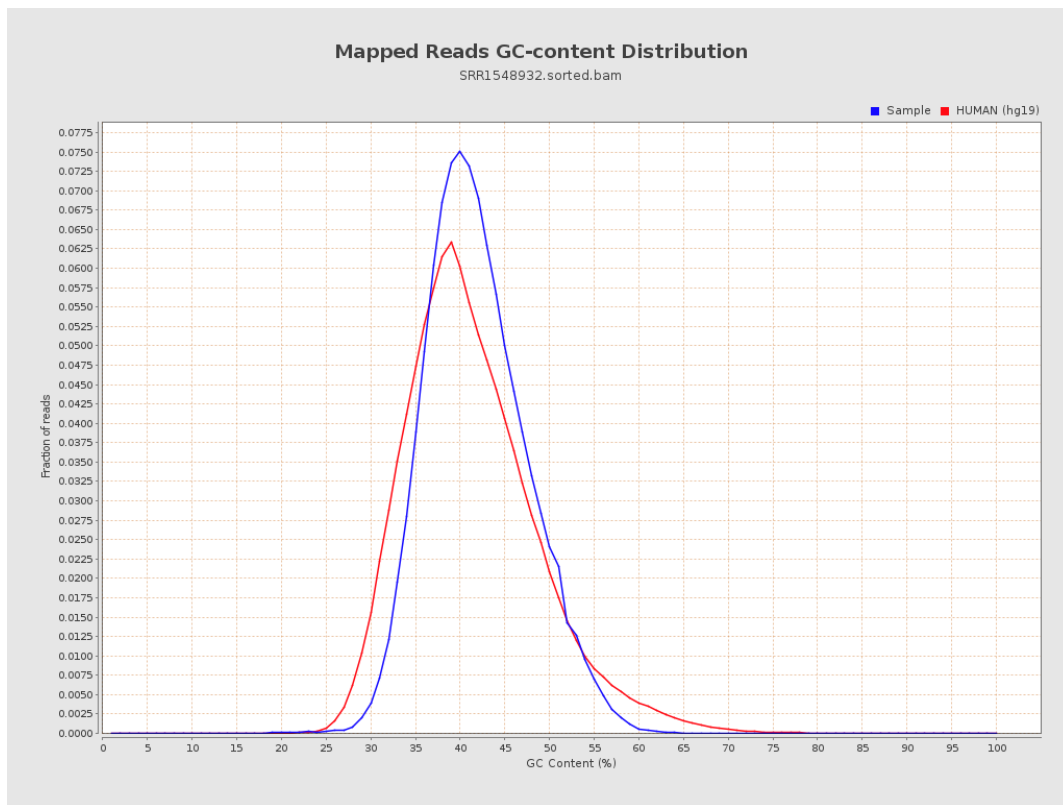
7. Results : Duplication Rate Histogram



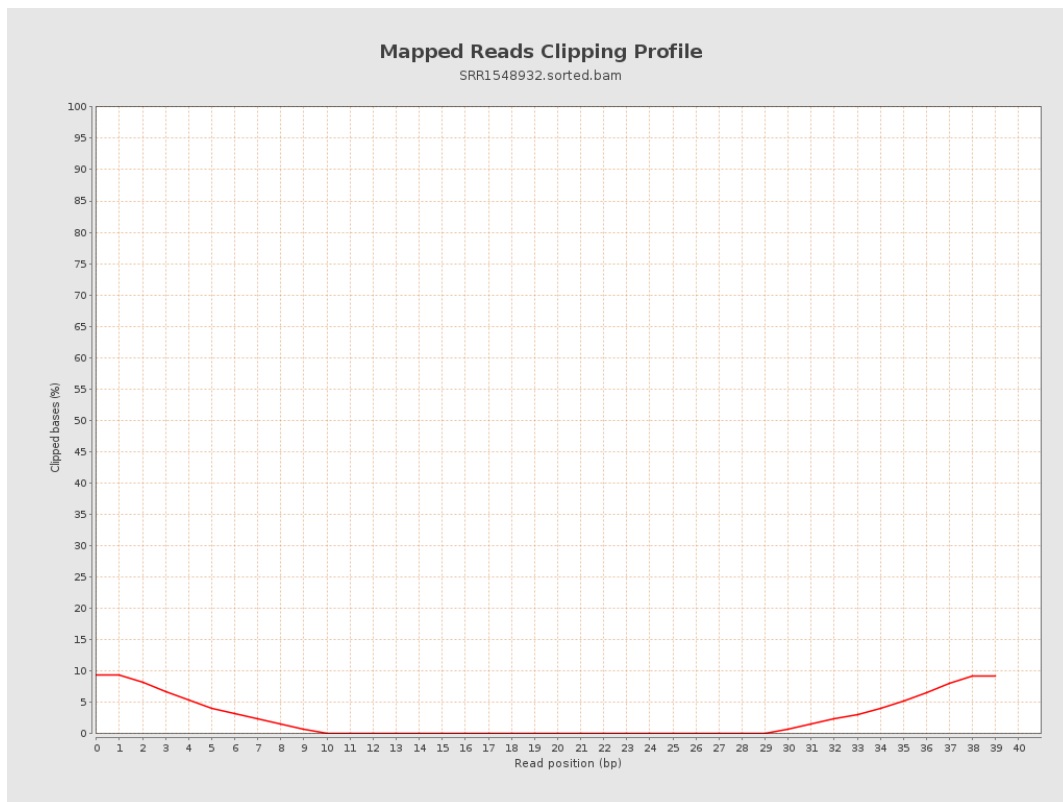
8. Results : Mapped Reads Nucleotide Content



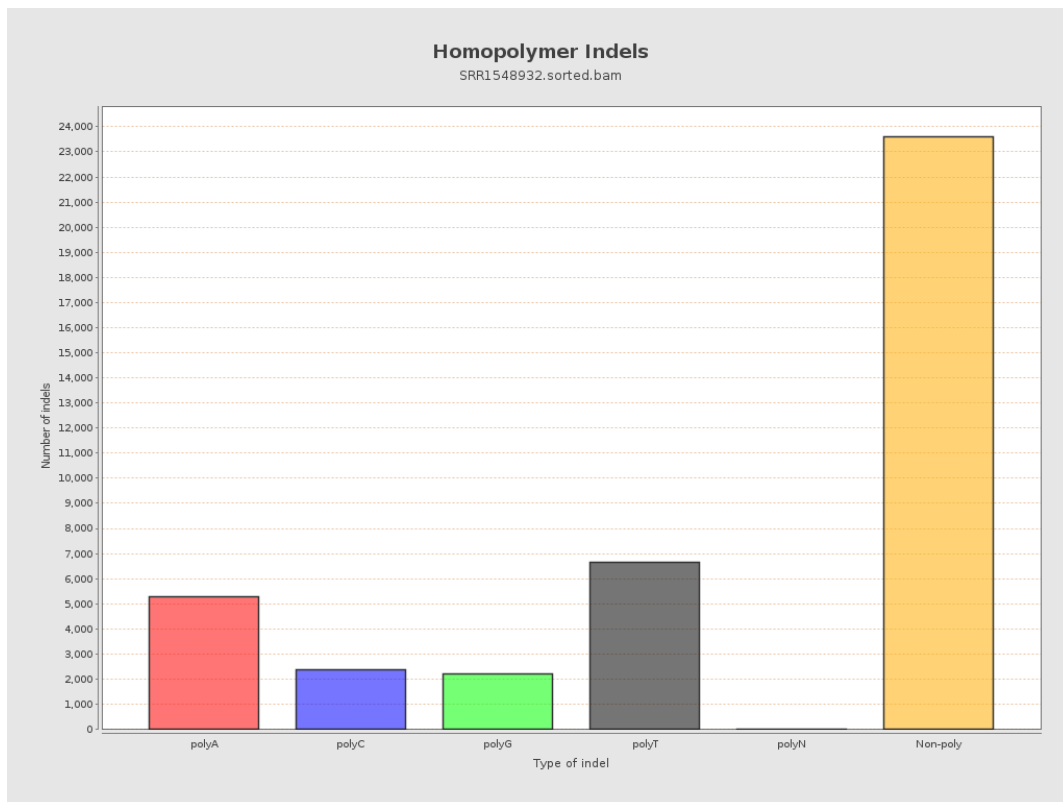
9. Results : Mapped Reads GC-content Distribution



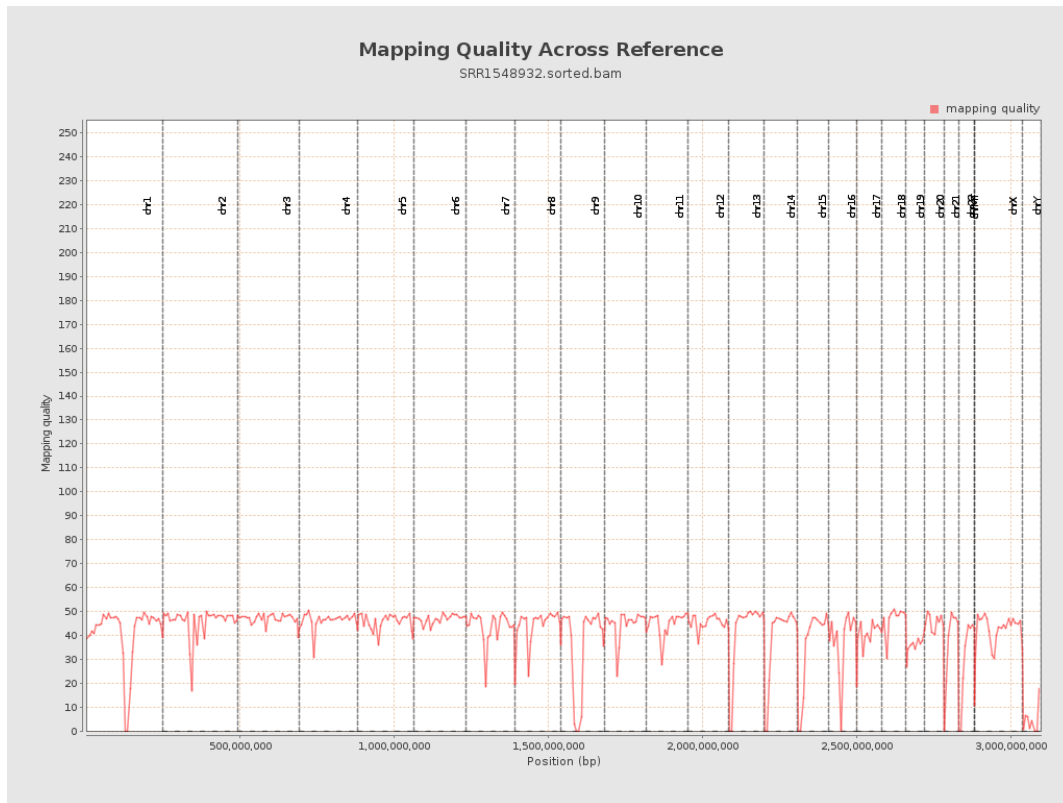
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

