Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 08:53:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1549006.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_SRR1549006 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1549006.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 08:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1549006.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,339,405
Mapped reads	9,819,262 / 86.59%
Unmapped reads	1,520,143 / 13.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	910,942 / 8.03%
Duplication rate	8.56%
Clipped reads	522,350 / 4.61%

2.2. ACGT Content

Number/percentage of A's	116,894,288 / 30%
Number/percentage of C's	77,018,638 / 19.77%
Number/percentage of T's	117,469,054 / 30.15%
Number/percentage of G's	78,253,766 / 20.08%
Number/percentage of N's	3,955 / 0%
GC Percentage	39.85%

2.3. Coverage

Mean	0.1259
Standard Deviation	0.9232

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Mismatches and indels

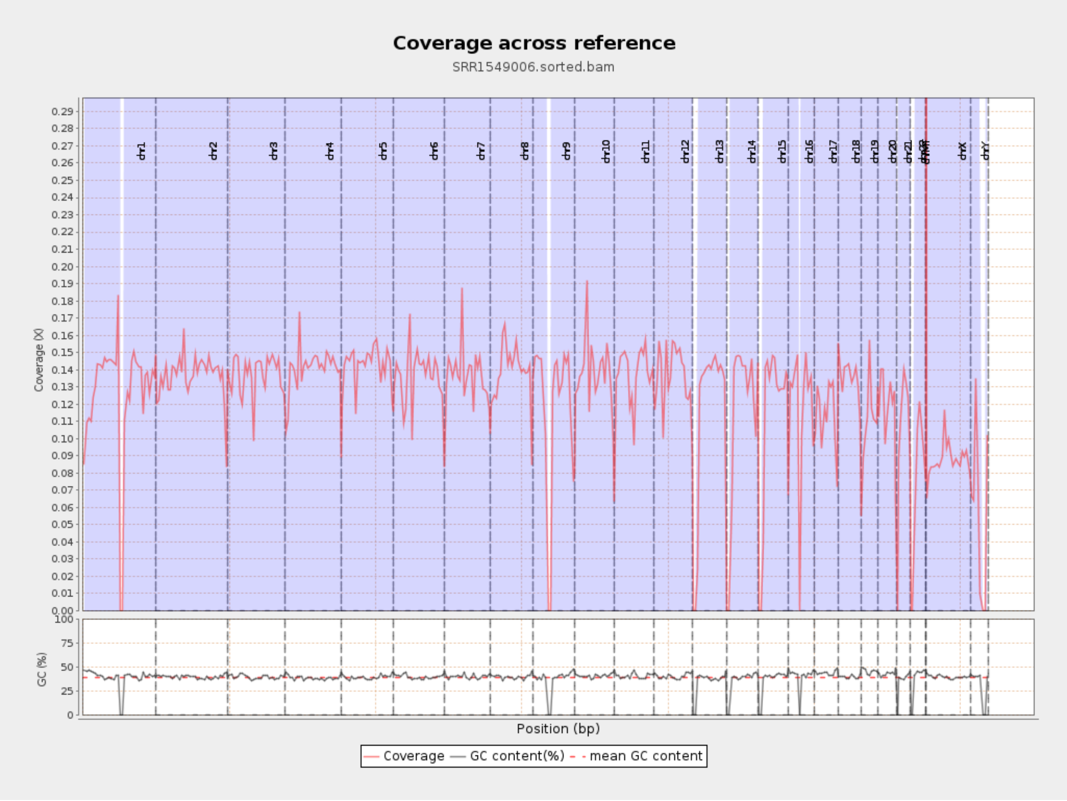
General error rate	0.3%
Mismatches	1,142,499
Insertions	12,250
Mapped reads with at least one insertion	0.12%
Deletions	33,355
Mapped reads with at least one deletion	0.34%
Homopolymer indels	43.02%

2.6. Chromosome stats

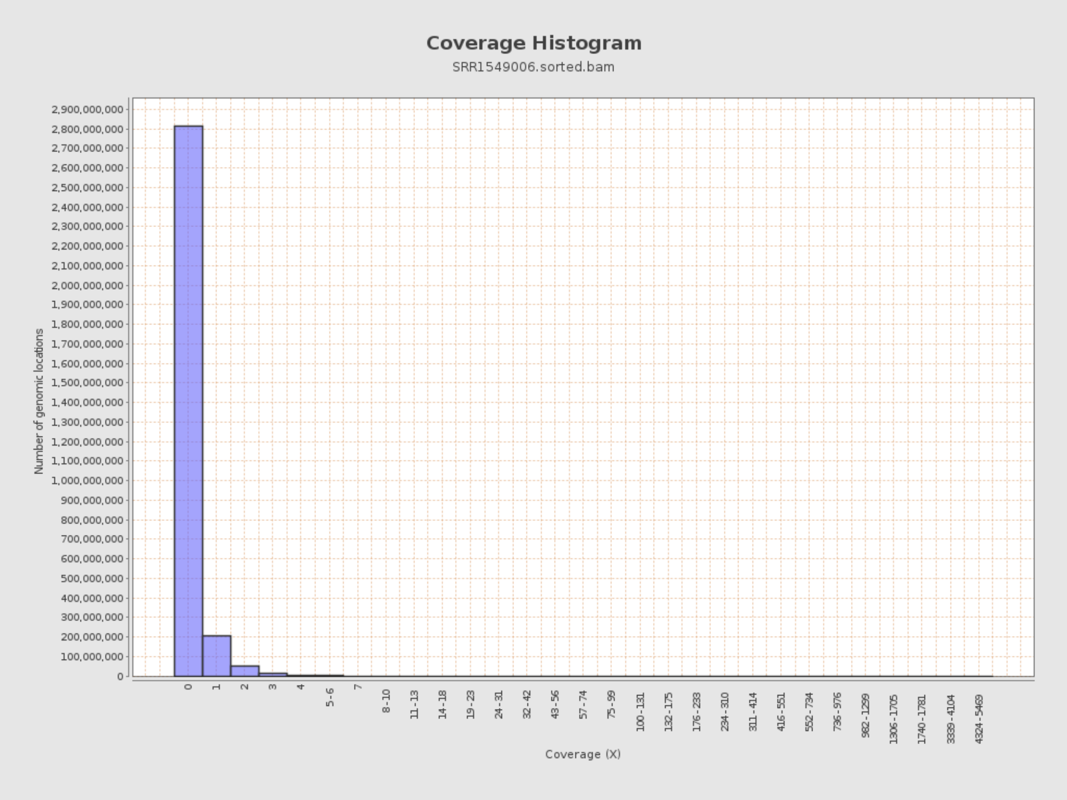
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	31408357	0.126	1.3602
chr2	243199373	33234684	0.1367	0.6872
chr3	198022430	27209739	0.1374	0.4821
chr4	191154276	27009918	0.1413	0.5419
chr5	180915260	25722197	0.1422	0.4949
chr6	171115067	23402812	0.1368	0.564
chr7	159138663	21674168	0.1362	0.9921
chr8	146364022	20338494	0.139	2.7178

chr9	141213431	16634098	0.1178	0.6312
chr10	135534747	18859285	0.1391	0.7345
chr11	135006516	18510025	0.1371	0.6374
chr12	133851895	18357126	0.1371	0.5038
chr13	115169878	13325235	0.1157	0.4393
chr14	107349540	12233164	0.114	0.5435
chr15	102531392	11312743	0.1103	0.4282
chr16	90354753	10376165	0.1148	0.4969
chr17	81195210	9338997	0.115	0.4884
chr18	78077248	10637703	0.1362	1.2858
chr19	59128983	6607816	0.1118	1.0702
chr20	63025520	7586814	0.1204	0.481
chr21	48129895	5066935	0.1053	0.5274
chr22	51304566	3798164	0.074	0.3959
chrMT	16571	22624	1.3653	1.8299
chrX	155270560	13637630	0.0878	0.4922
chrY	59373566	3378461	0.0569	0.573

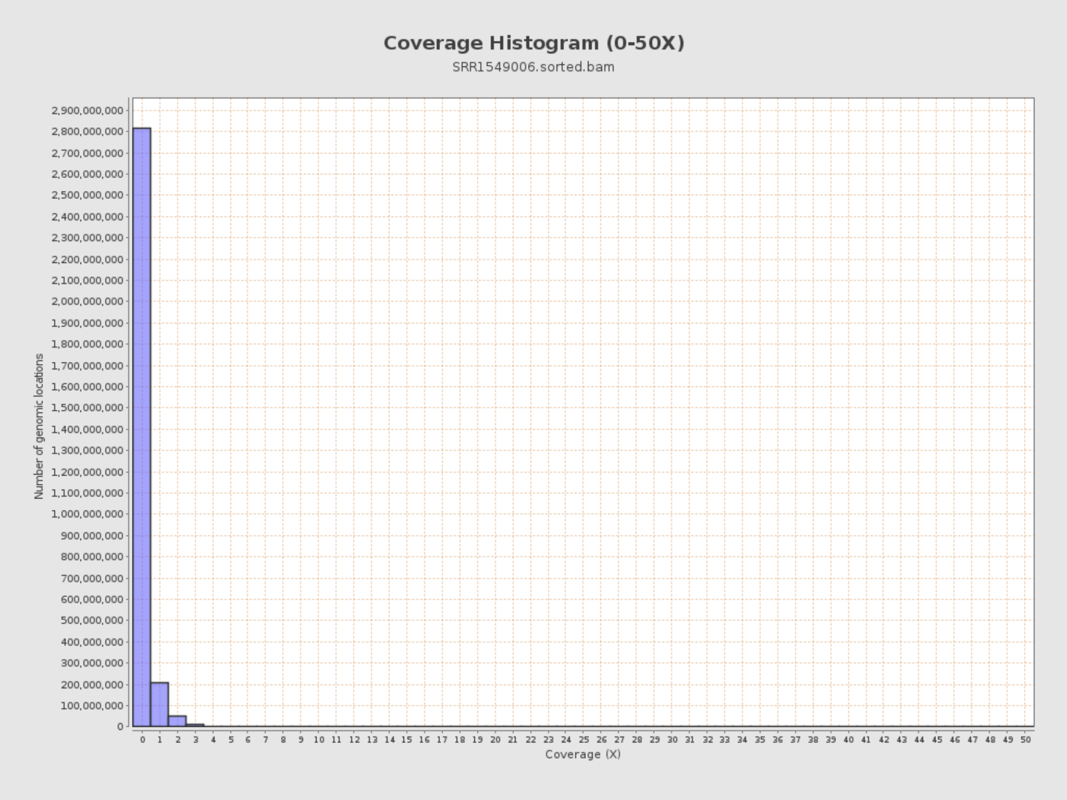
3. Results : Coverage across reference



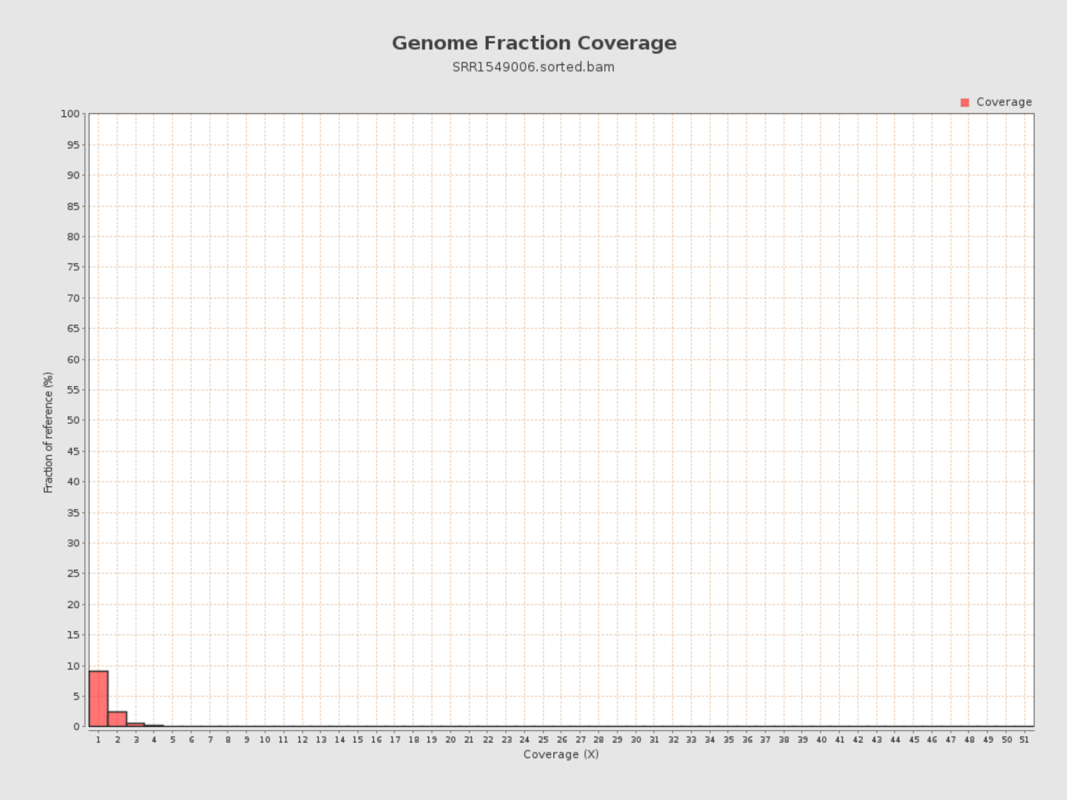
4. Results : Coverage Histogram



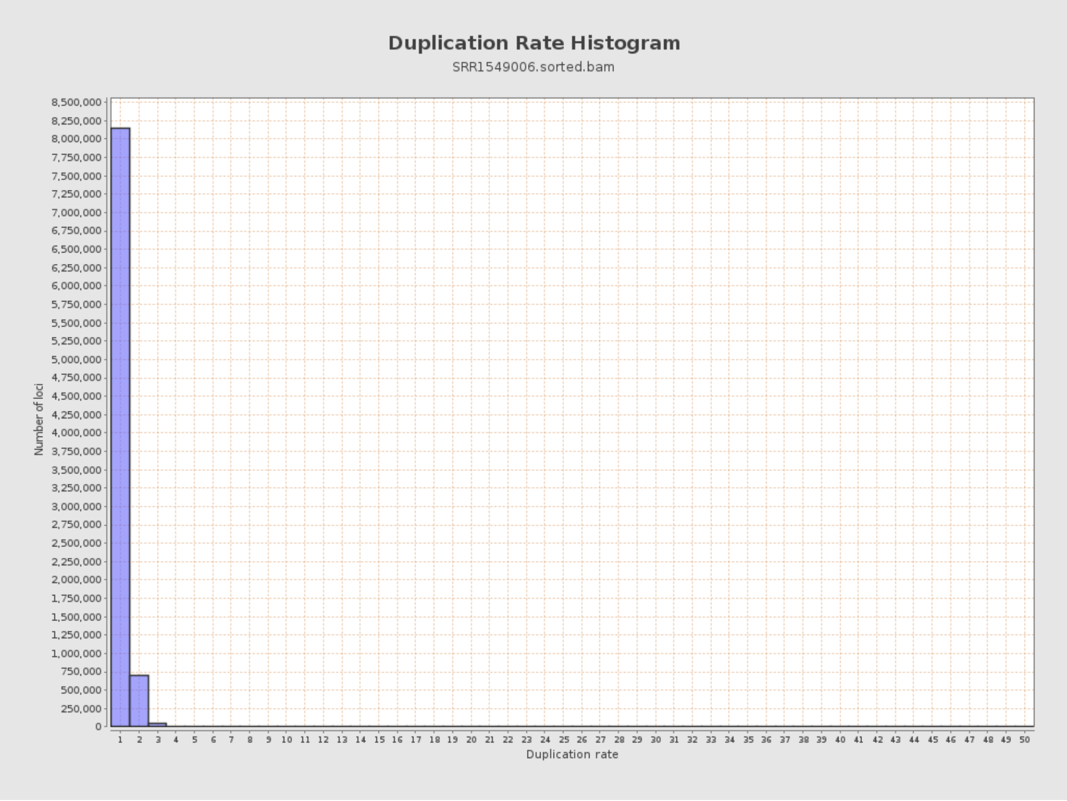
5. Results : Coverage Histogram (0-50X)



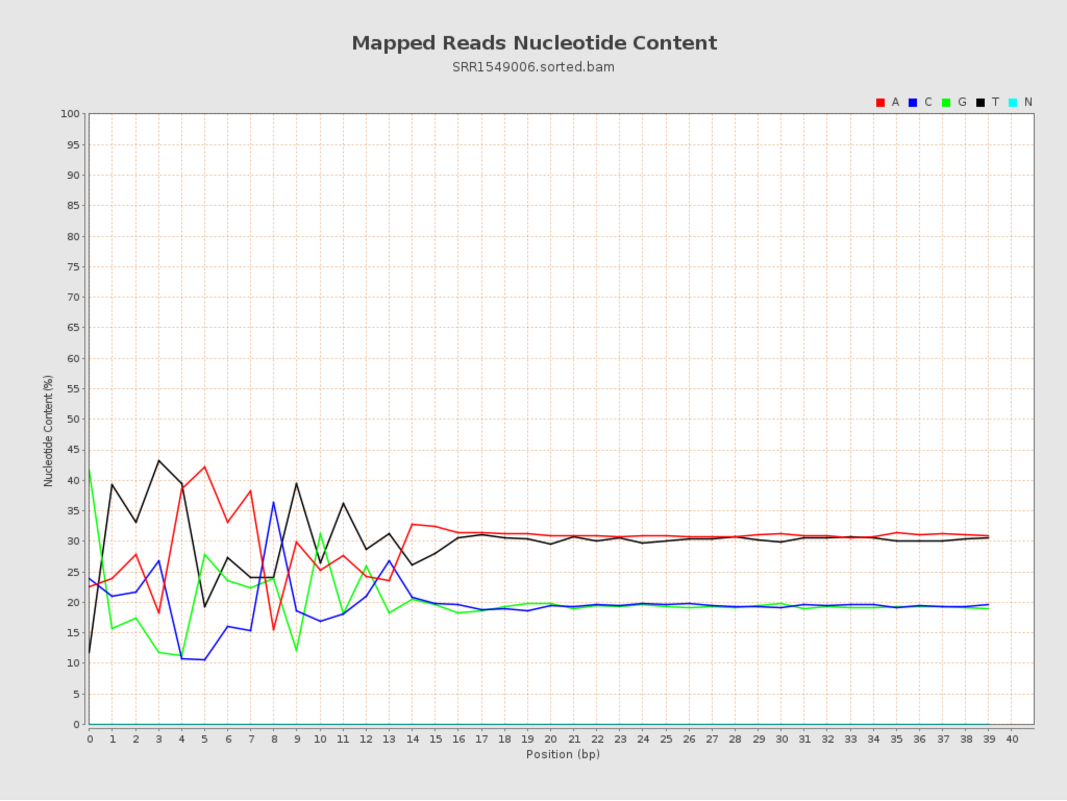
6. Results : Genome Fraction Coverage



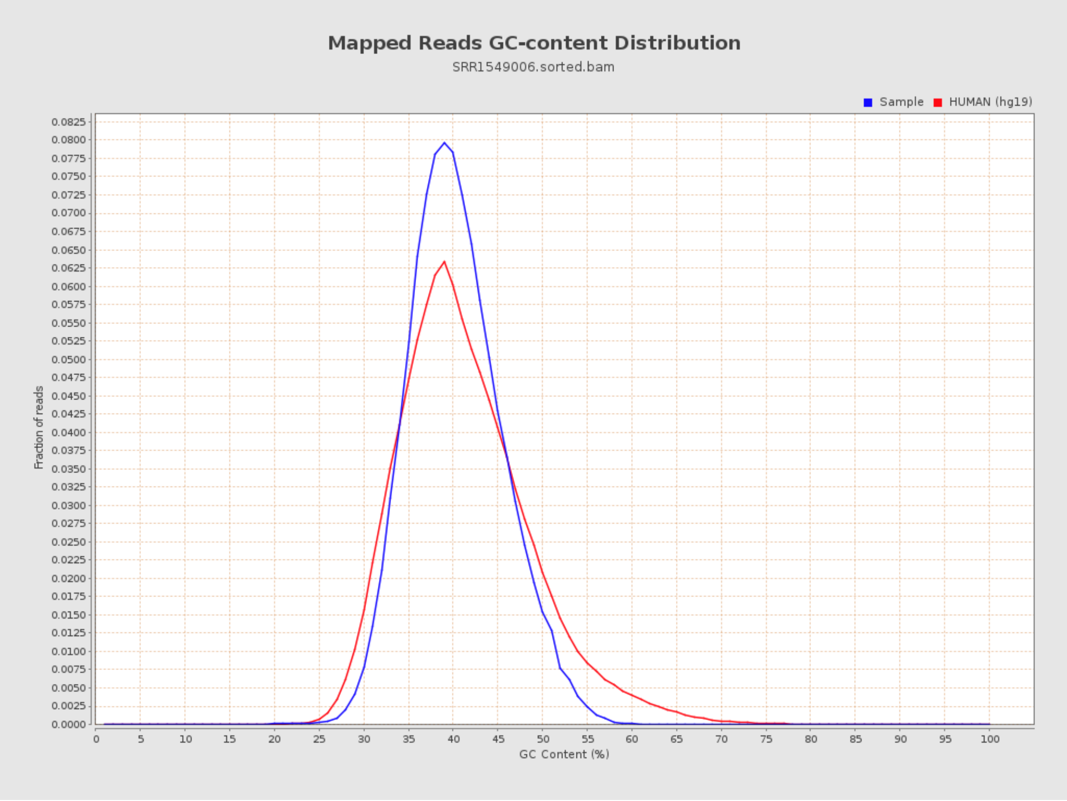
7. Results : Duplication Rate Histogram



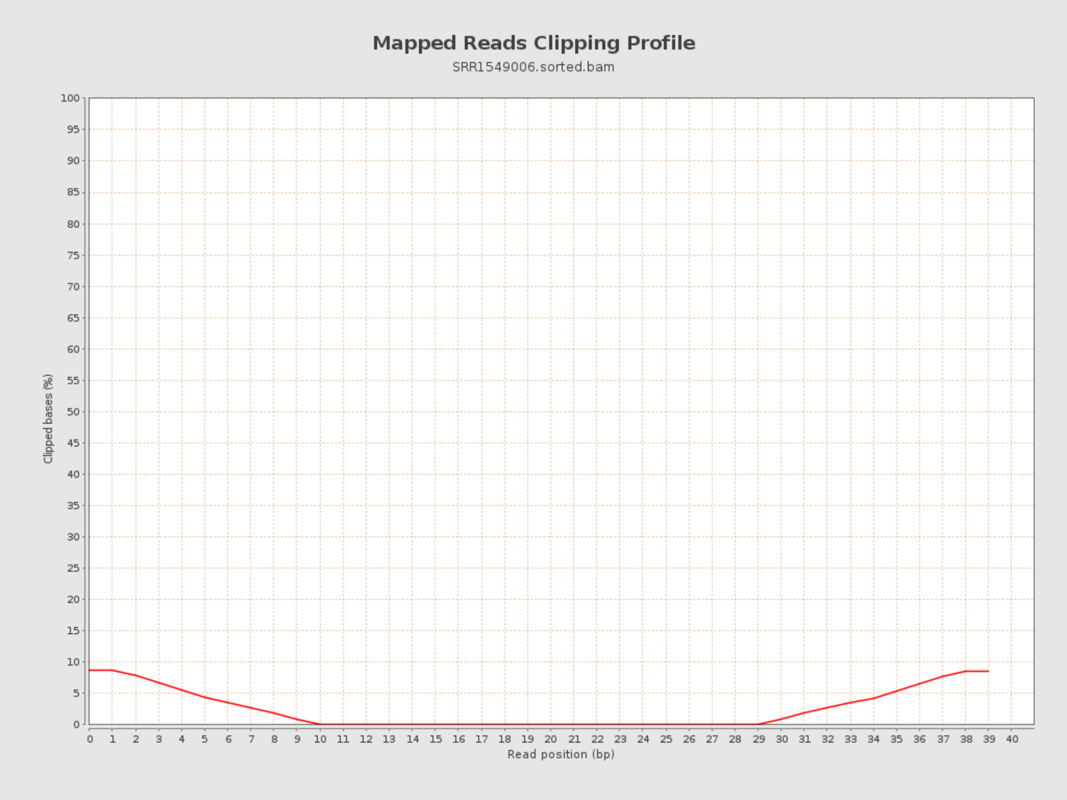
8. Results : Mapped Reads Nucleotide Content



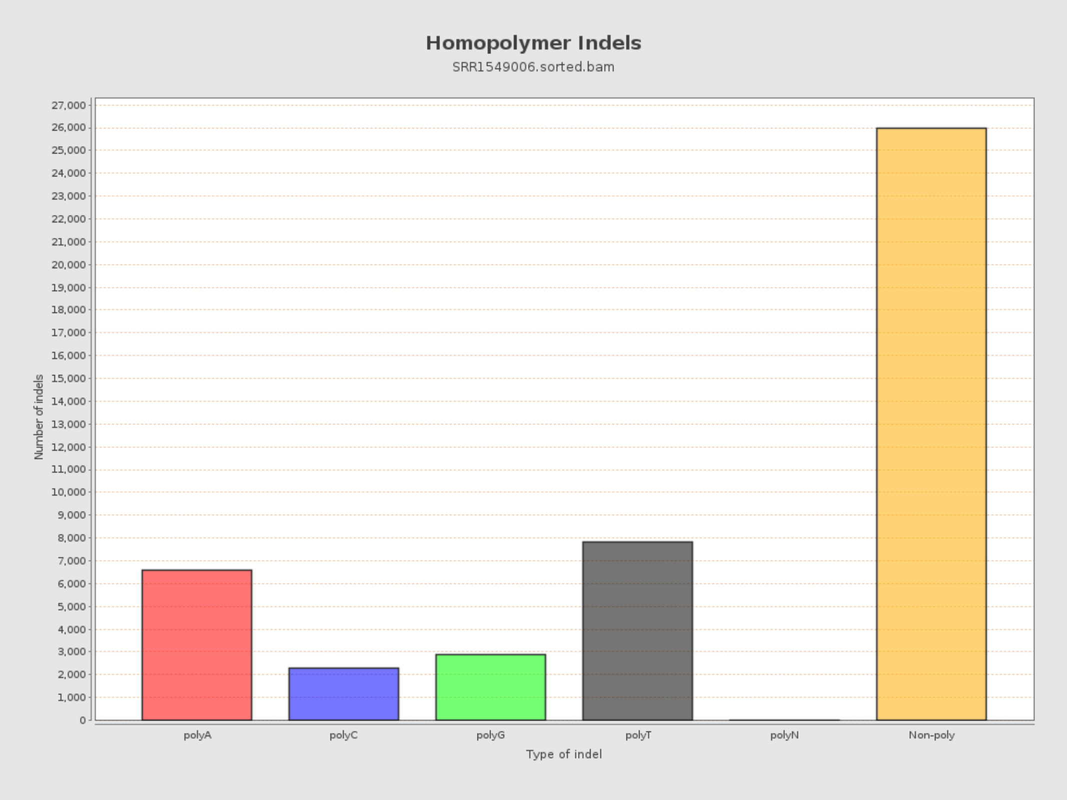
9. Results : Mapped Reads GC-content Distribution



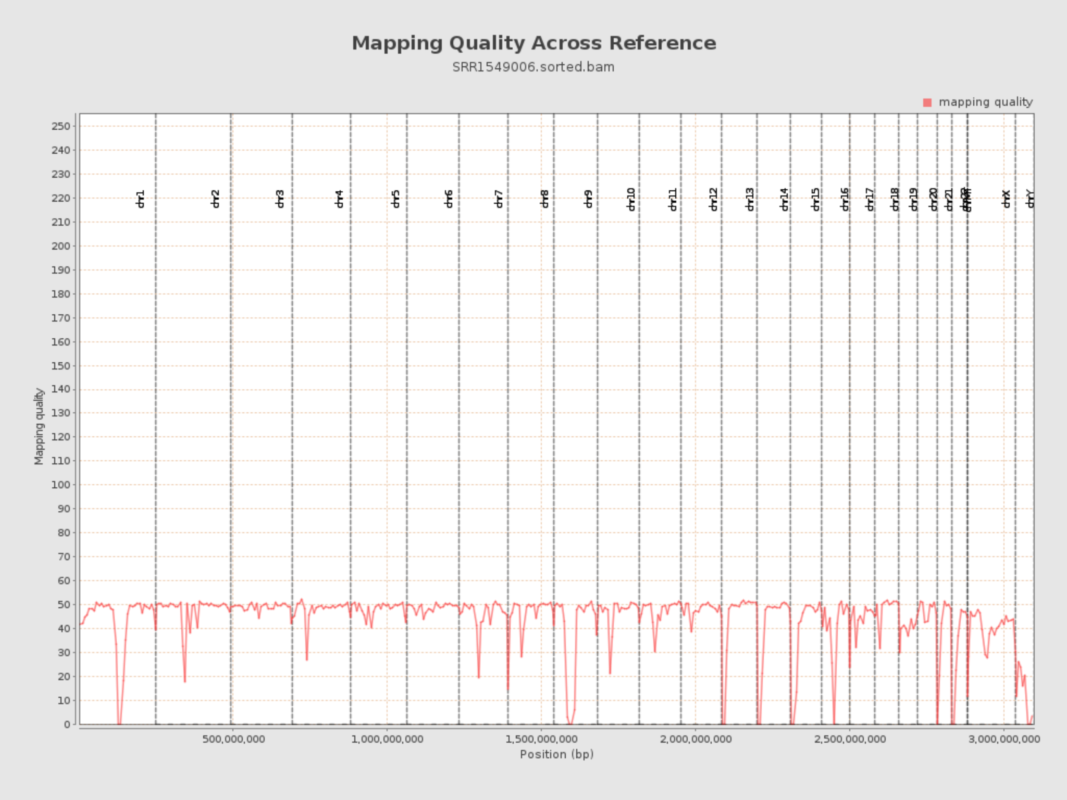
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram