Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:35:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505988.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_SRR1505988 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505988.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:35:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505988.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,969,306
Mapped reads	4,319,185 / 72.36%
Unmapped reads	1,650,121 / 27.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	209 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	406,291 / 6.81%
Duplication rate	7.2%
Clipped reads	528,643 / 8.86%

2.2. ACGT Content

Number/percentage of A's	60,916,958 / 30.11%
Number/percentage of C's	39,950,751 / 19.75%
Number/percentage of T's	61,095,658 / 30.2%
Number/percentage of G's	40,339,561 / 19.94%
Number/percentage of N's	845 / 0%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0654

Standard Deviation	0.6714

2.4. Mapping Quality

Mean Mapping Quality	44.4

2.5. Mismatches and indels

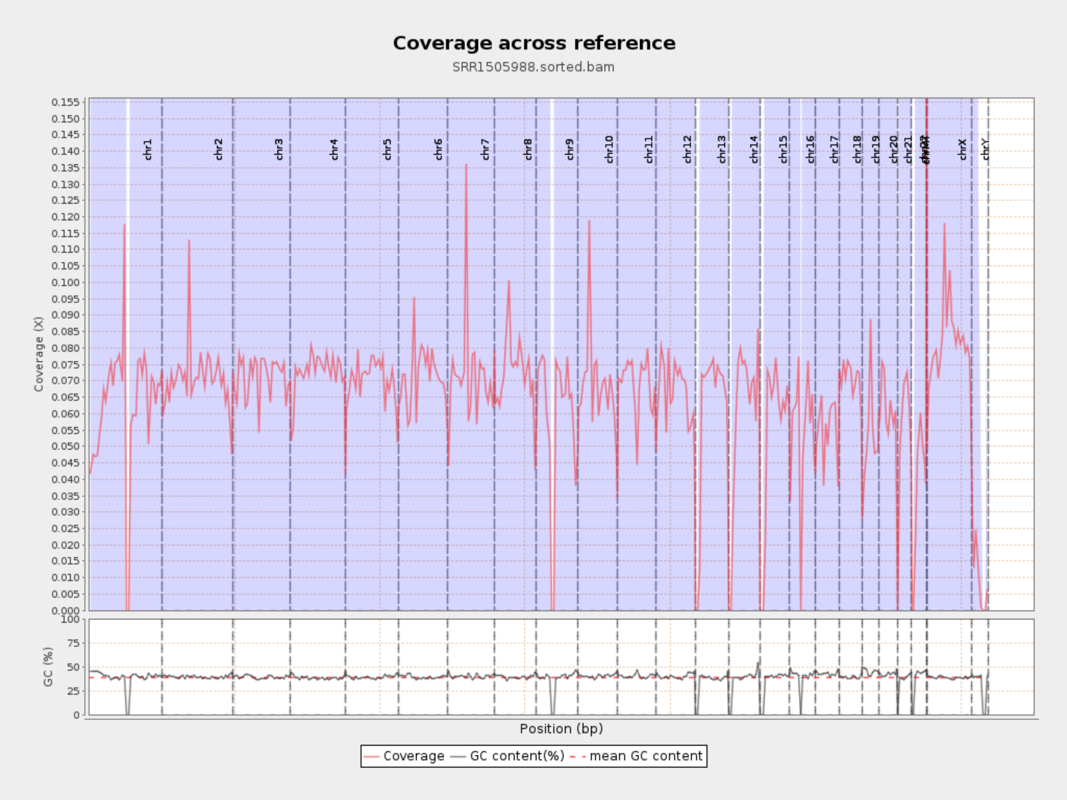
General error rate	0.53%
Mismatches	1,050,029
Insertions	9,394
Mapped reads with at least one insertion	0.22%
Deletions	29,725
Mapped reads with at least one deletion	0.69%
Homopolymer indels	45.41%

2.6. Chromosome stats

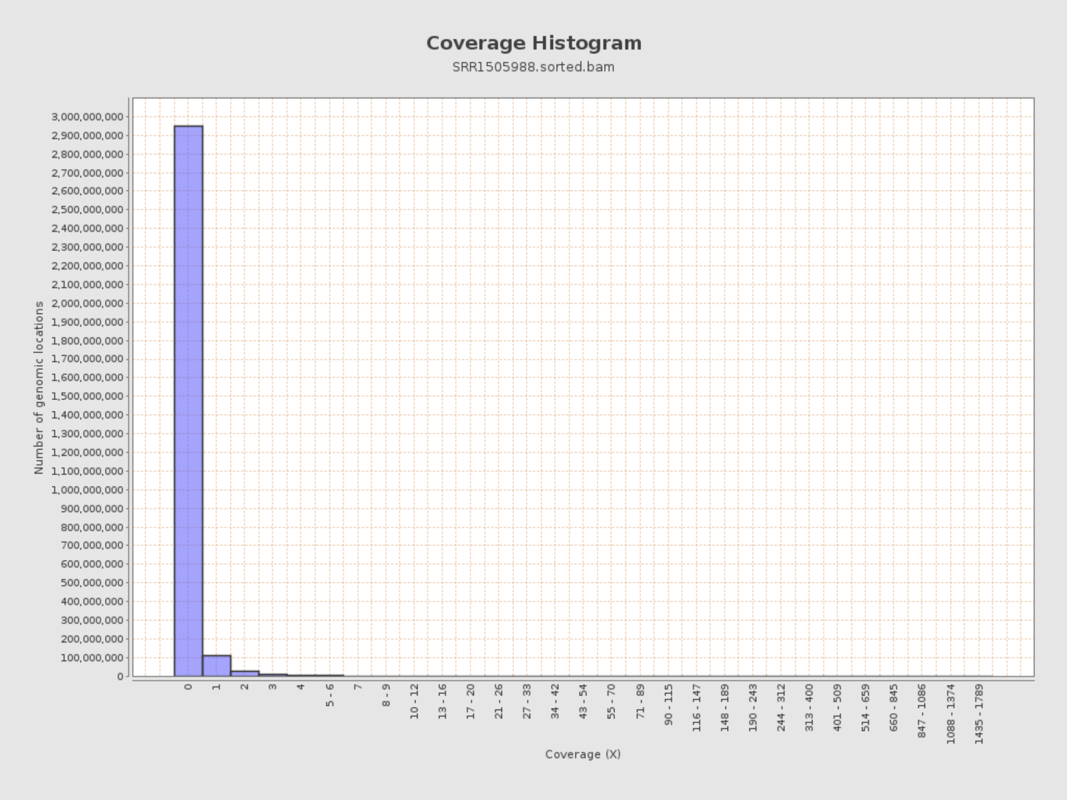
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15633931	0.0627	1.1786
chr2	243199373	17226837	0.0708	0.5254
chr3	198022430	14128281	0.0713	0.3571
chr4	191154276	13916322	0.0728	0.3607
chr5	180915260	12761918	0.0705	0.3582
chr6	171115067	12206288	0.0713	0.4479
chr7	159138663	11437758	0.0719	0.9105

chr8	146364022	10621247	0.0726	1.0202
chr9	141213431	8384087	0.0594	0.4819
chr10	135534747	9409058	0.0694	0.6224
chr11	135006516	9245276	0.0685	0.5523
chr12	133851895	8950196	0.0669	0.3697
chr13	115169878	6820248	0.0592	0.3236
chr14	107349540	6403358	0.0596	1.4754
chr15	102531392	5519710	0.0538	0.306
chr16	90354753	4958800	0.0549	0.3579
chr17	81195210	4411230	0.0543	0.3631
chr18	78077248	5551564	0.0711	0.9958
chr19	59128983	3201304	0.0541	0.8447
chr20	63025520	3860782	0.0613	0.3615
chr21	48129895	2650777	0.0551	0.3312
chr22	51304566	1807923	0.0352	0.2471
chrMT	16571	5570	0.3361	0.7337
chrX	155270560	12670465	0.0816	0.4394
chrY	59373566	561244	0.0095	0.1413

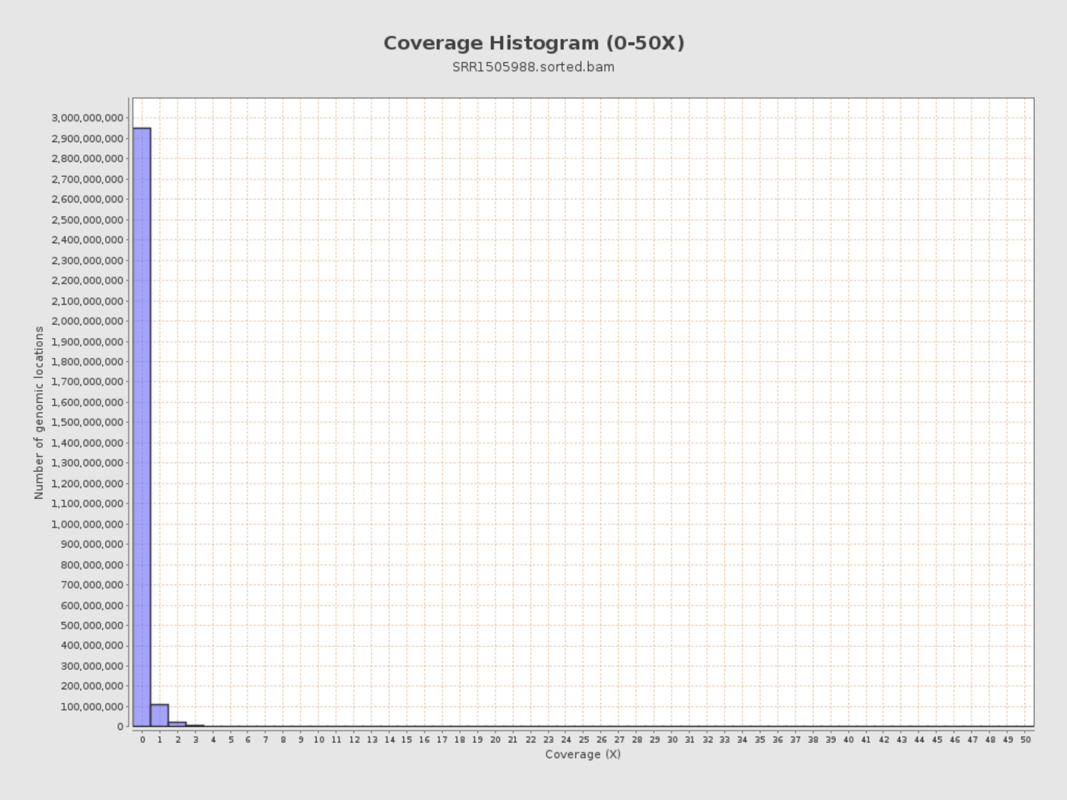
3. Results : Coverage across reference



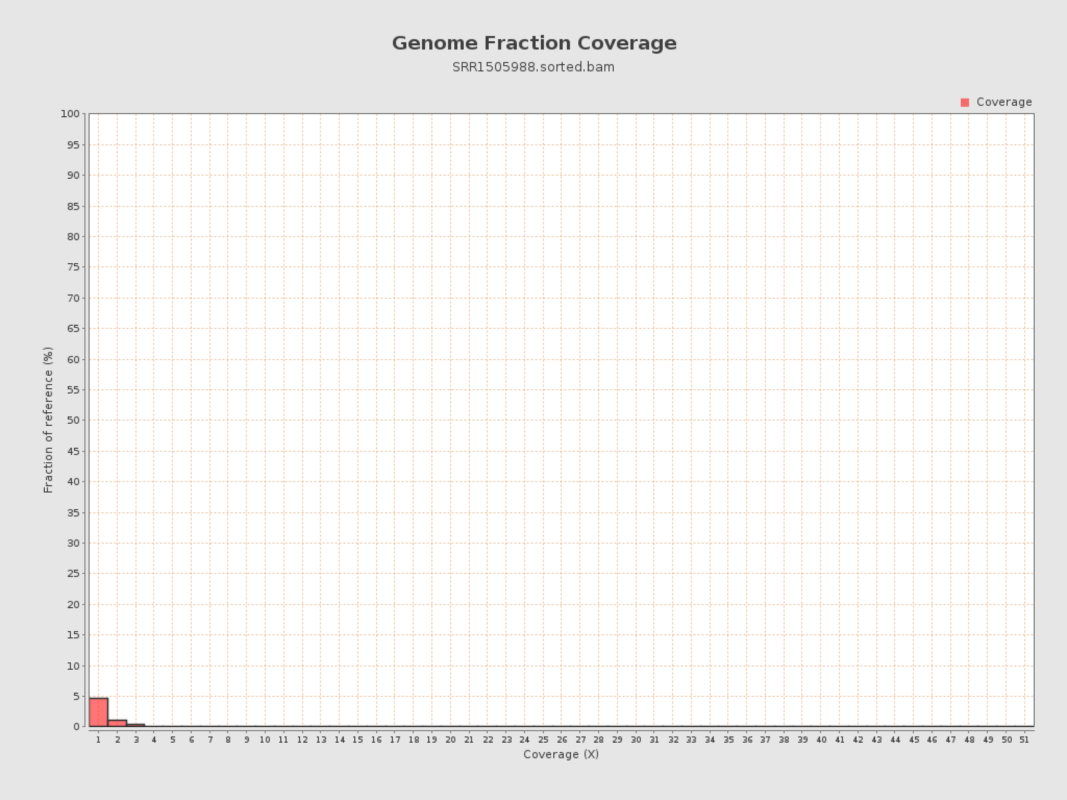
4. Results : Coverage Histogram



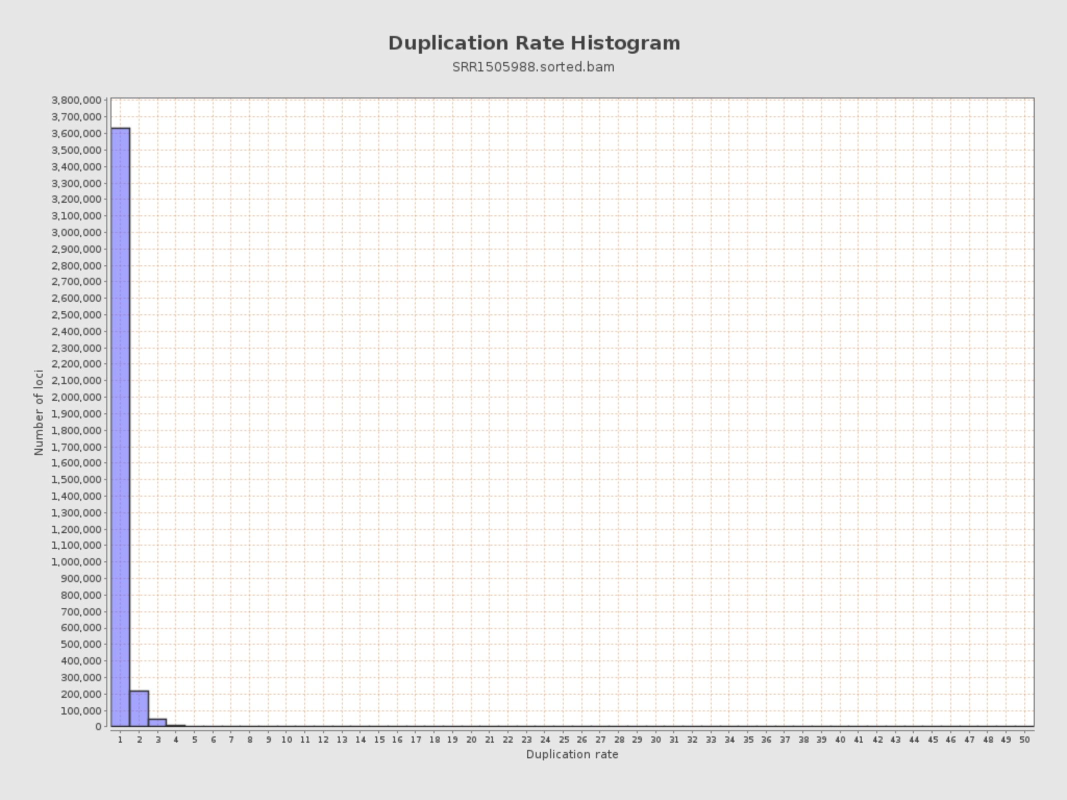
5. Results : Coverage Histogram (0-50X)



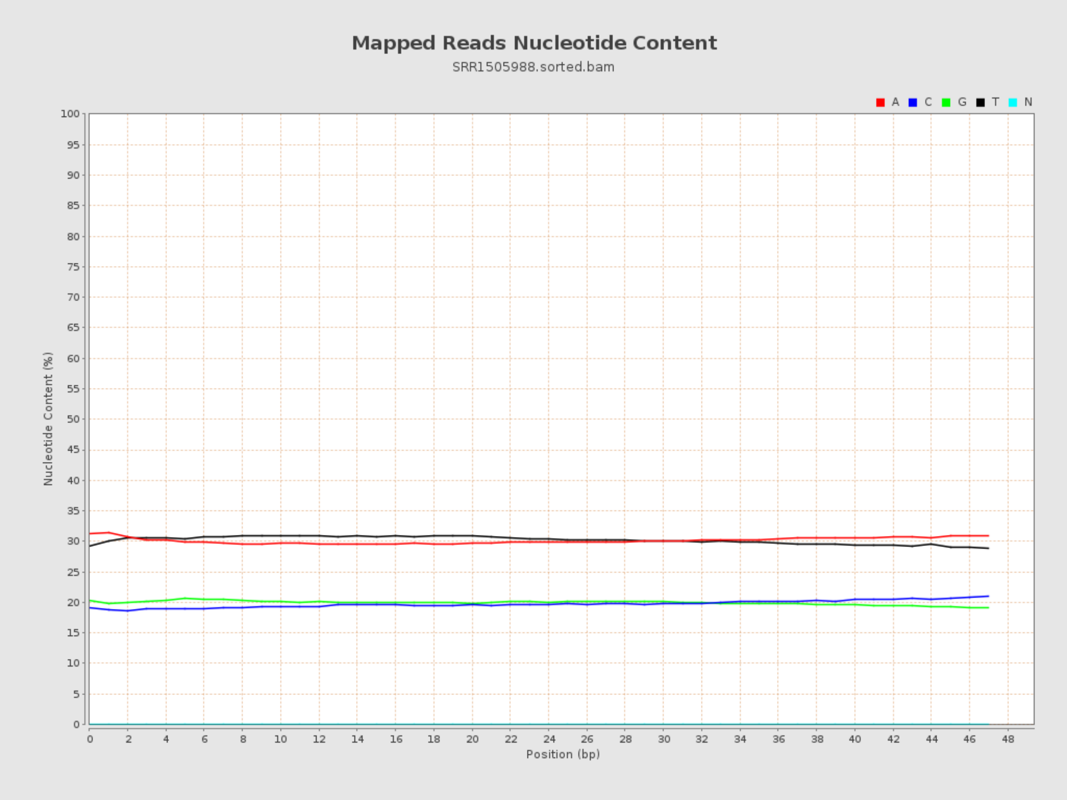
6. Results : Genome Fraction Coverage



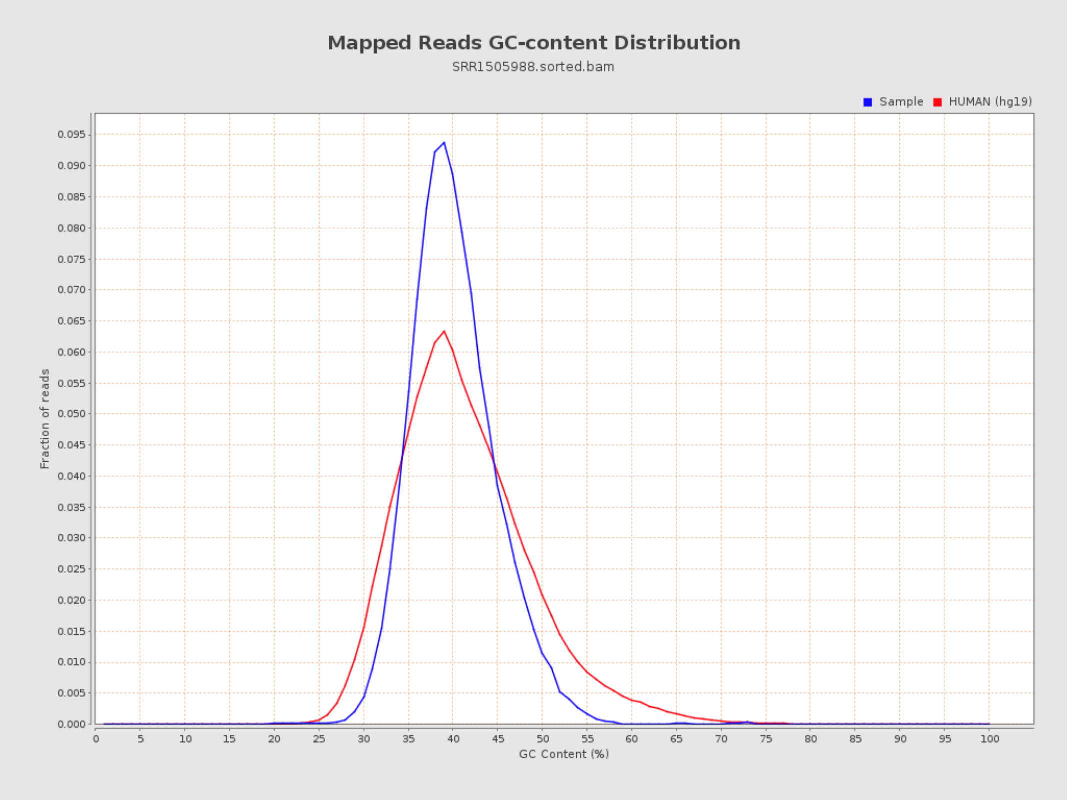
7. Results : Duplication Rate Histogram



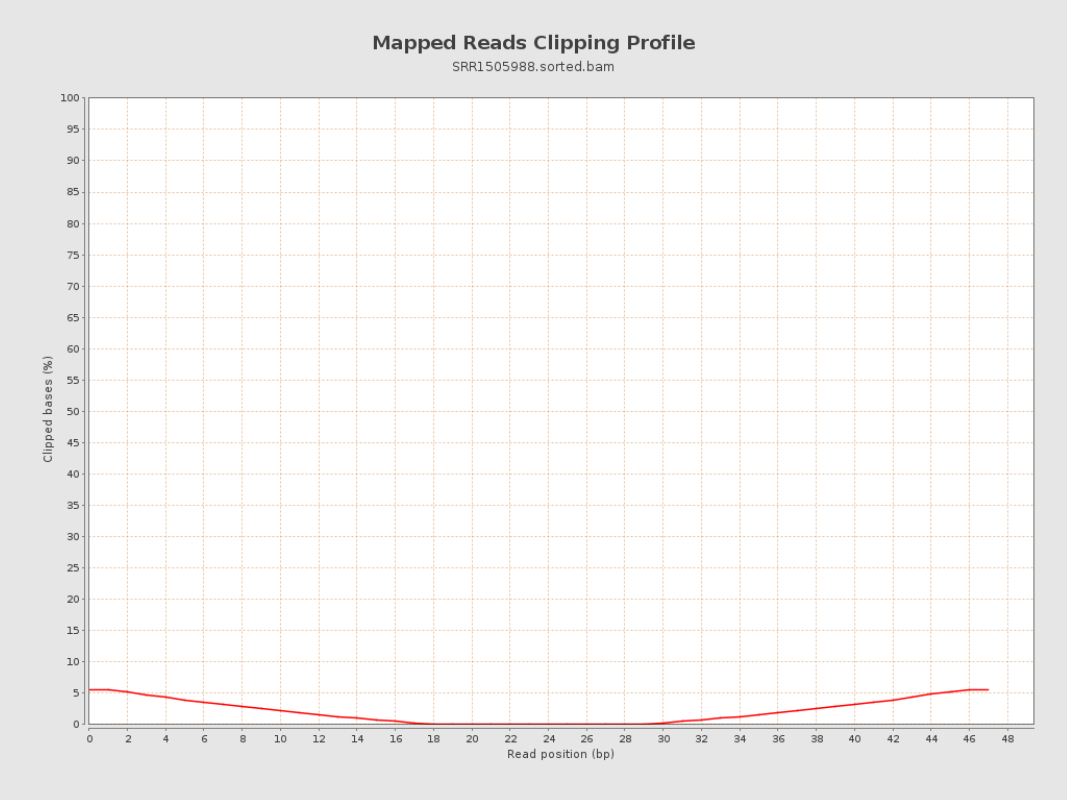
8. Results : Mapped Reads Nucleotide Content



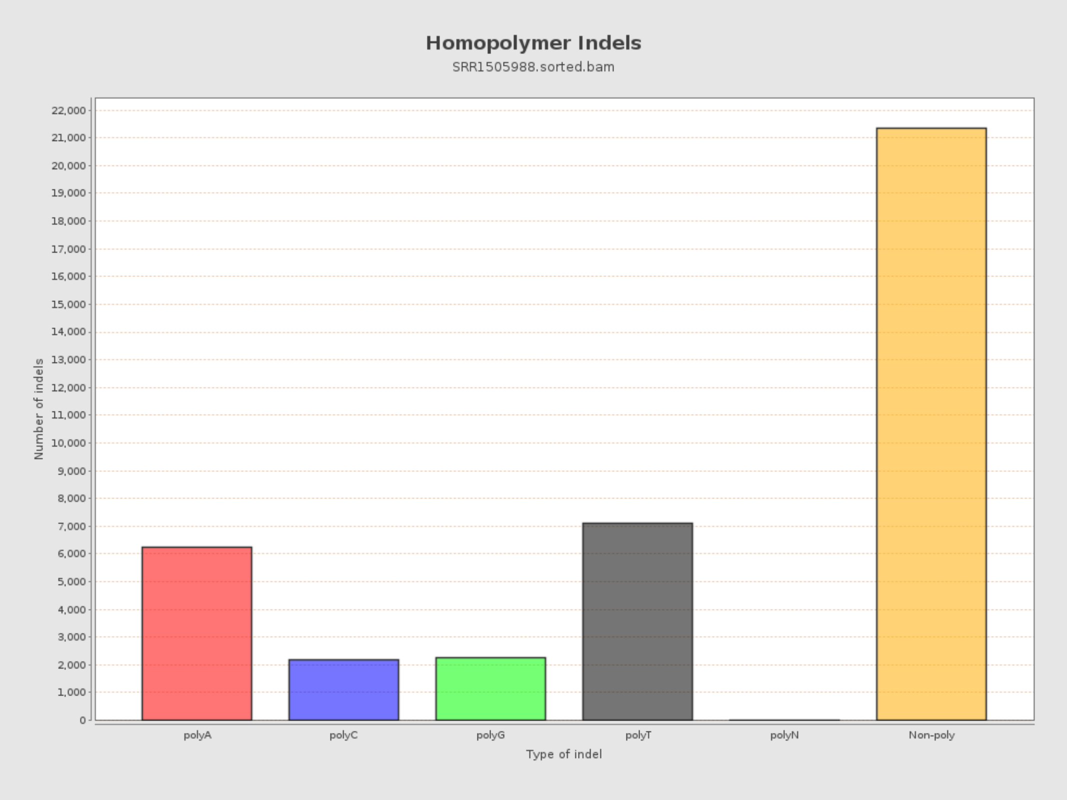
9. Results : Mapped Reads GC-content Distribution



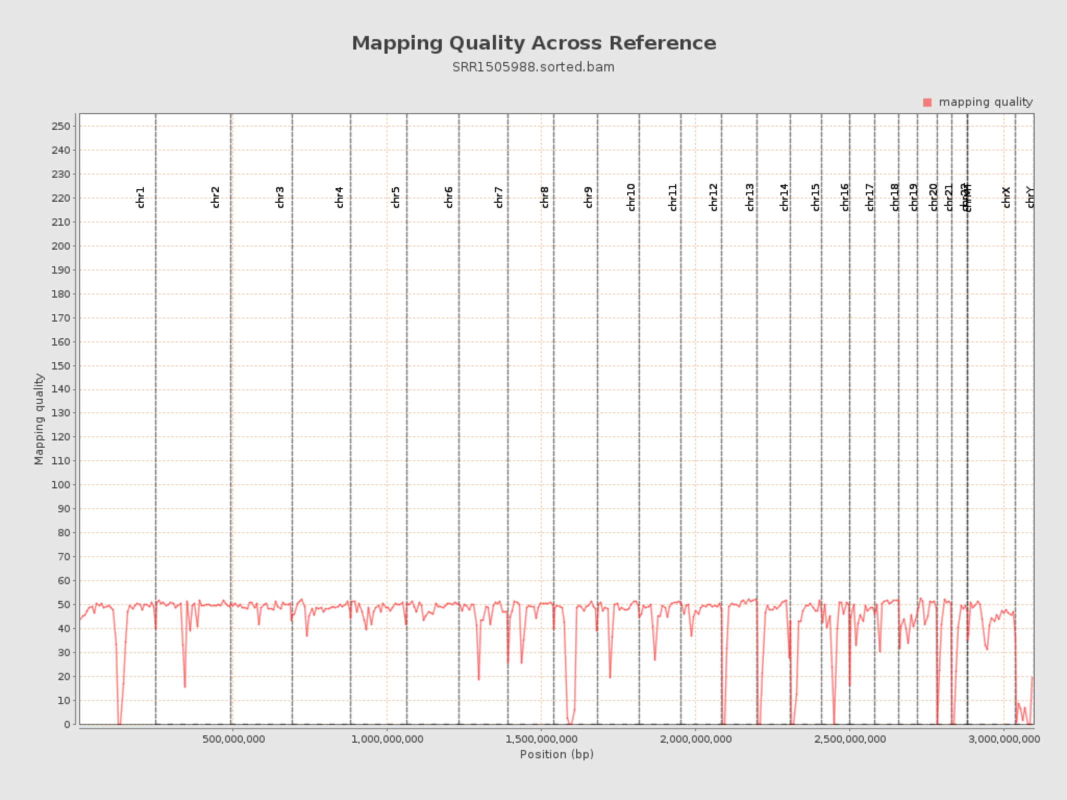
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram