Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:24:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505920.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_SRR1505920 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505920.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:24:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505920.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,757,471
Mapped reads	5,755,739 / 53.5%
Unmapped reads	5,001,732 / 46.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	276 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	292,738 / 2.72%
Duplication rate	3.72%
Clipped reads	731,230 / 6.8%

2.2. ACGT Content

Number/percentage of A's	79,575,109 / 29.55%
Number/percentage of C's	54,898,197 / 20.39%
Number/percentage of T's	79,090,745 / 29.37%
Number/percentage of G's	55,723,848 / 20.69%
Number/percentage of N's	948 / 0%
GC Percentage	41.08%

2.3. Coverage

Mean	0.087

Standard Deviation	0.7693

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

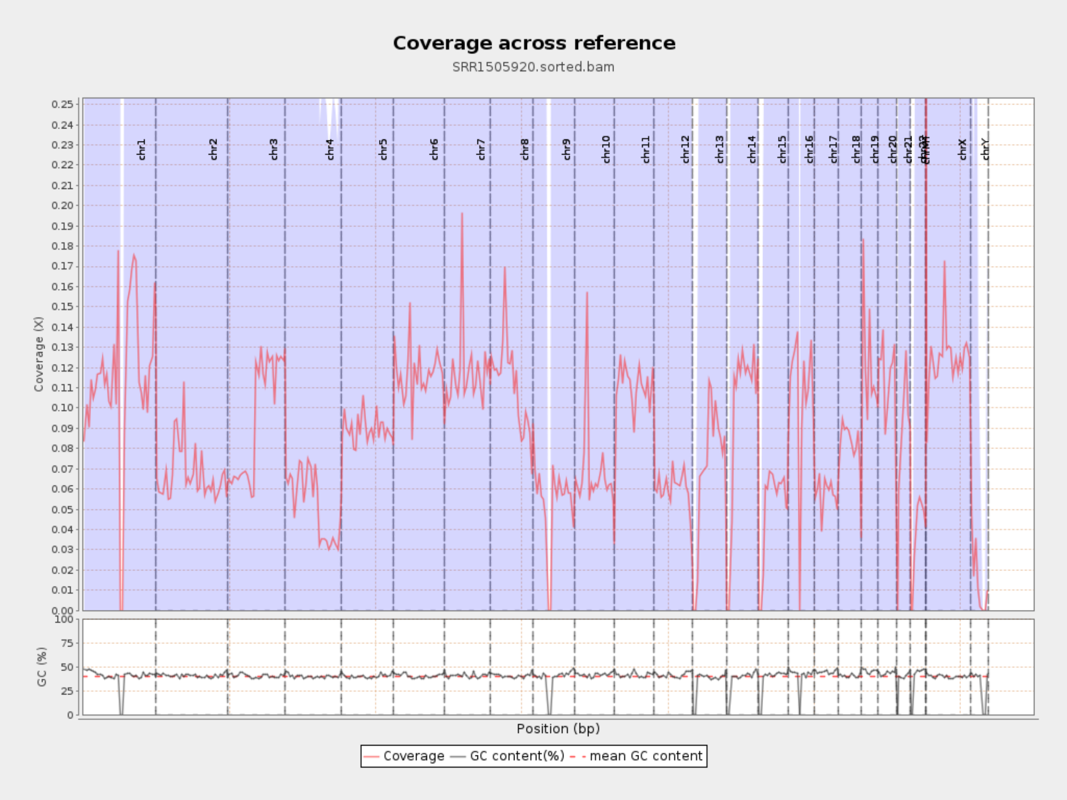
General error rate	0.53%
Mismatches	1,399,486
Insertions	12,183
Mapped reads with at least one insertion	0.21%
Deletions	41,463
Mapped reads with at least one deletion	0.72%
Homopolymer indels	46.11%

2.6. Chromosome stats

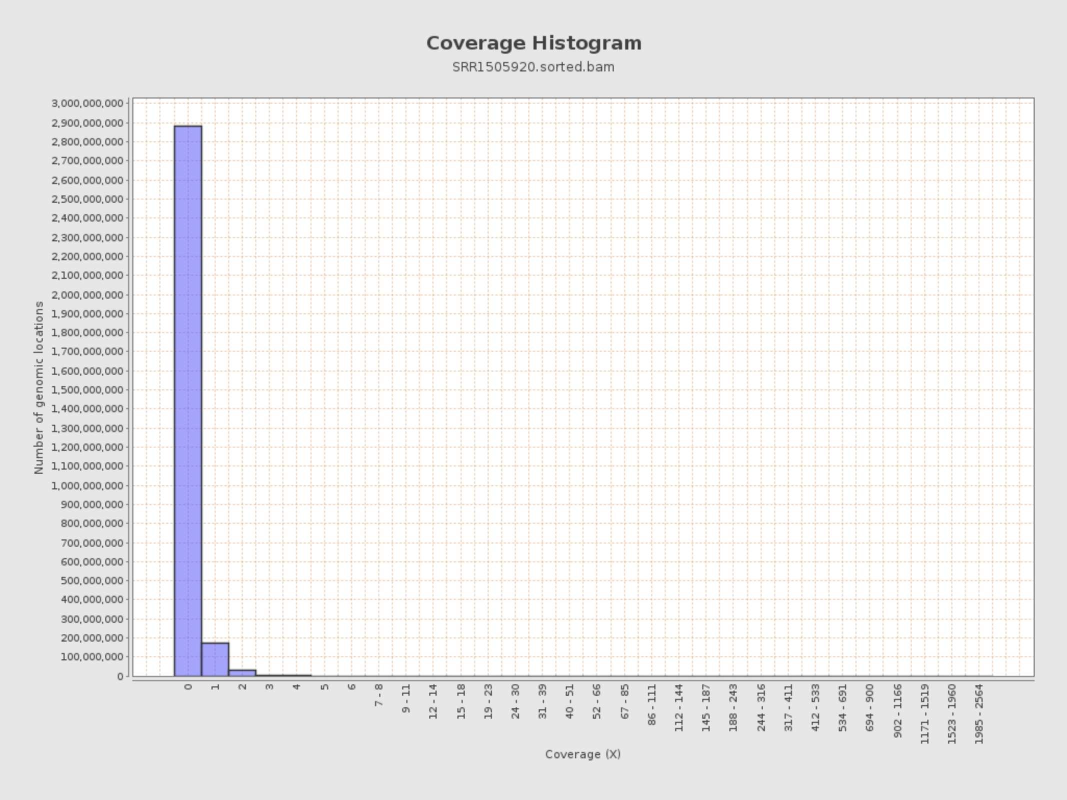
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28597493	0.1147	1.7446
chr2	243199373	16398679	0.0674	0.5235
chr3	198022430	18532227	0.0936	0.3758
chr4	191154276	10005822	0.0523	0.2857
chr5	180915260	16190168	0.0895	0.3682
chr6	171115067	20062018	0.1172	0.5566
chr7	159138663	18686090	0.1174	1.2902

chr8	146364022	16304359	0.1114	0.9618
chr9	141213431	7435070	0.0527	0.4402
chr10	135534747	9299785	0.0686	0.8021
chr11	135006516	14810736	0.1097	0.6724
chr12	133851895	8065699	0.0603	0.3239
chr13	115169878	8166571	0.0709	0.3182
chr14	107349540	10556829	0.0983	0.5652
chr15	102531392	5076961	0.0495	0.2642
chr16	90354753	9426437	0.1043	0.5045
chr17	81195210	4730092	0.0583	0.349
chr18	78077248	6551481	0.0839	0.9211
chr19	59128983	7026226	0.1188	1.1415
chr20	63025520	7311919	0.116	0.4276
chr21	48129895	4080411	0.0848	0.3804
chr22	51304566	1918033	0.0374	0.2322
chrMT	16571	6496	0.392	0.7401
chrX	155270560	19276862	0.1242	0.5121
chrY	59373566	830350	0.014	0.1949

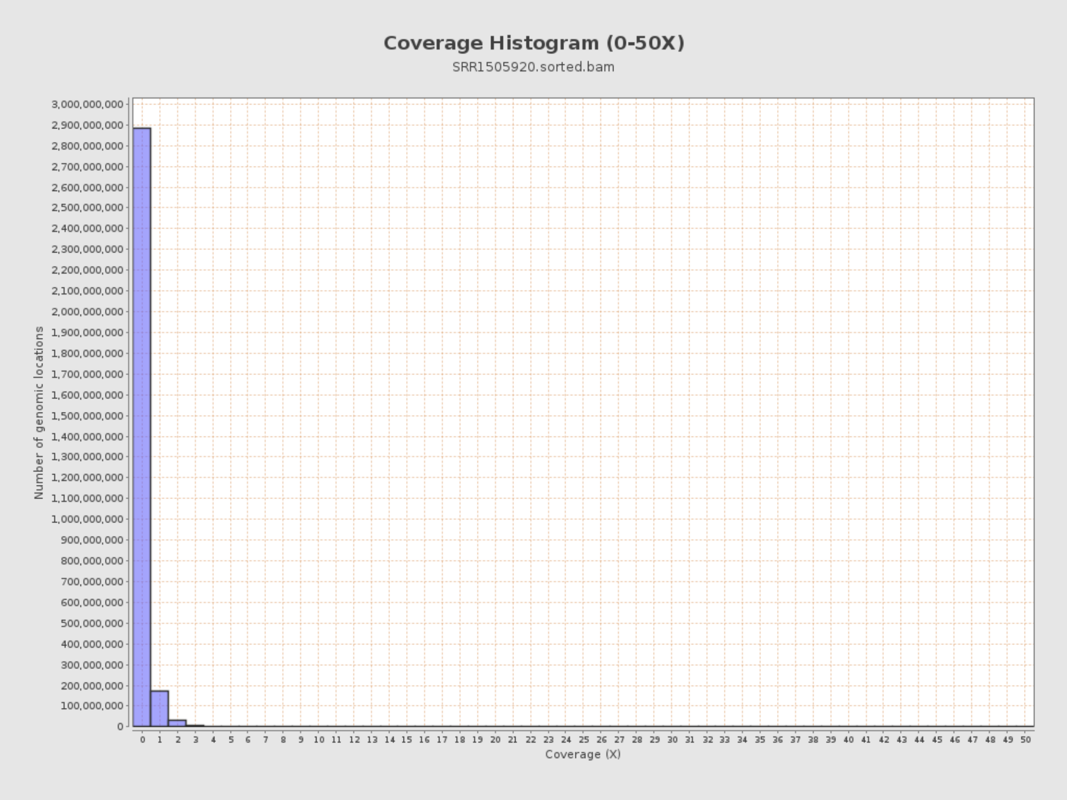
3. Results : Coverage across reference



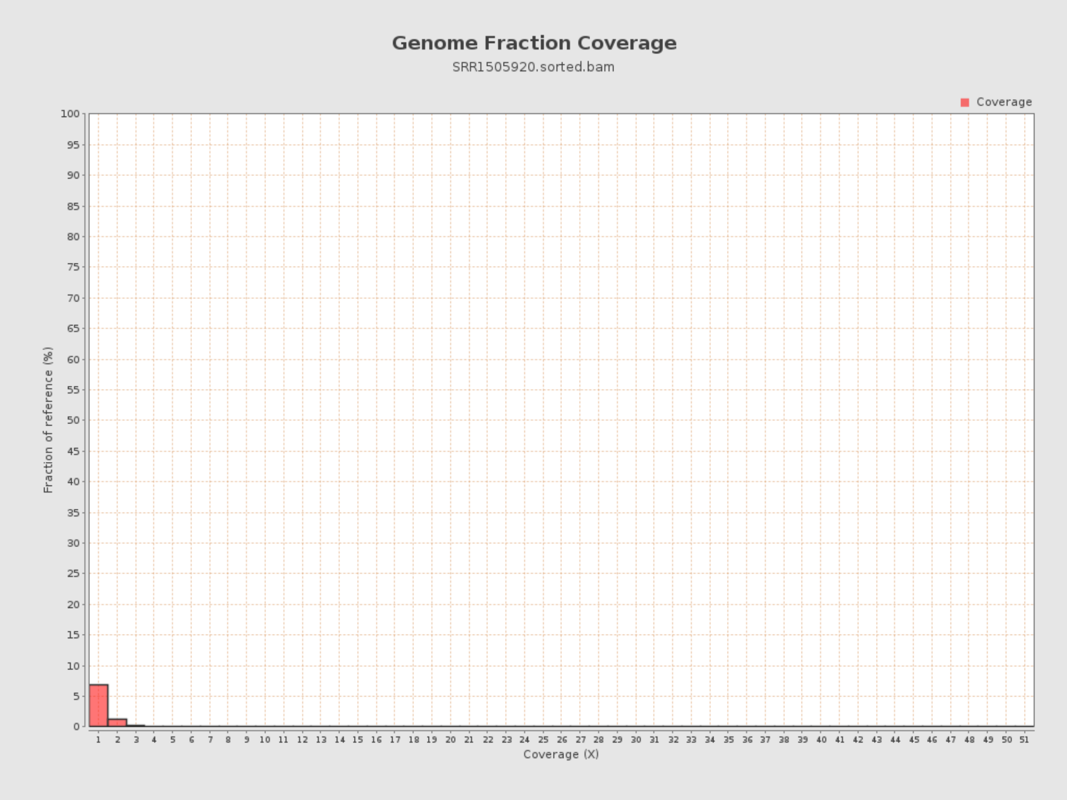
4. Results : Coverage Histogram



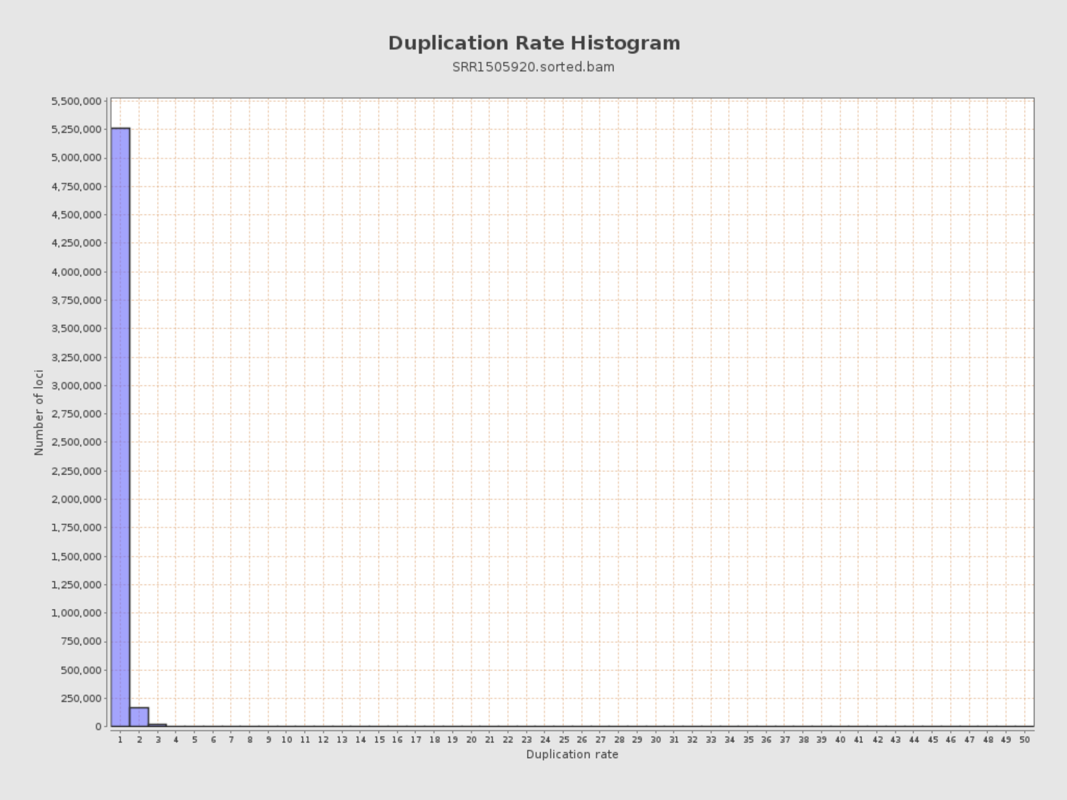
5. Results : Coverage Histogram (0-50X)



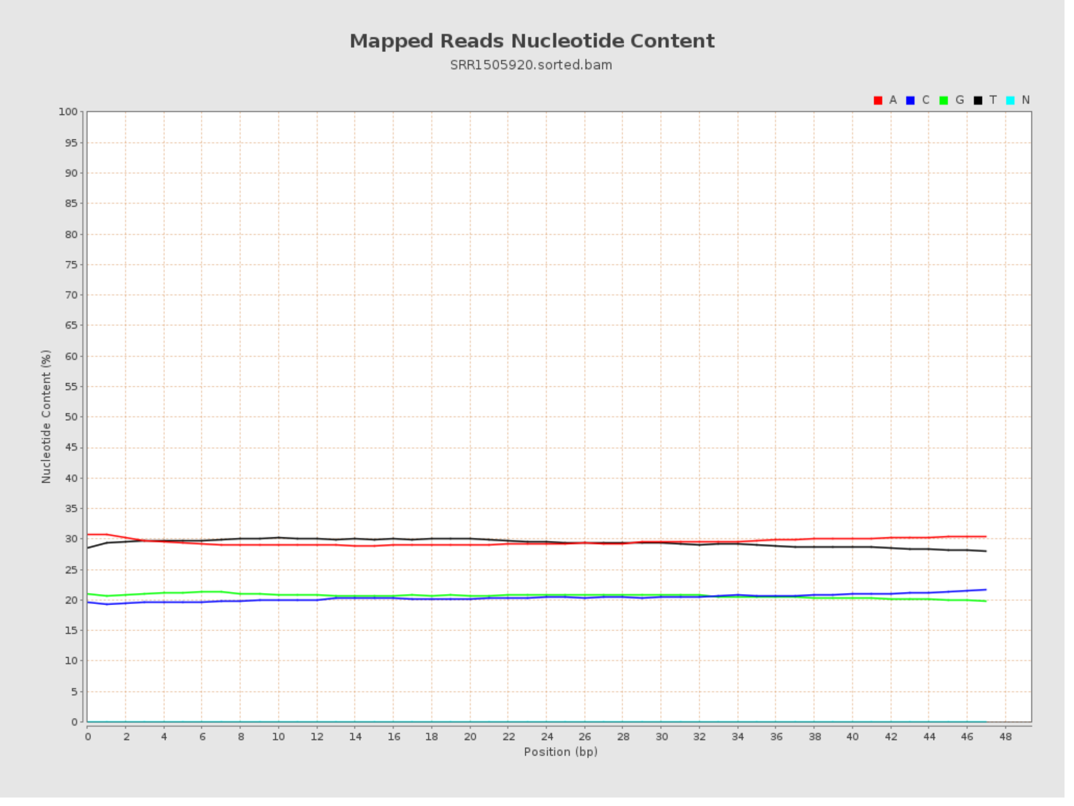
6. Results : Genome Fraction Coverage



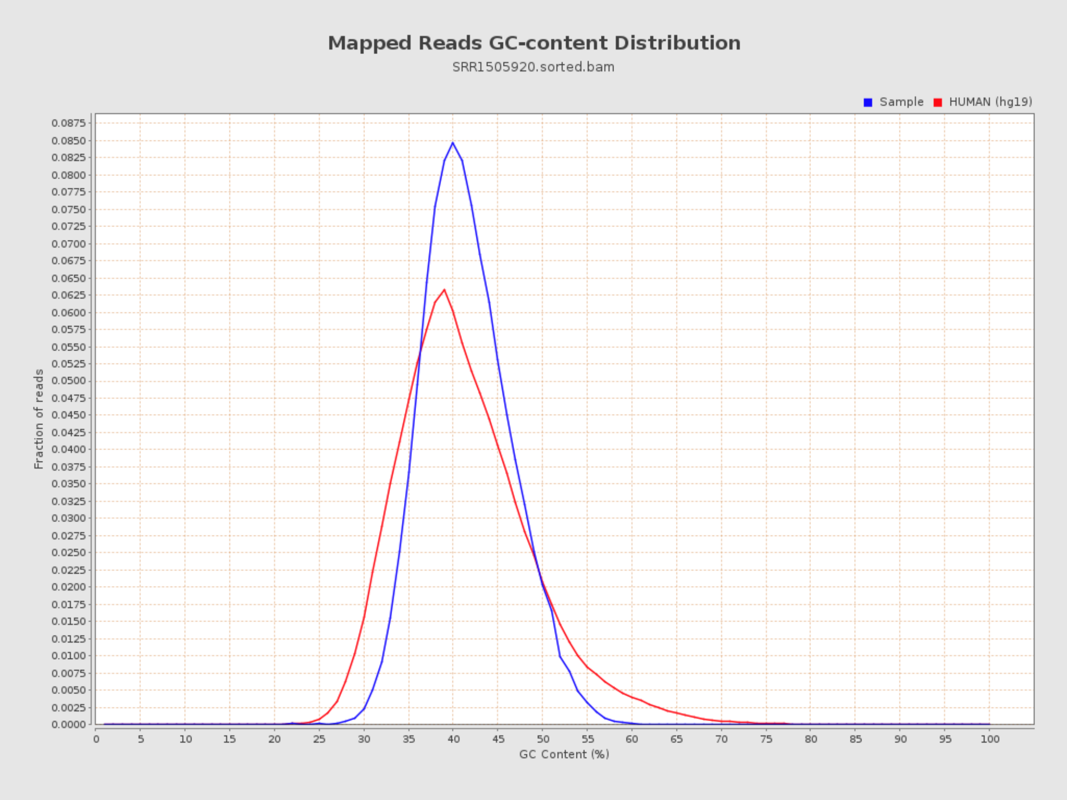
7. Results : Duplication Rate Histogram



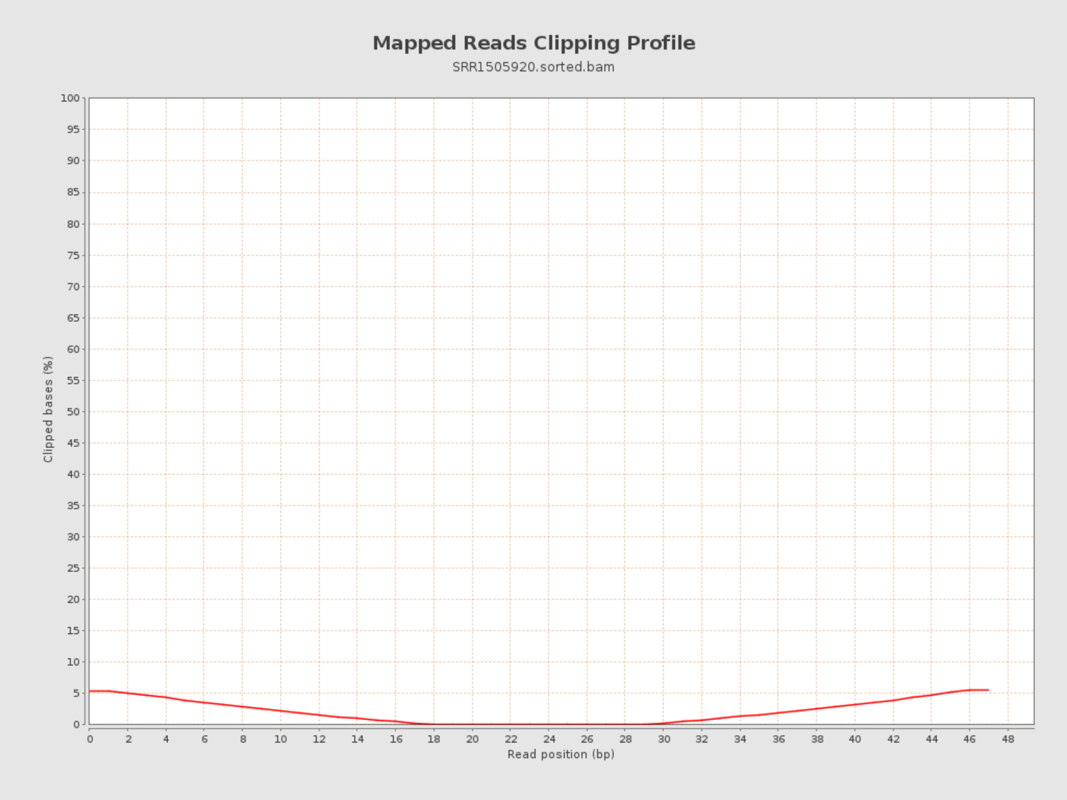
8. Results : Mapped Reads Nucleotide Content



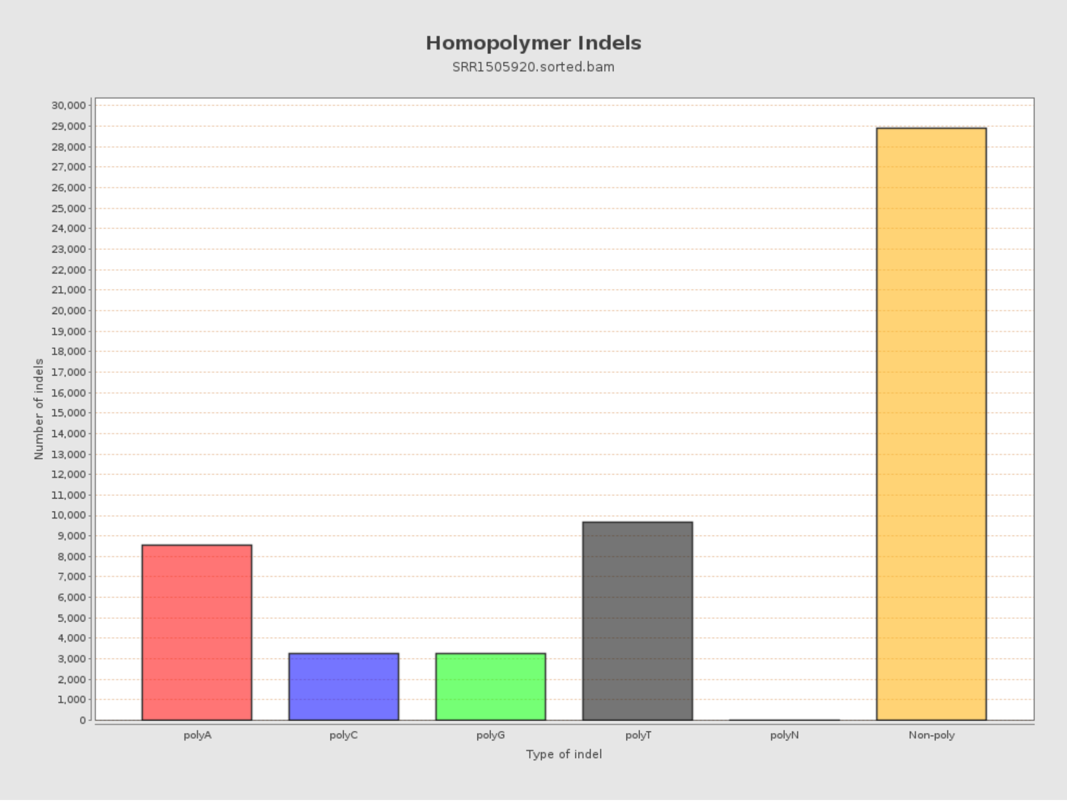
9. Results : Mapped Reads GC-content Distribution



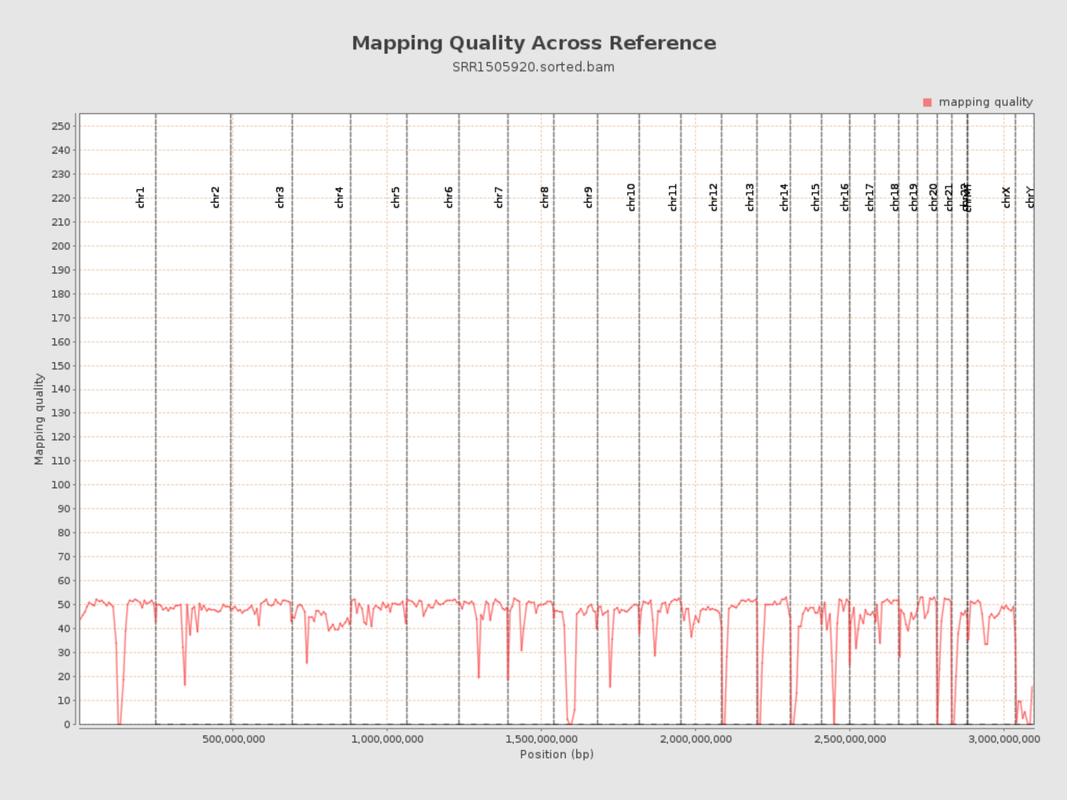
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram