Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:44:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505990.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_SRR1505990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:44:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,828,064
Mapped reads	3,992,195 / 68.5%
Unmapped reads	1,835,869 / 31.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	231 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	287,965 / 4.94%
Duplication rate	5.63%
Clipped reads	646,887 / 11.1%

2.2. ACGT Content

Number/percentage of A's	55,844,986 / 30.15%
Number/percentage of C's	36,009,754 / 19.44%
Number/percentage of T's	56,510,862 / 30.51%
Number/percentage of G's	36,876,888 / 19.91%
Number/percentage of N's	787 / 0%
GC Percentage	39.35%

2.3. Coverage

Mean	0.0599

Standard Deviation	0.5999

2.4. Mapping Quality

Mean Mapping Quality	43.73

2.5. Mismatches and indels

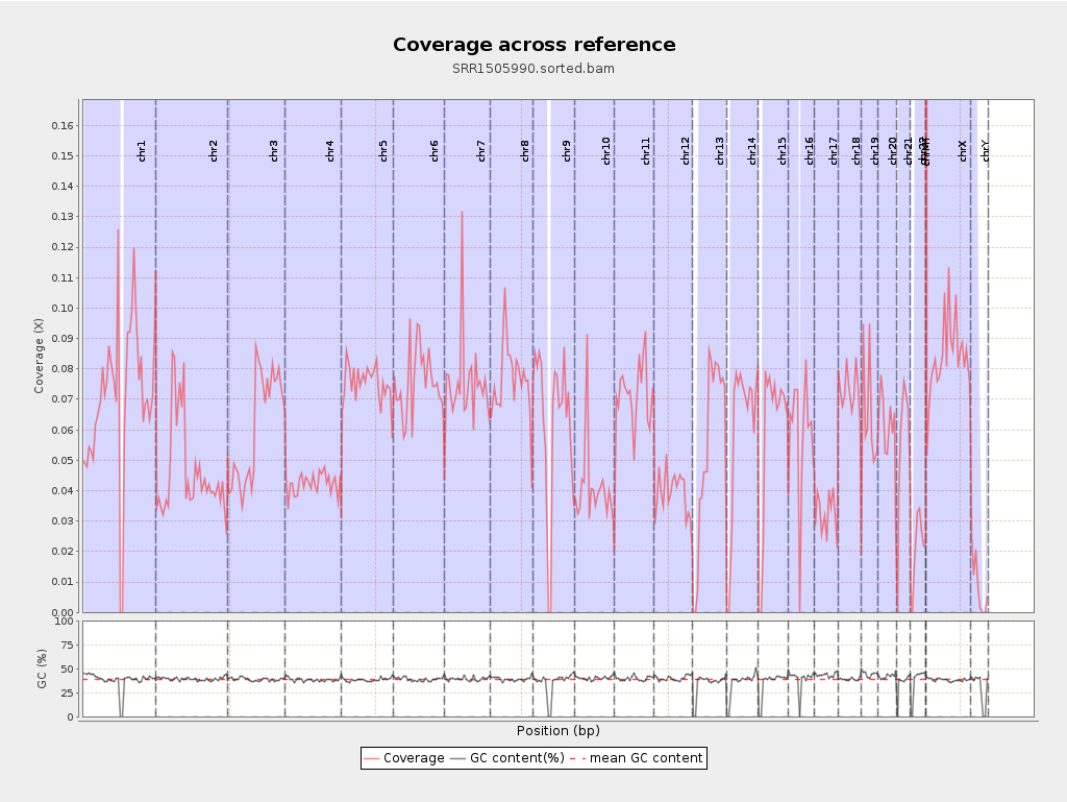
General error rate	0.52%
Mismatches	950,891
Insertions	9,043
Mapped reads with at least one insertion	0.23%
Deletions	29,202
Mapped reads with at least one deletion	0.73%
Homopolymer indels	46.58%

2.6. Chromosome stats

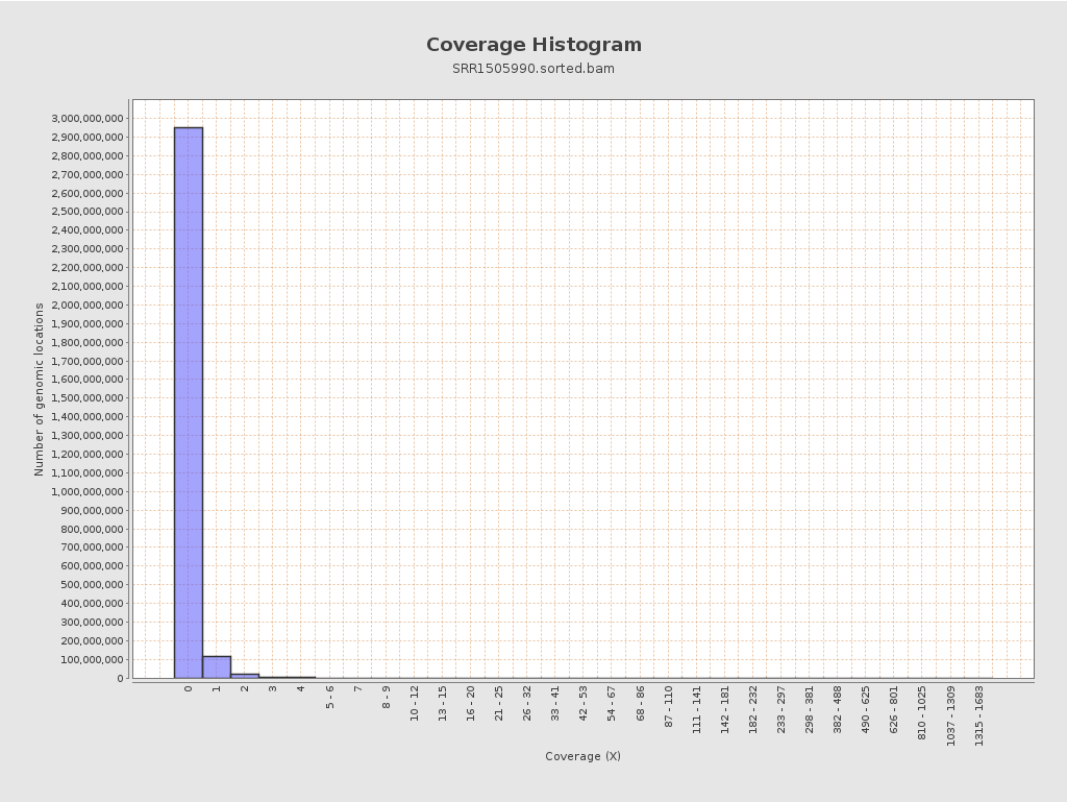
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	17775219	0.0713	1.254
chr2	243199373	11309584	0.0465	0.416
chr3	198022430	11992854	0.0606	0.3035
chr4	191154276	8105819	0.0424	0.2517
chr5	180915260	13510193	0.0747	0.3413
chr6	171115067	12957032	0.0757	0.4482
chr7	159138663	11910666	0.0748	0.8778

chr8	146364022	11095107	0.0758	0.8476
chr9	141213431	8847726	0.0627	0.4097
chr10	135534747	5521677	0.0407	0.5145
chr11	135006516	9610158	0.0712	0.4295
chr12	133851895	5231114	0.0391	0.2676
chr13	115169878	6346457	0.0551	0.2886
chr14	107349540	6466169	0.0602	1.0072
chr15	102531392	5966471	0.0582	0.2976
chr16	90354753	5191760	0.0575	0.343
chr17	81195210	2655890	0.0327	0.2592
chr18	78077248	5723356	0.0733	0.6758
chr19	59128983	3790364	0.0641	0.9211
chr20	63025520	3900928	0.0619	0.3235
chr21	48129895	2646099	0.055	0.306
chr22	51304566	1061254	0.0207	0.1729
chrMT	16571	185976	11.223	8.2658
chrX	155270560	12976815	0.0836	0.4051
chrY	59373566	505418	0.0085	0.1231

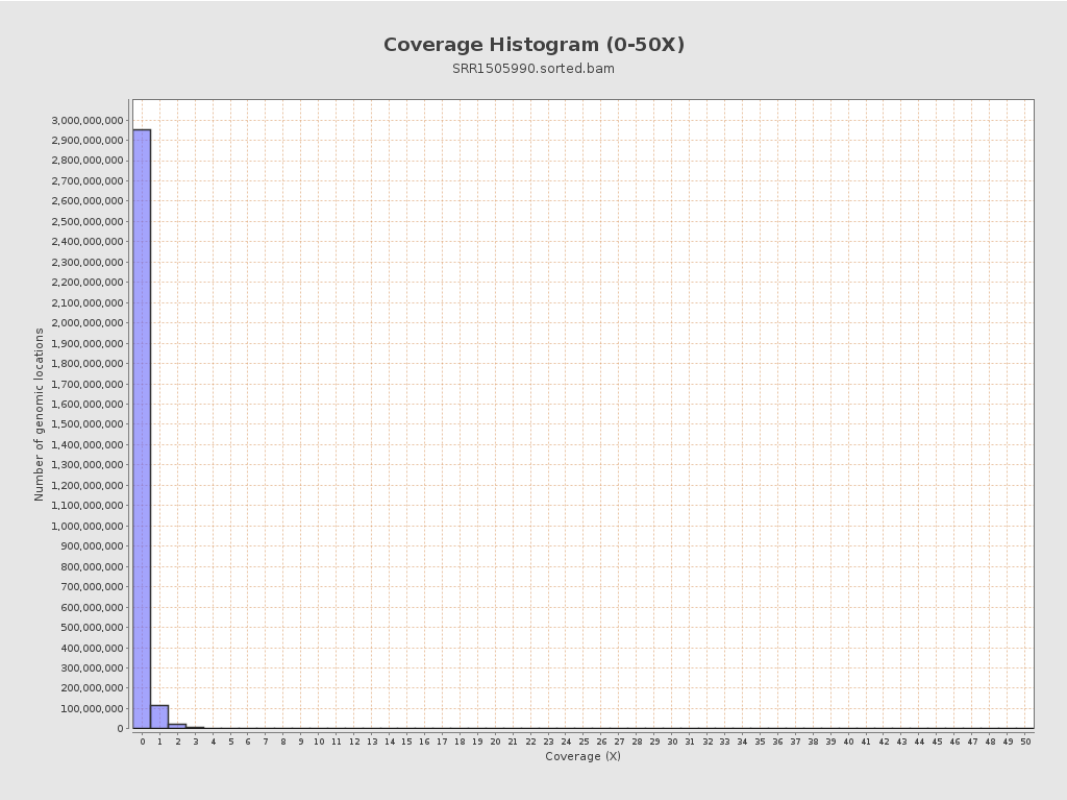
3. Results : Coverage across reference



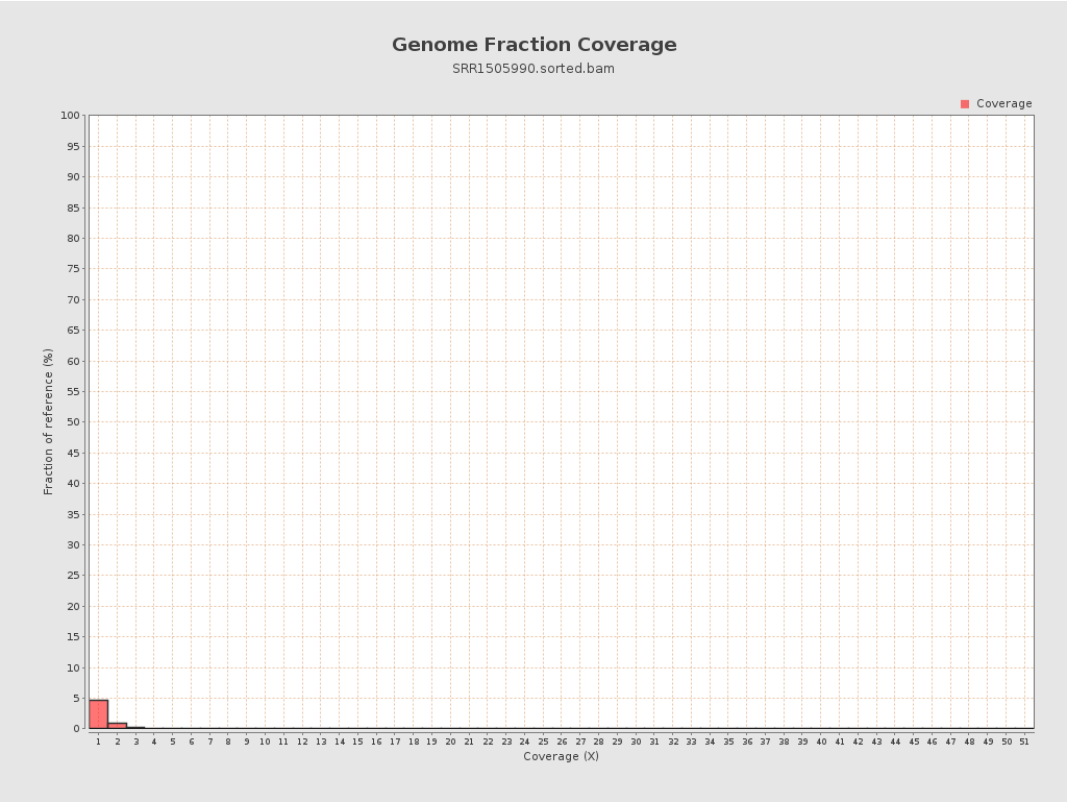
4. Results : Coverage Histogram



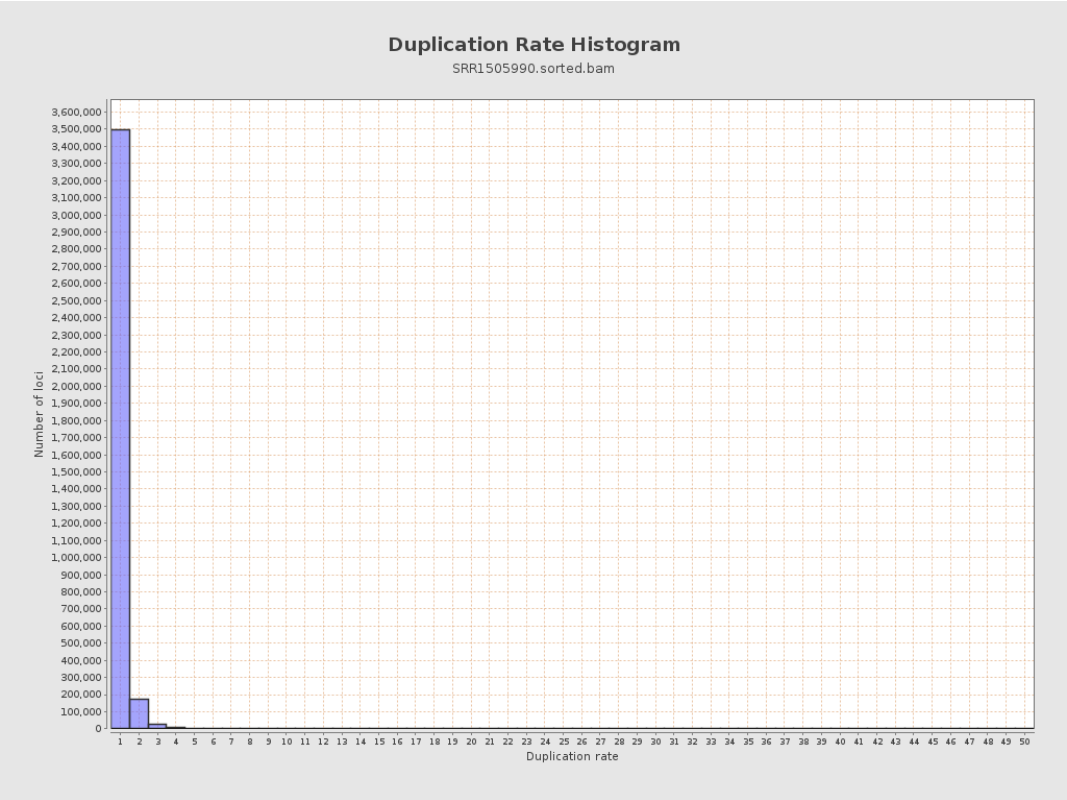
5. Results : Coverage Histogram (0-50X)



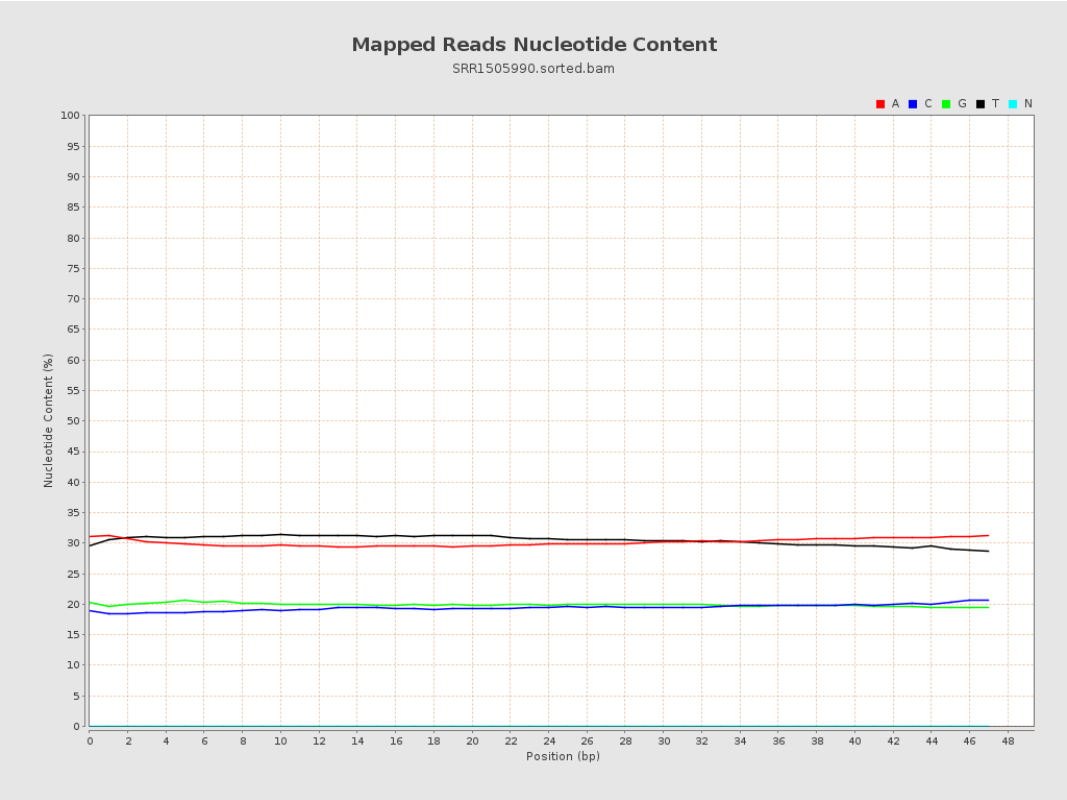
6. Results : Genome Fraction Coverage



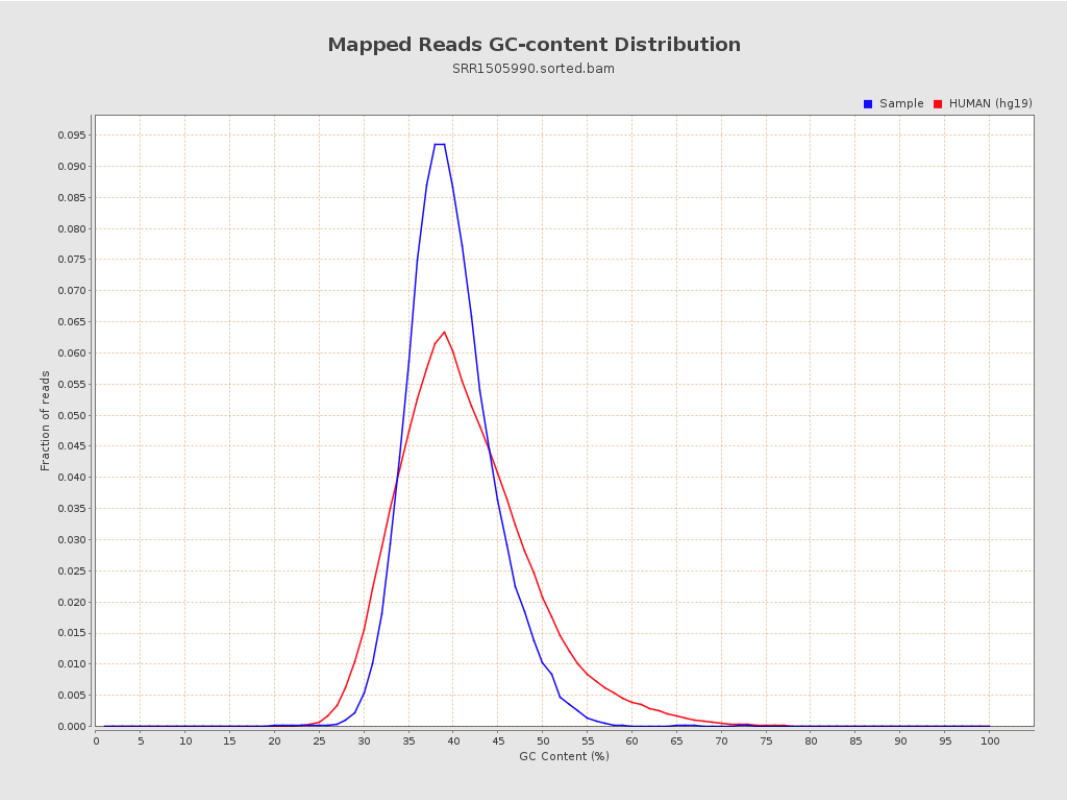
7. Results : Duplication Rate Histogram



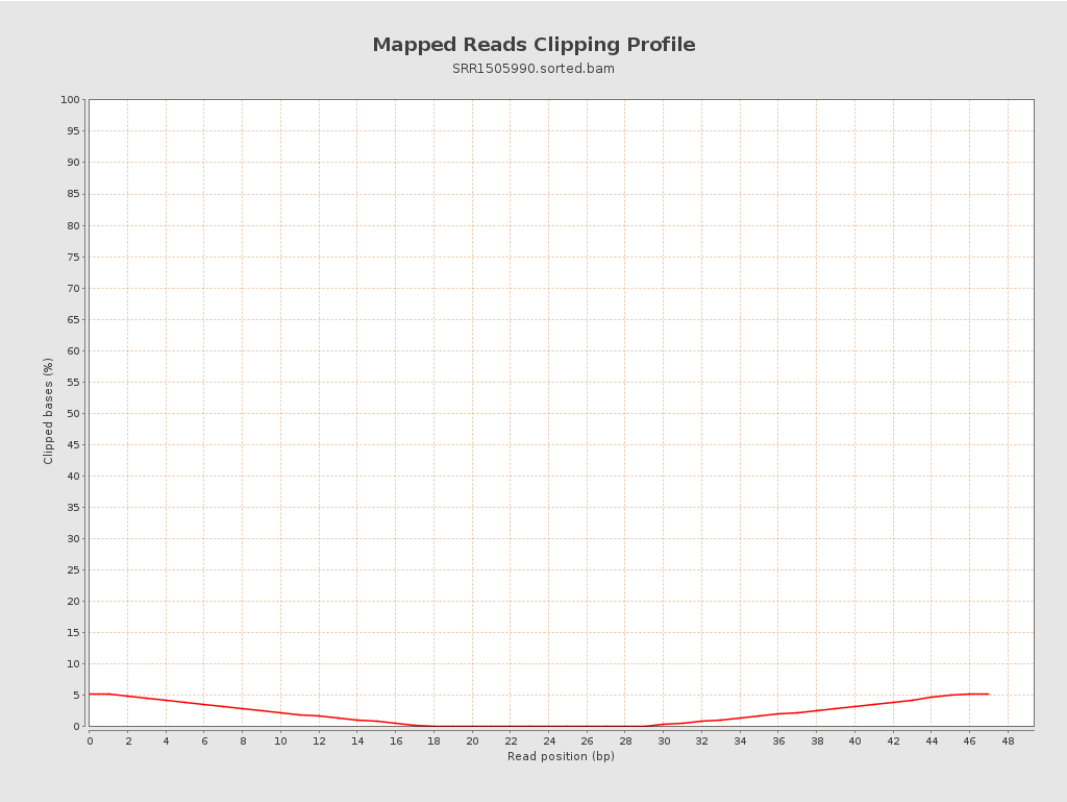
8. Results : Mapped Reads Nucleotide Content



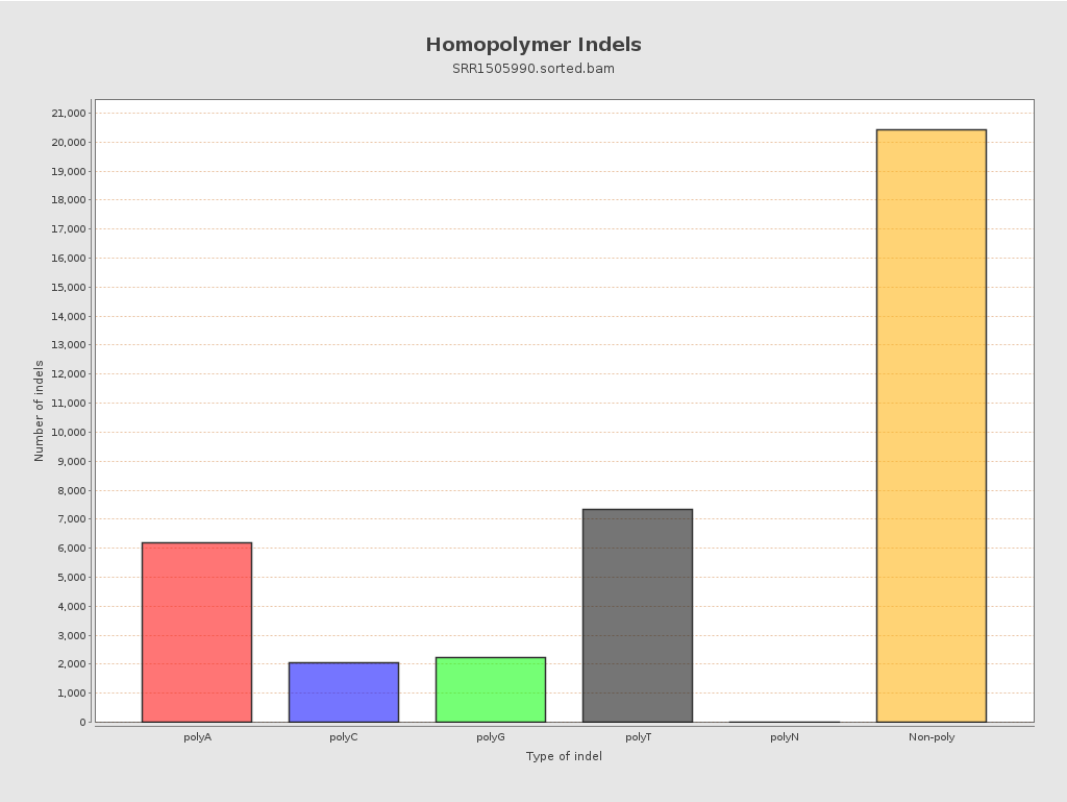
9. Results : Mapped Reads GC-content Distribution



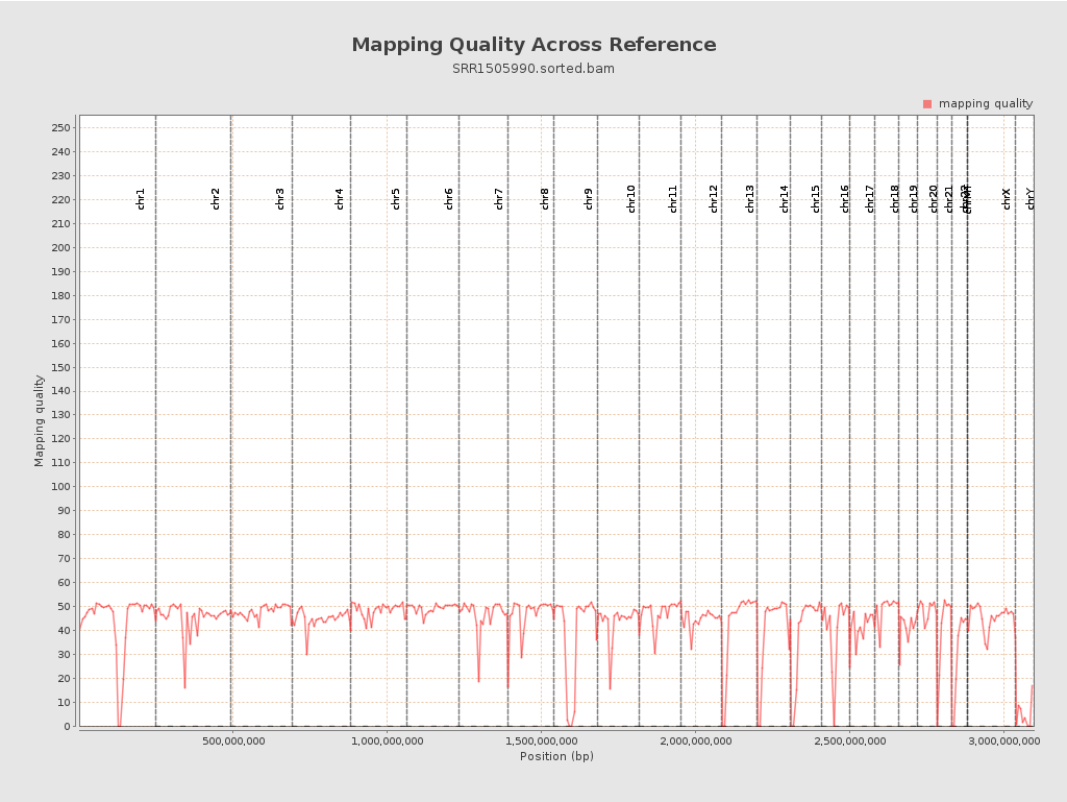
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram