Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:07:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505983.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_SRR1505983 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505983.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:07:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505983.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,218,699
Mapped reads	7,286,868 / 79.04%
Unmapped reads	1,931,831 / 20.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	257 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	366,742 / 3.98%
Duplication rate	3.71%
Clipped reads	782,373 / 8.49%

2.2. ACGT Content

Number/percentage of A's	104,248,959 / 30.46%
Number/percentage of C's	67,012,497 / 19.58%
Number/percentage of T's	102,802,827 / 30.04%
Number/percentage of G's	68,152,256 / 19.91%
Number/percentage of N's	1,453 / 0%
GC Percentage	39.5%

2.3. Coverage

Mean	0.1106

Standard Deviation	0.8742

2.4. Mapping Quality

Mean Mapping Quality	45.93

2.5. Mismatches and indels

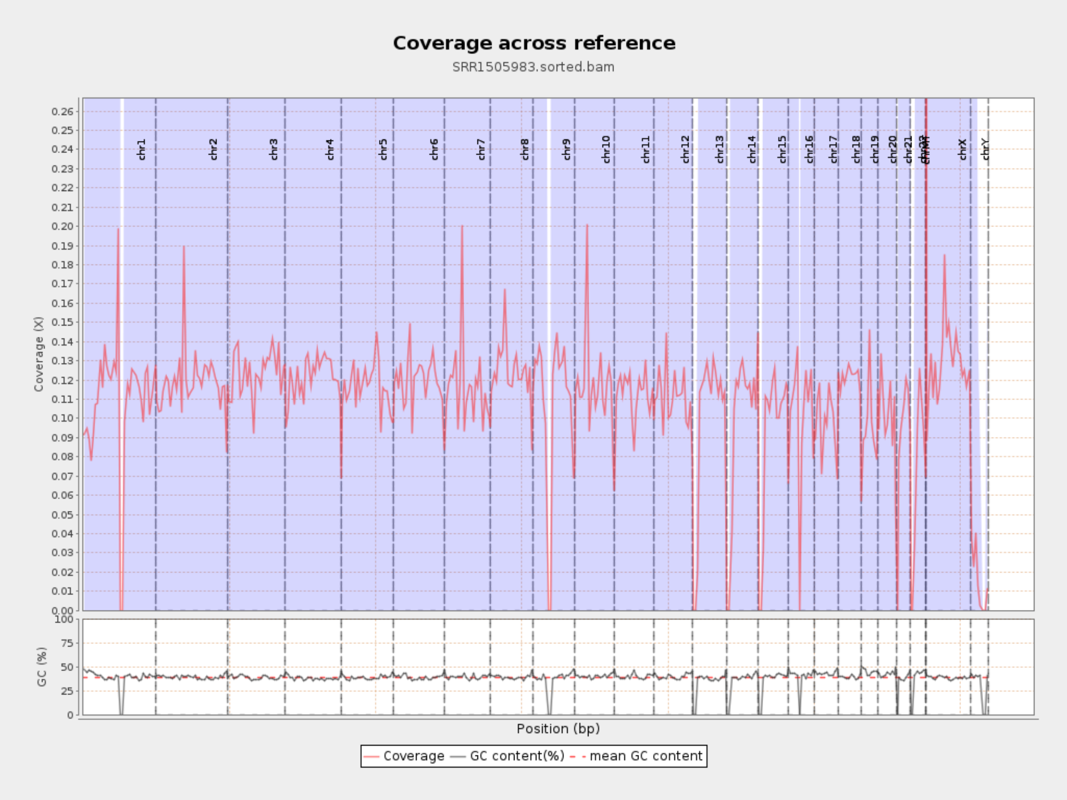
General error rate	0.47%
Mismatches	1,590,407
Insertions	16,545
Mapped reads with at least one insertion	0.23%
Deletions	49,203
Mapped reads with at least one deletion	0.67%
Homopolymer indels	47.59%

2.6. Chromosome stats

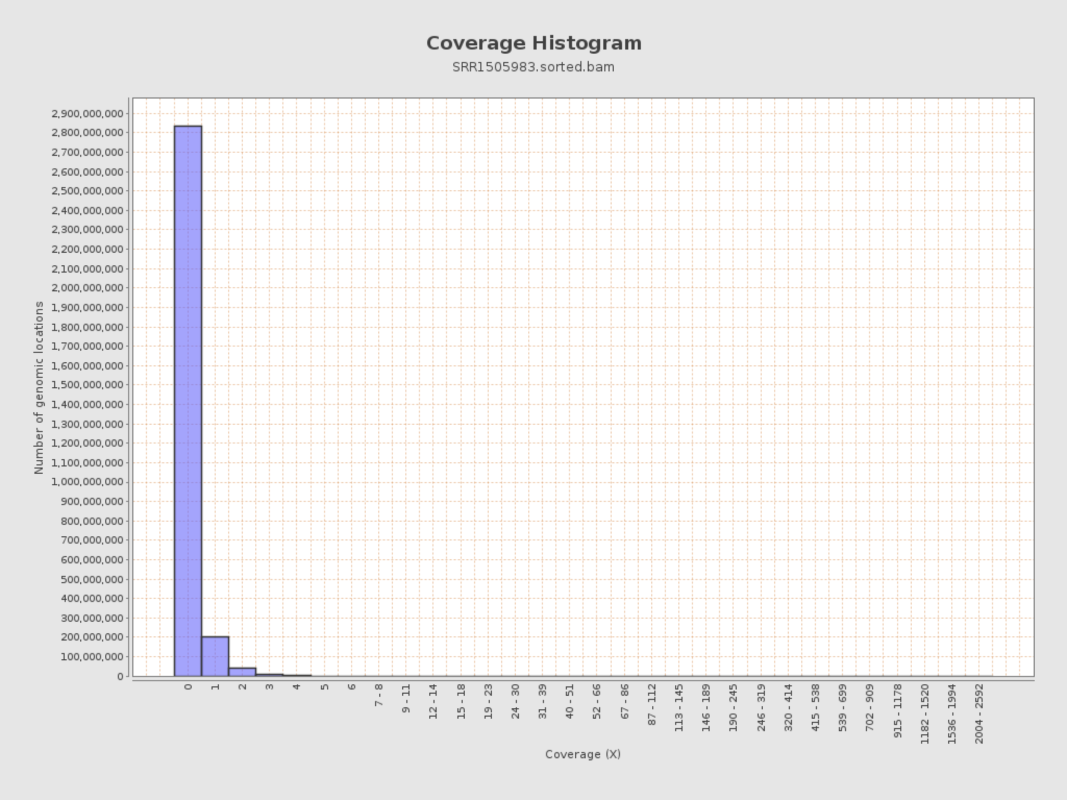
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27179285	0.109	1.9235
chr2	243199373	29021721	0.1193	0.7012
chr3	198022430	24521694	0.1238	0.4433
chr4	191154276	23303342	0.1219	0.4432
chr5	180915260	21114857	0.1167	0.4337
chr6	171115067	20672670	0.1208	0.5858
chr7	159138663	18431954	0.1158	1.1302

chr8	146364022	18214521	0.1244	1.3287
chr9	141213431	15225912	0.1078	0.6335
chr10	135534747	15978144	0.1179	0.8944
chr11	135006516	15168431	0.1124	0.6955
chr12	133851895	14884194	0.1112	0.4588
chr13	115169878	11320297	0.0983	0.3832
chr14	107349540	10372295	0.0966	0.471
chr15	102531392	9162743	0.0894	0.367
chr16	90354753	8888060	0.0984	0.4833
chr17	81195210	8027030	0.0989	0.4839
chr18	78077248	9514024	0.1219	1.467
chr19	59128983	5758688	0.0974	1.2542
chr20	63025520	6512352	0.1033	0.4195
chr21	48129895	4453404	0.0925	0.4237
chr22	51304566	3667267	0.0715	0.3273
chrMT	16571	21584	1.3025	1.3766
chrX	155270560	19982405	0.1287	0.5686
chrY	59373566	888415	0.015	0.2078

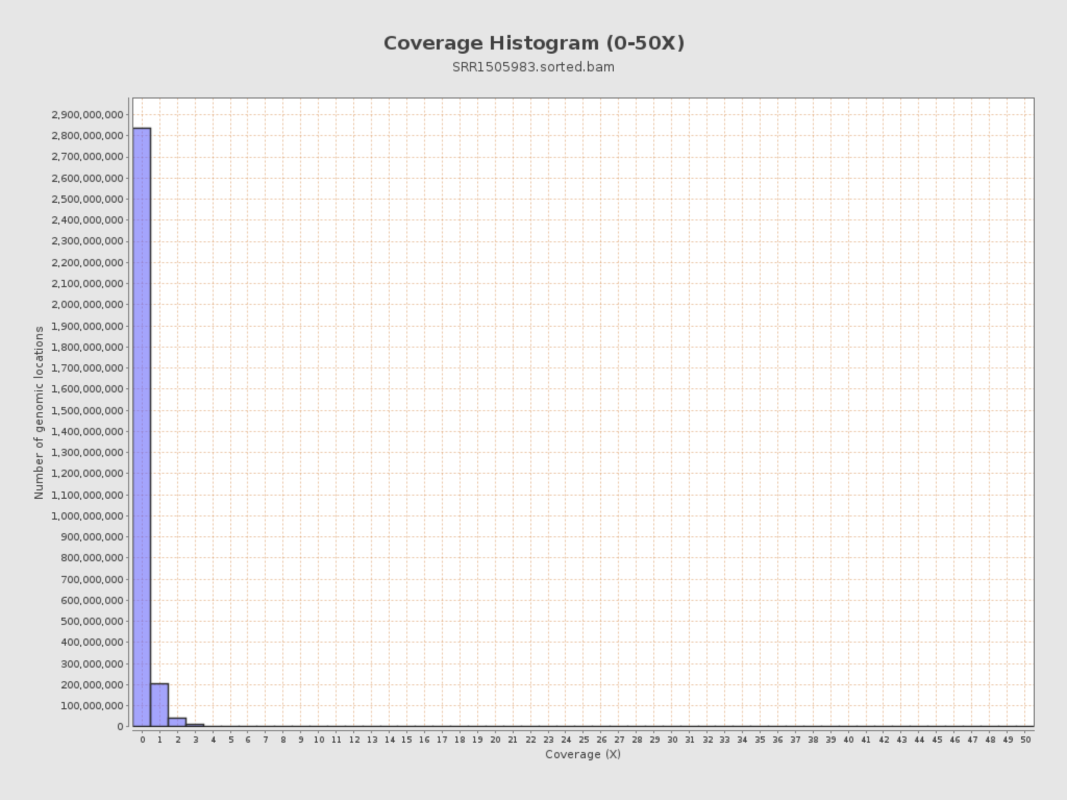
3. Results : Coverage across reference



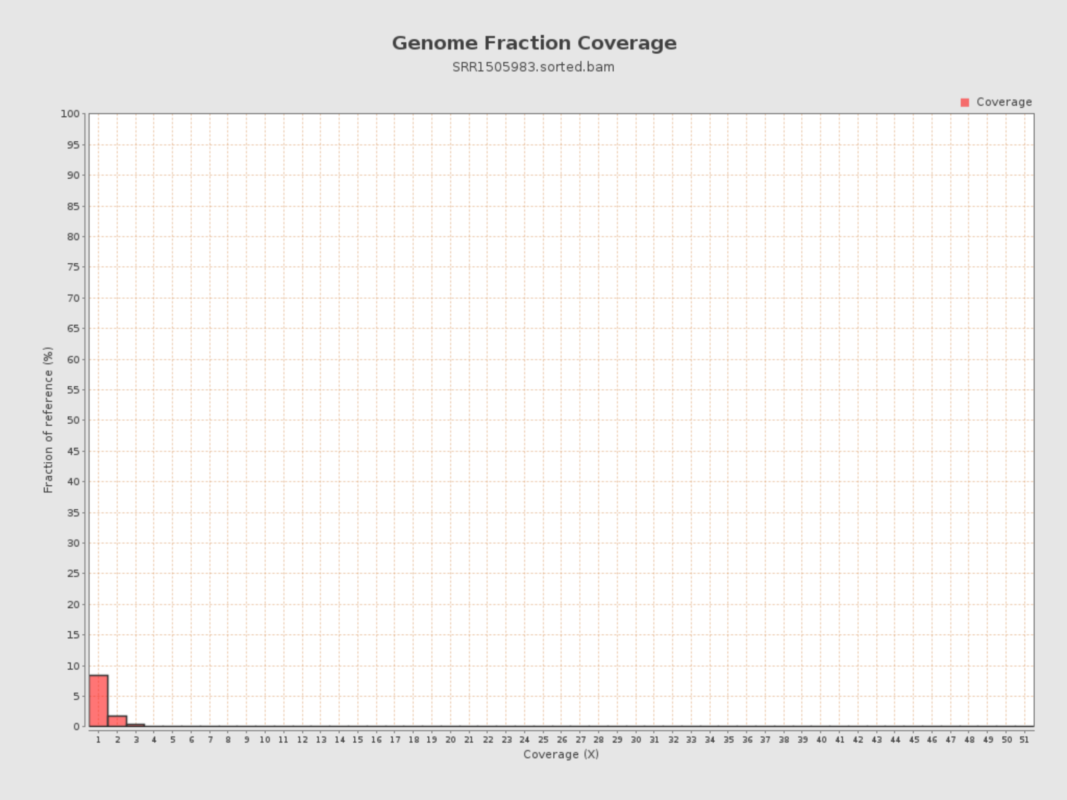
4. Results : Coverage Histogram



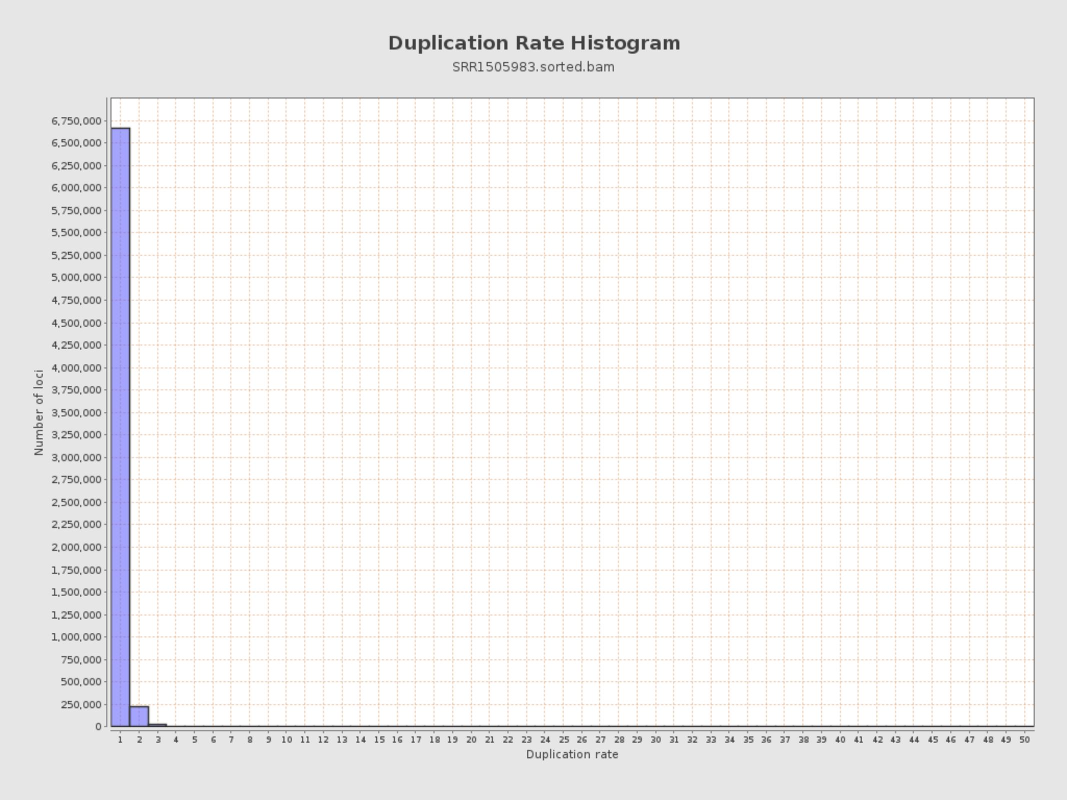
5. Results : Coverage Histogram (0-50X)



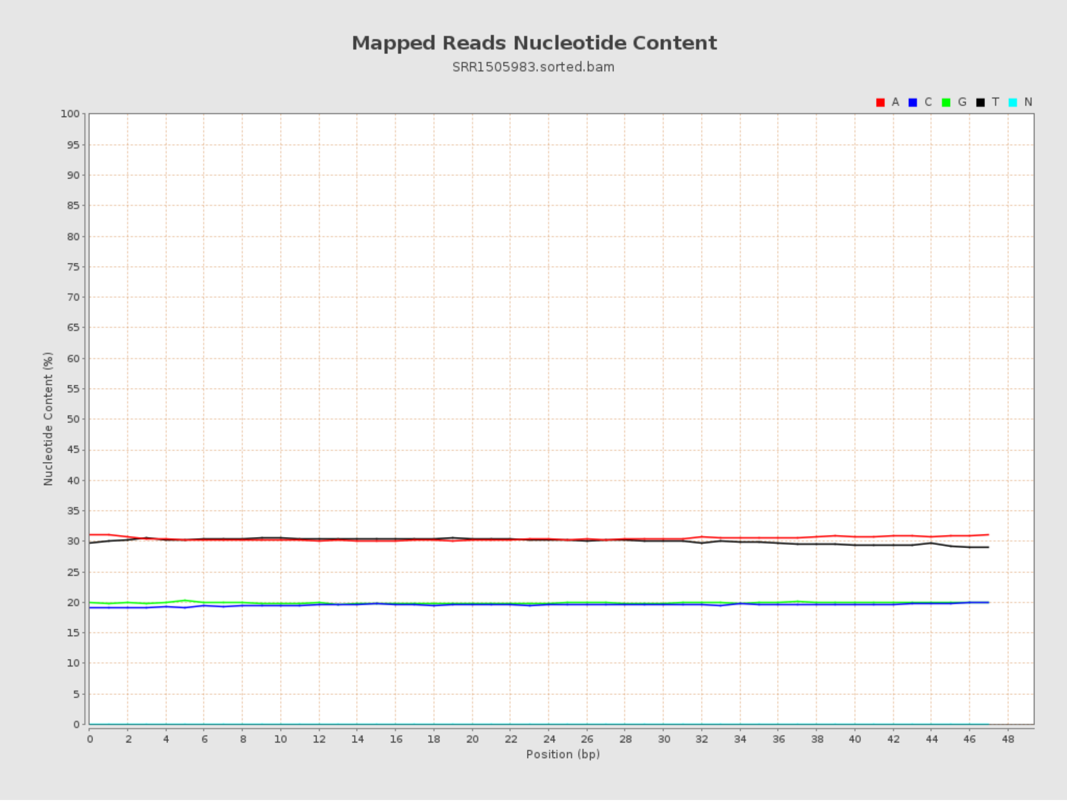
6. Results : Genome Fraction Coverage



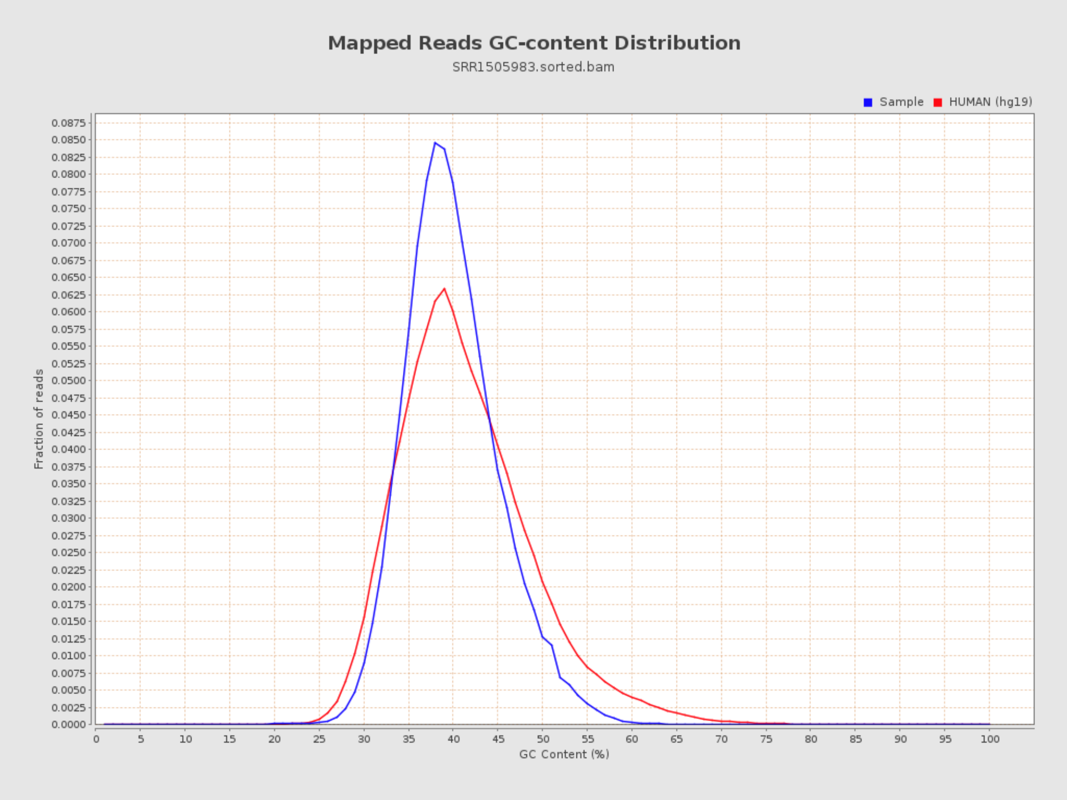
7. Results : Duplication Rate Histogram



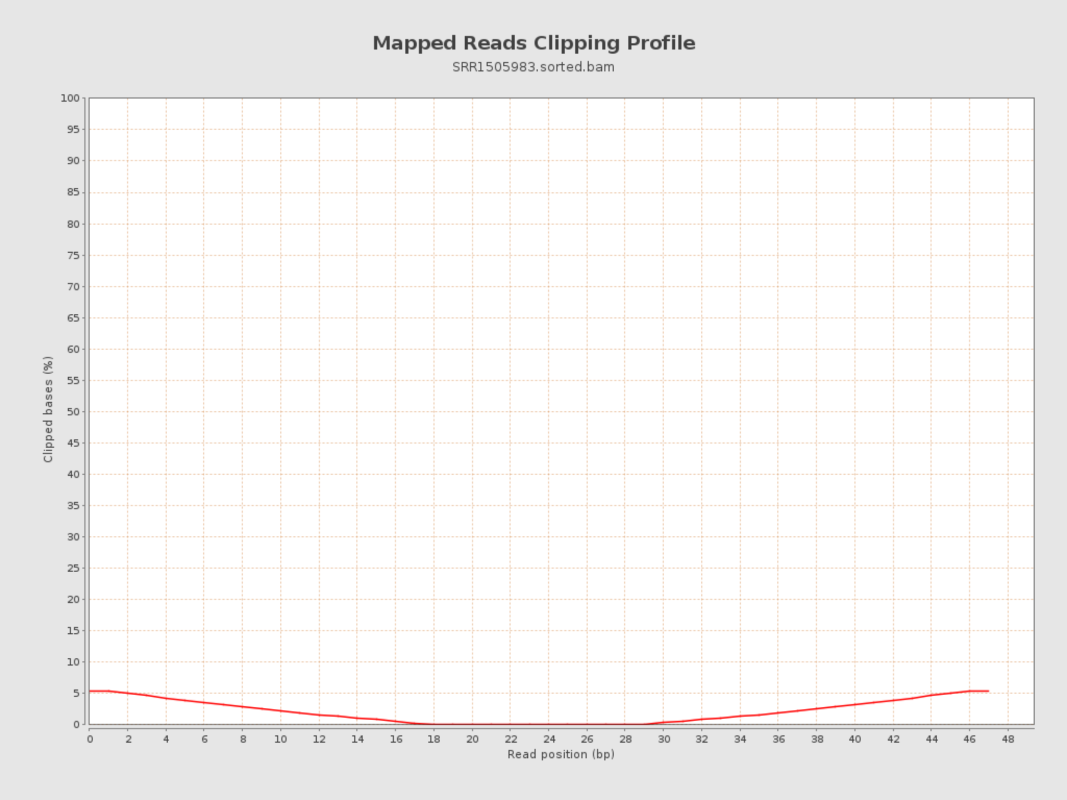
8. Results : Mapped Reads Nucleotide Content



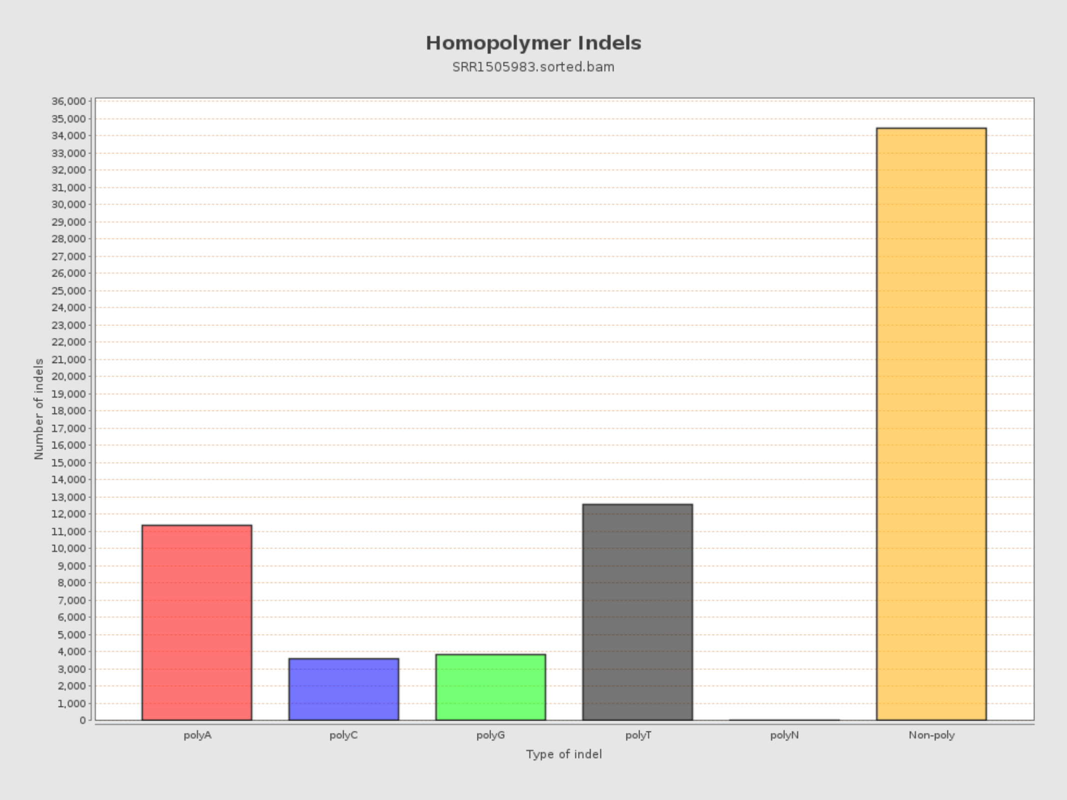
9. Results : Mapped Reads GC-content Distribution



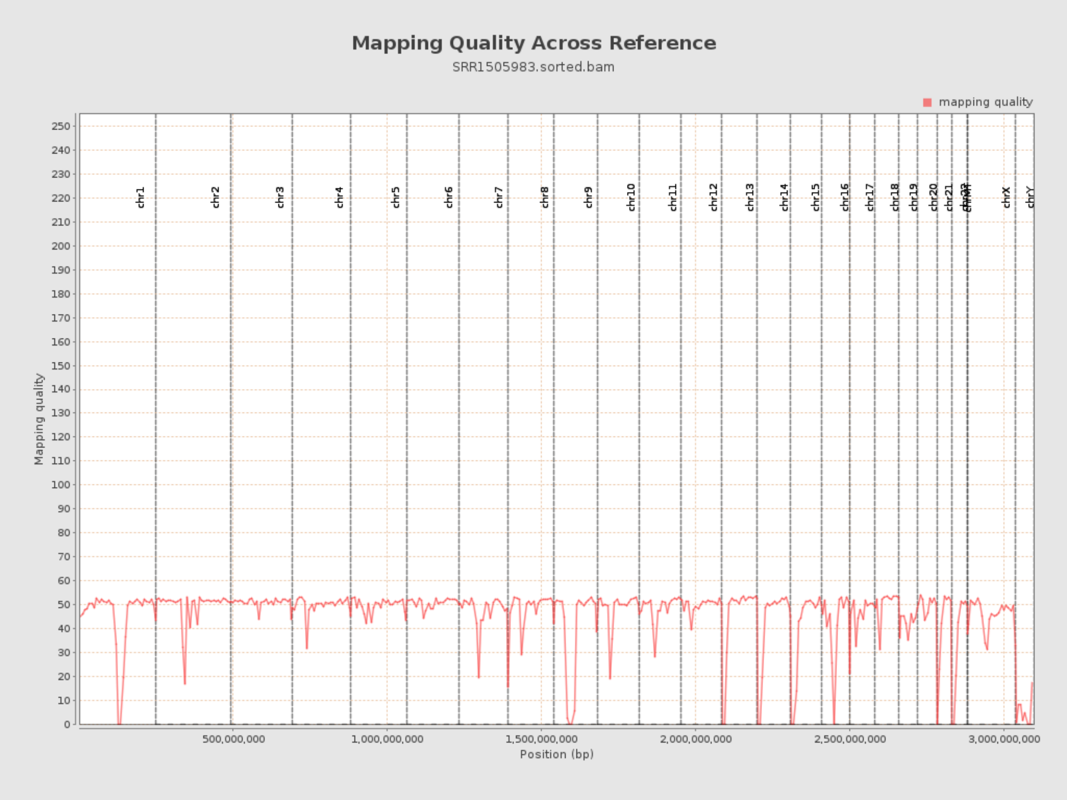
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram