Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 20:39:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505923.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_SRR1505923 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505923.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 20:39:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505923.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,229,522
Mapped reads	7,456,872 / 80.79%
Unmapped reads	1,772,650 / 19.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	258 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	254,512 / 2.76%
Duplication rate	1.96%
Clipped reads	834,029 / 9.04%

2.2. ACGT Content

Number/percentage of A's	106,818,316 / 30.53%
Number/percentage of C's	68,807,693 / 19.66%
Number/percentage of T's	103,939,330 / 29.71%
Number/percentage of G's	70,336,995 / 20.1%
Number/percentage of N's	1,092 / 0%
GC Percentage	39.77%

2.3. Coverage

Mean	0.1131

Standard Deviation	1.0054

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

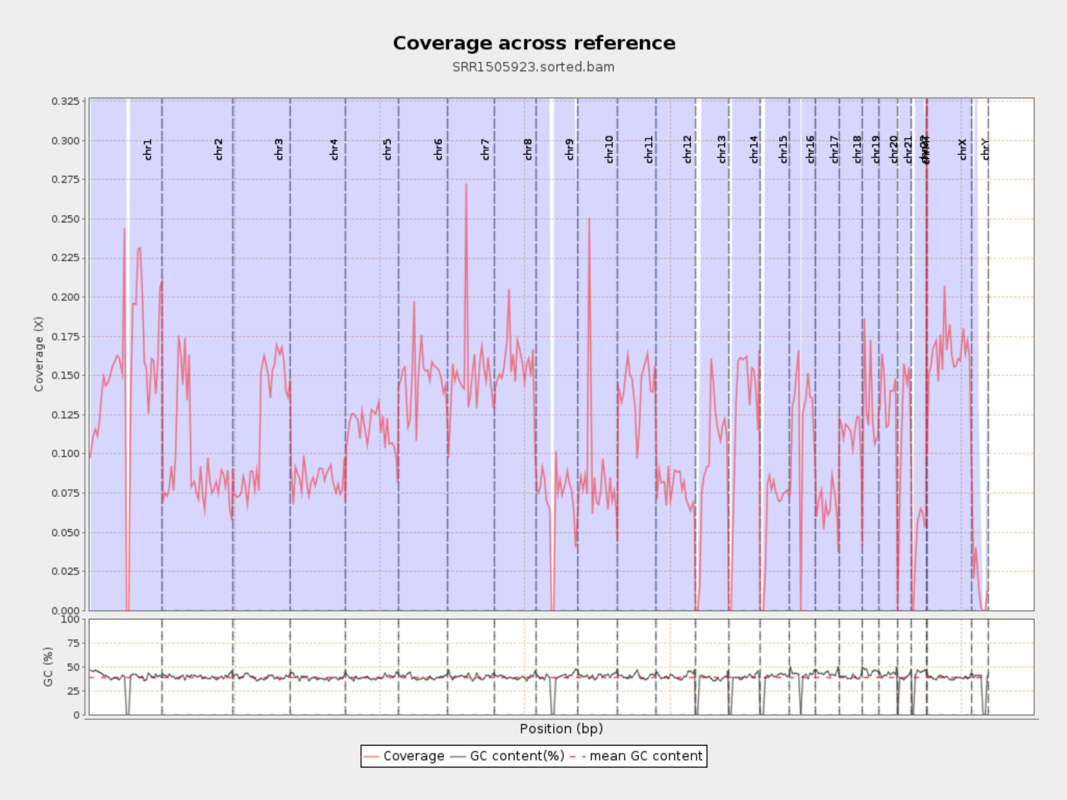
General error rate	0.47%
Mismatches	1,609,479
Insertions	14,985
Mapped reads with at least one insertion	0.2%
Deletions	53,611
Mapped reads with at least one deletion	0.72%
Homopolymer indels	48.36%

2.6. Chromosome stats

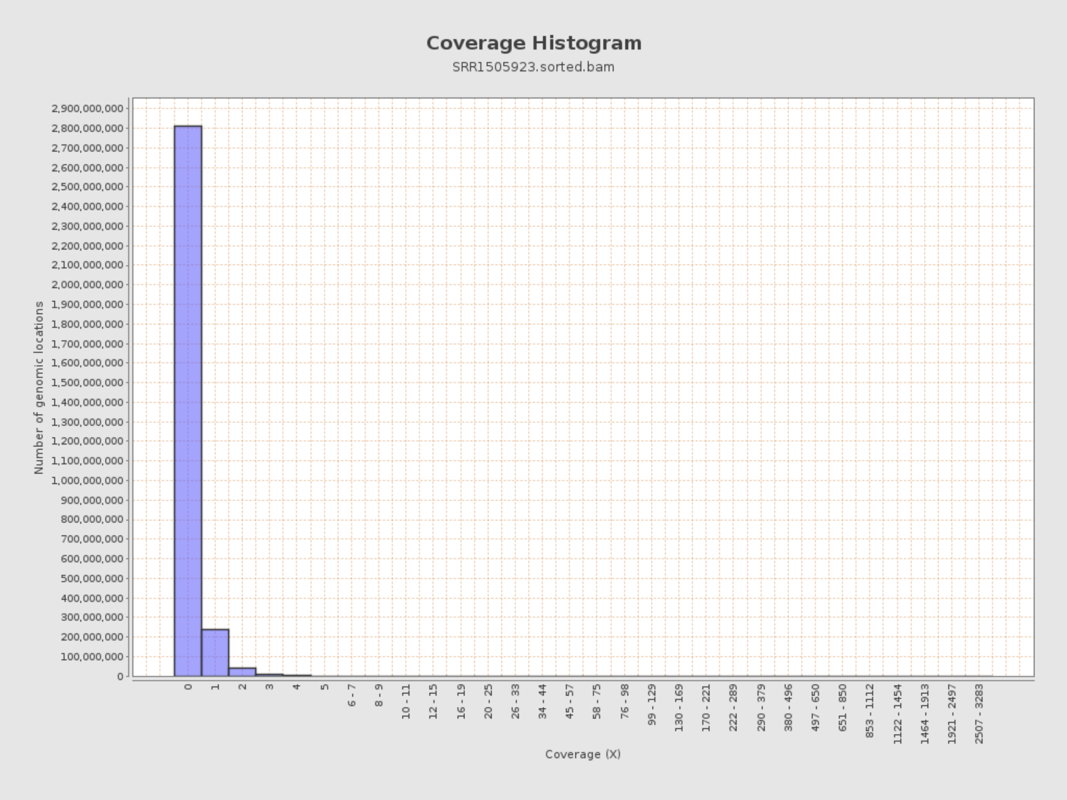
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	37305393	0.1497	2.2727
chr2	243199373	23054341	0.0948	0.6626
chr3	198022430	23357095	0.118	0.4395
chr4	191154276	16058649	0.084	0.3449
chr5	180915260	21021235	0.1162	0.4136
chr6	171115067	25438392	0.1487	0.6854
chr7	159138663	24202155	0.1521	1.6607

chr8	146364022	22836665	0.156	1.2956
chr9	141213431	9661861	0.0684	0.5592
chr10	135534747	11741558	0.0866	1.4707
chr11	135006516	19020267	0.1409	0.8574
chr12	133851895	10422203	0.0779	0.3733
chr13	115169878	10766808	0.0935	0.3483
chr14	107349540	13231293	0.1233	0.4595
chr15	102531392	6366091	0.0621	0.2855
chr16	90354753	11051565	0.1223	0.6215
chr17	81195210	5309984	0.0654	0.385
chr18	78077248	8967159	0.1148	1.144
chr19	59128983	7686200	0.13	1.5588
chr20	63025520	8543689	0.1356	0.4373
chr21	48129895	5494101	0.1142	0.4453
chr22	51304566	2198184	0.0428	0.2776
chrMT	16571	7615	0.4595	0.7783
chrX	155270560	25263419	0.1627	0.5866
chrY	59373566	972098	0.0164	0.2021

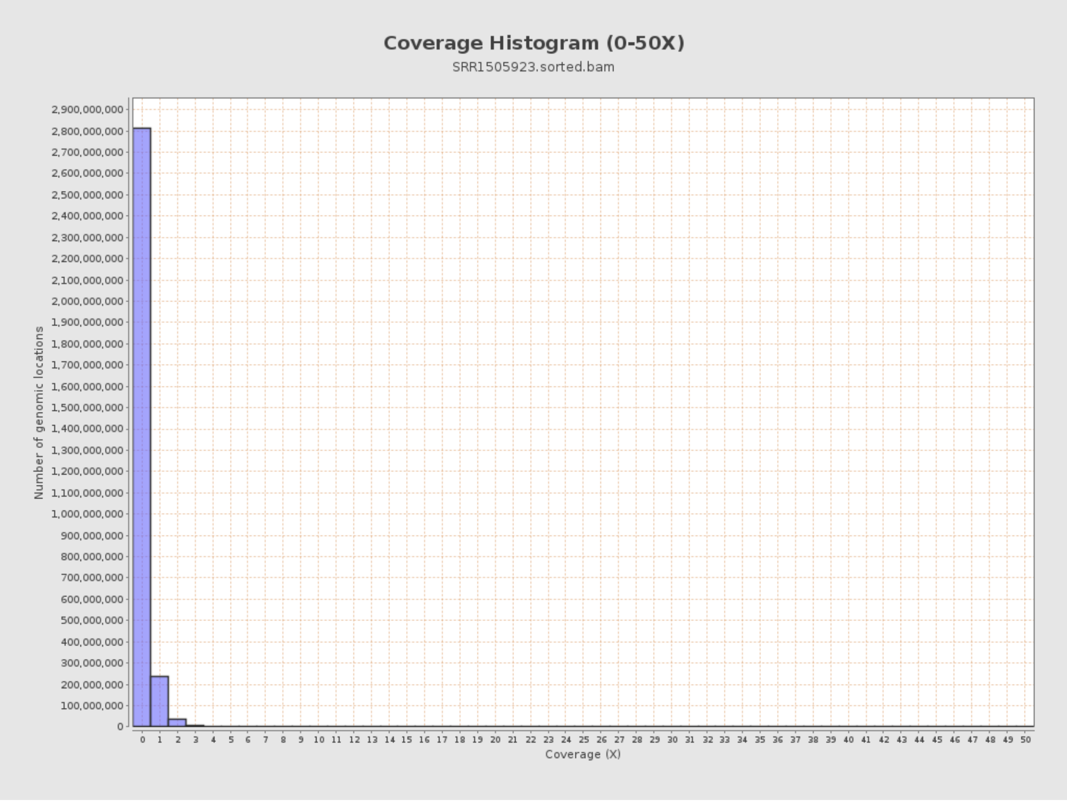
3. Results : Coverage across reference



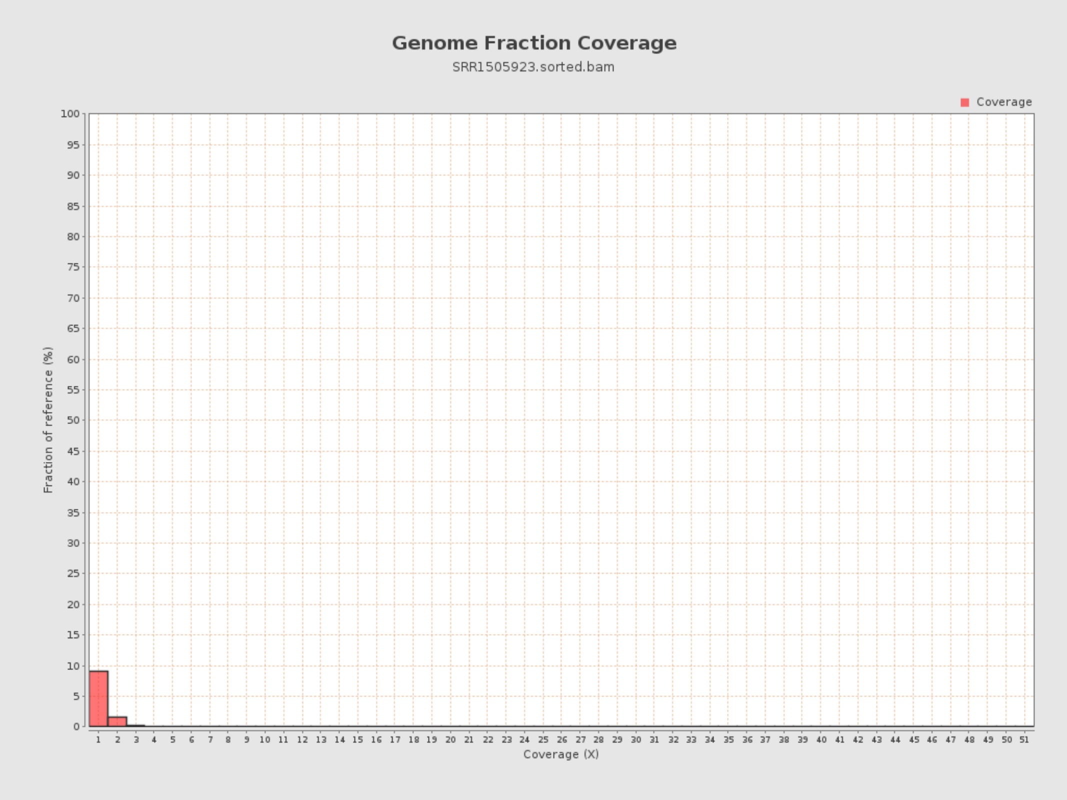
4. Results : Coverage Histogram



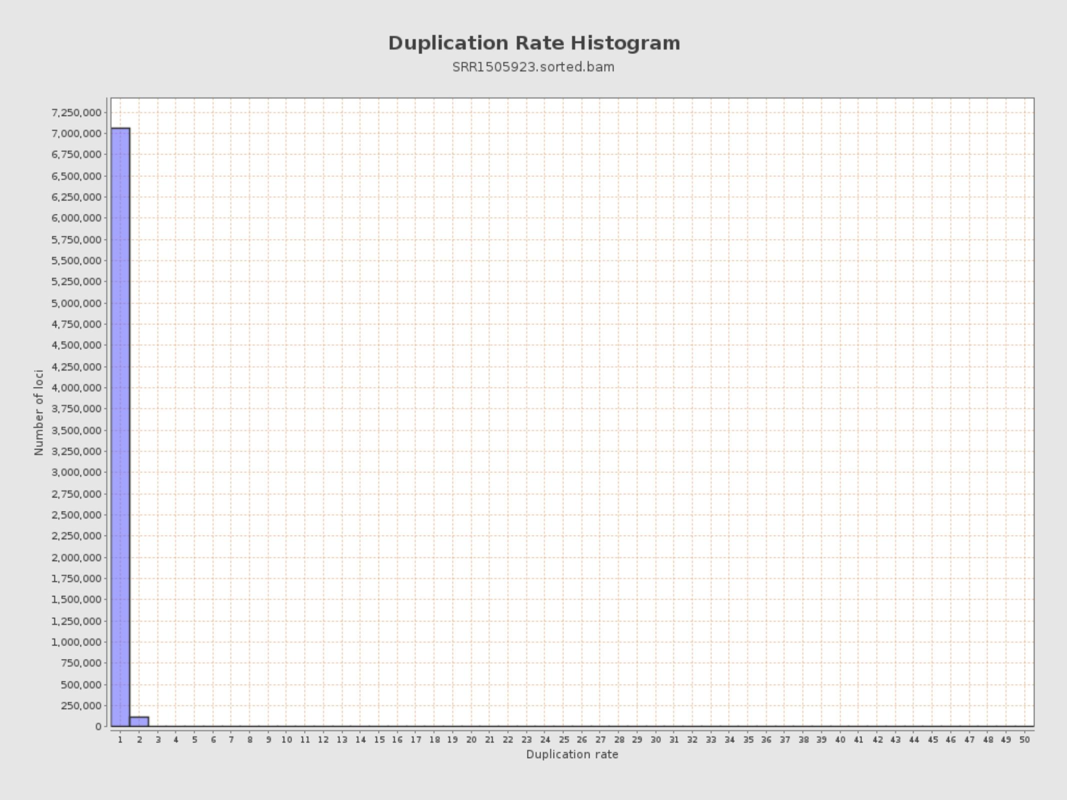
5. Results : Coverage Histogram (0-50X)



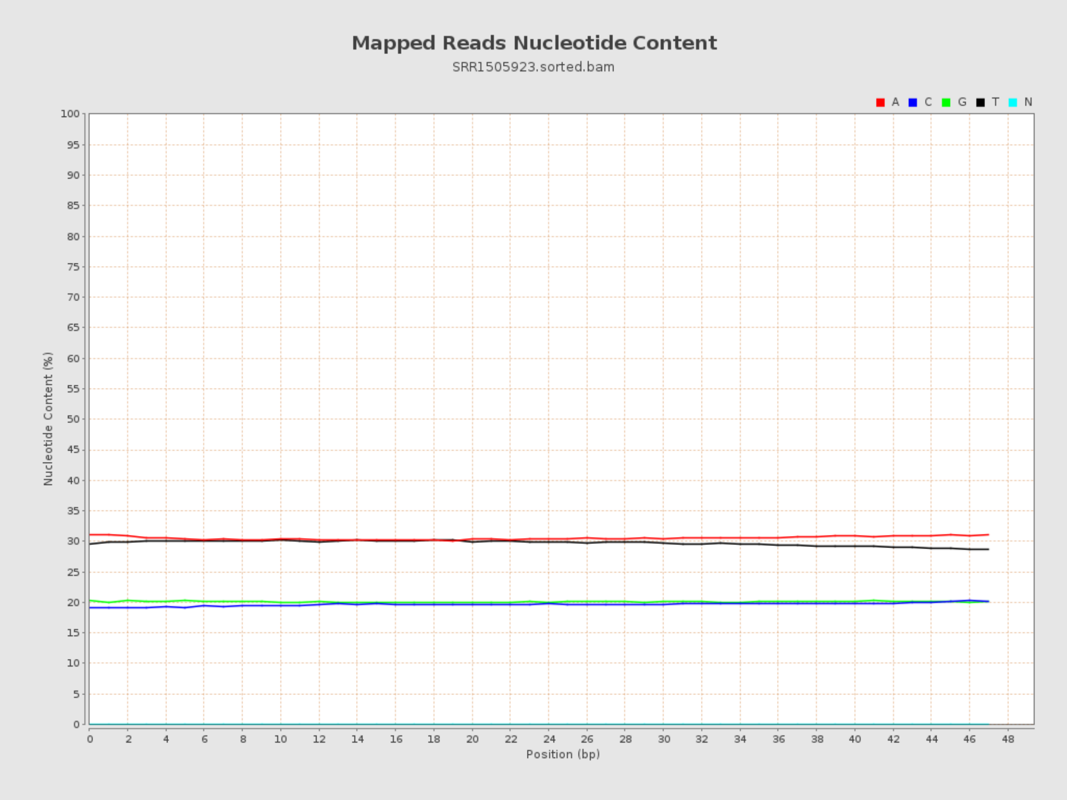
6. Results : Genome Fraction Coverage



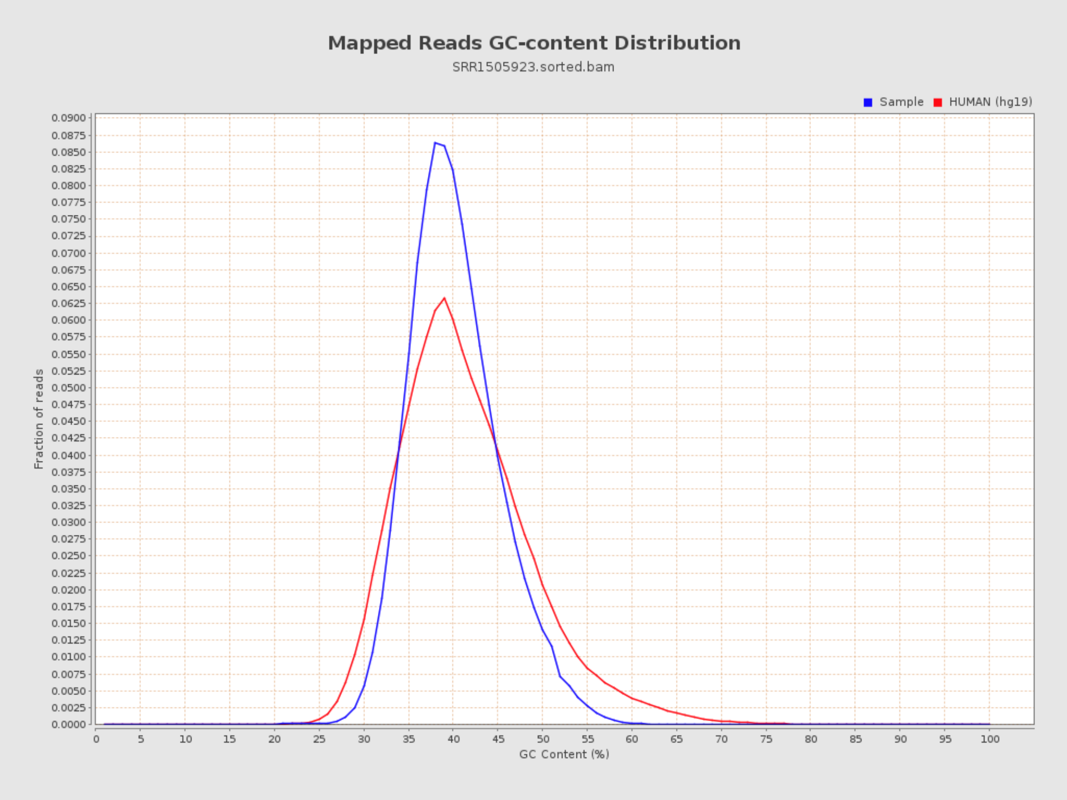
7. Results : Duplication Rate Histogram



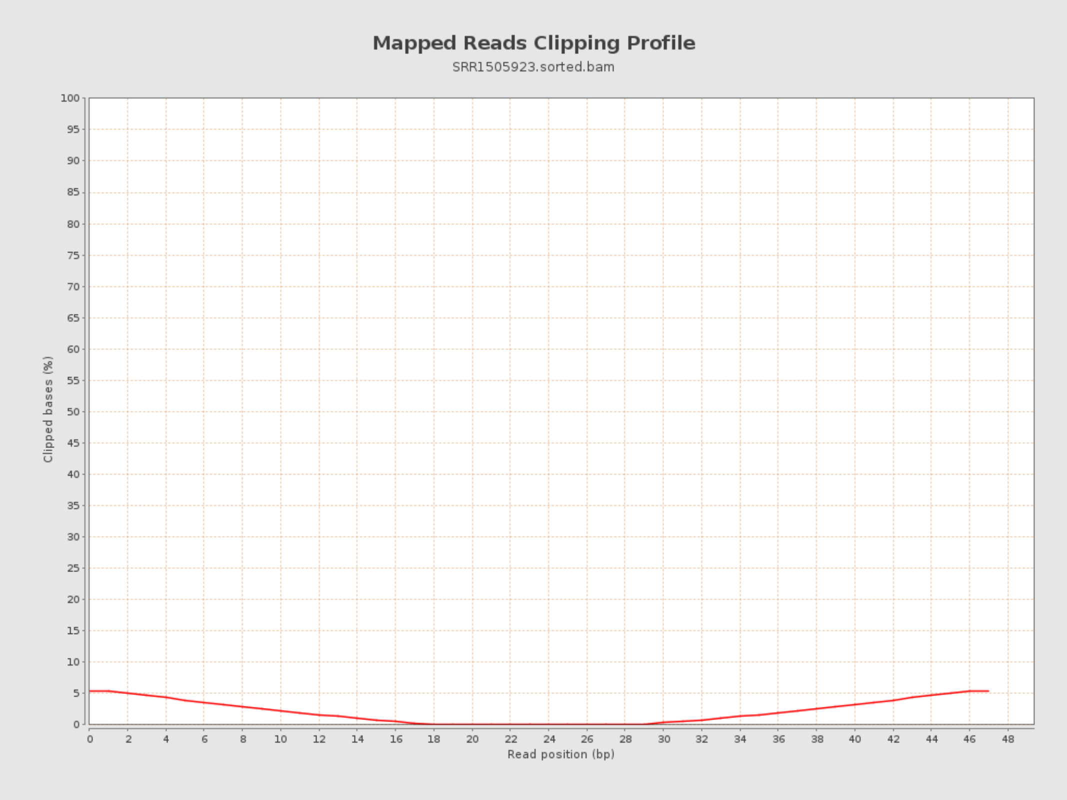
8. Results : Mapped Reads Nucleotide Content



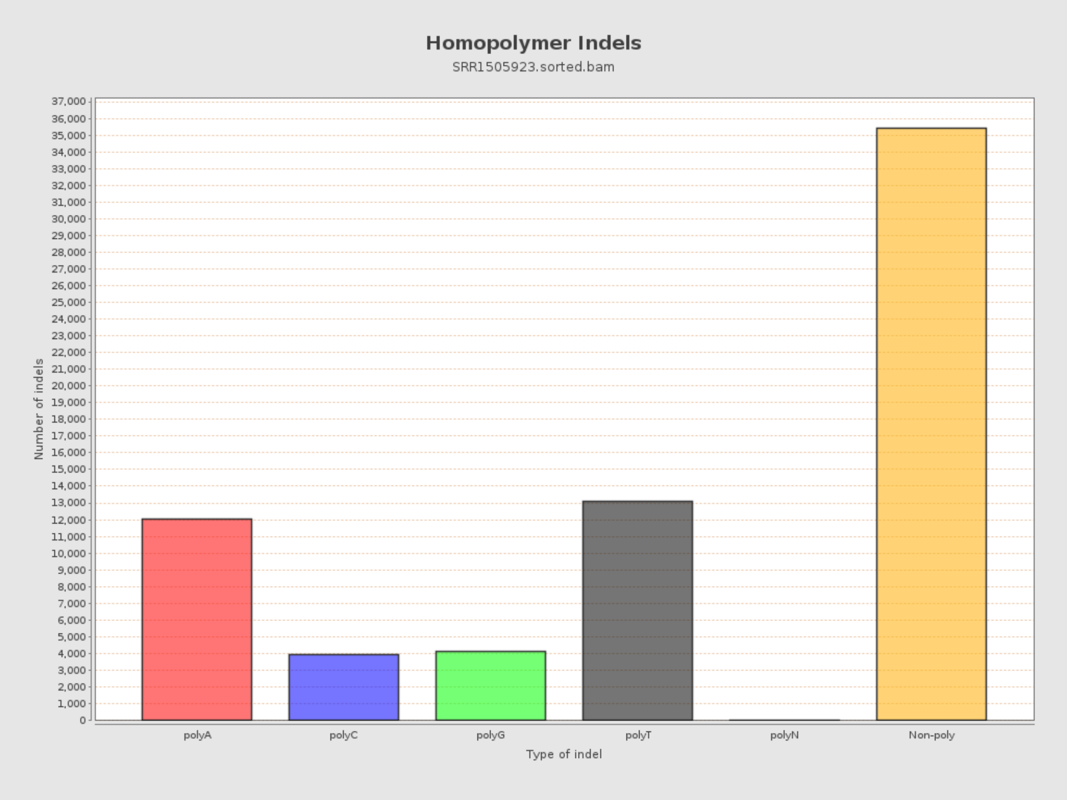
9. Results : Mapped Reads GC-content Distribution



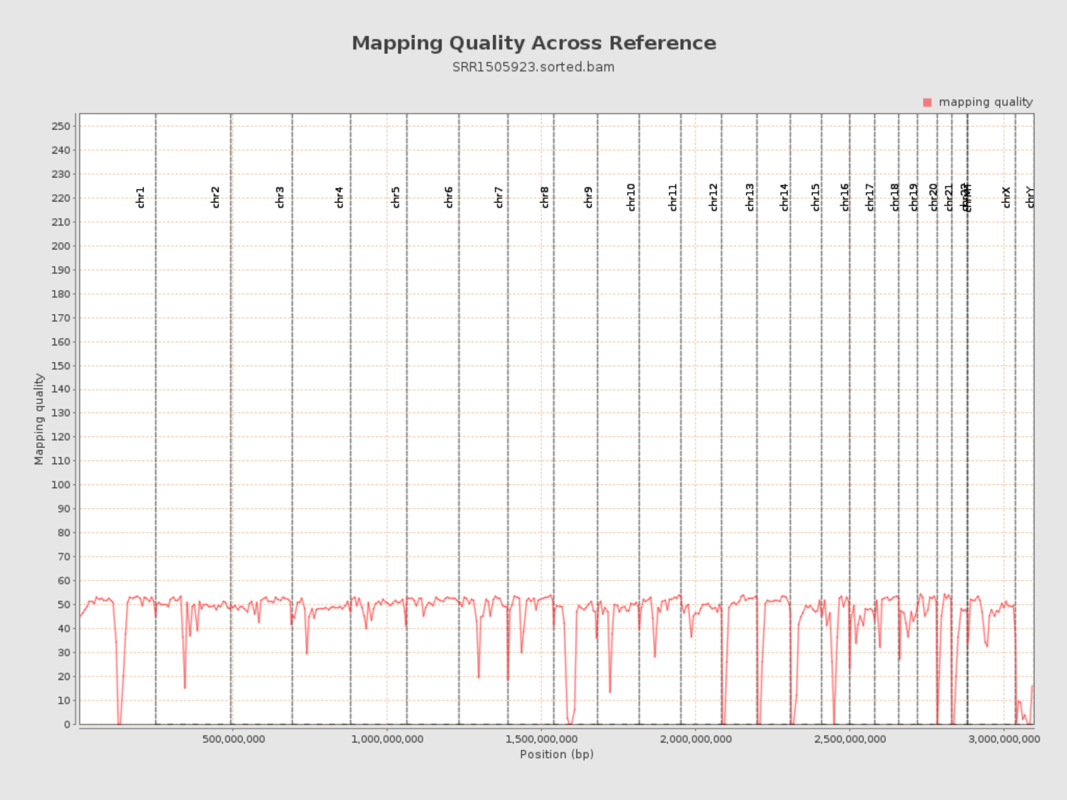
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram