Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:30:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505987.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_SRR1505987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:30:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,207,274
Mapped reads	4,525,141 / 72.9%
Unmapped reads	1,682,133 / 27.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	237 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	432,628 / 6.97%
Duplication rate	7.29%
Clipped reads	588,741 / 9.48%

2.2. ACGT Content

Number/percentage of A's	63,907,117 / 30.2%
Number/percentage of C's	42,138,786 / 19.91%
Number/percentage of T's	63,376,462 / 29.95%
Number/percentage of G's	42,205,292 / 19.94%
Number/percentage of N's	955 / 0%
GC Percentage	39.85%

2.3. Coverage

Mean	0.0684

Standard Deviation	0.6714

2.4. Mapping Quality

Mean Mapping Quality	44.45

2.5. Mismatches and indels

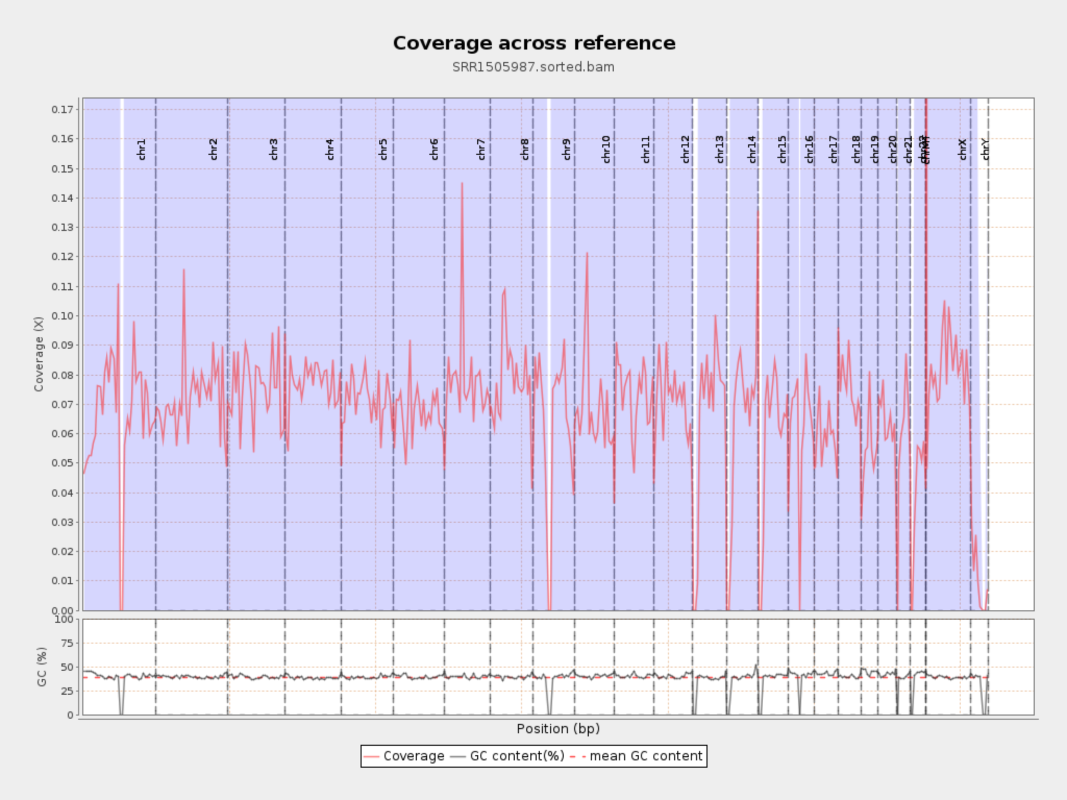
General error rate	0.53%
Mismatches	1,116,310
Insertions	9,808
Mapped reads with at least one insertion	0.22%
Deletions	30,790
Mapped reads with at least one deletion	0.68%
Homopolymer indels	44.93%

2.6. Chromosome stats

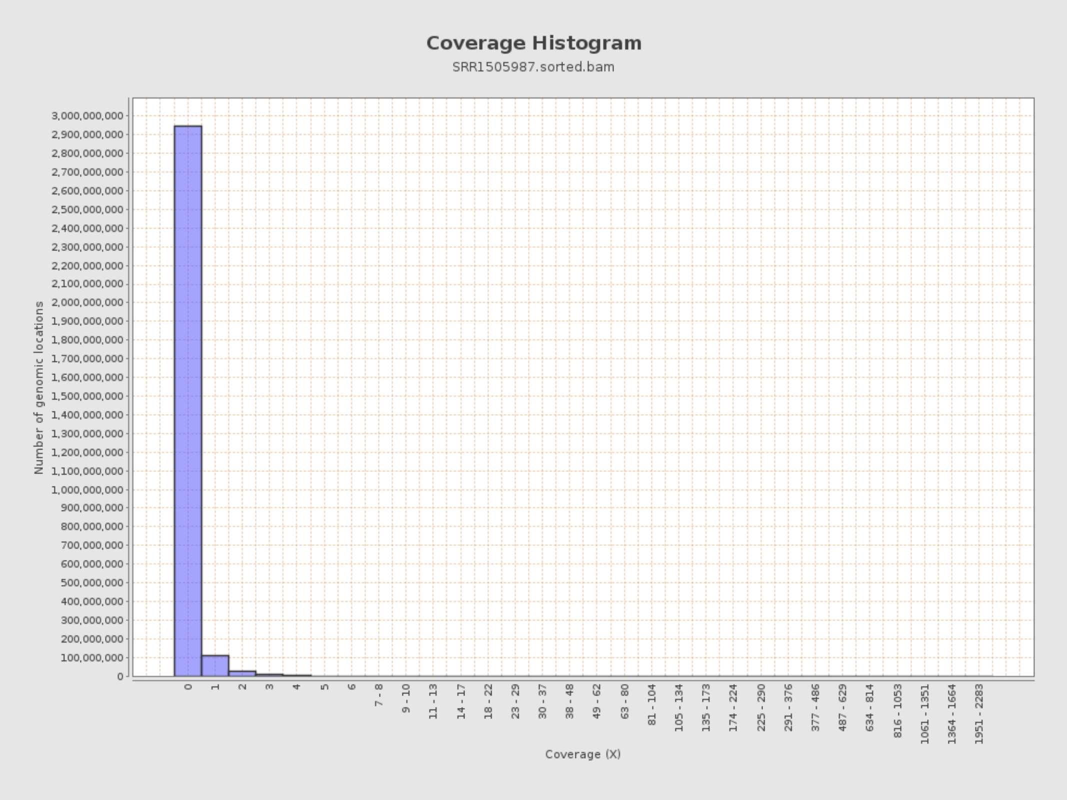
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16539060	0.0664	1.0417
chr2	243199373	17514593	0.072	0.5597
chr3	198022430	14996071	0.0757	0.3766
chr4	191154276	14729696	0.0771	0.3801
chr5	180915260	12945529	0.0716	0.3689
chr6	171115067	11534665	0.0674	0.431
chr7	159138663	12406225	0.078	1.0125

chr8	146364022	11428454	0.0781	1.2549
chr9	141213431	8996539	0.0637	0.526
chr10	135534747	9264333	0.0684	0.6426
chr11	135006516	9872097	0.0731	0.6307
chr12	133851895	9528858	0.0712	0.3903
chr13	115169878	7505132	0.0652	0.3488
chr14	107349540	6801219	0.0634	1.1317
chr15	102531392	5889908	0.0574	0.3245
chr16	90354753	5514561	0.061	0.3825
chr17	81195210	4832762	0.0595	0.3936
chr18	78077248	5935423	0.076	1.1052
chr19	59128983	3256920	0.0551	0.7795
chr20	63025520	4042123	0.0641	0.3663
chr21	48129895	2806477	0.0583	0.3527
chr22	51304566	1994377	0.0389	0.268
chrMT	16571	61608	3.7178	3.7155
chrX	155270560	12677519	0.0816	0.469
chrY	59373566	596323	0.01	0.1478

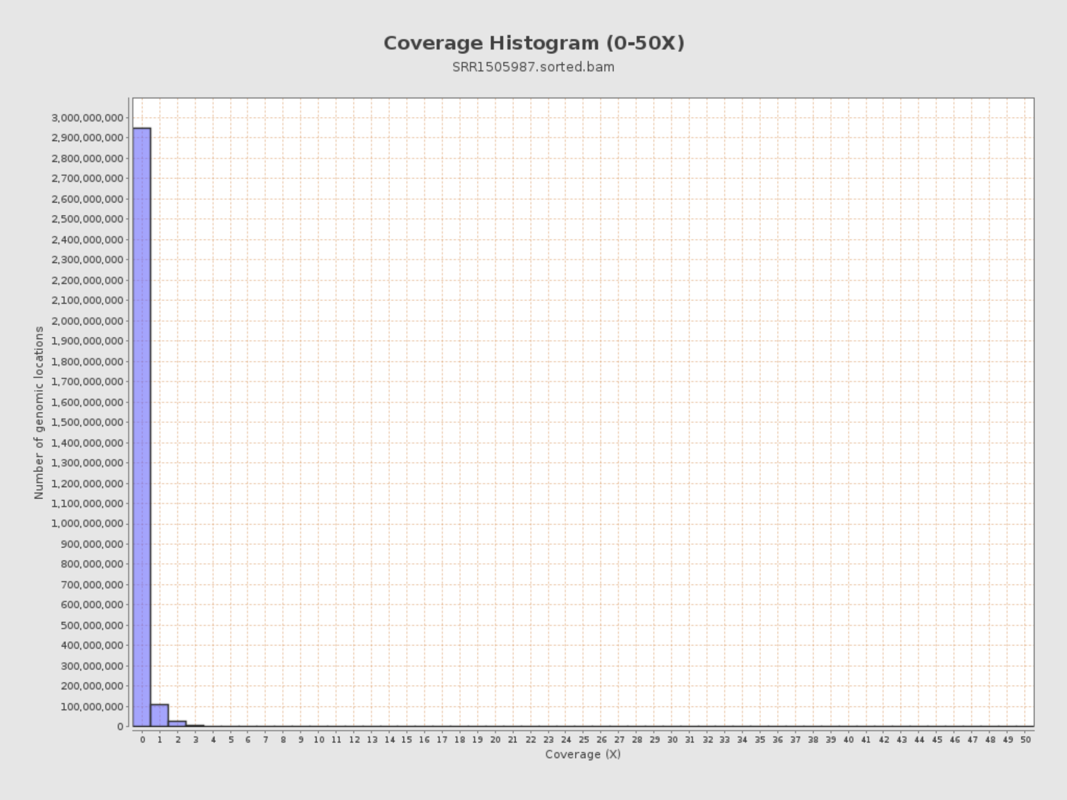
3. Results : Coverage across reference



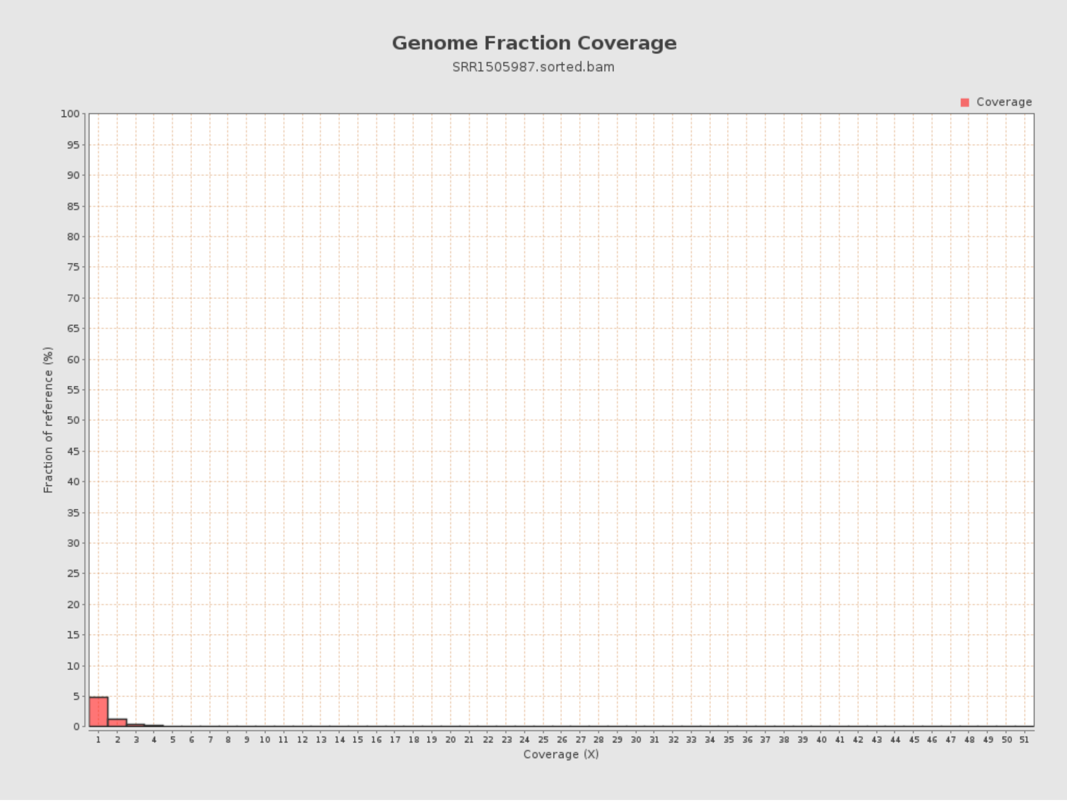
4. Results : Coverage Histogram



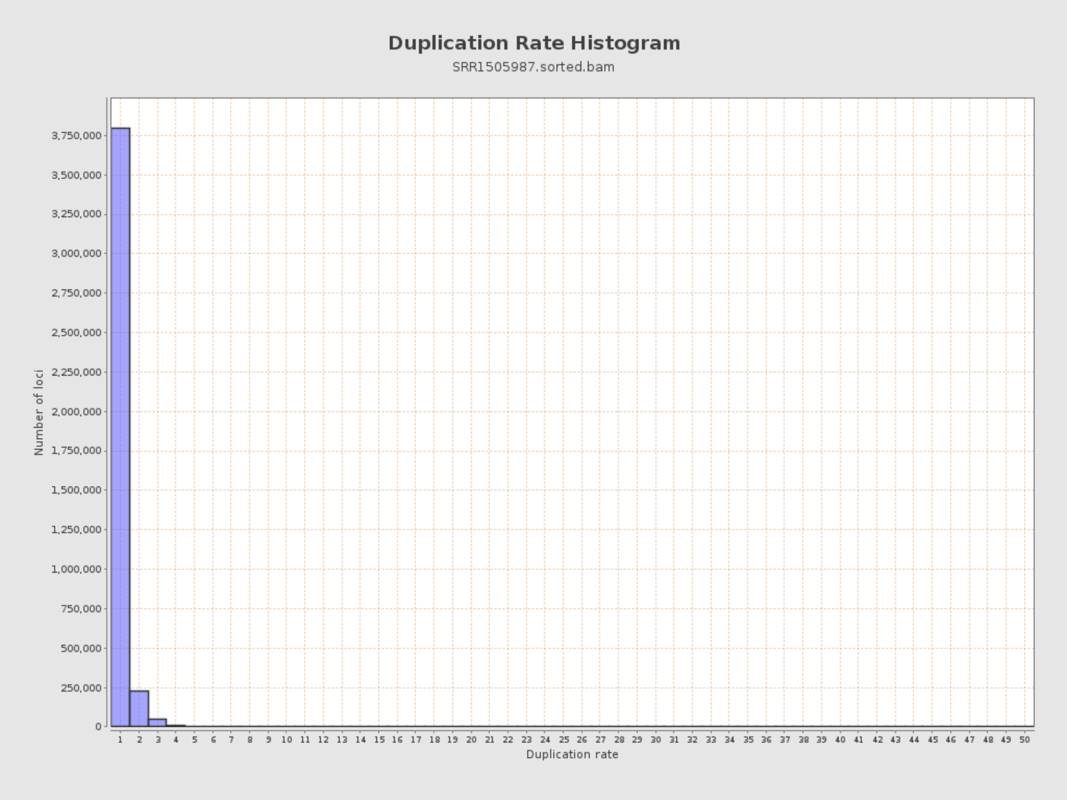
5. Results : Coverage Histogram (0-50X)



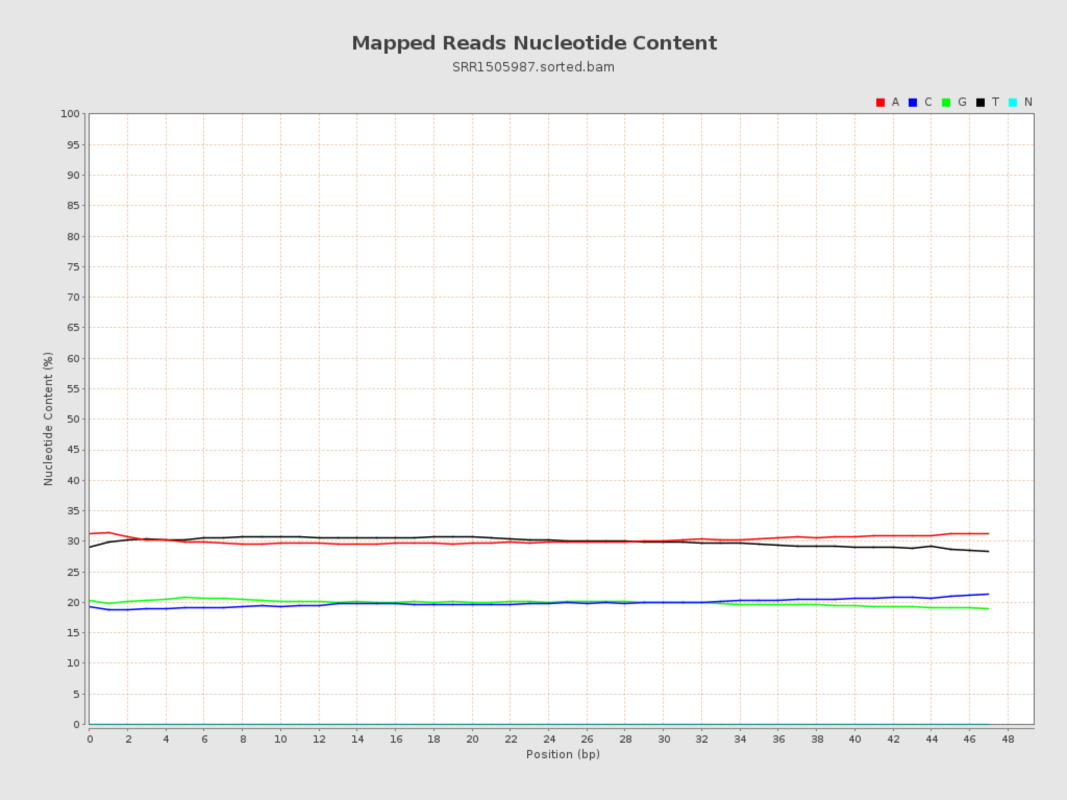
6. Results : Genome Fraction Coverage



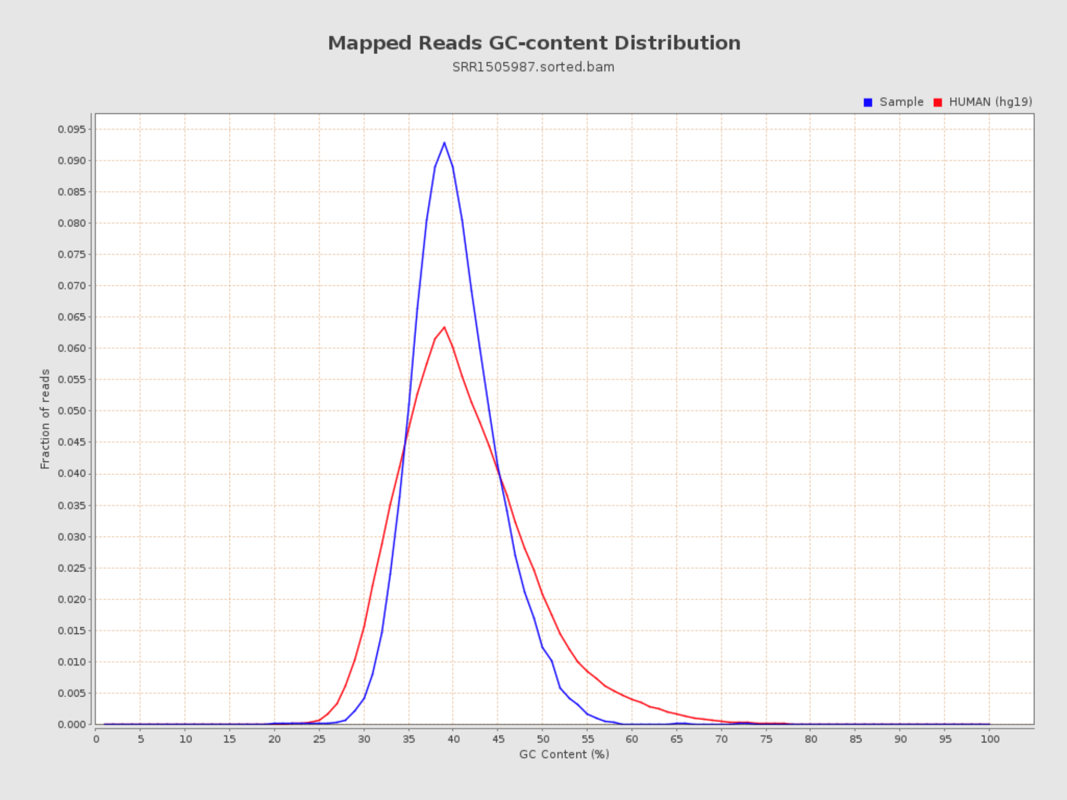
7. Results : Duplication Rate Histogram



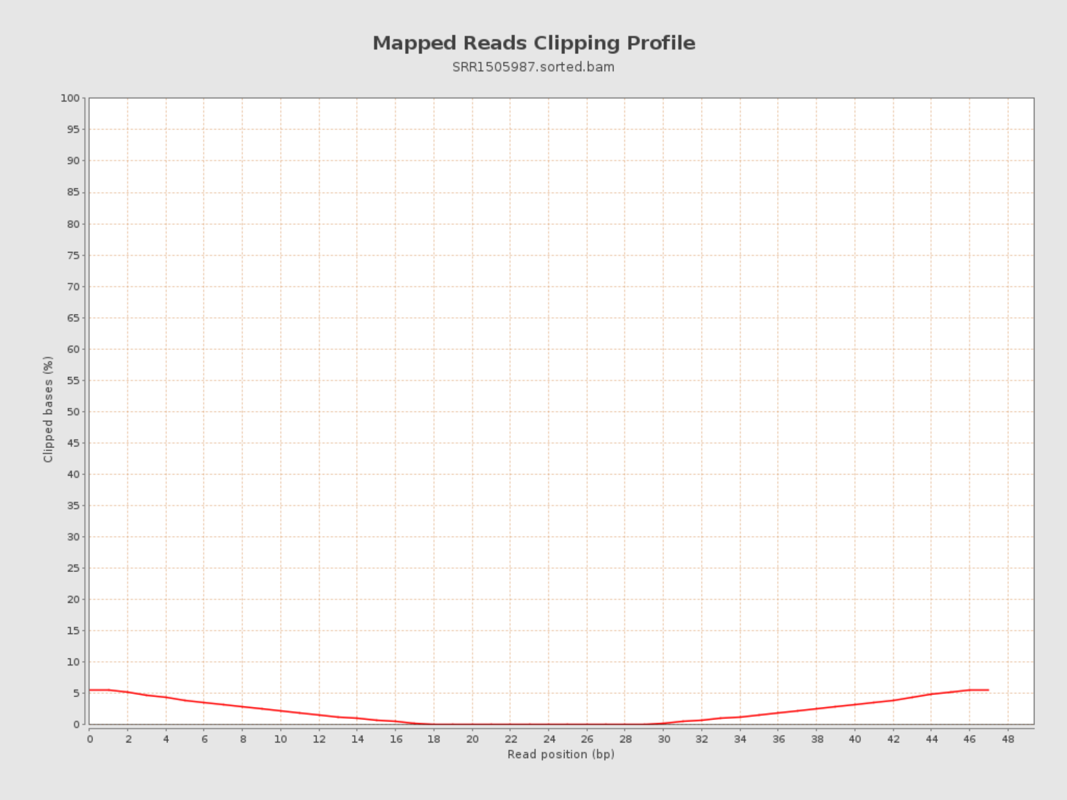
8. Results : Mapped Reads Nucleotide Content



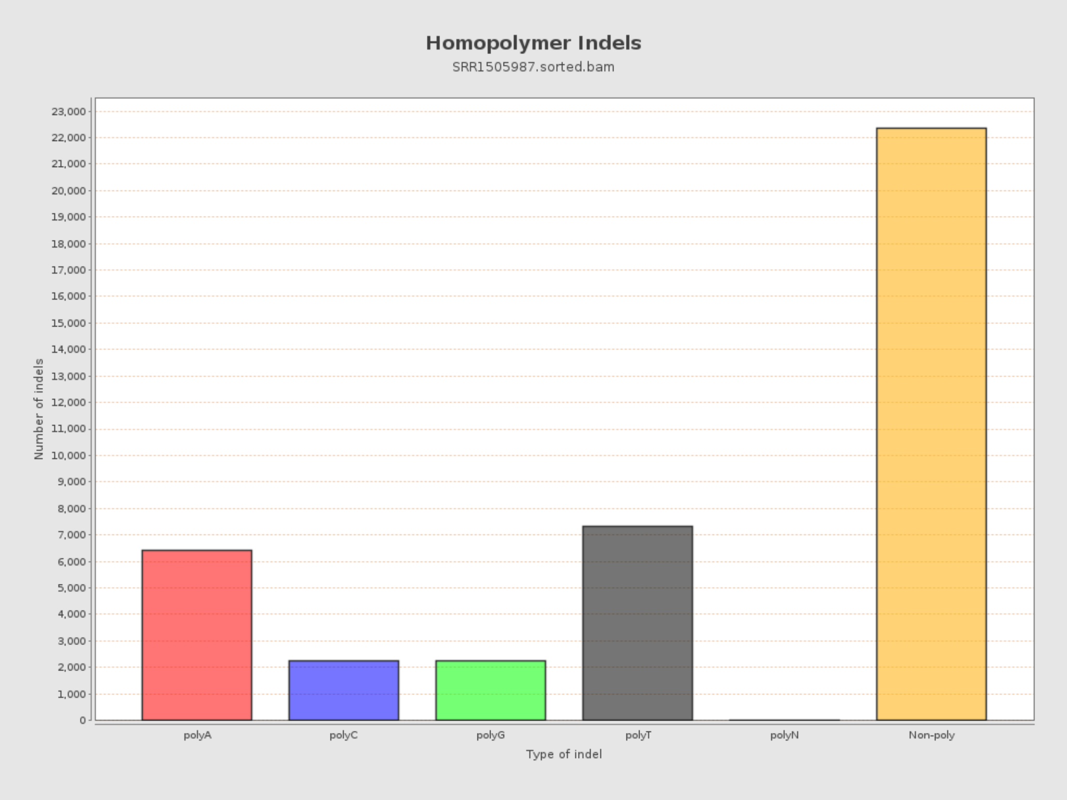
9. Results : Mapped Reads GC-content Distribution



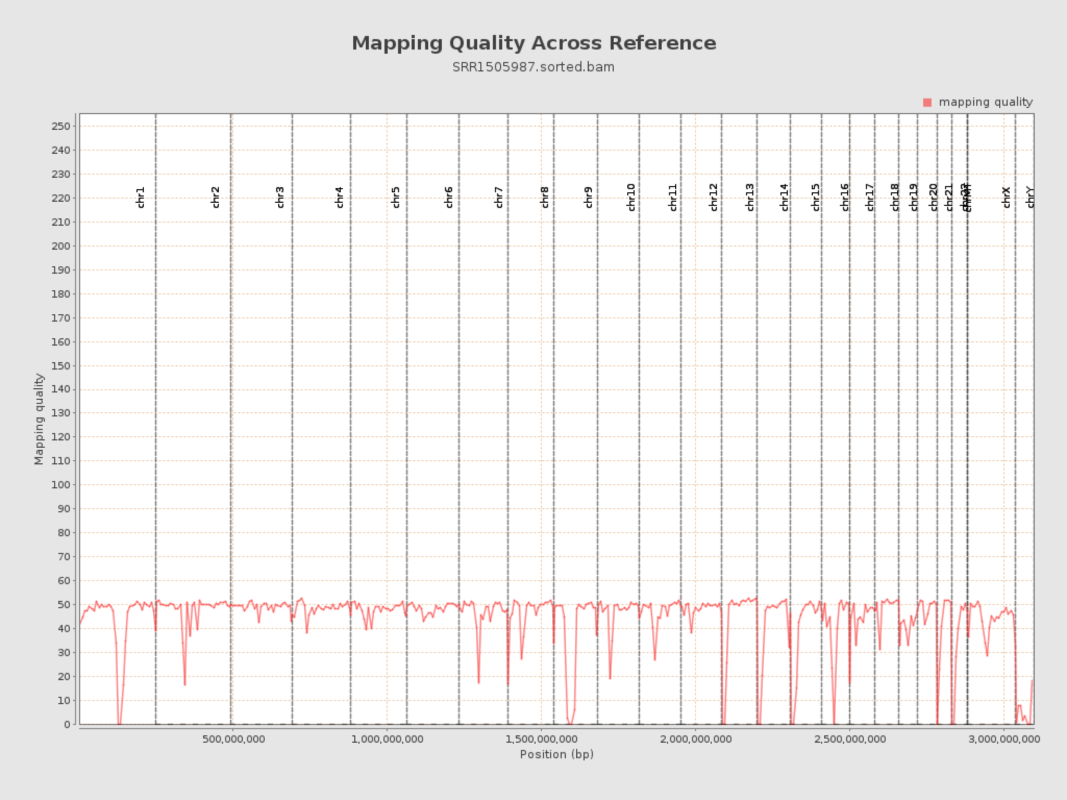
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram