Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:40:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505989.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_SRR1505989 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505989.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:40:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505989.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,672,424
Mapped reads	5,741,035 / 74.83%
Unmapped reads	1,931,389 / 25.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	228 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	337,585 / 4.4%
Duplication rate	4.36%
Clipped reads	791,392 / 10.31%

2.2. ACGT Content

Number/percentage of A's	81,358,200 / 30.38%
Number/percentage of C's	53,316,495 / 19.91%
Number/percentage of T's	79,229,097 / 29.58%
Number/percentage of G's	53,904,999 / 20.13%
Number/percentage of N's	1,138 / 0%
GC Percentage	40.04%

2.3. Coverage

Mean	0.0865

Standard Deviation	0.8046

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

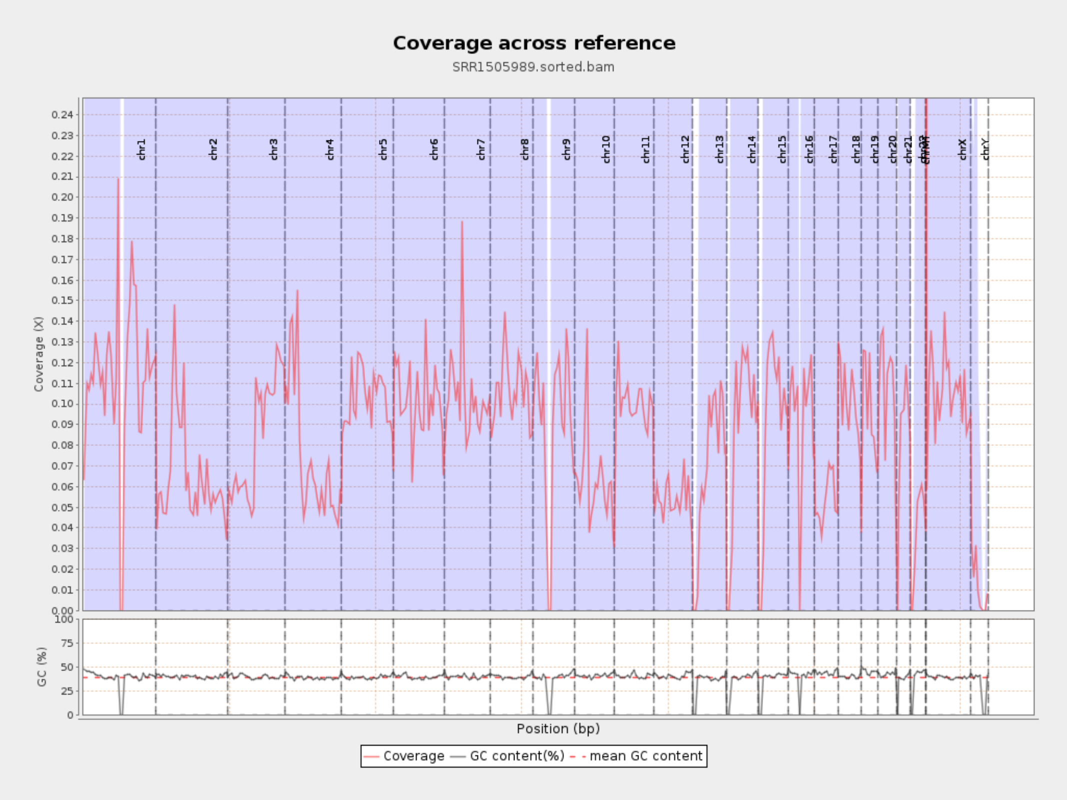
General error rate	0.47%
Mismatches	1,239,819
Insertions	11,720
Mapped reads with at least one insertion	0.2%
Deletions	41,023
Mapped reads with at least one deletion	0.71%
Homopolymer indels	48.2%

2.6. Chromosome stats

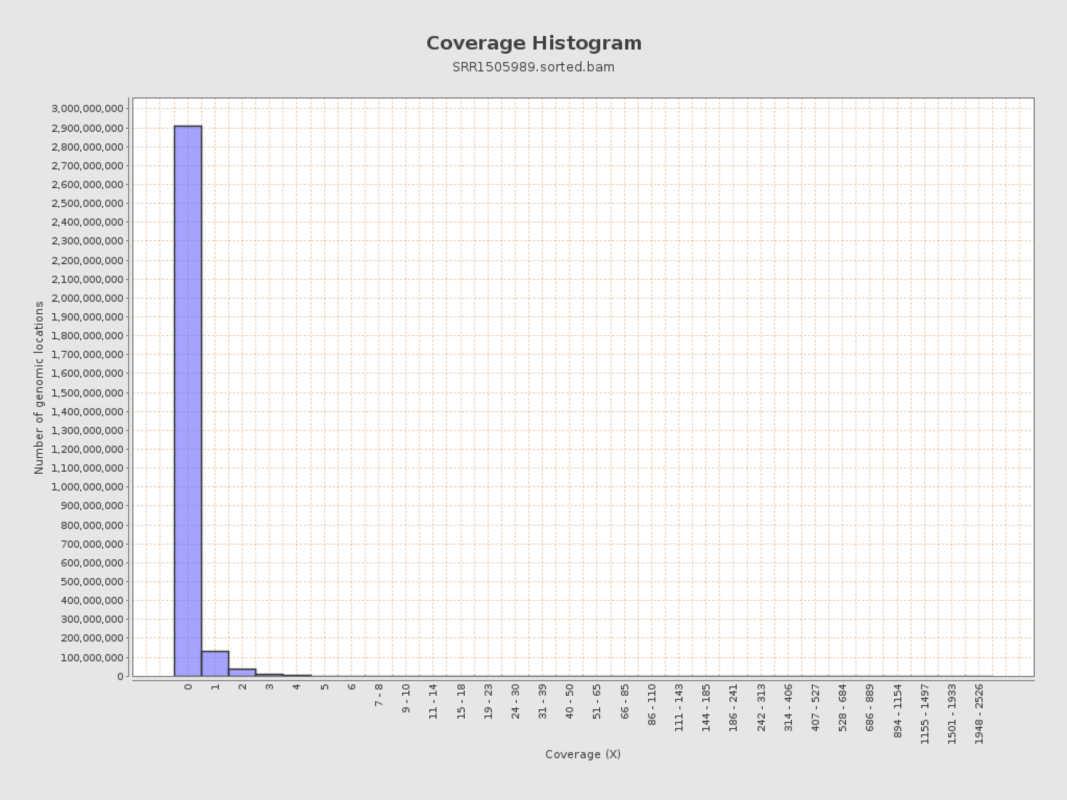
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	28283323	0.1135	1.8042
chr2	243199373	15983420	0.0657	0.5493
chr3	198022430	16582949	0.0837	0.3948
chr4	191154276	14060170	0.0736	0.3784
chr5	180915260	18564926	0.1026	0.4448
chr6	171115067	17457450	0.102	0.563
chr7	159138663	16573185	0.1041	1.2424

chr8	146364022	15503260	0.1059	1.2321
chr9	141213431	12851389	0.091	0.5658
chr10	135534747	8444354	0.0623	0.6886
chr11	135006516	13421280	0.0994	0.6562
chr12	133851895	7244147	0.0541	0.3499
chr13	115169878	7953275	0.0691	0.3484
chr14	107349540	9502706	0.0885	0.4584
chr15	102531392	9134884	0.0891	0.3971
chr16	90354753	8232619	0.0911	0.4469
chr17	81195210	4384063	0.054	0.3482
chr18	78077248	7948821	0.1018	1.0277
chr19	59128983	5680808	0.0961	1.1614
chr20	63025520	6900125	0.1095	0.4512
chr21	48129895	3993151	0.083	0.4309
chr22	51304566	1949212	0.038	0.251
chrMT	16571	106655	6.4362	5.2315
chrX	155270560	16424516	0.1058	0.5483
chrY	59373566	686629	0.0116	0.1964

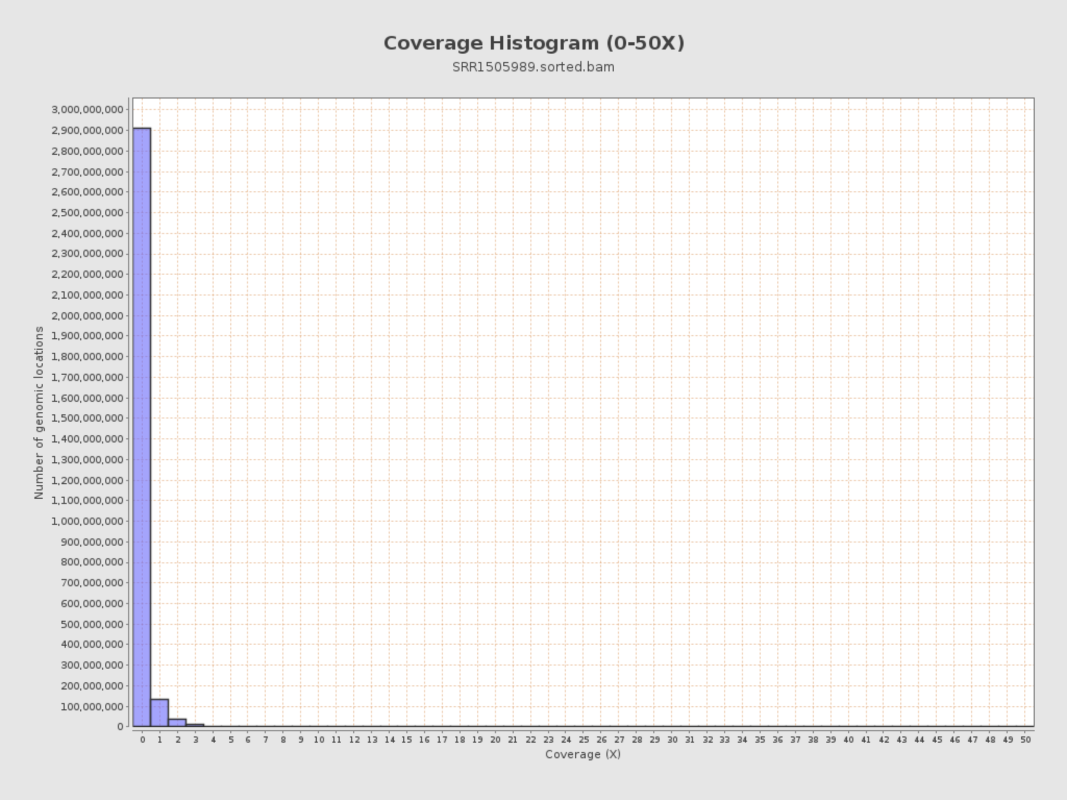
3. Results : Coverage across reference



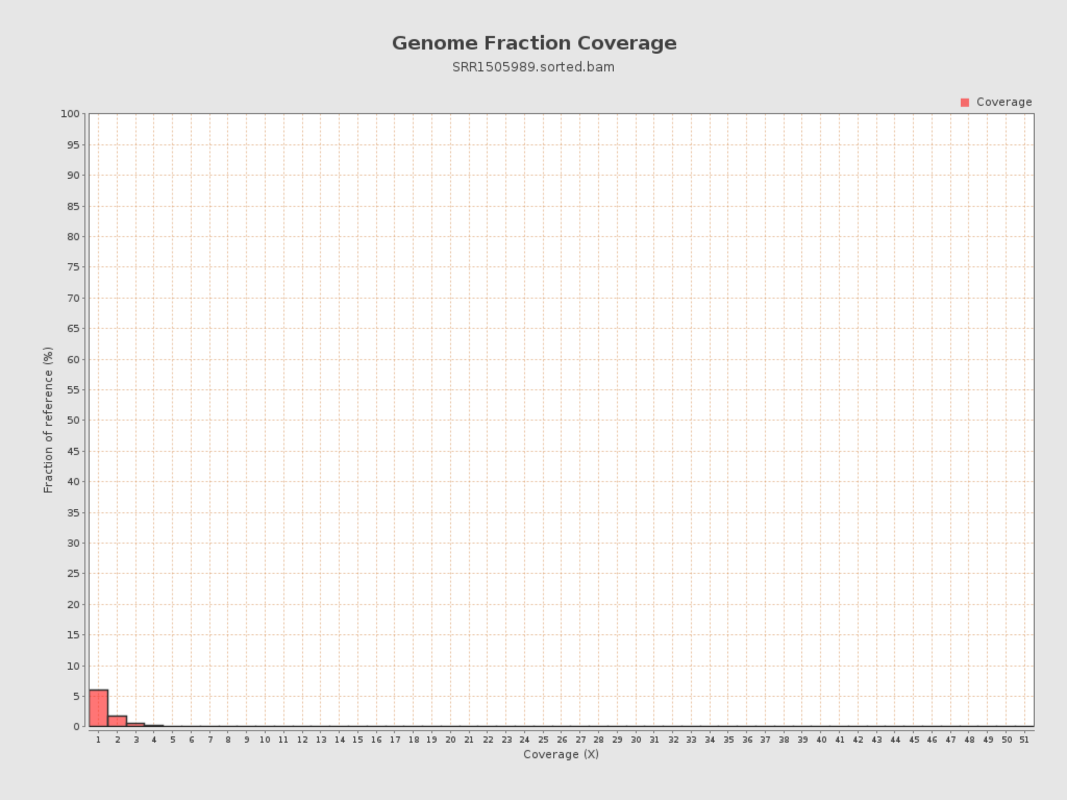
4. Results : Coverage Histogram



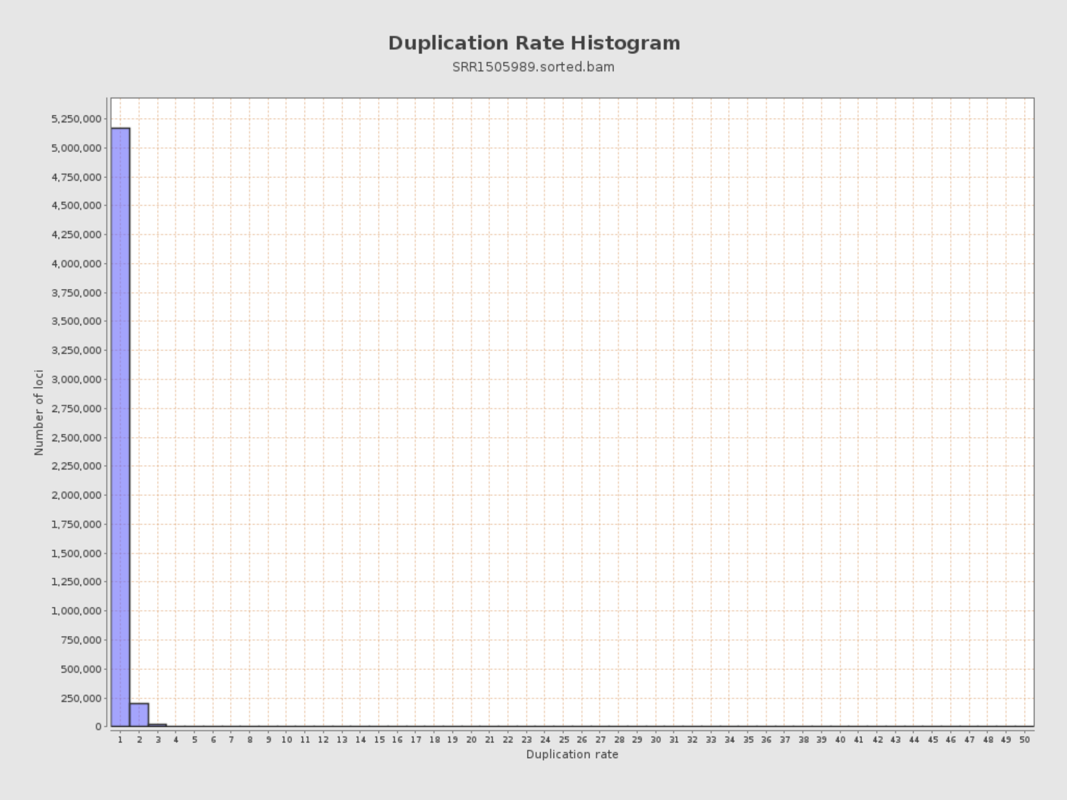
5. Results : Coverage Histogram (0-50X)



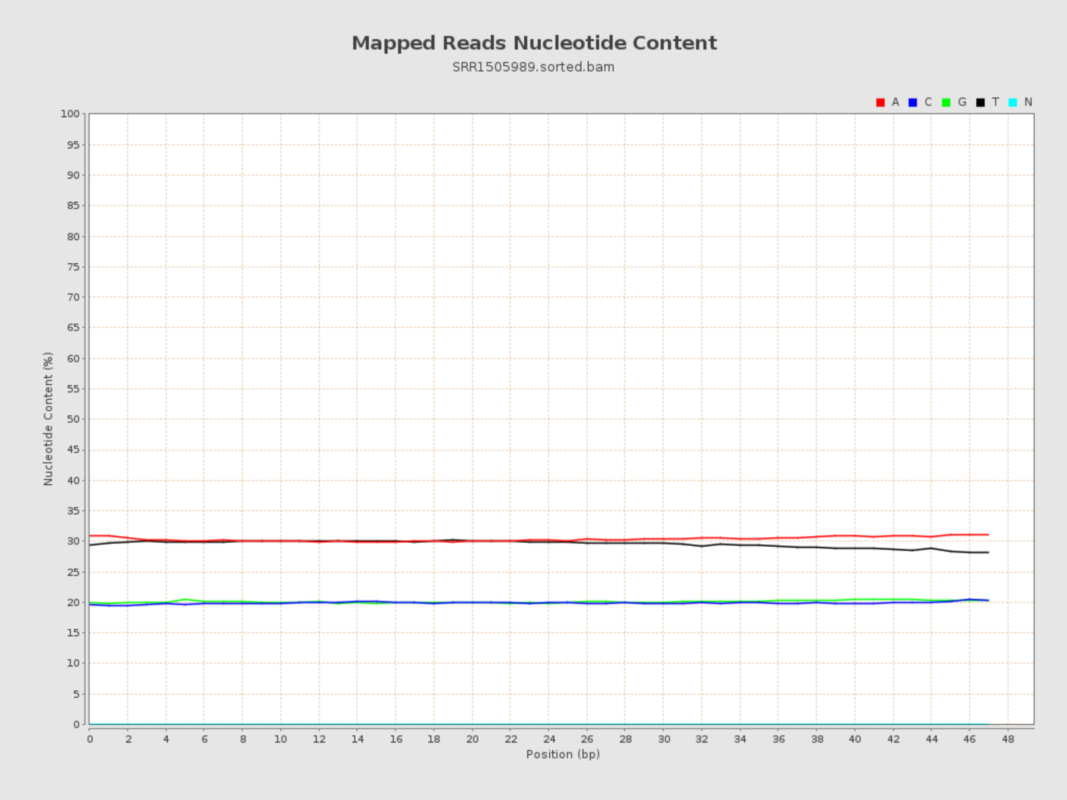
6. Results : Genome Fraction Coverage



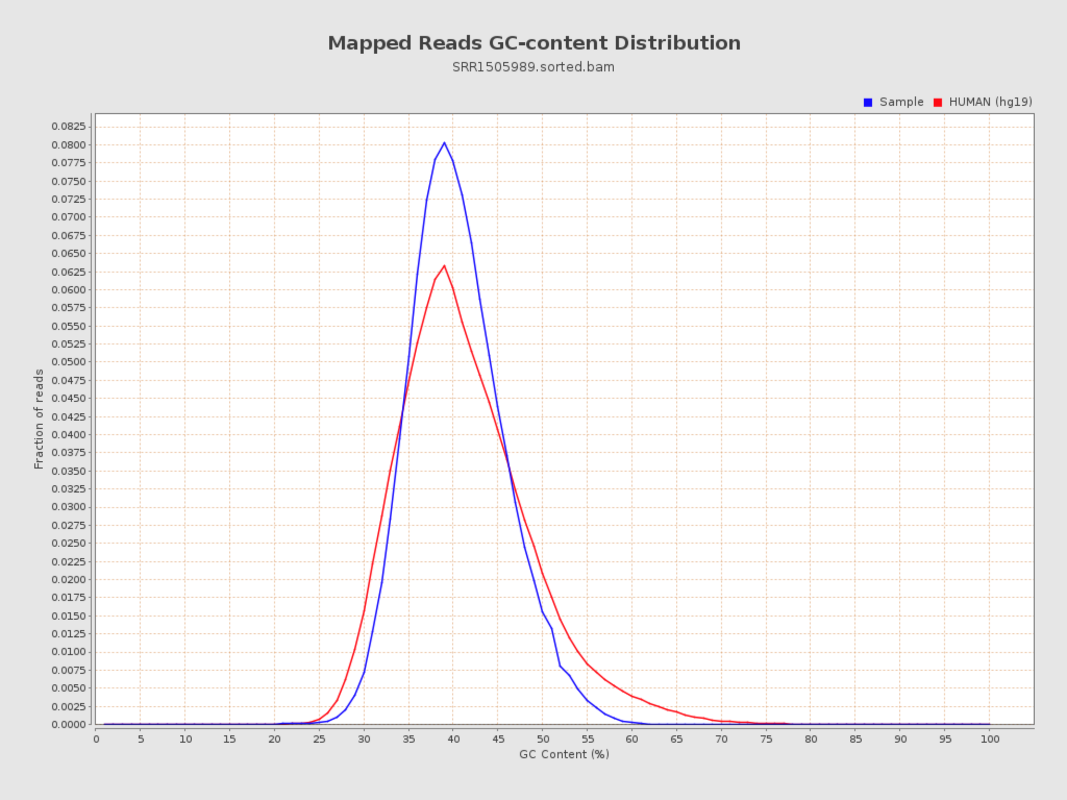
7. Results : Duplication Rate Histogram



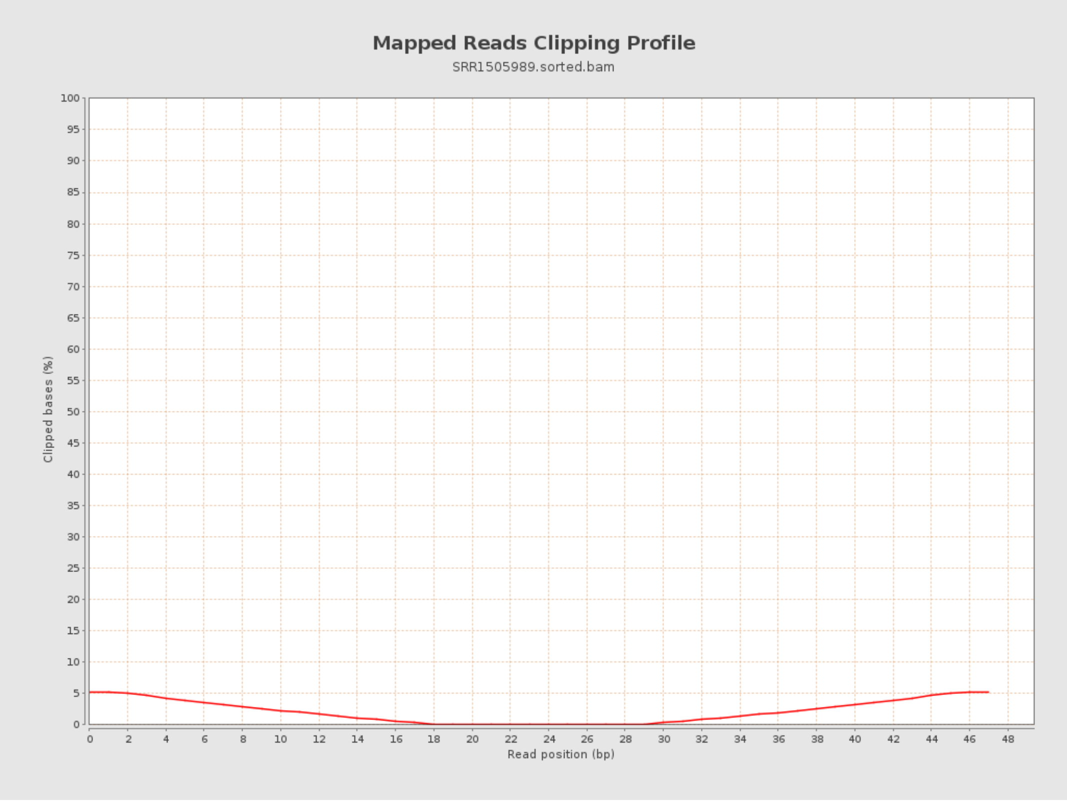
8. Results : Mapped Reads Nucleotide Content



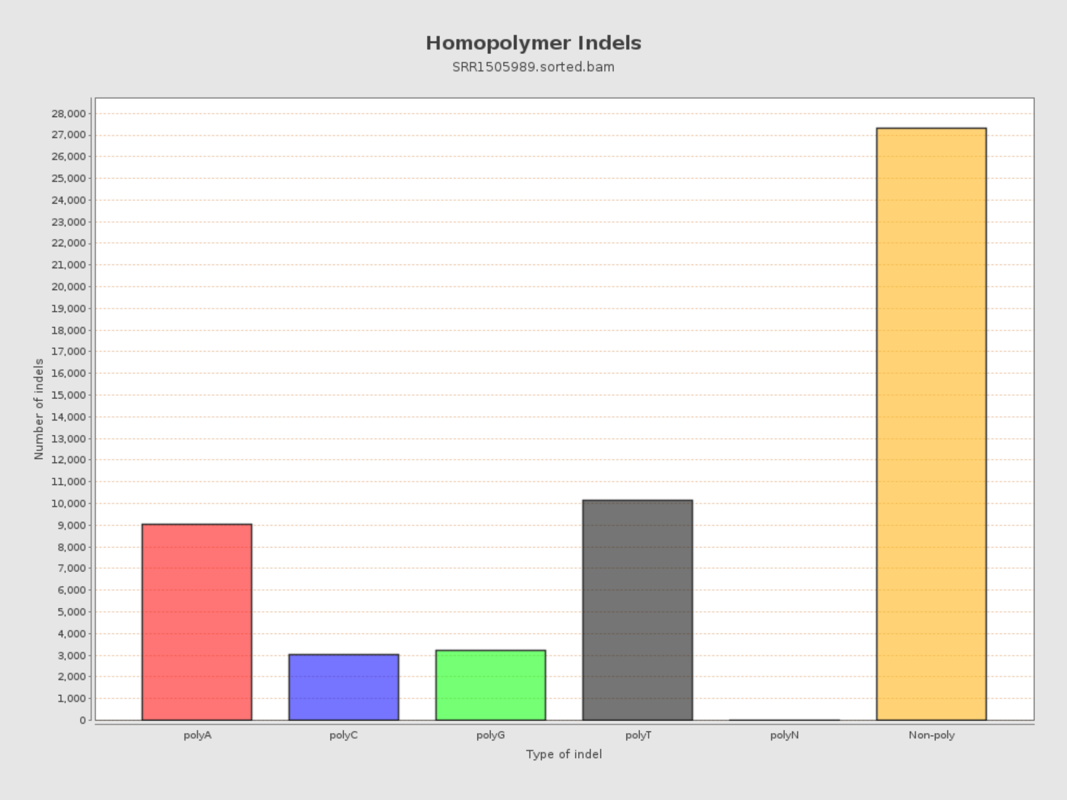
9. Results : Mapped Reads GC-content Distribution



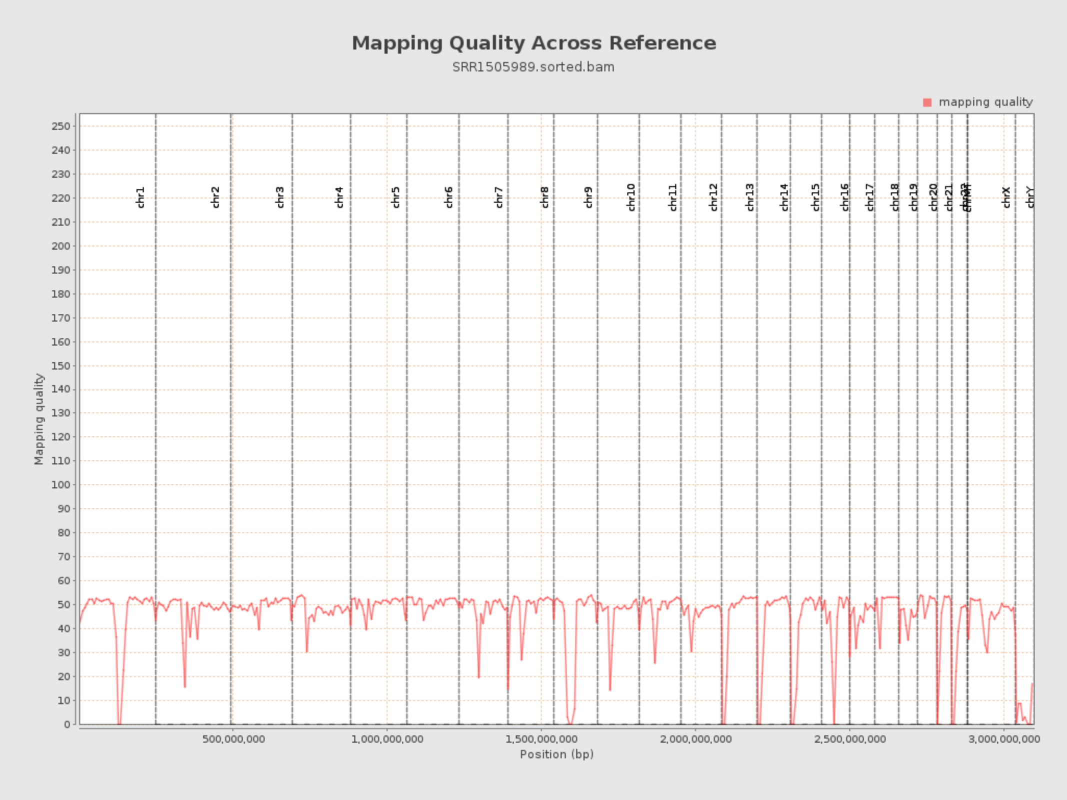
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram