Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:37:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505976.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_SRR1505976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:37:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,155,603
Mapped reads	3,114,641 / 60.41%
Unmapped reads	2,040,962 / 39.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	124 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	244,634 / 4.75%
Duplication rate	5.82%
Clipped reads	463,232 / 8.99%

2.2. ACGT Content

Number/percentage of A's	42,831,478 / 29.53%
Number/percentage of C's	30,077,800 / 20.74%
Number/percentage of T's	41,985,667 / 28.94%
Number/percentage of G's	30,159,362 / 20.79%
Number/percentage of N's	594 / 0%
GC Percentage	41.53%

2.3. Coverage

Mean	0.0469

Standard Deviation	0.8518

2.4. Mapping Quality

Mean Mapping Quality	44.08

2.5. Mismatches and indels

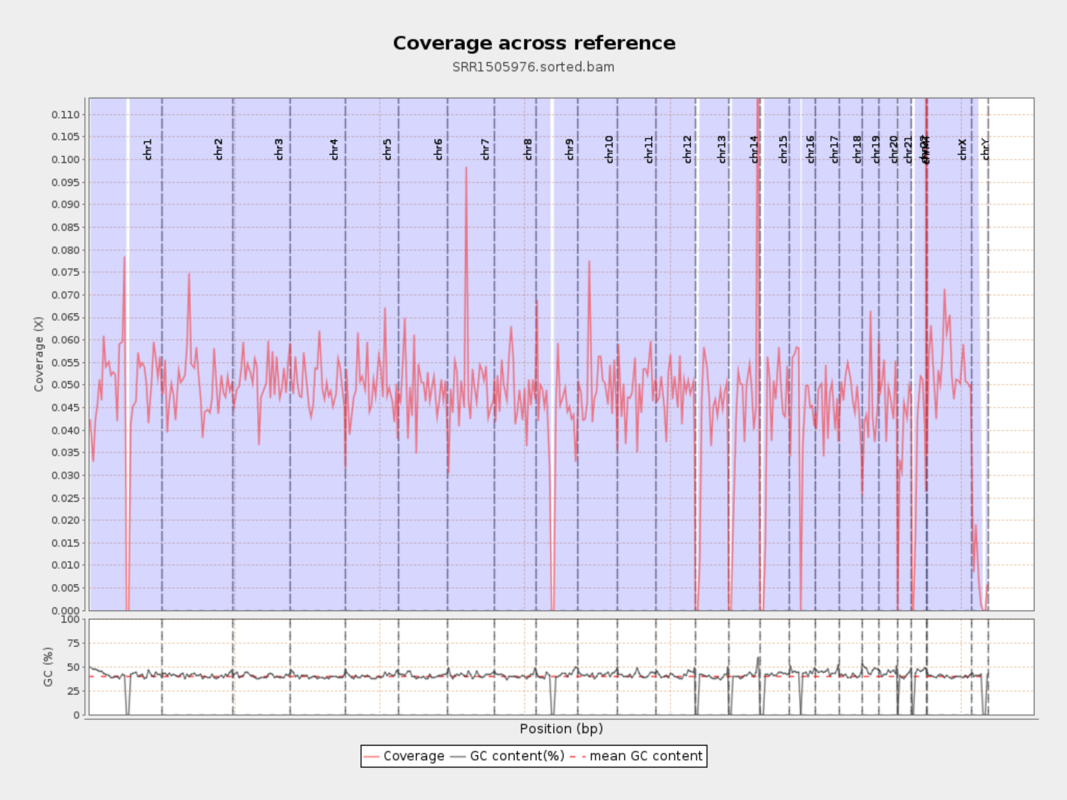
General error rate	0.53%
Mismatches	763,439
Insertions	6,934
Mapped reads with at least one insertion	0.22%
Deletions	21,014
Mapped reads with at least one deletion	0.67%
Homopolymer indels	43.4%

2.6. Chromosome stats

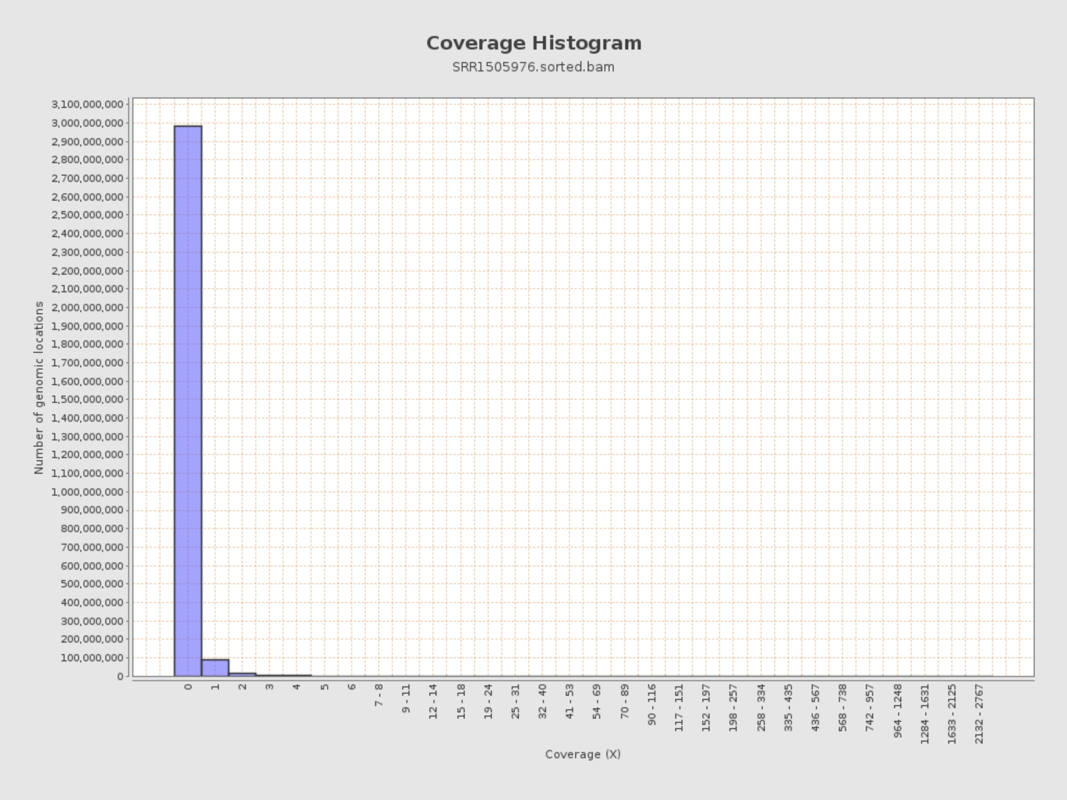
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12050608	0.0483	0.8101
chr2	243199373	12215796	0.0502	0.3776
chr3	198022430	10153102	0.0513	0.284
chr4	191154276	9568462	0.0501	0.2834
chr5	180915260	9033032	0.0499	0.2871
chr6	171115067	8384072	0.049	0.4952
chr7	159138663	8037290	0.0505	0.8012

chr8	146364022	7114467	0.0486	0.5617
chr9	141213431	5696032	0.0403	0.3151
chr10	135534747	6812154	0.0503	0.4476
chr11	135006516	6582729	0.0488	0.3455
chr12	133851895	6496406	0.0485	0.2884
chr13	115169878	4574266	0.0397	0.2486
chr14	107349540	4983943	0.0464	3.8948
chr15	102531392	4044265	0.0394	0.2466
chr16	90354753	4034686	0.0447	0.2845
chr17	81195210	3644801	0.0449	0.296
chr18	78077248	3726386	0.0477	0.5593
chr19	59128983	2644467	0.0447	0.5825
chr20	63025520	3032906	0.0481	0.5562
chr21	48129895	1802903	0.0375	0.2542
chr22	51304566	1623044	0.0316	0.2227
chrMT	16571	61379	3.704	3.138
chrX	155270560	8347106	0.0538	0.315
chrY	59373566	419516	0.0071	0.1251

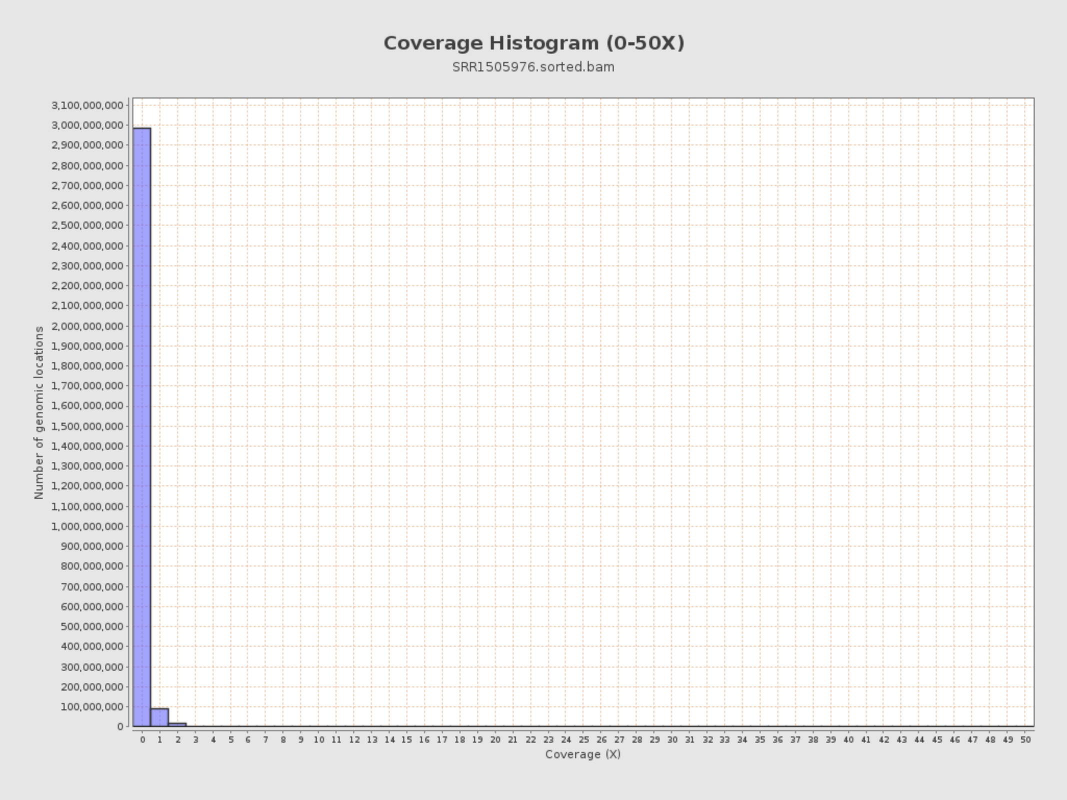
3. Results : Coverage across reference



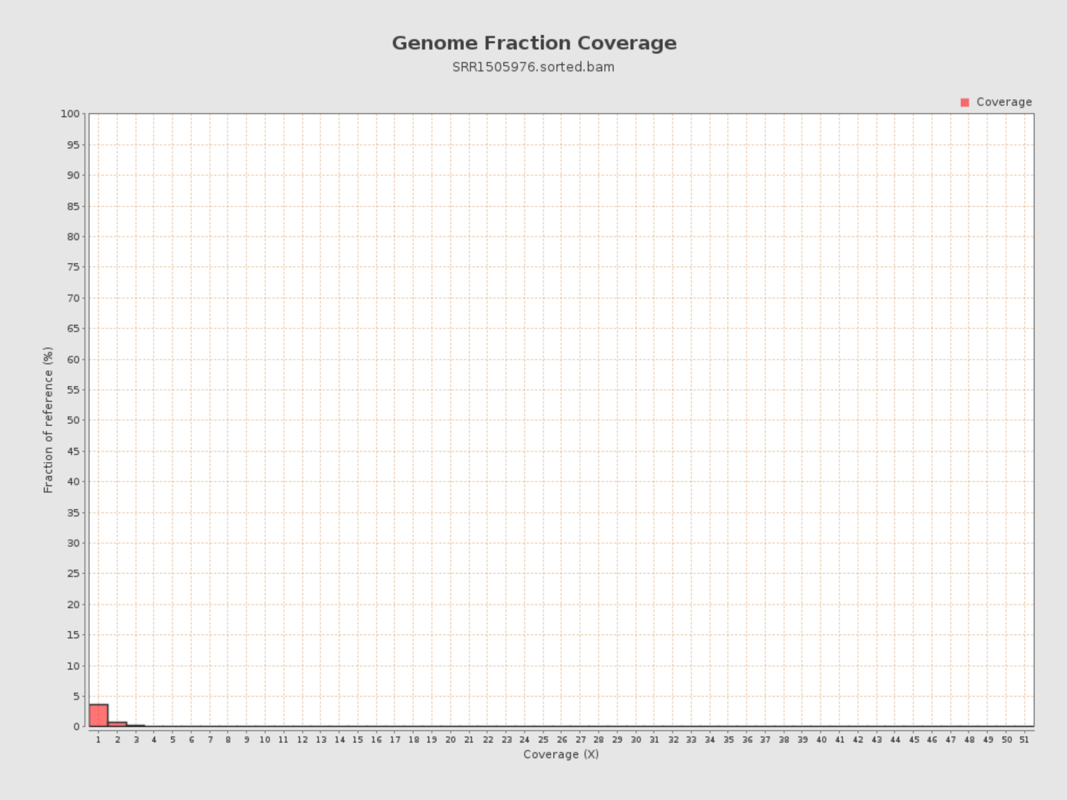
4. Results : Coverage Histogram



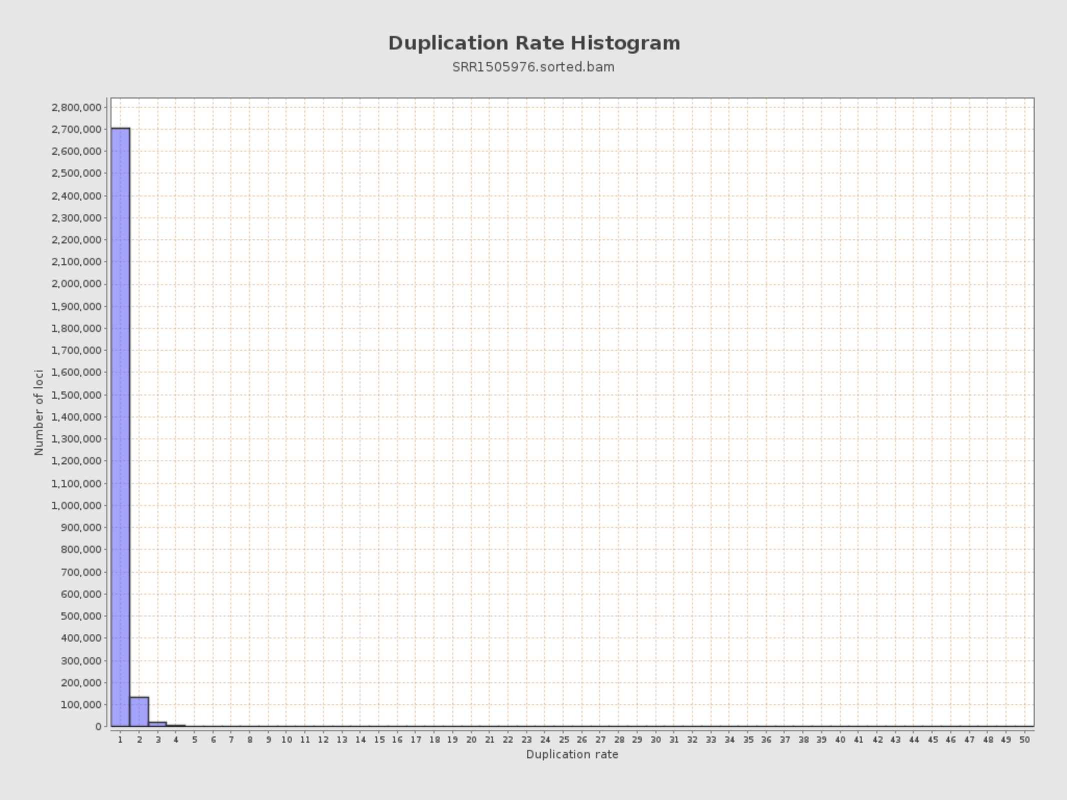
5. Results : Coverage Histogram (0-50X)



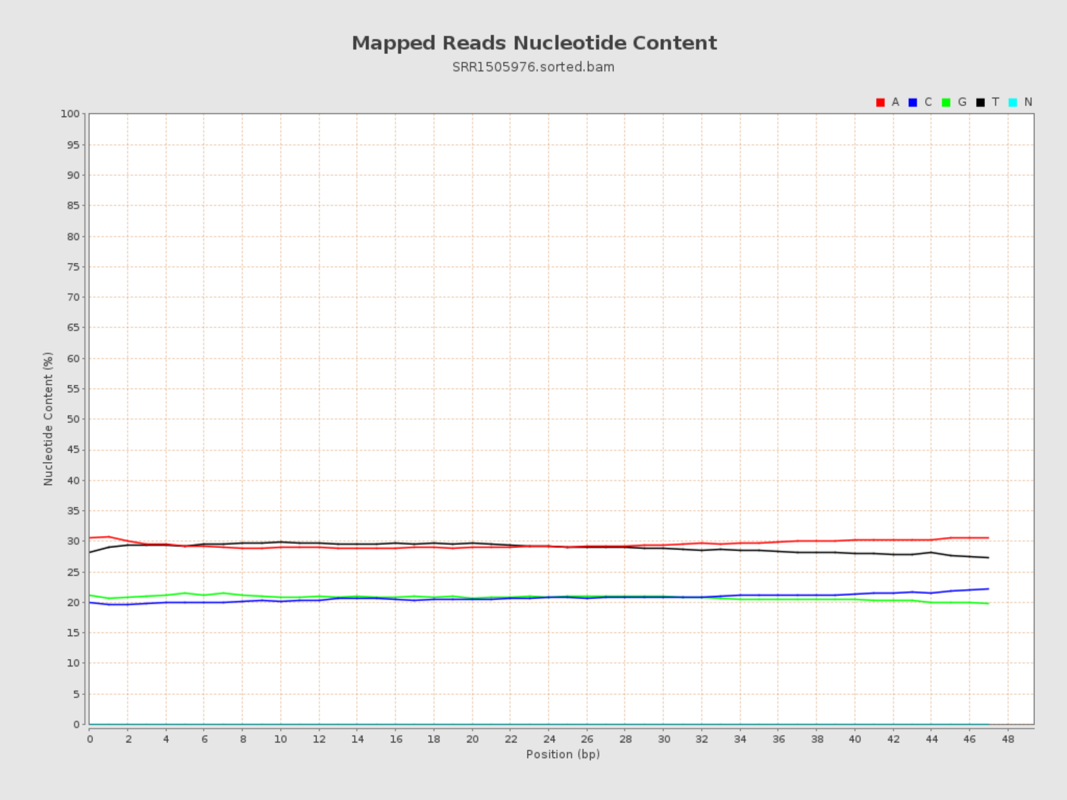
6. Results : Genome Fraction Coverage



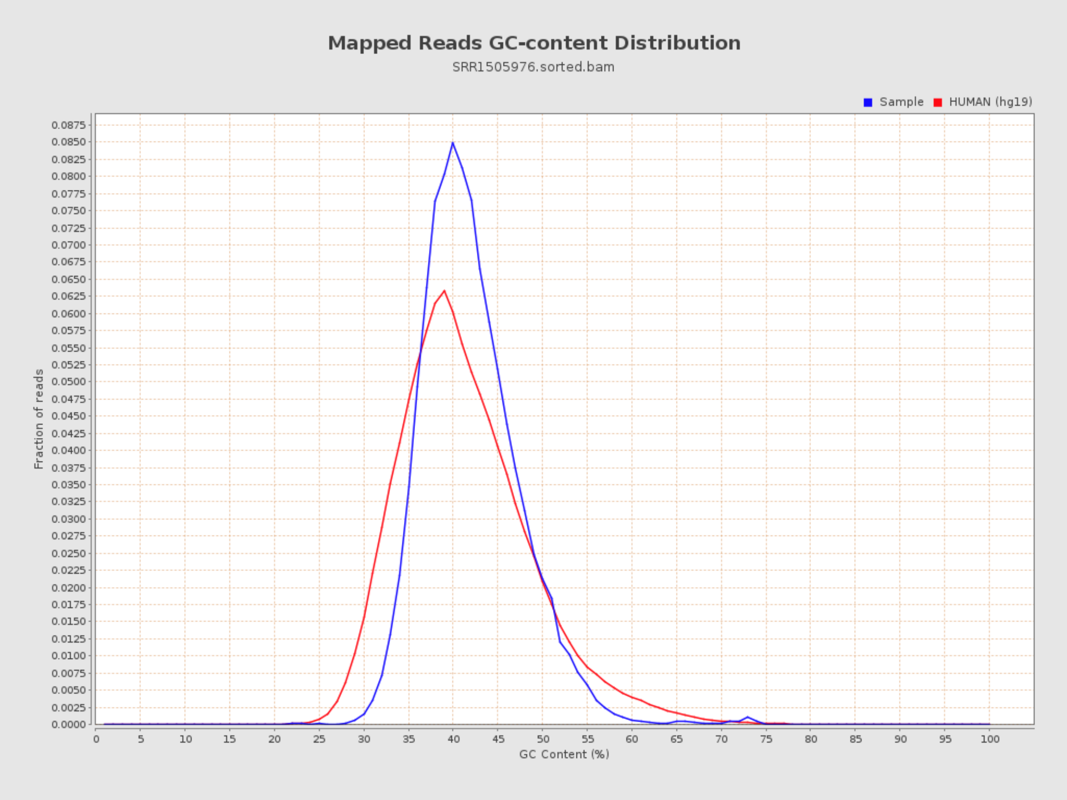
7. Results : Duplication Rate Histogram



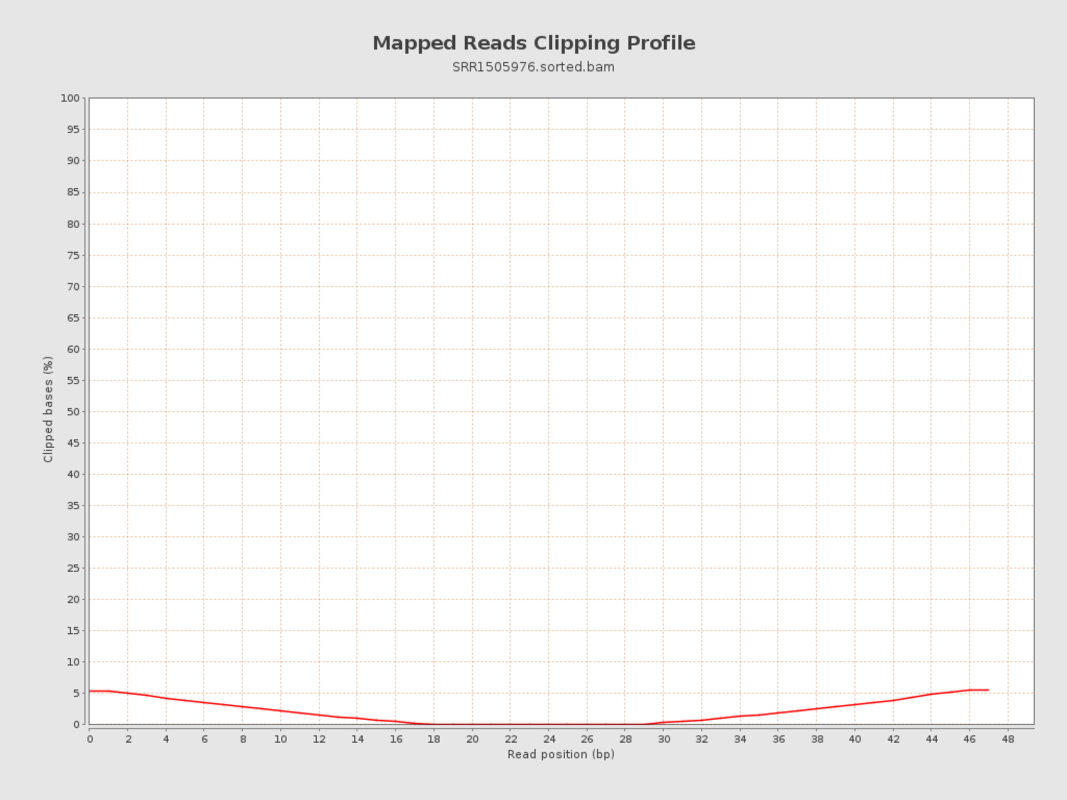
8. Results : Mapped Reads Nucleotide Content



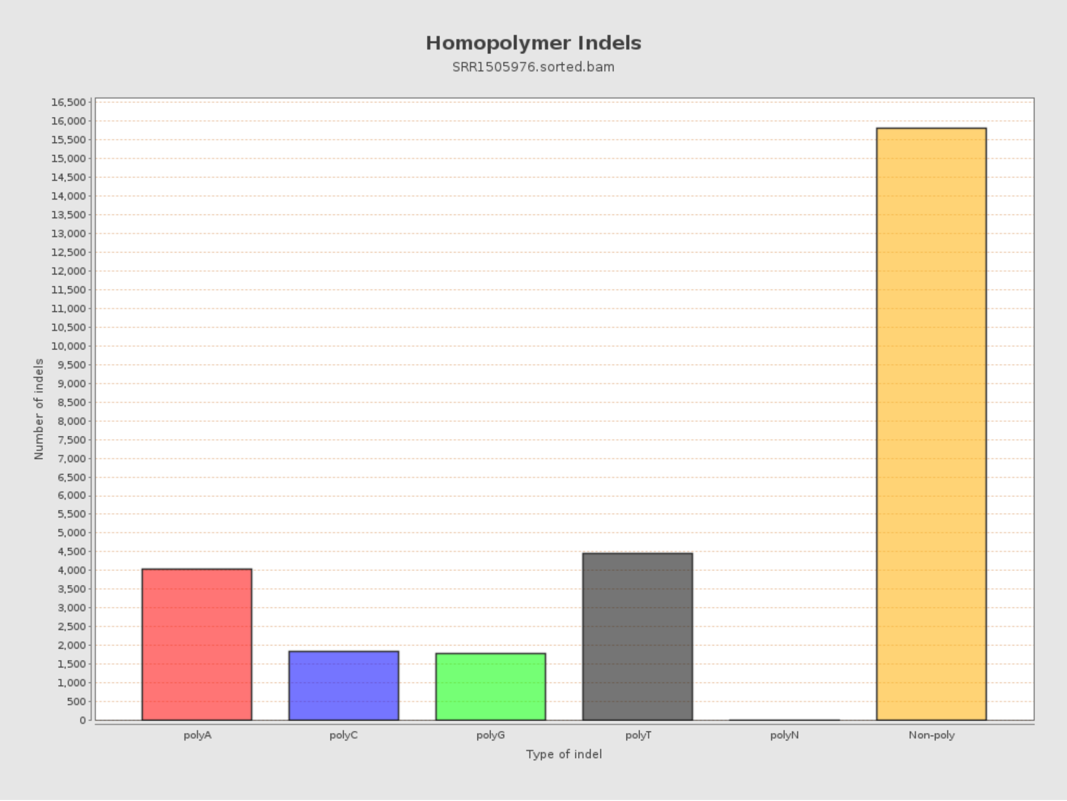
9. Results : Mapped Reads GC-content Distribution



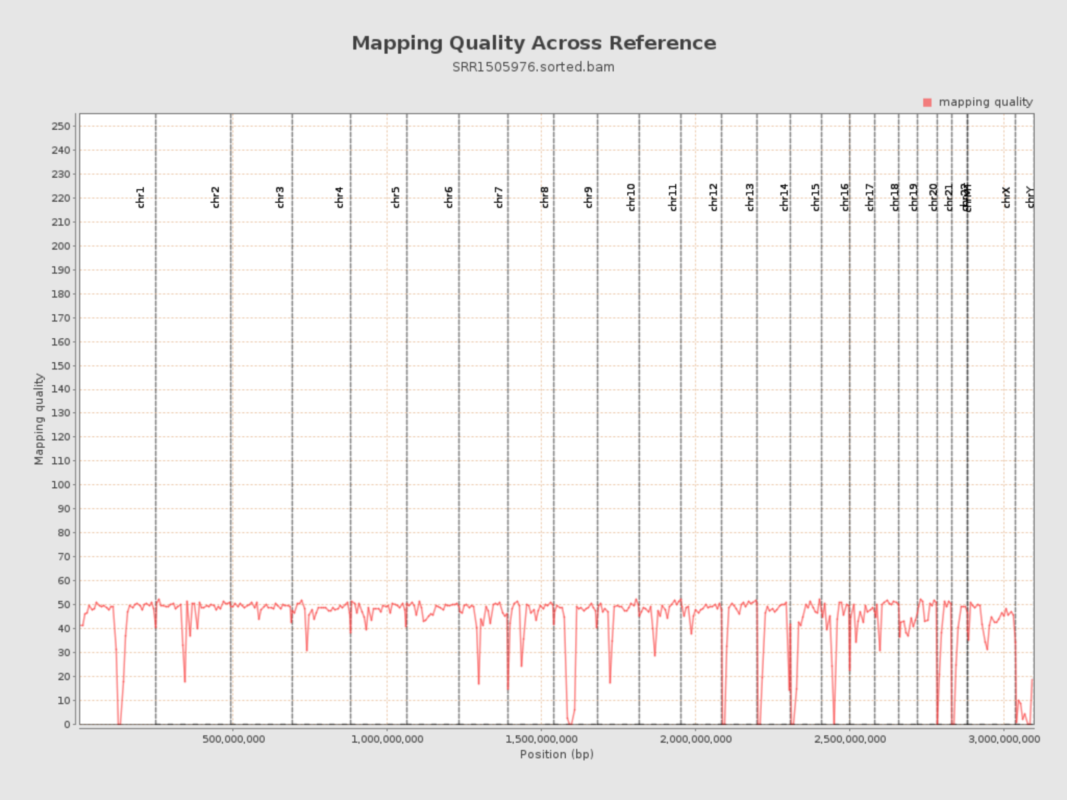
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram