Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 22:33:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004047.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_SRR6004047 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004047.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 22:33:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004047.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,700,896
Mapped reads	2,458,617 / 91.03%
Unmapped reads	242,279 / 8.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	24,125 / 0.89%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	119,624 / 4.43%
Duplication rate	4%
Clipped reads	1,232,323 / 45.63%

2.2. ACGT Content

Number/percentage of A's	44,631,876 / 27.69%
Number/percentage of C's	30,405,292 / 18.86%
Number/percentage of T's	50,110,934 / 31.09%
Number/percentage of G's	36,015,520 / 22.34%
Number/percentage of N's	19,324 / 0.01%
GC Percentage	41.21%

2.3. Coverage

Mean	0.0521

Standard Deviation	0.3855

2.4. Mapping Quality

Mean Mapping Quality	45.44

2.5. Mismatches and indels

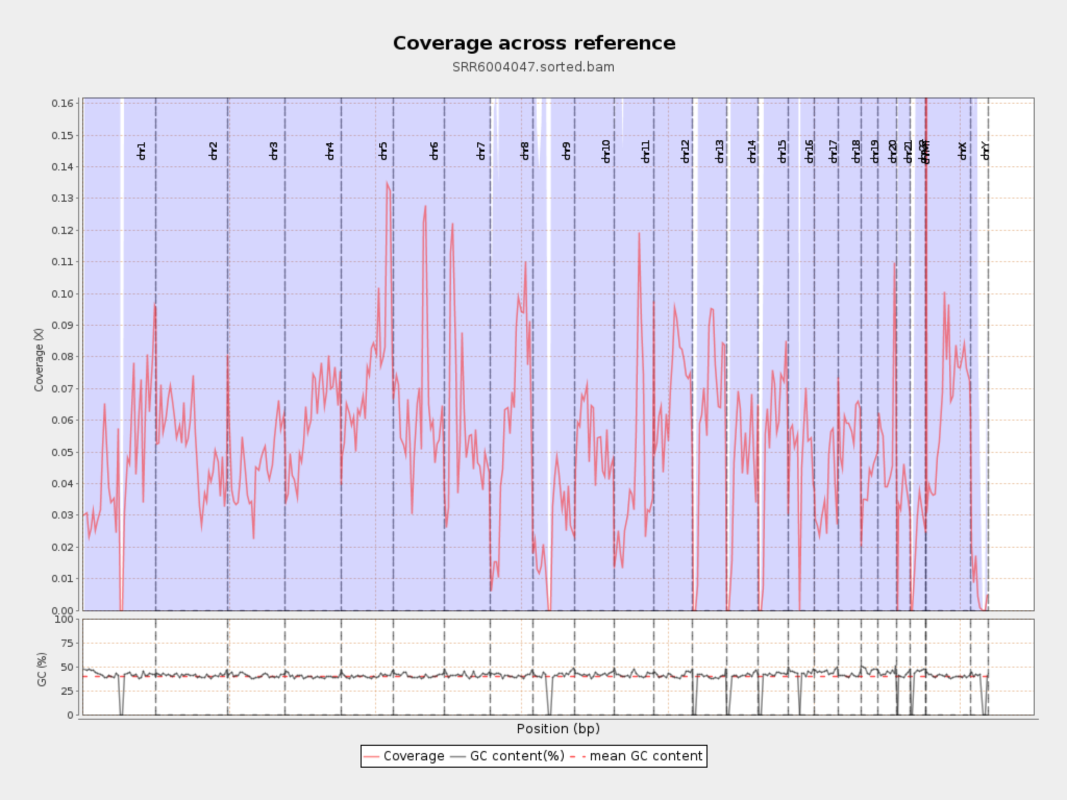
General error rate	0.73%
Mismatches	1,157,605
Insertions	10,866
Mapped reads with at least one insertion	0.44%
Deletions	39,631
Mapped reads with at least one deletion	1.6%
Homopolymer indels	45.3%

2.6. Chromosome stats

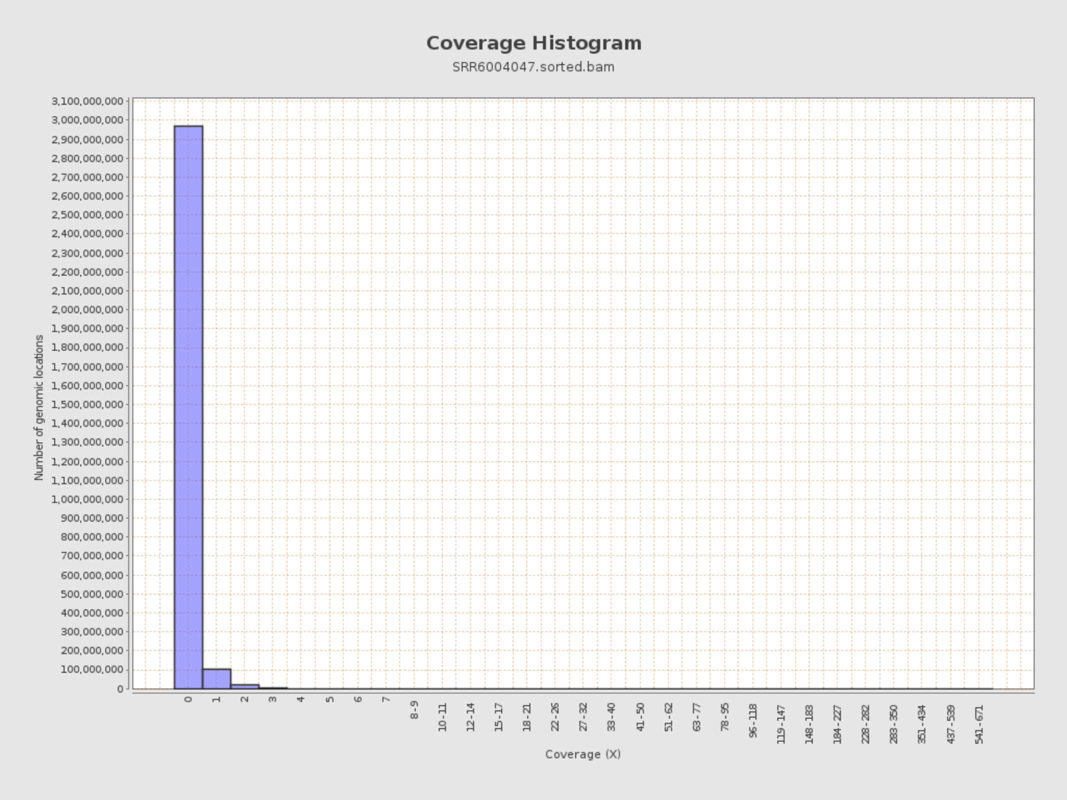
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11328081	0.0454	0.615
chr2	243199373	12547781	0.0516	0.4361
chr3	198022430	9178578	0.0464	0.2575
chr4	191154276	11516059	0.0602	0.3126
chr5	180915260	13647900	0.0754	0.3342
chr6	171115067	10892468	0.0637	0.3374
chr7	159138663	9032423	0.0568	0.6186

chr8	146364022	8858289	0.0605	0.4545
chr9	141213431	3519484	0.0249	0.2649
chr10	135534747	7331857	0.0541	0.3592
chr11	135006516	5516445	0.0409	0.3546
chr12	133851895	9337948	0.0698	0.3202
chr13	115169878	7135444	0.062	0.3011
chr14	107349540	4702811	0.0438	0.2559
chr15	102531392	5405108	0.0527	0.2907
chr16	90354753	4371729	0.0484	0.2767
chr17	81195210	2975892	0.0367	0.2458
chr18	78077248	4543155	0.0582	0.4826
chr19	59128983	2392456	0.0405	0.4682
chr20	63025520	3643274	0.0578	0.2949
chr21	48129895	1600454	0.0333	0.2331
chr22	51304566	1127964	0.022	0.175
chrMT	16571	20200	1.219	1.438
chrX	155270560	10243791	0.066	0.3437
chrY	59373566	382776	0.0064	0.1264

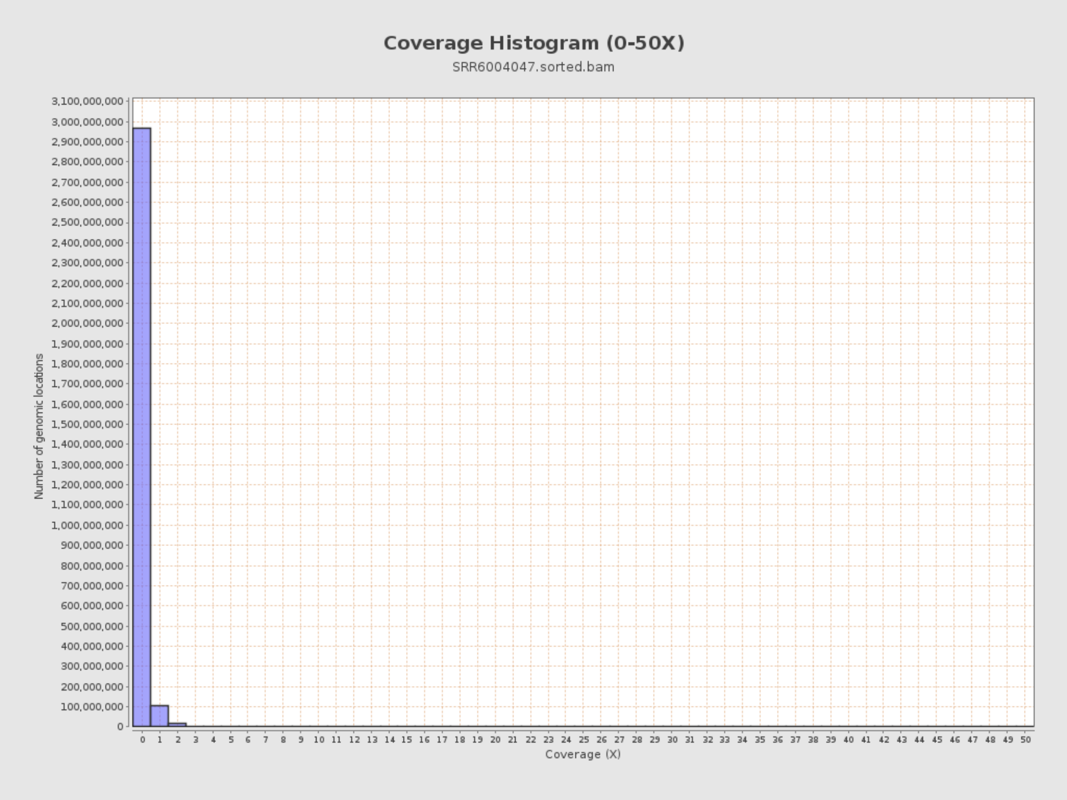
3. Results : Coverage across reference



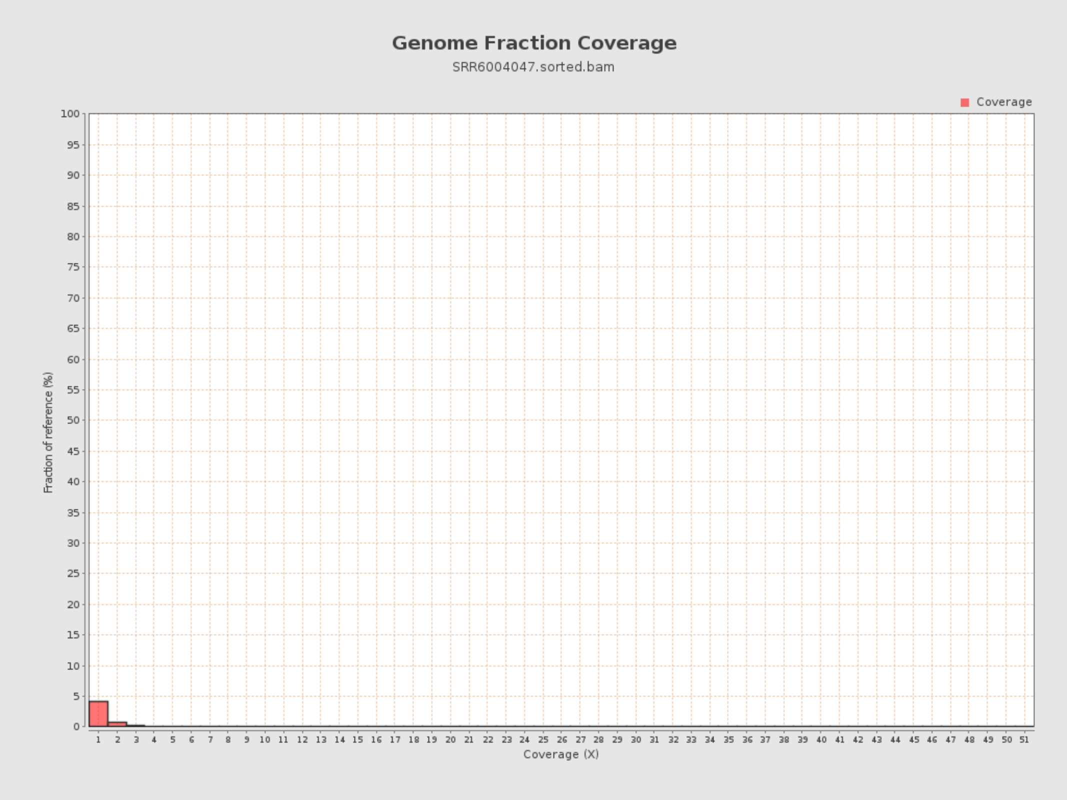
4. Results : Coverage Histogram



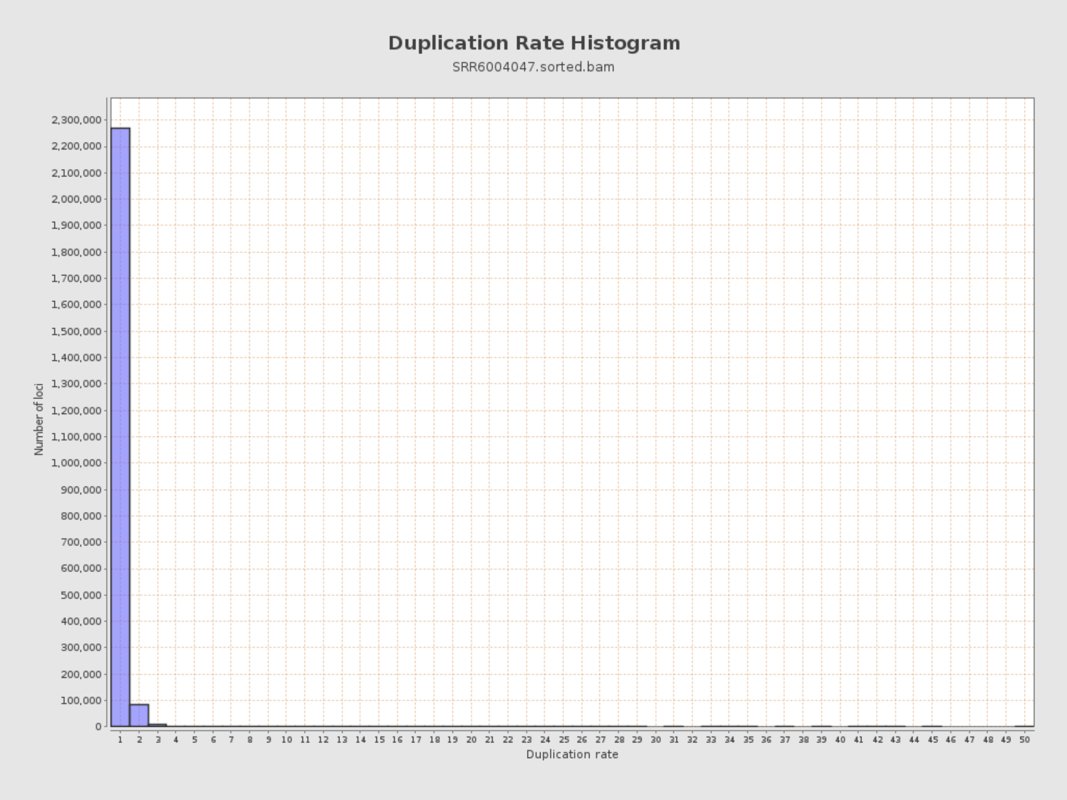
5. Results : Coverage Histogram (0-50X)



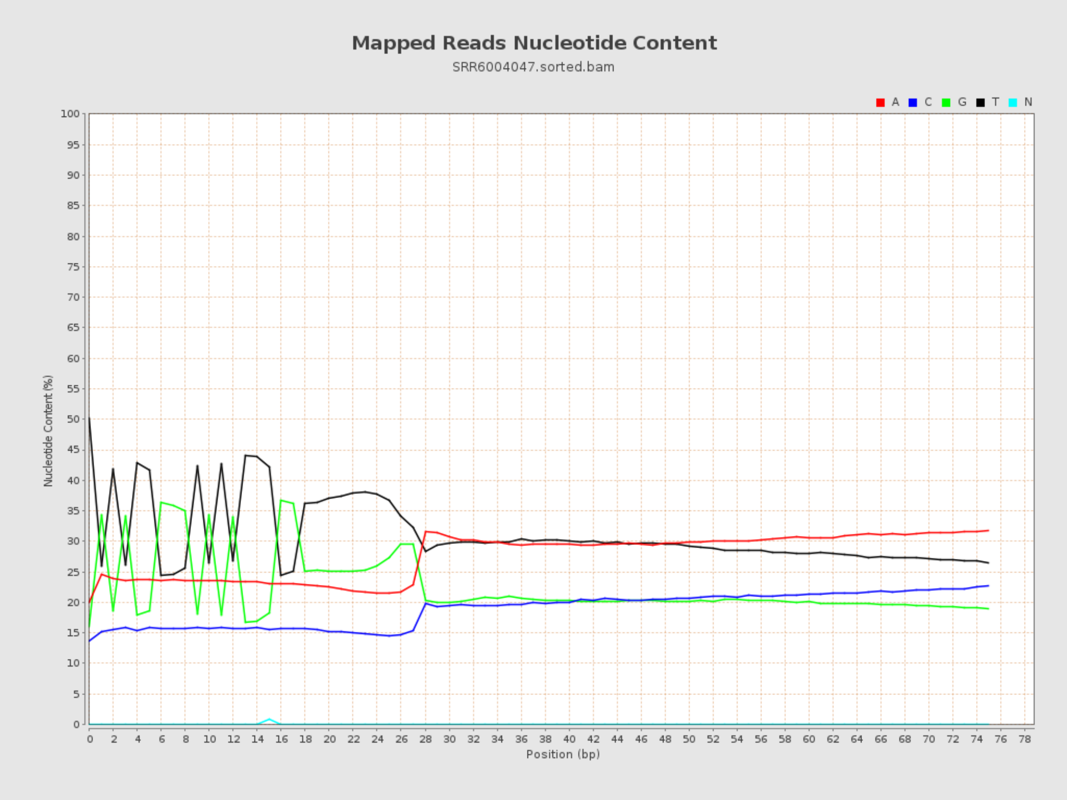
6. Results : Genome Fraction Coverage



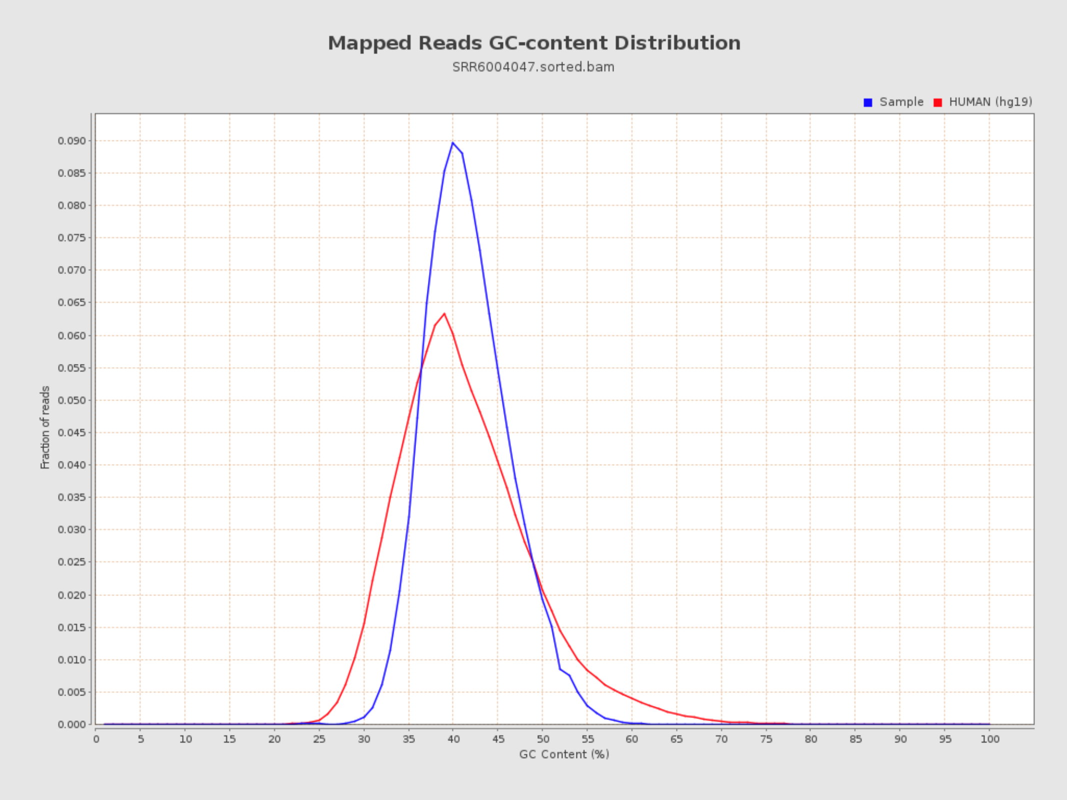
7. Results : Duplication Rate Histogram



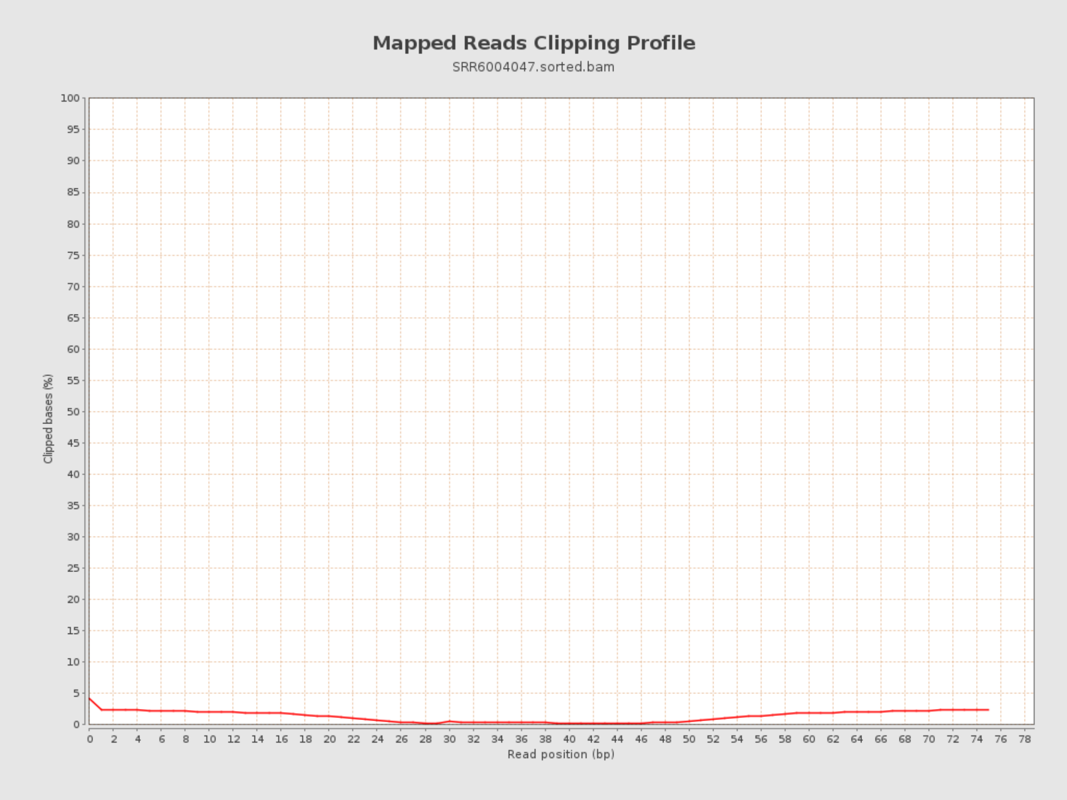
8. Results : Mapped Reads Nucleotide Content



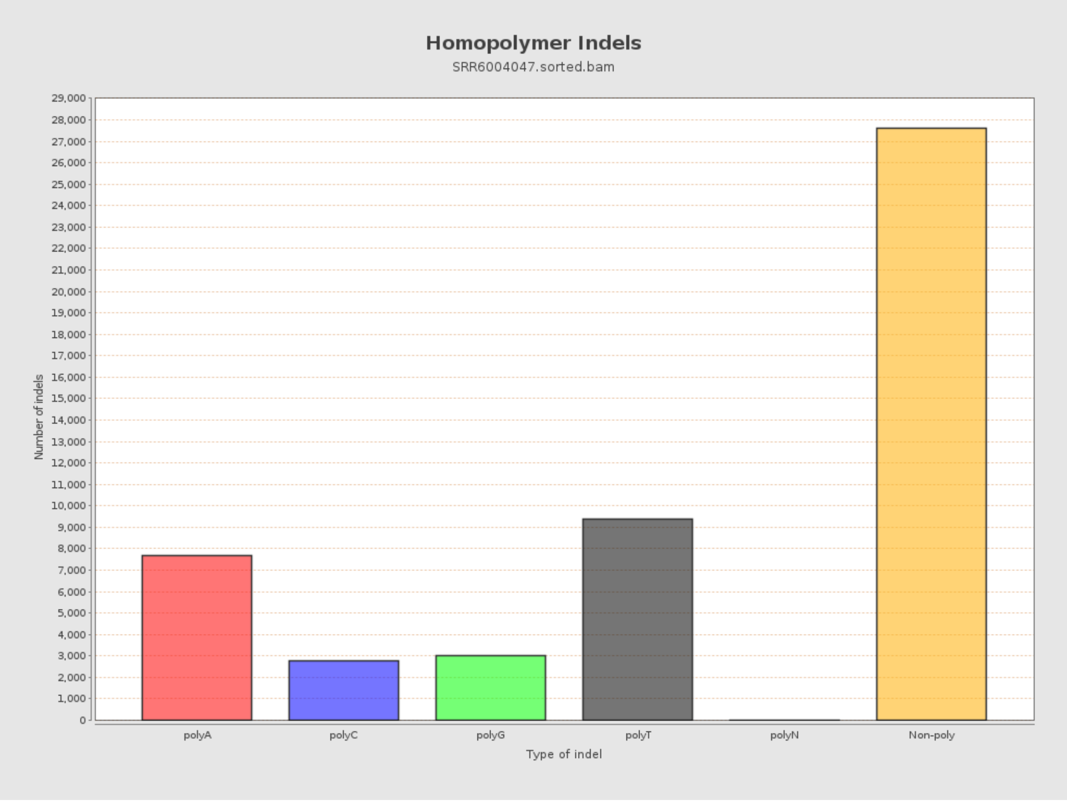
9. Results : Mapped Reads GC-content Distribution



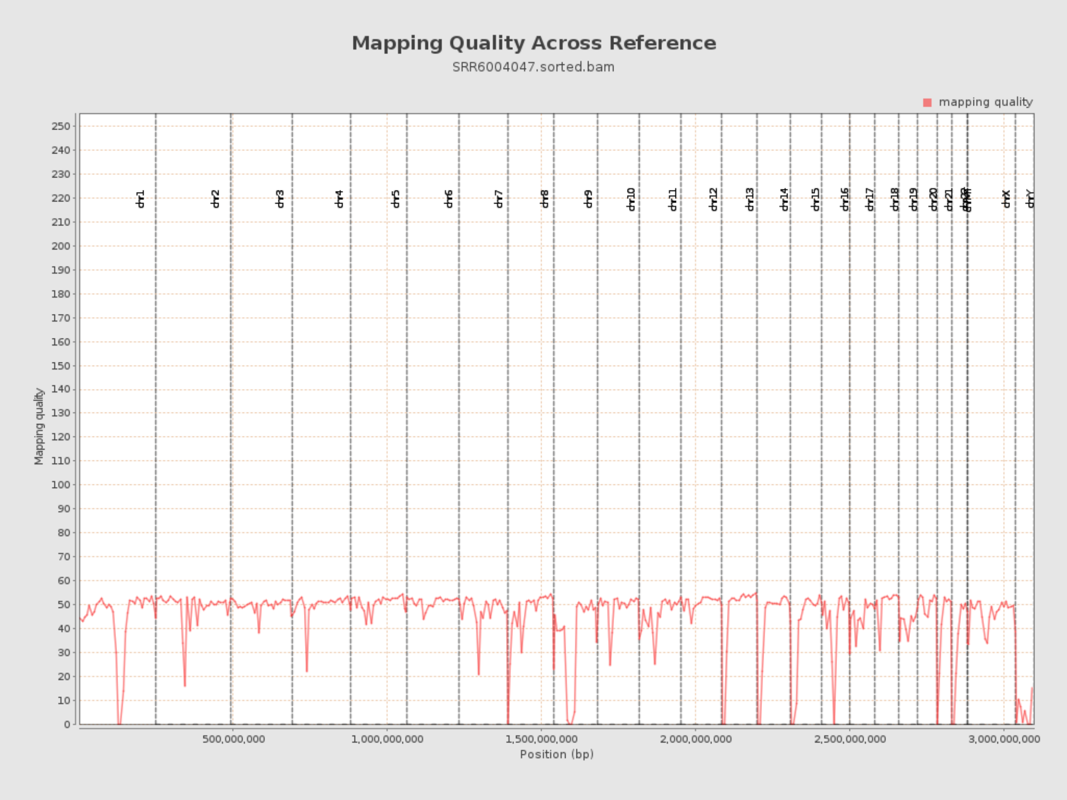
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram