Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:07:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004002.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_SRR6004002 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004002.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:07:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,683,337
Mapped reads	3,357,832 / 91.16%
Unmapped reads	325,505 / 8.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,759 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	126,885 / 3.44%
Duplication rate	2.57%
Clipped reads	1,661,618 / 45.11%

2.2. ACGT Content

Number/percentage of A's	59,387,631 / 26.92%
Number/percentage of C's	42,547,824 / 19.28%
Number/percentage of T's	66,928,273 / 30.33%
Number/percentage of G's	51,726,453 / 23.44%
Number/percentage of N's	42,817 / 0.02%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0713

Standard Deviation	0.5954

2.4. Mapping Quality

Mean Mapping Quality	42.91

2.5. Mismatches and indels

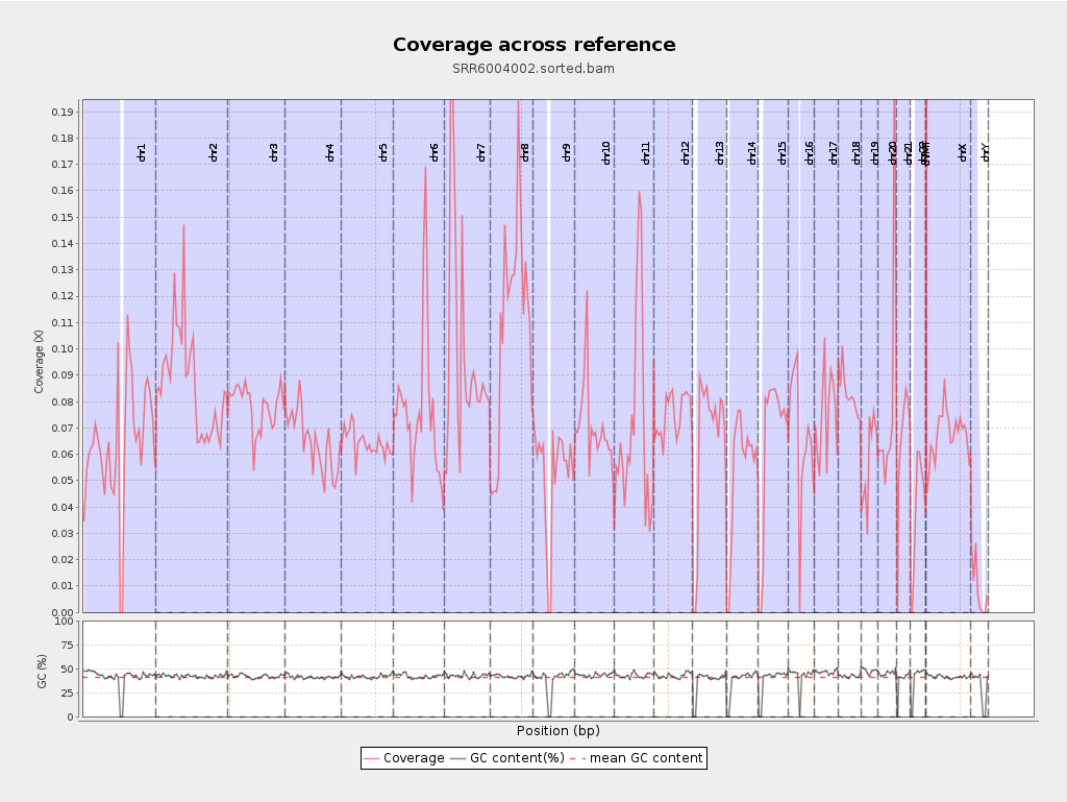
General error rate	0.84%
Mismatches	1,831,402
Insertions	17,635
Mapped reads with at least one insertion	0.52%
Deletions	56,812
Mapped reads with at least one deletion	1.67%
Homopolymer indels	45.55%

2.6. Chromosome stats

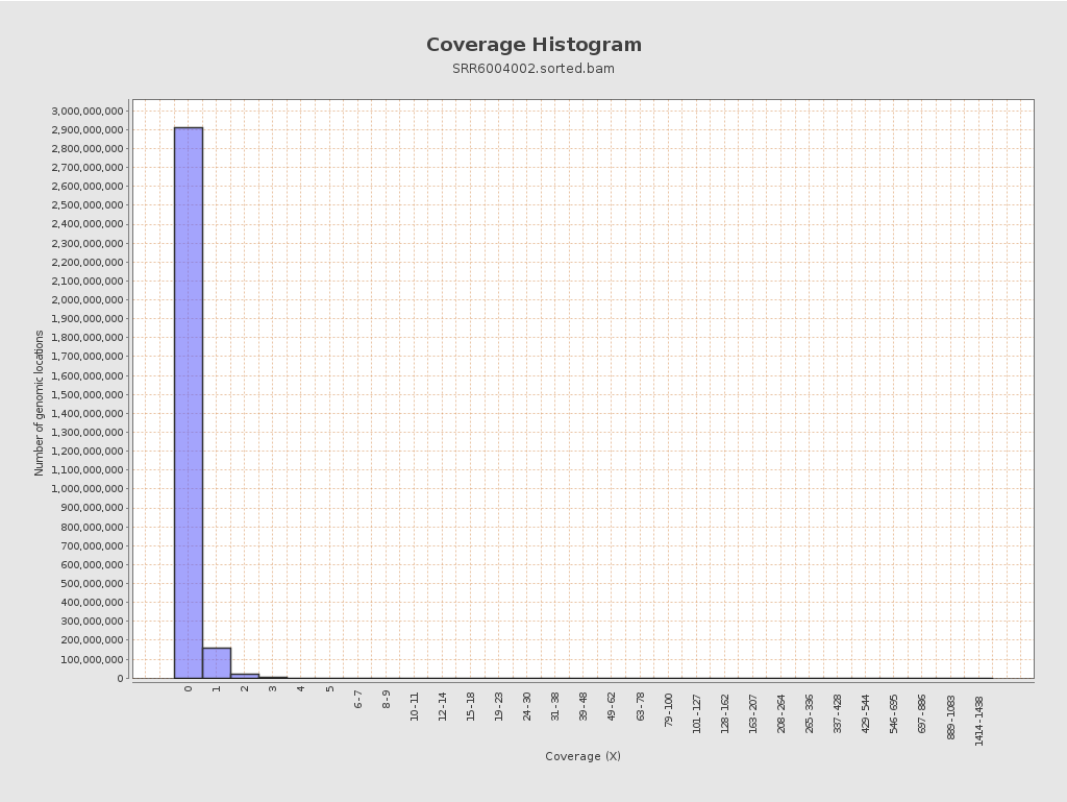
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15842815	0.0636	0.9689
chr2	243199373	21057023	0.0866	0.8484
chr3	198022430	15533730	0.0784	0.3246
chr4	191154276	12428917	0.065	0.3201
chr5	180915260	11620312	0.0642	0.2914
chr6	171115067	13068849	0.0764	0.3949
chr7	159138663	15385945	0.0967	1.1175

chr8	146364022	16021156	0.1095	0.6082
chr9	141213431	7384343	0.0523	0.5287
chr10	135534747	9551958	0.0705	0.5804
chr11	135006516	9426734	0.0698	0.4786
chr12	133851895	10076253	0.0753	0.3219
chr13	115169878	7521951	0.0653	0.2928
chr14	107349540	5883991	0.0548	0.3405
chr15	102531392	6539087	0.0638	0.3147
chr16	90354753	5925291	0.0656	0.3632
chr17	81195210	6059225	0.0746	0.3633
chr18	78077248	6509472	0.0834	1.0837
chr19	59128983	3379773	0.0572	0.783
chr20	63025520	5309333	0.0842	0.3685
chr21	48129895	3119107	0.0648	0.3269
chr22	51304566	1981630	0.0386	0.2255
chrMT	16571	110654	6.6776	4.577
chrX	155270560	10445512	0.0673	0.3605
chrY	59373566	543463	0.0092	0.1717

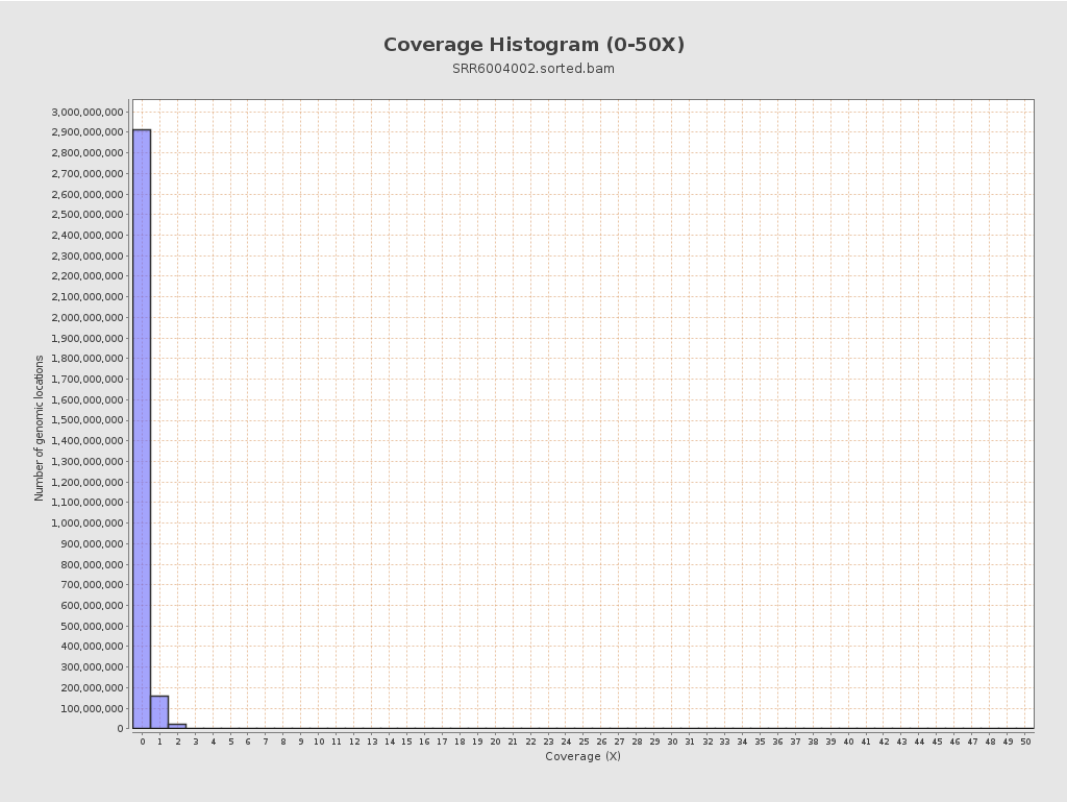
3. Results : Coverage across reference



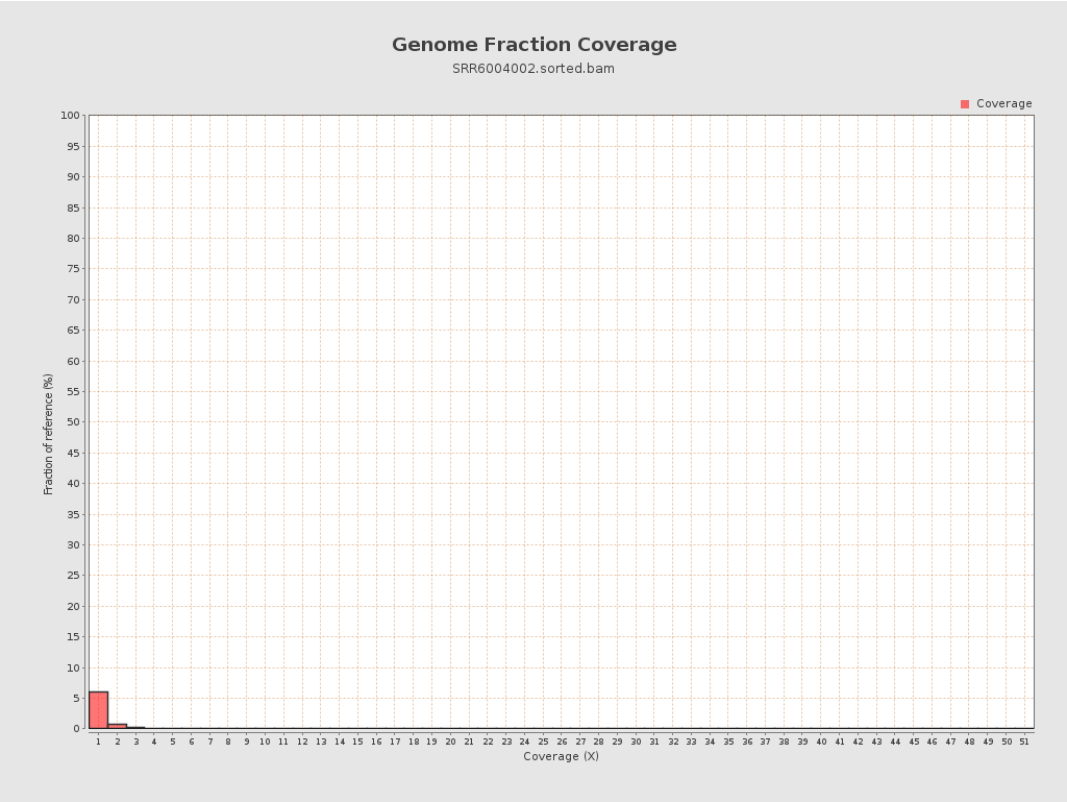
4. Results : Coverage Histogram



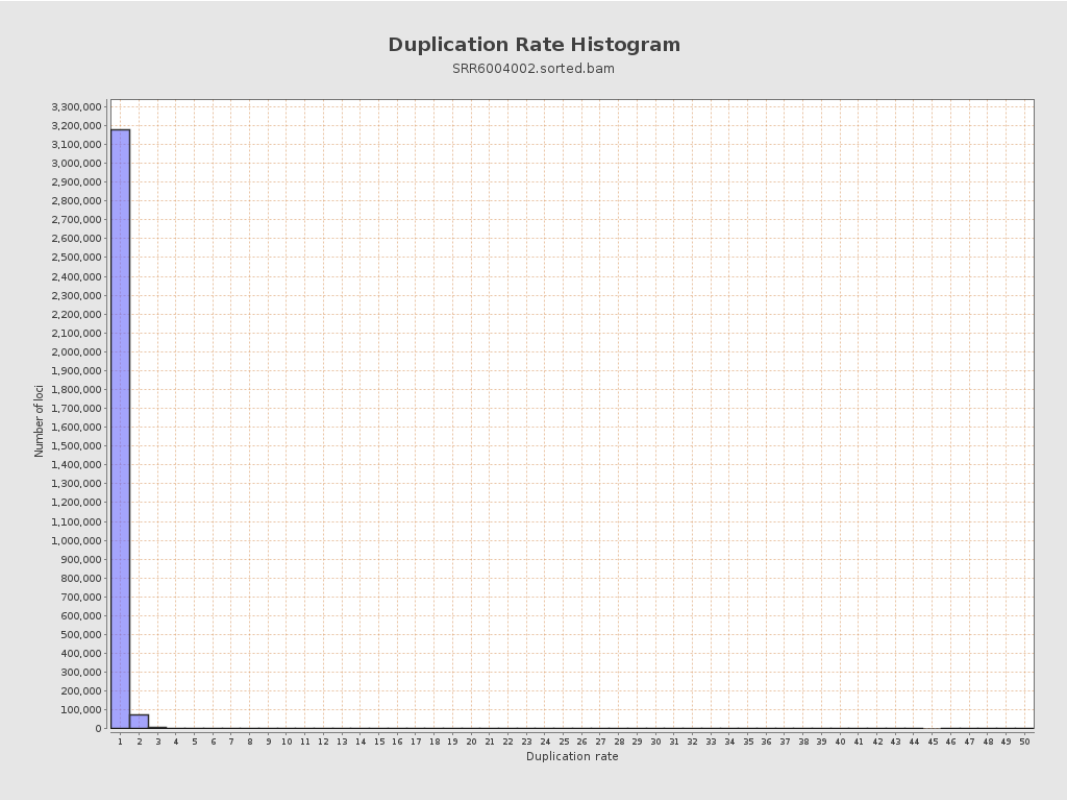
5. Results : Coverage Histogram (0-50X)



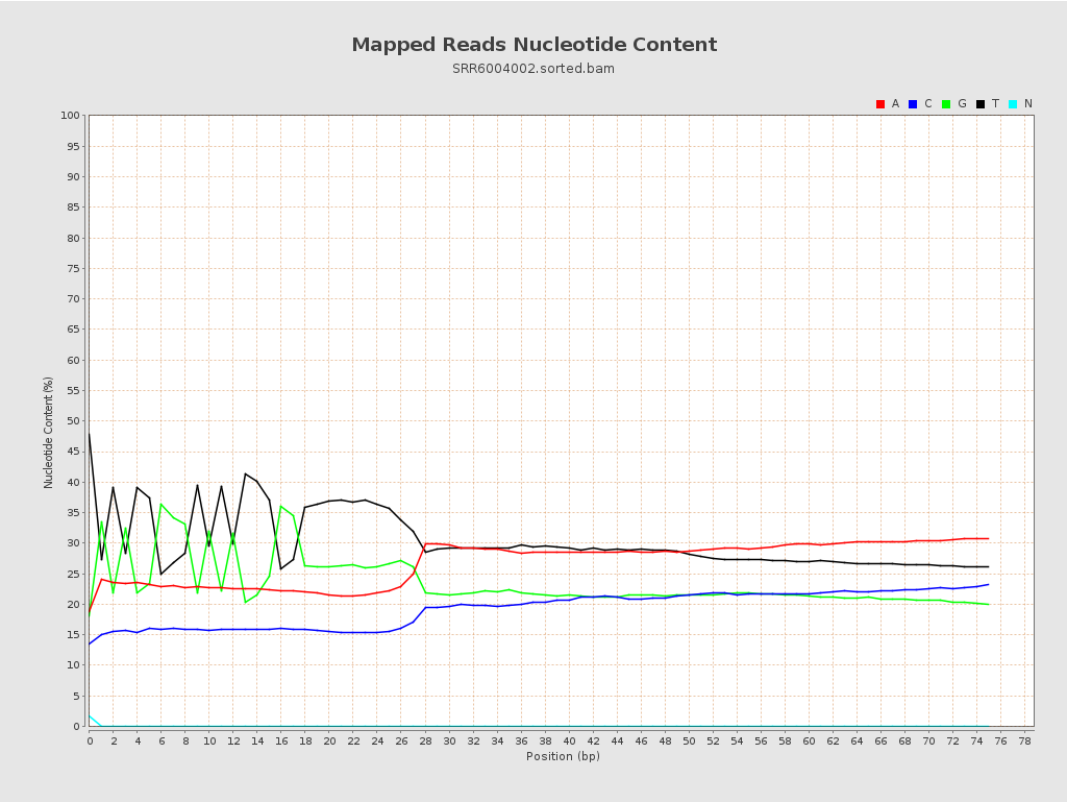
6. Results : Genome Fraction Coverage



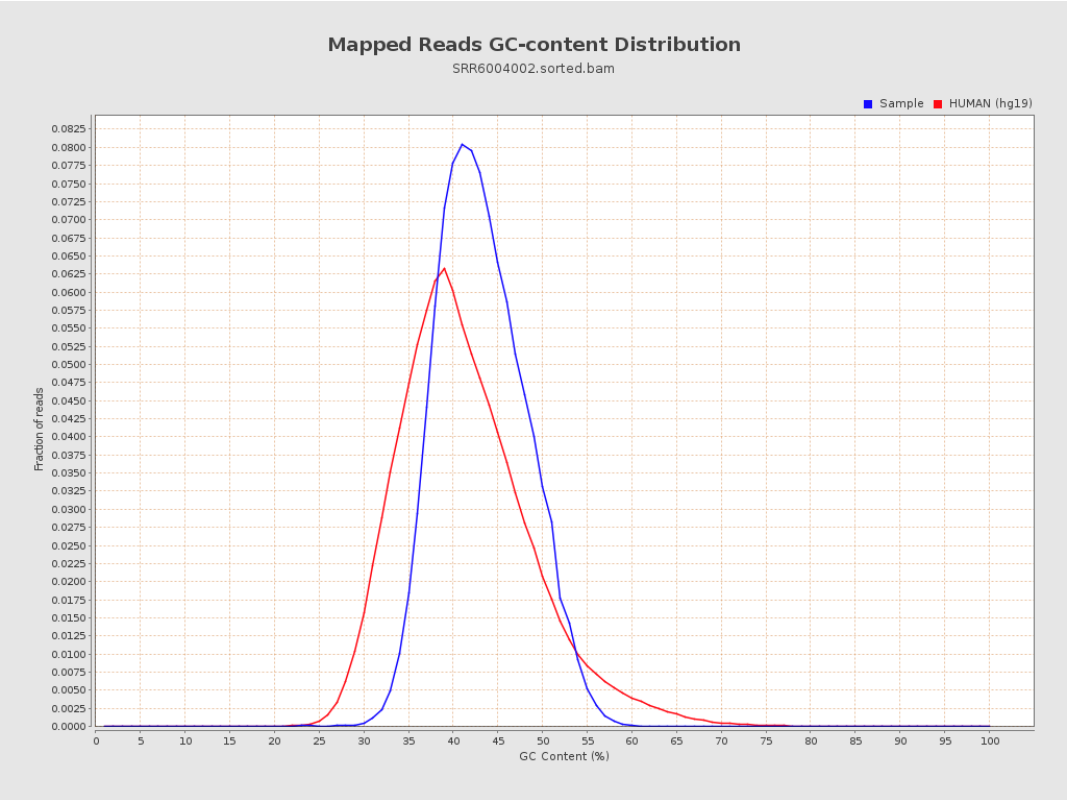
7. Results : Duplication Rate Histogram



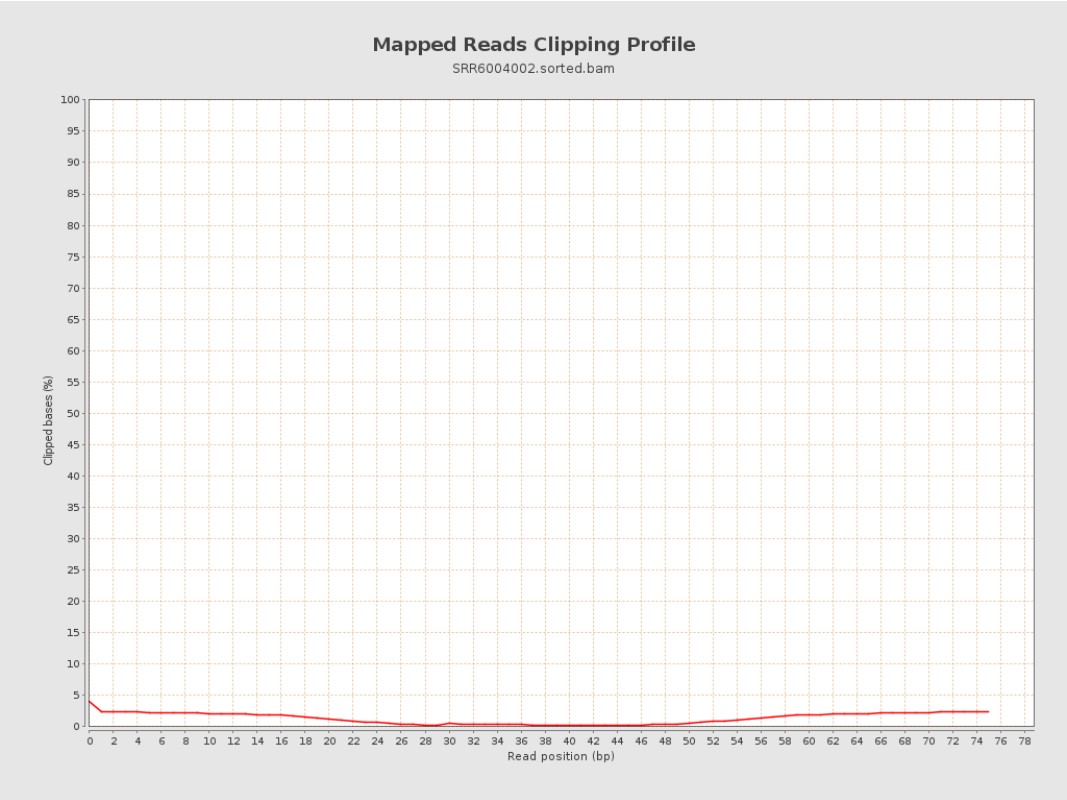
8. Results : Mapped Reads Nucleotide Content



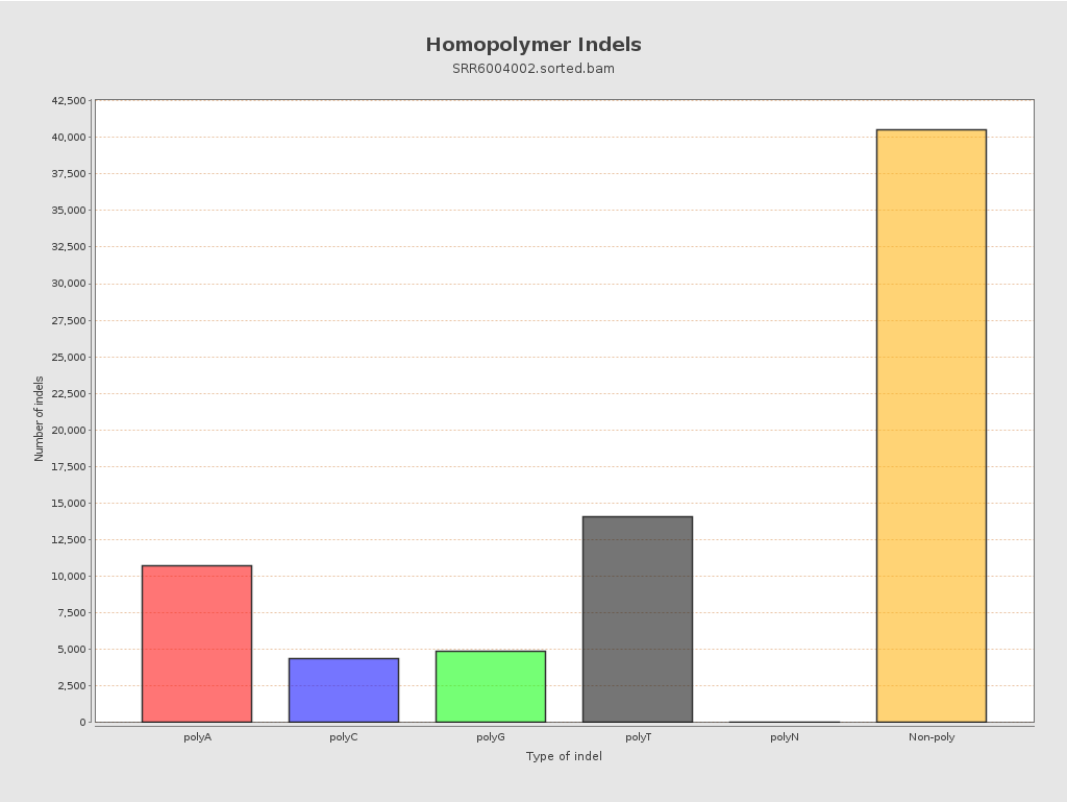
9. Results : Mapped Reads GC-content Distribution



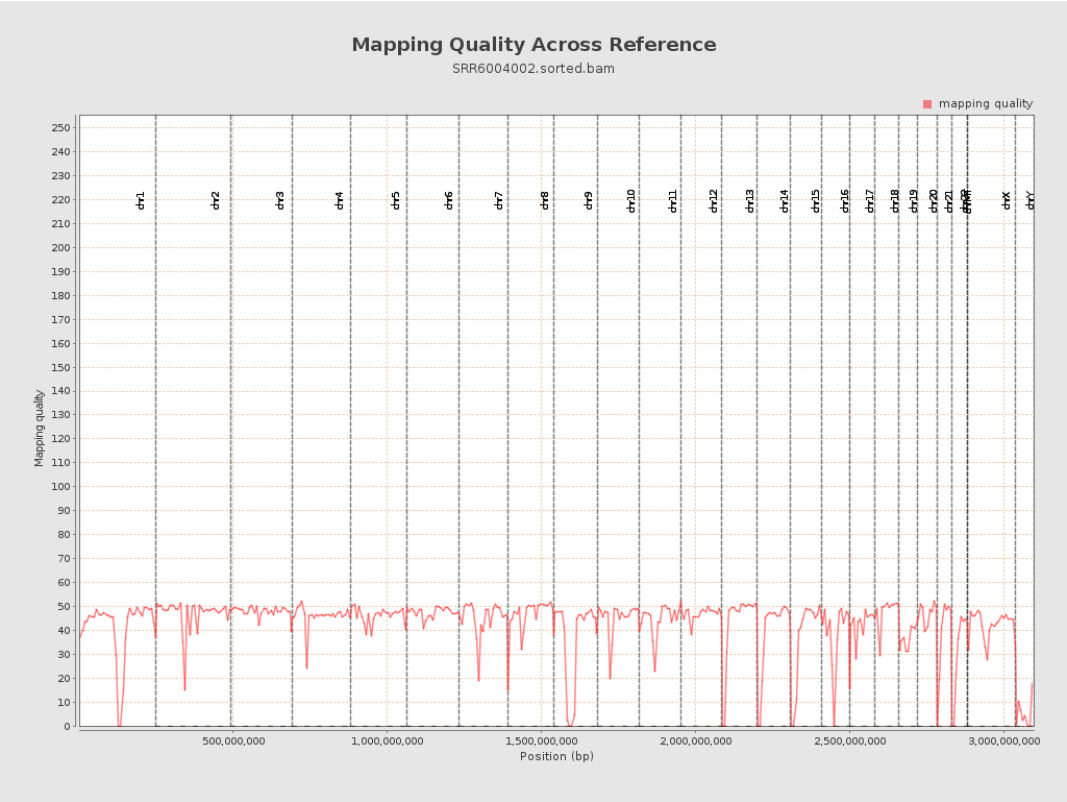
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram