Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 23:45:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525219.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_SRR10525219 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525219.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 23:45:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525219.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,301,072
Mapped reads	1,190,258 / 91.48%
Unmapped reads	110,814 / 8.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,339 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	32,344 / 2.49%
Duplication rate	1.91%
Clipped reads	1,192,813 / 91.68%

2.2. ACGT Content

Number/percentage of A's	17,804,390 / 25.23%
Number/percentage of C's	13,963,799 / 19.79%
Number/percentage of T's	21,678,021 / 30.72%
Number/percentage of G's	17,110,003 / 24.25%
Number/percentage of N's	1,797 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0228

Standard Deviation	0.2377

2.4. Mapping Quality

Mean Mapping Quality	45.26

2.5. Mismatches and indels

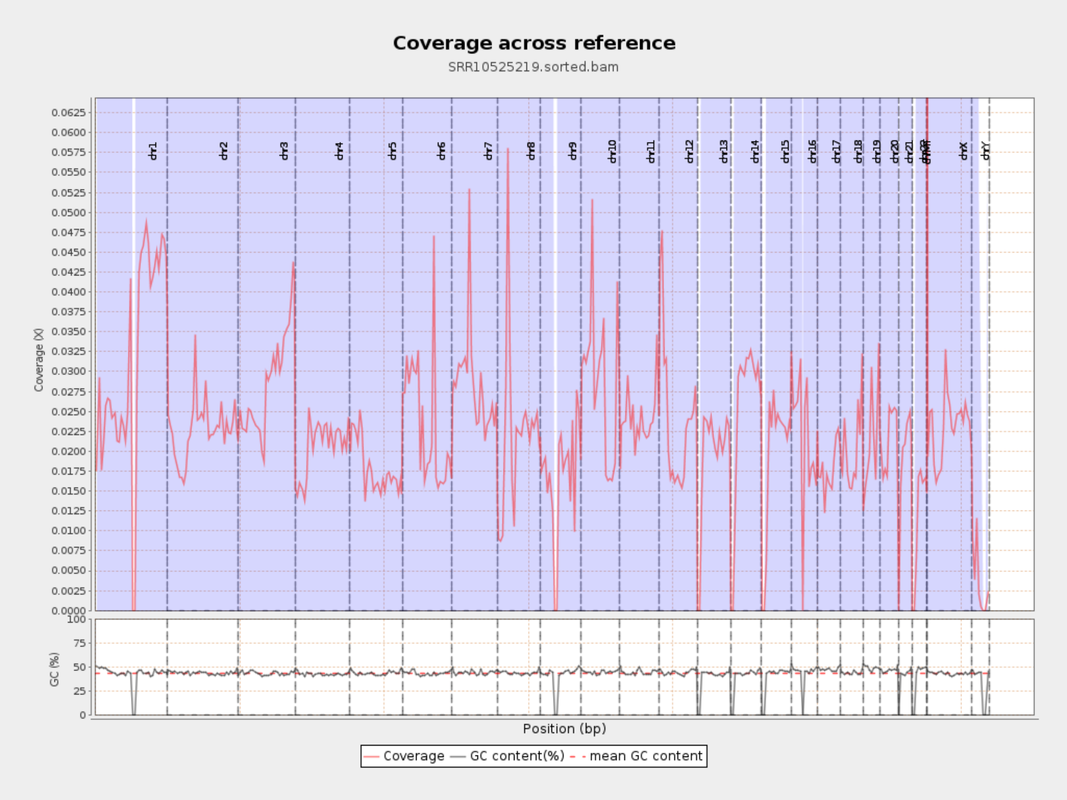
General error rate	0.51%
Mismatches	351,655
Insertions	4,162
Mapped reads with at least one insertion	0.35%
Deletions	14,405
Mapped reads with at least one deletion	1.2%
Homopolymer indels	43.66%

2.6. Chromosome stats

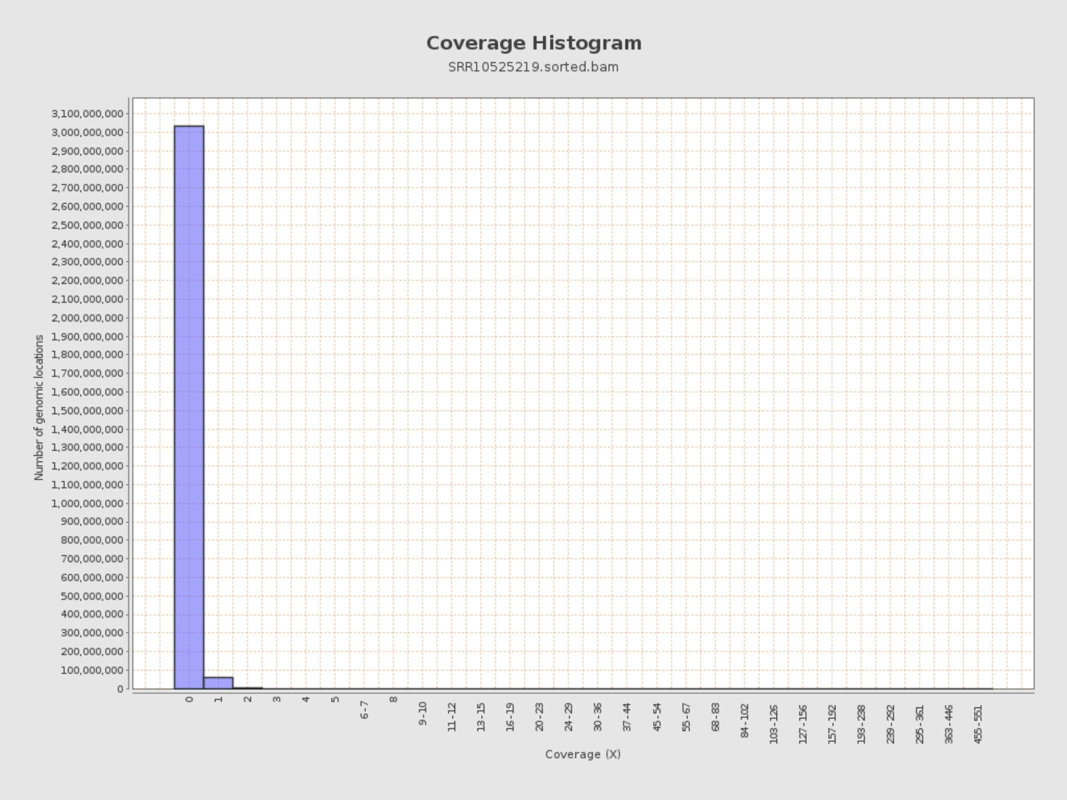
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7797012	0.0313	0.4398
chr2	243199373	5513021	0.0227	0.2768
chr3	198022430	5624625	0.0284	0.1807
chr4	191154276	3942211	0.0206	0.158
chr5	180915260	3248217	0.018	0.1421
chr6	171115067	4040603	0.0236	0.1848
chr7	159138663	4529398	0.0285	0.4057

chr8	146364022	3272819	0.0224	0.1866
chr9	141213431	2356138	0.0167	0.1666
chr10	135534747	3916572	0.0289	0.263
chr11	135006516	3260476	0.0242	0.1947
chr12	133851895	3243137	0.0242	0.166
chr13	115169878	2218708	0.0193	0.1491
chr14	107349540	2707609	0.0252	0.1716
chr15	102531392	1975889	0.0193	0.1468
chr16	90354753	1957065	0.0217	0.1711
chr17	81195210	1449516	0.0179	0.1467
chr18	78077248	1550994	0.0199	0.3189
chr19	59128983	1284442	0.0217	0.295
chr20	63025520	1344613	0.0213	0.1562
chr21	48129895	924603	0.0192	0.1516
chr22	51304566	601521	0.0117	0.1143
chrMT	16571	4541	0.274	0.5563
chrX	155270560	3613209	0.0233	0.1711
chrY	59373566	204635	0.0034	0.1007

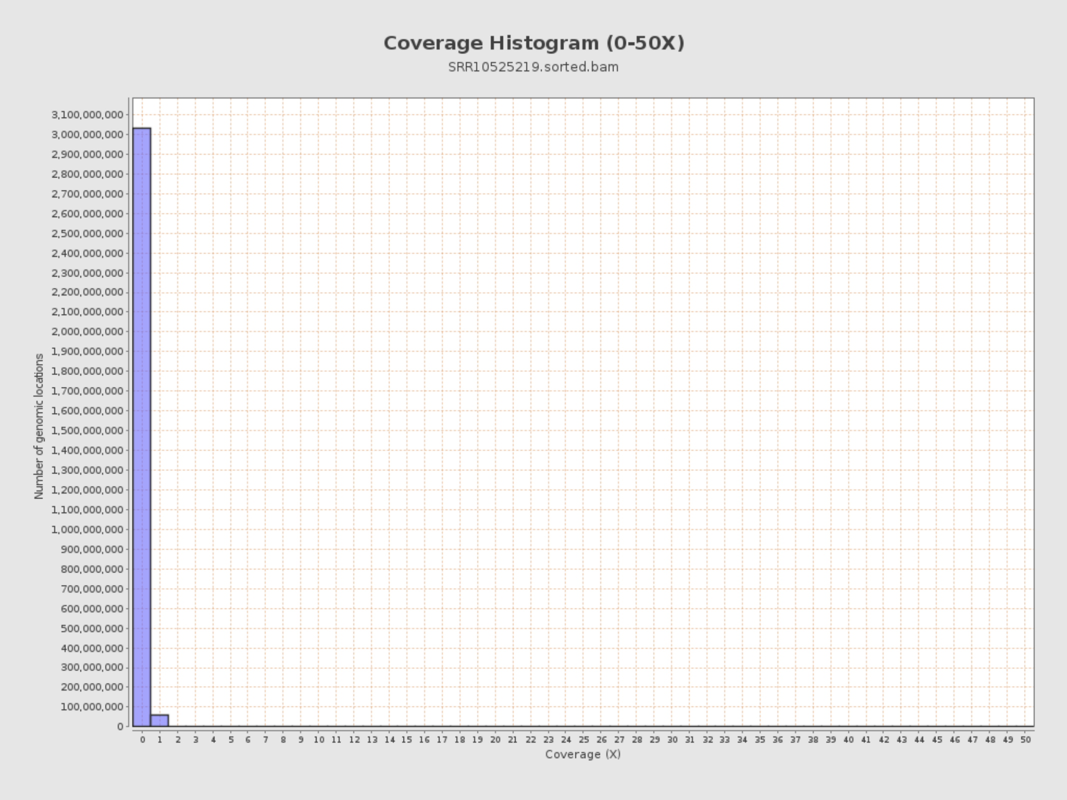
3. Results : Coverage across reference



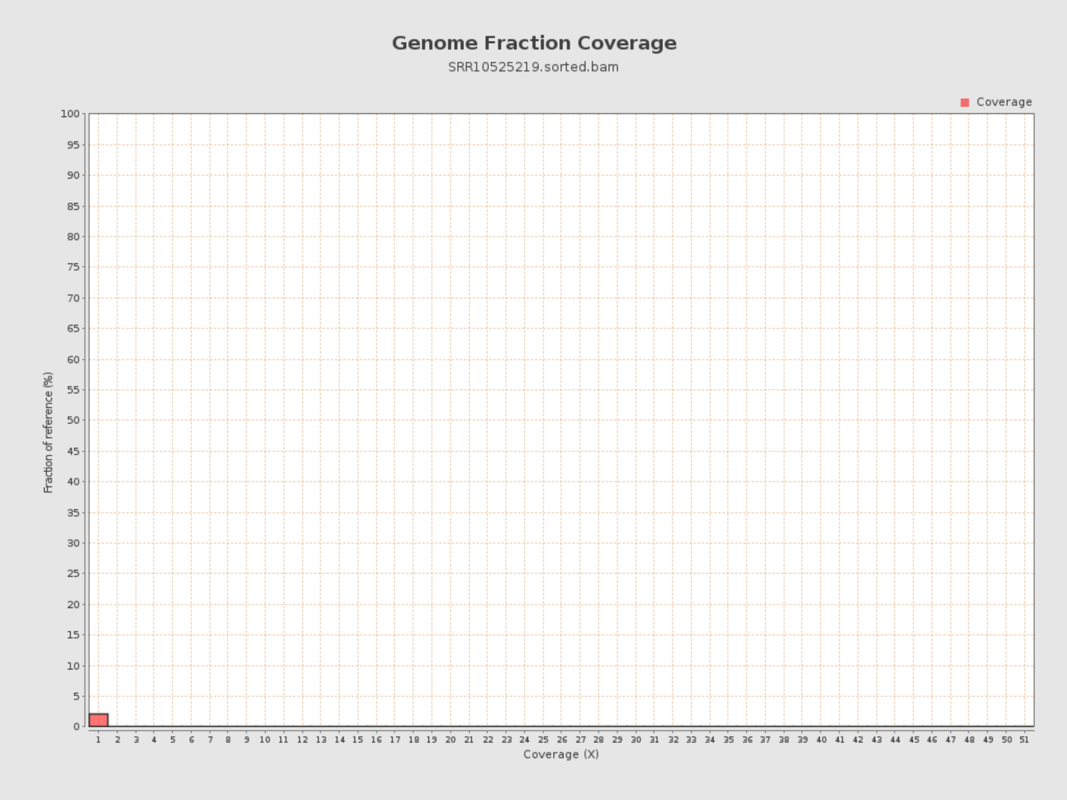
4. Results : Coverage Histogram



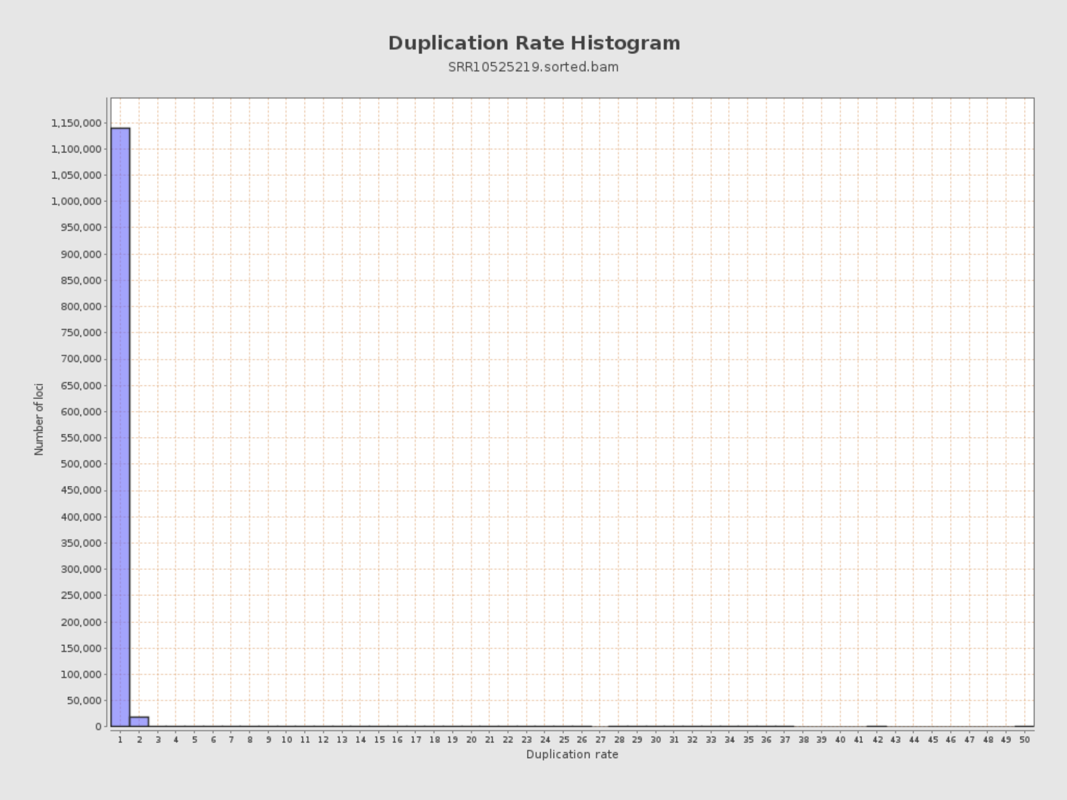
5. Results : Coverage Histogram (0-50X)



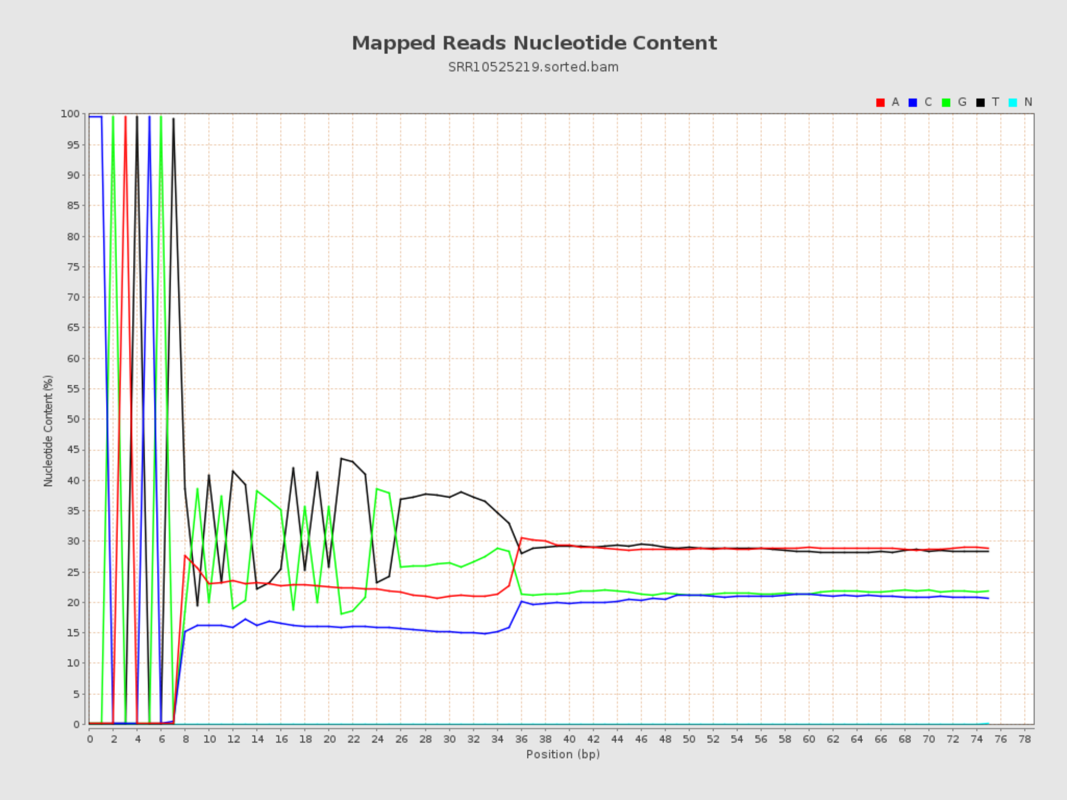
6. Results : Genome Fraction Coverage



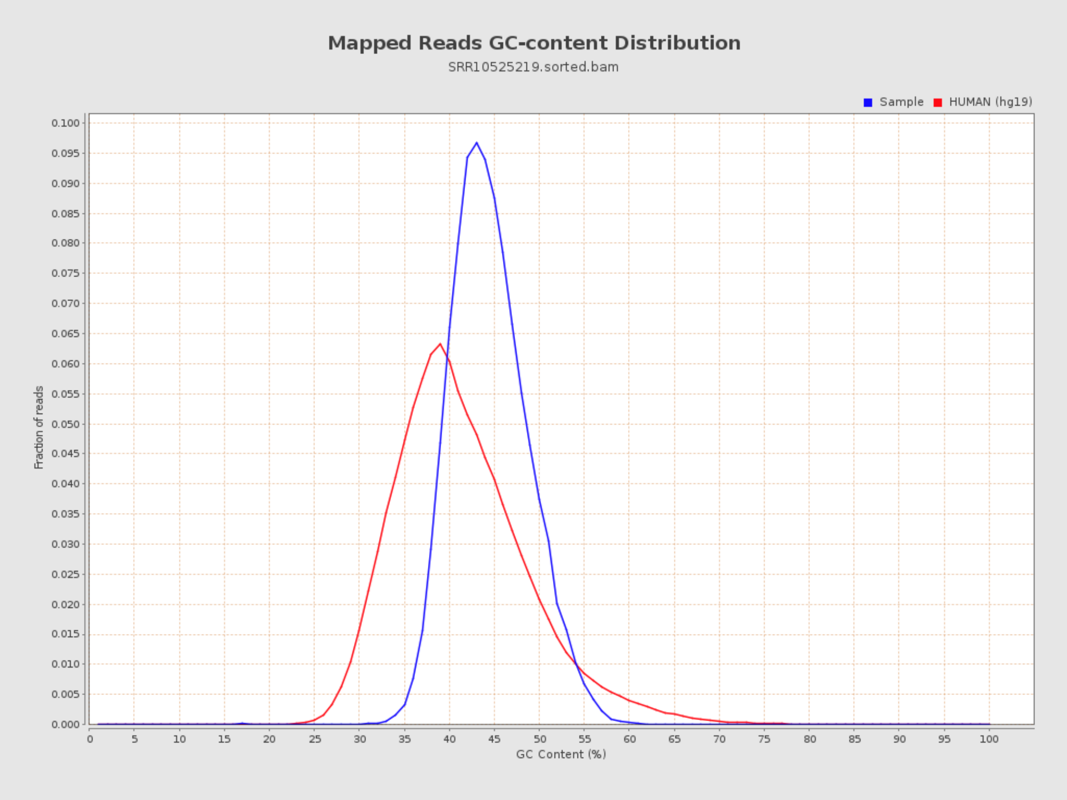
7. Results : Duplication Rate Histogram



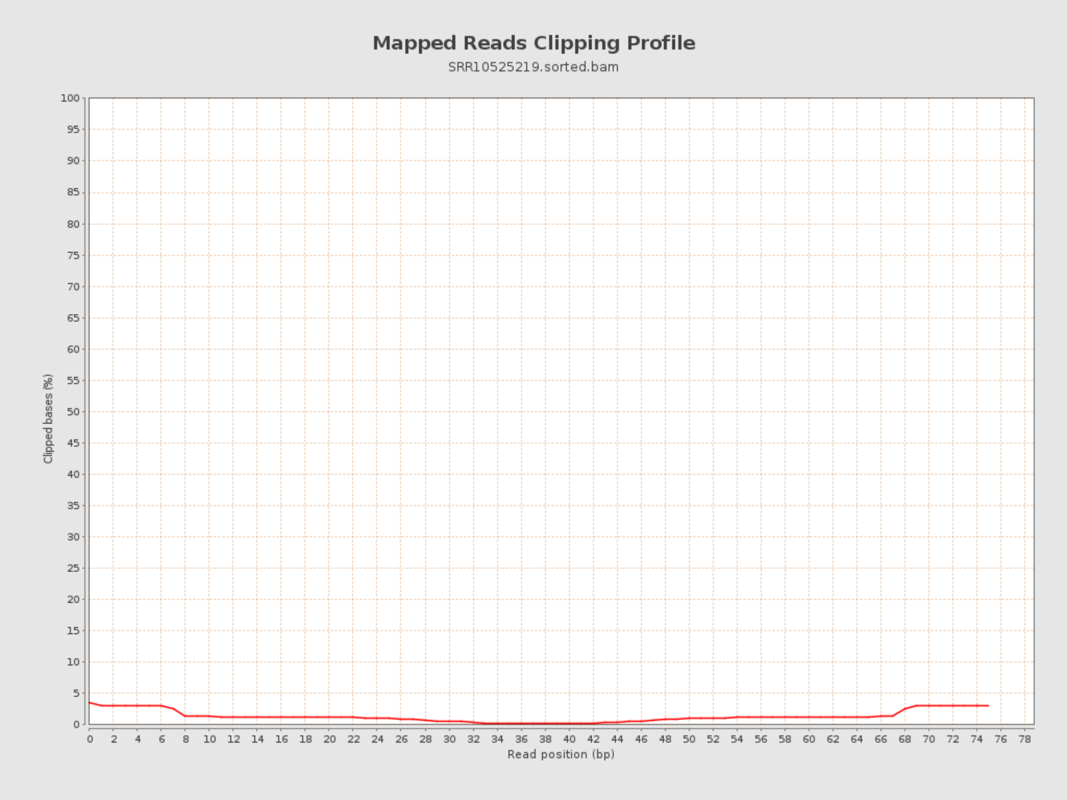
8. Results : Mapped Reads Nucleotide Content



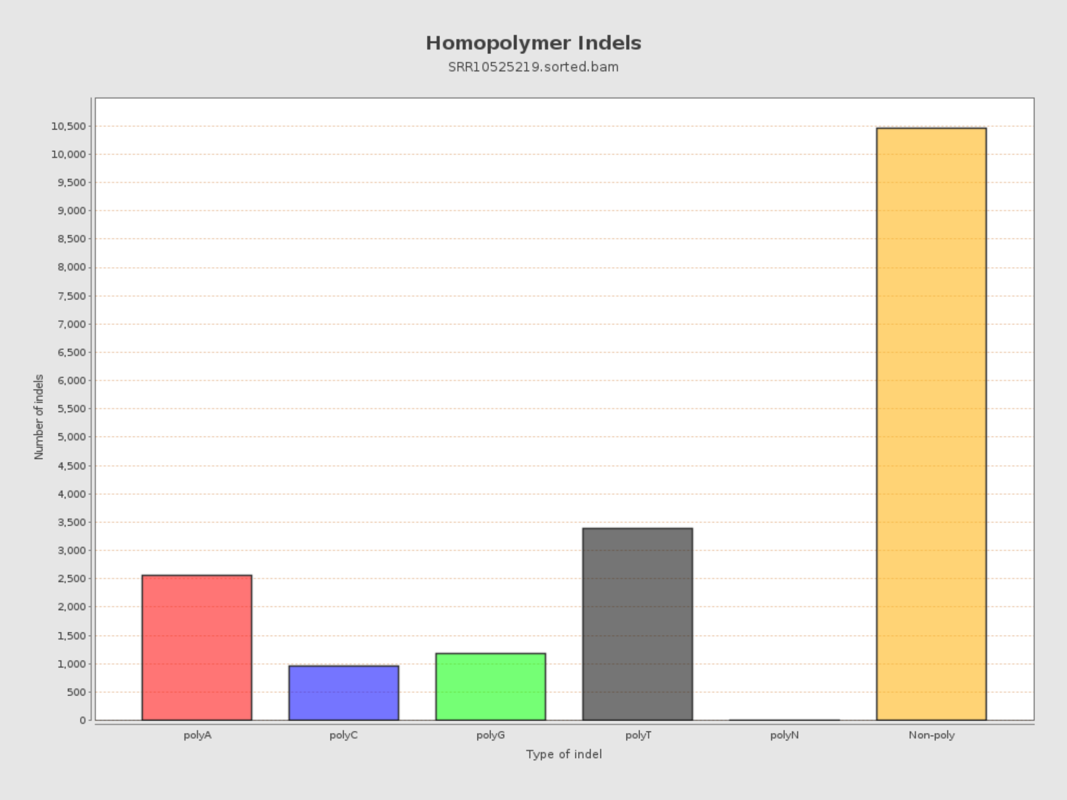
9. Results : Mapped Reads GC-content Distribution



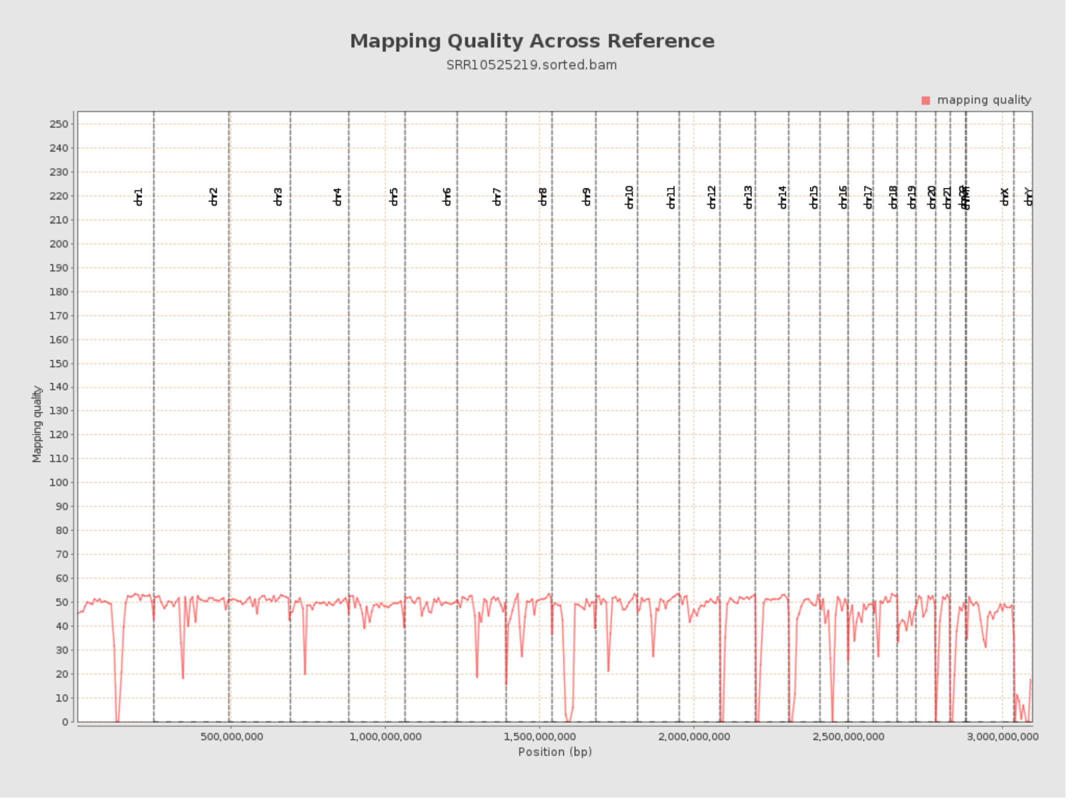
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram