Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:04:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524468.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_SRR10524468 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524468.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:04:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524468.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,409,019
Mapped reads	1,300,832 / 92.32%
Unmapped reads	108,187 / 7.68%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,772 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	52,835 / 3.75%
Duplication rate	3.1%
Clipped reads	1,300,697 / 92.31%

2.2. ACGT Content

Number/percentage of A's	18,751,423 / 24.79%
Number/percentage of C's	14,033,486 / 18.55%
Number/percentage of T's	24,269,855 / 32.08%
Number/percentage of G's	18,588,245 / 24.57%
Number/percentage of N's	1,578 / 0%
GC Percentage	43.13%

2.3. Coverage

Mean	0.0244

Standard Deviation	0.2413

2.4. Mapping Quality

Mean Mapping Quality	45.31

2.5. Mismatches and indels

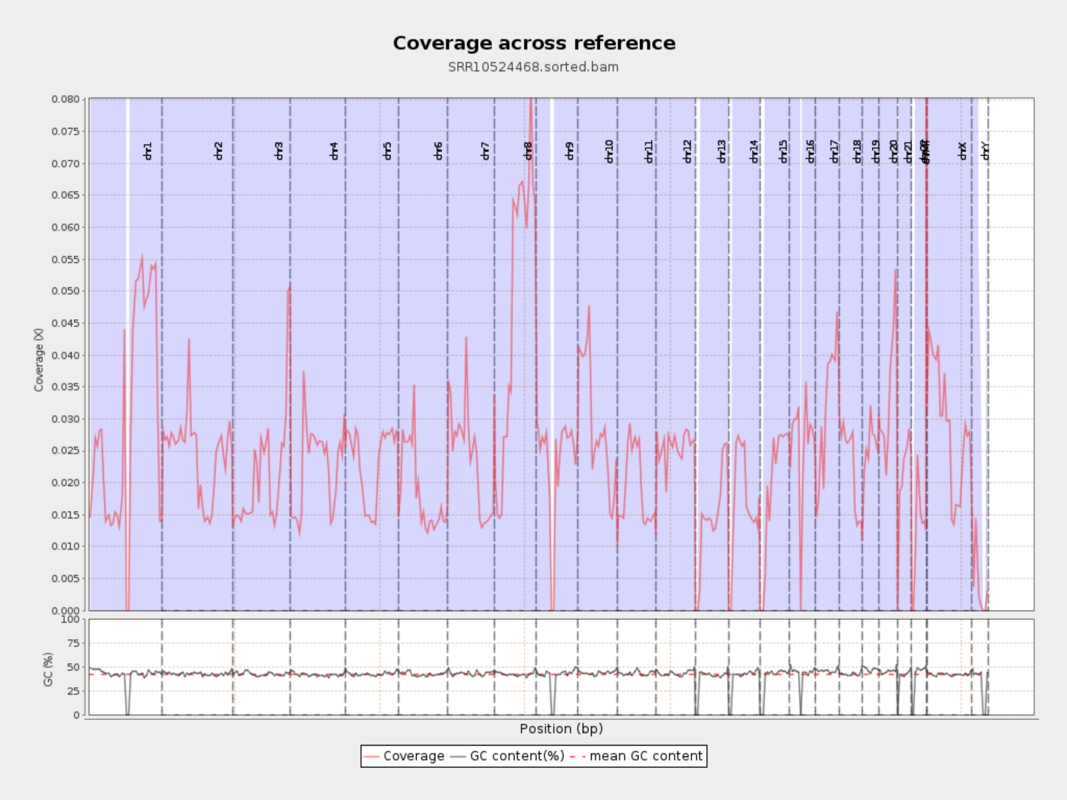
General error rate	0.48%
Mismatches	354,004
Insertions	4,819
Mapped reads with at least one insertion	0.37%
Deletions	13,899
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.05%

2.6. Chromosome stats

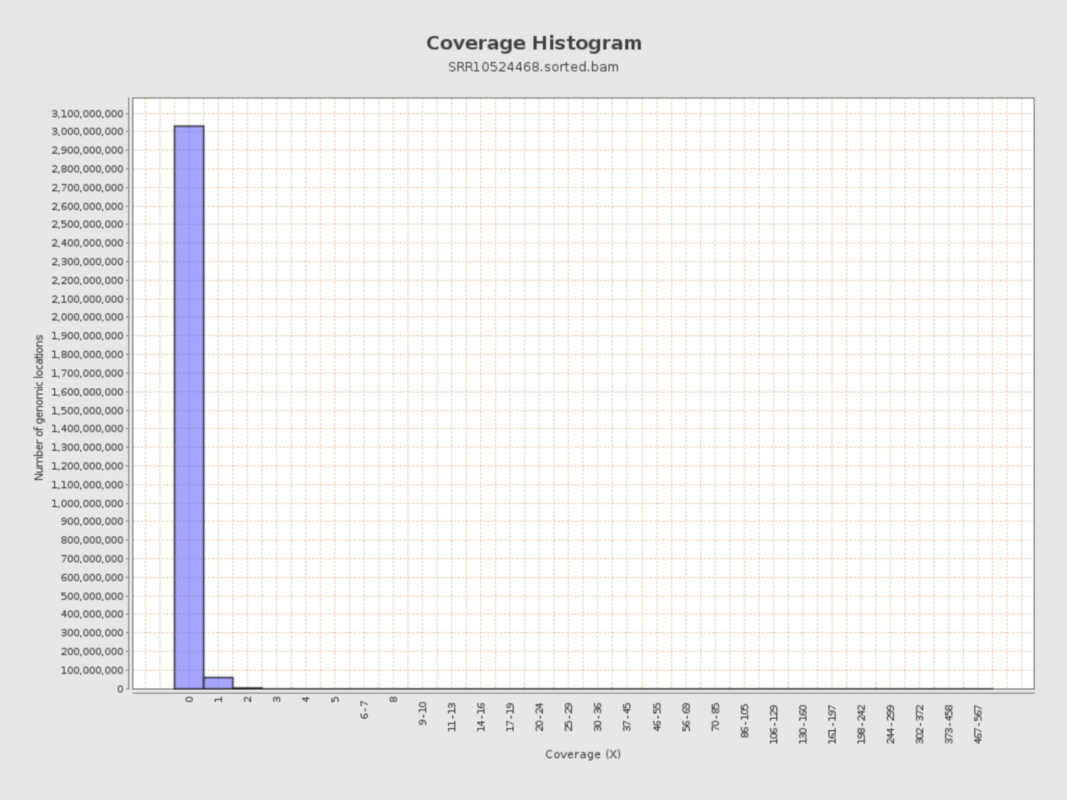
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7475800	0.03	0.4387
chr2	243199373	5991297	0.0246	0.2704
chr3	198022430	4148928	0.021	0.1588
chr4	191154276	4304863	0.0225	0.1847
chr5	180915260	4210422	0.0233	0.1681
chr6	171115067	3178758	0.0186	0.1866
chr7	159138663	3802180	0.0239	0.3135

chr8	146364022	7039306	0.0481	0.2744
chr9	141213431	3247755	0.023	0.2175
chr10	135534747	3977818	0.0293	0.2532
chr11	135006516	2584122	0.0191	0.2154
chr12	133851895	3448900	0.0258	0.1771
chr13	115169878	1672928	0.0145	0.1322
chr14	107349540	1796737	0.0167	0.1449
chr15	102531392	1993100	0.0194	0.1605
chr16	90354753	2345732	0.026	0.1849
chr17	81195210	2608668	0.0321	0.2049
chr18	78077248	1787075	0.0229	0.3323
chr19	59128983	1512021	0.0256	0.2983
chr20	63025520	2153263	0.0342	0.2069
chr21	48129895	1018886	0.0212	0.1687
chr22	51304566	611156	0.0119	0.119
chrMT	16571	4522	0.2729	0.5436
chrX	155270560	4505195	0.029	0.2034
chrY	59373566	248776	0.0042	0.1176

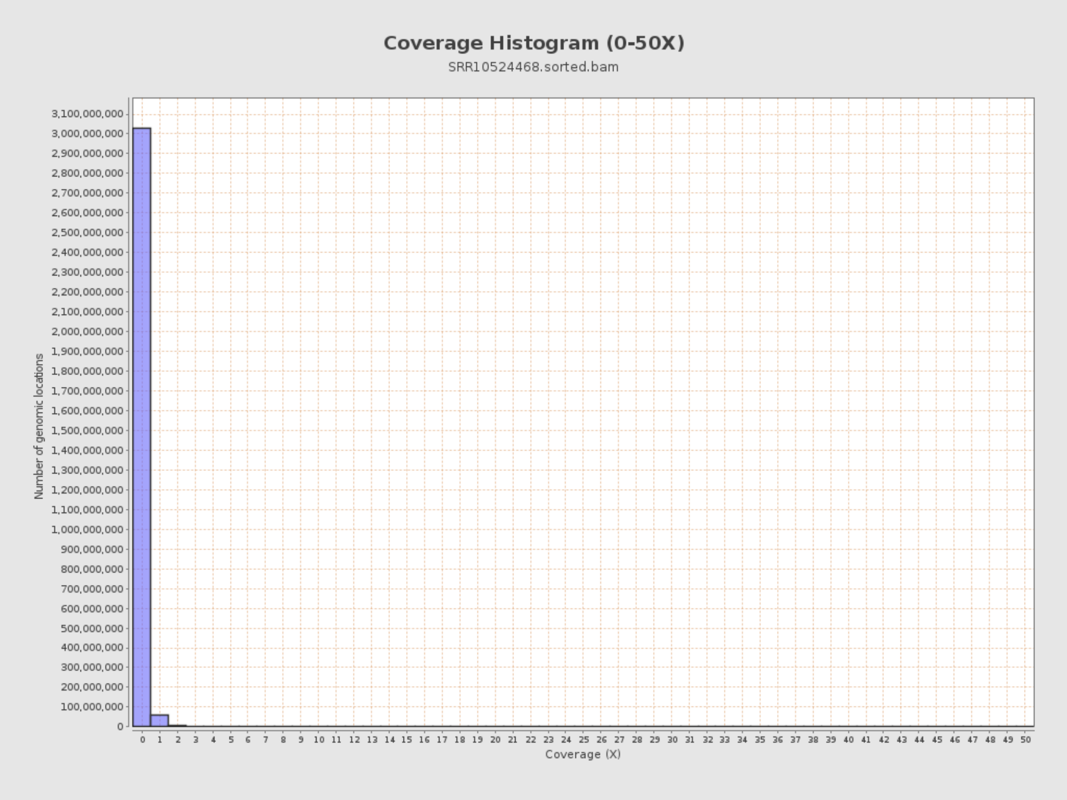
3. Results : Coverage across reference



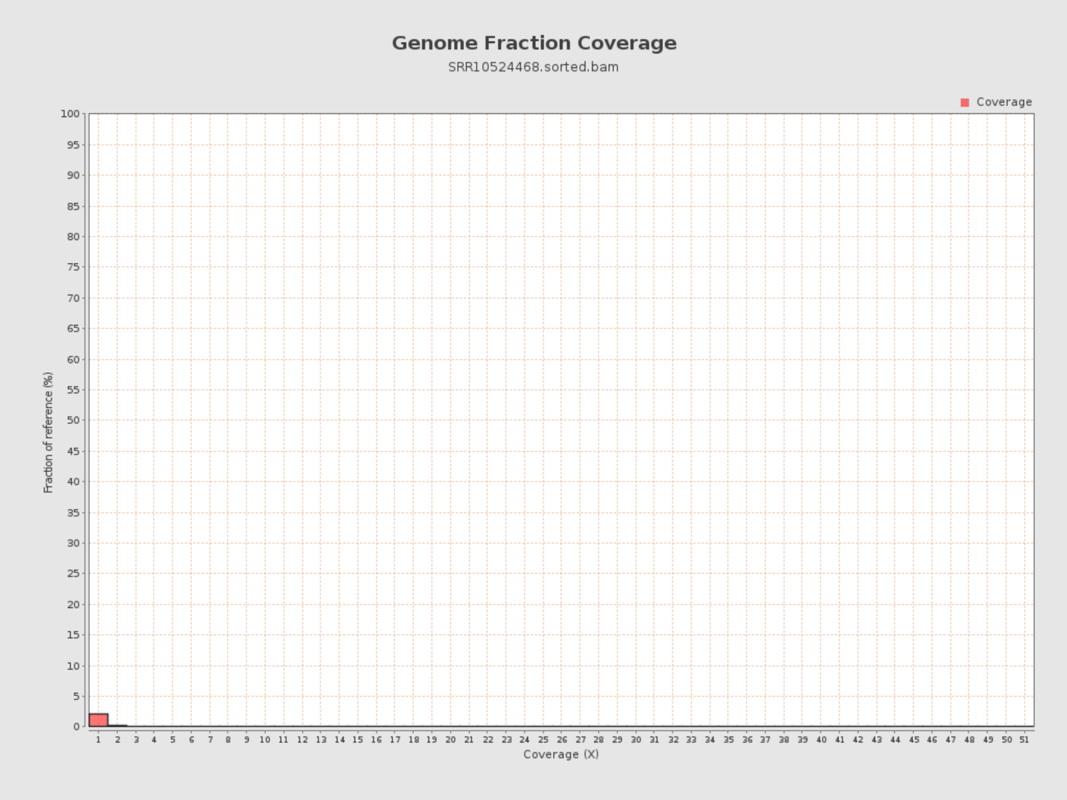
4. Results : Coverage Histogram



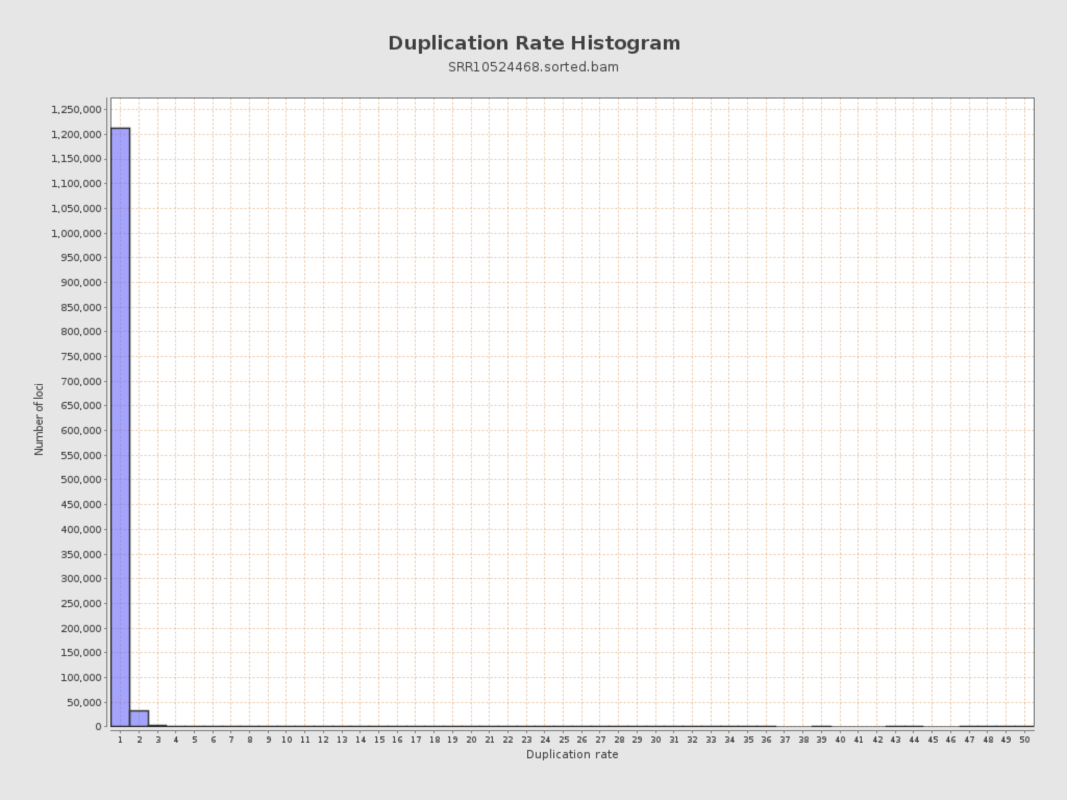
5. Results : Coverage Histogram (0-50X)



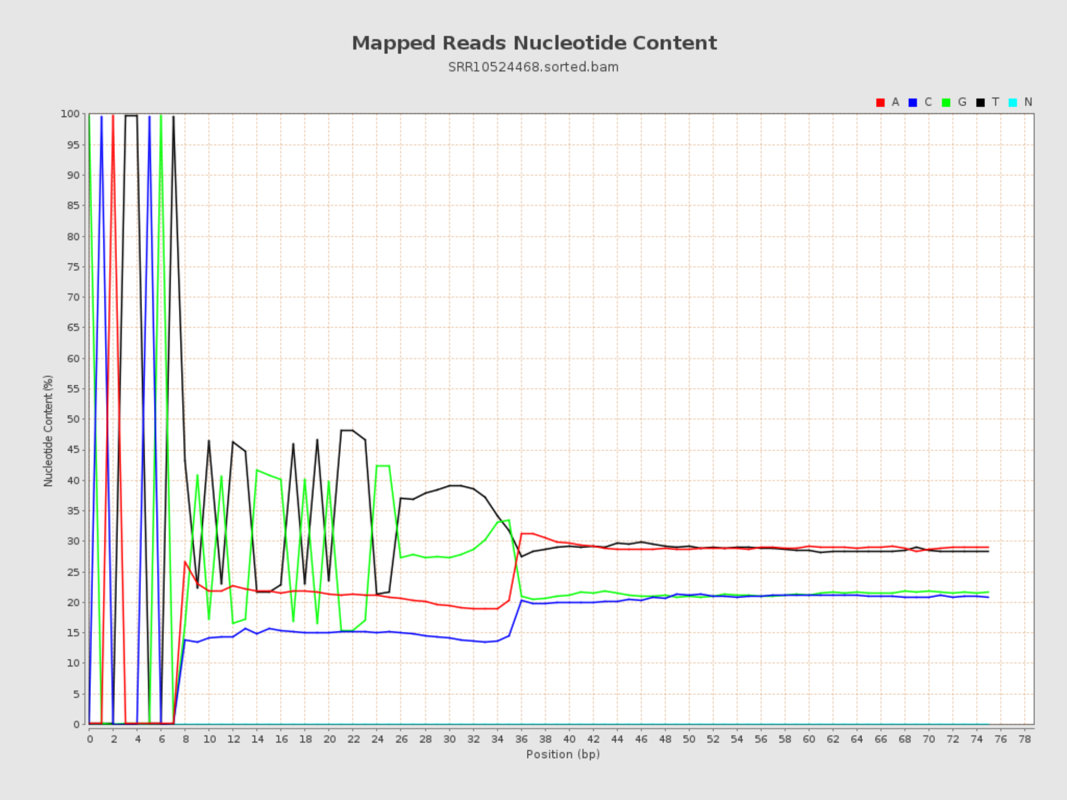
6. Results : Genome Fraction Coverage



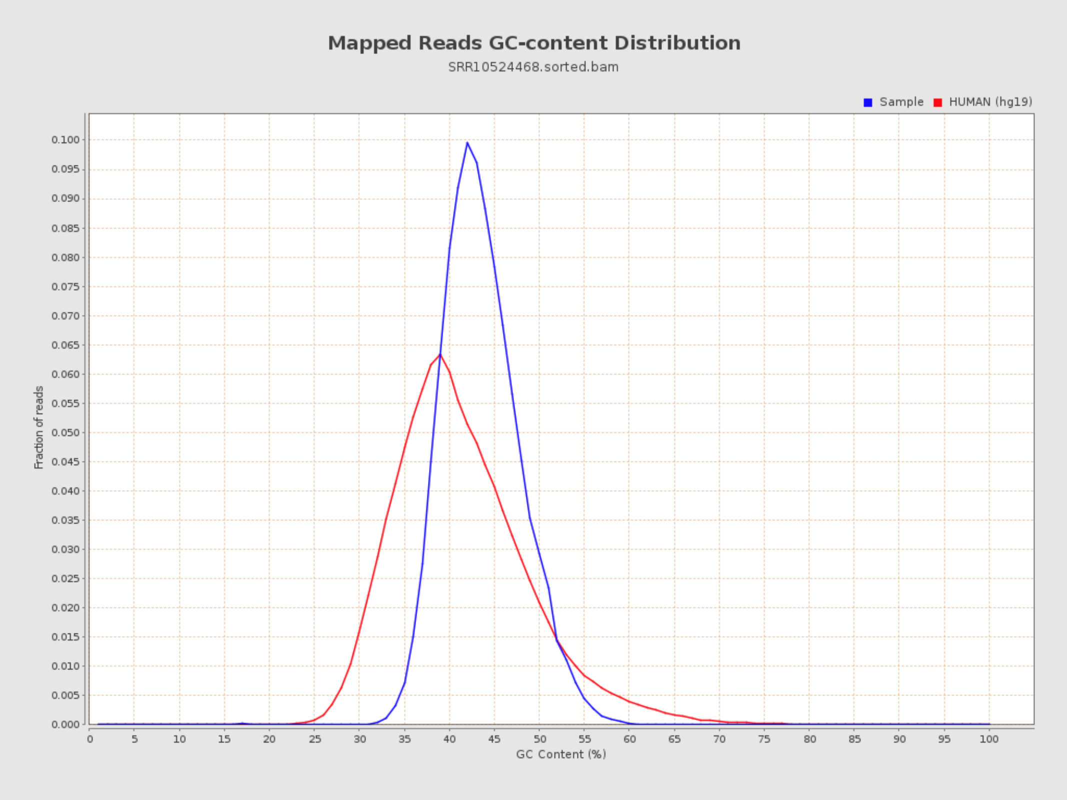
7. Results : Duplication Rate Histogram



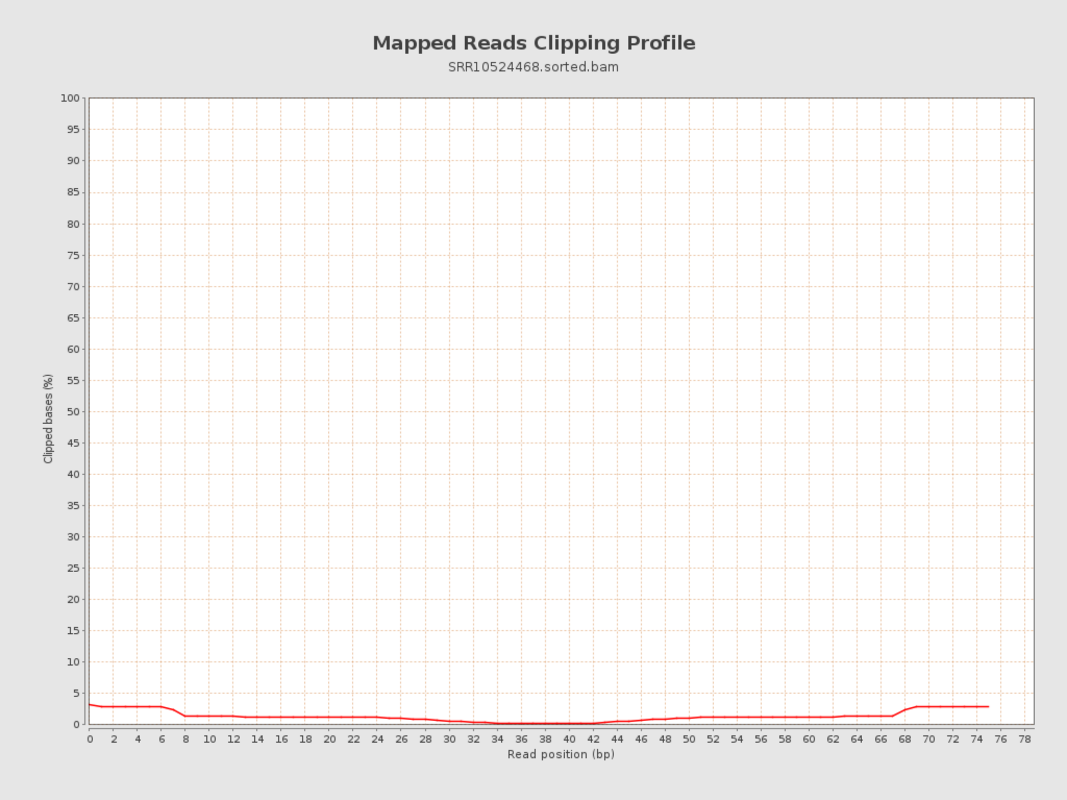
8. Results : Mapped Reads Nucleotide Content



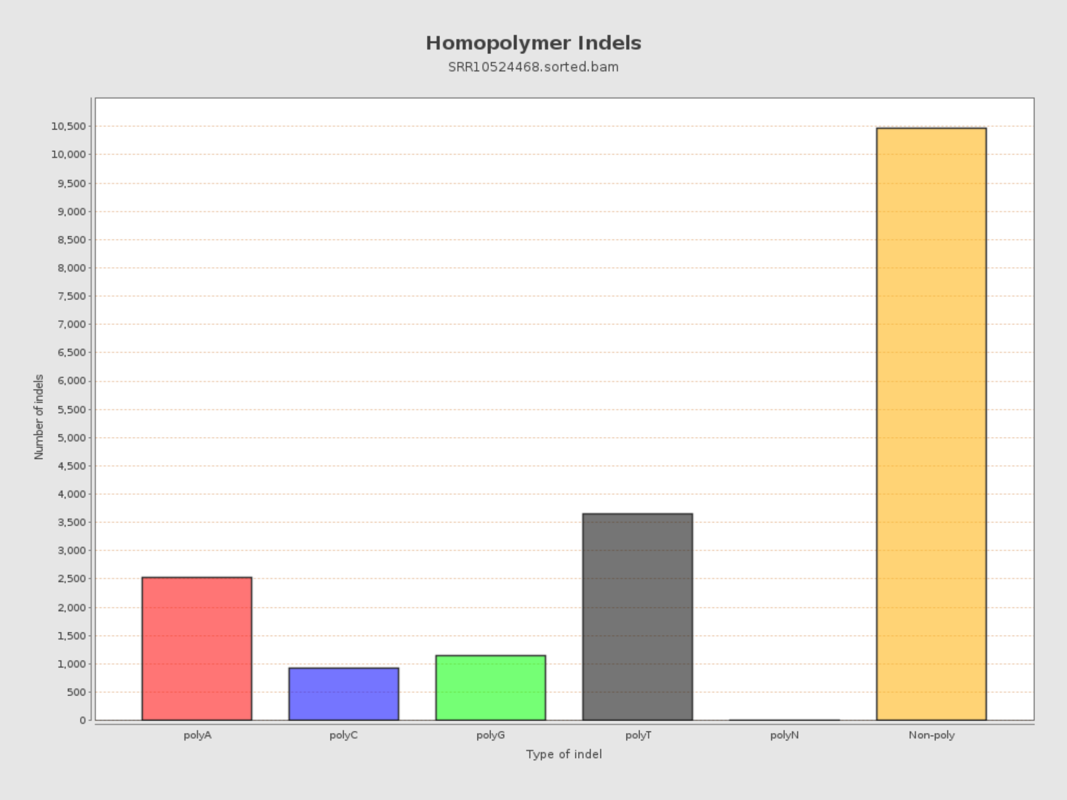
9. Results : Mapped Reads GC-content Distribution



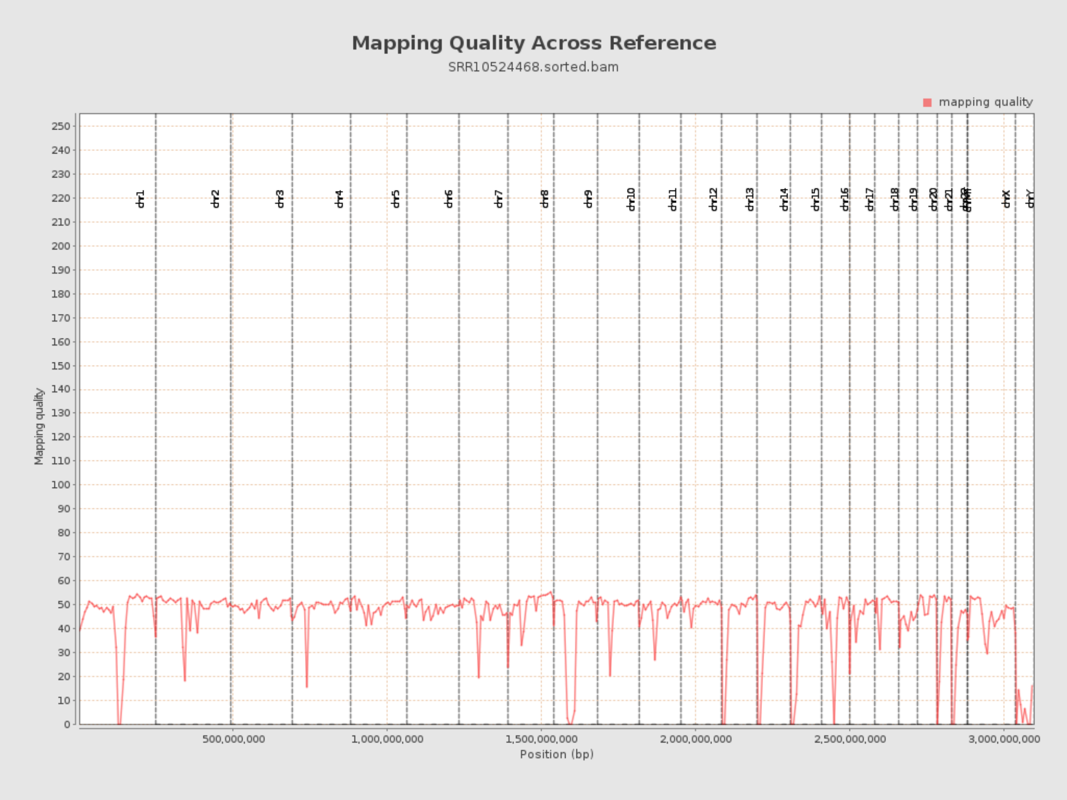
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram