Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:52:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524987.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_SRR10524987 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524987.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:52:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524987.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,897,541
Mapped reads	1,728,375 / 91.08%
Unmapped reads	169,166 / 8.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,130 / 0.22%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	67,162 / 3.54%
Duplication rate	2.92%
Clipped reads	1,730,317 / 91.19%

2.2. ACGT Content

Number/percentage of A's	25,511,692 / 25.15%
Number/percentage of C's	19,738,914 / 19.46%
Number/percentage of T's	31,495,023 / 31.05%
Number/percentage of G's	24,678,448 / 24.33%
Number/percentage of N's	1,225 / 0%
GC Percentage	43.79%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.2812

2.4. Mapping Quality

Mean Mapping Quality	45.88

2.5. Mismatches and indels

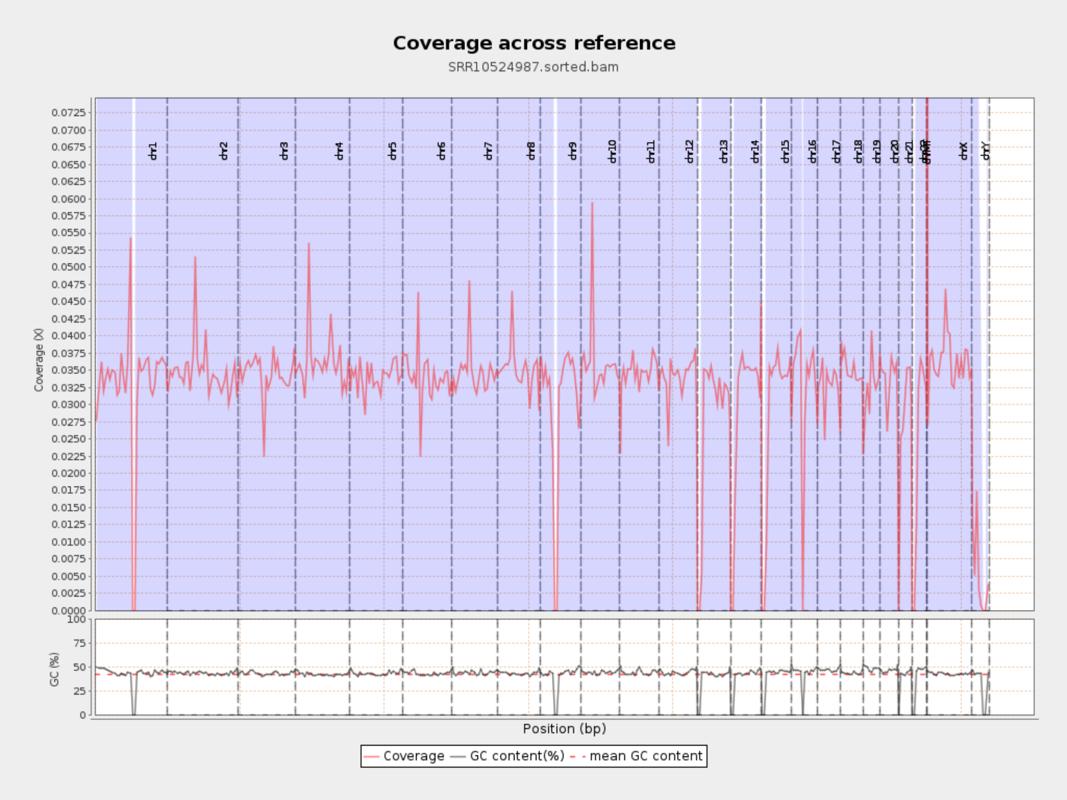
General error rate	0.49%
Mismatches	480,928
Insertions	5,670
Mapped reads with at least one insertion	0.33%
Deletions	19,368
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.66%

2.6. Chromosome stats

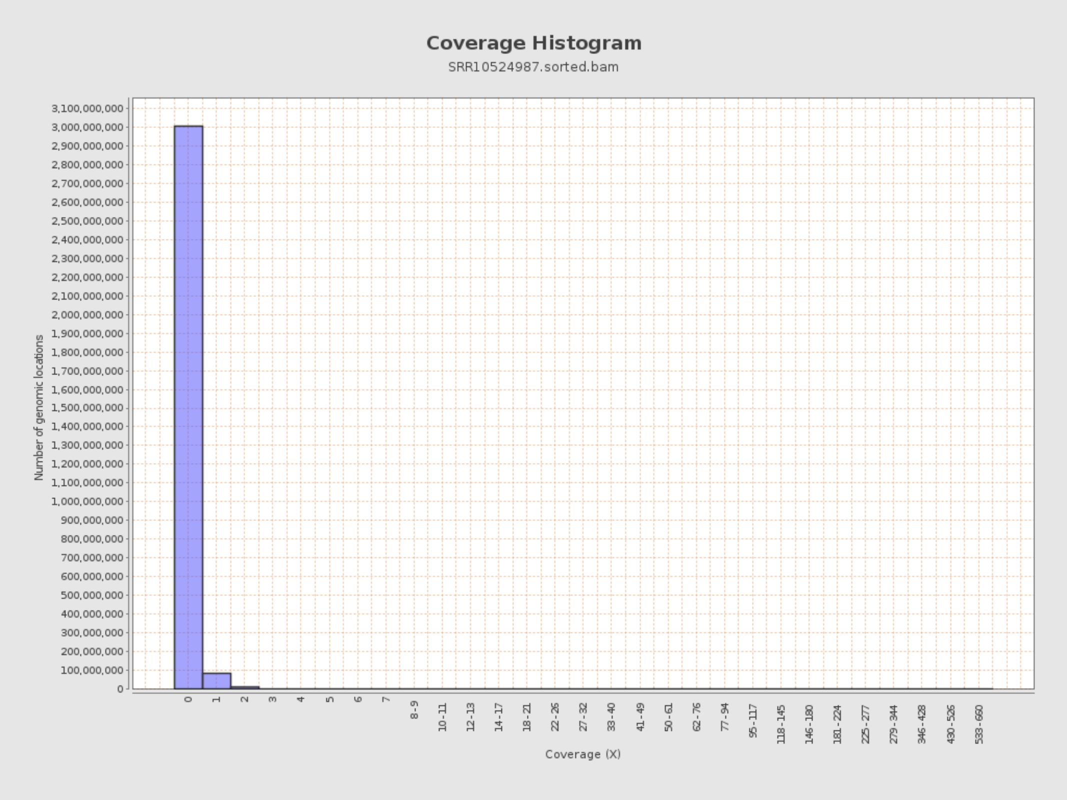
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8152327	0.0327	0.5087
chr2	243199373	8464052	0.0348	0.3106
chr3	198022430	6812346	0.0344	0.2055
chr4	191154276	6933018	0.0363	0.2348
chr5	180915260	6167947	0.0341	0.2049
chr6	171115067	5824214	0.034	0.2547
chr7	159138663	5525823	0.0347	0.3074

chr8	146364022	5152956	0.0352	0.2964
chr9	141213431	4210956	0.0298	0.2349
chr10	135534747	4910498	0.0362	0.2952
chr11	135006516	4689463	0.0347	0.289
chr12	133851895	4559132	0.0341	0.2059
chr13	115169878	3164625	0.0275	0.1832
chr14	107349540	3144965	0.0293	0.1952
chr15	102531392	2897192	0.0283	0.1967
chr16	90354753	2907738	0.0322	0.2079
chr17	81195210	2655403	0.0327	0.2216
chr18	78077248	2740679	0.0351	0.4044
chr19	59128983	1939912	0.0328	0.3305
chr20	63025520	2104741	0.0334	0.2054
chr21	48129895	1333388	0.0277	0.2052
chr22	51304566	1206832	0.0235	0.1691
chrMT	16571	11021	0.6651	1.0636
chrX	155270560	5650365	0.0364	0.2326
chrY	59373566	298794	0.005	0.1386

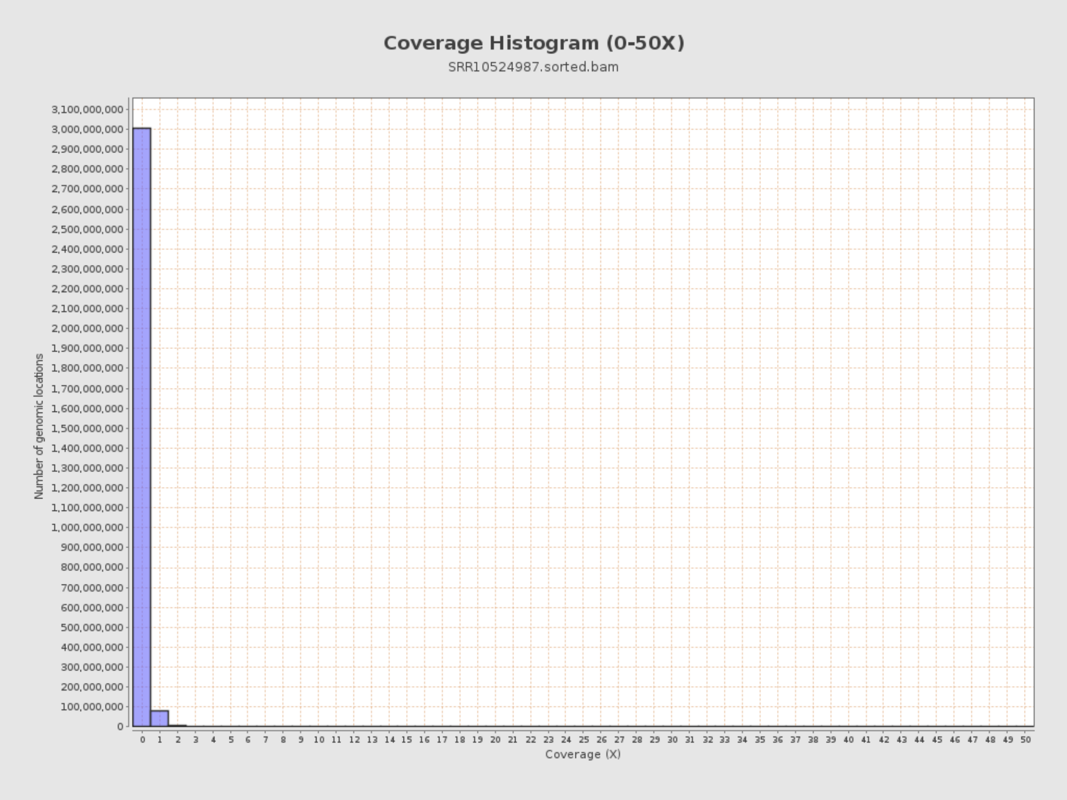
3. Results : Coverage across reference



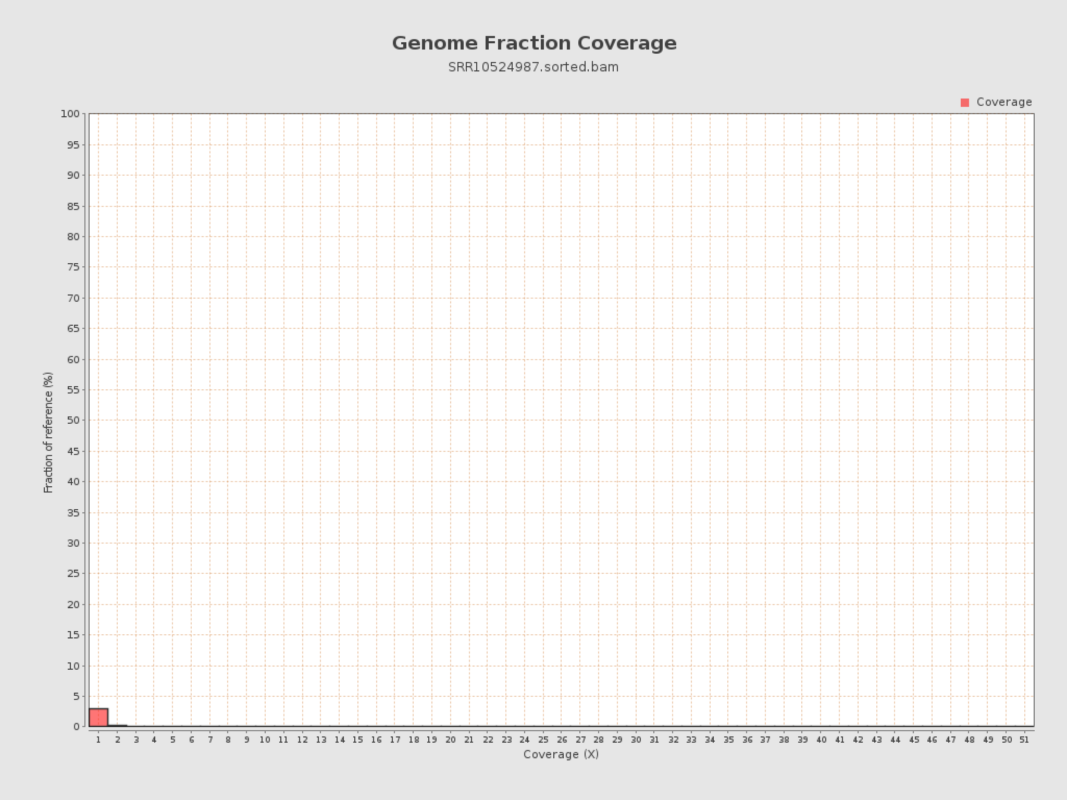
4. Results : Coverage Histogram



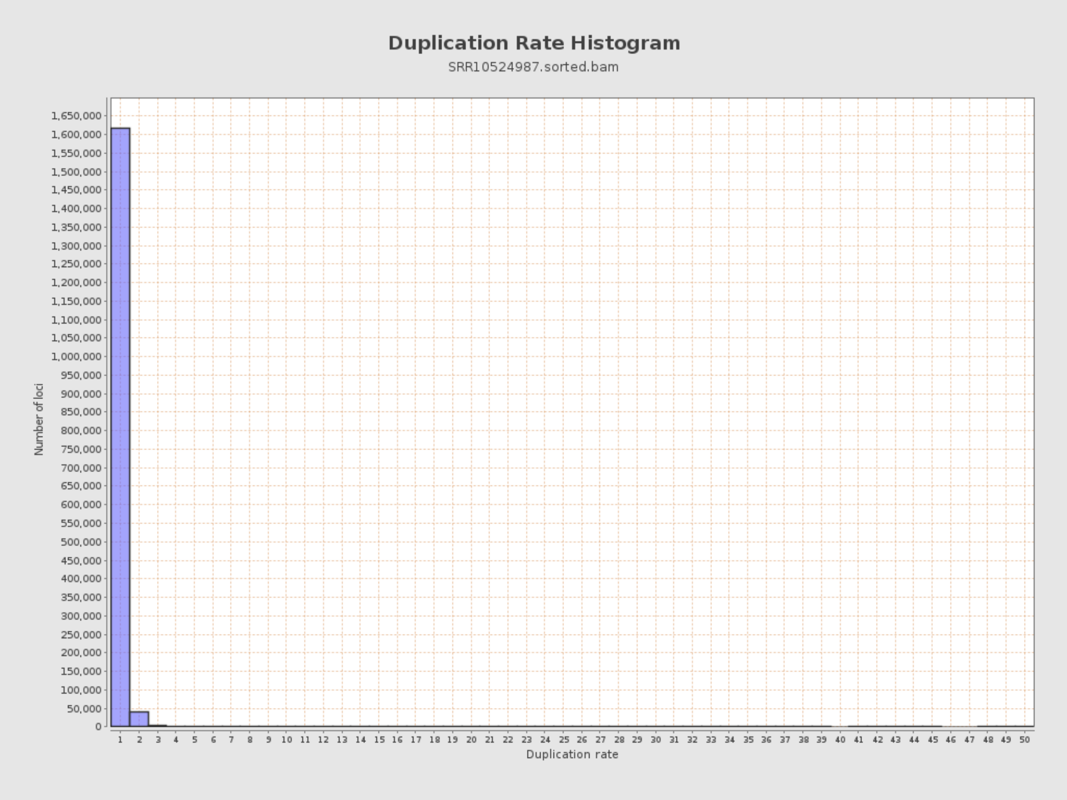
5. Results : Coverage Histogram (0-50X)



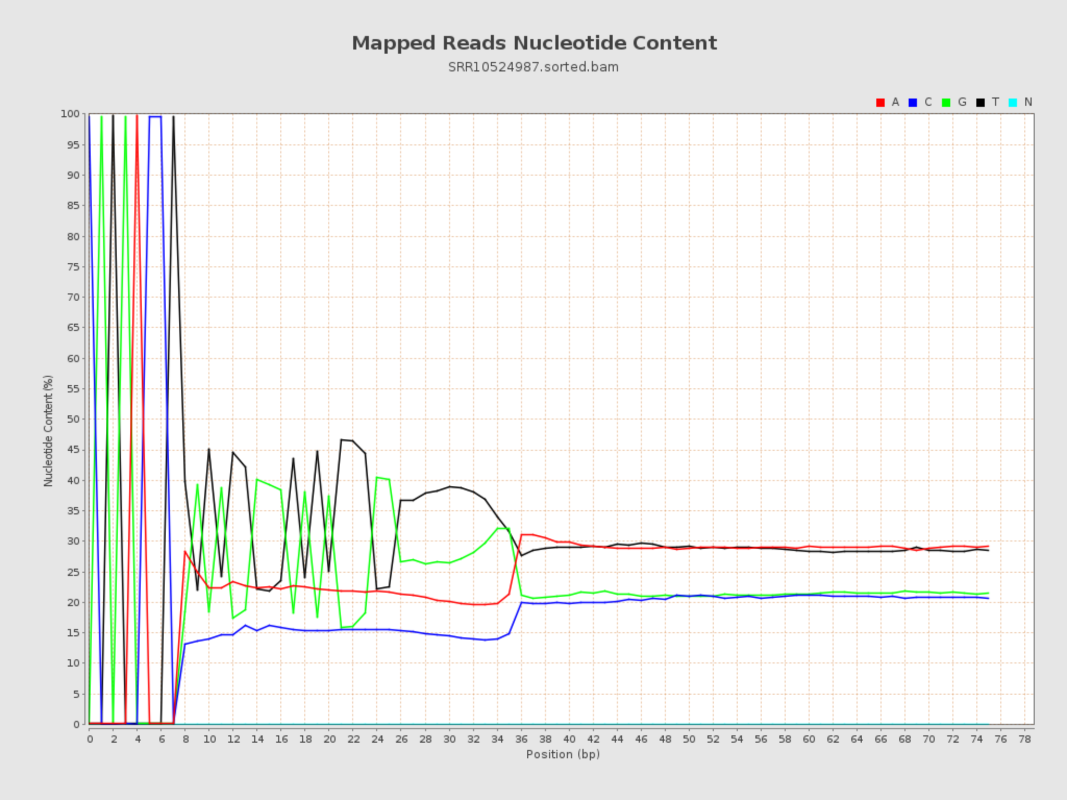
6. Results : Genome Fraction Coverage



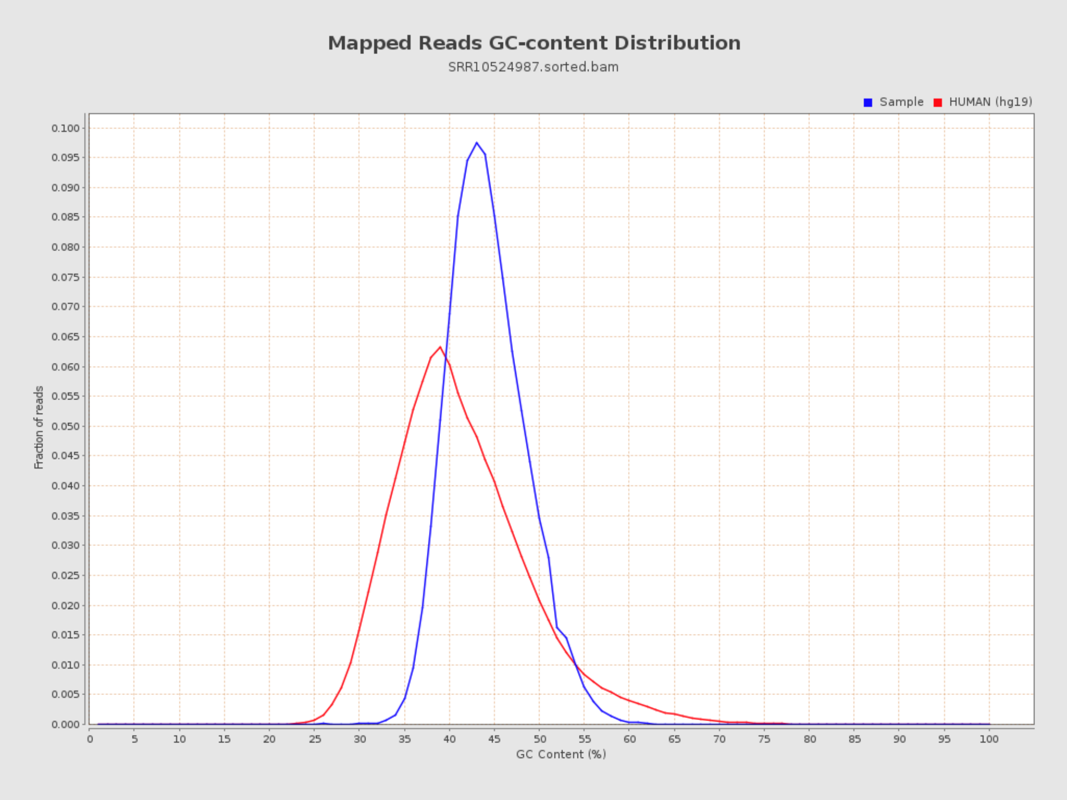
7. Results : Duplication Rate Histogram



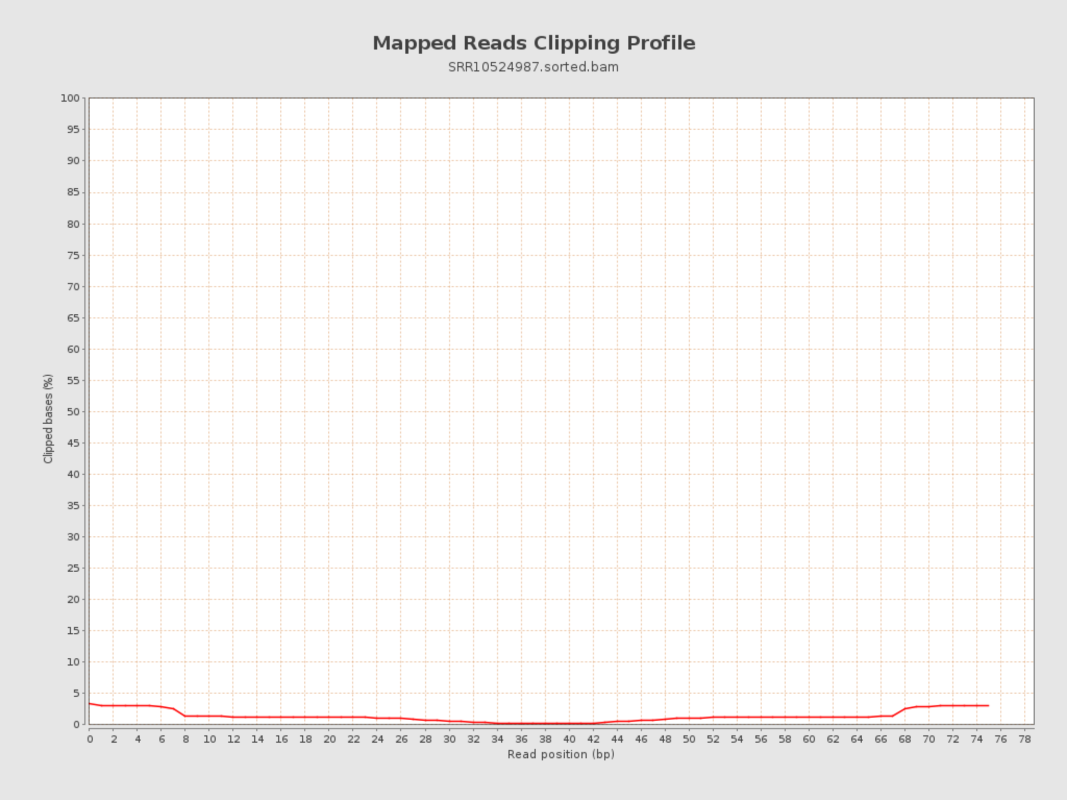
8. Results : Mapped Reads Nucleotide Content



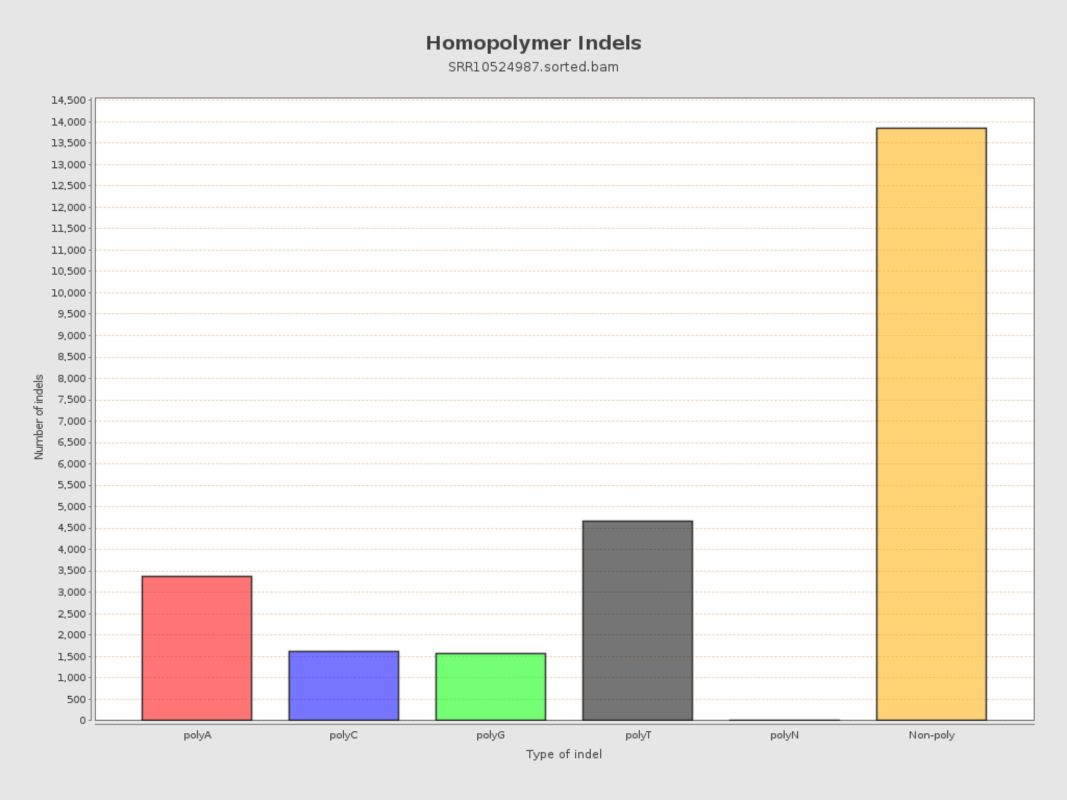
9. Results : Mapped Reads GC-content Distribution



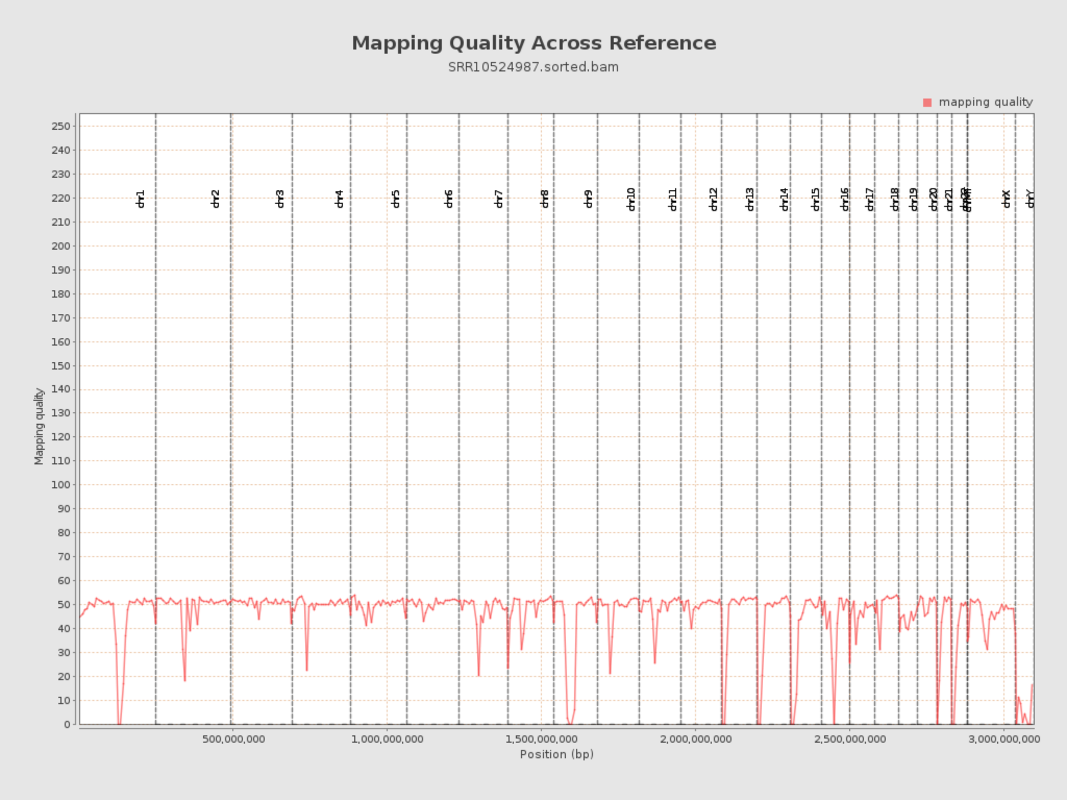
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram