Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 02:45:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524907.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_SRR10524907 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524907.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 02:45:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524907.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,004,883
Mapped reads	1,857,808 / 92.66%
Unmapped reads	147,075 / 7.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,133 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	104,263 / 5.2%
Duplication rate	4.34%
Clipped reads	1,859,025 / 92.72%

2.2. ACGT Content

Number/percentage of A's	26,330,712 / 24.42%
Number/percentage of C's	20,140,809 / 18.68%
Number/percentage of T's	34,799,706 / 32.28%
Number/percentage of G's	26,547,617 / 24.62%
Number/percentage of N's	828 / 0%
GC Percentage	43.3%

2.3. Coverage

Mean	0.0348

Standard Deviation	0.3088

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

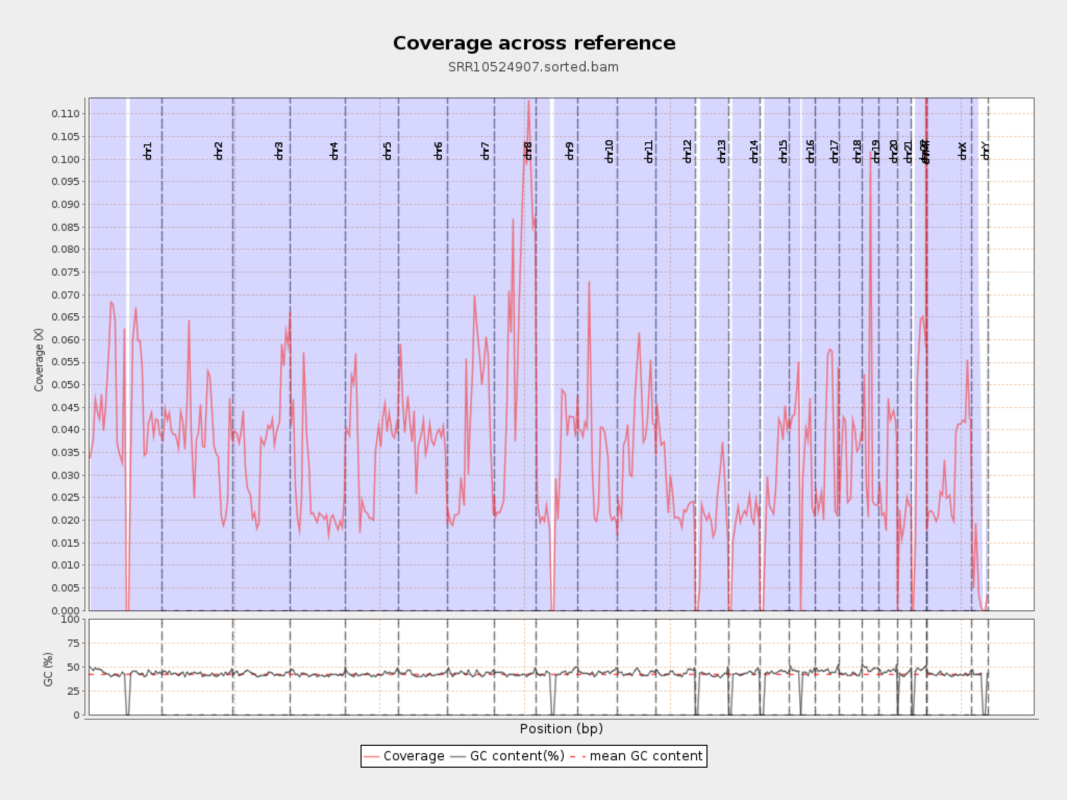
General error rate	0.52%
Mismatches	545,823
Insertions	7,172
Mapped reads with at least one insertion	0.38%
Deletions	21,058
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.15%

2.6. Chromosome stats

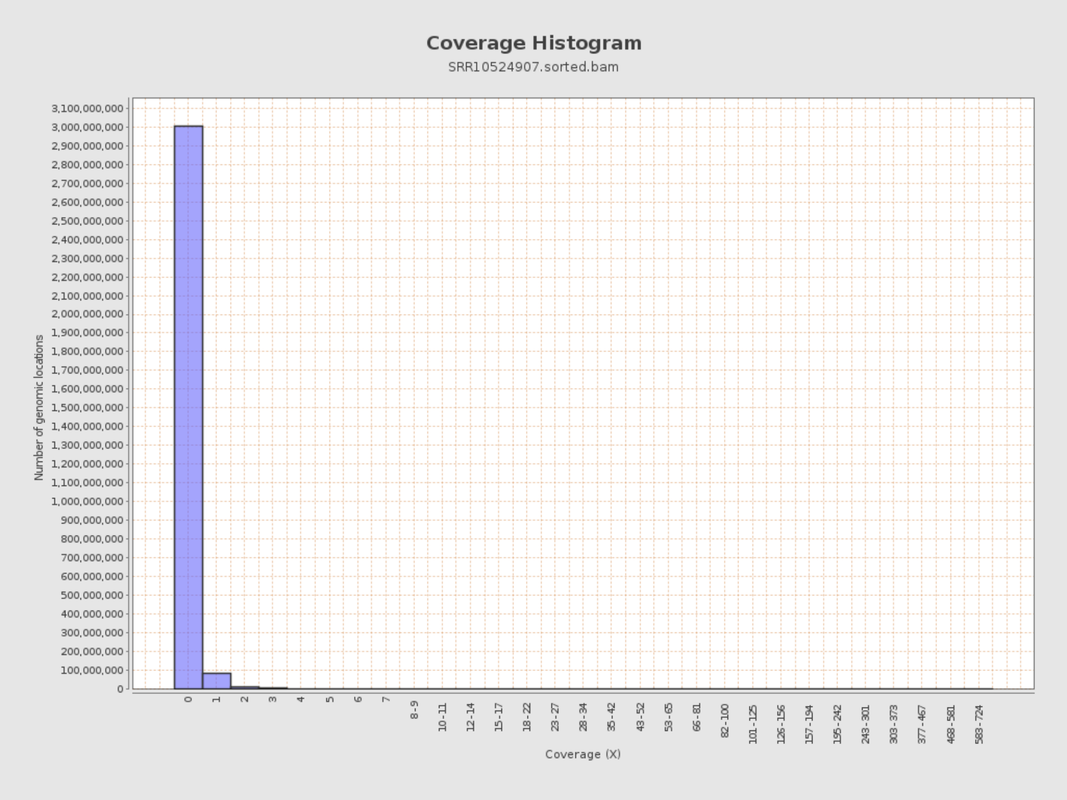
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11005976	0.0442	0.5582
chr2	243199373	9412584	0.0387	0.3806
chr3	198022430	7596020	0.0384	0.2231
chr4	191154276	4817093	0.0252	0.2261
chr5	180915260	6504412	0.036	0.2147
chr6	171115067	6818100	0.0398	0.243
chr7	159138663	6352843	0.0399	0.3775

chr8	146364022	9298197	0.0635	0.3929
chr9	141213431	3994406	0.0283	0.2457
chr10	135534747	4585026	0.0338	0.3444
chr11	135006516	5418170	0.0401	0.2716
chr12	133851895	3609303	0.027	0.1925
chr13	115169878	2265924	0.0197	0.1585
chr14	107349540	1983724	0.0185	0.1612
chr15	102531392	2795996	0.0273	0.1887
chr16	90354753	3208611	0.0355	0.2286
chr17	81195210	2938101	0.0362	0.2244
chr18	78077248	2755958	0.0353	0.4114
chr19	59128983	2279994	0.0386	0.4254
chr20	63025520	2104921	0.0334	0.2136
chr21	48129895	928414	0.0193	0.2045
chr22	51304566	2108811	0.0411	0.2342
chrMT	16571	21814	1.3164	1.4215
chrX	155270560	4753080	0.0306	0.2203
chrY	59373566	296974	0.005	0.1697

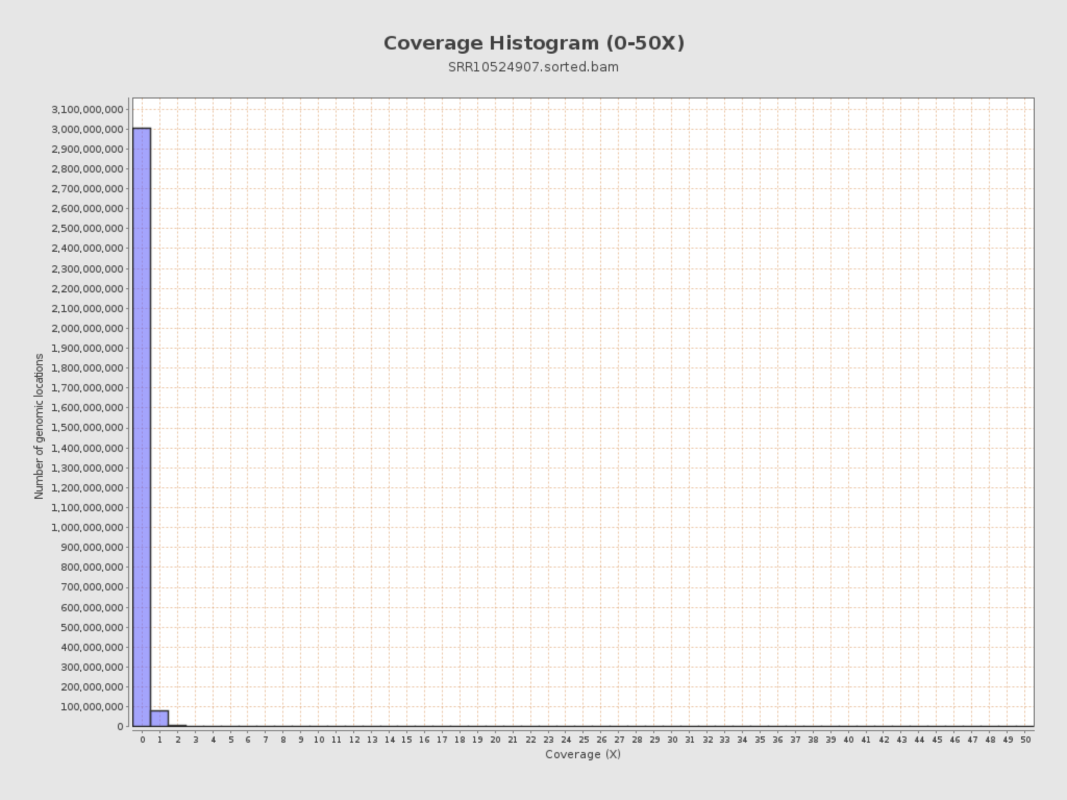
3. Results : Coverage across reference



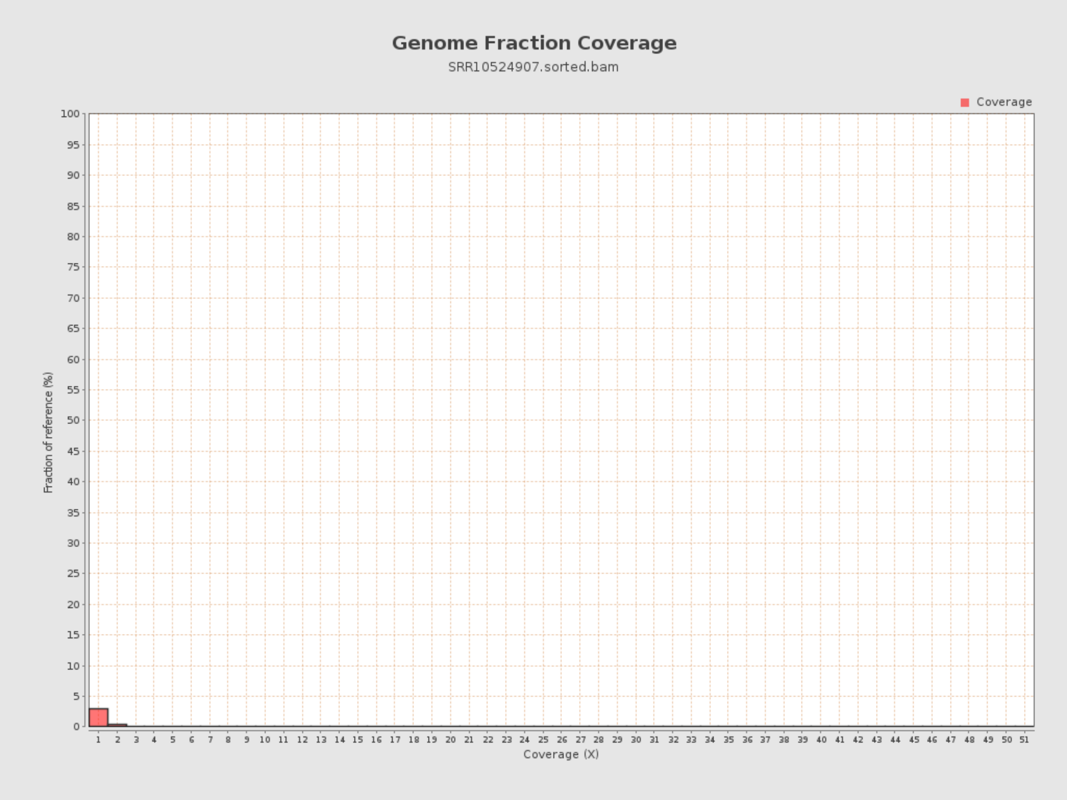
4. Results : Coverage Histogram



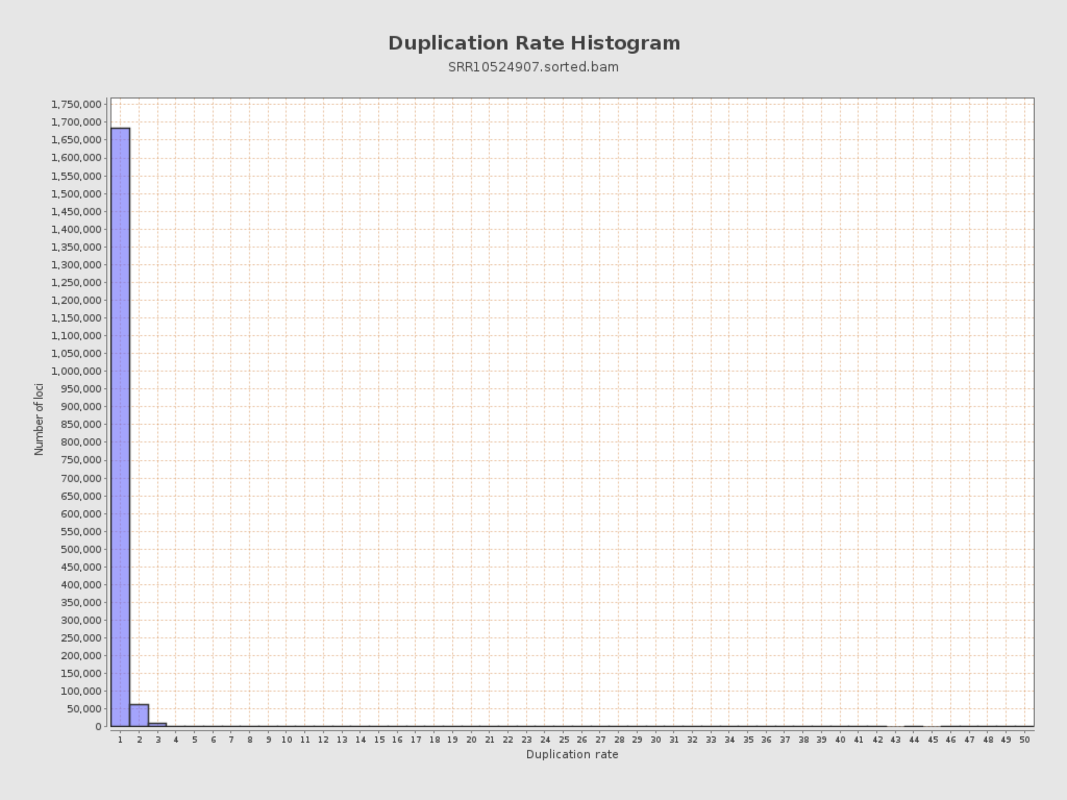
5. Results : Coverage Histogram (0-50X)



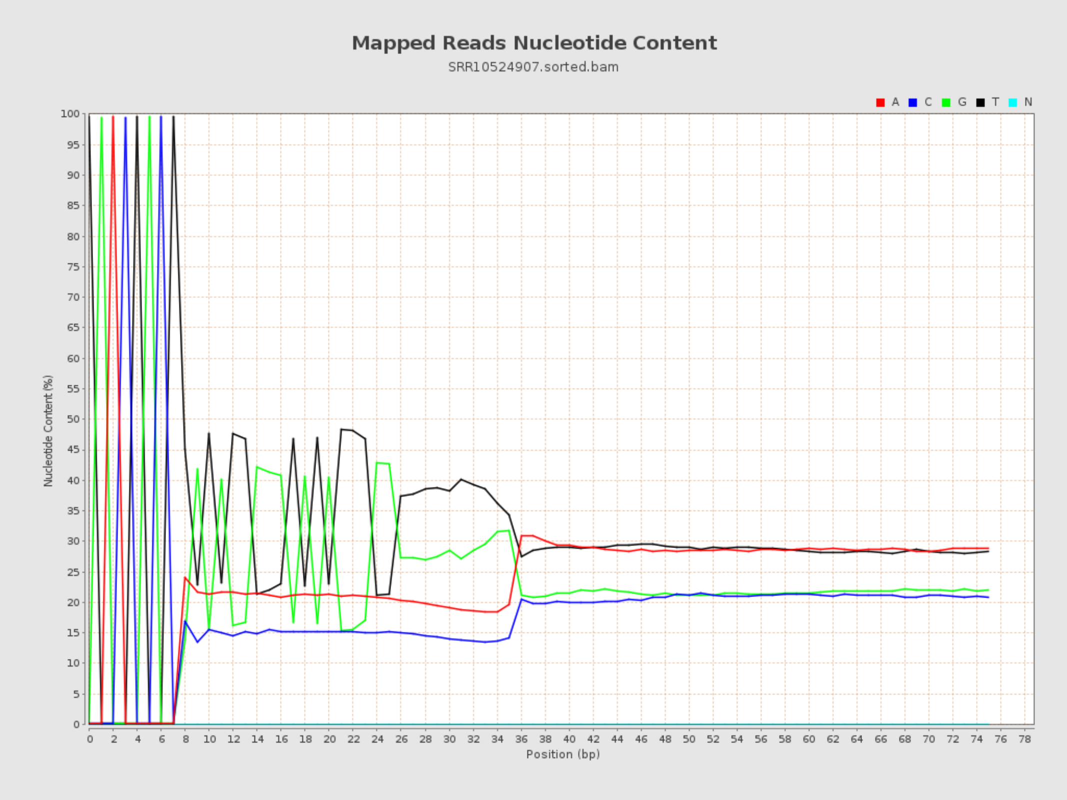
6. Results : Genome Fraction Coverage



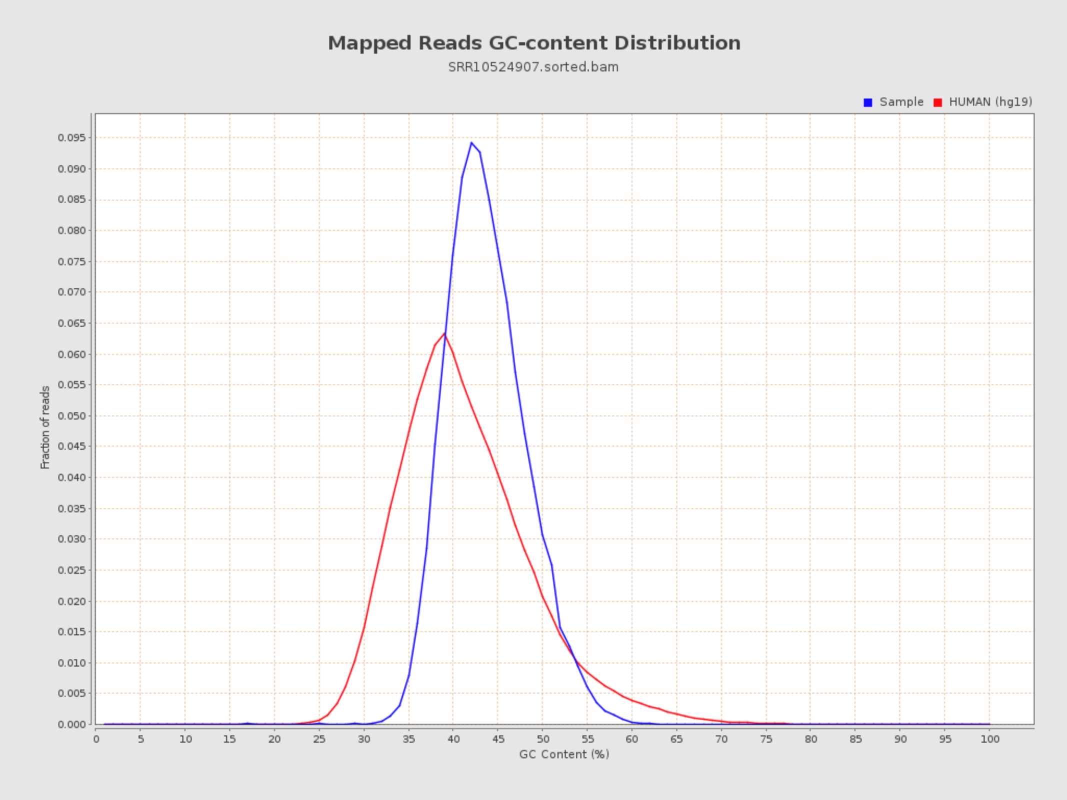
7. Results : Duplication Rate Histogram



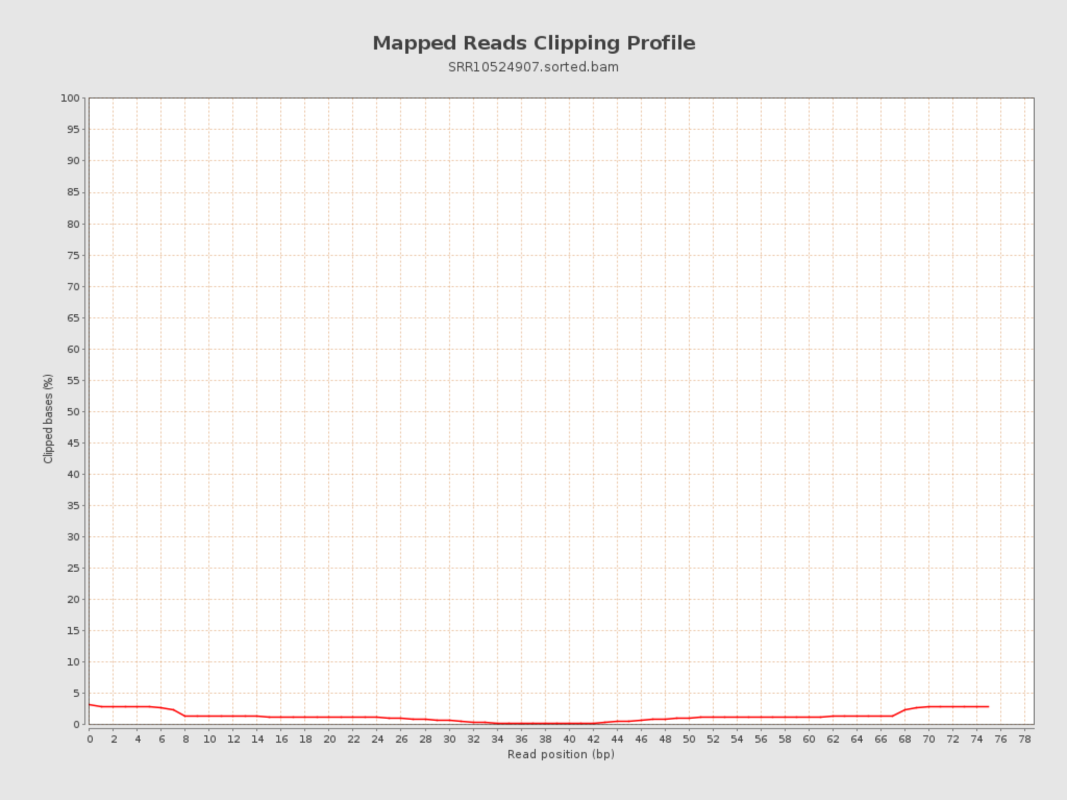
8. Results : Mapped Reads Nucleotide Content



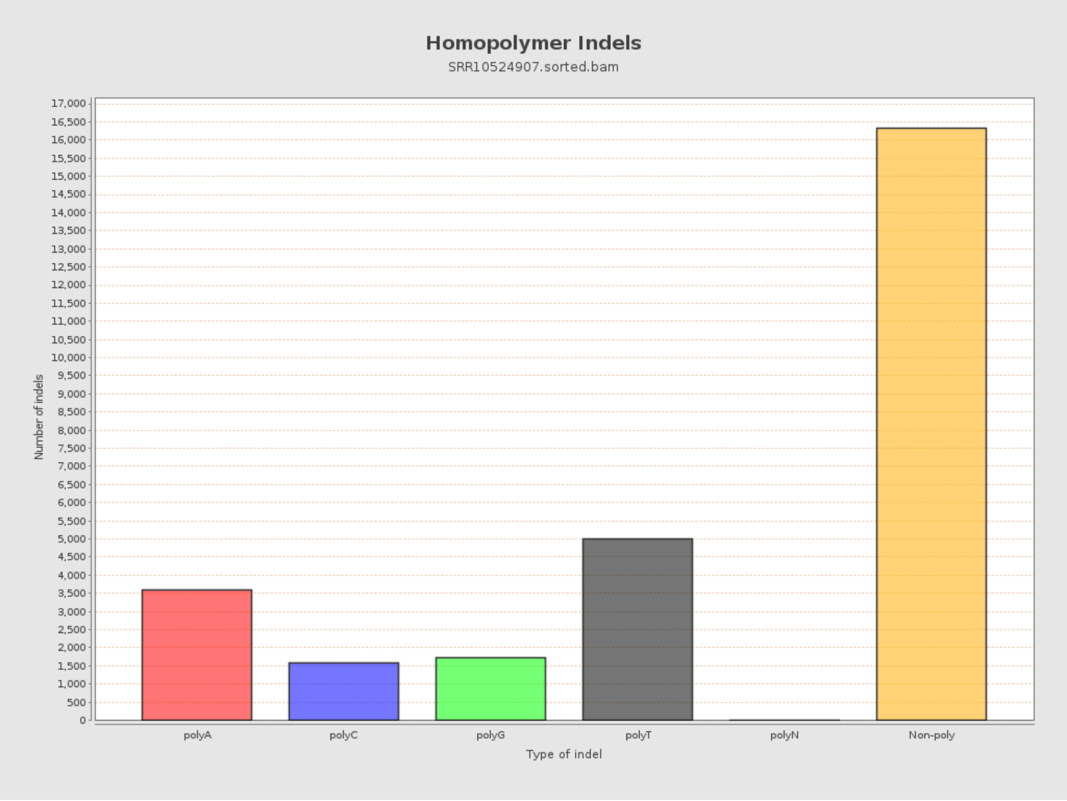
9. Results : Mapped Reads GC-content Distribution



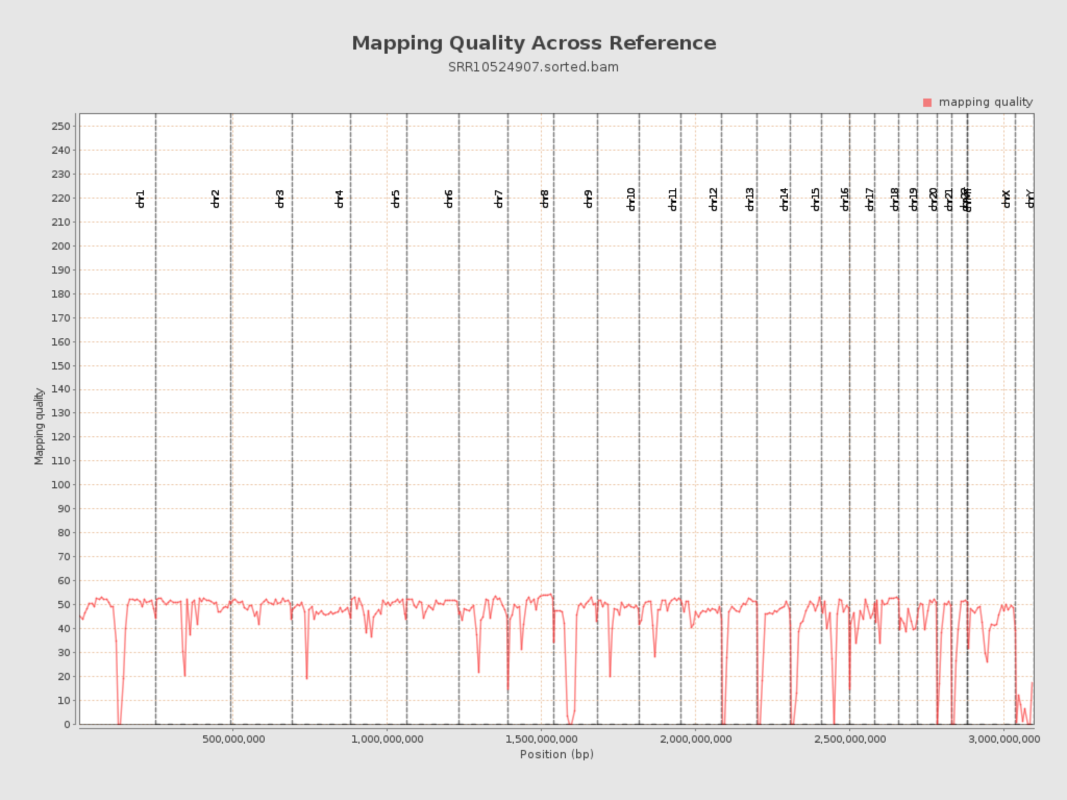
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram