Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 03:25:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1548974.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_SRR1548974 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1548974.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 03:25:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1548974.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,301,773
Mapped reads	2,371,493 / 44.73%
Unmapped reads	2,930,280 / 55.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	55,700 / 1.05%
Duplication rate	1.69%
Clipped reads	242,418 / 4.57%

2.2. ACGT Content

Number/percentage of A's	29,077,169 / 31.07%
Number/percentage of C's	17,730,230 / 18.94%
Number/percentage of T's	28,900,969 / 30.88%
Number/percentage of G's	17,883,253 / 19.11%
Number/percentage of N's	4,150 / 0%
GC Percentage	38.05%

2.3. Coverage

Mean	0.0302
Standard Deviation	0.2595

2.4. Mapping Quality

Mean Mapping Quality	43.78

2.5. Mismatches and indels

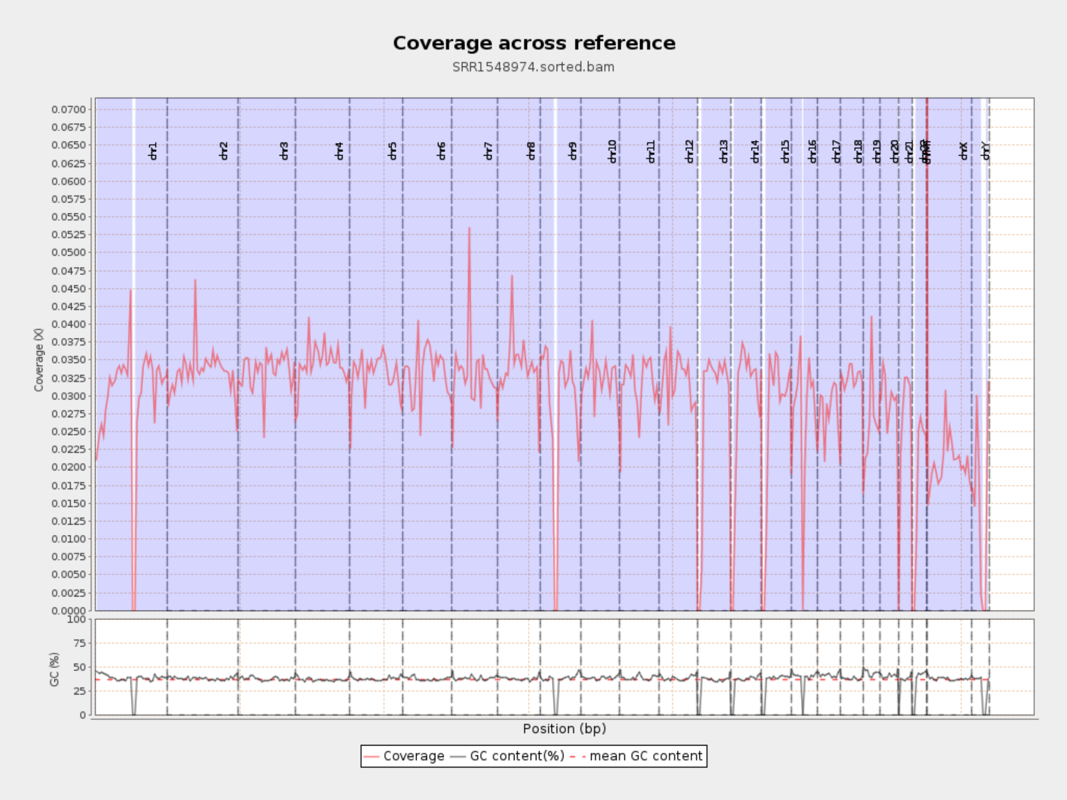
General error rate	0.33%
Mismatches	304,297
Insertions	4,357
Mapped reads with at least one insertion	0.18%
Deletions	10,404
Mapped reads with at least one deletion	0.44%
Homopolymer indels	44.8%

2.6. Chromosome stats

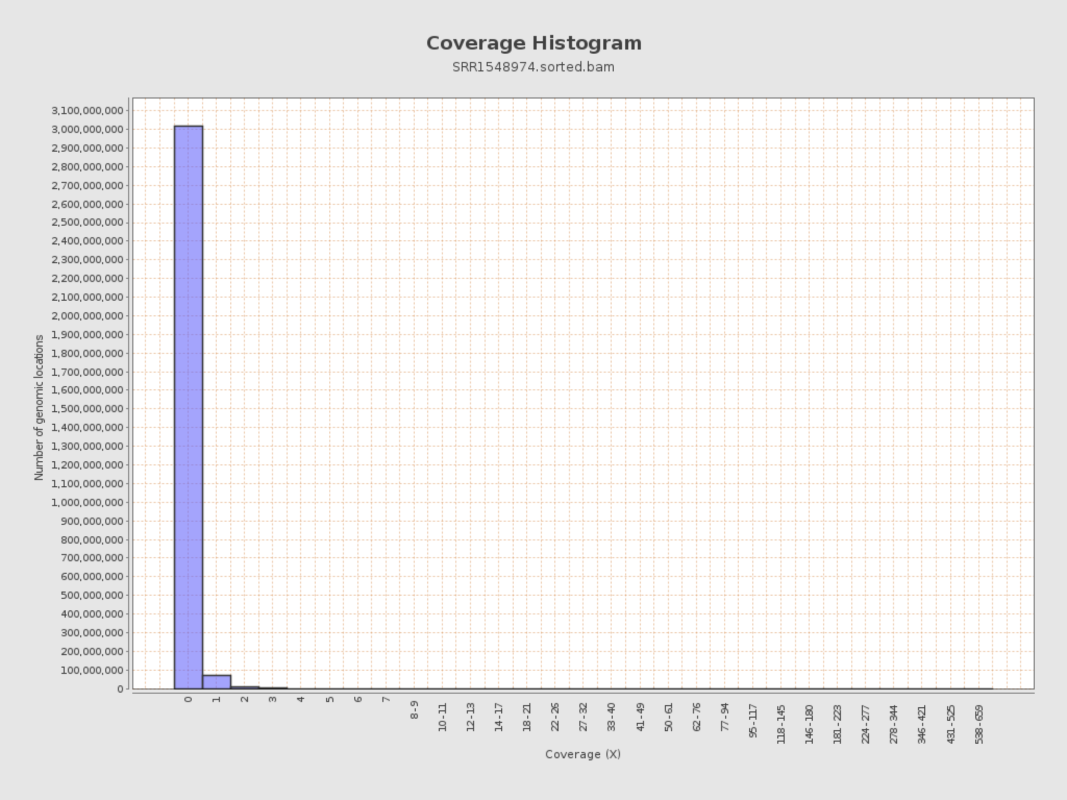
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7391129	0.0297	0.3942
chr2	243199373	8138635	0.0335	0.2513
chr3	198022430	6643469	0.0335	0.2083
chr4	191154276	6582194	0.0344	0.2151
chr5	180915260	6022772	0.0333	0.209
chr6	171115067	5706898	0.0334	0.22
chr7	159138663	5303194	0.0333	0.3476
chr8	146364022	5000286	0.0342	0.392

chr9	141213431	4014178	0.0284	0.233
chr10	135534747	4416881	0.0326	0.2304
chr11	135006516	4303394	0.0319	0.2459
chr12	133851895	4297000	0.0321	0.209
chr13	115169878	3199802	0.0278	0.1886
chr14	107349540	2987882	0.0278	0.204
chr15	102531392	2703733	0.0264	0.1825
chr16	90354753	2432814	0.0269	0.1919
chr17	81195210	2248810	0.0277	0.1925
chr18	78077248	2552800	0.0327	0.3621
chr19	59128983	1574288	0.0266	0.3736
chr20	63025520	1852033	0.0294	0.1982
chr21	48129895	1256943	0.0261	0.1953
chr22	51304566	902246	0.0176	0.1551
chrMT	16571	3130	0.1889	0.4875
chrX	155270560	3219856	0.0207	0.1869
chrY	59373566	854479	0.0144	0.1982

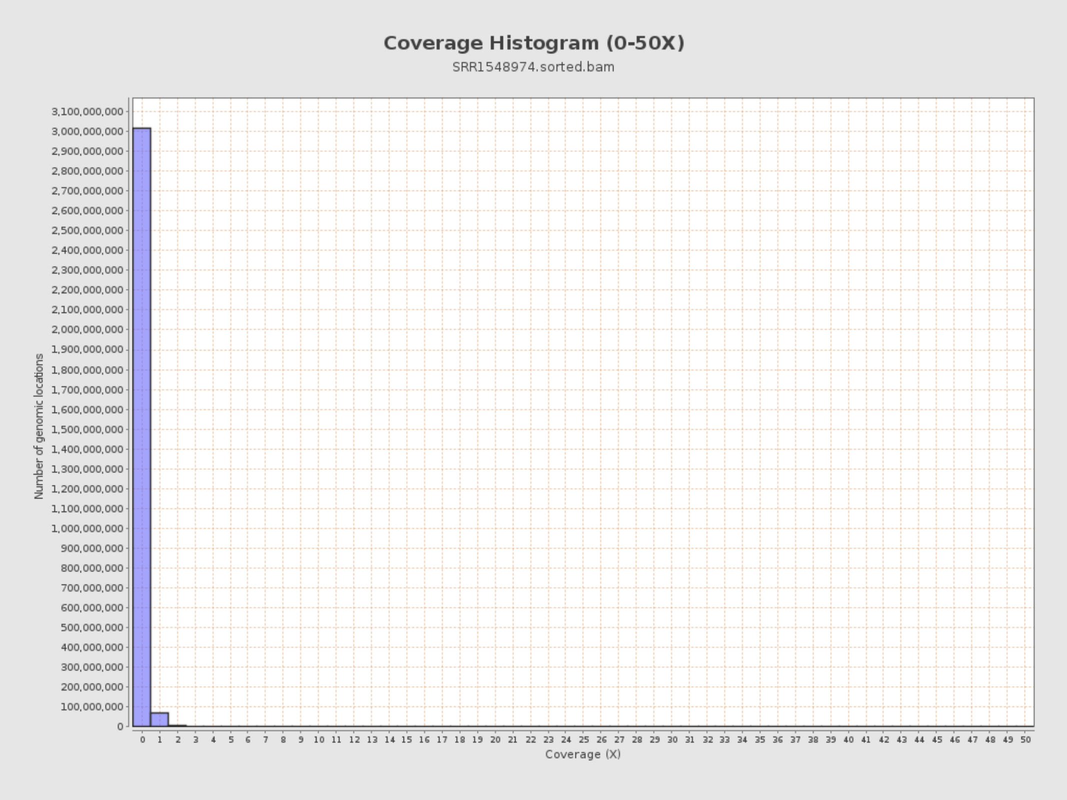
3. Results : Coverage across reference



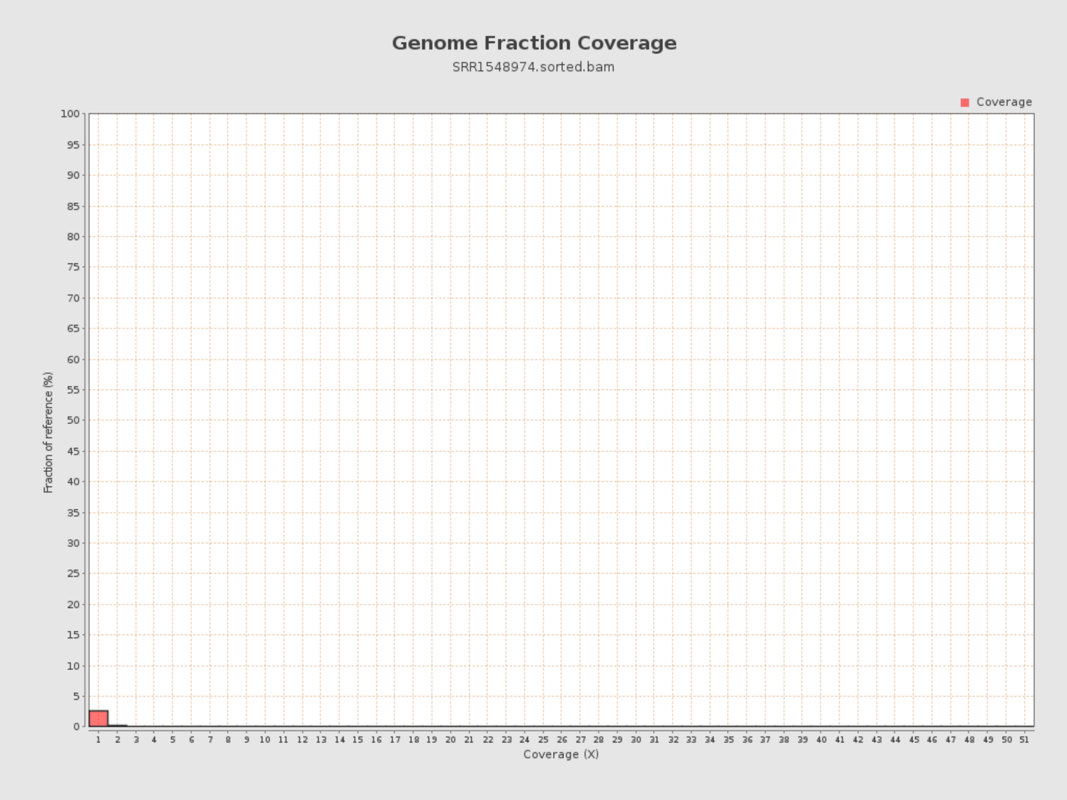
4. Results : Coverage Histogram



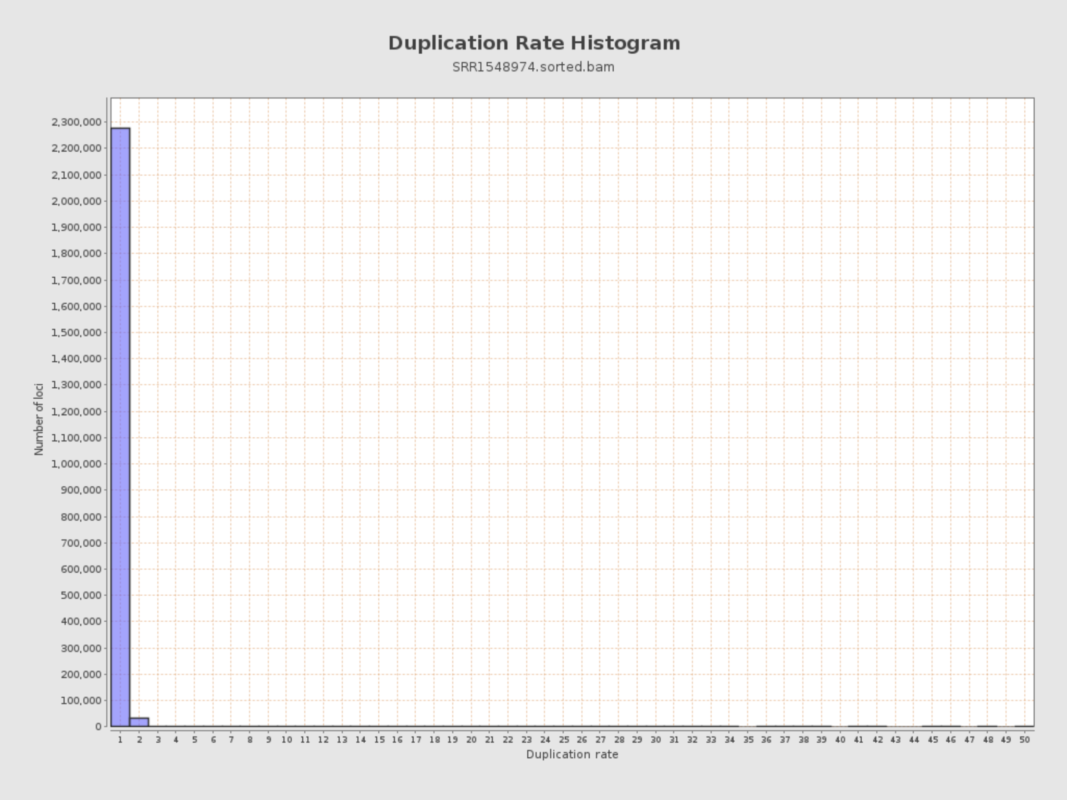
5. Results : Coverage Histogram (0-50X)



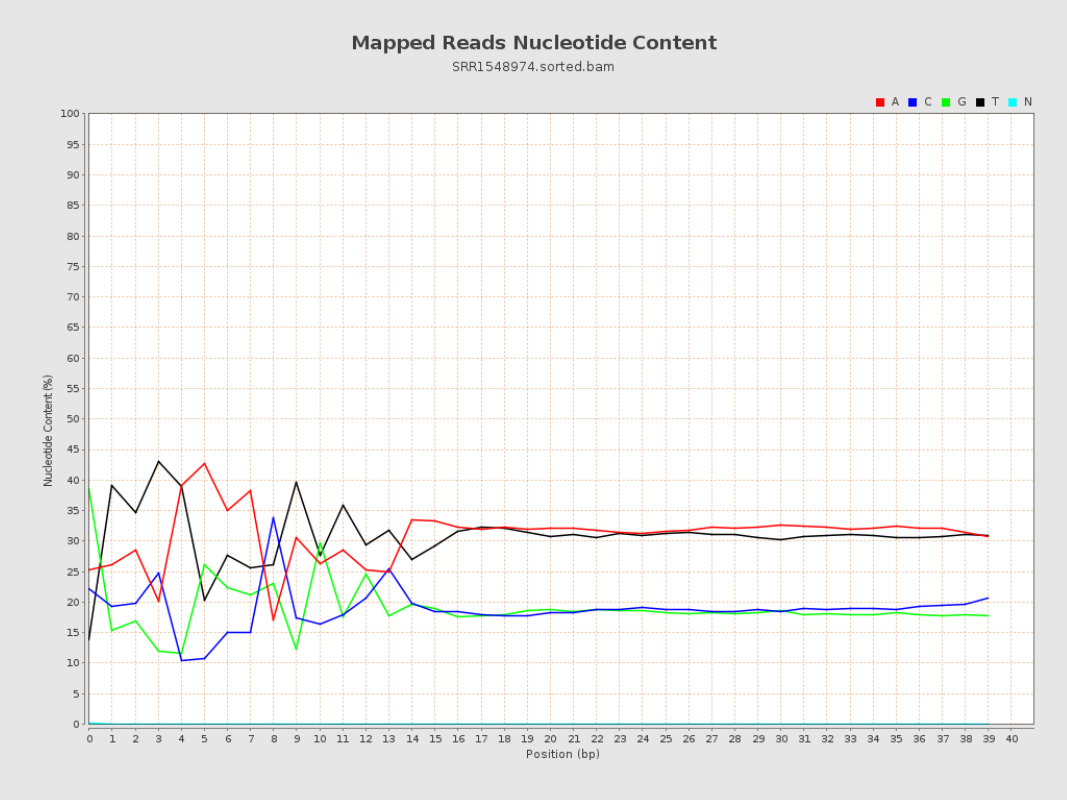
6. Results : Genome Fraction Coverage



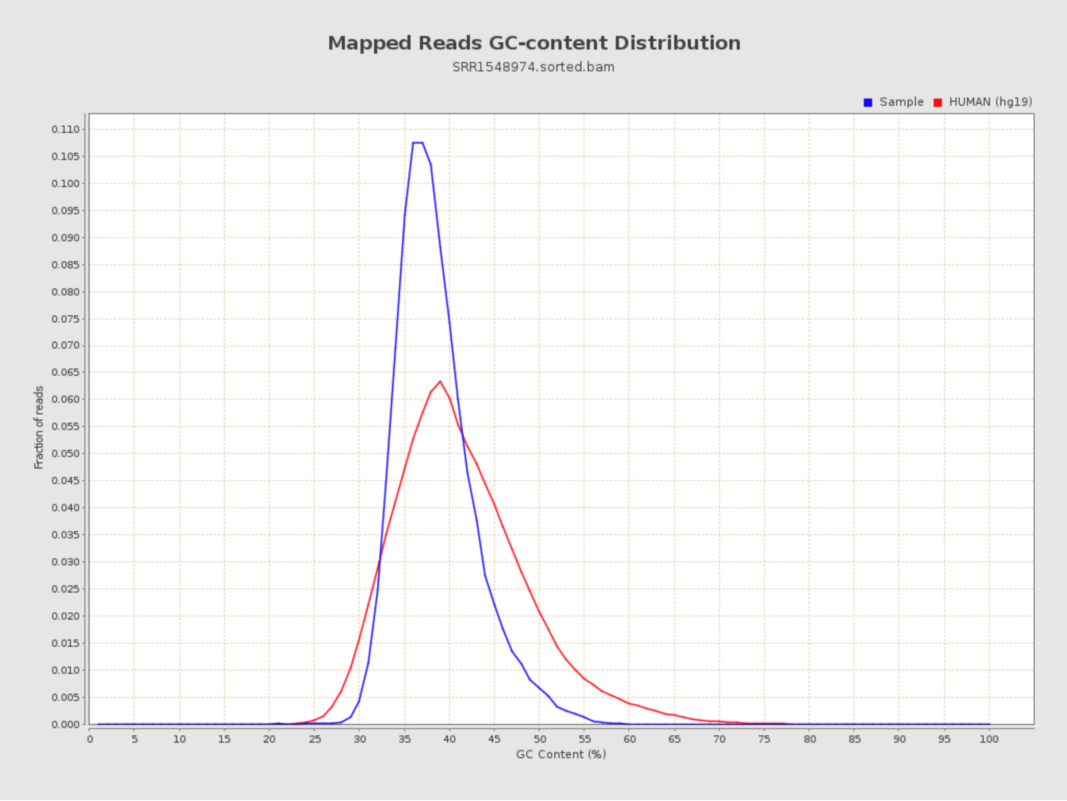
7. Results : Duplication Rate Histogram



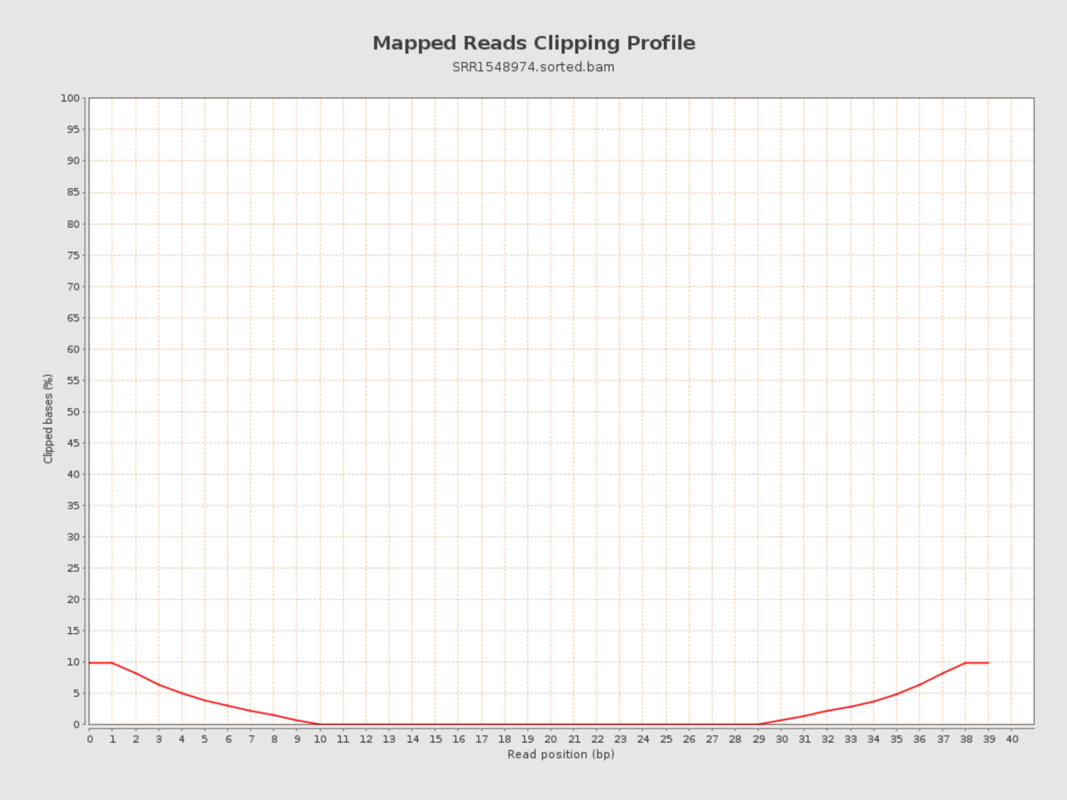
8. Results : Mapped Reads Nucleotide Content



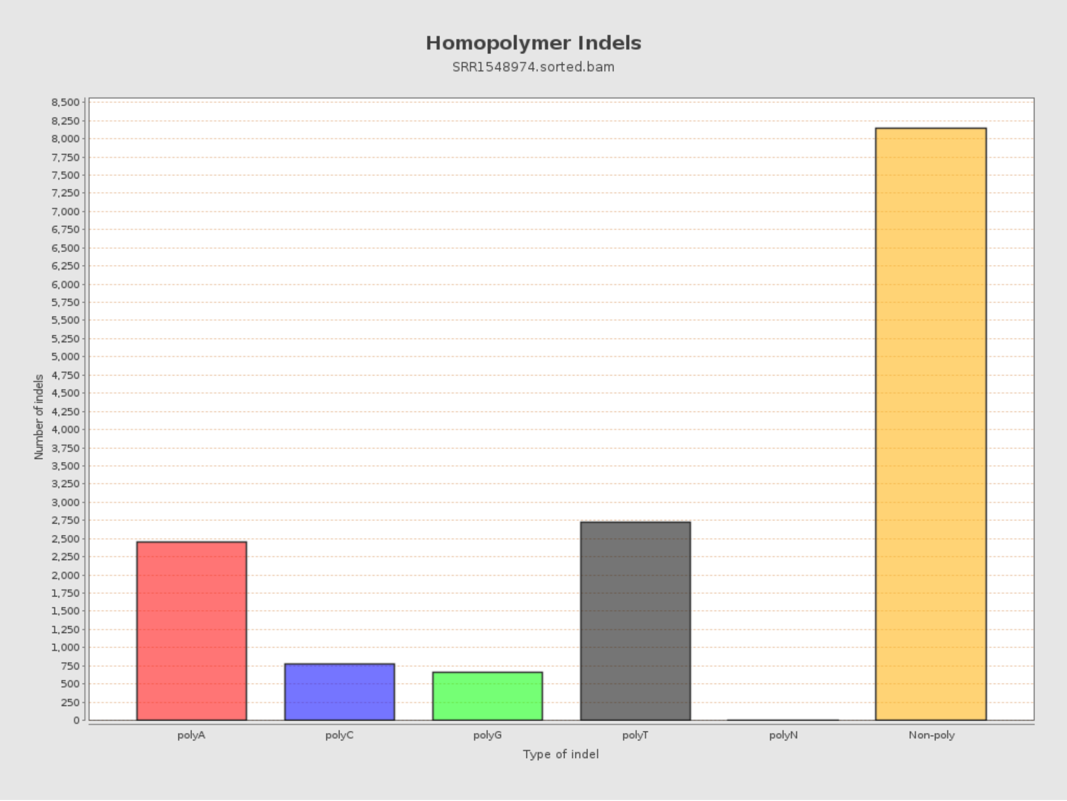
9. Results : Mapped Reads GC-content Distribution



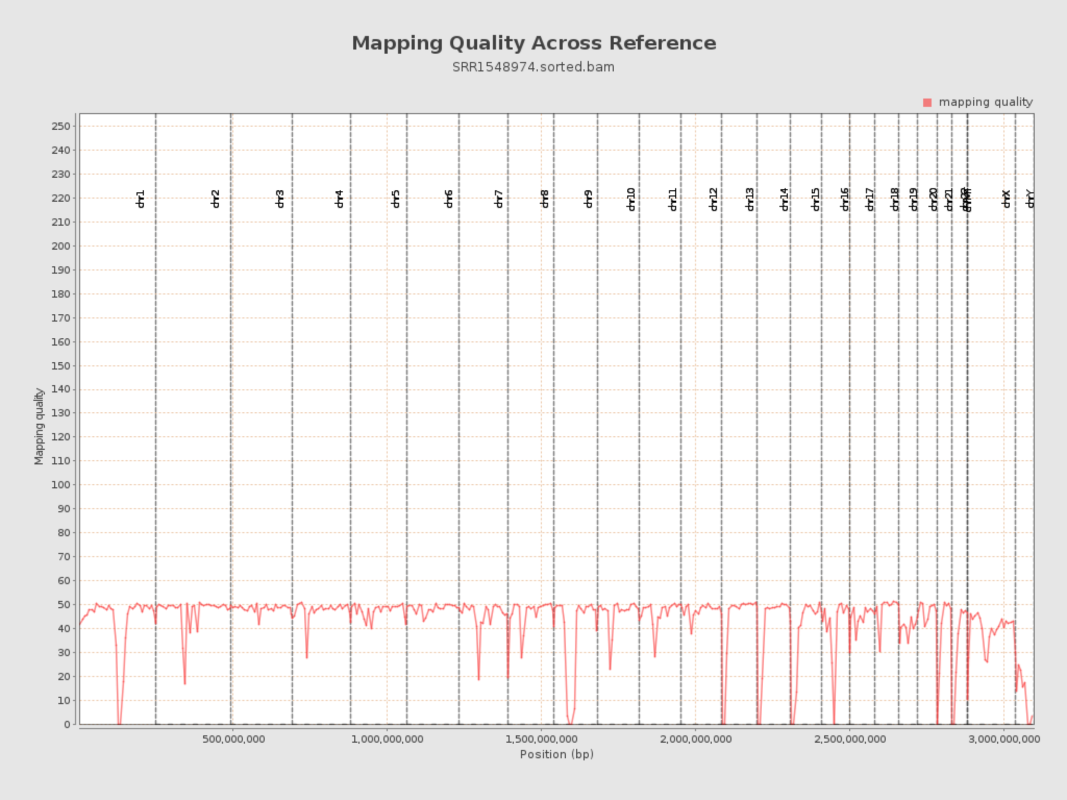
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram