Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:38:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971323.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_SRR2971323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:38:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	86,738,332
Mapped reads	75,181,671 / 86.68%
Unmapped reads	11,556,661 / 13.32%
Mapped paired reads	0 / 0%
Secondary alignments	0
Read min/max/mean length	40 / 40 / 40
Duplicated reads (estimated)	25,035,950 / 28.86%
Duplication rate	30.52%
Clipped reads	10,229,750 / 11.79%

2.2. ACGT Content

Number/percentage of A's	793,670,312 / 26.92%
Number/percentage of C's	657,324,278 / 22.29%
Number/percentage of T's	824,022,769 / 27.95%
Number/percentage of G's	673,507,153 / 22.84%
Number/percentage of N's	25,602 / 0%
GC Percentage	45.14%

2.3. Coverage

Mean	0.9526
Standard Deviation	6.7256

2.4. Mapping Quality

Mean Mapping Quality	28.94

2.5. Mismatches and indels

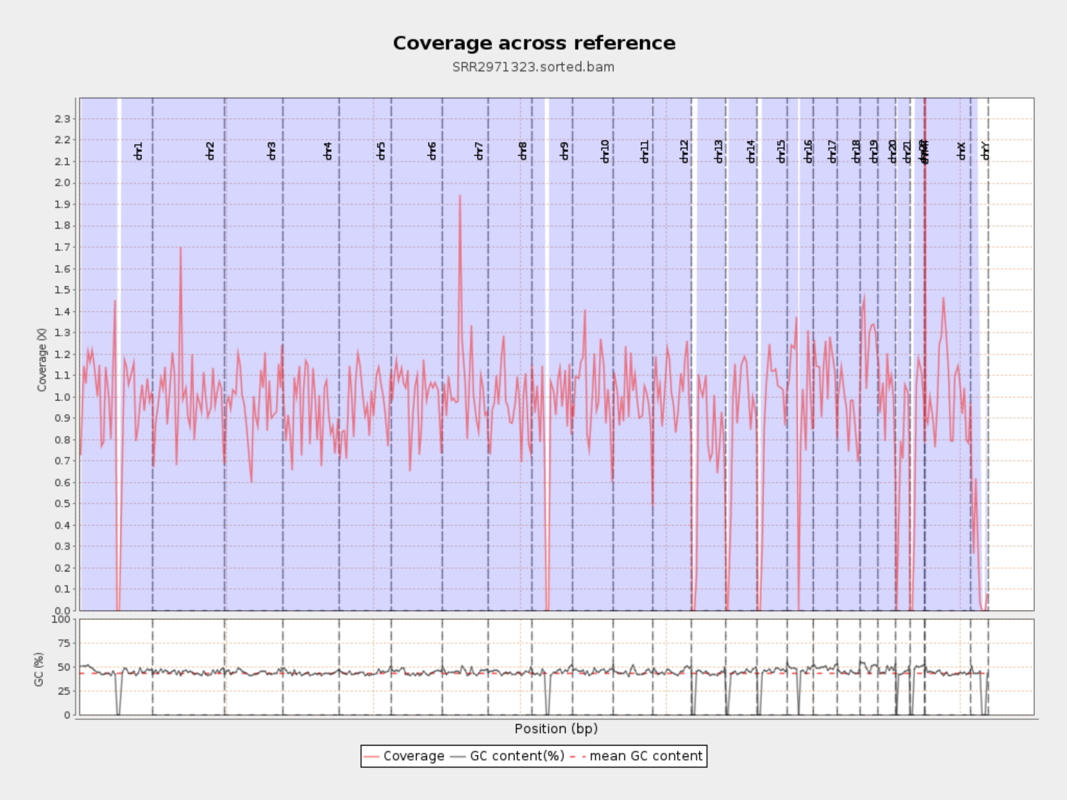
General error rate	0.43%
Mismatches	12,656,049
Insertions	134,778
Mapped reads with at least one insertion	0.18%
Deletions	246,699
Mapped reads with at least one deletion	0.33%
Homopolymer indels	34.05%

2.6. Chromosome stats

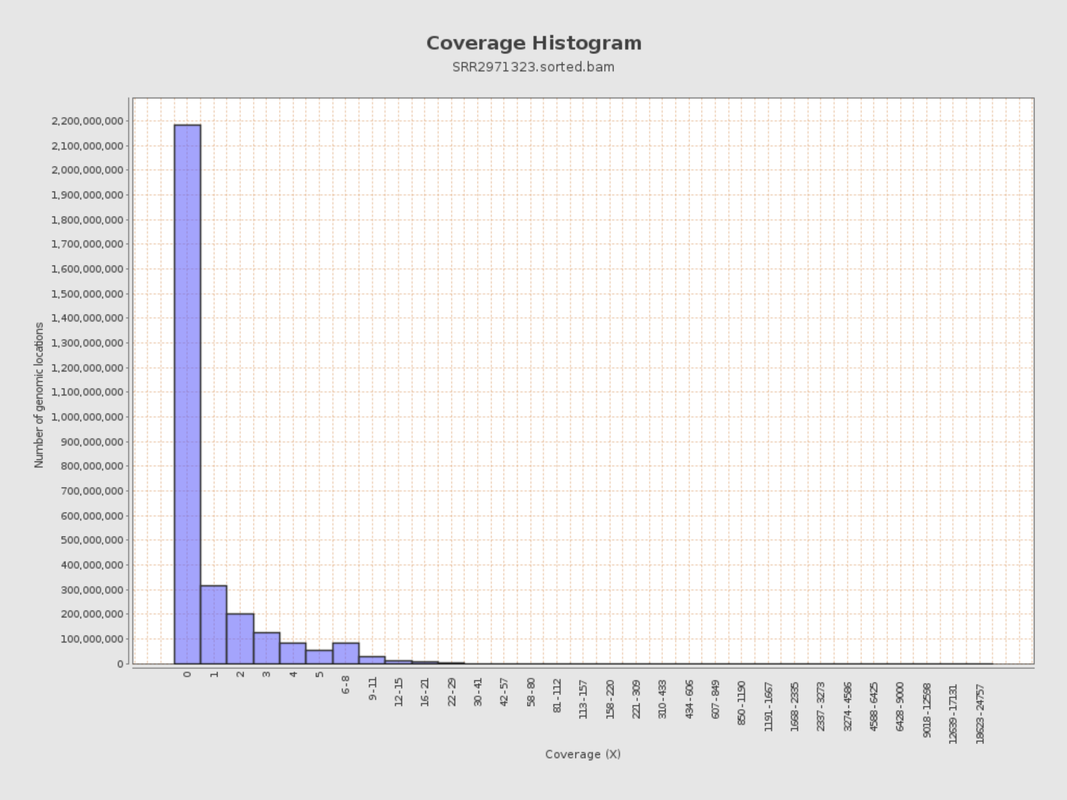
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	241156874	0.9675	11.7365
chr2	243199373	244075977	1.0036	6.5311
chr3	198022430	193365464	0.9765	2.5711
chr4	191154276	177526129	0.9287	3.1885
chr5	180915260	175120488	0.968	2.7207
chr6	171115067	172234504	1.0065	3.0347
chr7	159138663	168145767	1.0566	10.2149
chr8	146364022	140872747	0.9625	12.5985

chr9	141213431	124998301	0.8852	6.727
chr10	135534747	139724525	1.0309	5.5237
chr11	135006516	134457074	0.9959	5.7707
chr12	133851895	139257683	1.0404	2.9853
chr13	115169878	84657711	0.7351	2.0122
chr14	107349540	91762399	0.8548	4.1178
chr15	102531392	86499767	0.8436	2.6476
chr16	90354753	88307106	0.9773	3.395
chr17	81195210	91235234	1.1237	3.041
chr18	78077248	72329743	0.9264	13.3949
chr19	59128983	76466571	1.2932	12.8441
chr20	63025520	63590734	1.009	3.1829
chr21	48129895	34797164	0.723	3.1594
chr22	51304566	37788645	0.7366	2.3059
chrMT	16571	76220	4.5996	5.5181
chrX	155270560	156788211	1.0098	4.2934
chrY	59373566	13623089	0.2294	1.9702

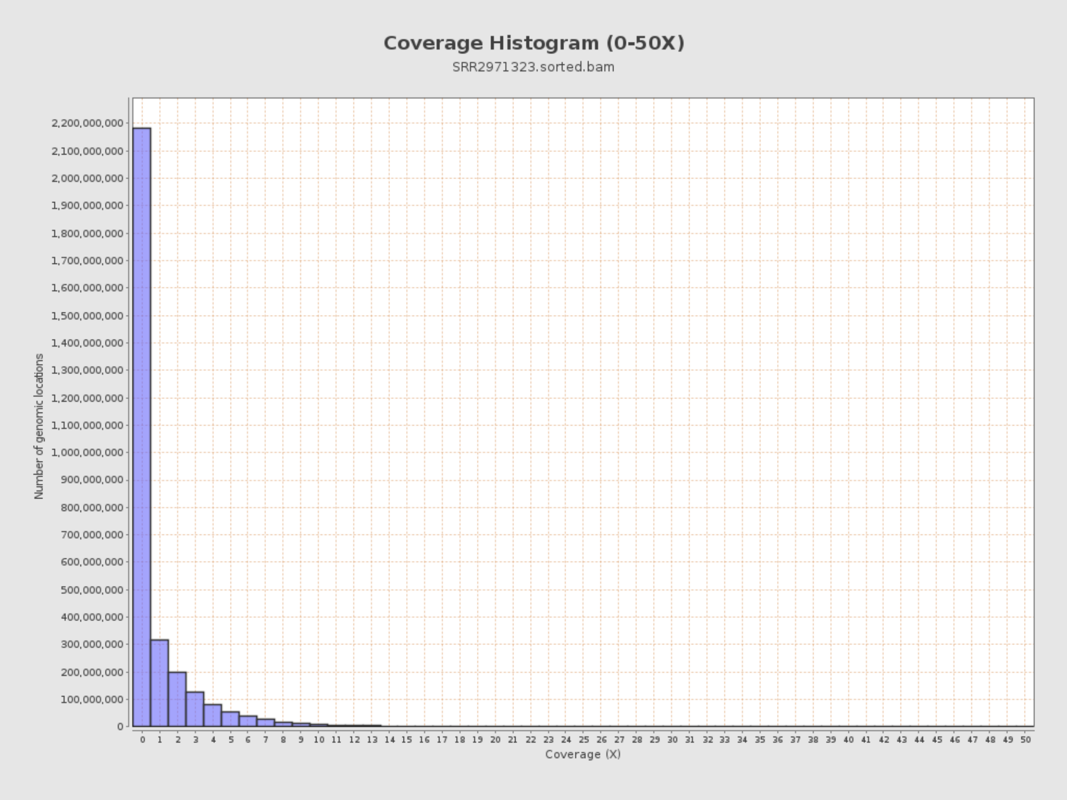
3. Results : Coverage across reference



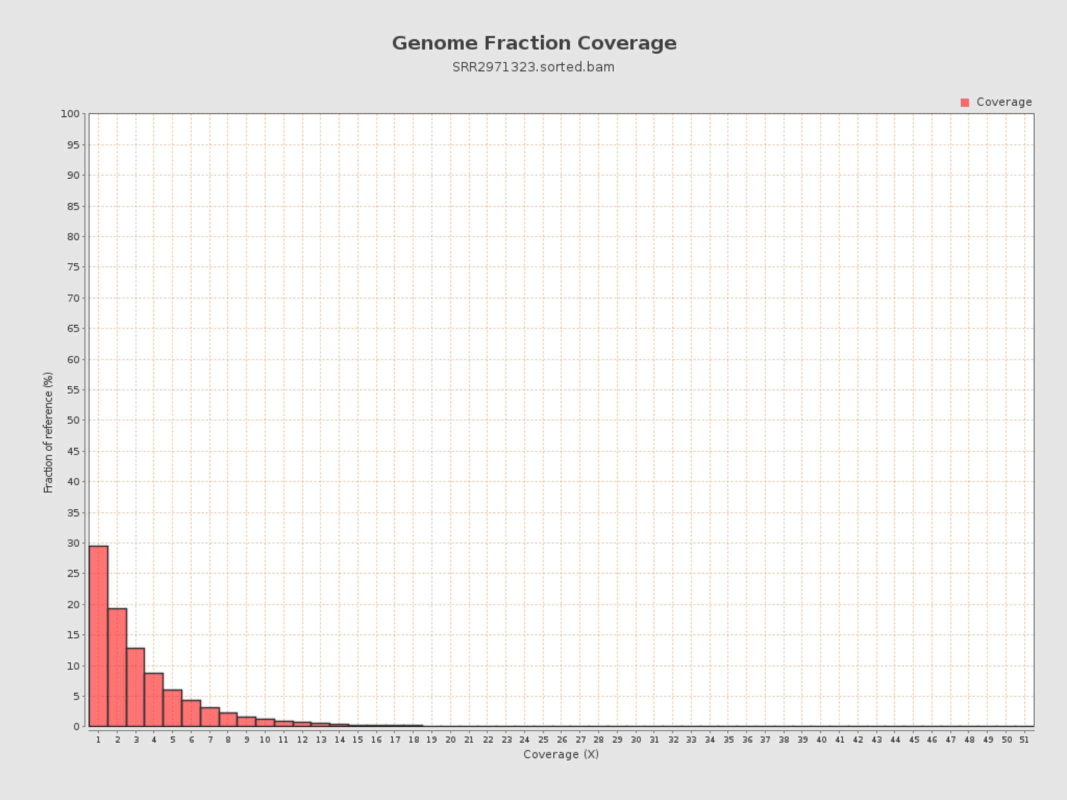
4. Results : Coverage Histogram



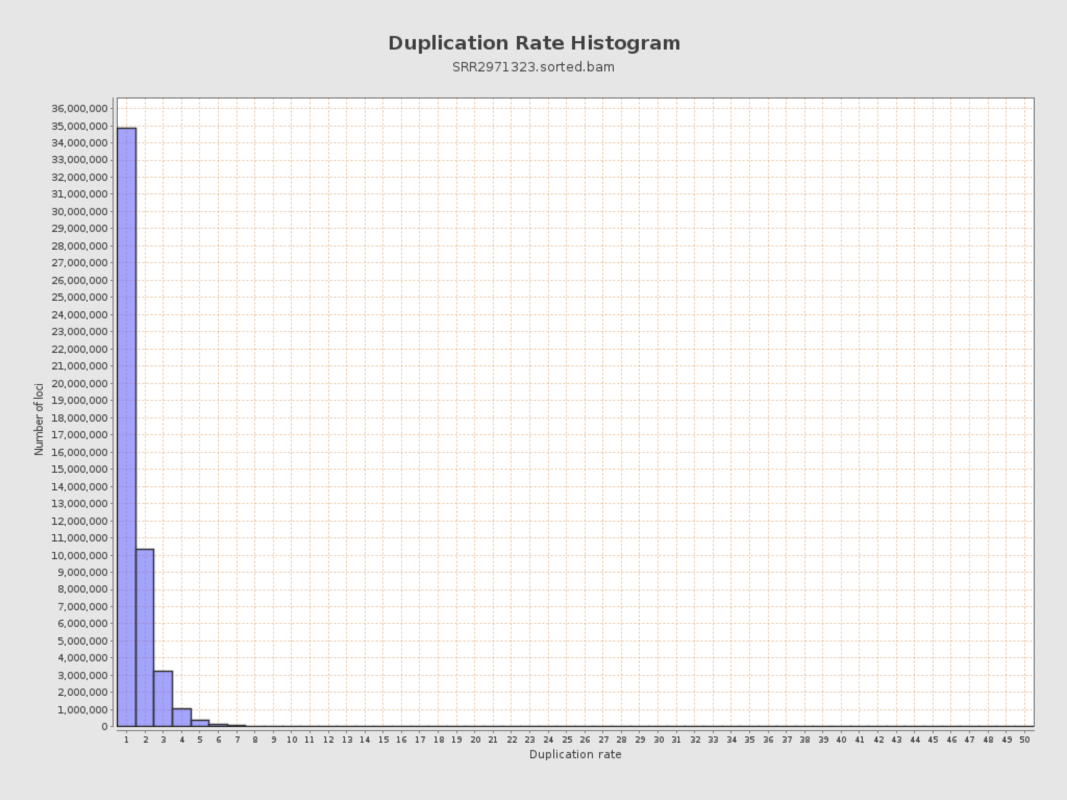
5. Results : Coverage Histogram (0-50X)



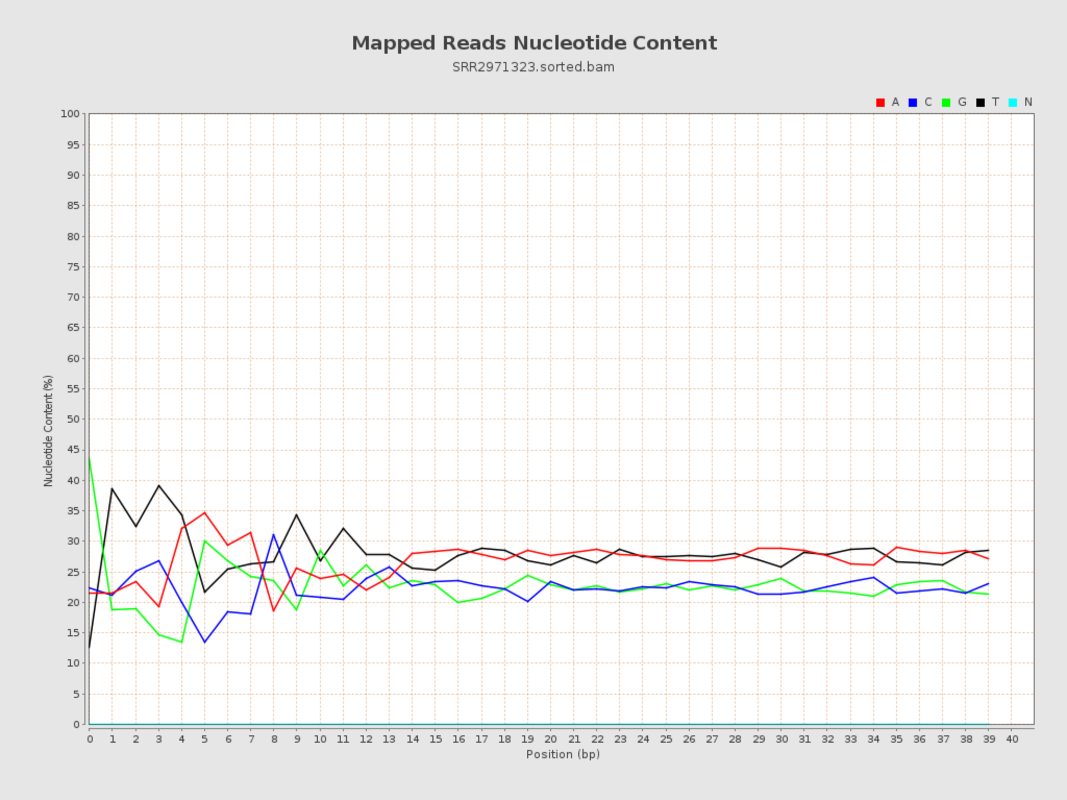
6. Results : Genome Fraction Coverage



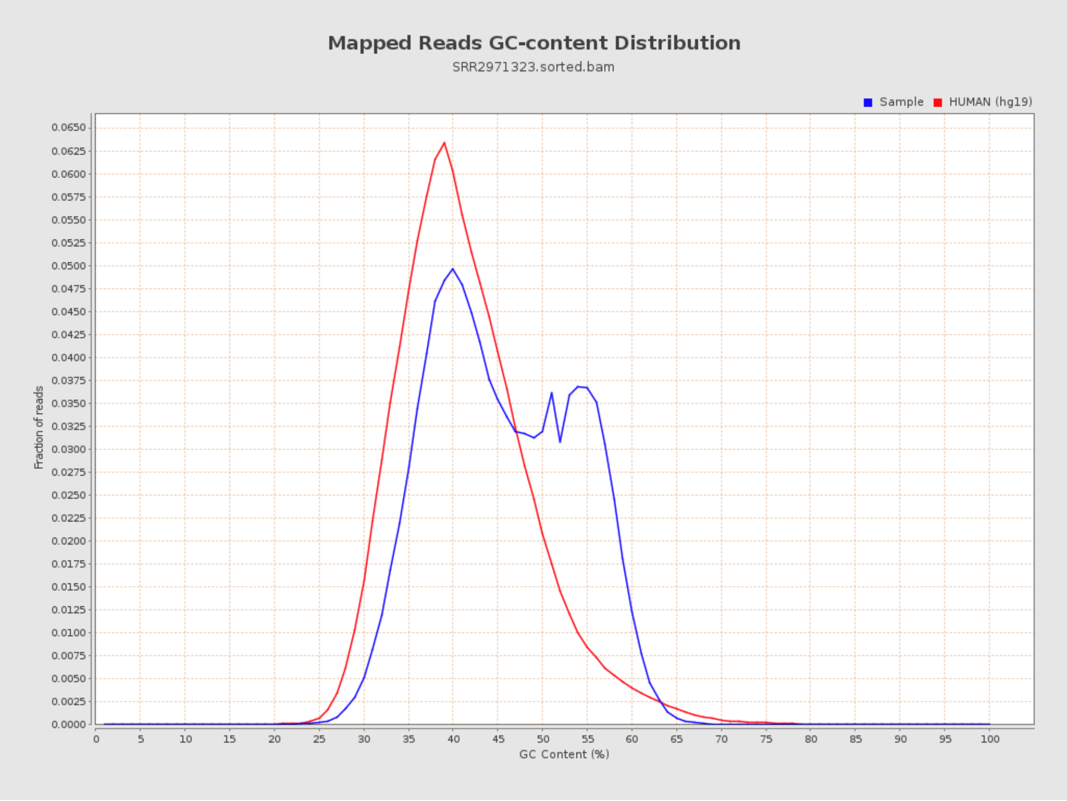
7. Results : Duplication Rate Histogram



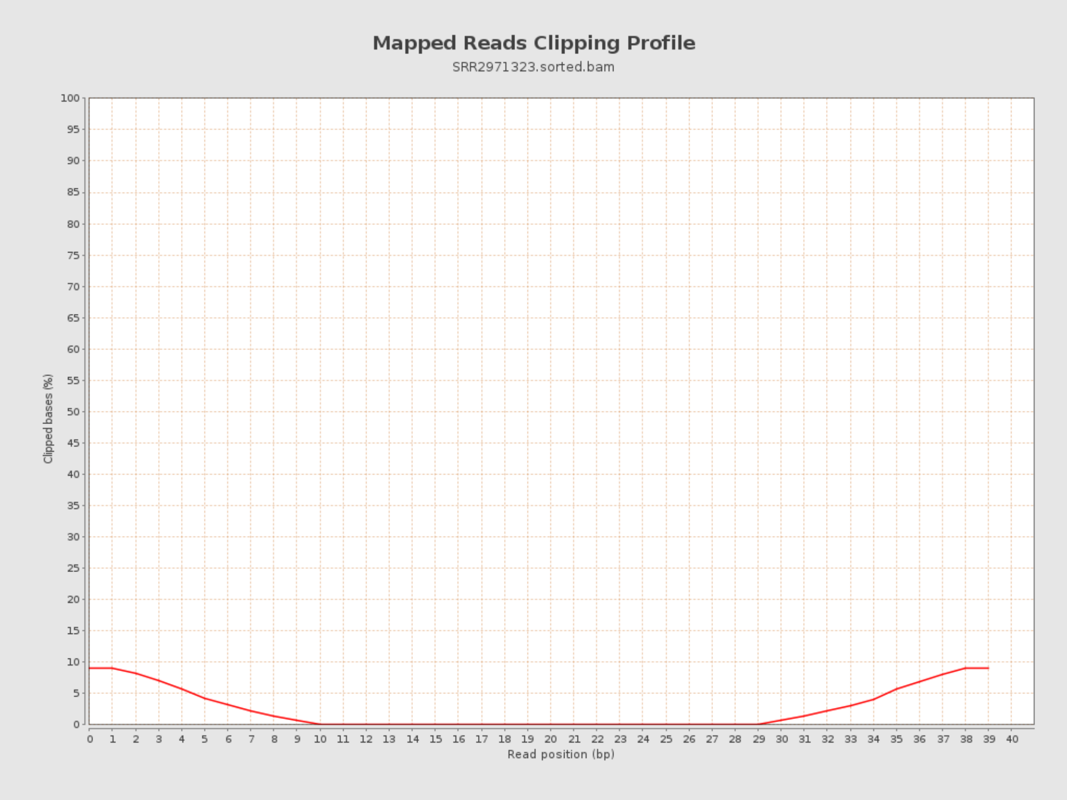
8. Results : Mapped Reads Nucleotide Content



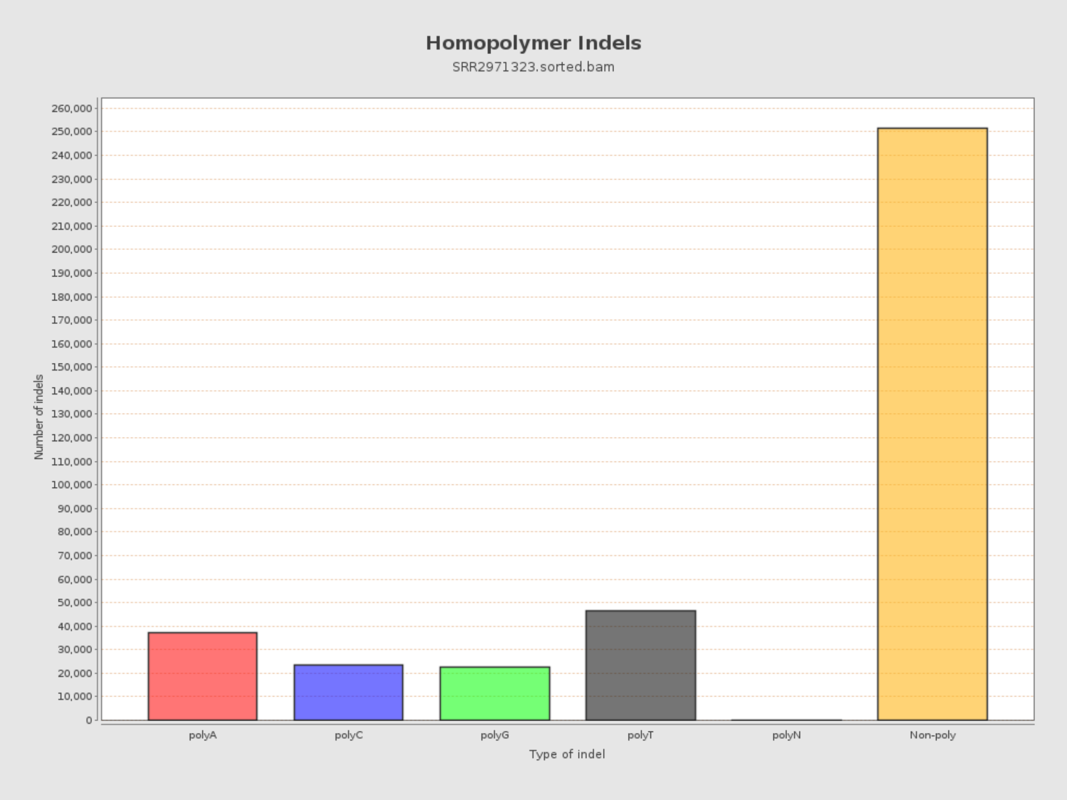
9. Results : Mapped Reads GC-content Distribution



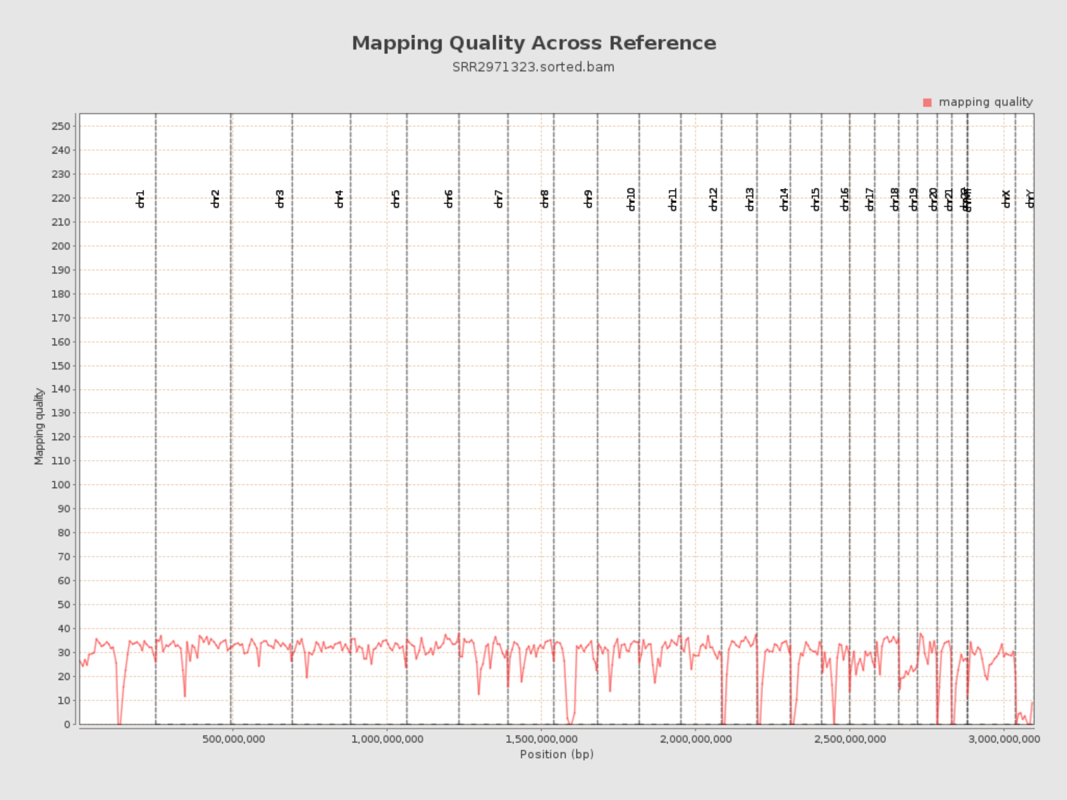
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram