Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 04:03:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004139.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_SRR6004139 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004139.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 04:02:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004139.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,079,547
Mapped reads	1,856,916 / 89.29%
Unmapped reads	222,631 / 10.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,702 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	53,373 / 2.57%
Duplication rate	1.78%
Clipped reads	1,018,965 / 49%

2.2. ACGT Content

Number/percentage of A's	33,280,447 / 27.71%
Number/percentage of C's	22,435,126 / 18.68%
Number/percentage of T's	36,060,118 / 30.03%
Number/percentage of G's	28,298,777 / 23.56%
Number/percentage of N's	24,338 / 0.02%
GC Percentage	42.24%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.3902

2.4. Mapping Quality

Mean Mapping Quality	42.36

2.5. Mismatches and indels

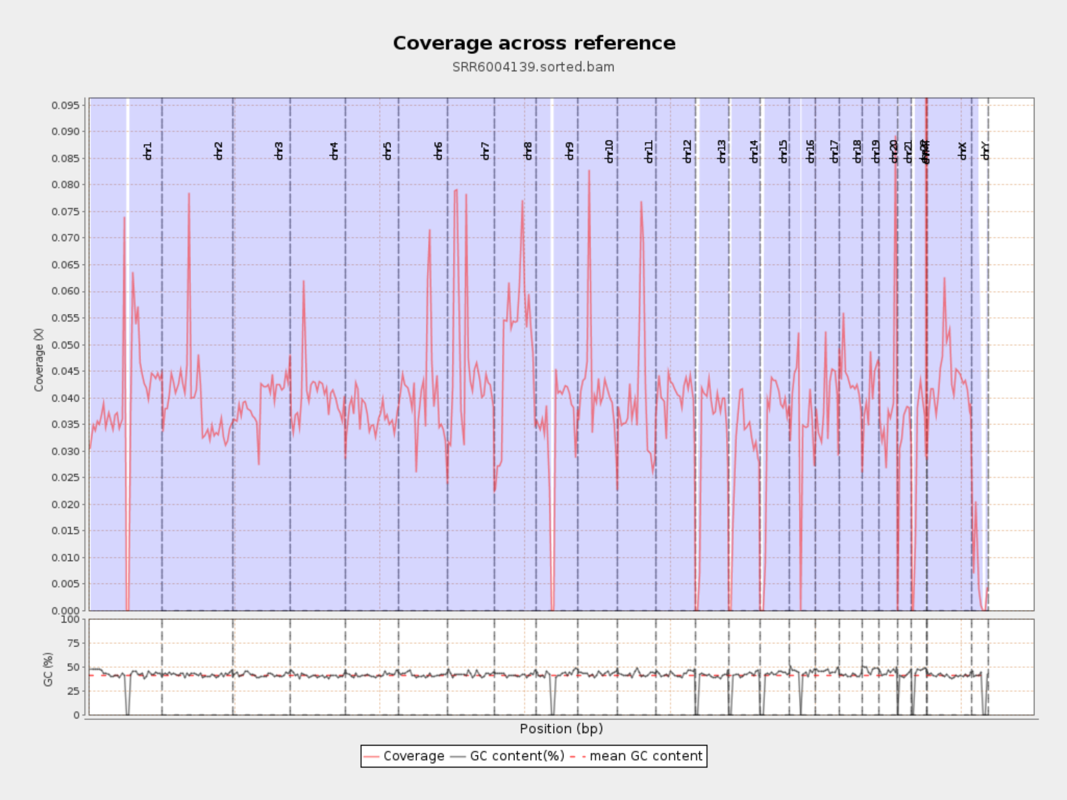
General error rate	0.9%
Mismatches	1,061,886
Insertions	10,879
Mapped reads with at least one insertion	0.58%
Deletions	35,350
Mapped reads with at least one deletion	1.88%
Homopolymer indels	43.81%

2.6. Chromosome stats

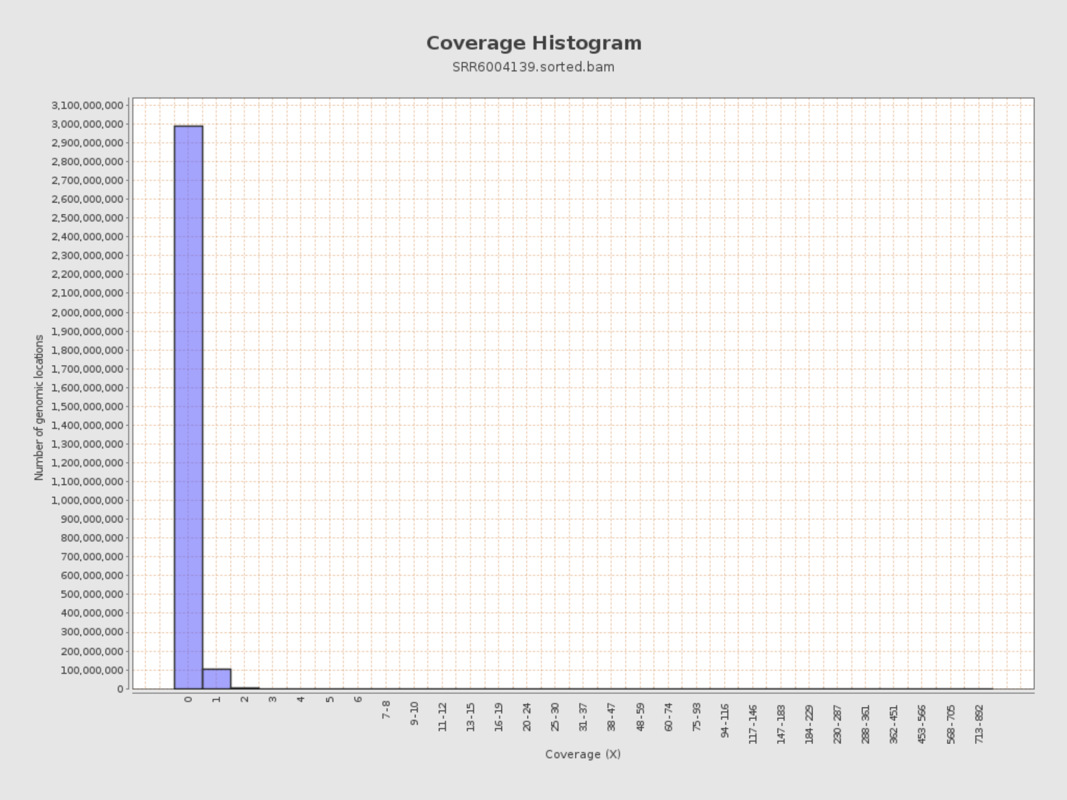
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9766534	0.0392	0.7515
chr2	243199373	9547359	0.0393	0.4188
chr3	198022430	7812504	0.0395	0.2132
chr4	191154276	7726317	0.0404	0.2448
chr5	180915260	6636558	0.0367	0.2092
chr6	171115067	7024386	0.0411	0.2515
chr7	159138663	7509566	0.0472	0.5445

chr8	146364022	7248942	0.0495	0.4214
chr9	141213431	4704002	0.0333	0.3694
chr10	135534747	5744275	0.0424	0.4104
chr11	135006516	5412906	0.0401	0.3194
chr12	133851895	5469124	0.0409	0.2208
chr13	115169878	3768095	0.0327	0.1918
chr14	107349540	3100487	0.0289	0.2346
chr15	102531392	3296389	0.0322	0.193
chr16	90354753	3201631	0.0354	0.2532
chr17	81195210	3193955	0.0393	0.2395
chr18	78077248	3432464	0.044	0.6851
chr19	59128983	2427212	0.041	0.5243
chr20	63025520	2681308	0.0425	0.2432
chr21	48129895	1517863	0.0315	0.2245
chr22	51304566	1375976	0.0268	0.1722
chrMT	16571	427823	25.8176	17.1618
chrX	155270560	6767247	0.0436	0.2606
chrY	59373566	365420	0.0062	0.1617

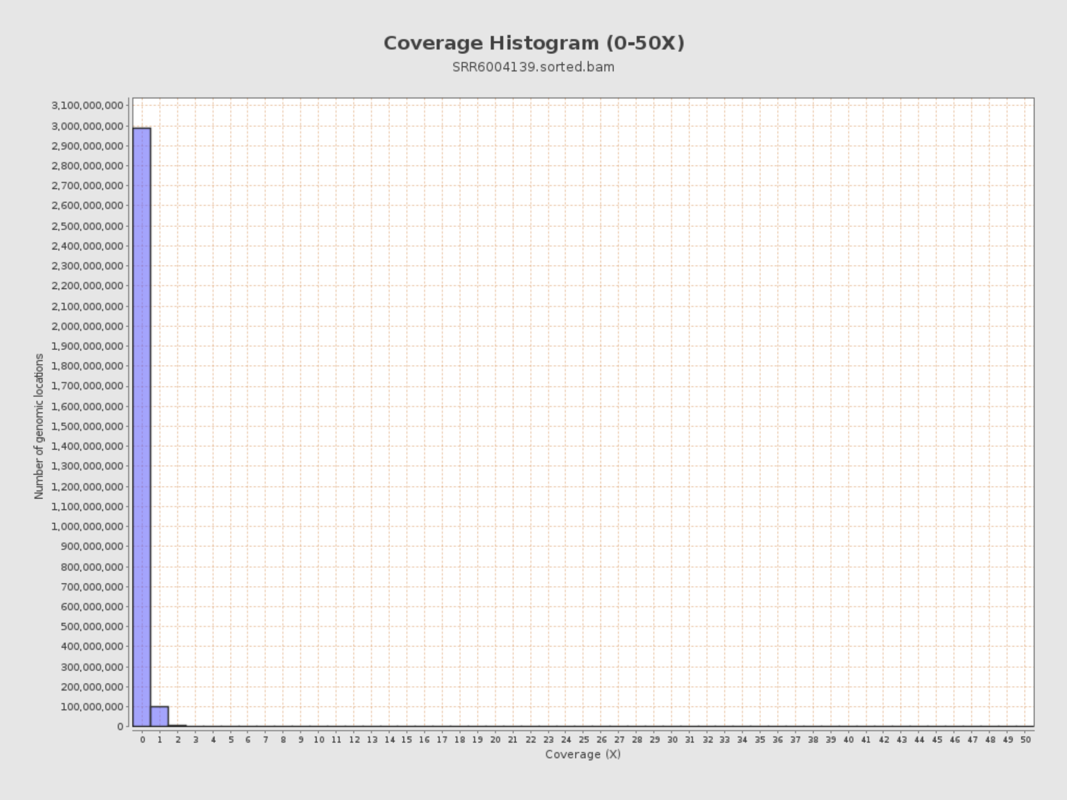
3. Results : Coverage across reference



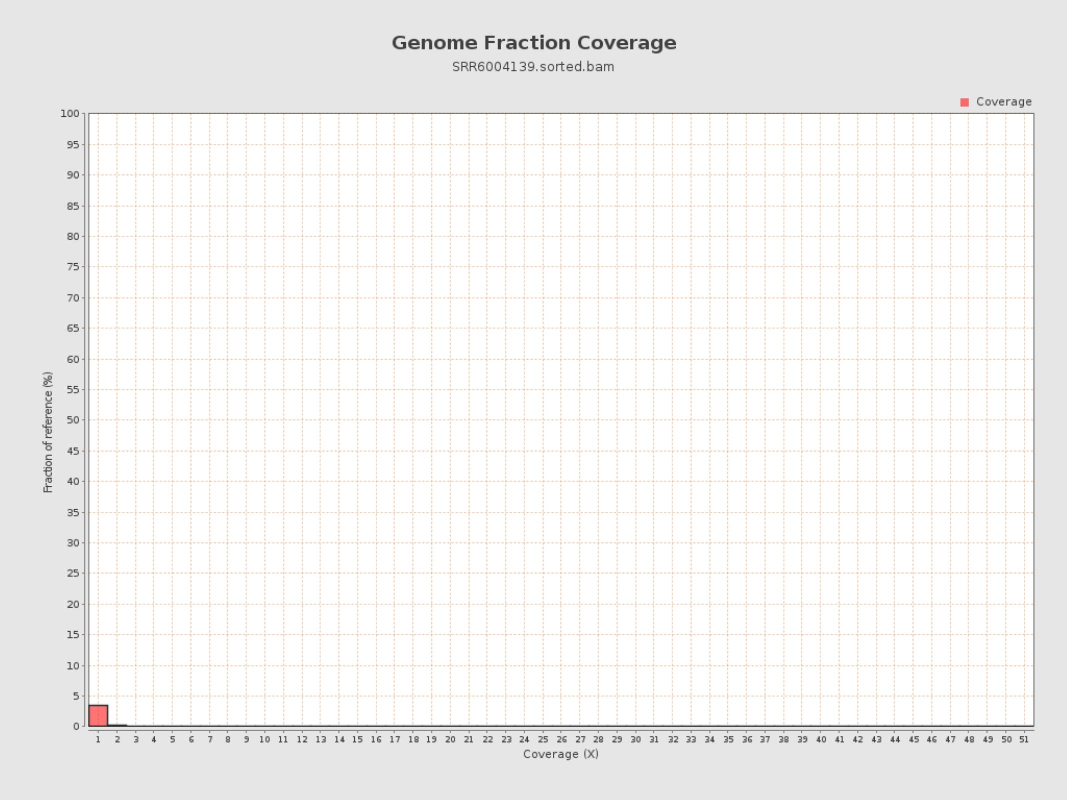
4. Results : Coverage Histogram



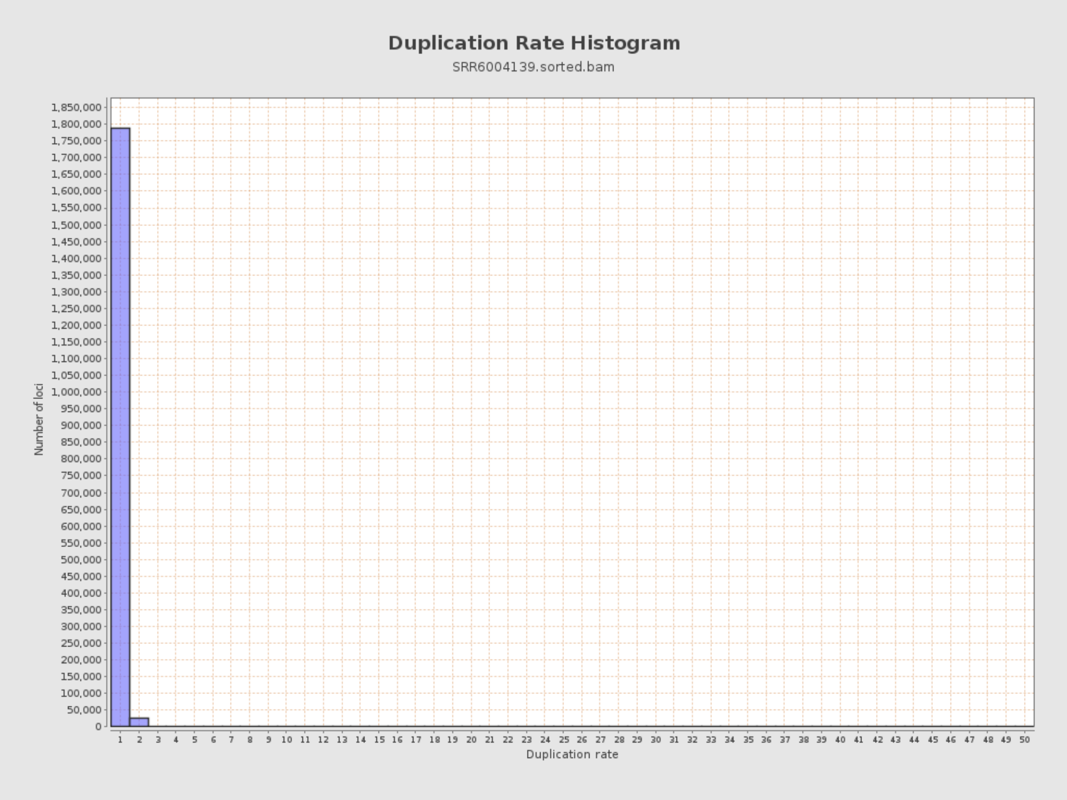
5. Results : Coverage Histogram (0-50X)



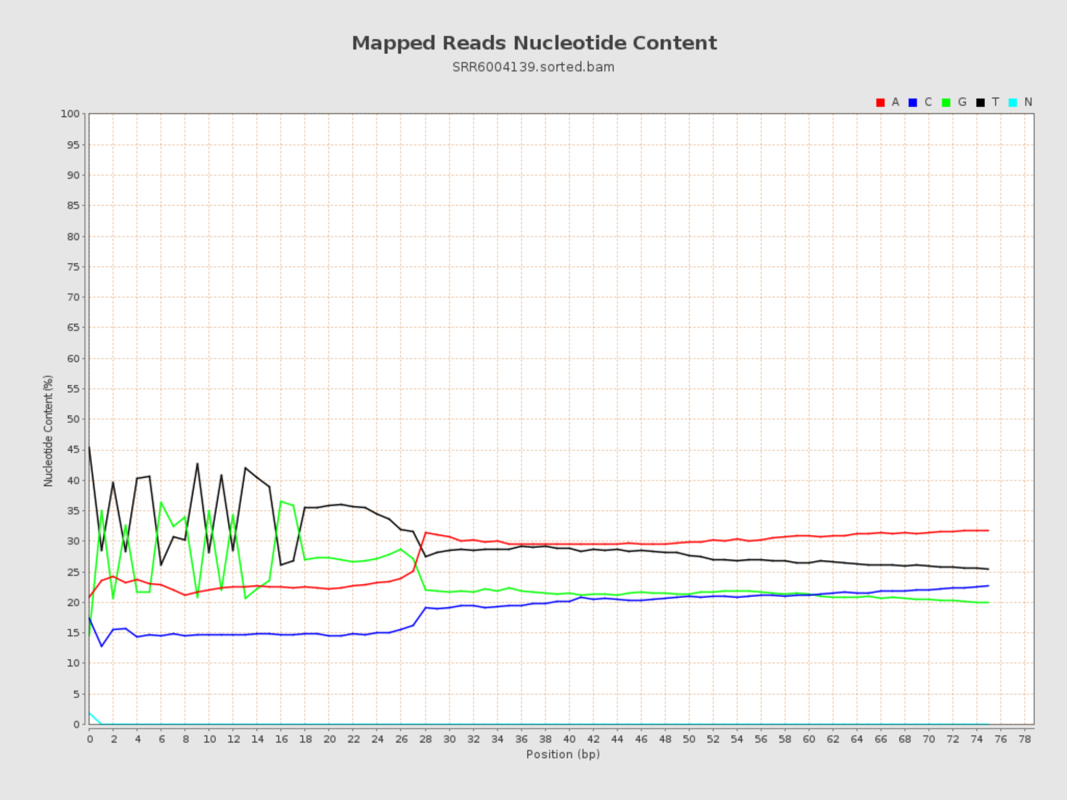
6. Results : Genome Fraction Coverage



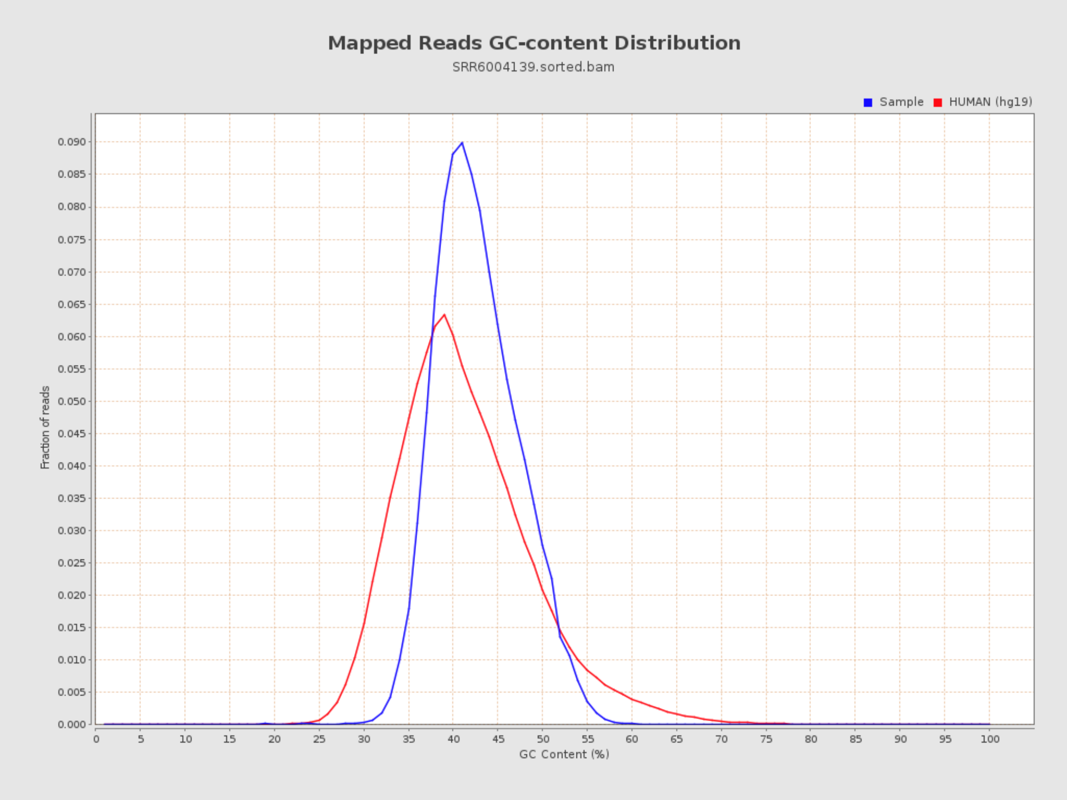
7. Results : Duplication Rate Histogram



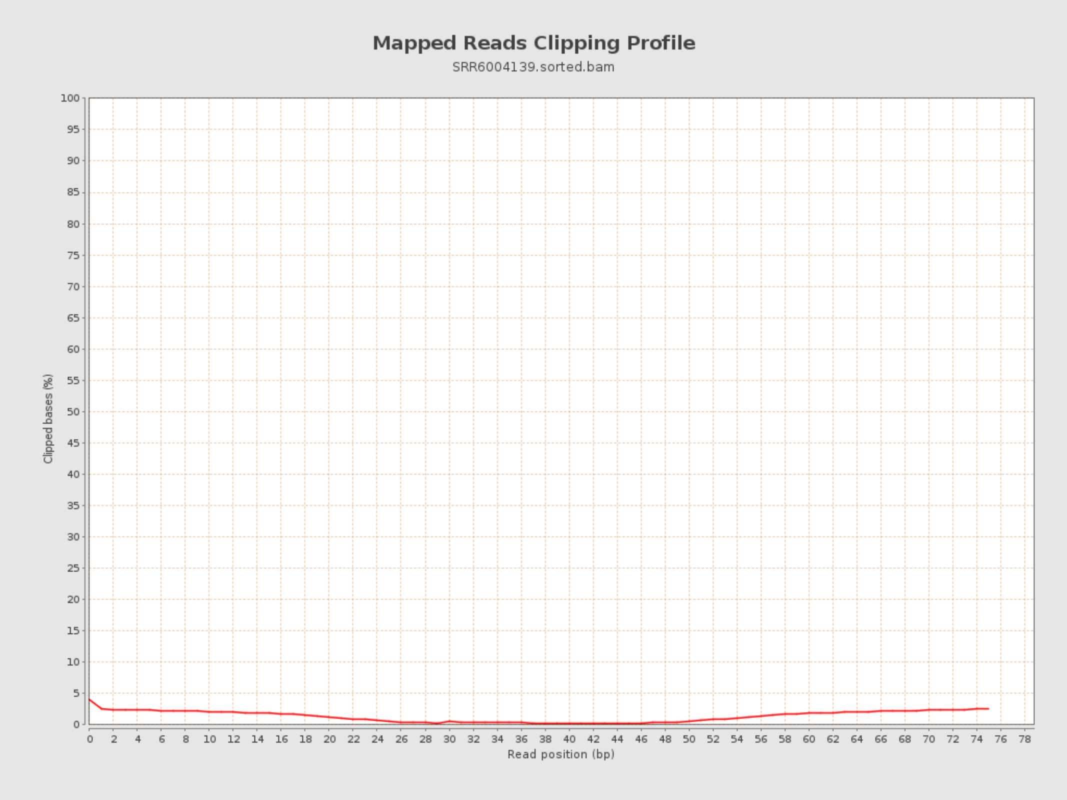
8. Results : Mapped Reads Nucleotide Content



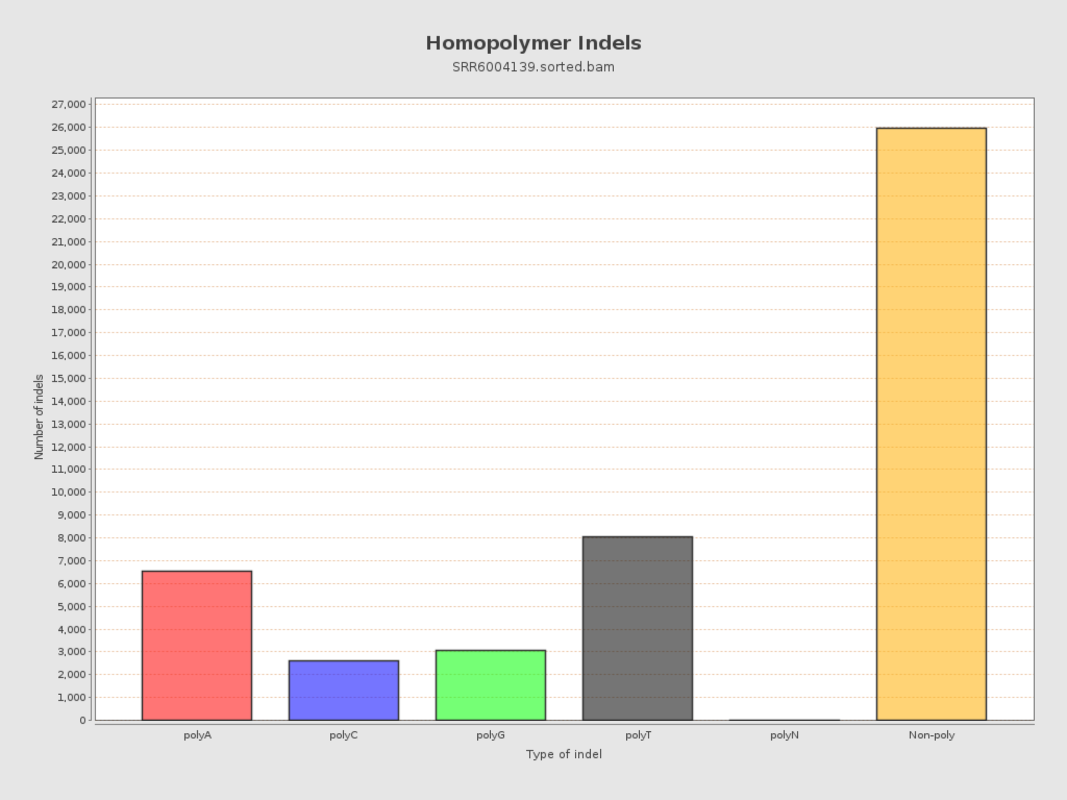
9. Results : Mapped Reads GC-content Distribution



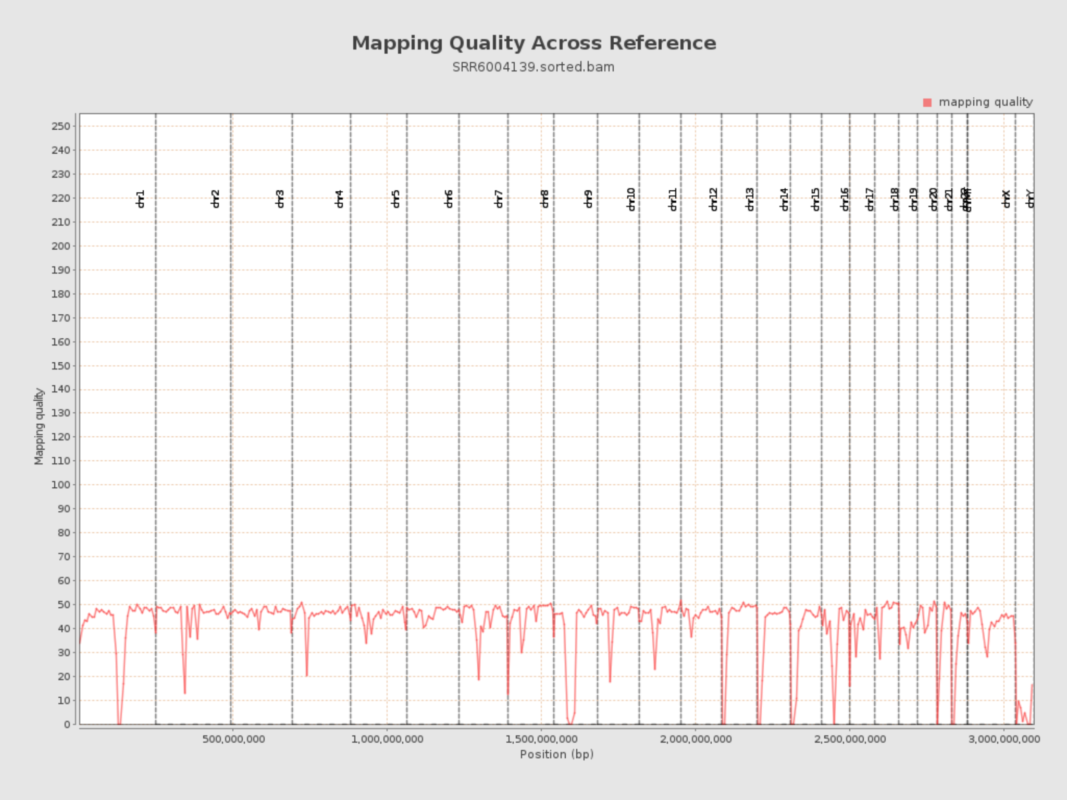
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram