Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 13:09:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008826.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_SRR6008826 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008826.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 13:09:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008826.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,464,237
Mapped reads	169,253 / 11.56%
Unmapped reads	1,294,984 / 88.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,910 / 0.13%
Read min/max/mean length	30 / 76 / 76.05
Duplicated reads (estimated)	13,278 / 0.91%
Duplication rate	6.21%
Clipped reads	83,001 / 5.67%

2.2. ACGT Content

Number/percentage of A's	3,056,357 / 27.76%
Number/percentage of C's	1,986,478 / 18.04%
Number/percentage of T's	3,566,837 / 32.4%
Number/percentage of G's	2,384,899 / 21.66%
Number/percentage of N's	14,495 / 0.13%
GC Percentage	39.71%

2.3. Coverage

Mean	0.0036

Standard Deviation	0.0958

2.4. Mapping Quality

Mean Mapping Quality	44.11

2.5. Mismatches and indels

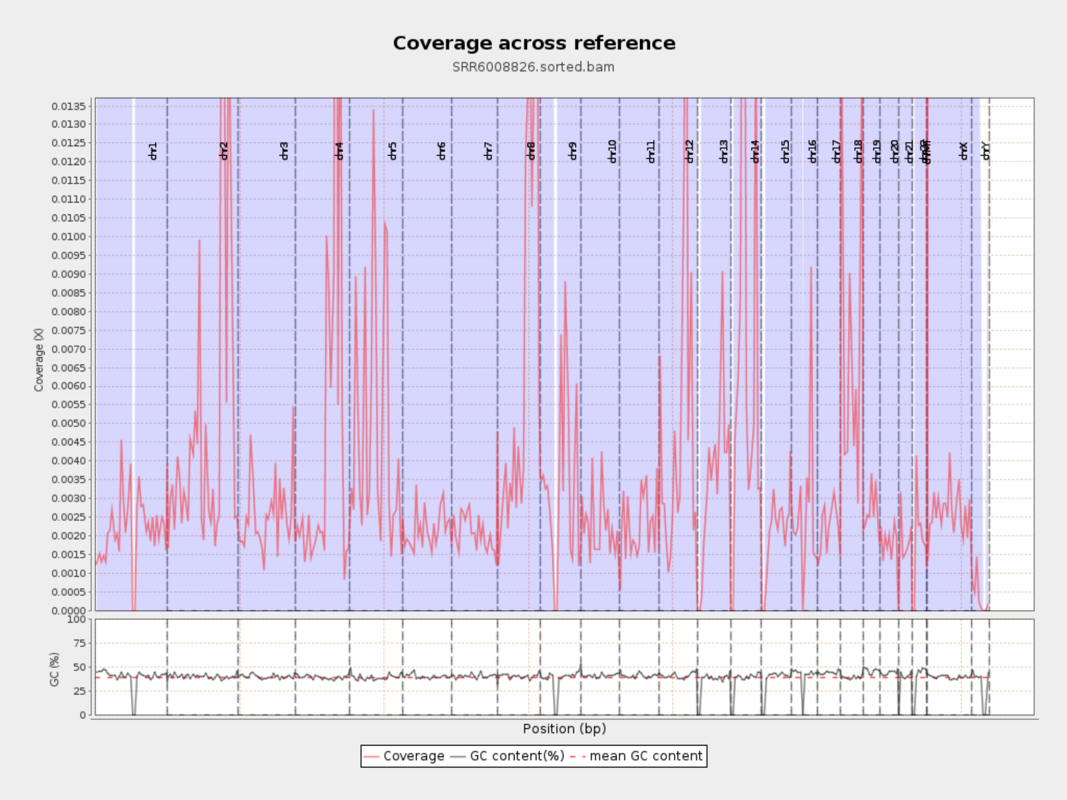
General error rate	0.9%
Mismatches	97,846
Insertions	832
Mapped reads with at least one insertion	0.49%
Deletions	3,355
Mapped reads with at least one deletion	1.96%
Homopolymer indels	45.4%

2.6. Chromosome stats

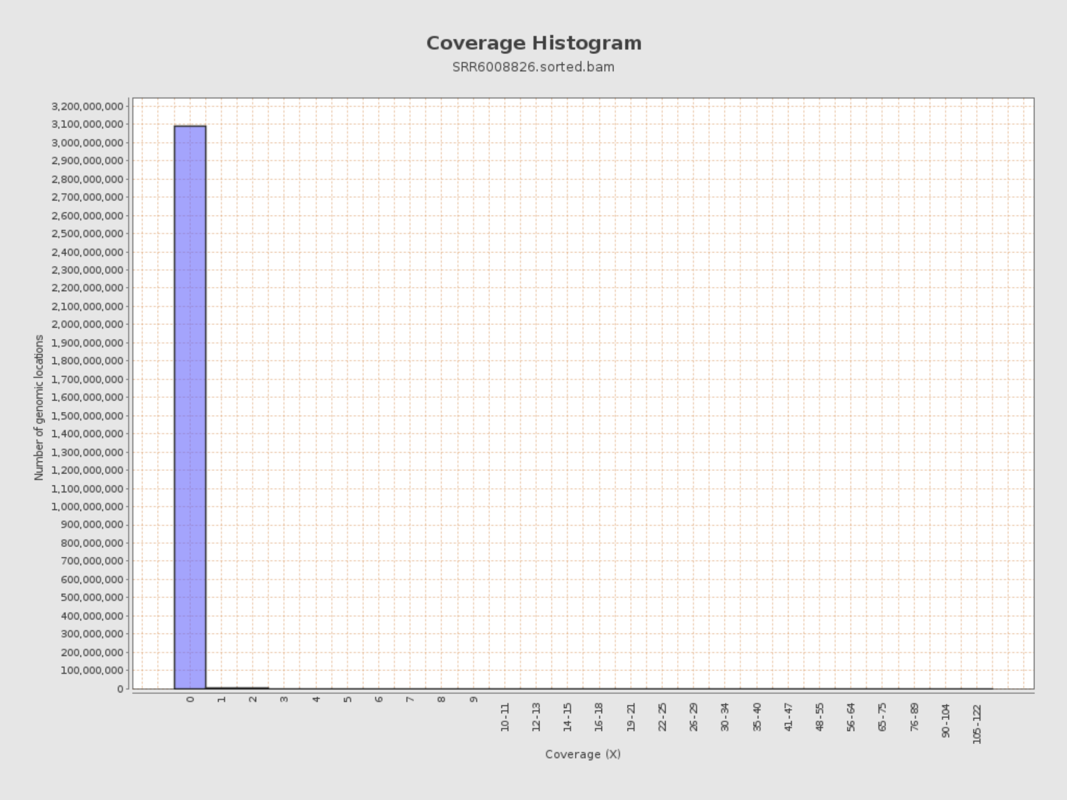
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	539182	0.0022	0.1013
chr2	243199373	1238602	0.0051	0.126
chr3	198022430	512669	0.0026	0.0712
chr4	191154276	996401	0.0052	0.1086
chr5	180915260	914575	0.0051	0.1036
chr6	171115067	371242	0.0022	0.0675
chr7	159138663	332406	0.0021	0.0642

chr8	146364022	1003958	0.0069	0.1316
chr9	141213431	473658	0.0034	0.0837
chr10	135534747	308491	0.0023	0.0669
chr11	135006516	312897	0.0023	0.0777
chr12	133851895	696947	0.0052	0.1097
chr13	115169878	408986	0.0036	0.0877
chr14	107349540	778866	0.0073	0.1382
chr15	102531392	208607	0.002	0.0661
chr16	90354753	244130	0.0027	0.0961
chr17	81195210	182458	0.0022	0.0647
chr18	78077248	594514	0.0076	0.1322
chr19	59128983	156486	0.0026	0.0737
chr20	63025520	113800	0.0018	0.0555
chr21	48129895	85650	0.0018	0.149
chr22	51304566	97690	0.0019	0.0589
chrMT	16571	12255	0.7395	1.1877
chrX	155270560	408171	0.0026	0.0804
chrY	59373566	22444	0.0004	0.0276

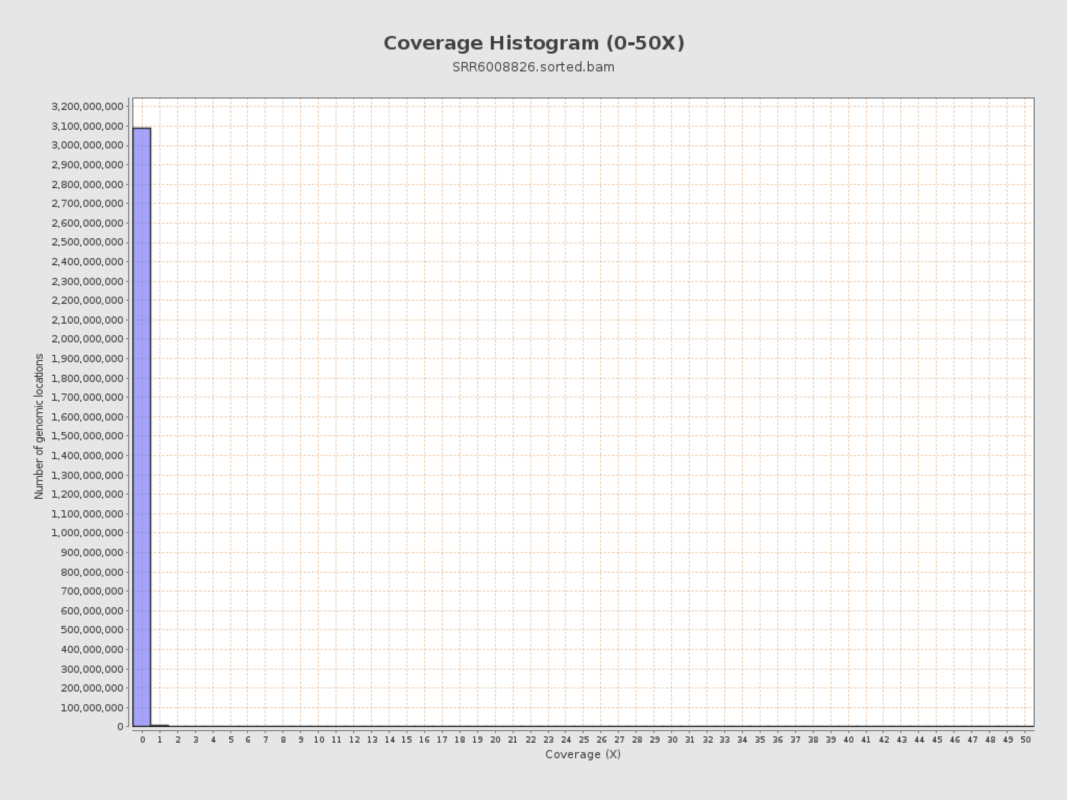
3. Results : Coverage across reference



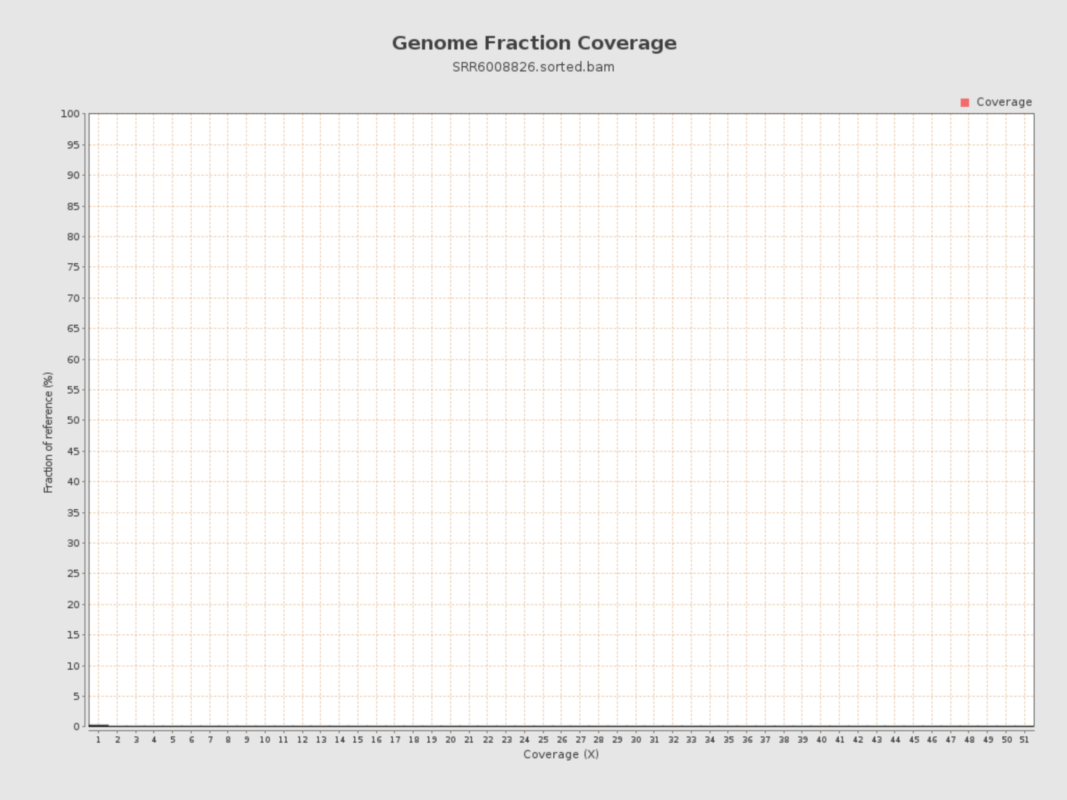
4. Results : Coverage Histogram



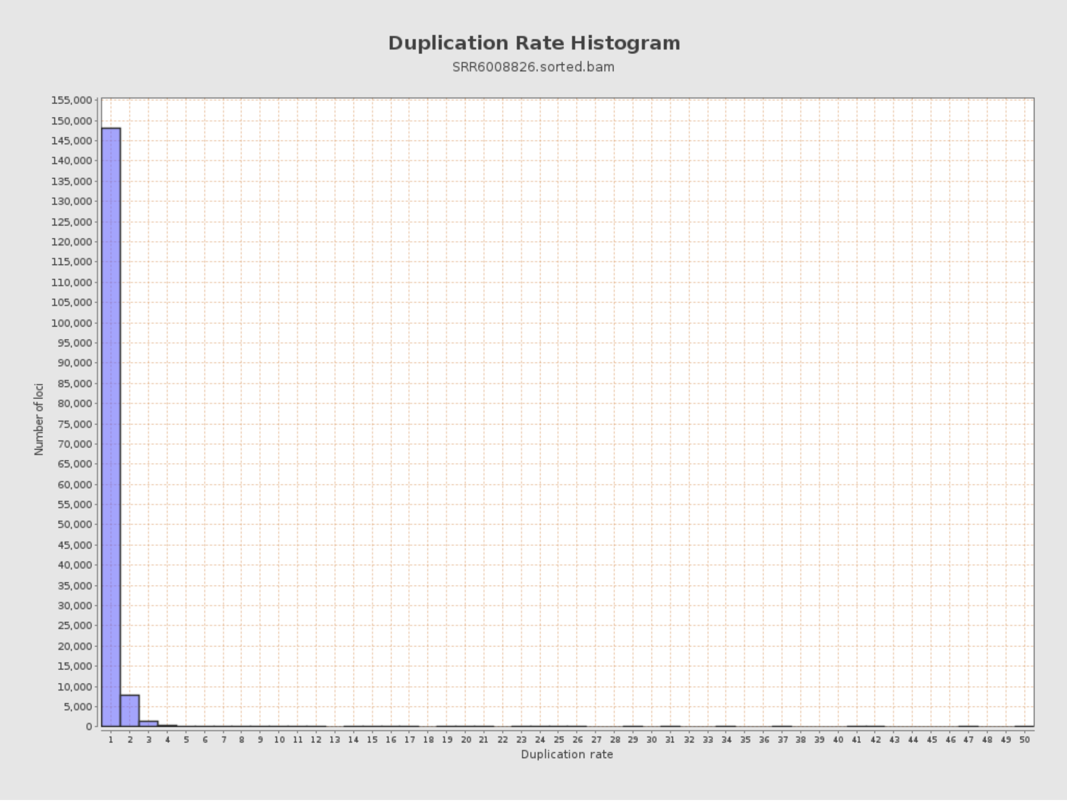
5. Results : Coverage Histogram (0-50X)



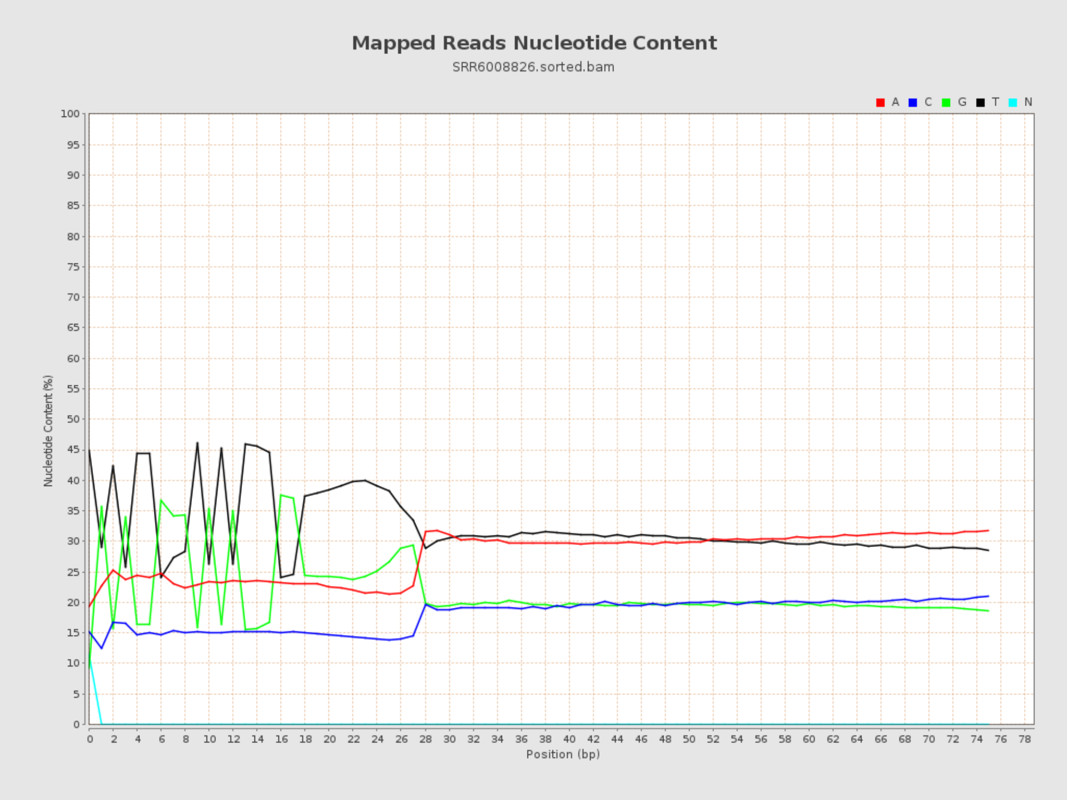
6. Results : Genome Fraction Coverage



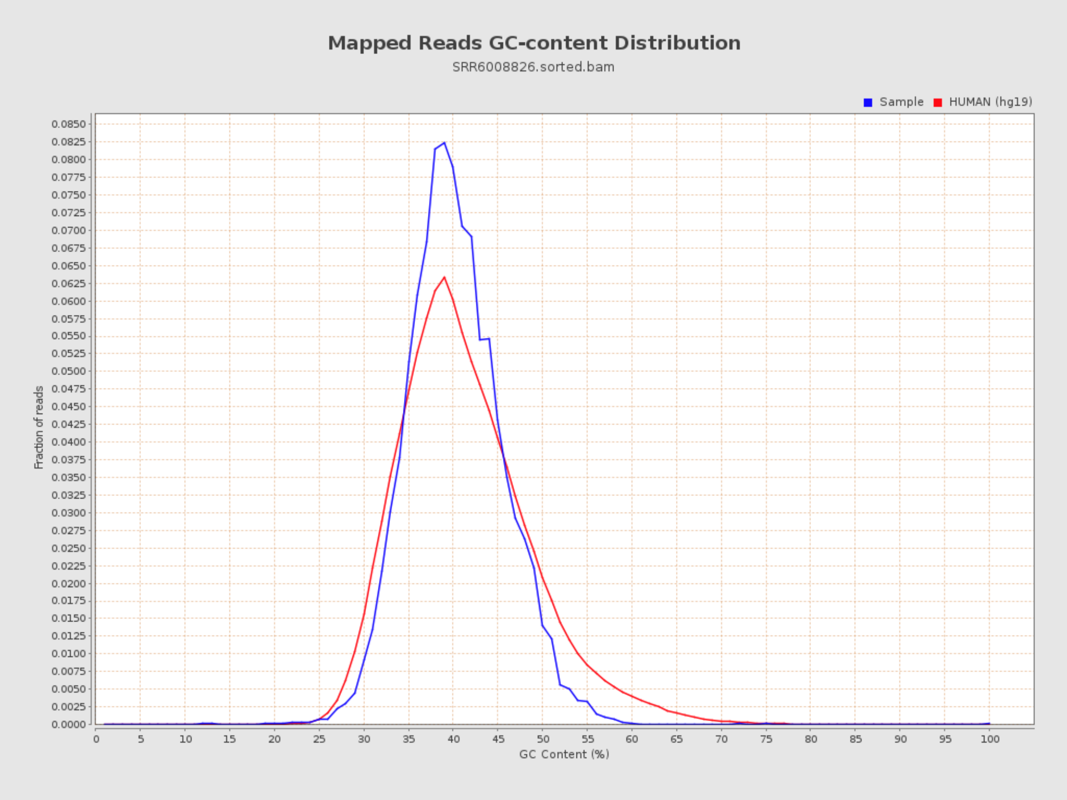
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content



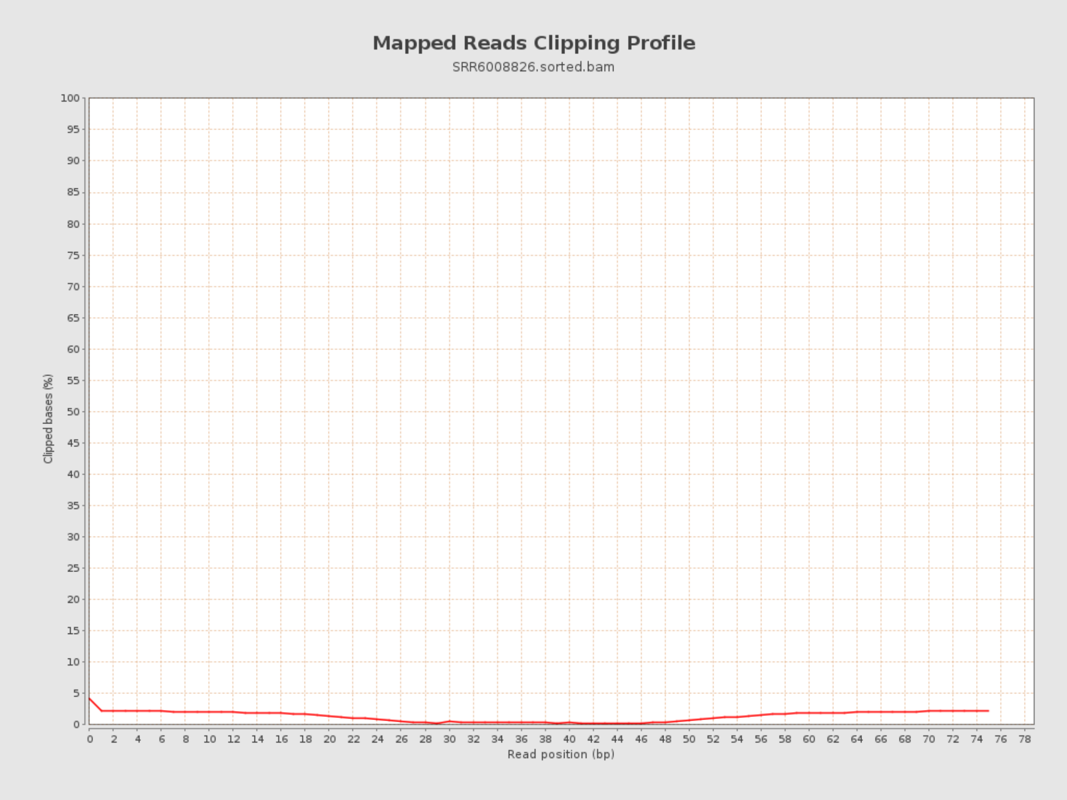
9. Results : Mapped Reads GC-content Distribution



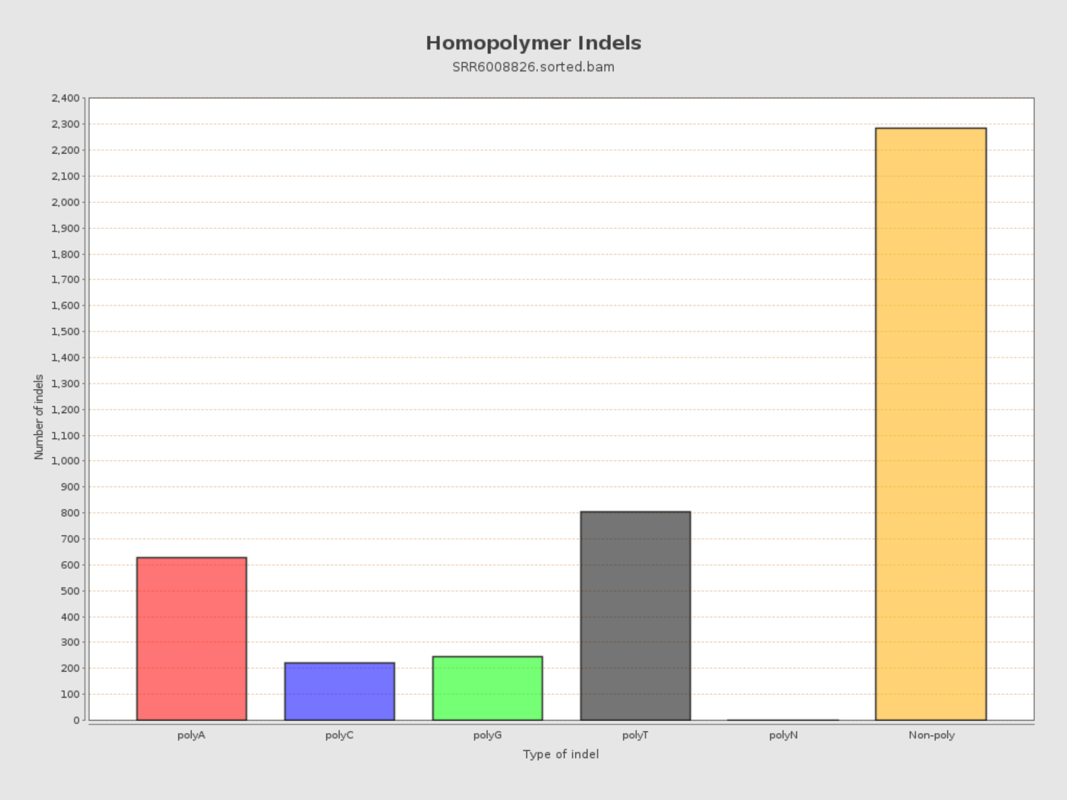
Mapped Reads GC-content Distribution

SRR6008826.sorted.bam

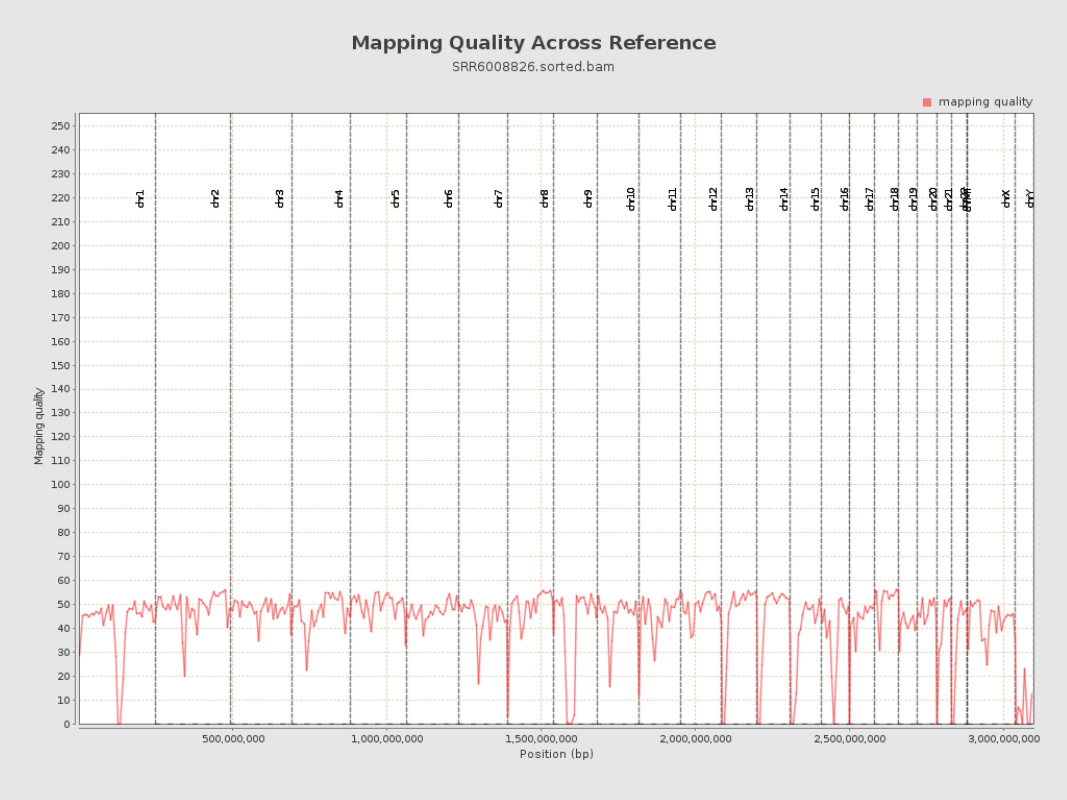
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram