Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:12:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068163.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_SRR6068163 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068163.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:12:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068163.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,235,025
Mapped reads	1,027,164 / 83.17%
Unmapped reads	207,861 / 16.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,495 / 0.77%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	76,332 / 6.18%
Duplication rate	6.27%
Clipped reads	512,128 / 41.47%

2.2. ACGT Content

Number/percentage of A's	20,351,913 / 29.89%
Number/percentage of C's	13,037,868 / 19.15%
Number/percentage of T's	20,777,129 / 30.51%
Number/percentage of G's	13,857,132 / 20.35%
Number/percentage of N's	70,393 / 0.1%
GC Percentage	39.5%

2.3. Coverage

Mean	0.022

Standard Deviation	0.2902

2.4. Mapping Quality

Mean Mapping Quality	47.37

2.5. Mismatches and indels

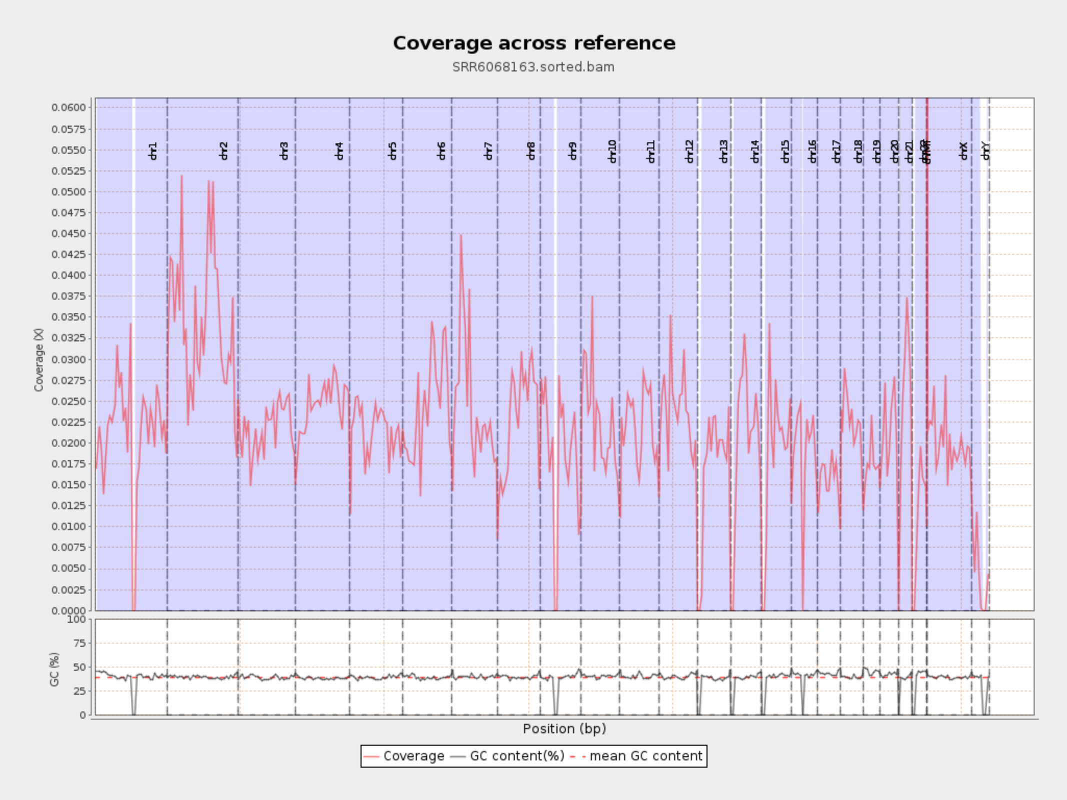
General error rate	0.91%
Mismatches	612,156
Insertions	4,925
Mapped reads with at least one insertion	0.48%
Deletions	18,525
Mapped reads with at least one deletion	1.78%
Homopolymer indels	47.97%

2.6. Chromosome stats

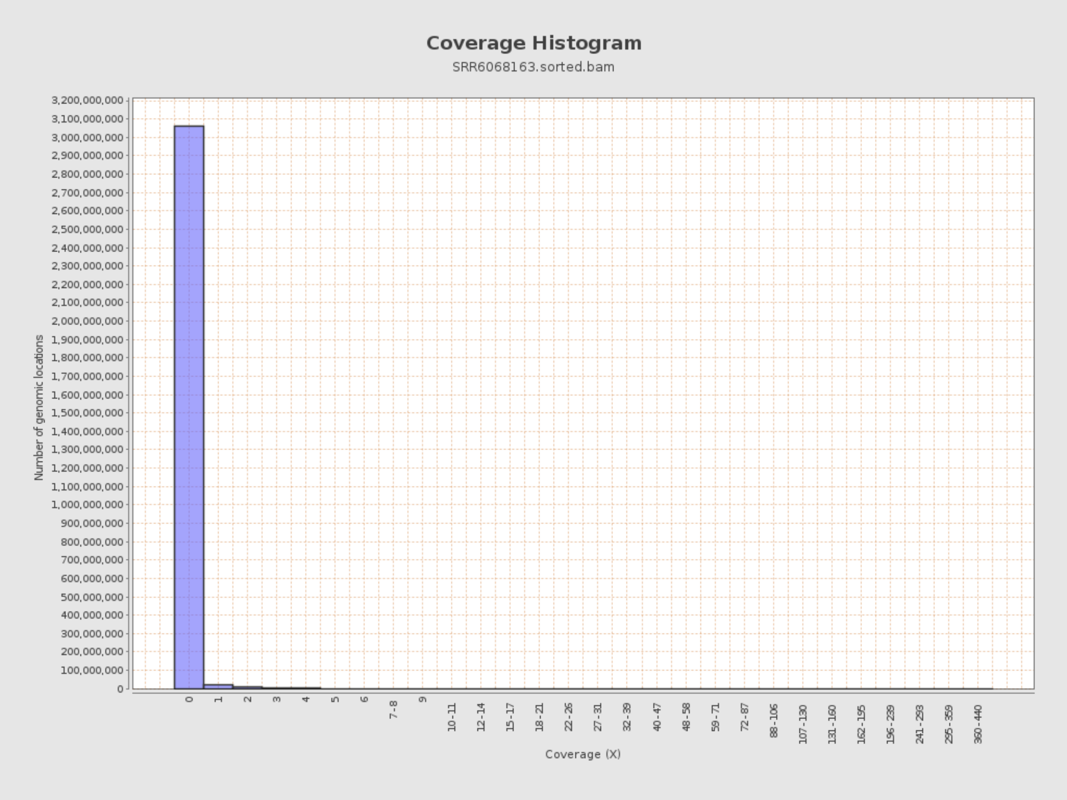
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5251543	0.0211	0.4279
chr2	243199373	8420797	0.0346	0.3428
chr3	198022430	4299587	0.0217	0.2453
chr4	191154276	4672757	0.0244	0.2644
chr5	180915260	3915342	0.0216	0.2449
chr6	171115067	4163376	0.0243	0.2687
chr7	159138663	3915874	0.0246	0.3523

chr8	146364022	3396844	0.0232	0.3581
chr9	141213431	2659263	0.0188	0.2526
chr10	135534747	3046364	0.0225	0.279
chr11	135006516	2968614	0.022	0.2742
chr12	133851895	3201863	0.0239	0.2594
chr13	115169878	1925120	0.0167	0.2168
chr14	107349540	2178173	0.0203	0.2441
chr15	102531392	1909158	0.0186	0.2294
chr16	90354753	1674137	0.0185	0.2273
chr17	81195210	1264910	0.0156	0.2081
chr18	78077248	1764983	0.0226	0.4065
chr19	59128983	1030076	0.0174	0.2705
chr20	63025520	1328540	0.0211	0.2437
chr21	48129895	1188624	0.0247	0.2642
chr22	51304566	570026	0.0111	0.1687
chrMT	16571	16259	0.9812	1.5444
chrX	155270560	3112779	0.02	0.2386
chrY	59373566	251564	0.0042	0.1025

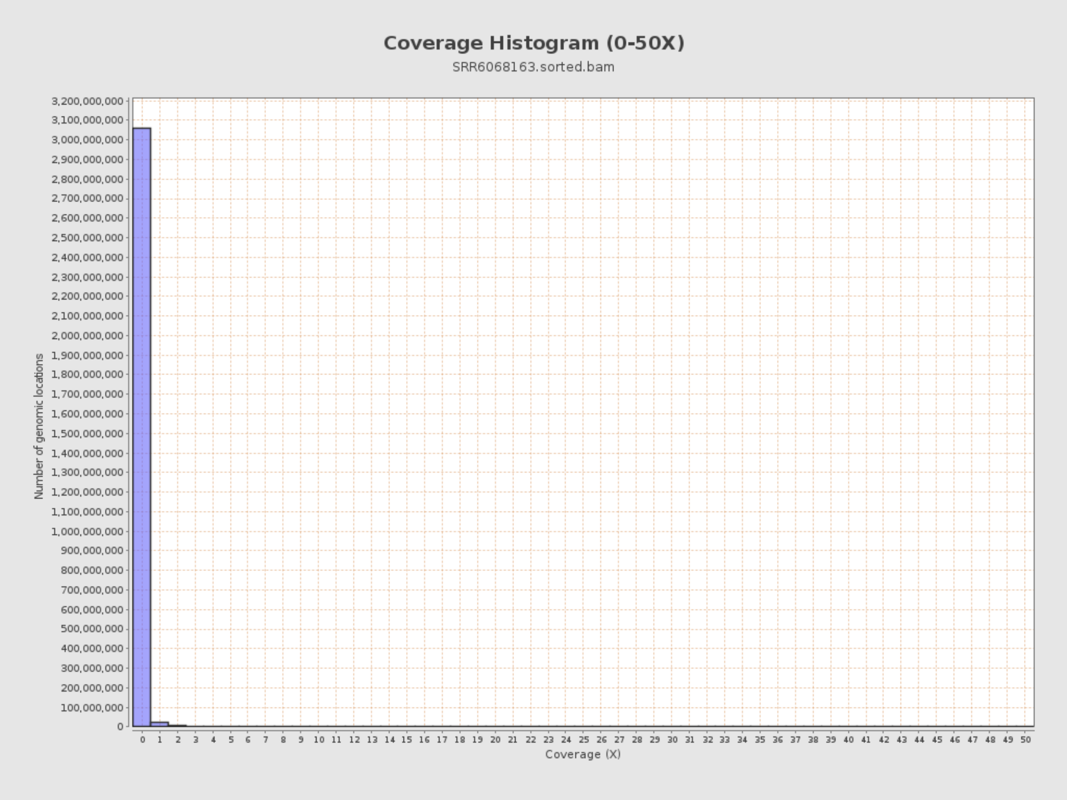
3. Results : Coverage across reference



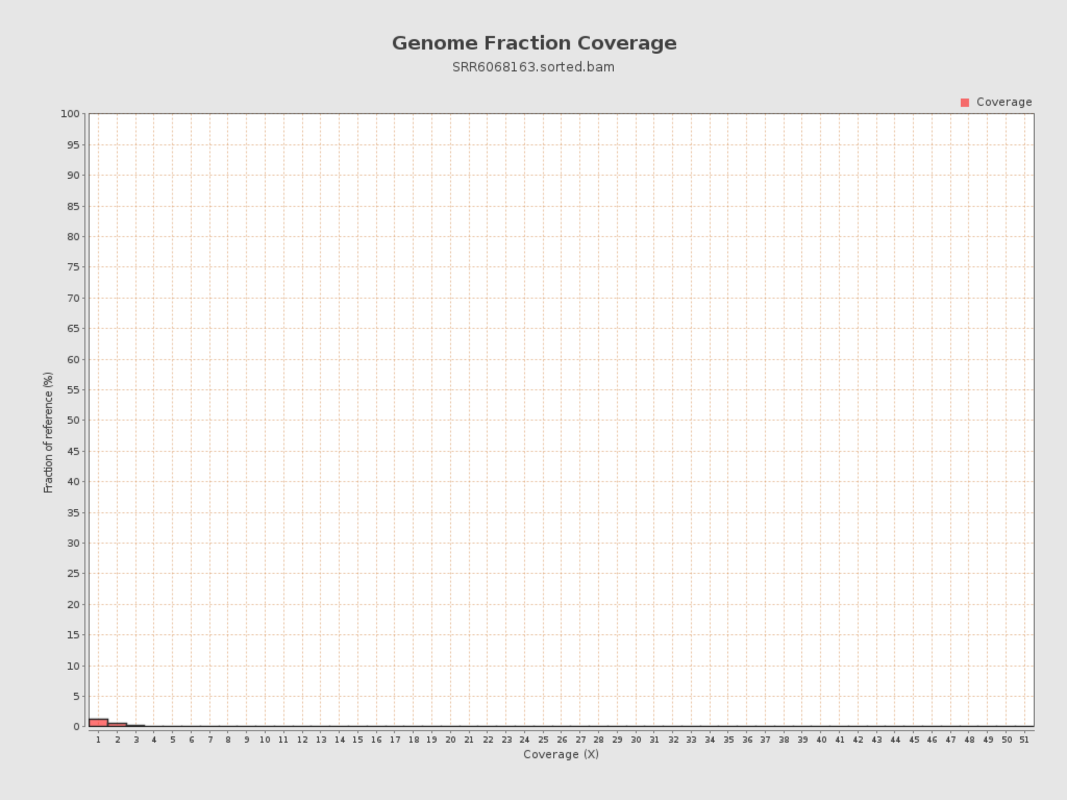
4. Results : Coverage Histogram



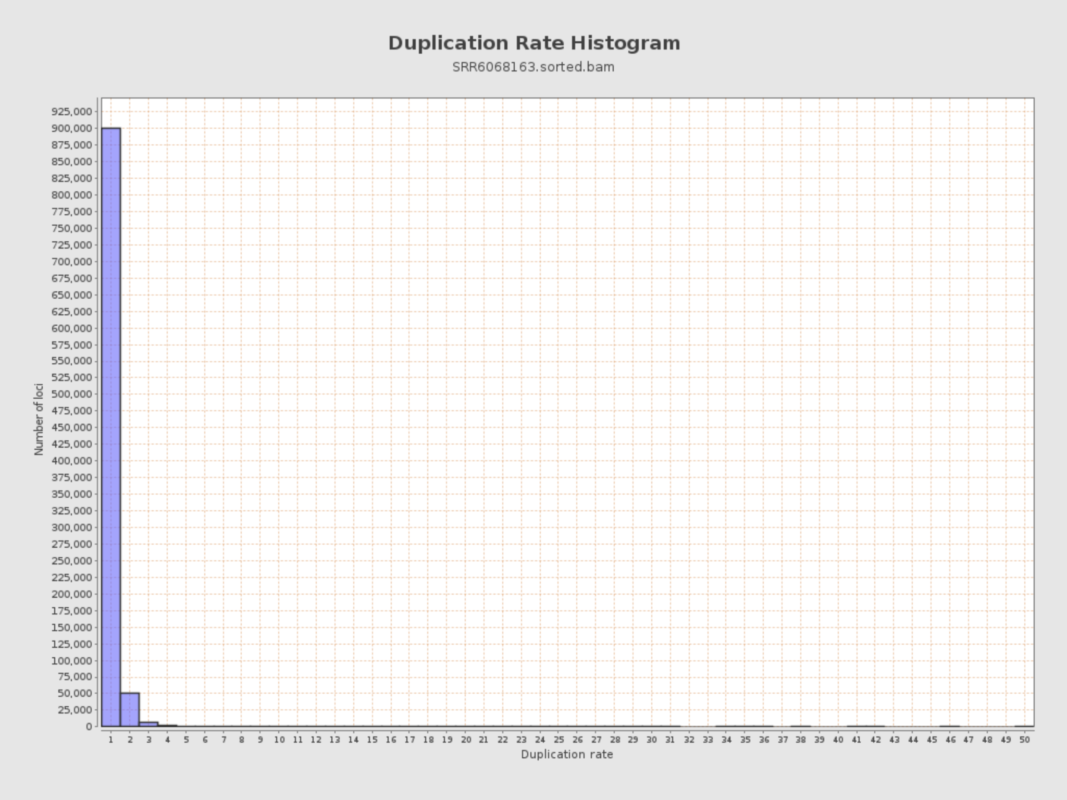
5. Results : Coverage Histogram (0-50X)



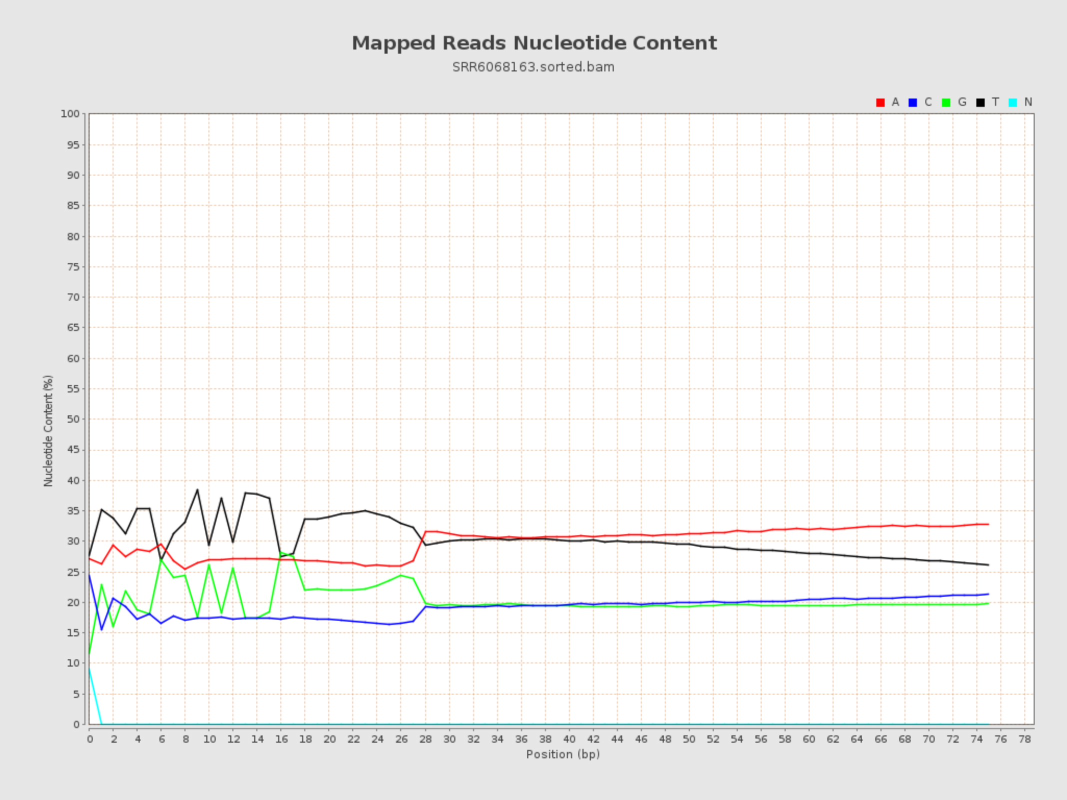
6. Results : Genome Fraction Coverage



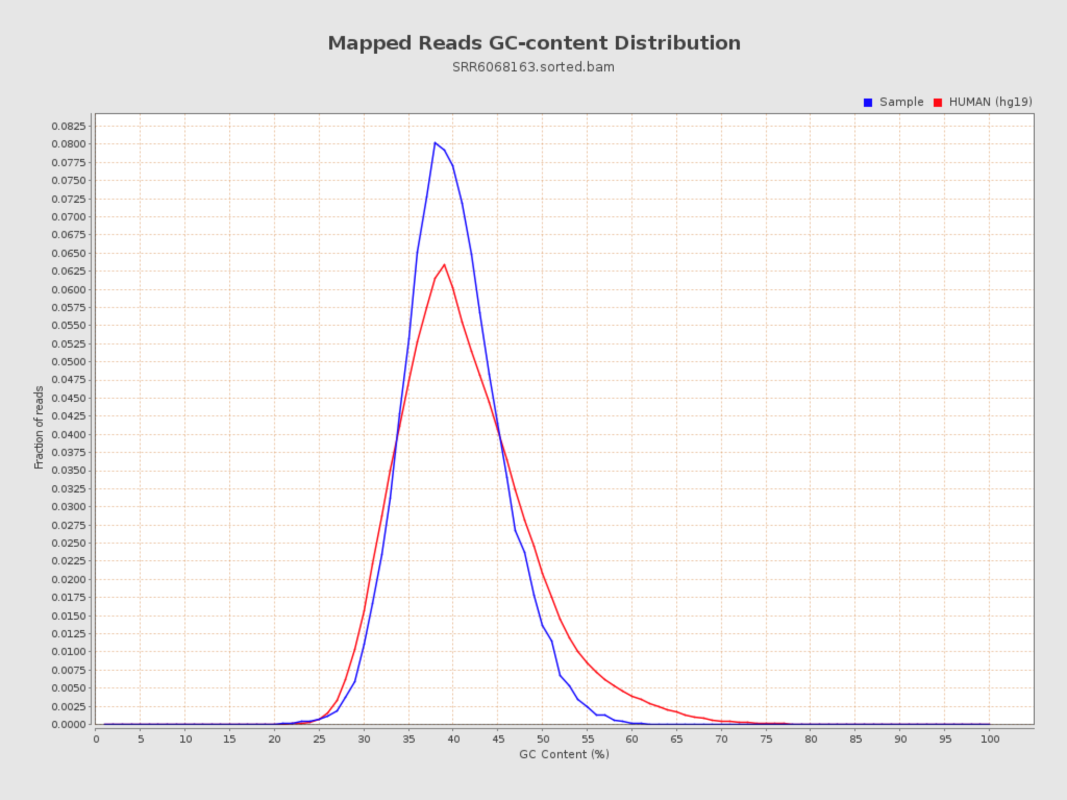
7. Results : Duplication Rate Histogram



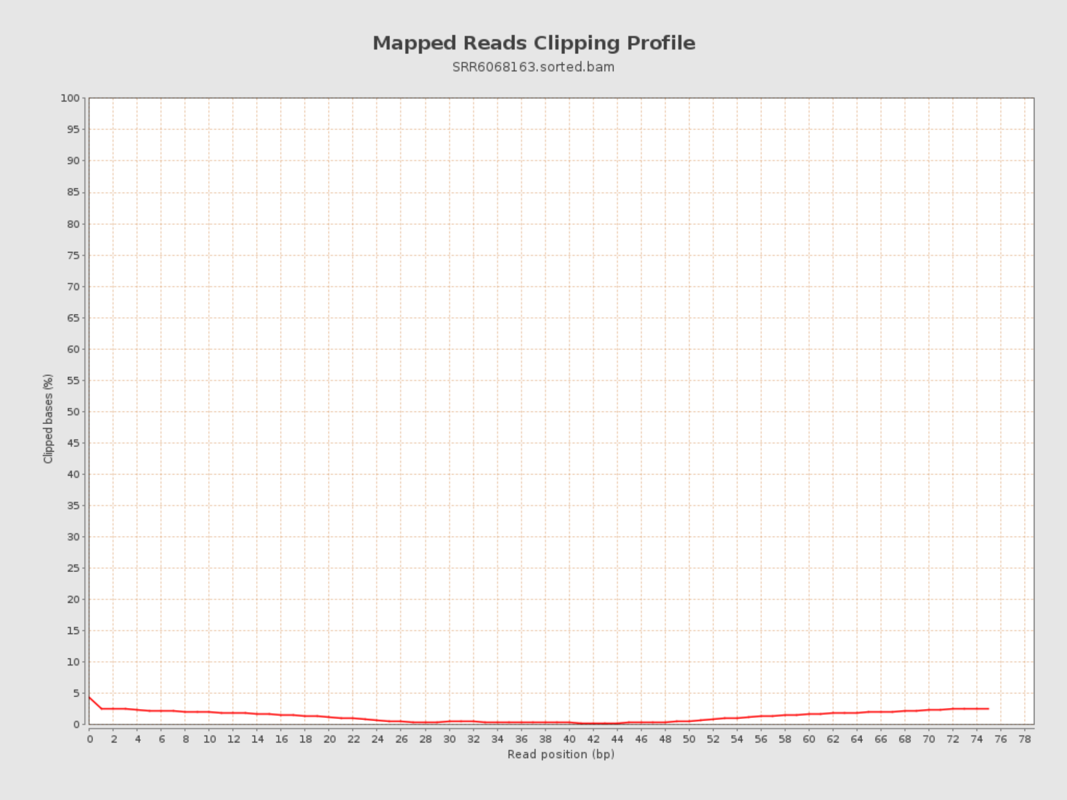
8. Results : Mapped Reads Nucleotide Content



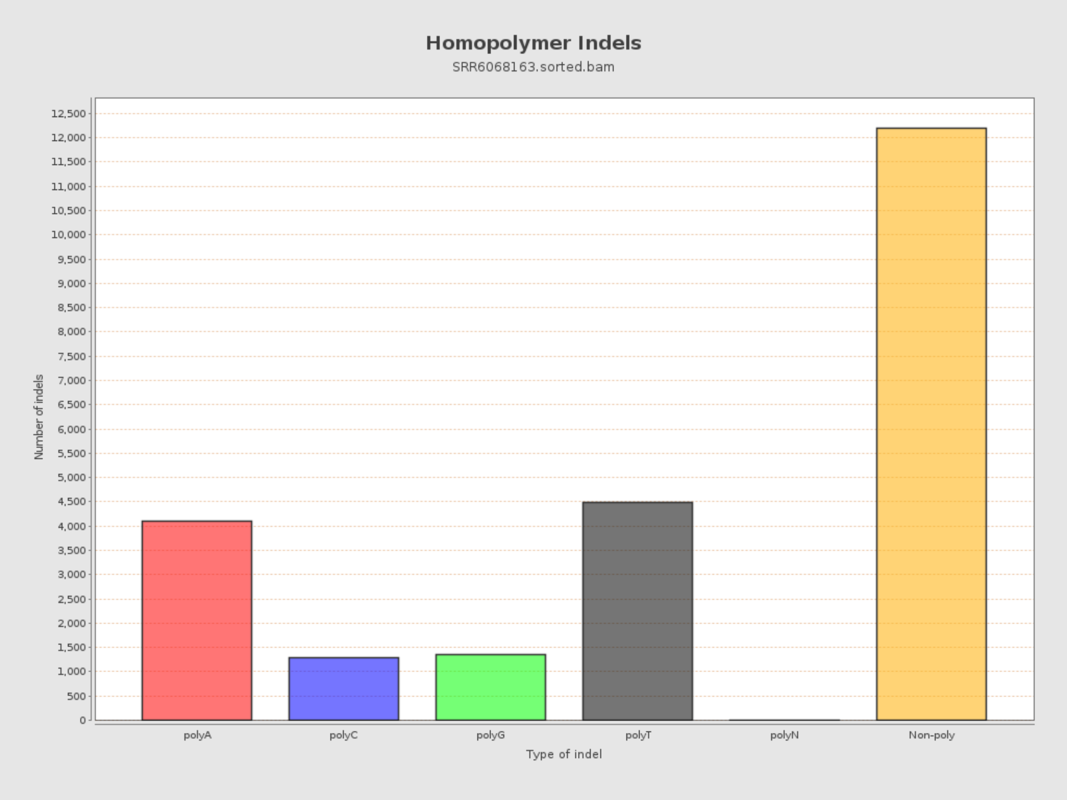
9. Results : Mapped Reads GC-content Distribution



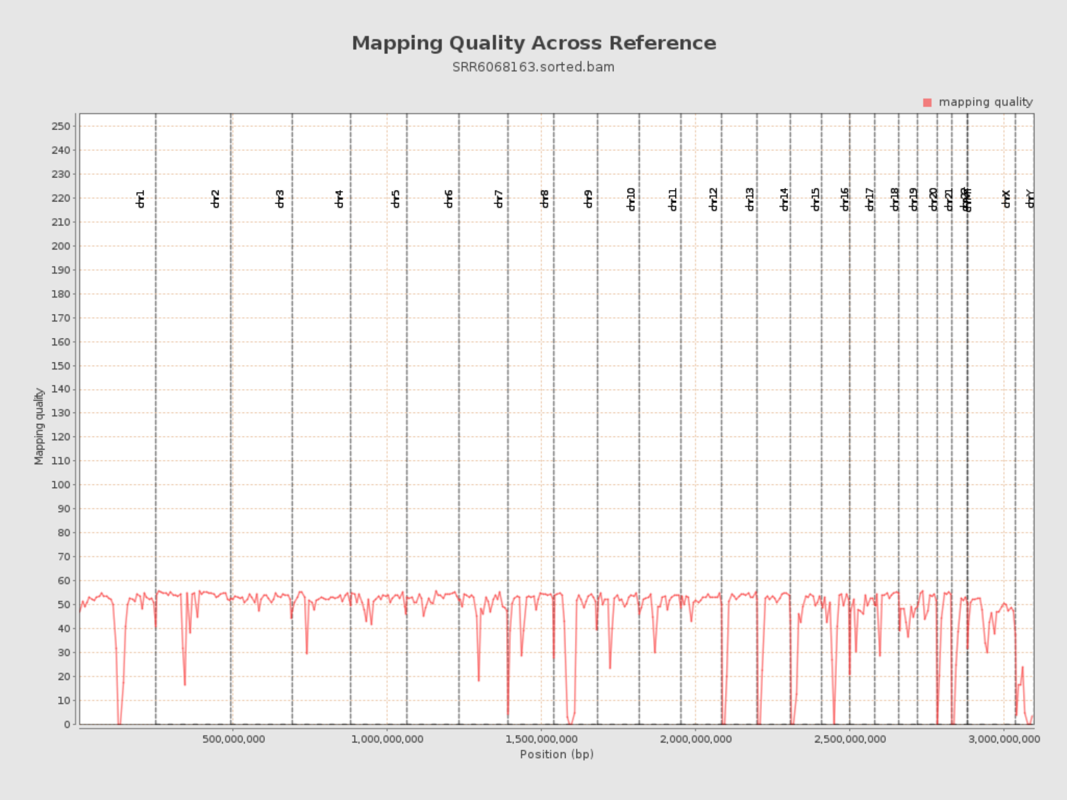
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram