Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:20:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083653.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_SRR3083653 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083653.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:20:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083653.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,518,721
Mapped reads	2,087,553 / 82.88%
Unmapped reads	431,168 / 17.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,616 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	72,705 / 2.89%
Duplication rate	2.91%
Clipped reads	1,558,555 / 61.88%

2.2. ACGT Content

Number/percentage of A's	36,770,917 / 29.95%
Number/percentage of C's	24,332,807 / 19.82%
Number/percentage of T's	35,662,887 / 29.05%
Number/percentage of G's	25,994,938 / 21.17%
Number/percentage of N's	15,866 / 0.01%
GC Percentage	40.99%

2.3. Coverage

Mean	0.0397

Standard Deviation	0.3203

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

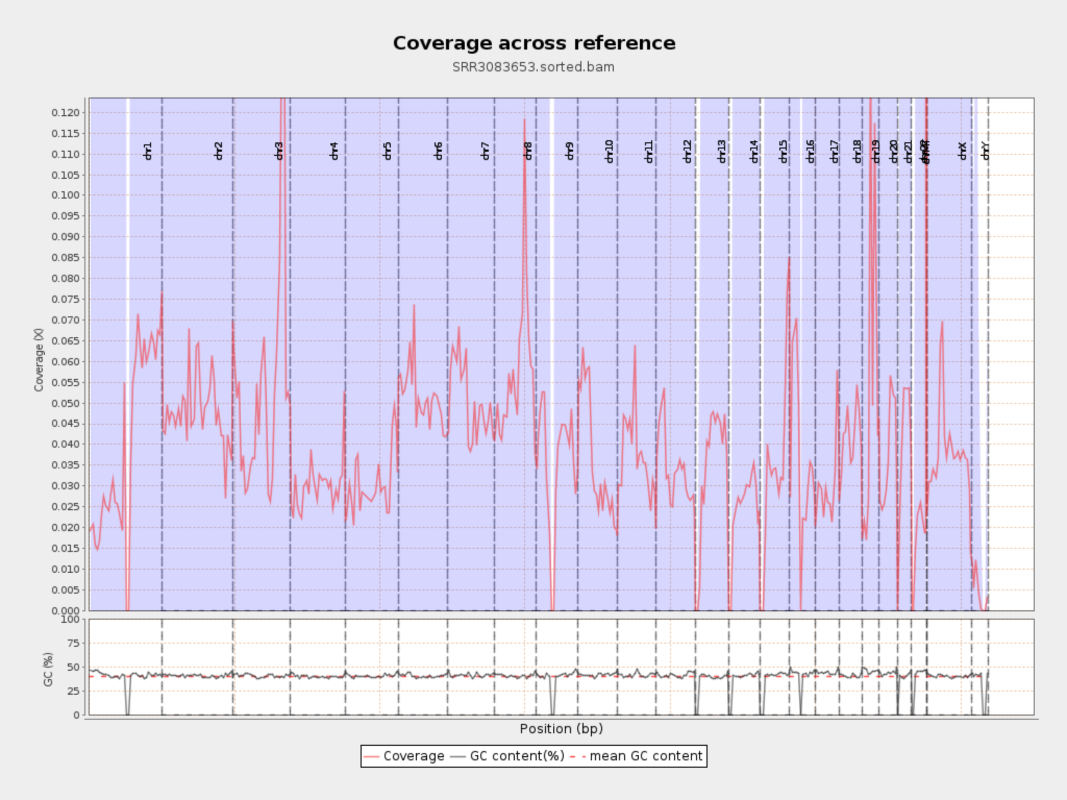
General error rate	0.82%
Mismatches	988,102
Insertions	8,339
Mapped reads with at least one insertion	0.4%
Deletions	23,085
Mapped reads with at least one deletion	1.1%
Homopolymer indels	46.18%

2.6. Chromosome stats

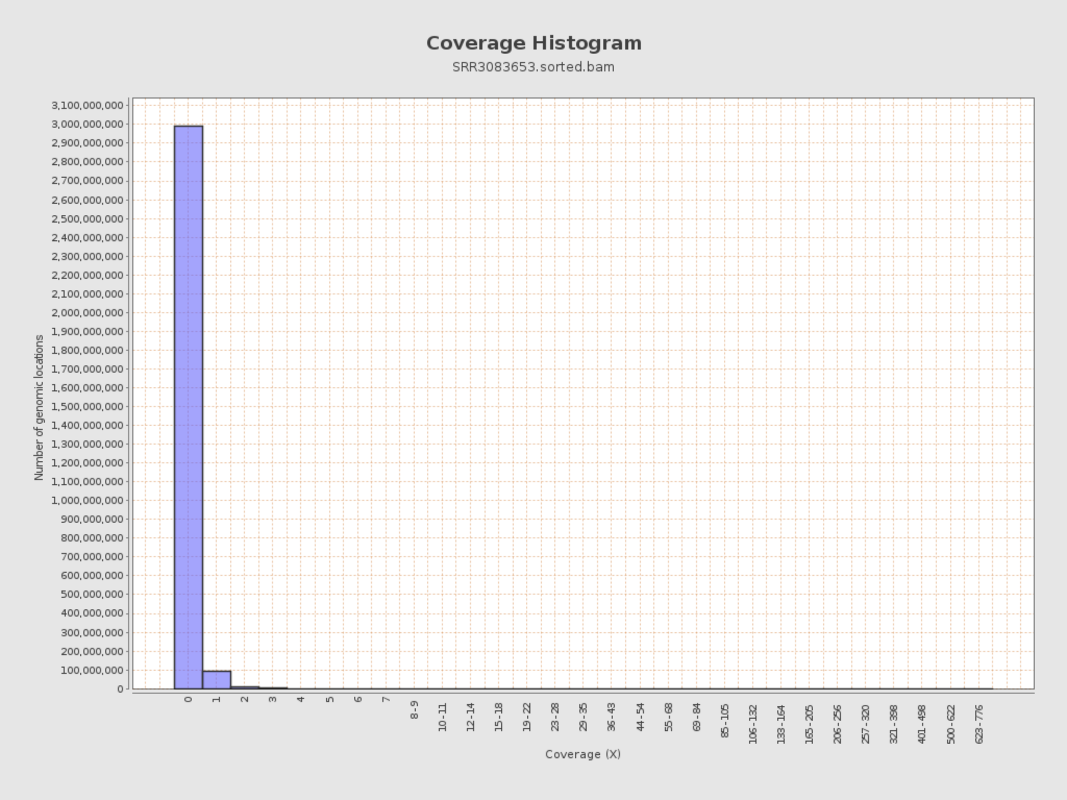
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9835833	0.0395	0.6597
chr2	243199373	11670642	0.048	0.2811
chr3	198022430	10954289	0.0553	0.266
chr4	191154276	5764547	0.0302	0.1958
chr5	180915260	5491950	0.0304	0.1948
chr6	171115067	8819293	0.0515	0.2906
chr7	159138663	8096304	0.0509	0.4149

chr8	146364022	8440633	0.0577	0.4068
chr9	141213431	5022472	0.0356	0.2381
chr10	135534747	5012830	0.037	0.2747
chr11	135006516	5052353	0.0374	0.2561
chr12	133851895	4559936	0.0341	0.2055
chr13	115169878	3903059	0.0339	0.2048
chr14	107349540	2604959	0.0243	0.1748
chr15	102531392	3457298	0.0337	0.2059
chr16	90354753	3429224	0.038	0.2247
chr17	81195210	2524961	0.0311	0.2071
chr18	78077248	3288082	0.0421	0.3781
chr19	59128983	3321441	0.0562	0.4629
chr20	63025520	2379725	0.0378	0.2202
chr21	48129895	1917024	0.0398	0.2259
chr22	51304566	844505	0.0165	0.1415
chrMT	16571	200338	12.0897	7.1933
chrX	155270560	5966894	0.0384	0.2268
chrY	59373566	254619	0.0043	0.086

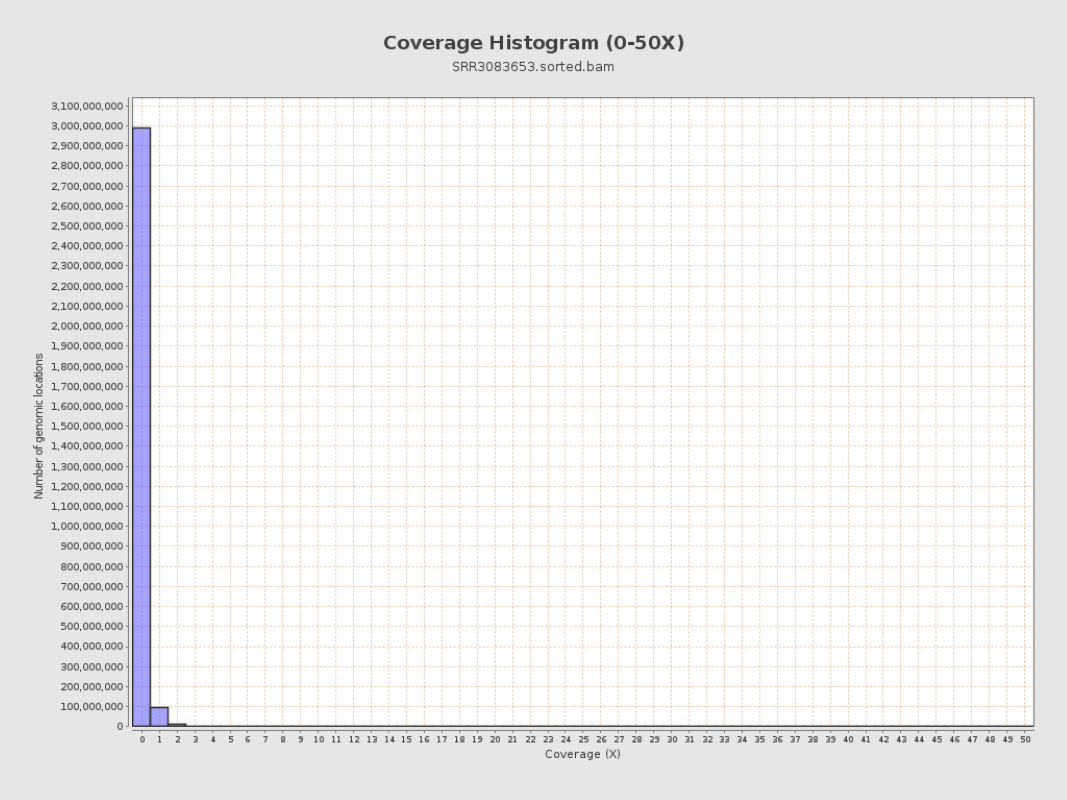
3. Results : Coverage across reference



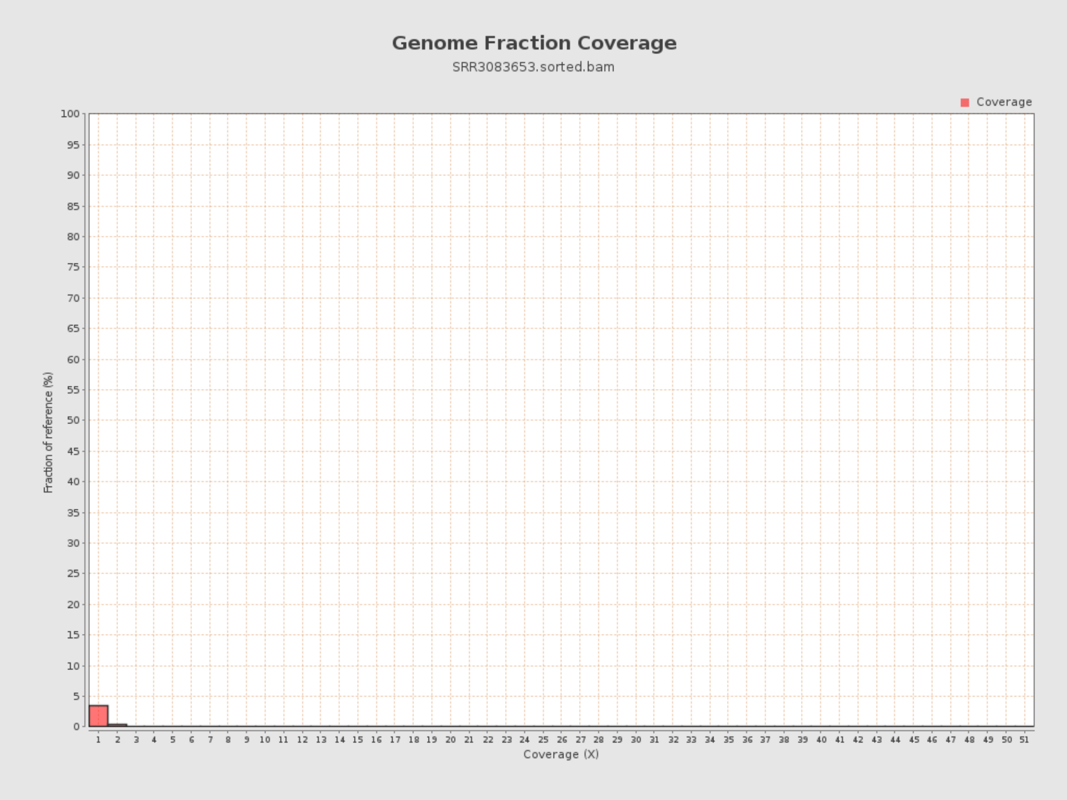
4. Results : Coverage Histogram



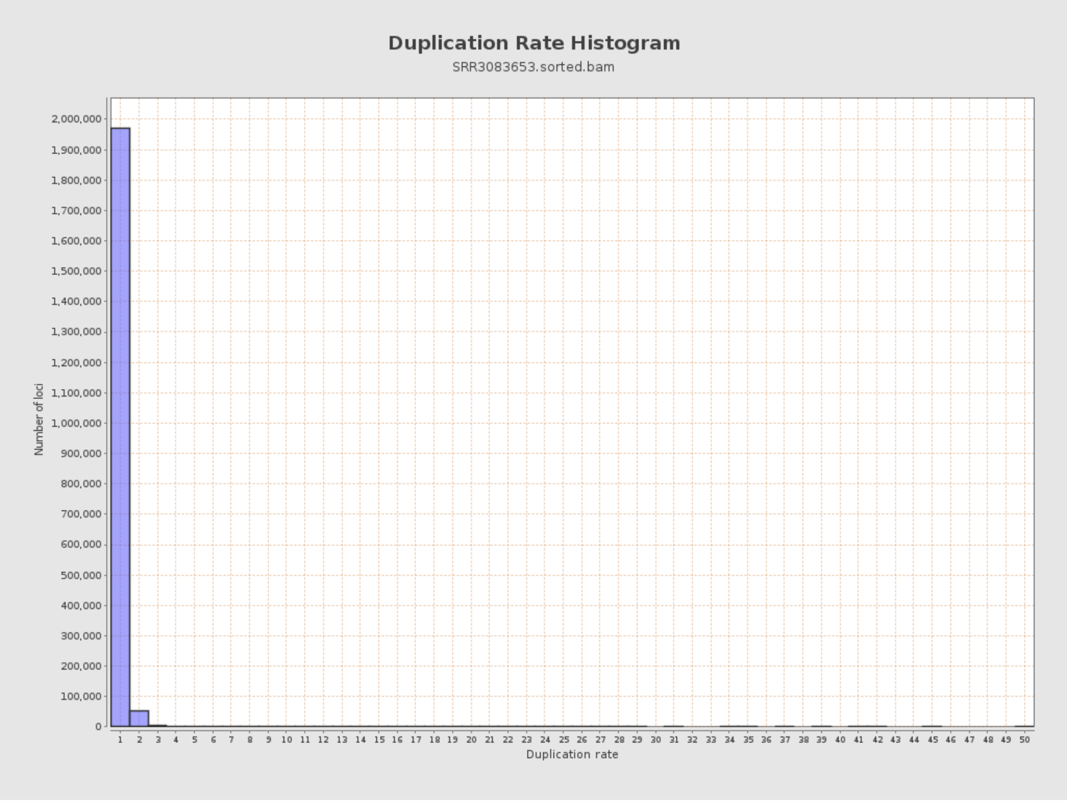
5. Results : Coverage Histogram (0-50X)



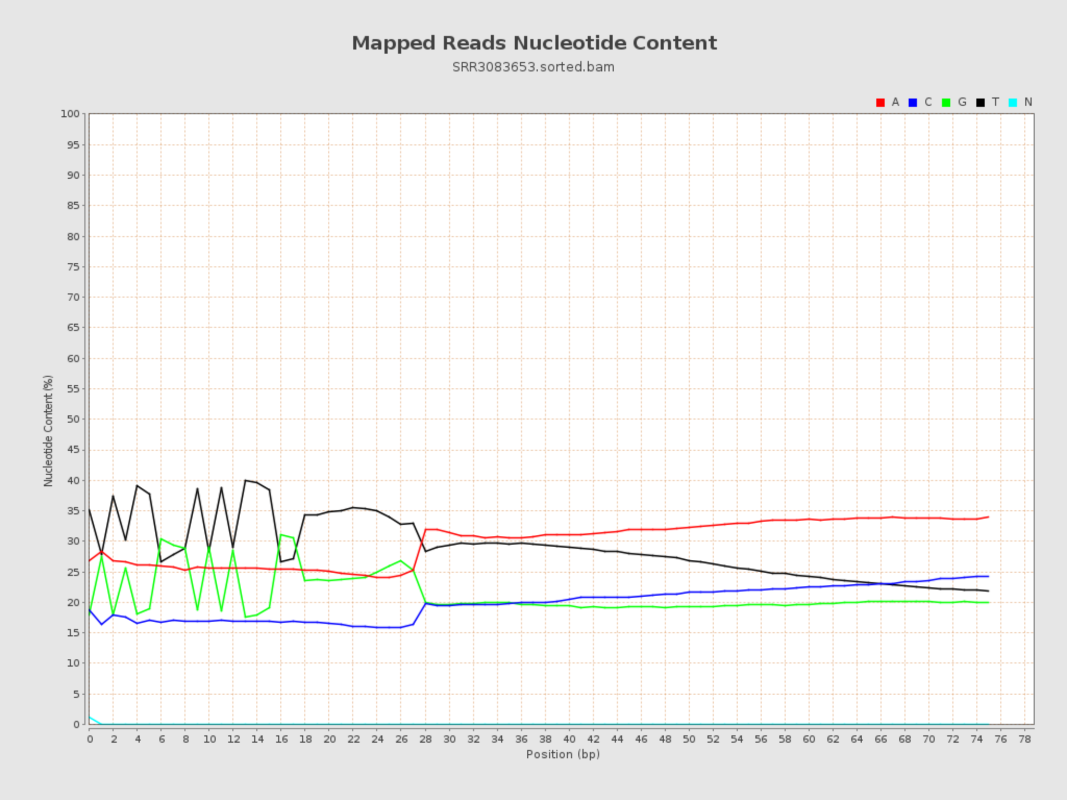
6. Results : Genome Fraction Coverage



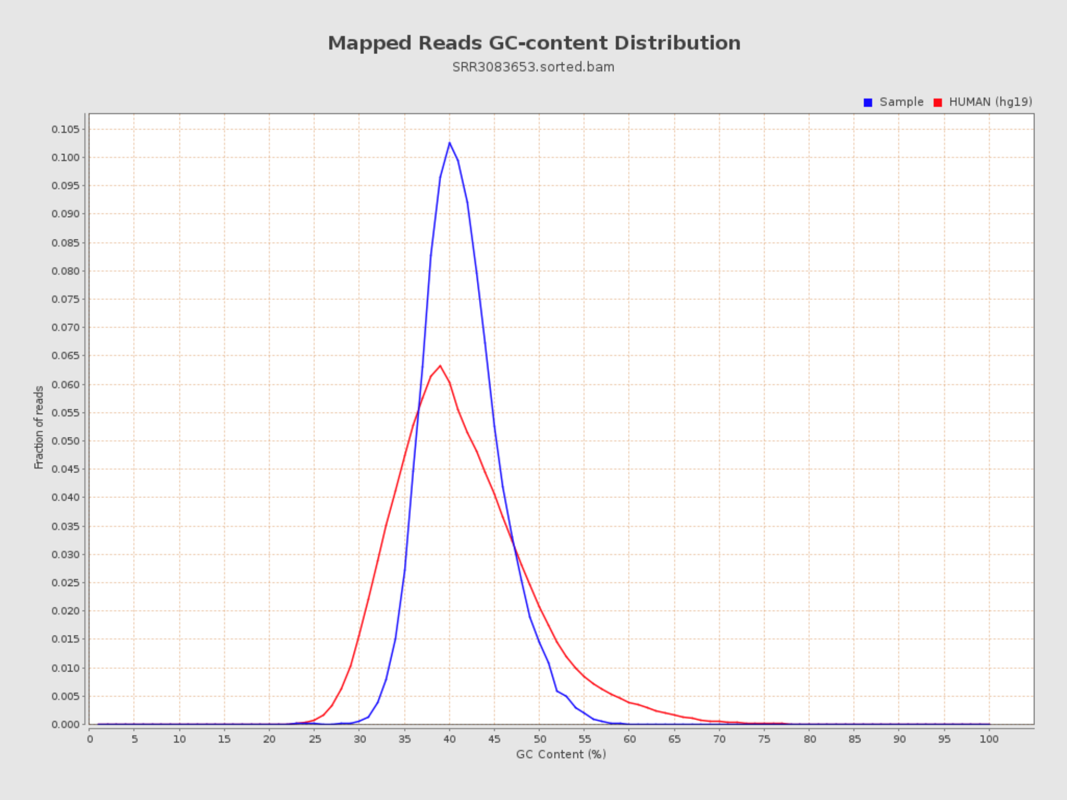
7. Results : Duplication Rate Histogram



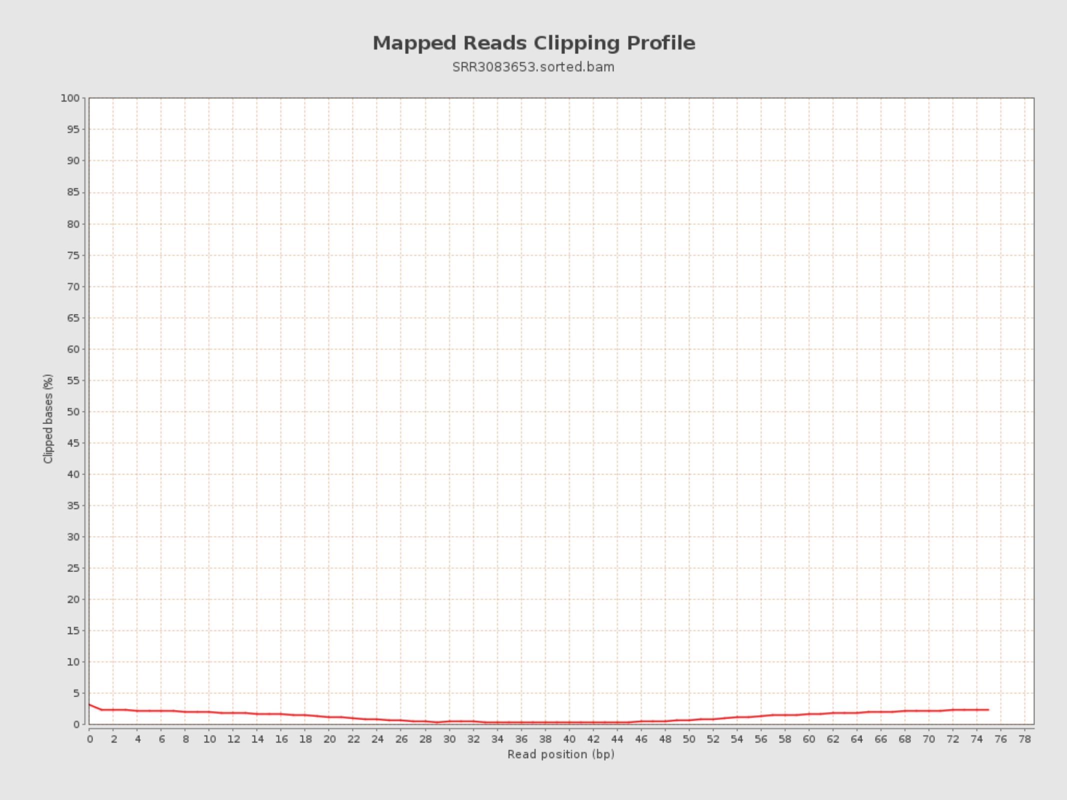
8. Results : Mapped Reads Nucleotide Content



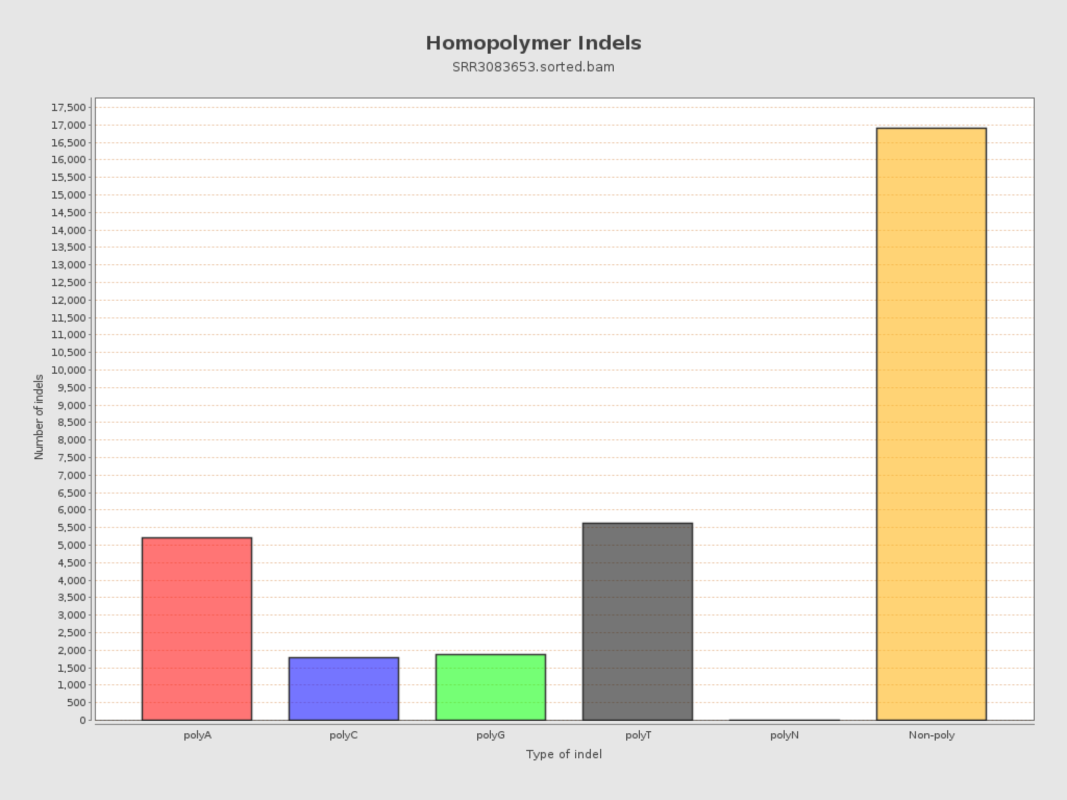
9. Results : Mapped Reads GC-content Distribution



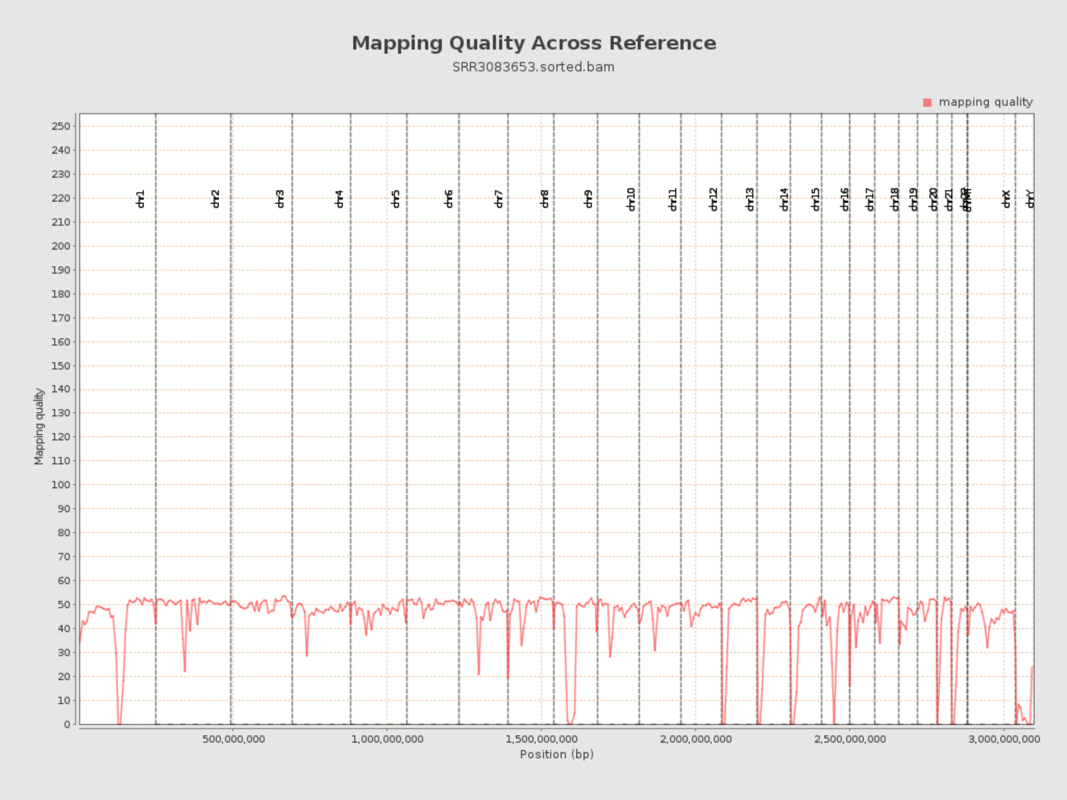
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram