Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 00:45:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083629.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_SRR3083629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083629.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 00:45:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,435,056
Mapped reads	1,296,750 / 90.36%
Unmapped reads	138,306 / 9.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,182 / 0.99%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	48,152 / 3.36%
Duplication rate	2.13%
Clipped reads	604,024 / 42.09%

2.2. ACGT Content

Number/percentage of A's	23,570,218 / 27.29%
Number/percentage of C's	16,585,876 / 19.2%
Number/percentage of T's	25,729,090 / 29.79%
Number/percentage of G's	20,484,228 / 23.72%
Number/percentage of N's	3,988 / 0%
GC Percentage	42.92%

2.3. Coverage

Mean	0.0279

Standard Deviation	0.4783

2.4. Mapping Quality

Mean Mapping Quality	42.15

2.5. Mismatches and indels

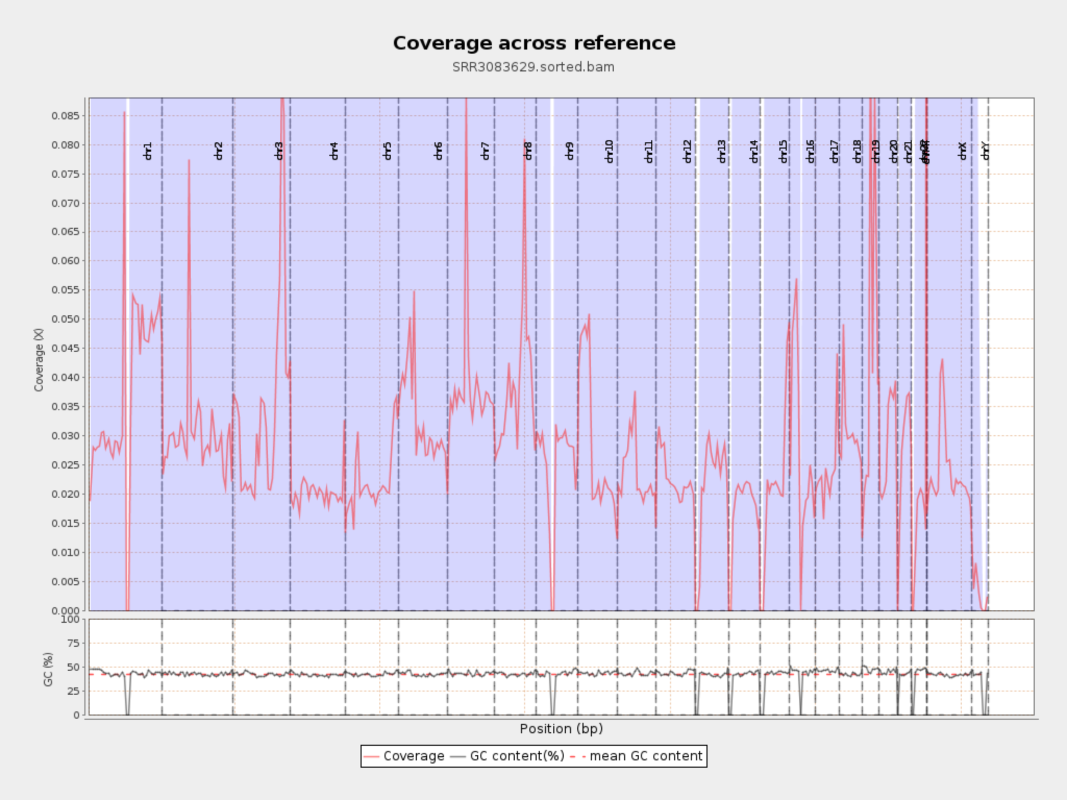
General error rate	0.76%
Mismatches	643,654
Insertions	7,702
Mapped reads with at least one insertion	0.59%
Deletions	17,850
Mapped reads with at least one deletion	1.36%
Homopolymer indels	42.89%

2.6. Chromosome stats

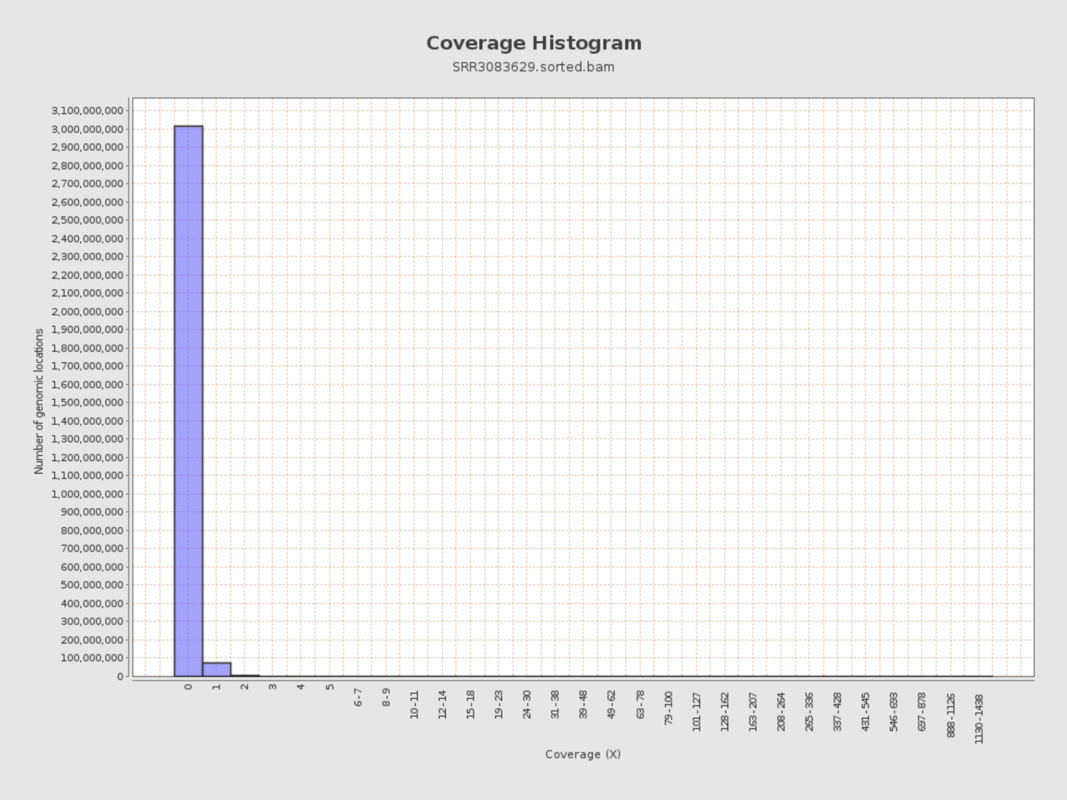
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9256240	0.0371	1.2206
chr2	243199373	7389990	0.0304	0.4935
chr3	198022430	6862231	0.0347	0.2004
chr4	191154276	3888898	0.0203	0.1767
chr5	180915260	4048836	0.0224	0.1623
chr6	171115067	5685868	0.0332	0.2703
chr7	159138663	6185890	0.0389	0.7803

chr8	146364022	5663257	0.0387	0.3392
chr9	141213431	3452641	0.0244	0.291
chr10	135534747	3945442	0.0291	0.3049
chr11	135006516	3171918	0.0235	0.2877
chr12	133851895	3035766	0.0227	0.1629
chr13	115169878	2452054	0.0213	0.1538
chr14	107349540	1843474	0.0172	0.1559
chr15	102531392	2161982	0.0211	0.17
chr16	90354753	2524141	0.0279	0.1973
chr17	81195210	1975977	0.0243	0.1821
chr18	78077248	2405763	0.0308	0.6179
chr19	59128983	2719742	0.046	0.8047
chr20	63025520	1819749	0.0289	0.1887
chr21	48129895	1285352	0.0267	0.1783
chr22	51304566	695415	0.0136	0.1212
chrMT	16571	7863	0.4745	0.8297
chrX	155270560	3745097	0.0241	0.1924
chrY	59373566	178775	0.003	0.0727

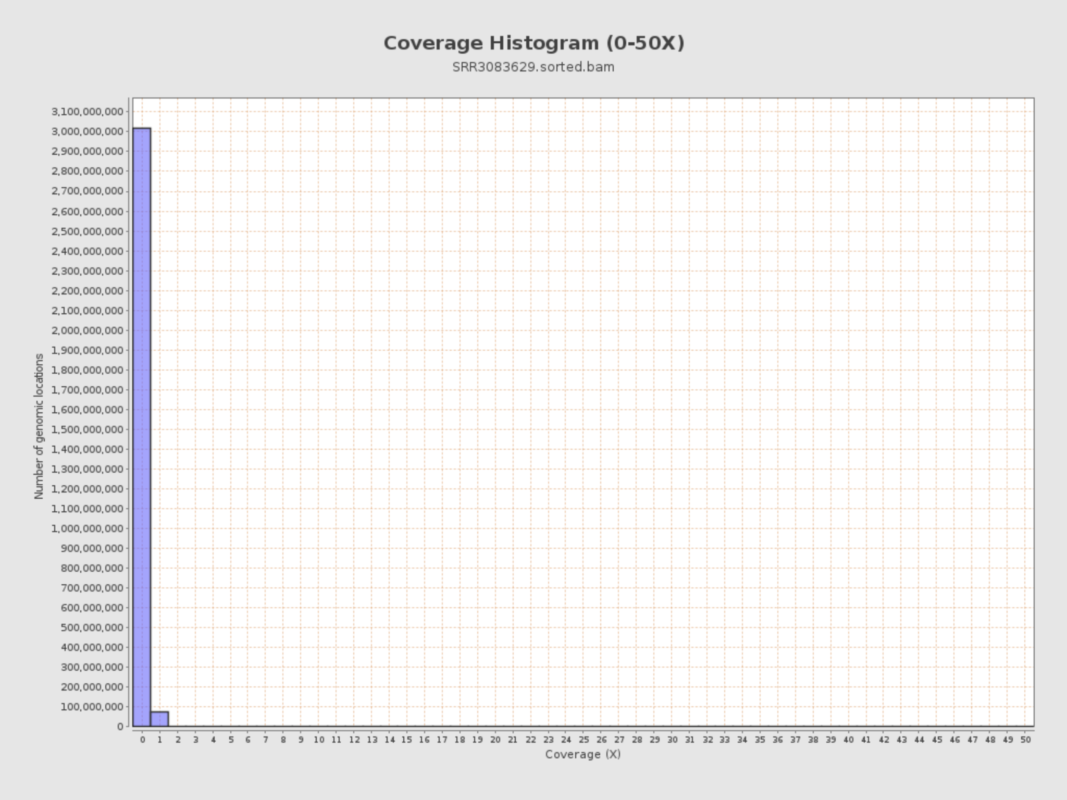
3. Results : Coverage across reference



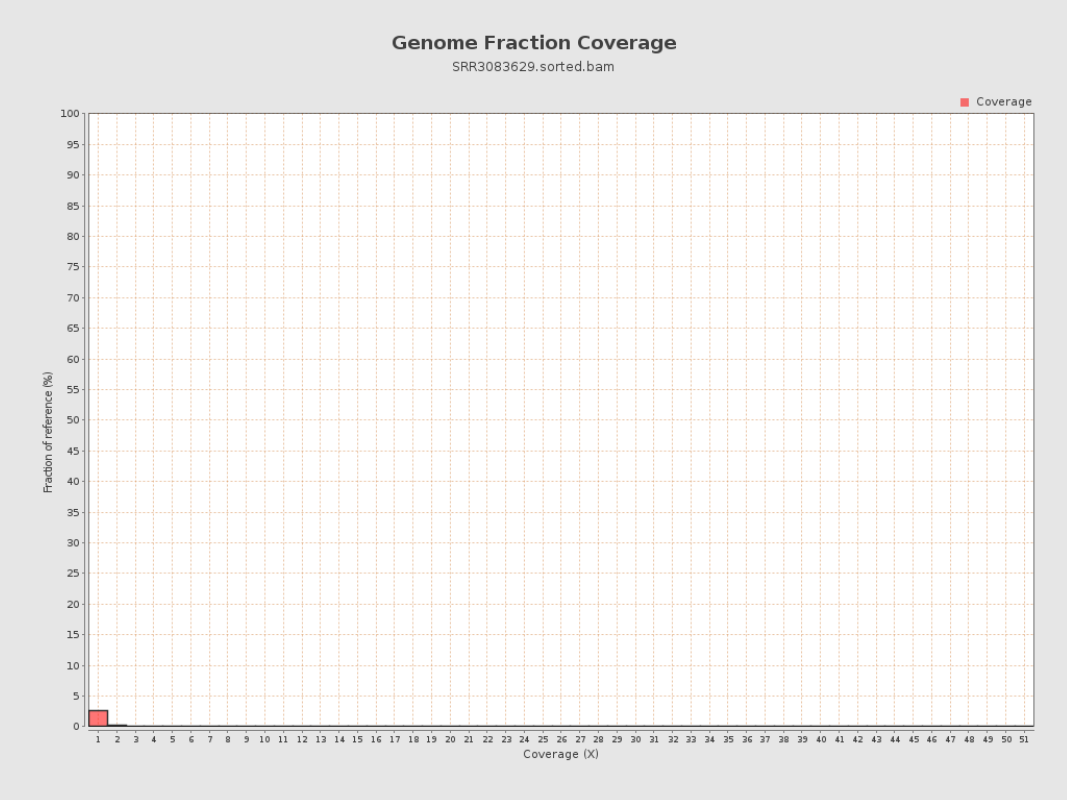
4. Results : Coverage Histogram



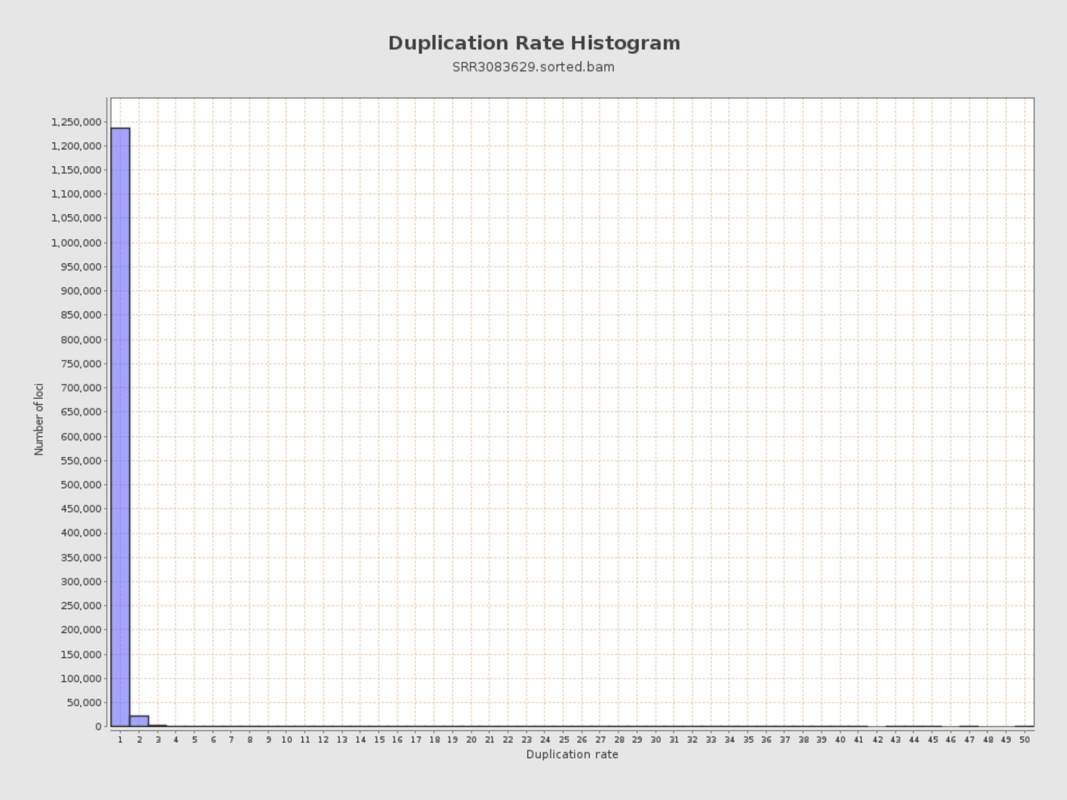
5. Results : Coverage Histogram (0-50X)



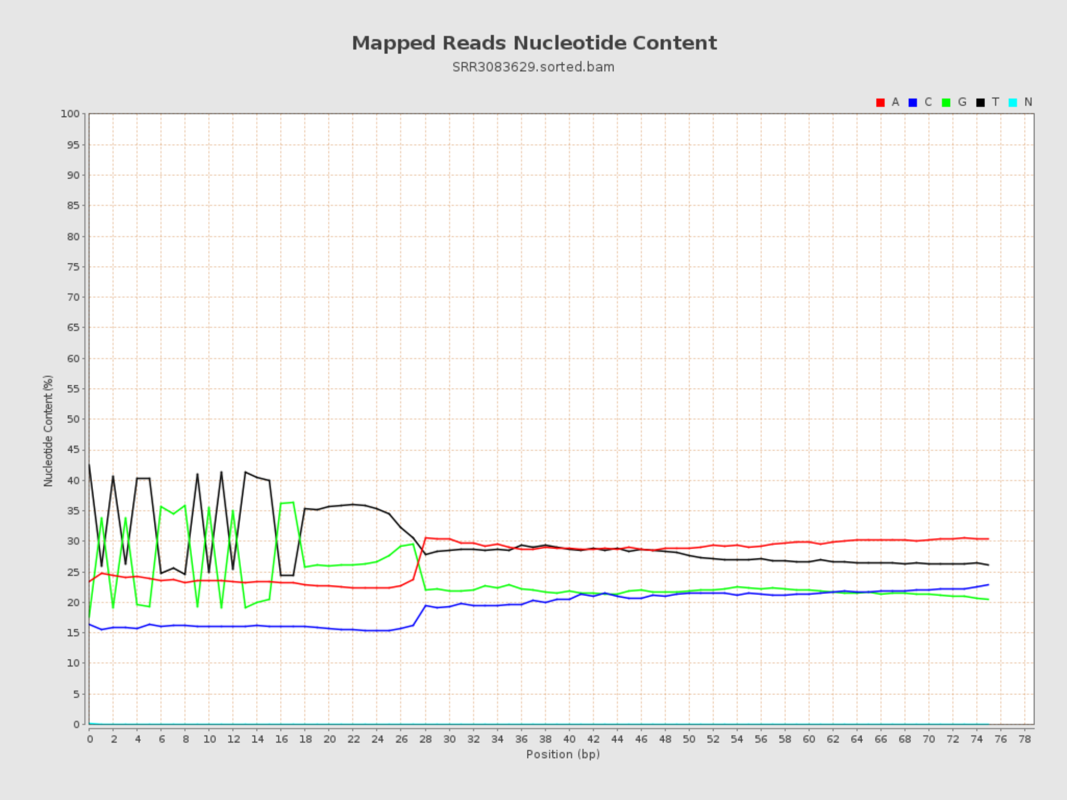
6. Results : Genome Fraction Coverage



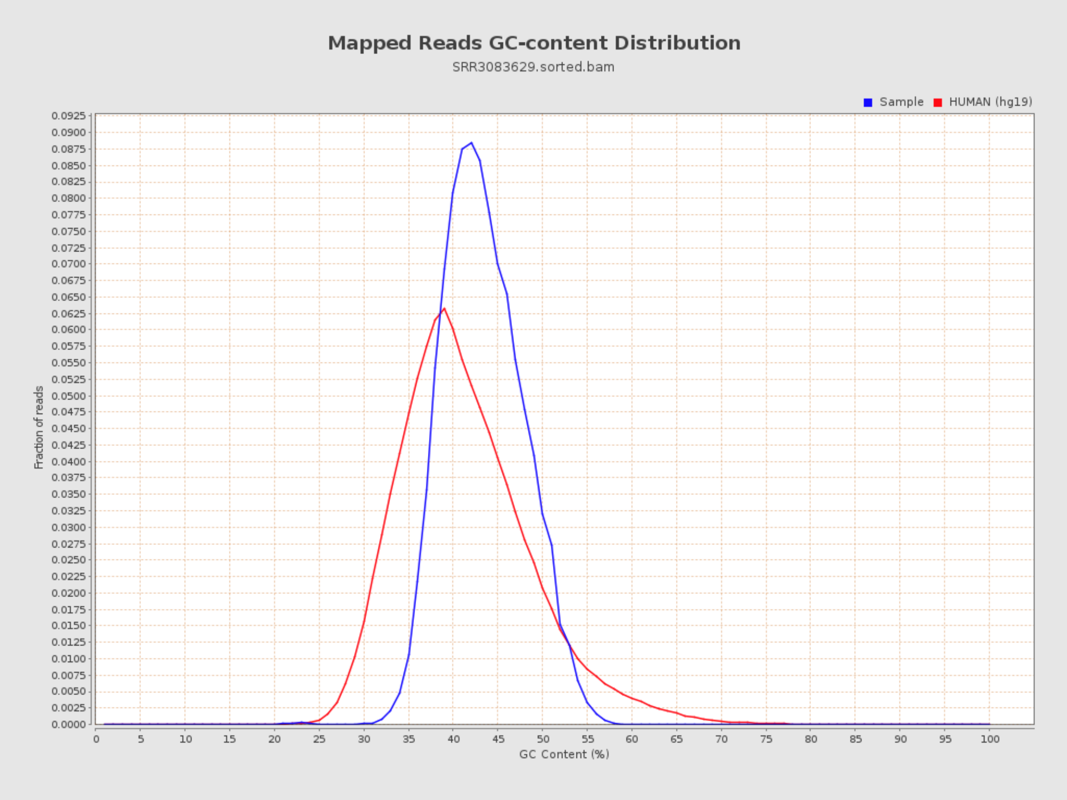
7. Results : Duplication Rate Histogram



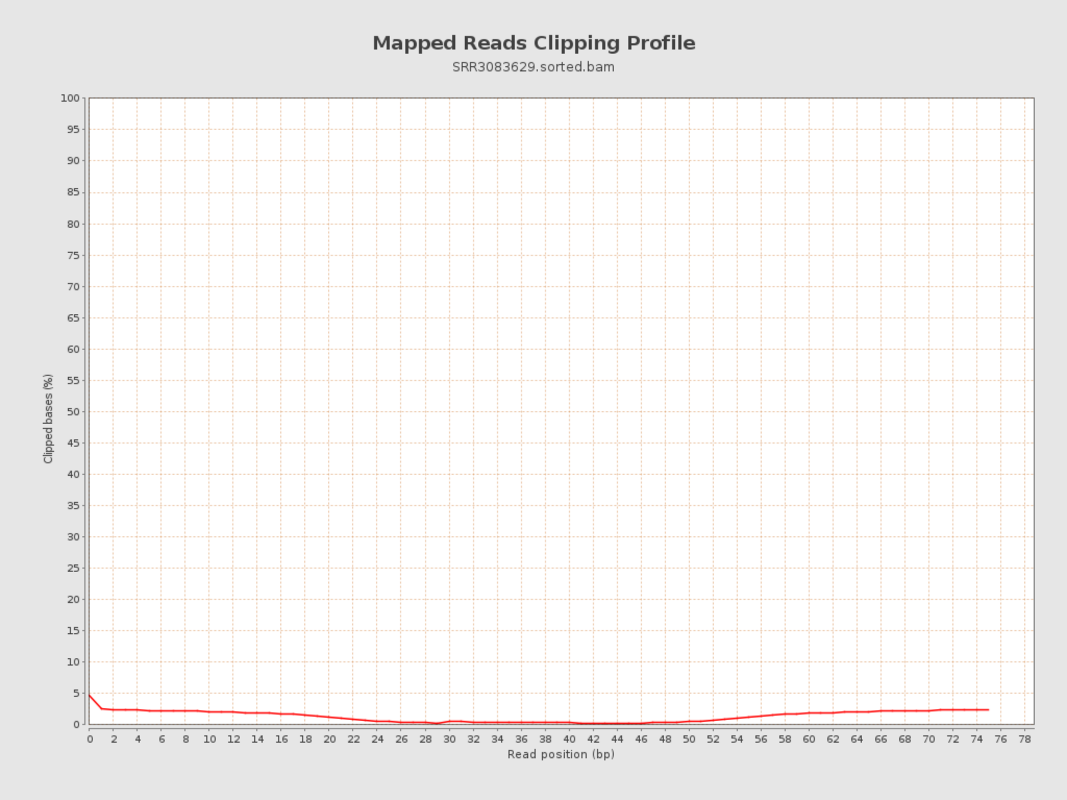
8. Results : Mapped Reads Nucleotide Content



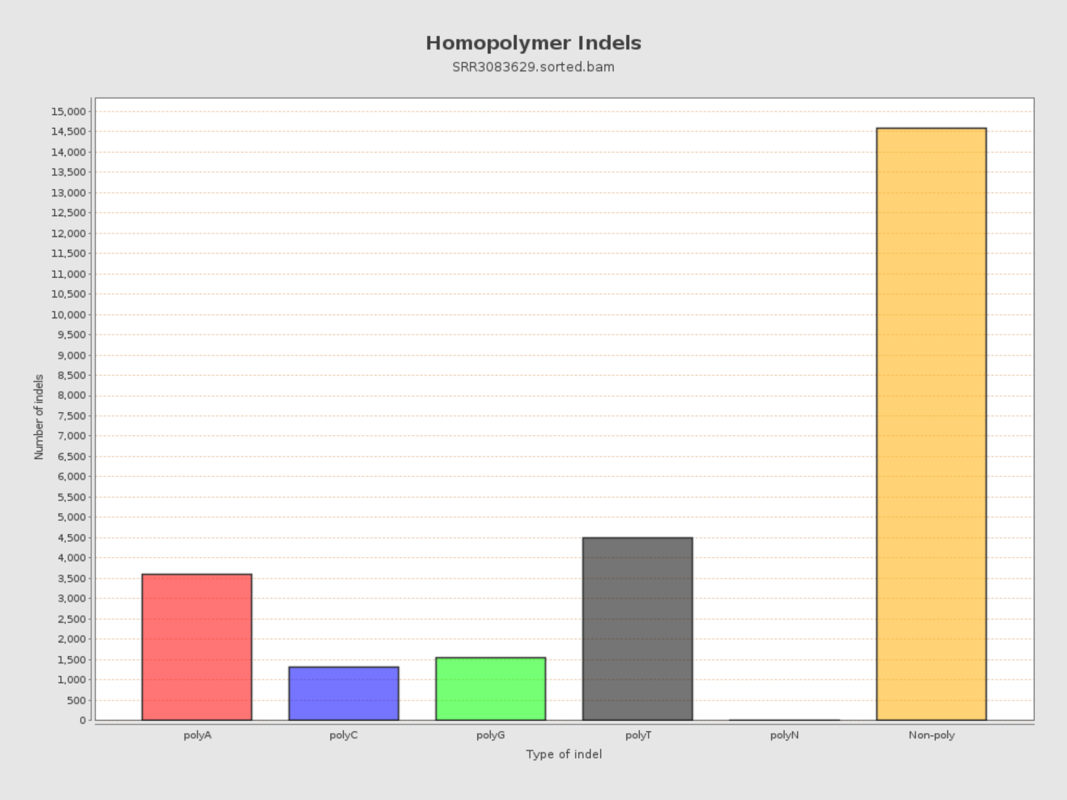
9. Results : Mapped Reads GC-content Distribution



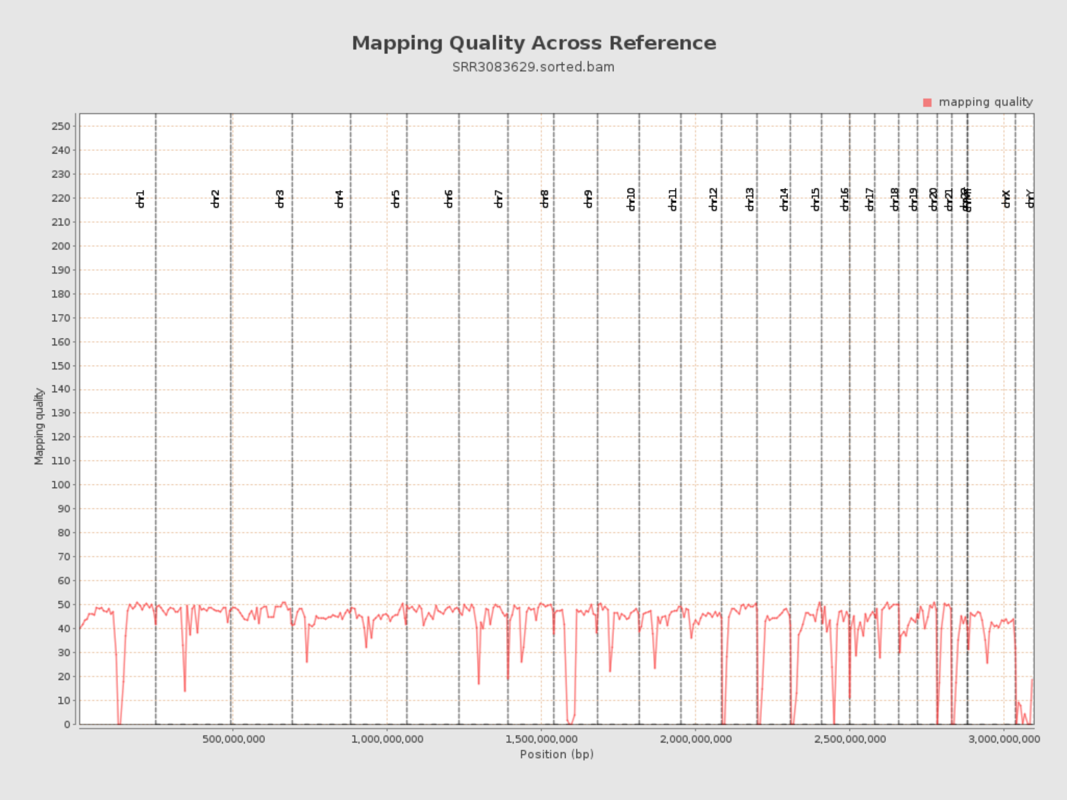
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram