Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 21:29:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013323.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_SRR6013323 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013323.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 21:29:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013323.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,209,853
Mapped reads	1,917,736 / 86.78%
Unmapped reads	292,117 / 13.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,936 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	79,300 / 3.59%
Duplication rate	3.06%
Clipped reads	824,007 / 37.29%

2.2. ACGT Content

Number/percentage of A's	35,636,589 / 27.84%
Number/percentage of C's	23,466,219 / 18.33%
Number/percentage of T's	40,663,514 / 31.77%
Number/percentage of G's	28,228,349 / 22.05%
Number/percentage of N's	1,799 / 0%
GC Percentage	40.39%

2.3. Coverage

Mean	0.0414

Standard Deviation	0.4069

2.4. Mapping Quality

Mean Mapping Quality	46.3

2.5. Mismatches and indels

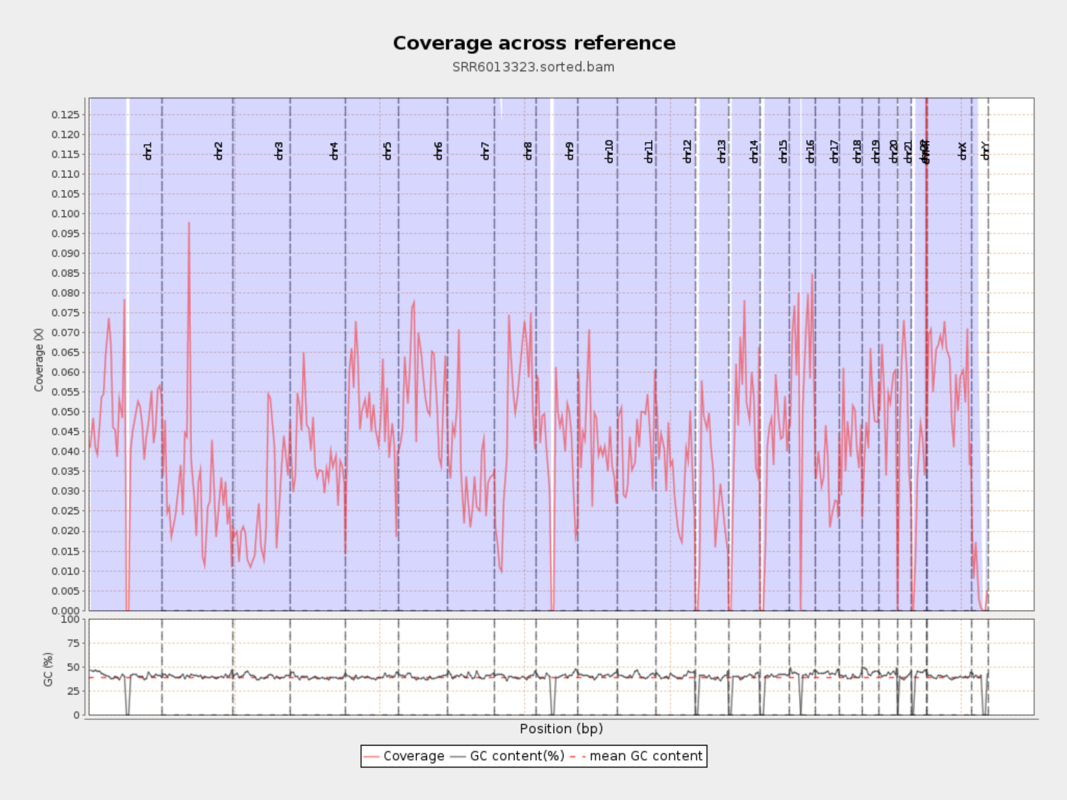
General error rate	0.73%
Mismatches	922,643
Insertions	9,197
Mapped reads with at least one insertion	0.48%
Deletions	31,215
Mapped reads with at least one deletion	1.61%
Homopolymer indels	47.29%

2.6. Chromosome stats

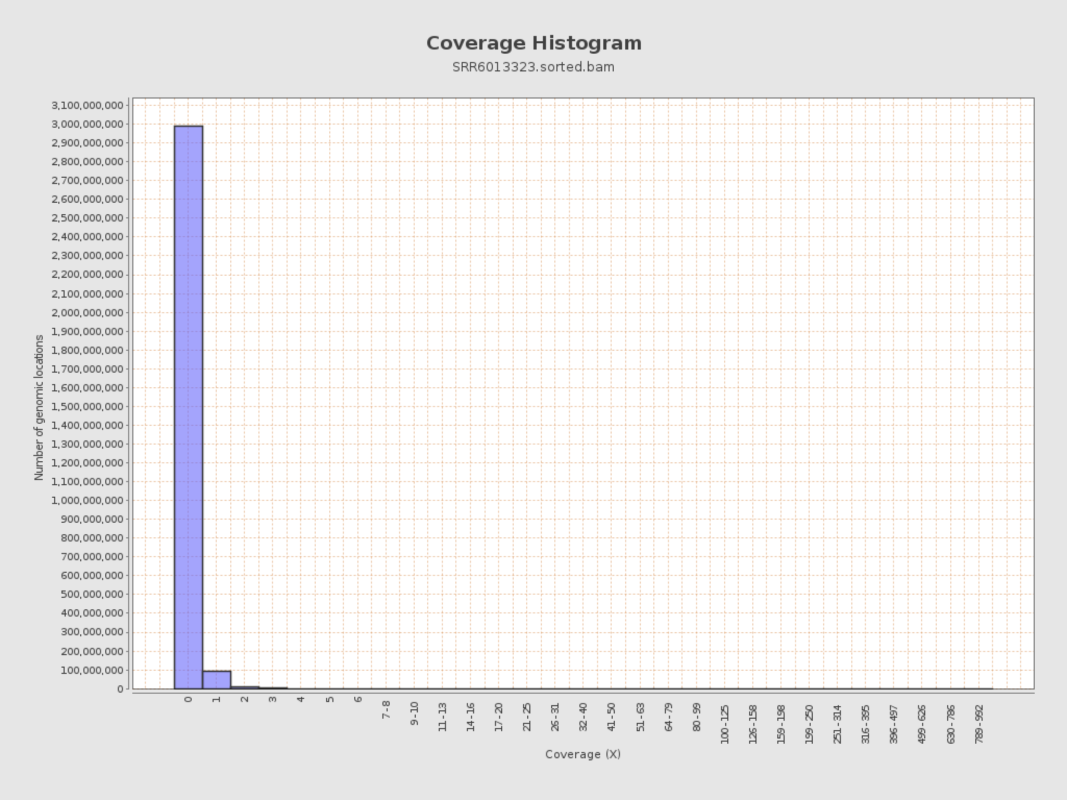
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11787508	0.0473	0.8345
chr2	243199373	7460735	0.0307	0.4468
chr3	198022430	5196517	0.0262	0.1865
chr4	191154276	7561501	0.0396	0.2421
chr5	180915260	8957913	0.0495	0.2573
chr6	171115067	9506804	0.0556	0.3651
chr7	159138663	5604739	0.0352	0.2891

chr8	146364022	7040352	0.0481	0.4613
chr9	141213431	5585964	0.0396	0.4065
chr10	135534747	5875636	0.0434	0.3635
chr11	135006516	5802938	0.043	0.3389
chr12	133851895	4668402	0.0349	0.2205
chr13	115169878	3320327	0.0288	0.1925
chr14	107349540	4894656	0.0456	0.2655
chr15	102531392	3822645	0.0373	0.2254
chr16	90354753	5537743	0.0613	0.3133
chr17	81195210	2593797	0.0319	0.2353
chr18	78077248	3409225	0.0437	0.7973
chr19	59128983	2828970	0.0478	0.6288
chr20	63025520	3354081	0.0532	0.2743
chr21	48129895	2265197	0.0471	0.2684
chr22	51304566	1394880	0.0272	0.1847
chrMT	16571	8384	0.5059	0.8493
chrX	155270560	9223123	0.0594	0.311
chrY	59373566	348266	0.0059	0.1282

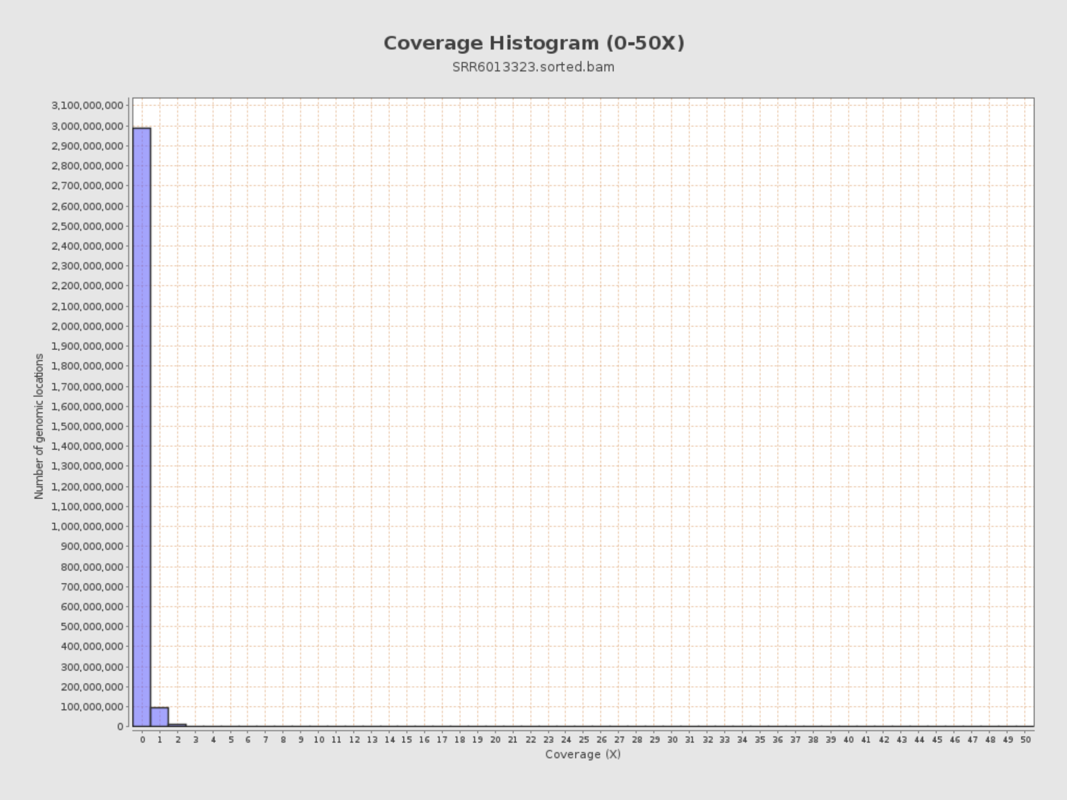
3. Results : Coverage across reference



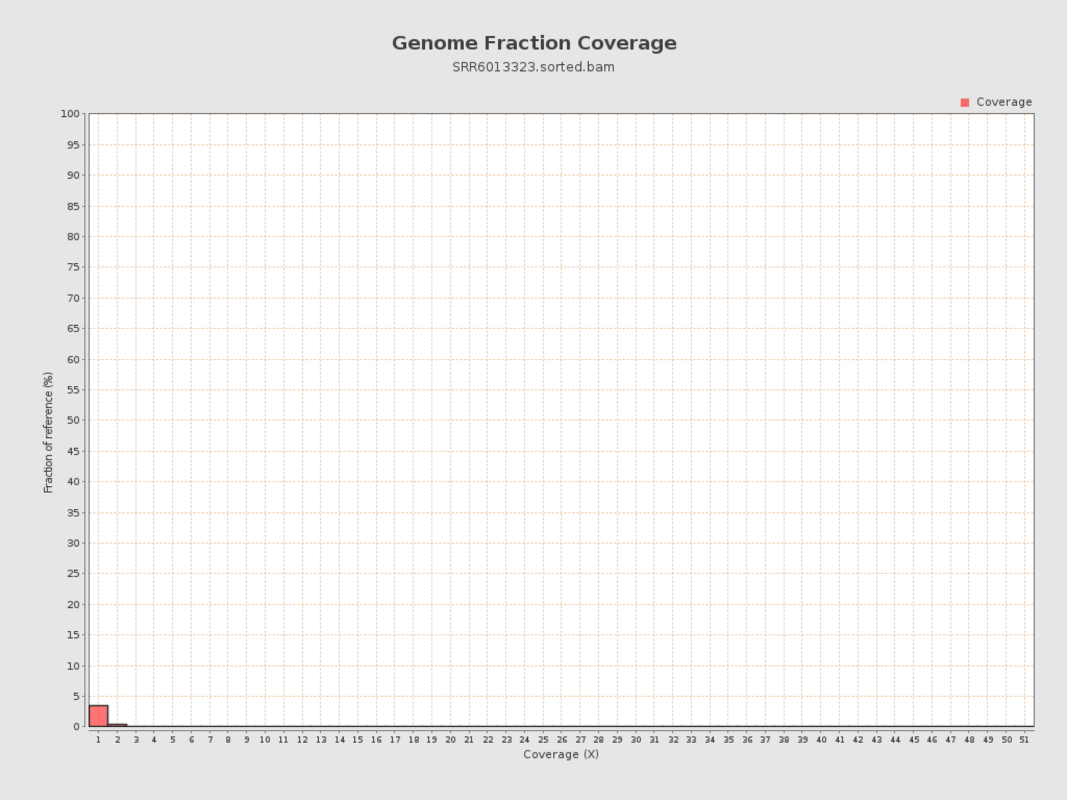
4. Results : Coverage Histogram



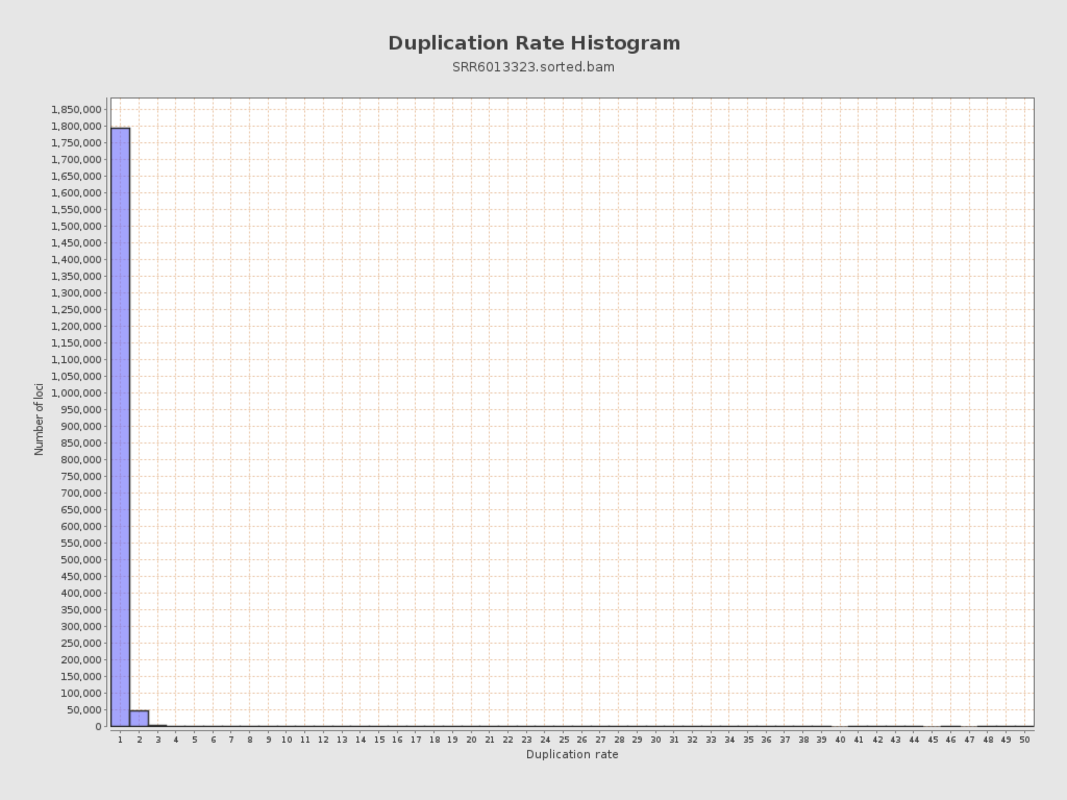
5. Results : Coverage Histogram (0-50X)



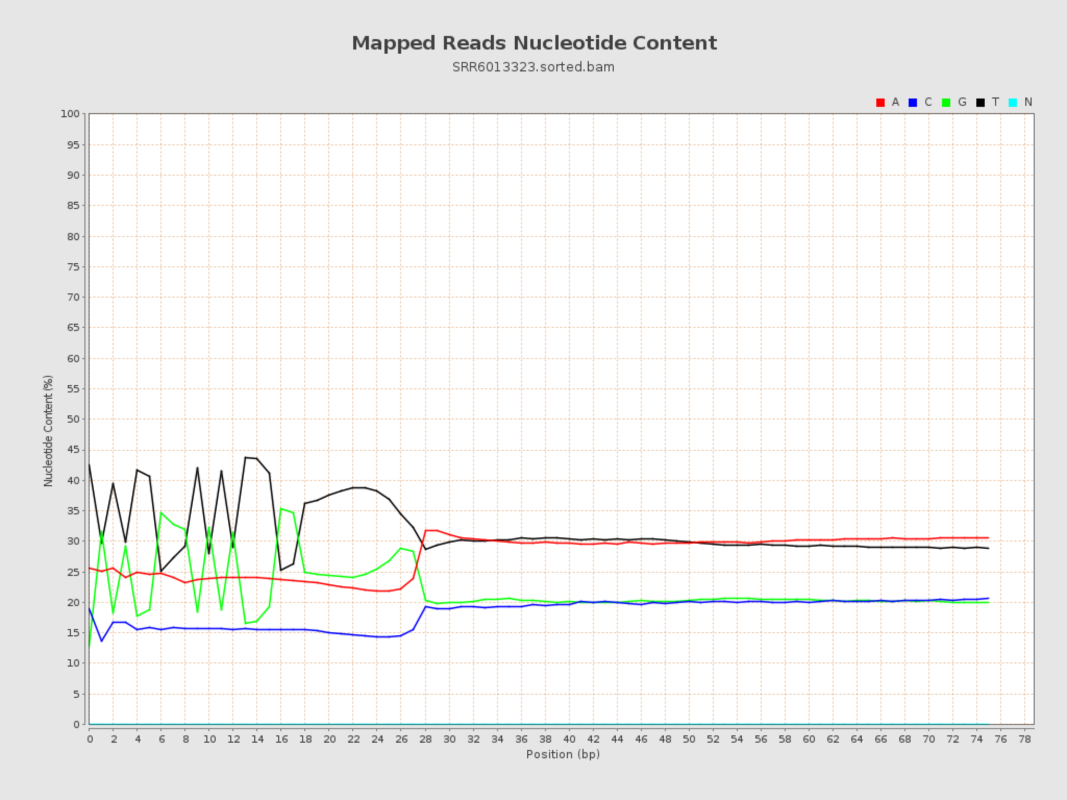
6. Results : Genome Fraction Coverage



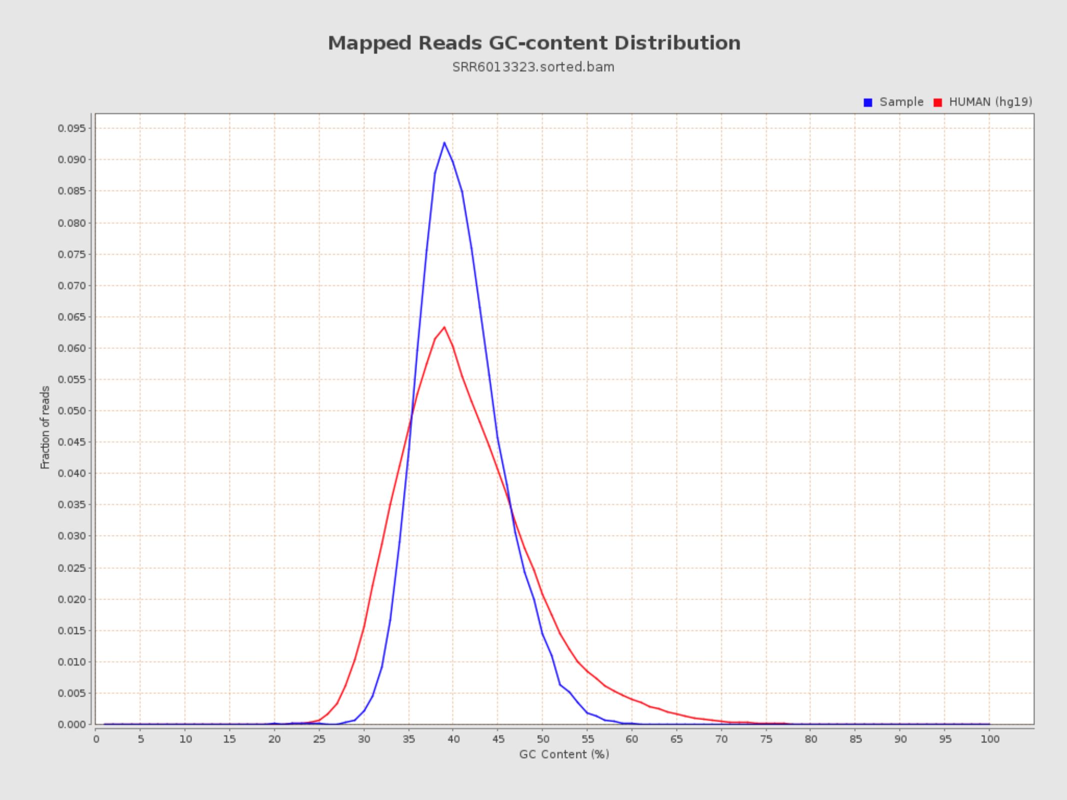
7. Results : Duplication Rate Histogram



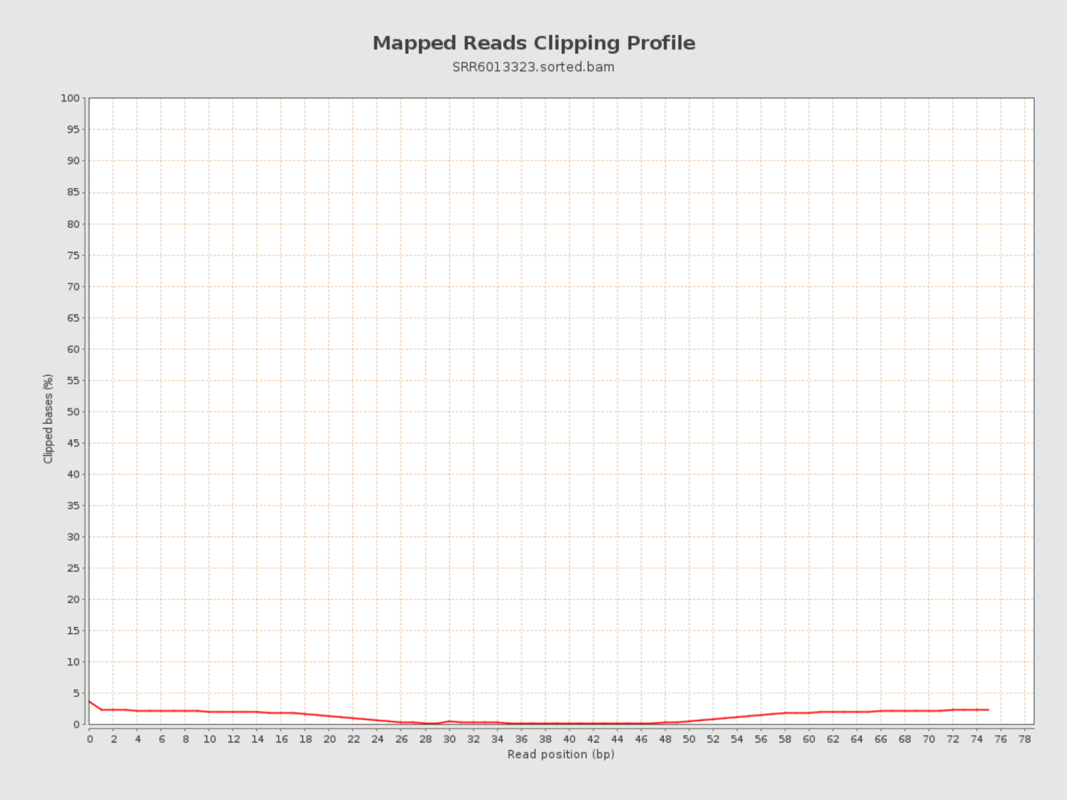
8. Results : Mapped Reads Nucleotide Content



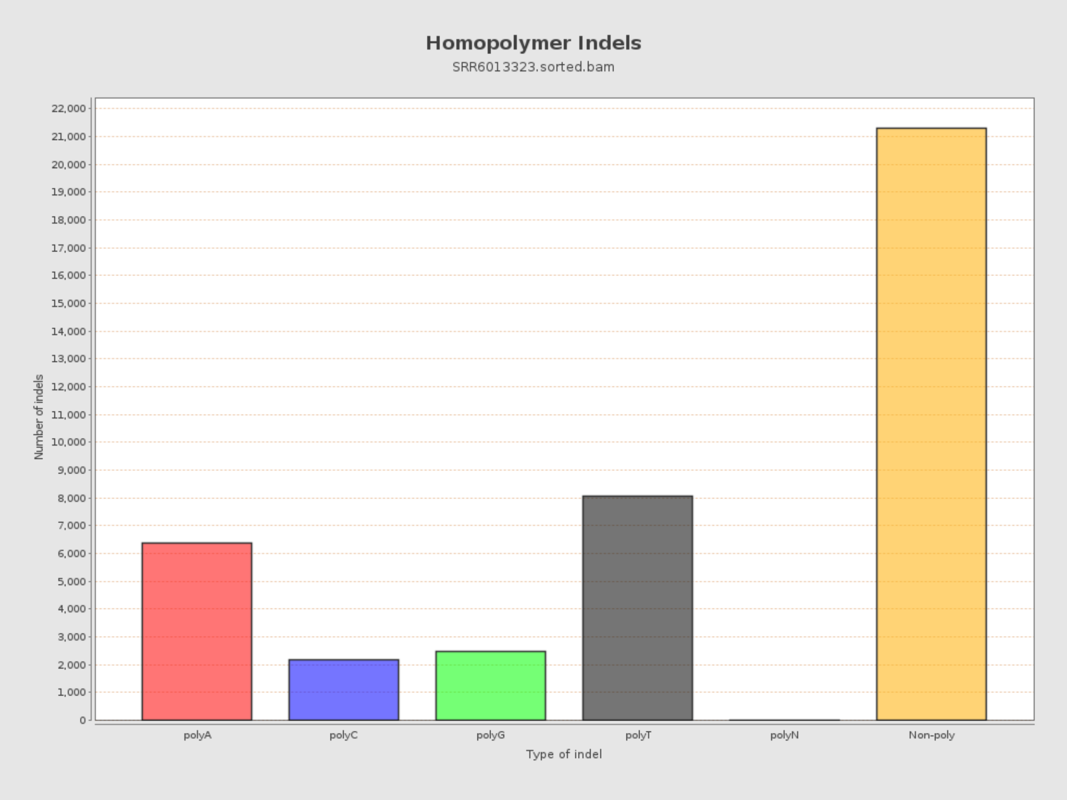
9. Results : Mapped Reads GC-content Distribution



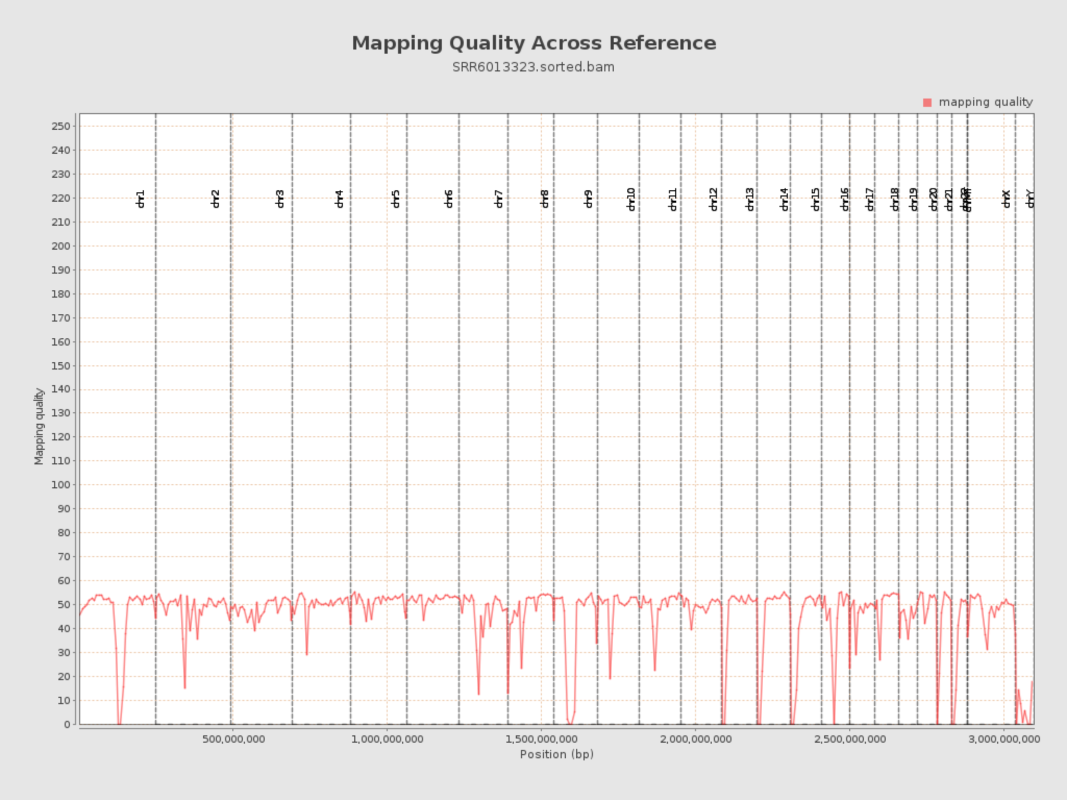
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram