Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/18 22:54:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR053602.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_SRR053602 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR053602.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 18 22:54:56 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR053602.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,879,714
Mapped reads	5,443,734 / 61.31%
Unmapped reads	3,435,980 / 38.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	184 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	1,185,219 / 13.35%
Duplication rate	15.89%
Clipped reads	771,251 / 8.69%

2.2. ACGT Content

Number/percentage of A's	76,938,460 / 30.27%
Number/percentage of C's	48,666,611 / 19.15%
Number/percentage of T's	76,356,485 / 30.04%
Number/percentage of G's	52,115,630 / 20.5%
Number/percentage of N's	111,403 / 0.04%
GC Percentage	39.65%

2.3. Coverage

Mean	0.0821

Standard Deviation	0.8636

2.4. Mapping Quality

Mean Mapping Quality	44.49

2.5. Mismatches and indels

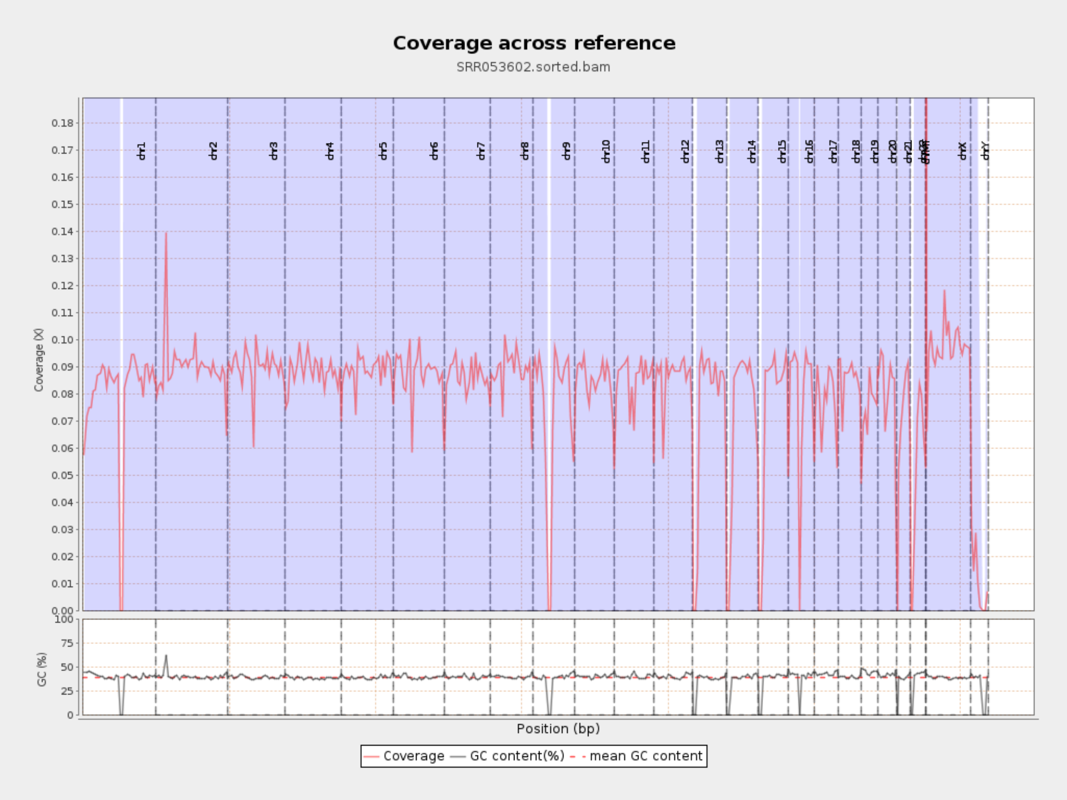
General error rate	0.95%
Mismatches	2,403,083
Insertions	14,138
Mapped reads with at least one insertion	0.26%
Deletions	38,203
Mapped reads with at least one deletion	0.7%
Homopolymer indels	45.47%

2.6. Chromosome stats

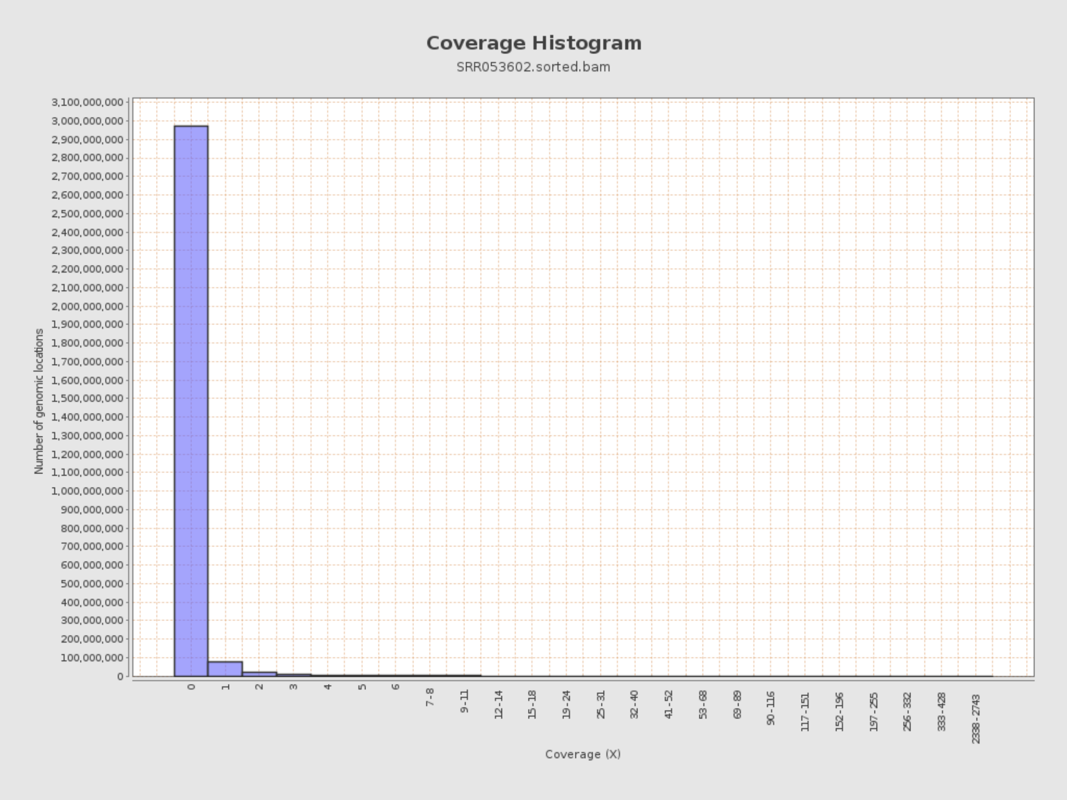
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19813580	0.0795	0.6886
chr2	243199373	21955528	0.0903	2.1141
chr3	198022430	17797532	0.0899	0.657
chr4	191154276	16918710	0.0885	0.6769
chr5	180915260	16037974	0.0886	0.6426
chr6	171115067	15072510	0.0881	0.695
chr7	159138663	13715424	0.0862	0.7525

chr8	146364022	12920141	0.0883	0.6827
chr9	141213431	10443714	0.074	0.6107
chr10	135534747	11605084	0.0856	0.6728
chr11	135006516	11494571	0.0851	0.6854
chr12	133851895	11590065	0.0866	0.636
chr13	115169878	8438314	0.0733	0.5903
chr14	107349540	7758001	0.0723	0.6321
chr15	102531392	7347896	0.0717	0.5804
chr16	90354753	6950583	0.0769	0.6178
chr17	81195210	6373634	0.0785	0.5954
chr18	78077248	6707457	0.0859	0.7098
chr19	59128983	4448197	0.0752	0.6487
chr20	63025520	5248017	0.0833	0.6327
chr21	48129895	3250449	0.0675	0.6071
chr22	51304566	2620839	0.0511	0.4527
chrMT	16571	17265	1.0419	3.0574
chrX	155270560	15078422	0.0971	0.7249
chrY	59373566	638494	0.0108	0.2153

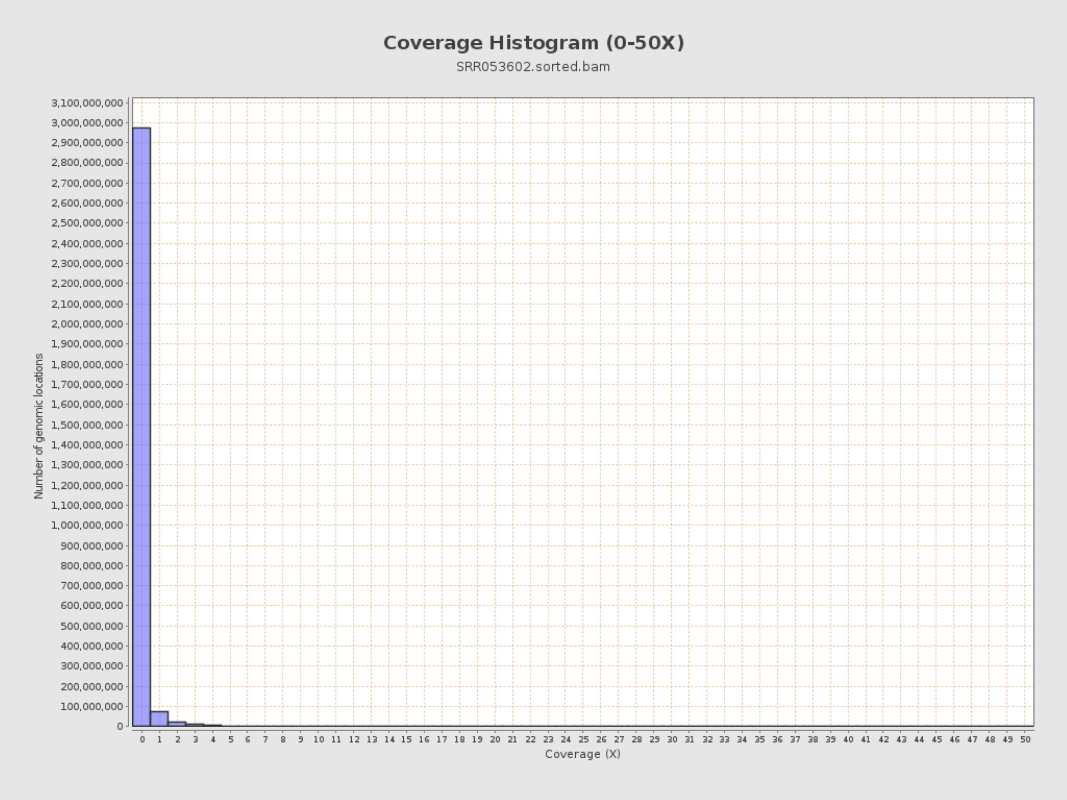
3. Results : Coverage across reference



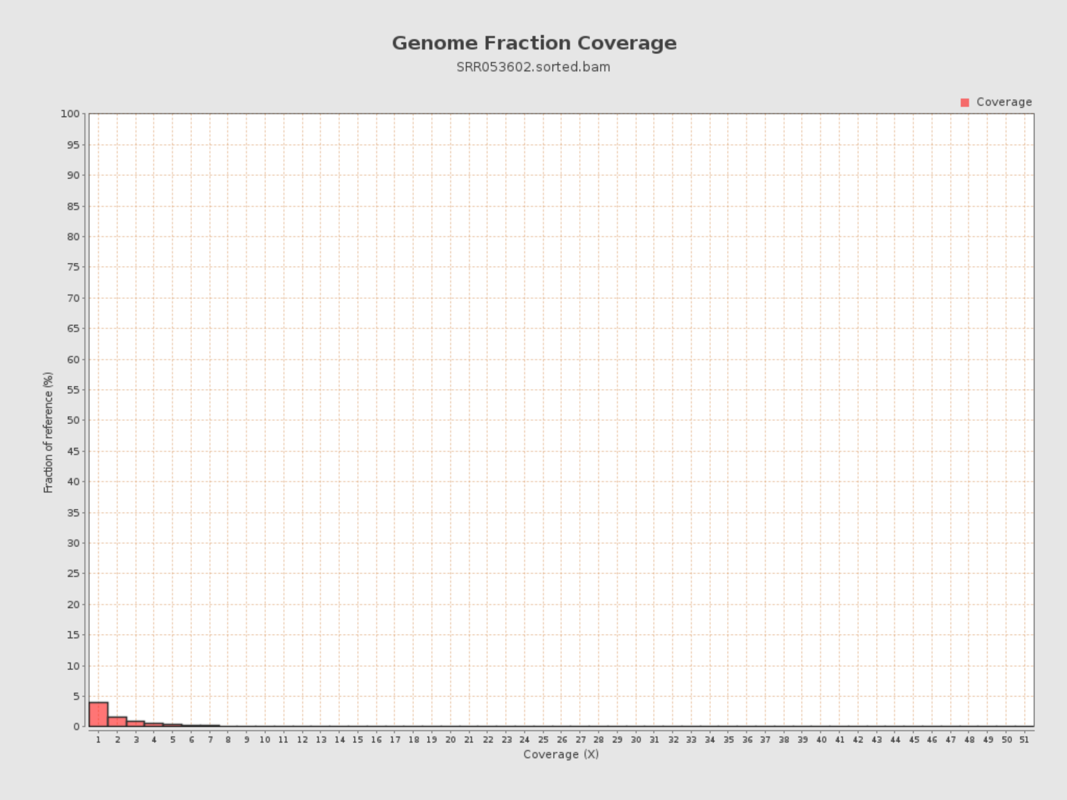
4. Results : Coverage Histogram



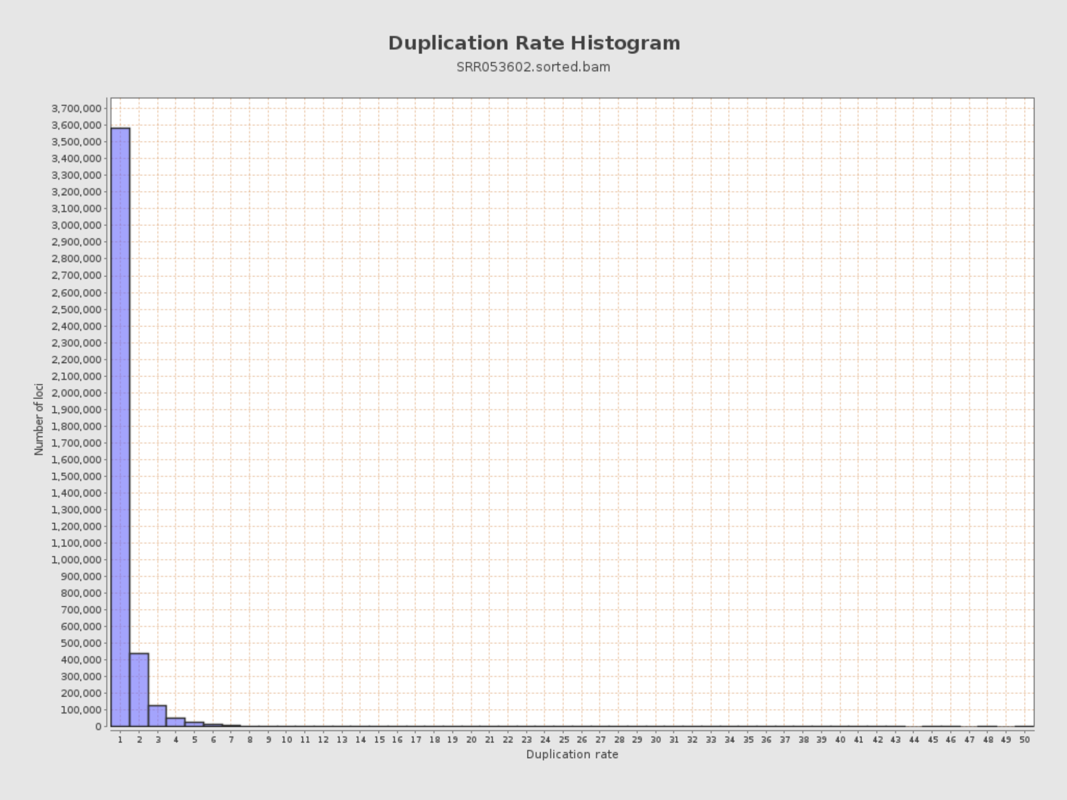
5. Results : Coverage Histogram (0-50X)



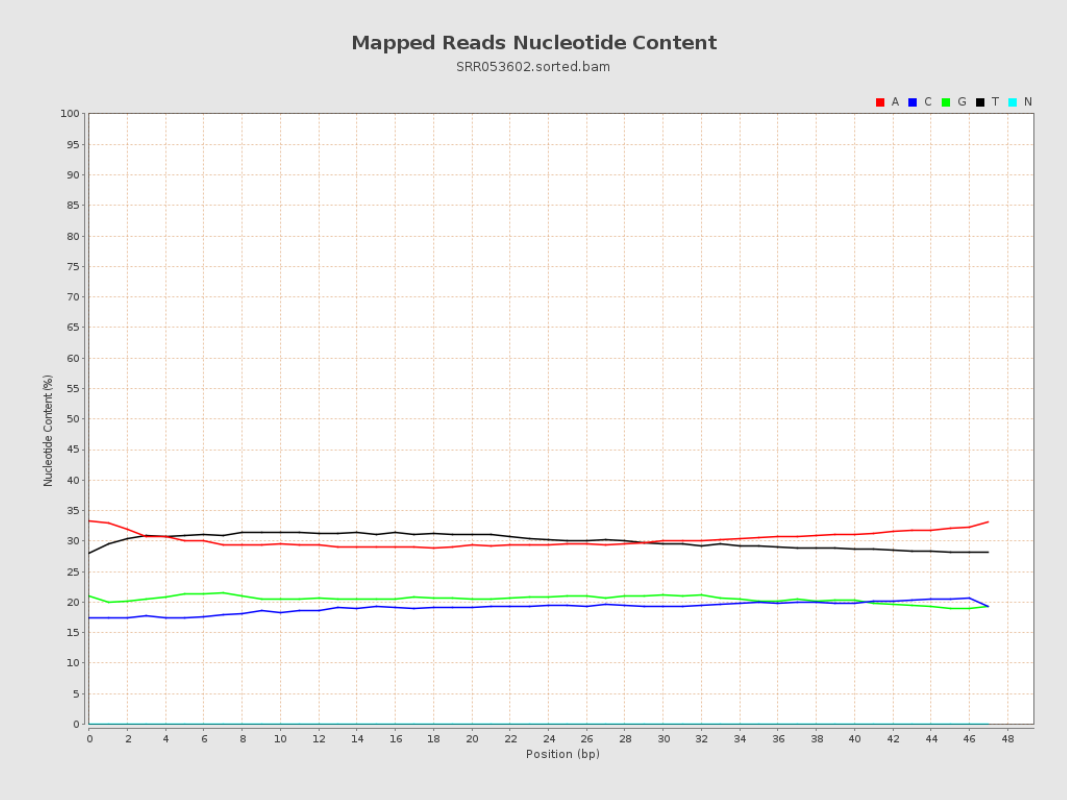
6. Results : Genome Fraction Coverage



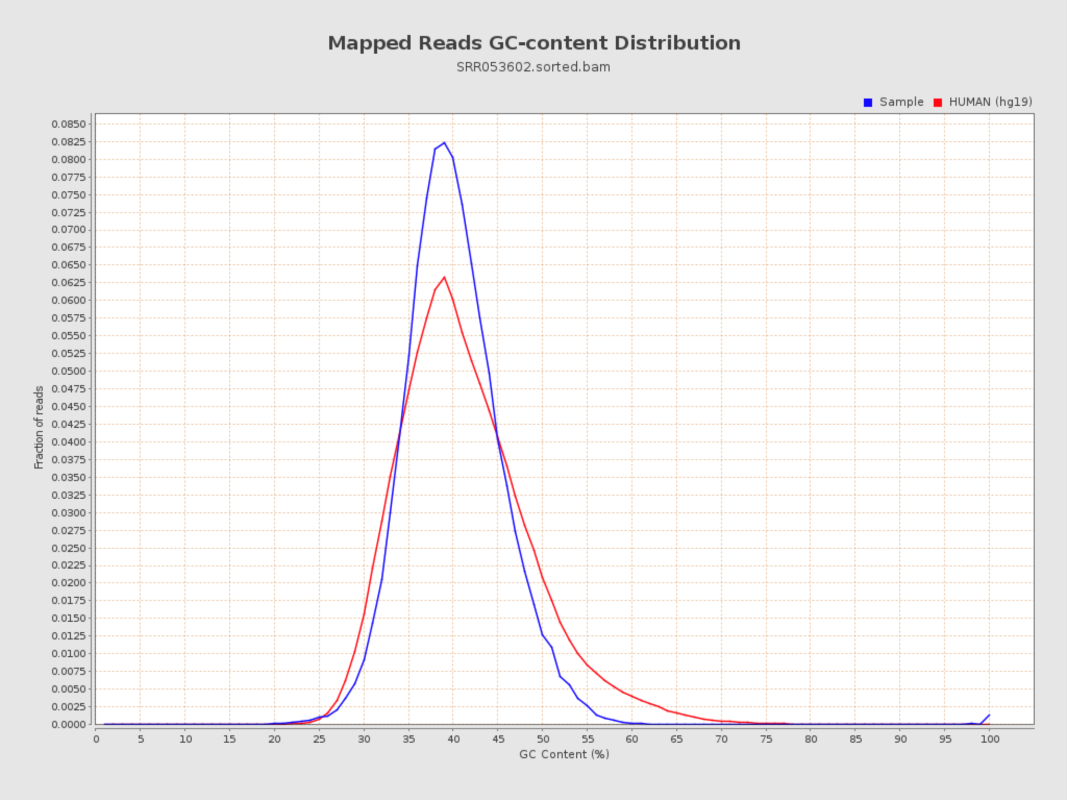
7. Results : Duplication Rate Histogram



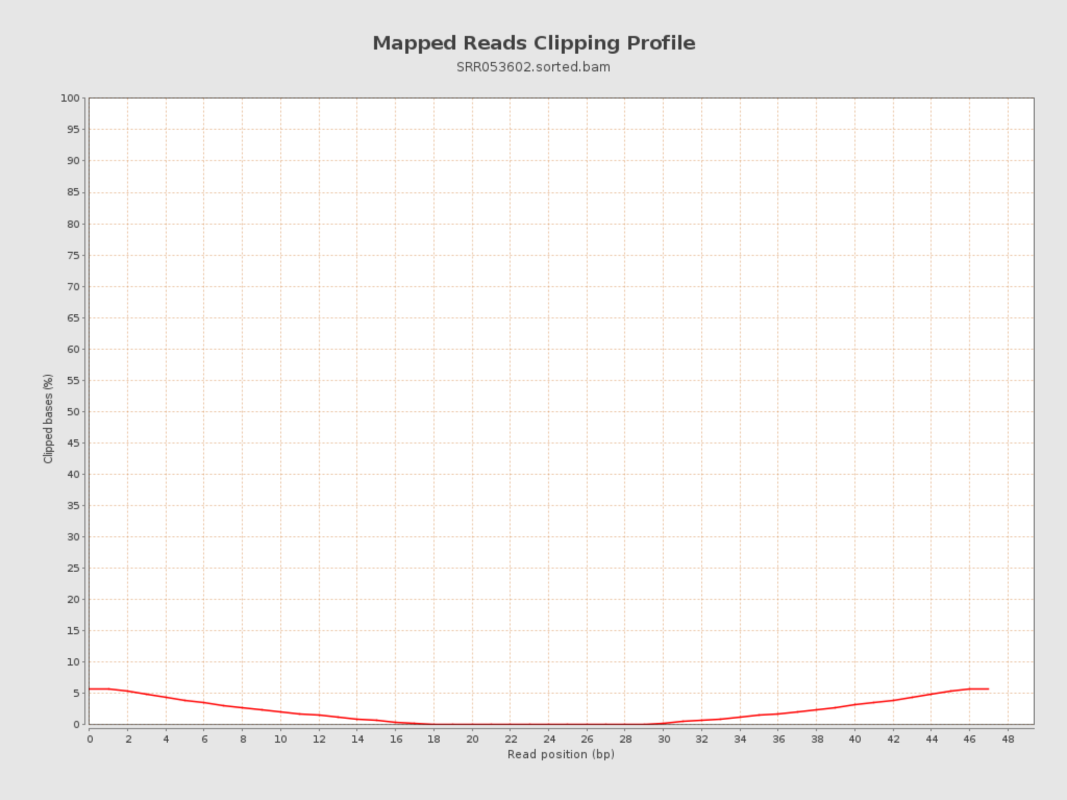
8. Results : Mapped Reads Nucleotide Content



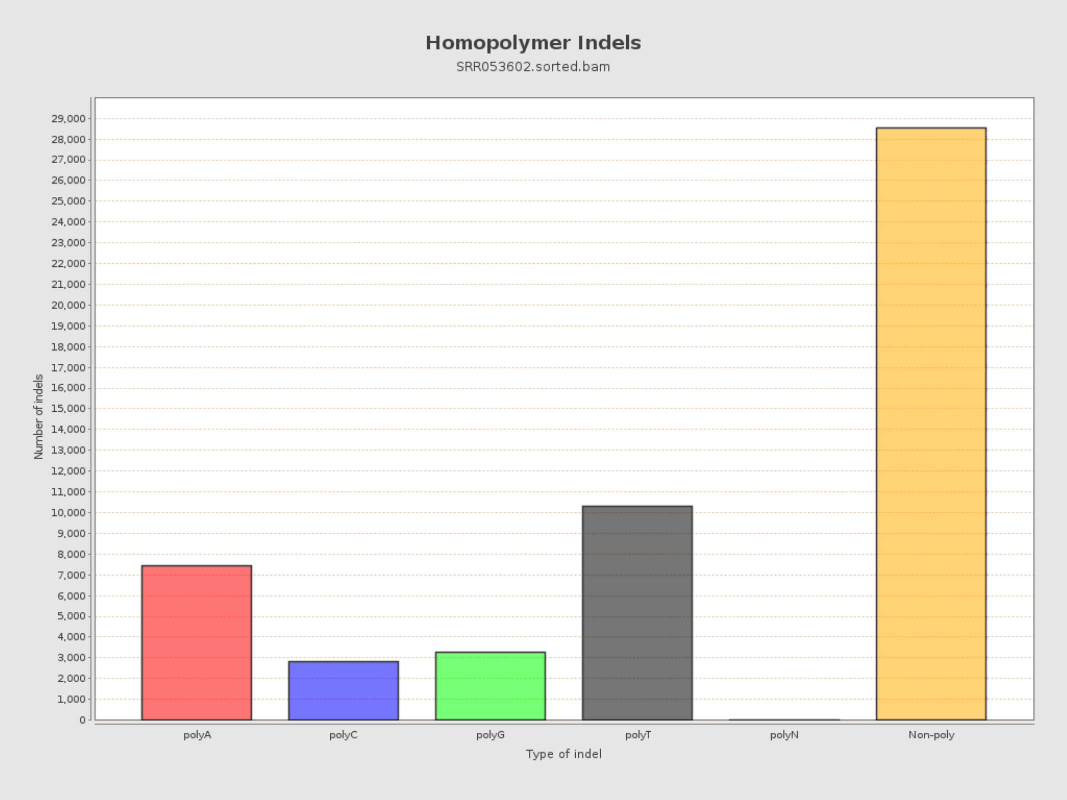
9. Results : Mapped Reads GC-content Distribution



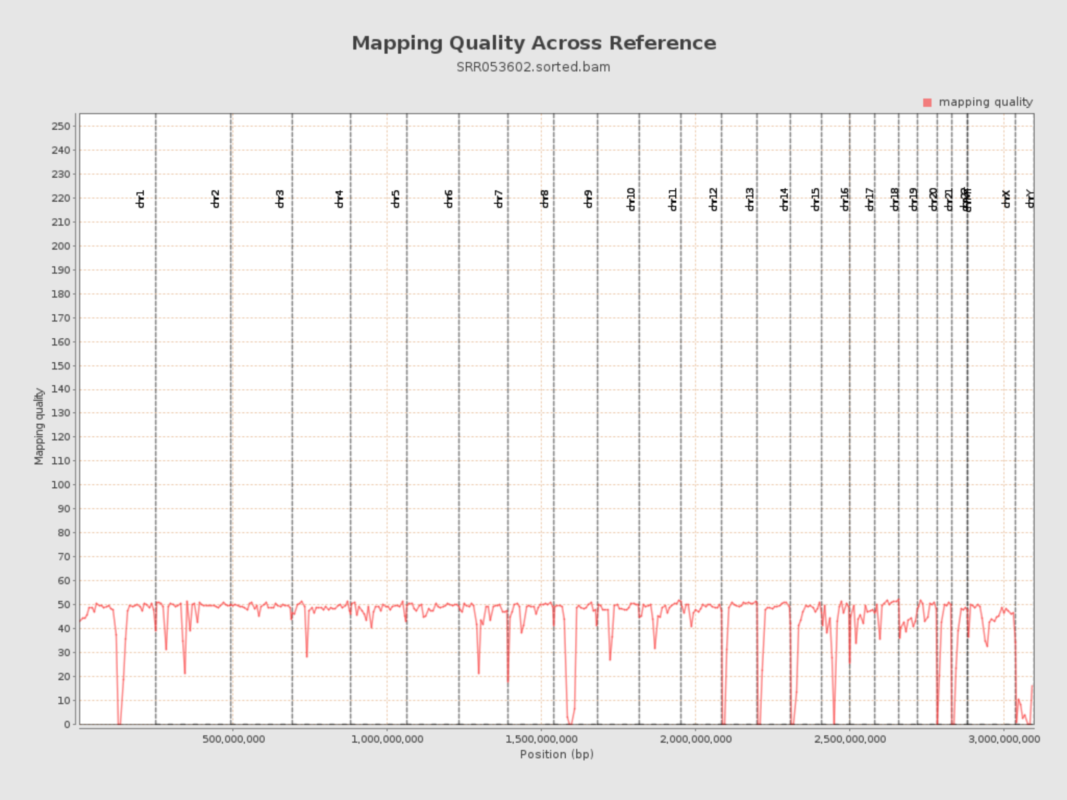
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram