Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 02:03:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063553.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_SRR6063553 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063553.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 02:03:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063553.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,310,744
Mapped reads	2,995,607 / 90.48%
Unmapped reads	315,137 / 9.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,291 / 0.76%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	176,356 / 5.33%
Duplication rate	4.67%
Clipped reads	1,465,716 / 44.27%

2.2. ACGT Content

Number/percentage of A's	55,046,821 / 27.89%
Number/percentage of C's	36,041,231 / 18.26%
Number/percentage of T's	62,633,322 / 31.73%
Number/percentage of G's	43,654,572 / 22.12%
Number/percentage of N's	4,844 / 0%
GC Percentage	40.38%

2.3. Coverage

Mean	0.0638

Standard Deviation	0.5575

2.4. Mapping Quality

Mean Mapping Quality	45.92

2.5. Mismatches and indels

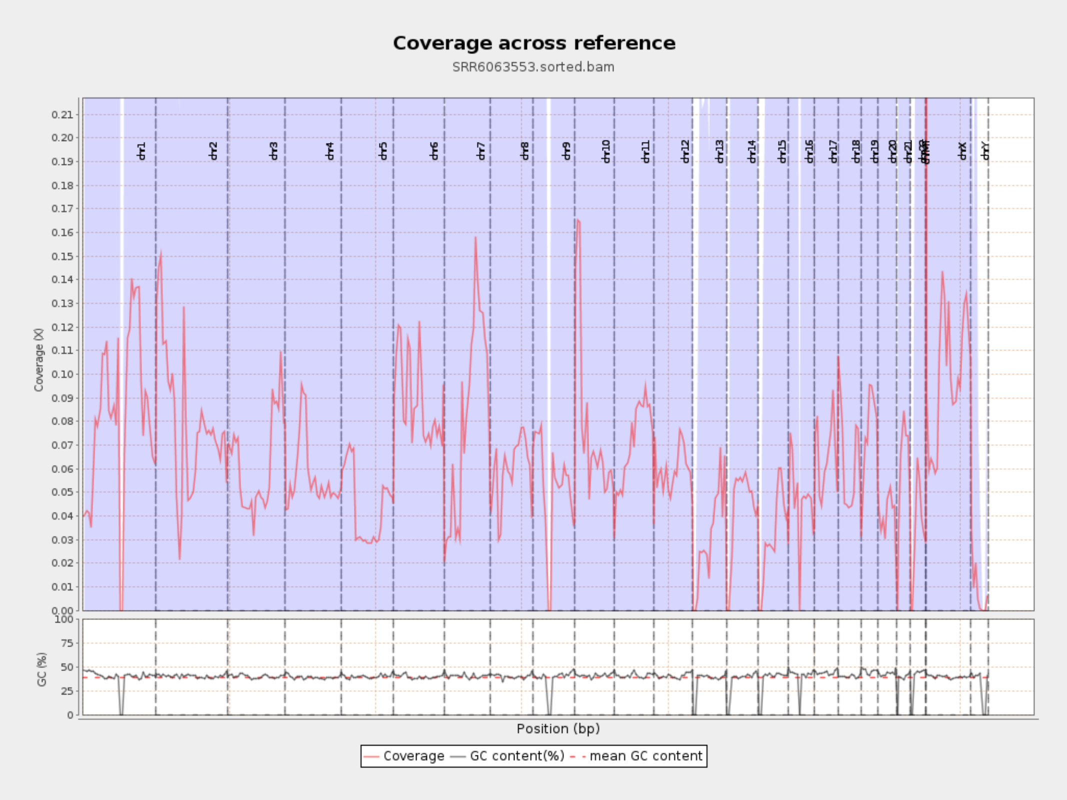
General error rate	0.82%
Mismatches	1,589,033
Insertions	14,999
Mapped reads with at least one insertion	0.5%
Deletions	51,308
Mapped reads with at least one deletion	1.69%
Homopolymer indels	46.53%

2.6. Chromosome stats

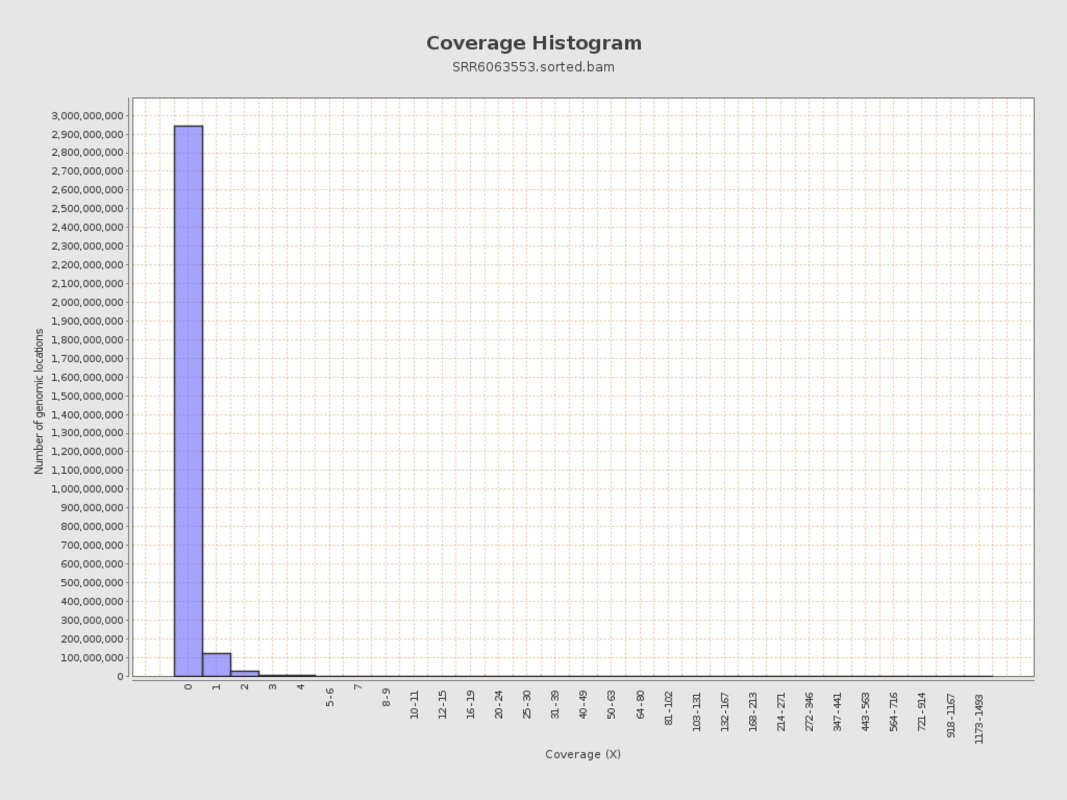
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20583429	0.0826	1.0675
chr2	243199373	19600207	0.0806	0.7266
chr3	198022430	12239416	0.0618	0.3065
chr4	191154276	10945202	0.0573	0.3108
chr5	180915260	7938812	0.0439	0.2617
chr6	171115067	15279131	0.0893	0.4427
chr7	159138663	13008696	0.0817	0.6912

chr8	146364022	8706576	0.0595	0.9074
chr9	141213431	7359256	0.0521	0.4854
chr10	135534747	10655805	0.0786	0.4537
chr11	135006516	9610504	0.0712	0.4683
chr12	133851895	8026320	0.06	0.3198
chr13	115169878	3646920	0.0317	0.2239
chr14	107349540	4640305	0.0432	0.3094
chr15	102531392	3194924	0.0312	0.2399
chr16	90354753	4127457	0.0457	0.2869
chr17	81195210	5445629	0.0671	0.3484
chr18	78077248	4937756	0.0632	0.771
chr19	59128983	4527259	0.0766	0.7474
chr20	63025520	2569612	0.0408	0.2656
chr21	48129895	2802947	0.0582	0.3211
chr22	51304566	1720086	0.0335	0.2197
chrMT	16571	44736	2.6997	2.5193
chrX	155270560	15358125	0.0989	0.4565
chrY	59373566	495391	0.0083	0.1491

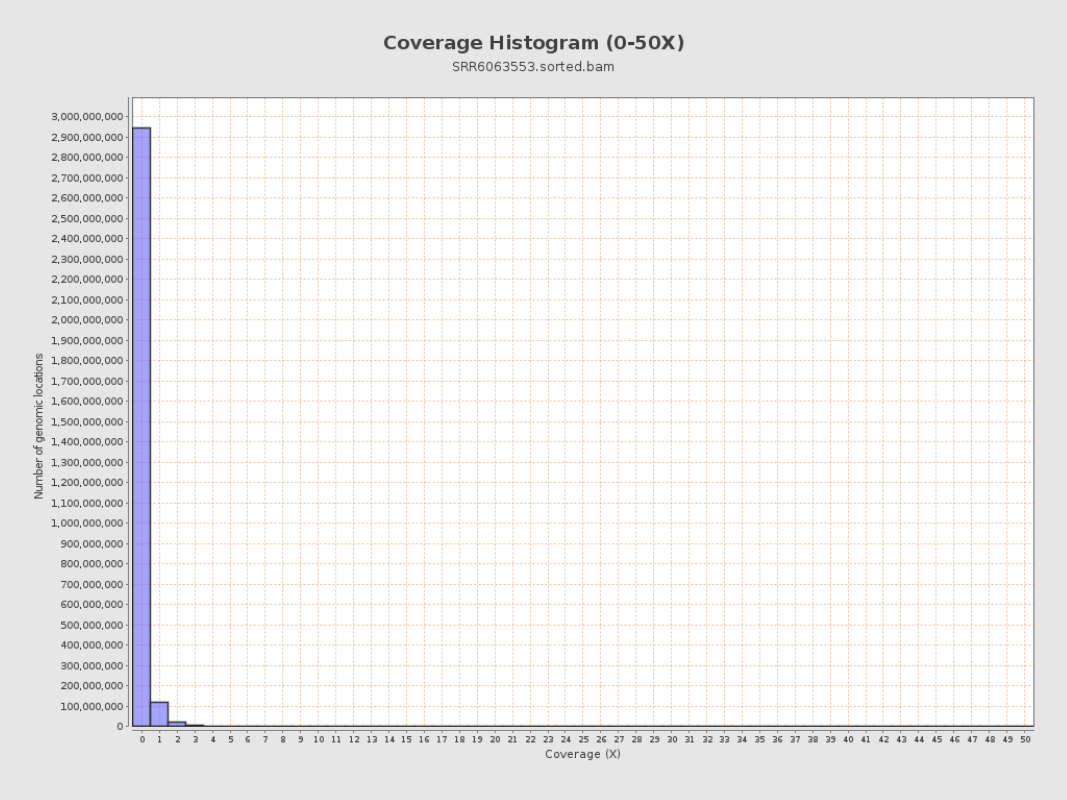
3. Results : Coverage across reference



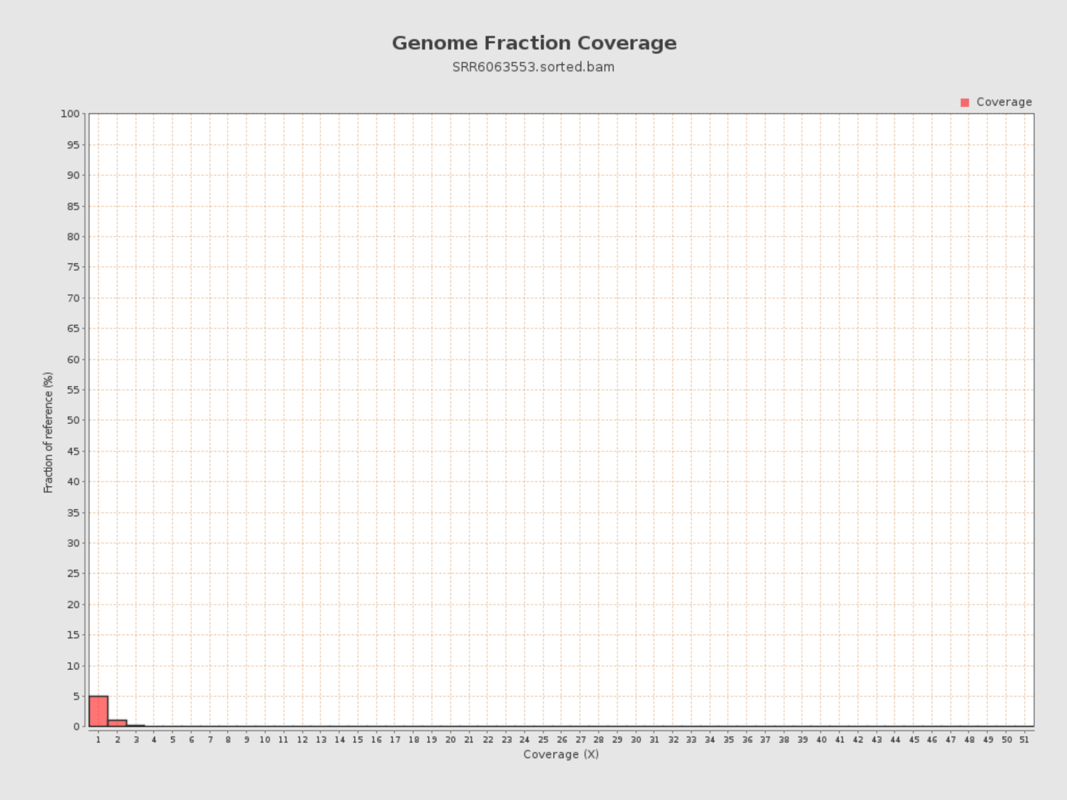
4. Results : Coverage Histogram



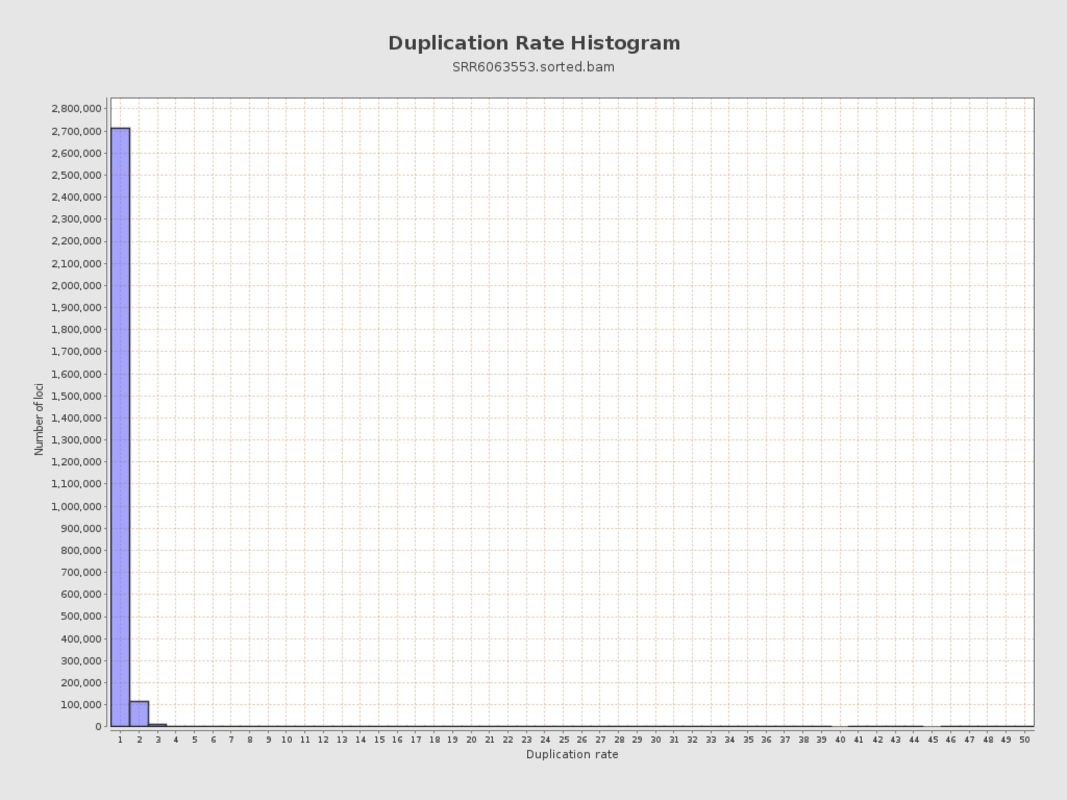
5. Results : Coverage Histogram (0-50X)



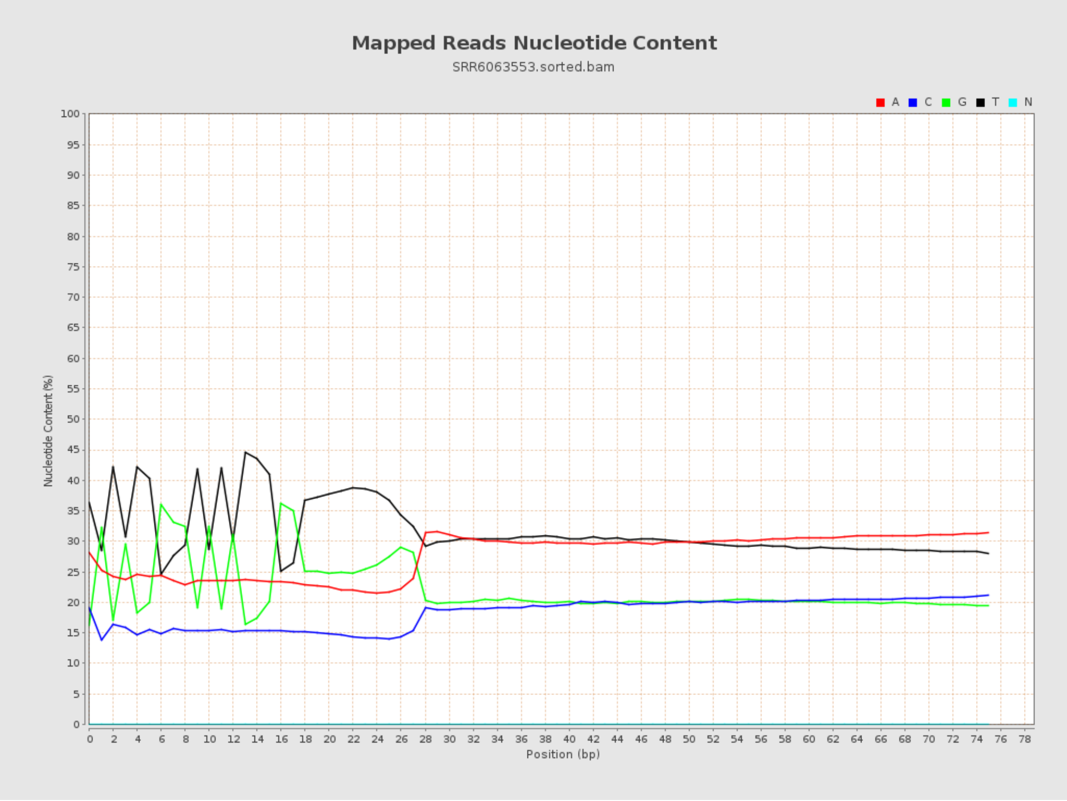
6. Results : Genome Fraction Coverage



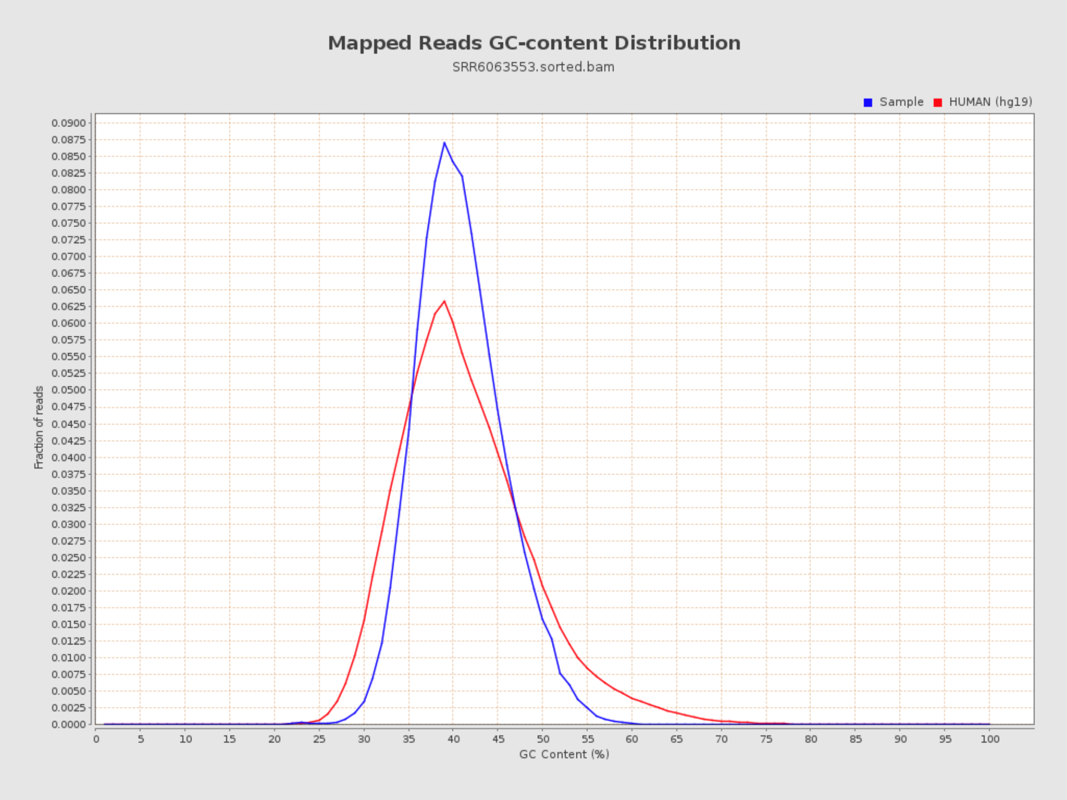
7. Results : Duplication Rate Histogram



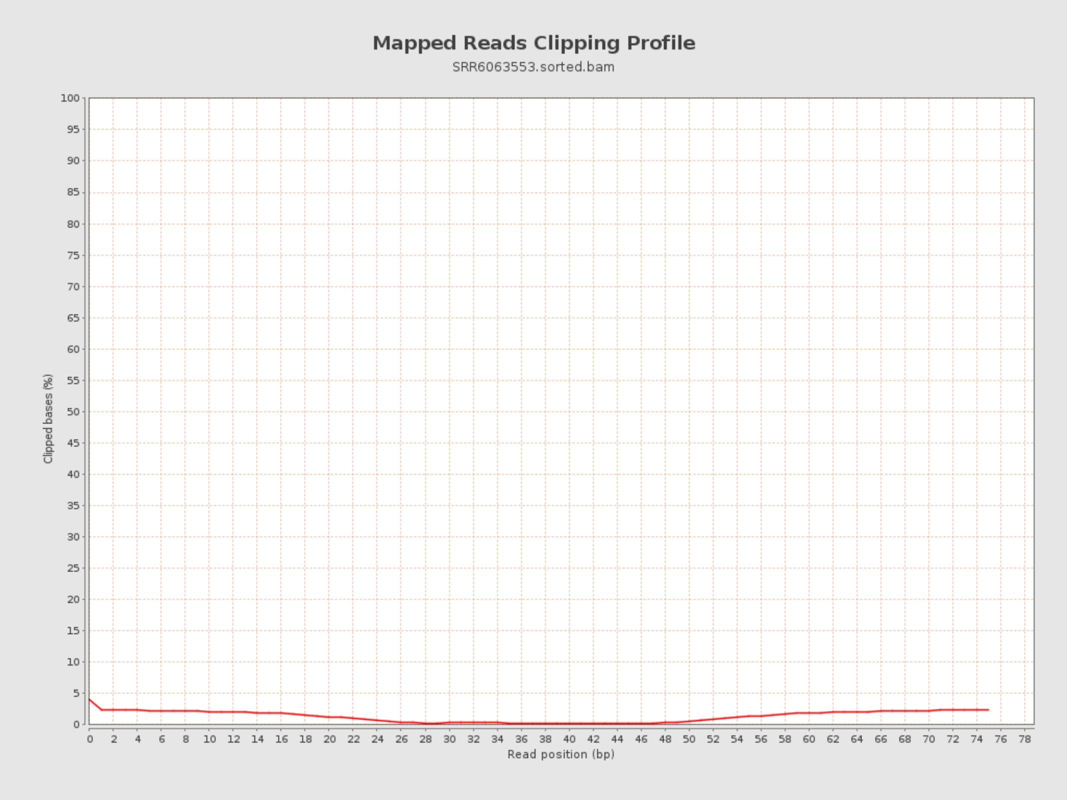
8. Results : Mapped Reads Nucleotide Content



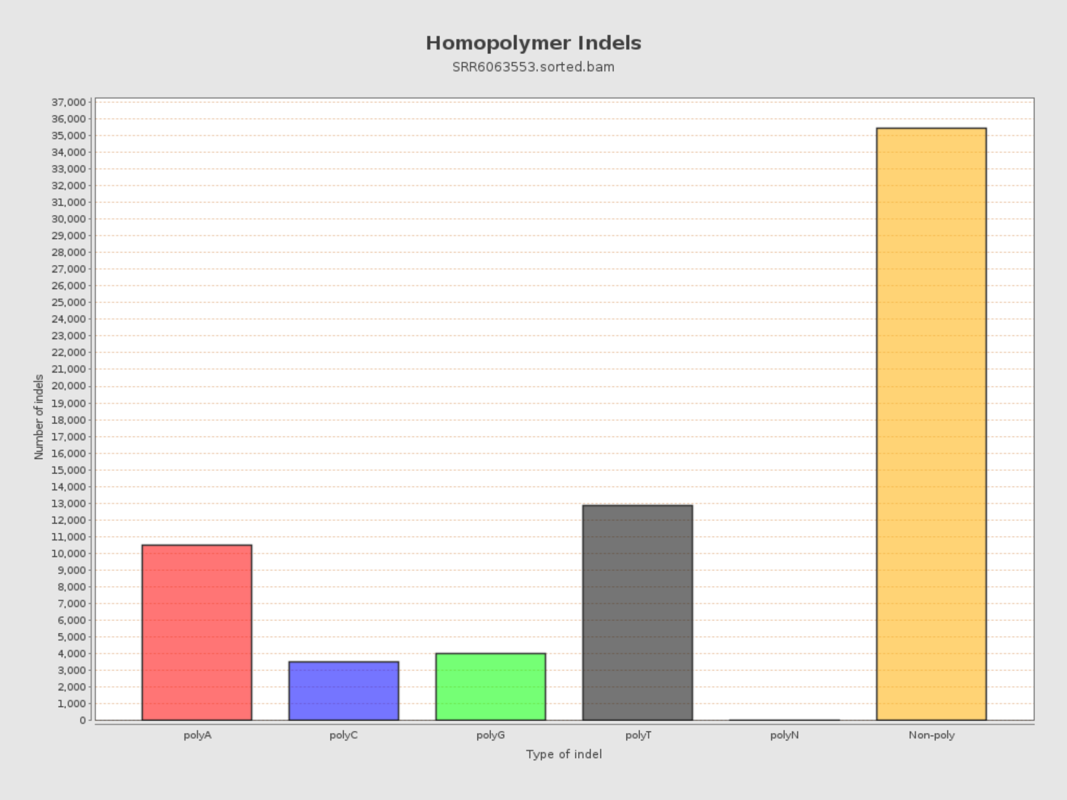
9. Results : Mapped Reads GC-content Distribution



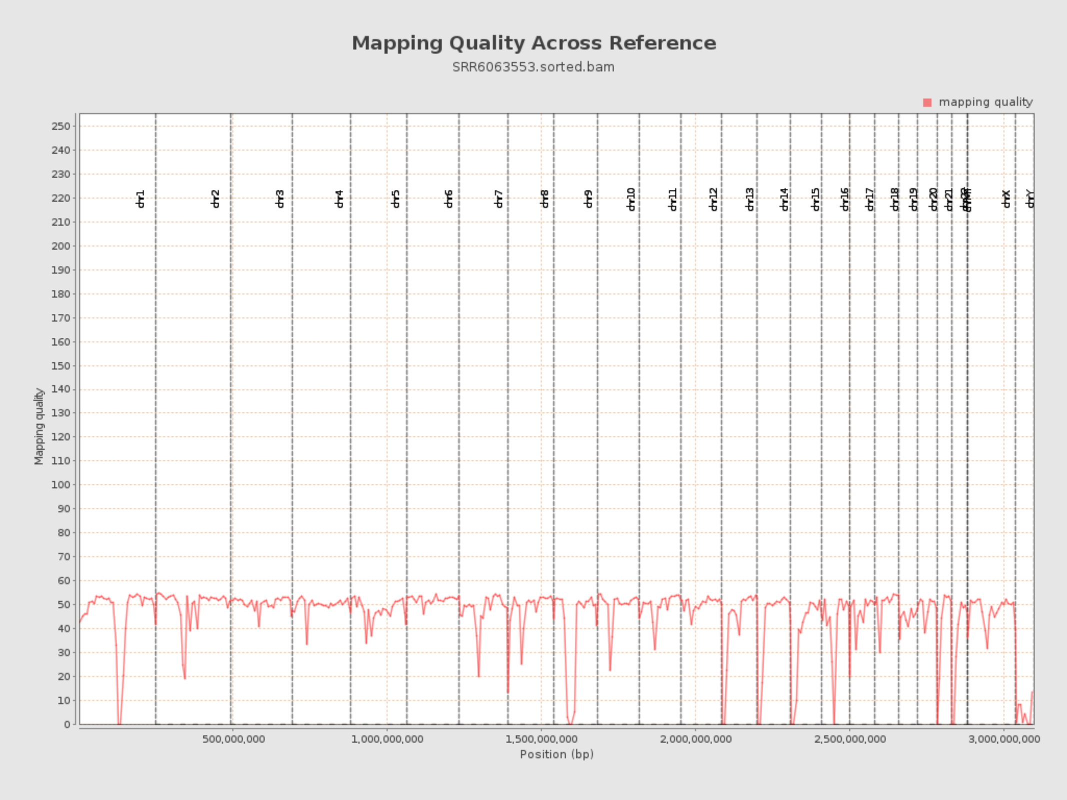
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram