Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 12:27:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163151.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_SRR1163151 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163151.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 12:27:30 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163151.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	78,902,294
Mapped reads	78,187,071 / 99.09%
Unmapped reads	715,223 / 0.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	386,781 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	40,833,102 / 51.75%
Duplication rate	41.52%
Clipped reads	6,756,651 / 8.56%

2.2. ACGT Content

Number/percentage of A's	1,884,344,831 / 24.44%
Number/percentage of C's	1,971,290,127 / 25.57%
Number/percentage of T's	1,888,377,786 / 24.5%
Number/percentage of G's	1,964,662,729 / 25.49%
Number/percentage of N's	254,776 / 0%
GC Percentage	51.06%

2.3. Coverage

Mean	2.4905

Standard Deviation	28.8746

2.4. Mapping Quality

Mean Mapping Quality	49.38

2.5. Mismatches and indels

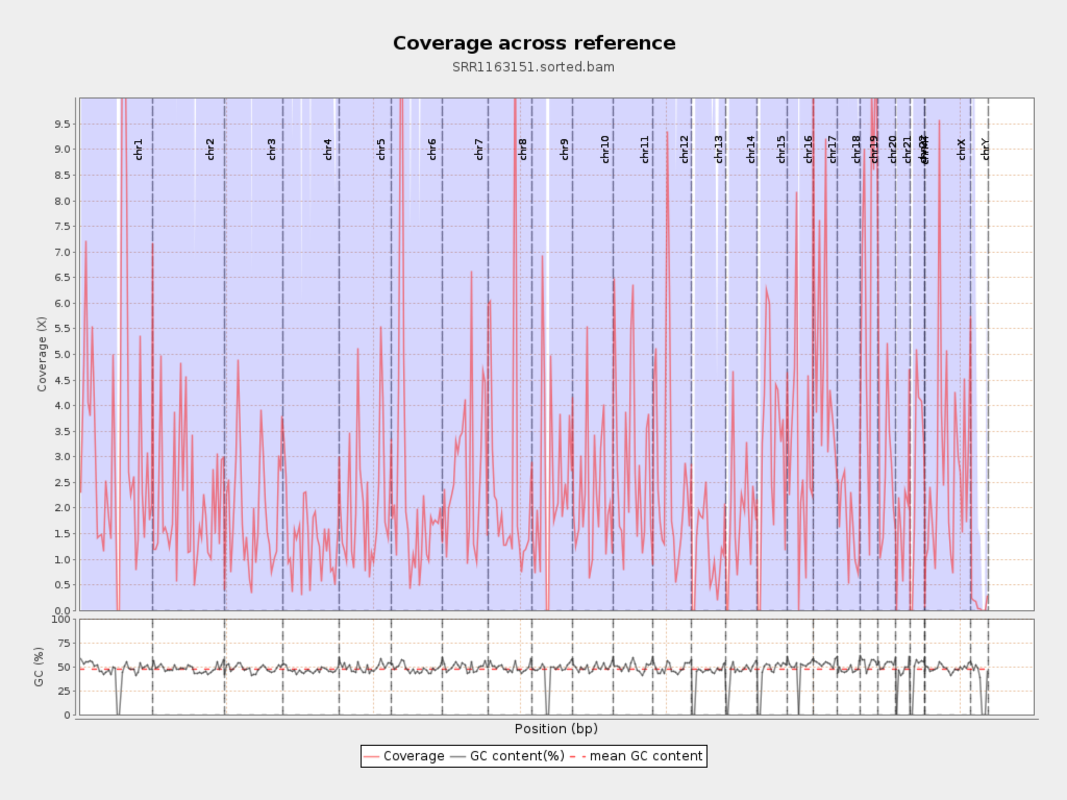
General error rate	0.32%
Mismatches	23,550,250
Insertions	557,288
Mapped reads with at least one insertion	0.7%
Deletions	388,673
Mapped reads with at least one deletion	0.49%
Homopolymer indels	45.93%

2.6. Chromosome stats

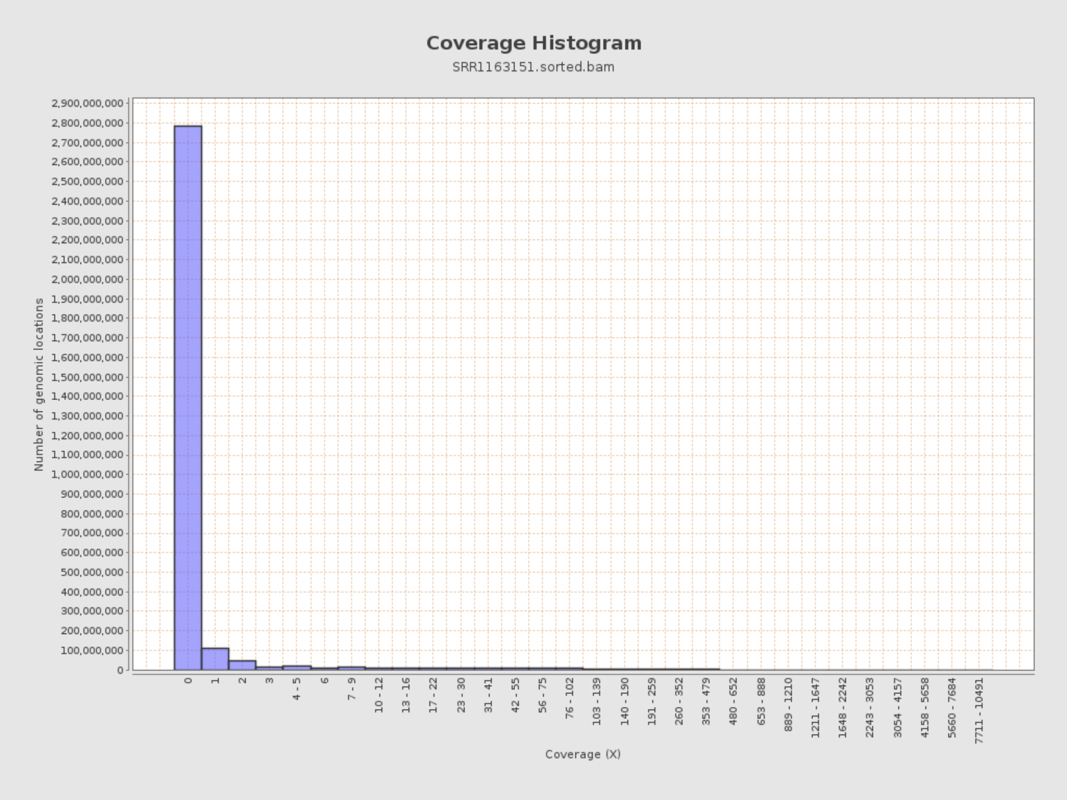
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	855500304	3.4323	33.4498
chr2	243199373	503581503	2.0707	22.3038
chr3	198022430	382048474	1.9293	21.4184
chr4	191154276	264018247	1.3812	17.7374
chr5	180915260	384066967	2.1229	31.9175
chr6	171115067	394048562	2.3028	27.6644
chr7	159138663	426775677	2.6818	33.9398

chr8	146364022	349407285	2.3872	40.0973
chr9	141213431	344984990	2.443	28.0751
chr10	135534747	300859613	2.2198	25.6405
chr11	135006516	396316529	2.9355	28.5936
chr12	133851895	367940765	2.7489	28.4189
chr13	115169878	129760690	1.1267	14.0303
chr14	107349540	195535577	1.8215	20.2672
chr15	102531392	324986075	3.1696	35.9334
chr16	90354753	282998652	3.1321	26.8779
chr17	81195210	391695577	4.8241	37.6801
chr18	78077248	129207143	1.6549	23.0256
chr19	59128983	430425919	7.2794	50.6287
chr20	63025520	174312994	2.7658	28.3313
chr21	48129895	91155726	1.894	29.2269
chr22	51304566	145695971	2.8398	25.2496
chrMT	16571	910	0.0549	0.3037
chrX	155270560	437708305	2.819	33.5382
chrY	59373566	6843895	0.1153	6.388

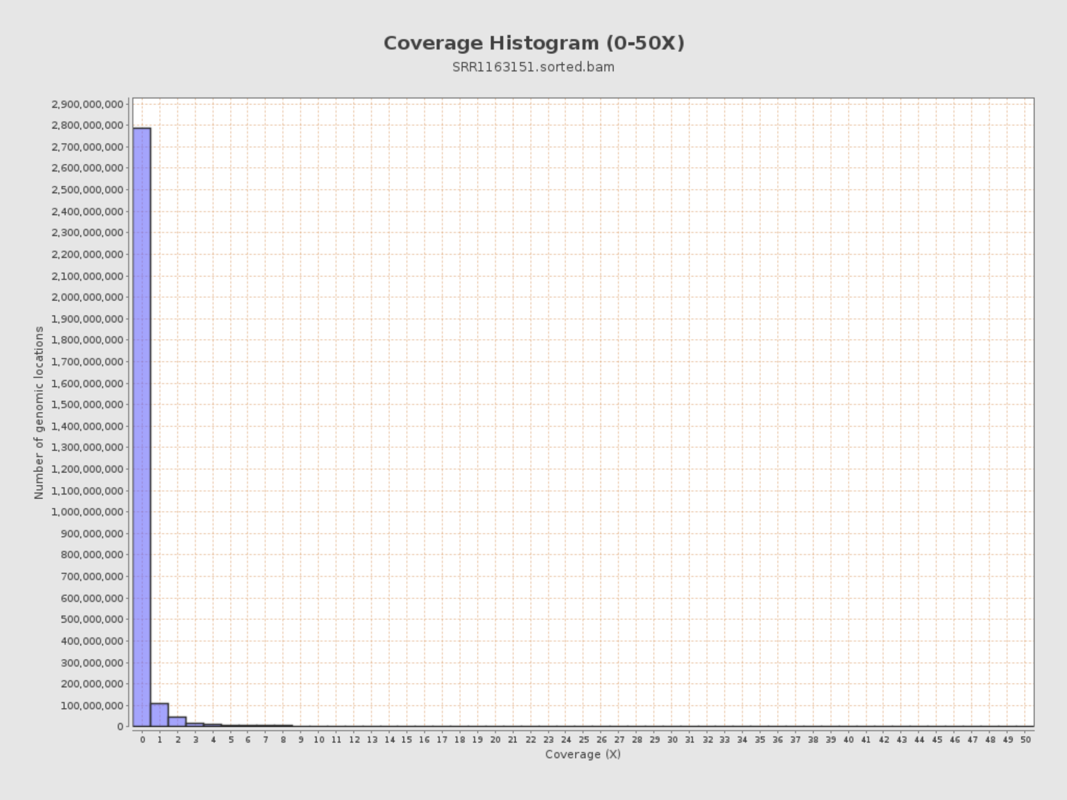
3. Results : Coverage across reference



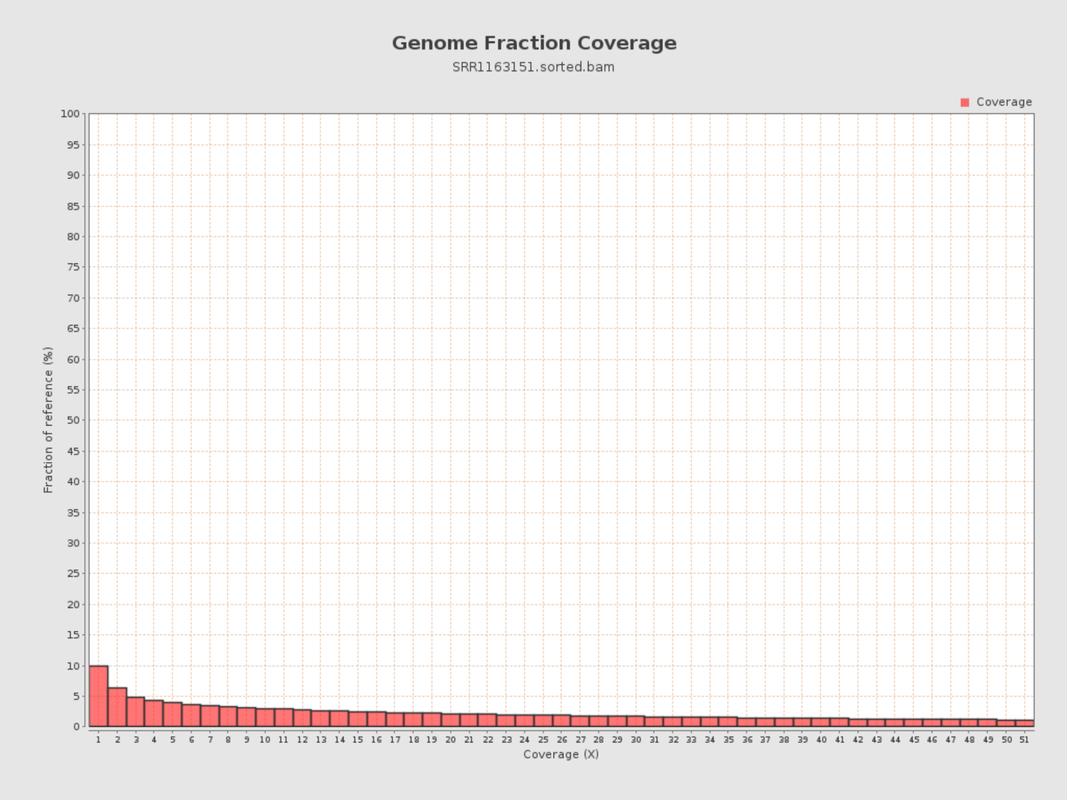
4. Results : Coverage Histogram



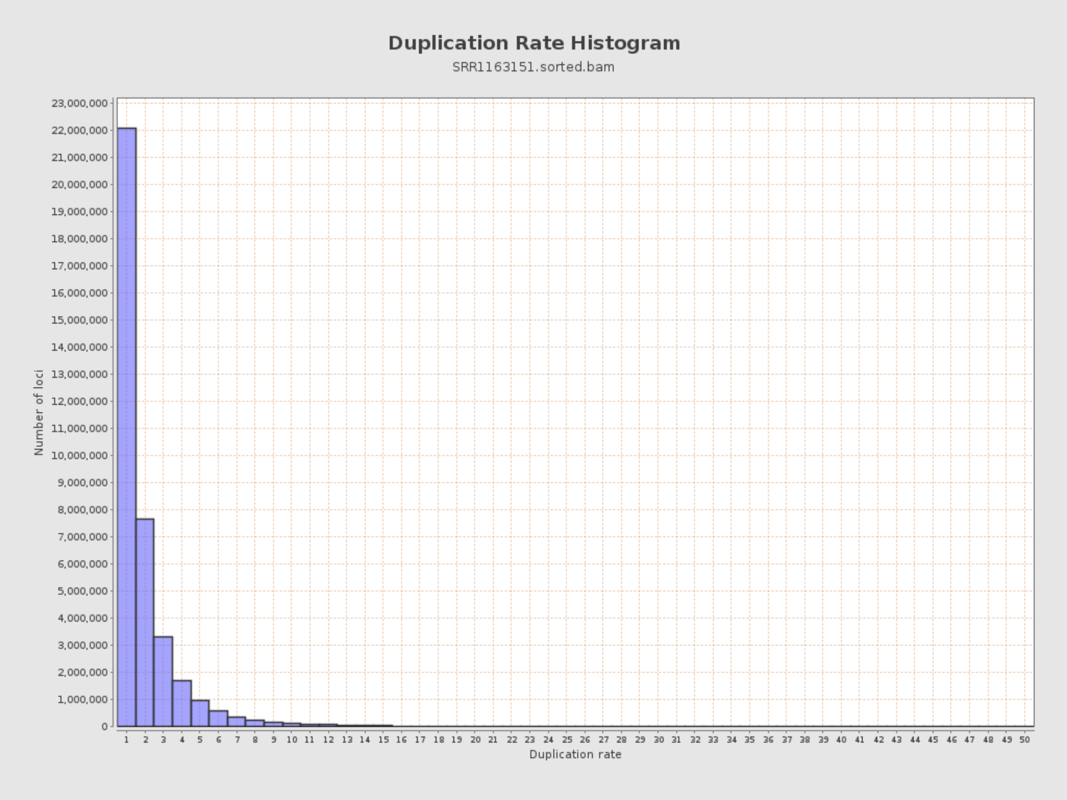
5. Results : Coverage Histogram (0-50X)



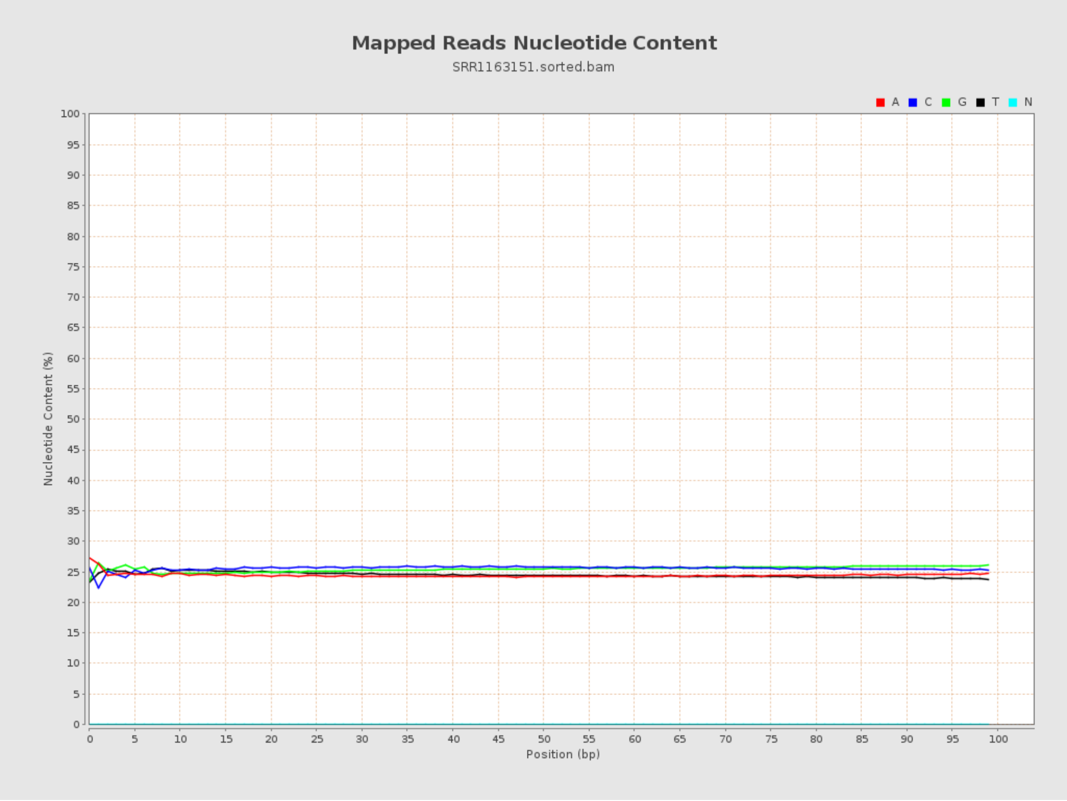
6. Results : Genome Fraction Coverage



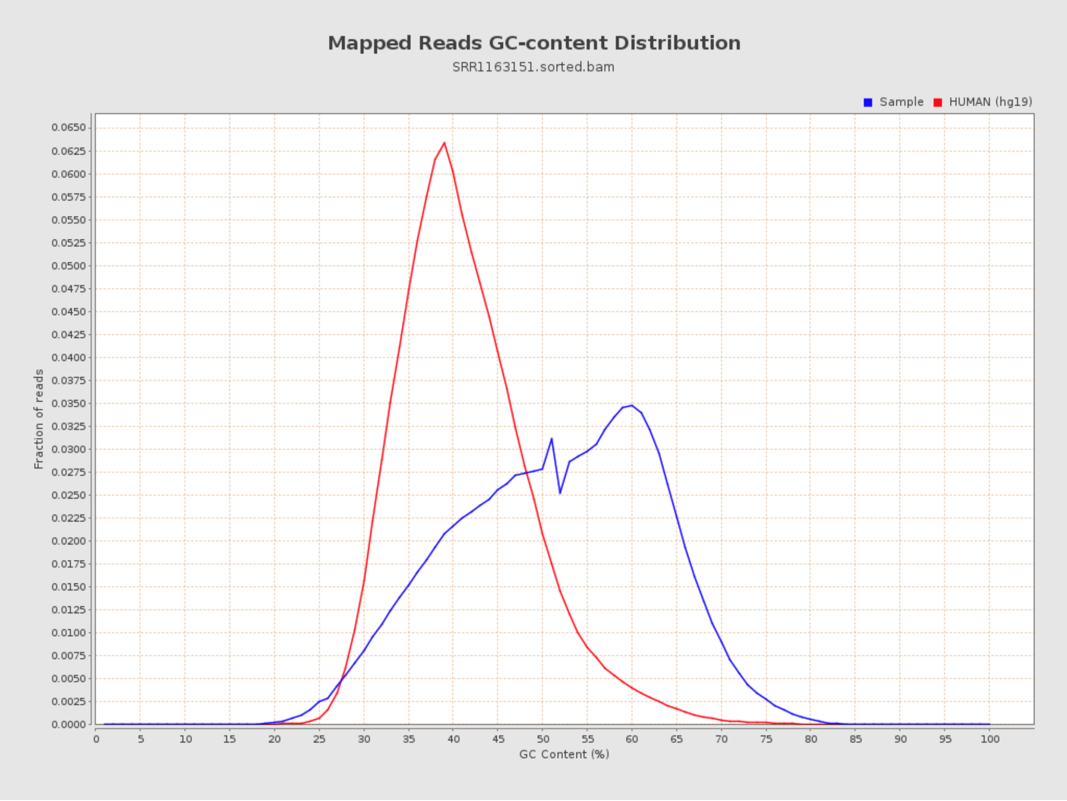
7. Results : Duplication Rate Histogram



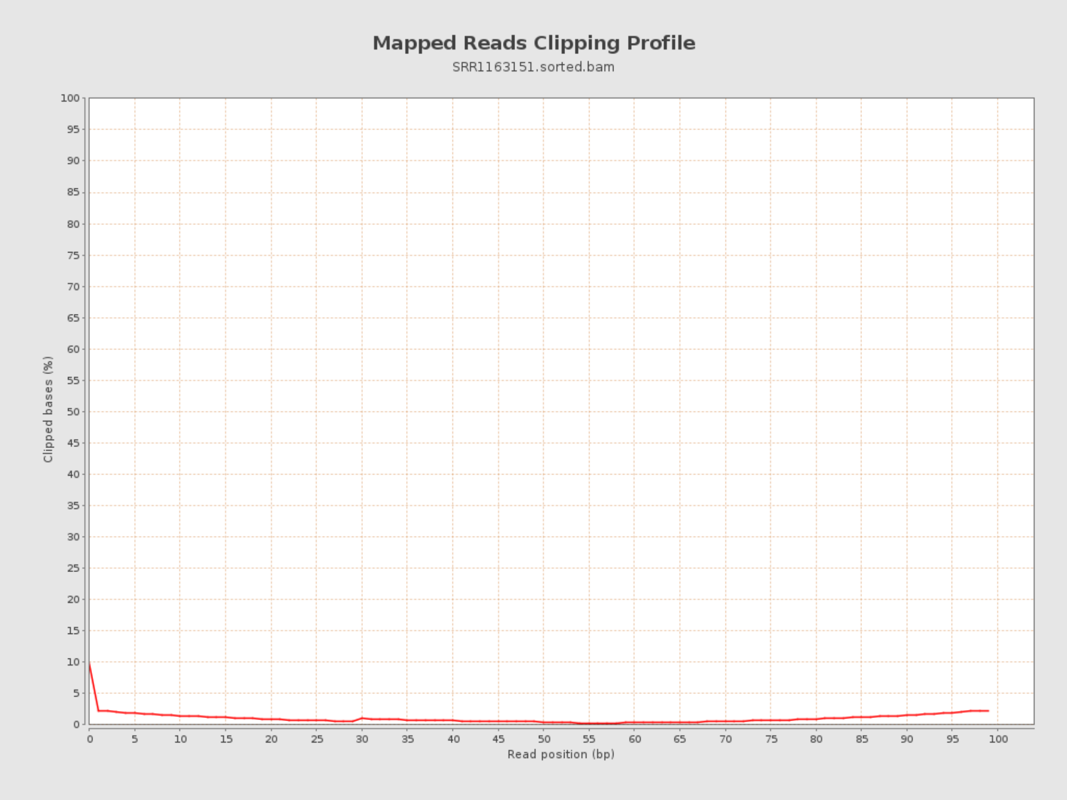
8. Results : Mapped Reads Nucleotide Content



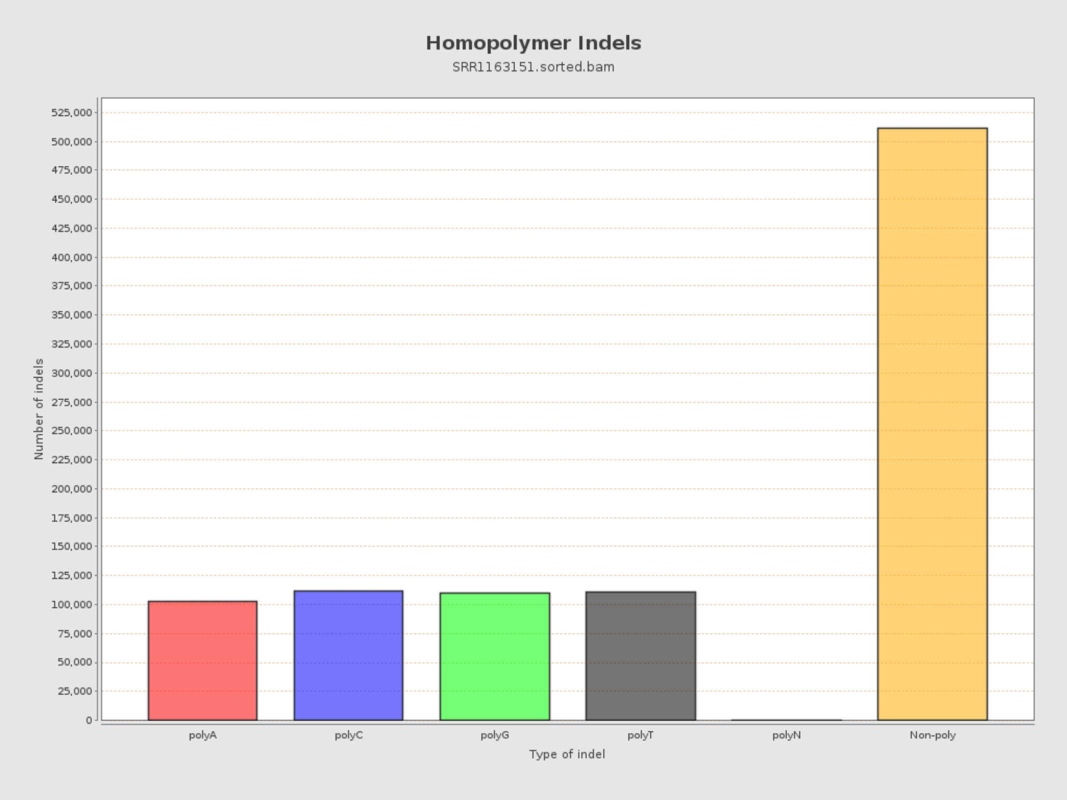
9. Results : Mapped Reads GC-content Distribution



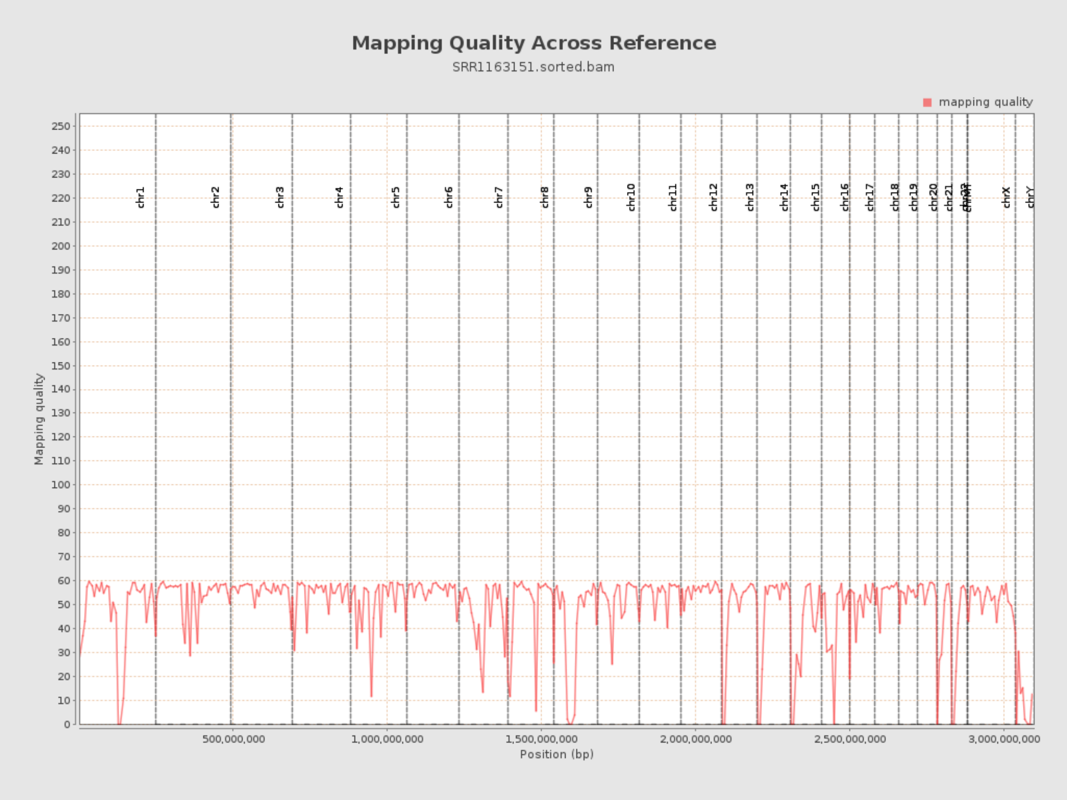
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram