Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 01:01:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163034.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_SRR1163034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 01:01:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	85,049,774
Mapped reads	83,043,957 / 97.64%
Unmapped reads	2,005,817 / 2.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	419,435 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	46,571,494 / 54.76%
Duplication rate	44.33%
Clipped reads	17,785,261 / 20.91%

2.2. ACGT Content

Number/percentage of A's	1,882,542,533 / 23.71%
Number/percentage of C's	2,087,635,907 / 26.3%
Number/percentage of T's	1,864,623,863 / 23.49%
Number/percentage of G's	2,099,887,066 / 26.45%
Number/percentage of N's	3,934,952 / 0.05%
GC Percentage	52.75%

2.3. Coverage

Mean	2.5647

Standard Deviation	33.2995

2.4. Mapping Quality

Mean Mapping Quality	49.03

2.5. Mismatches and indels

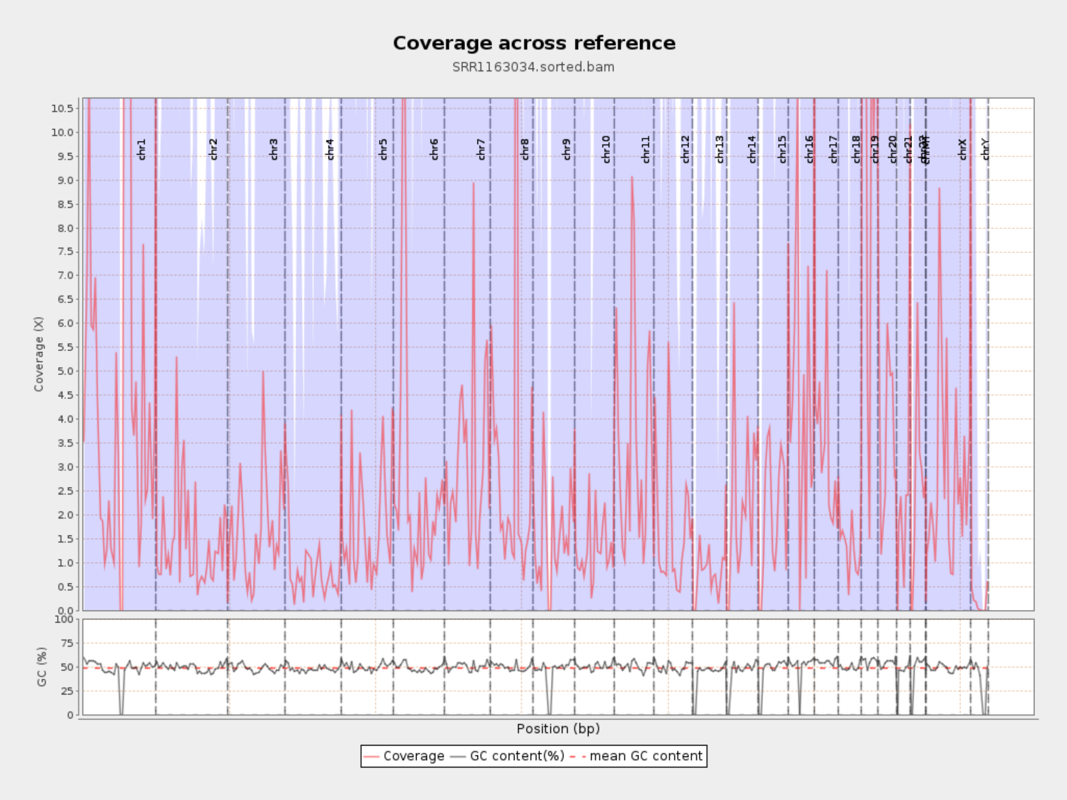
General error rate	0.54%
Mismatches	41,885,061
Insertions	512,774
Mapped reads with at least one insertion	0.61%
Deletions	440,426
Mapped reads with at least one deletion	0.52%
Homopolymer indels	45.21%

2.6. Chromosome stats

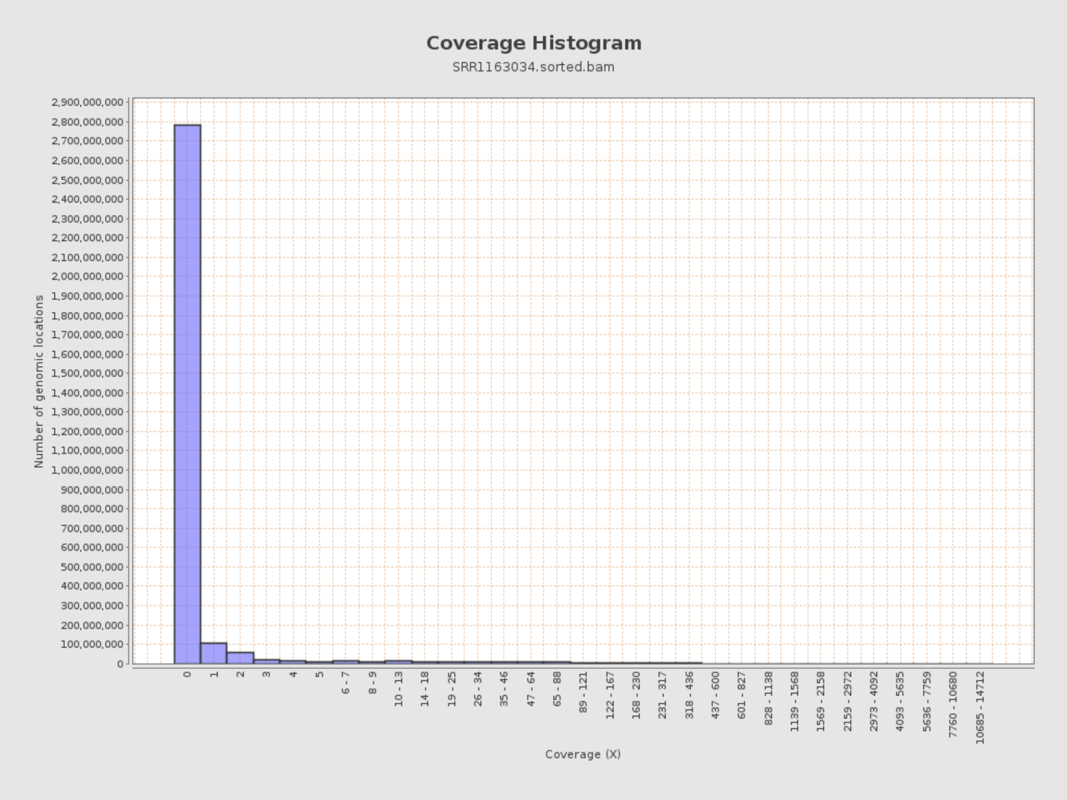
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1263673986	5.0699	47.0469
chr2	243199373	350709584	1.4421	18.0709
chr3	198022430	331925373	1.6762	18.9639
chr4	191154276	165323354	0.8649	12.56
chr5	180915260	325531252	1.7994	31.7054
chr6	171115067	462012995	2.7	29.1298
chr7	159138663	493411957	3.1005	33.2819

chr8	146364022	486038719	3.3208	72.5956
chr9	141213431	214121245	1.5163	18.5913
chr10	135534747	174292062	1.286	13.7775
chr11	135006516	482453545	3.5736	33.1274
chr12	133851895	247456004	1.8487	19.6085
chr13	115169878	92468212	0.8029	10.514
chr14	107349540	240677303	2.242	22.3369
chr15	102531392	198931441	1.9402	19.1394
chr16	90354753	393881652	4.3593	37.4796
chr17	81195210	277484503	3.4175	29.2441
chr18	78077248	103327138	1.3234	15.7773
chr19	59128983	690823218	11.6833	83.0448
chr20	63025520	228647584	3.6279	33.6484
chr21	48129895	122972386	2.555	56.8086
chr22	51304566	132516665	2.5829	25.6576
chrMT	16571	2997	0.1809	0.5085
chrX	155270560	450313549	2.9002	30.878
chrY	59373566	10623190	0.1789	9.8838

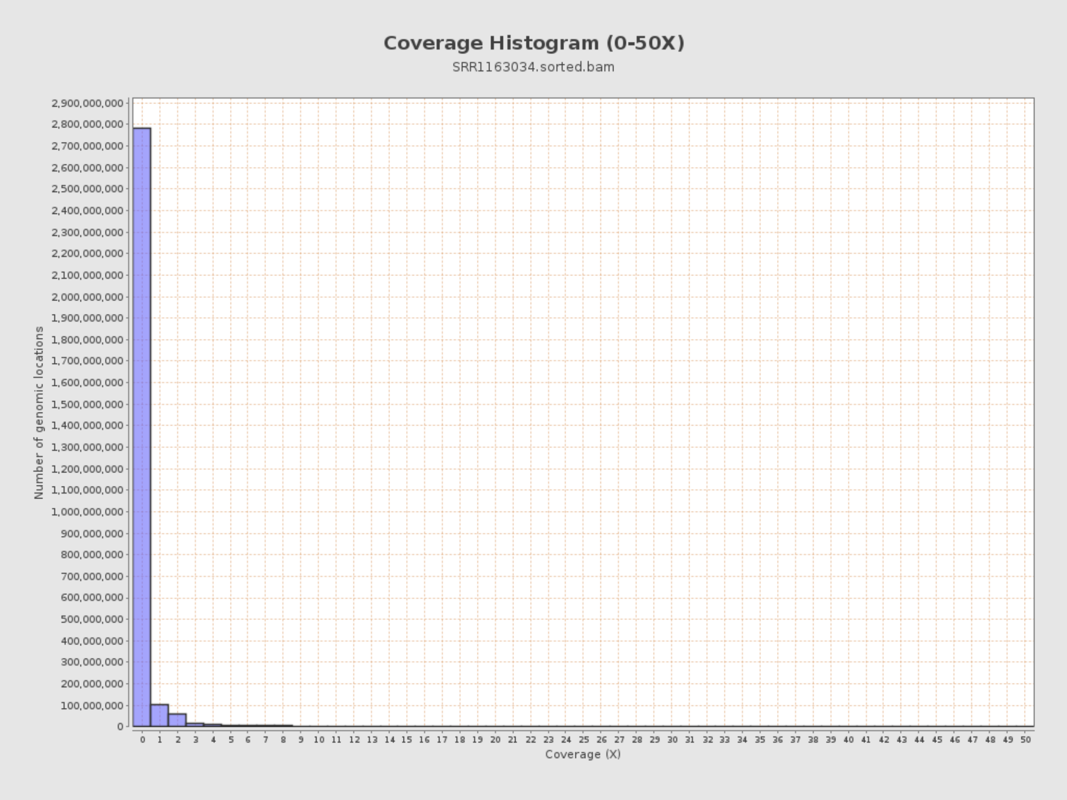
3. Results : Coverage across reference



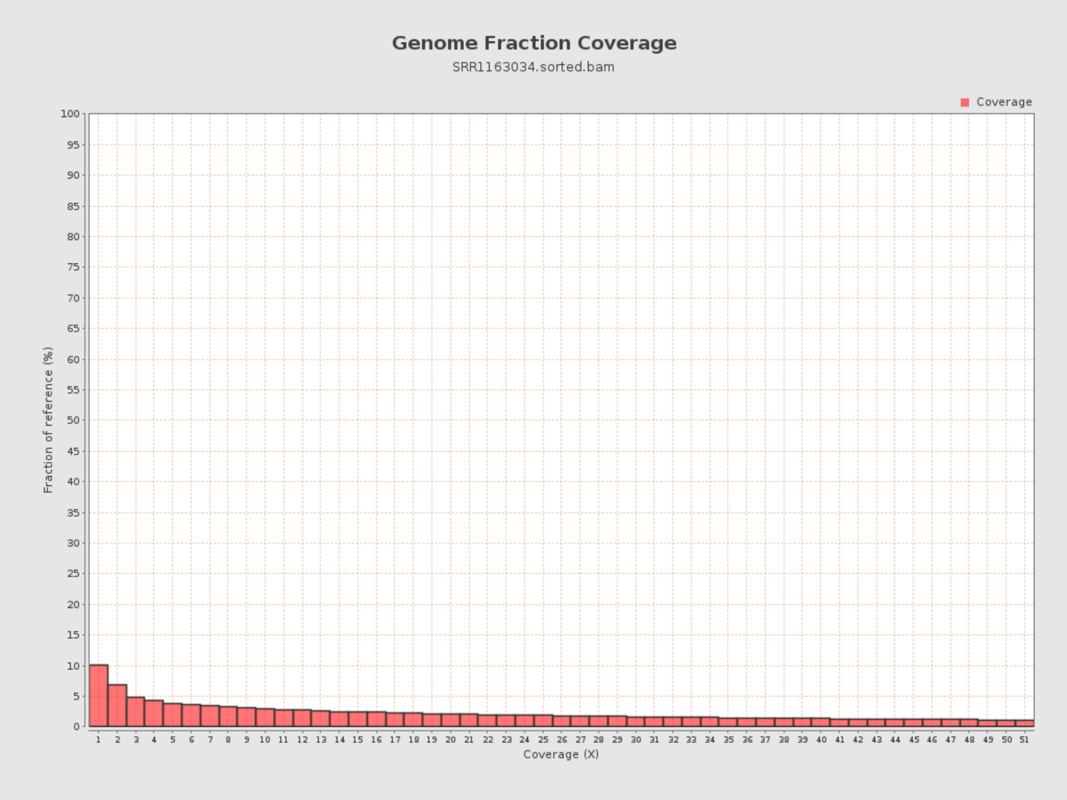
4. Results : Coverage Histogram



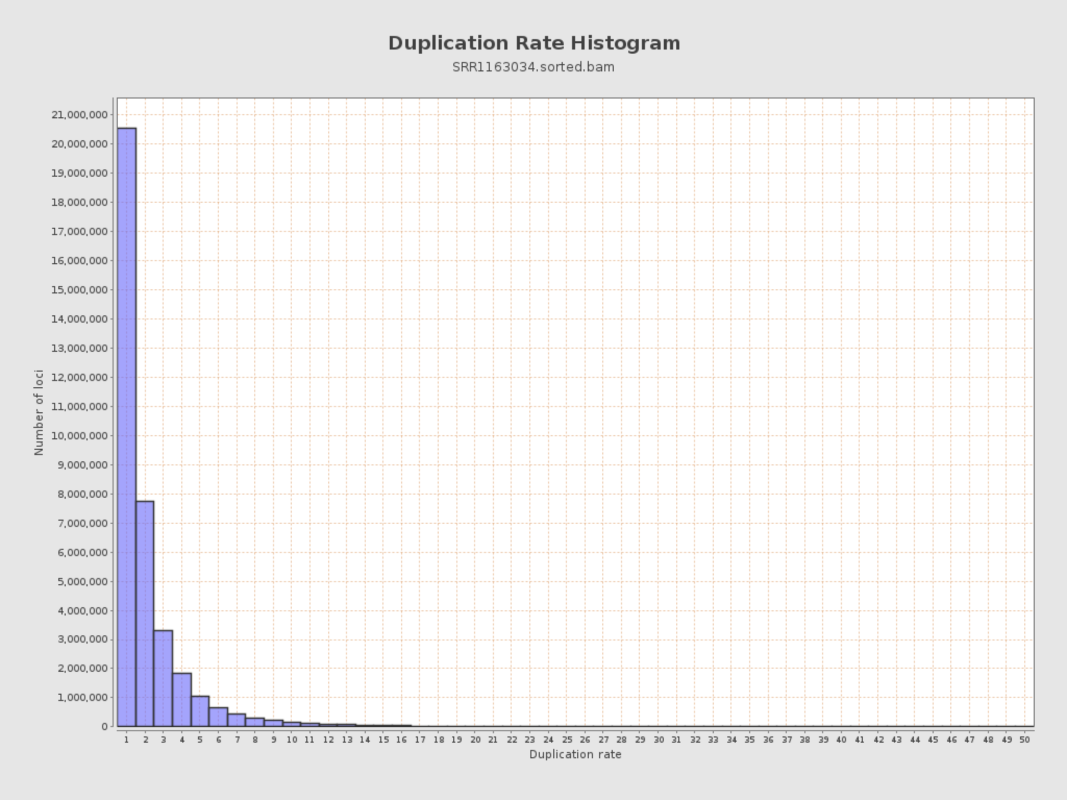
5. Results : Coverage Histogram (0-50X)



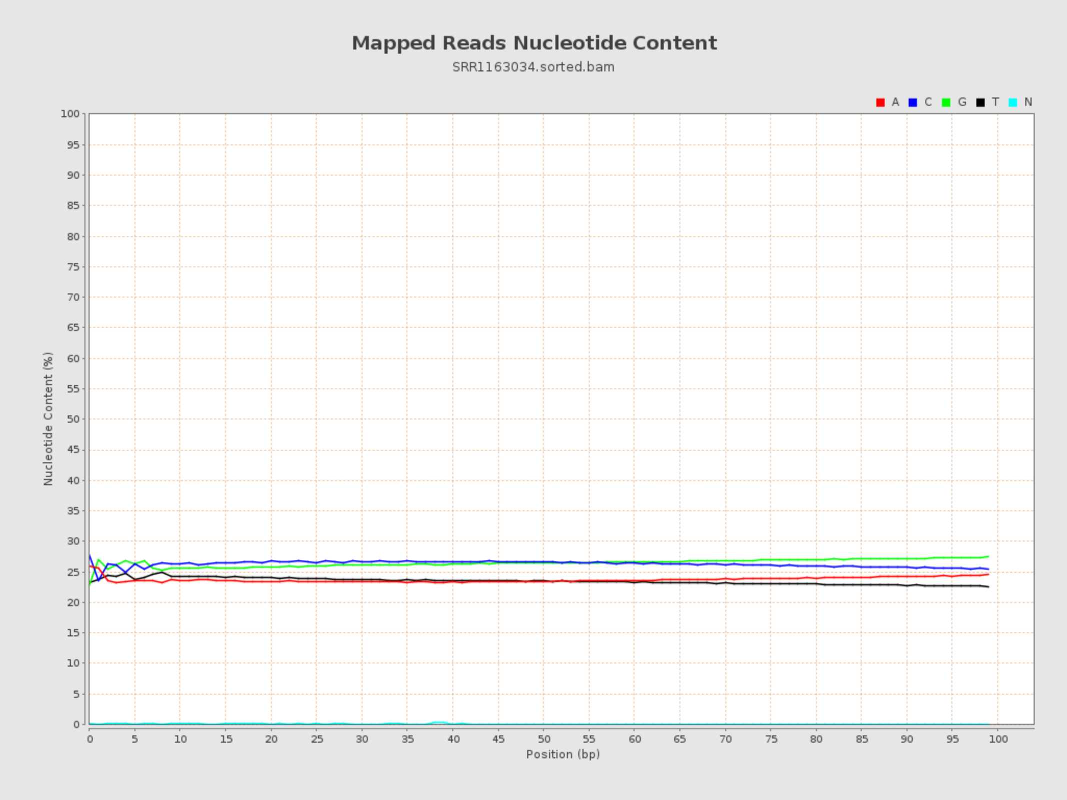
6. Results : Genome Fraction Coverage



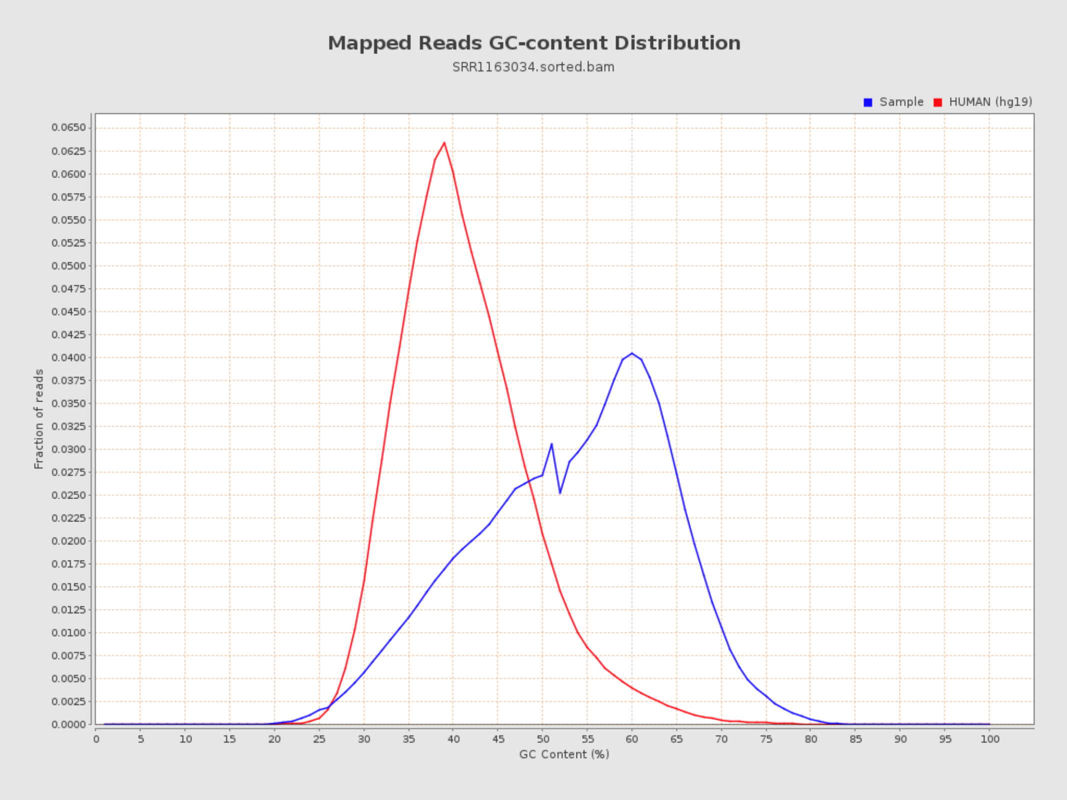
7. Results : Duplication Rate Histogram



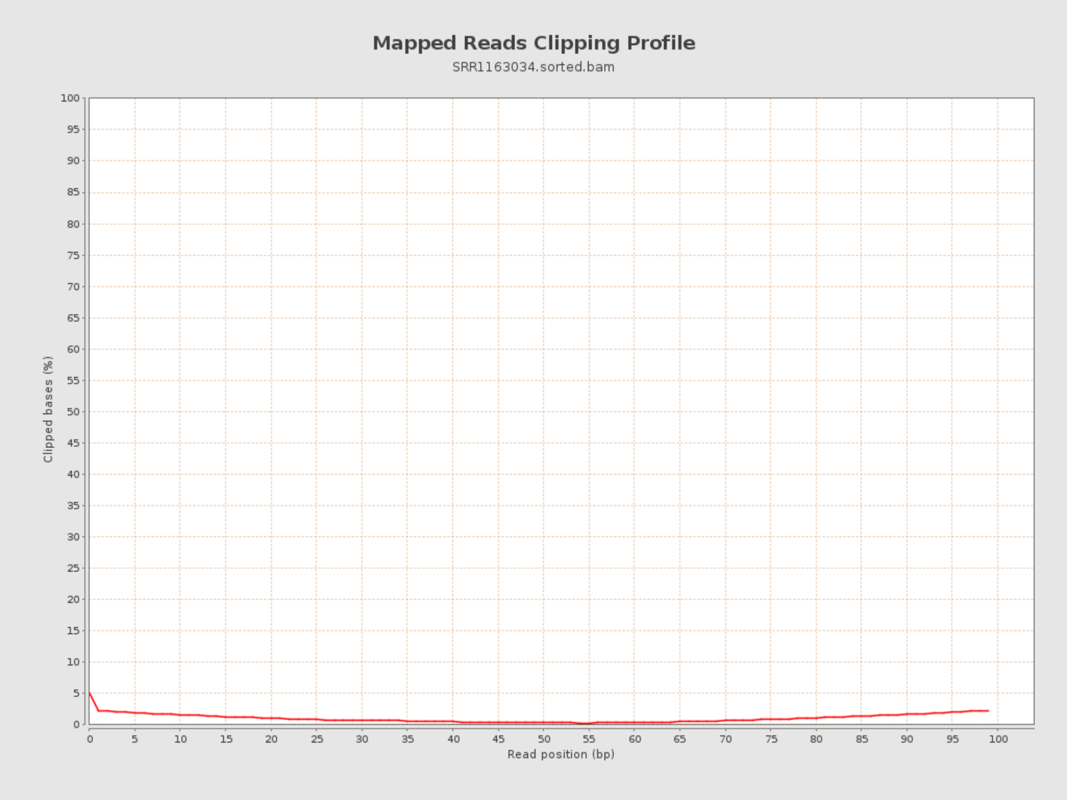
8. Results : Mapped Reads Nucleotide Content



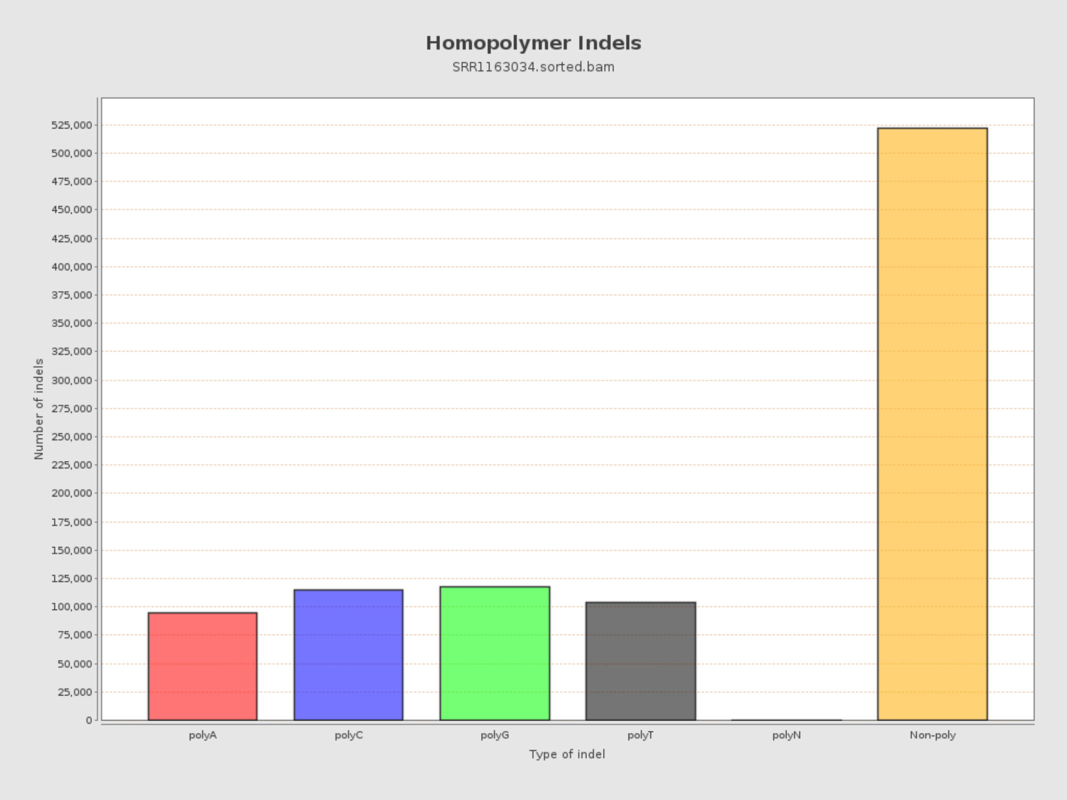
9. Results : Mapped Reads GC-content Distribution



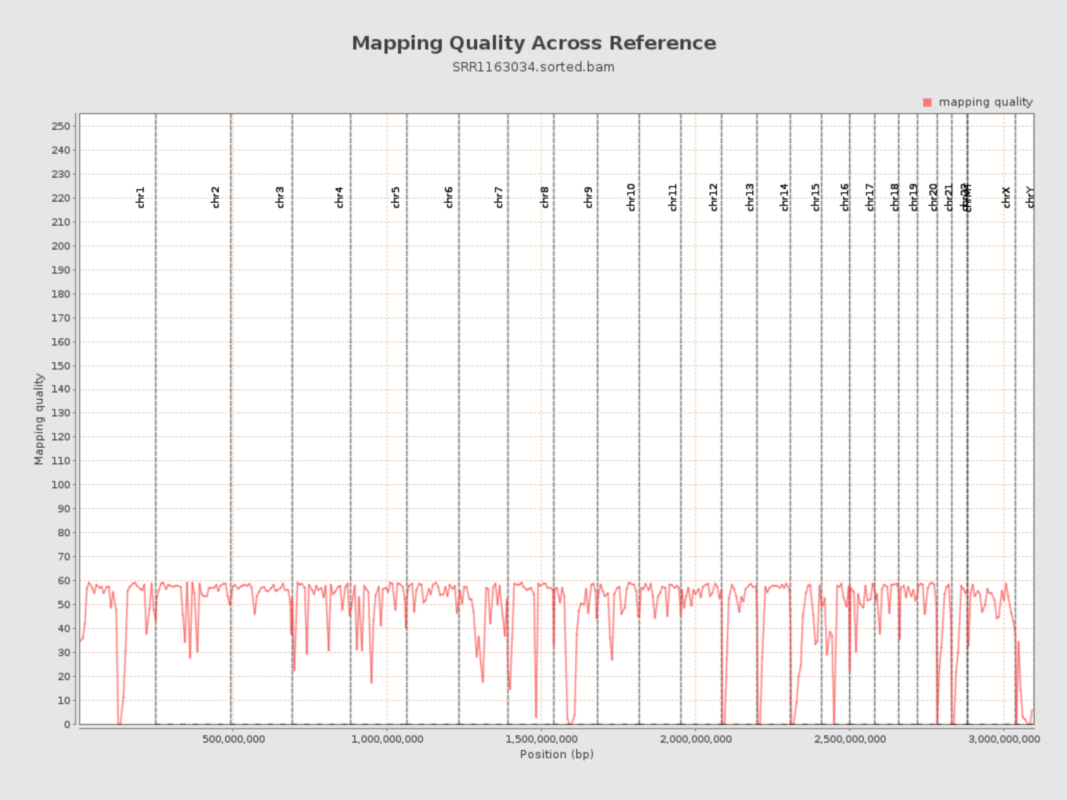
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram