Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 02:03:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163035.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_SRR1163035 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163035.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 02:03:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163035.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	84,034,230
Mapped reads	81,913,366 / 97.48%
Unmapped reads	2,120,864 / 2.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	372,748 / 0.44%
Read min/max/mean length	30 / 100 / 100.18
Duplicated reads (estimated)	45,501,109 / 54.15%
Duplication rate	45.32%
Clipped reads	19,643,787 / 23.38%

2.2. ACGT Content

Number/percentage of A's	1,836,365,660 / 23.64%
Number/percentage of C's	2,049,745,319 / 26.39%
Number/percentage of T's	1,813,469,209 / 23.34%
Number/percentage of G's	2,065,130,975 / 26.58%
Number/percentage of N's	3,827,527 / 0.05%
GC Percentage	52.97%

2.3. Coverage

Mean	2.5098

Standard Deviation	30.1828

2.4. Mapping Quality

Mean Mapping Quality	48.99

2.5. Mismatches and indels

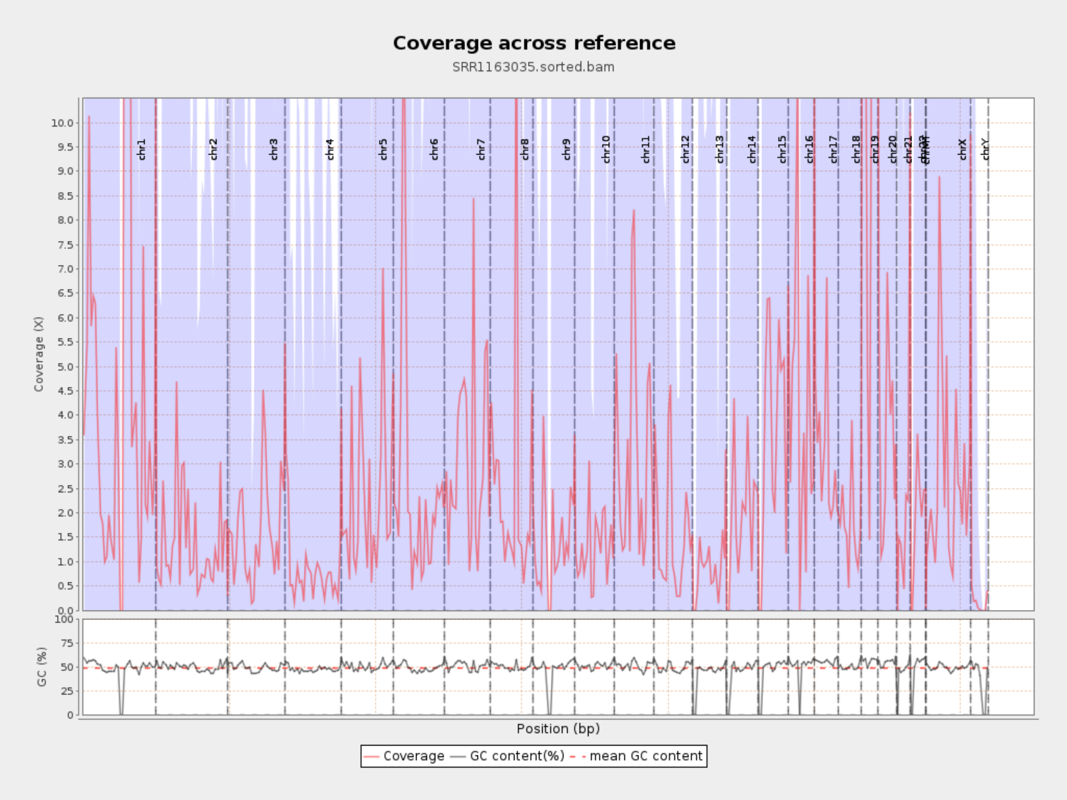
General error rate	0.54%
Mismatches	41,407,653
Insertions	471,507
Mapped reads with at least one insertion	0.57%
Deletions	410,116
Mapped reads with at least one deletion	0.49%
Homopolymer indels	44.88%

2.6. Chromosome stats

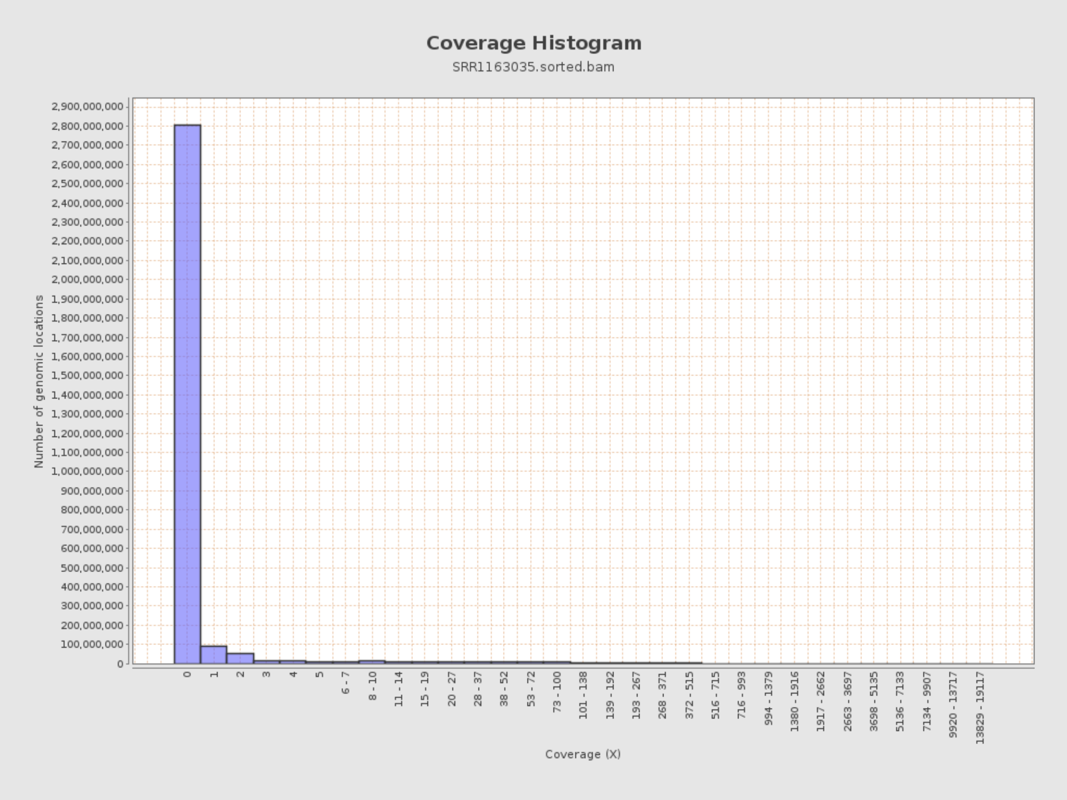
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1186895394	4.7619	44.6262
chr2	243199373	333547659	1.3715	15.3776
chr3	198022430	324405060	1.6382	17.3645
chr4	191154276	152813506	0.7994	12.8666
chr5	180915260	428723308	2.3697	37.1869
chr6	171115067	435186214	2.5432	25.9114
chr7	159138663	500944775	3.1479	36.1493

chr8	146364022	373298228	2.5505	43.4033
chr9	141213431	191384316	1.3553	15.1383
chr10	135534747	175105088	1.292	13.4517
chr11	135006516	437178552	3.2382	29.049
chr12	133851895	219237124	1.6379	16.6742
chr13	115169878	98759836	0.8575	10.3409
chr14	107349540	210135617	1.9575	18.5682
chr15	102531392	359343232	3.5047	28.4818
chr16	90354753	368907772	4.0829	31.2031
chr17	81195210	268642306	3.3086	25.1986
chr18	78077248	135114085	1.7305	19.2816
chr19	59128983	703506402	11.8978	88.5744
chr20	63025520	219317249	3.4798	30.6893
chr21	48129895	111300420	2.3125	48.5962
chr22	51304566	96463585	1.8802	16.9927
chrMT	16571	452	0.0273	0.2037
chrX	155270560	430011162	2.7694	31.3052
chrY	59373566	9239014	0.1556	8.0737

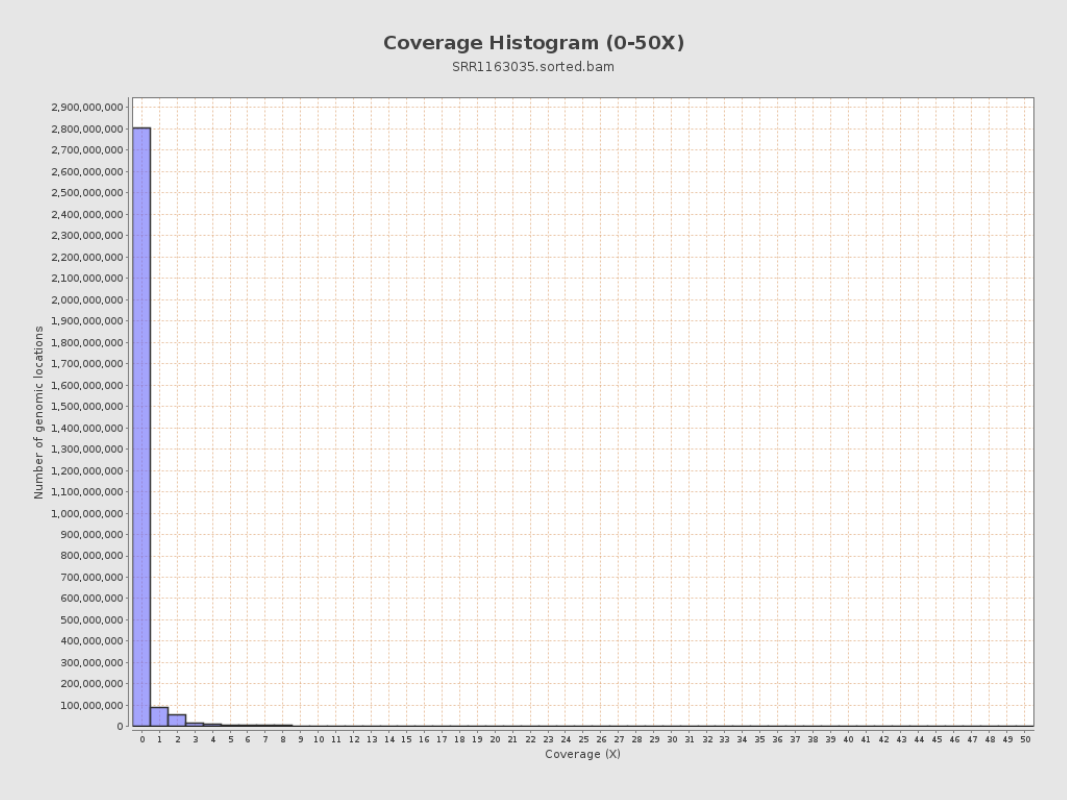
3. Results : Coverage across reference



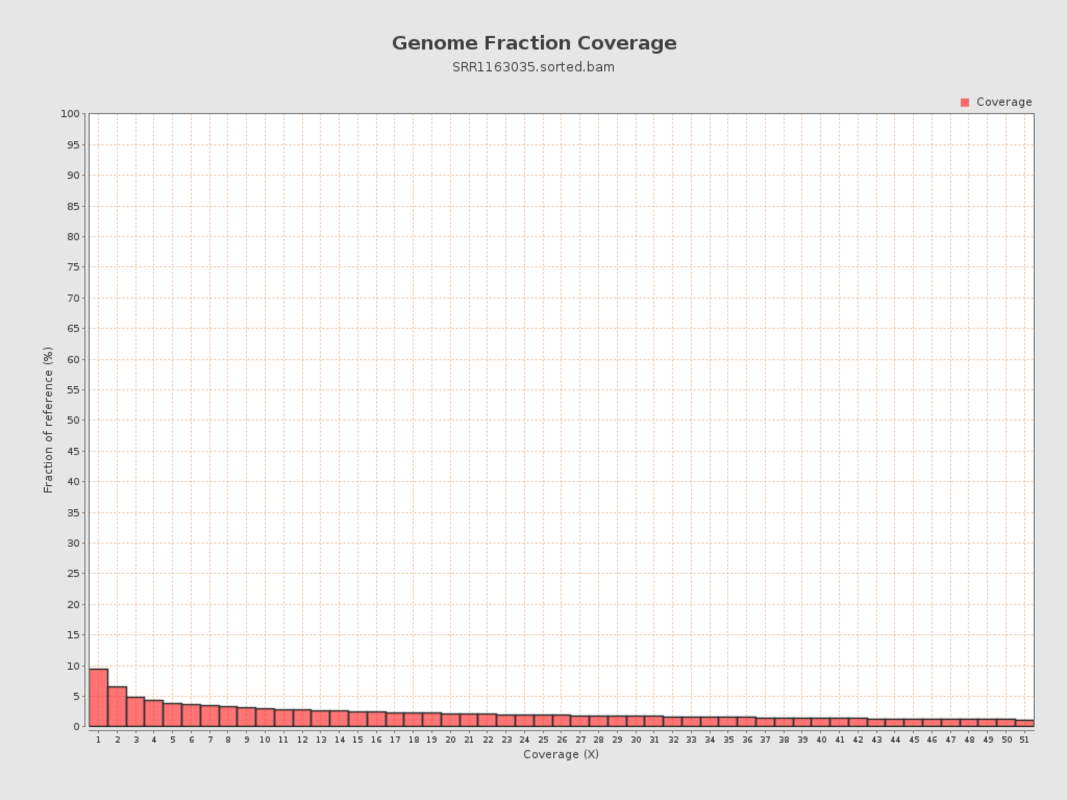
4. Results : Coverage Histogram



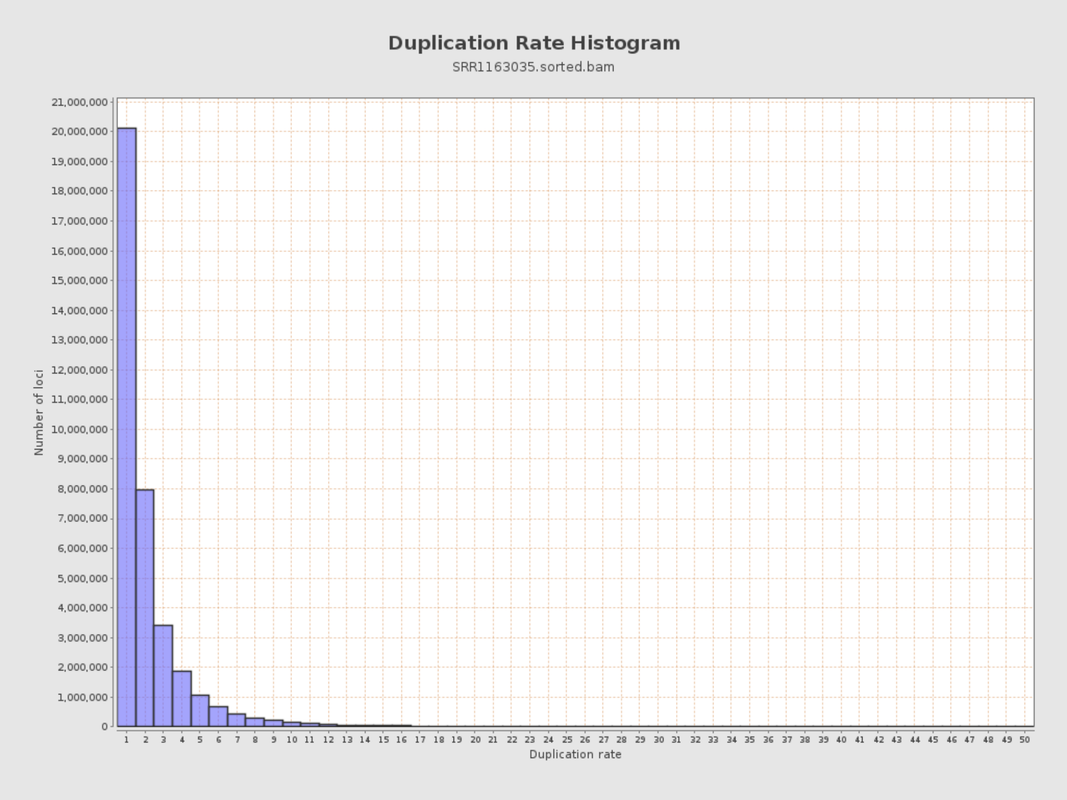
5. Results : Coverage Histogram (0-50X)



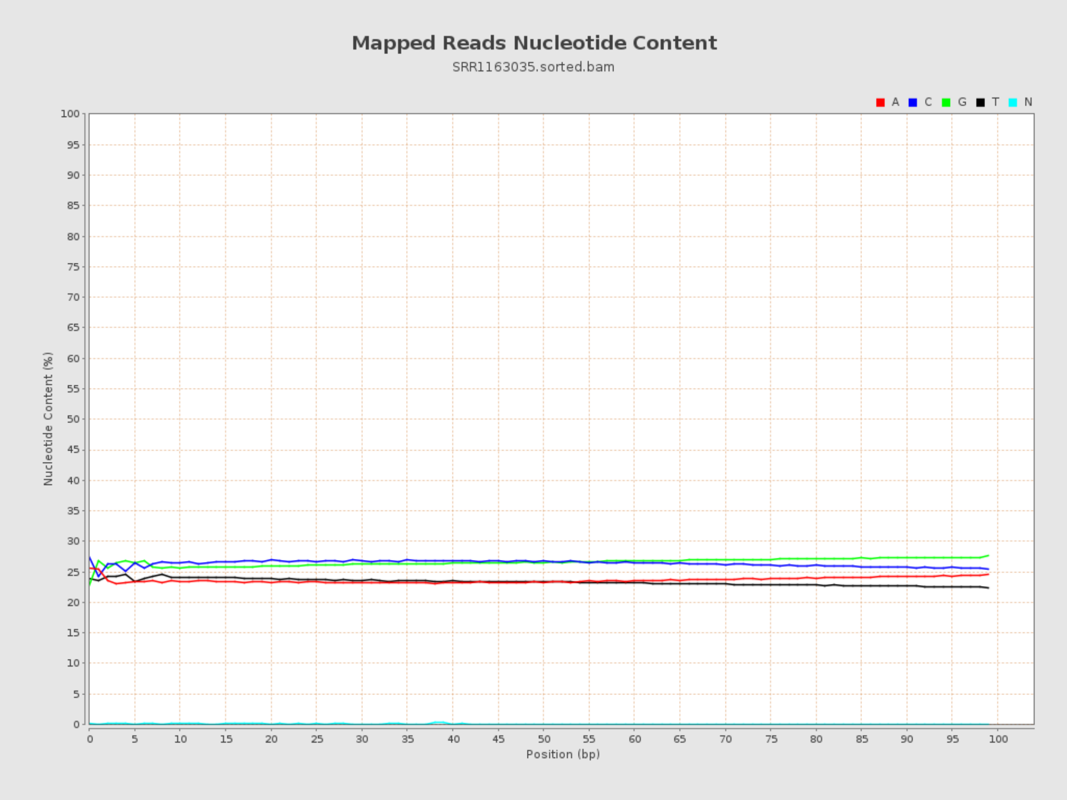
6. Results : Genome Fraction Coverage



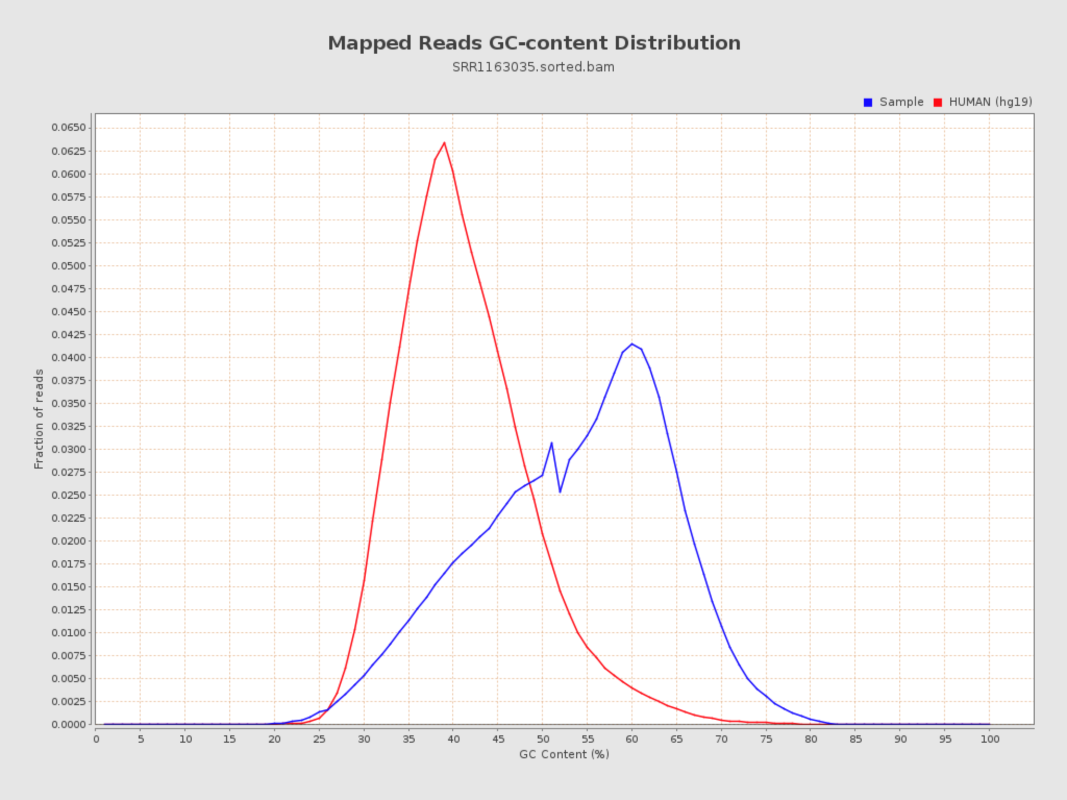
7. Results : Duplication Rate Histogram



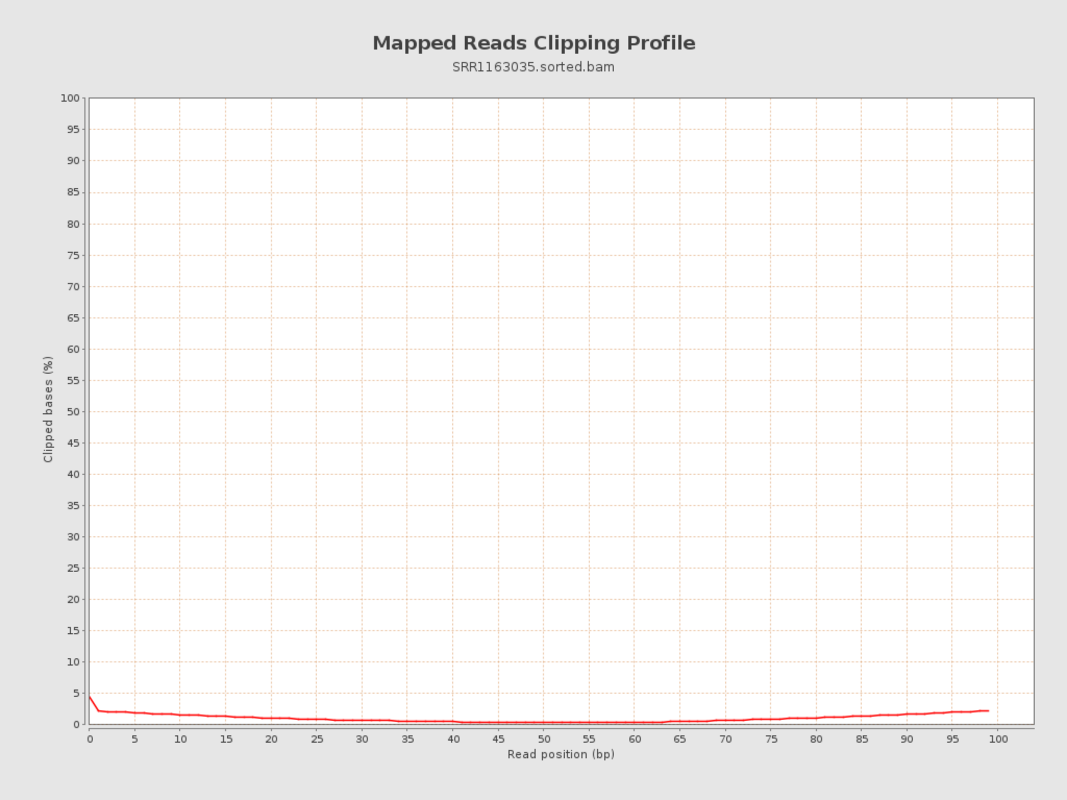
8. Results : Mapped Reads Nucleotide Content



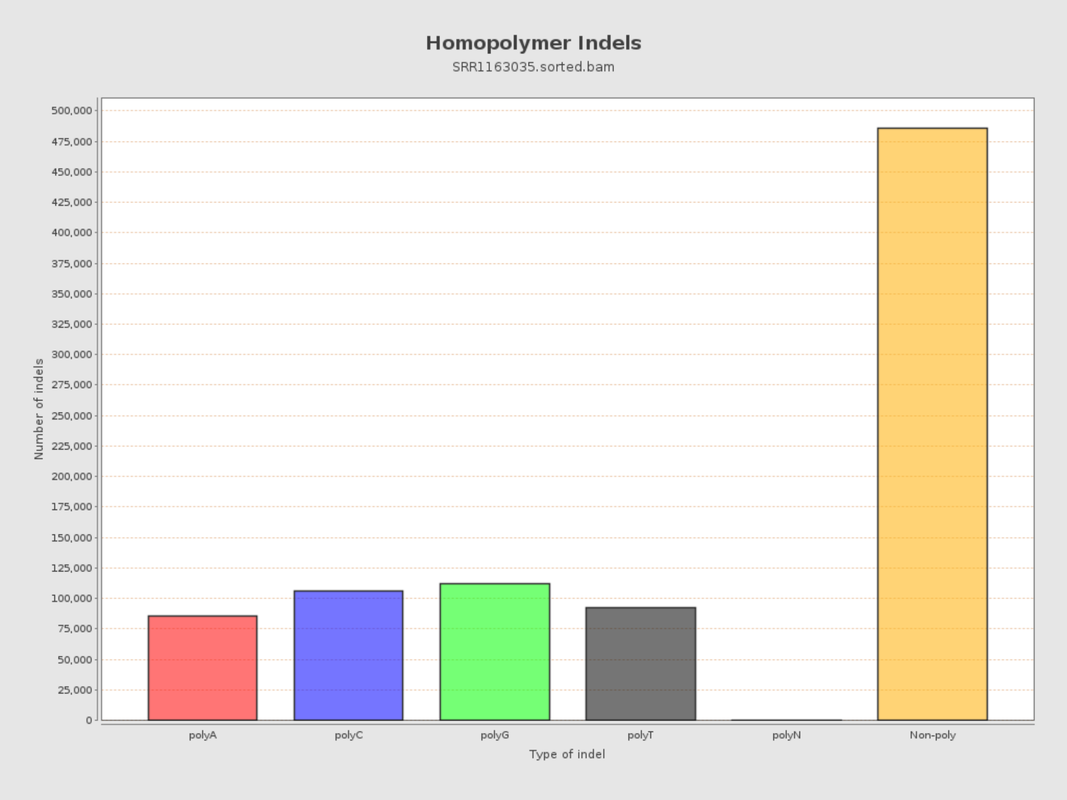
9. Results : Mapped Reads GC-content Distribution



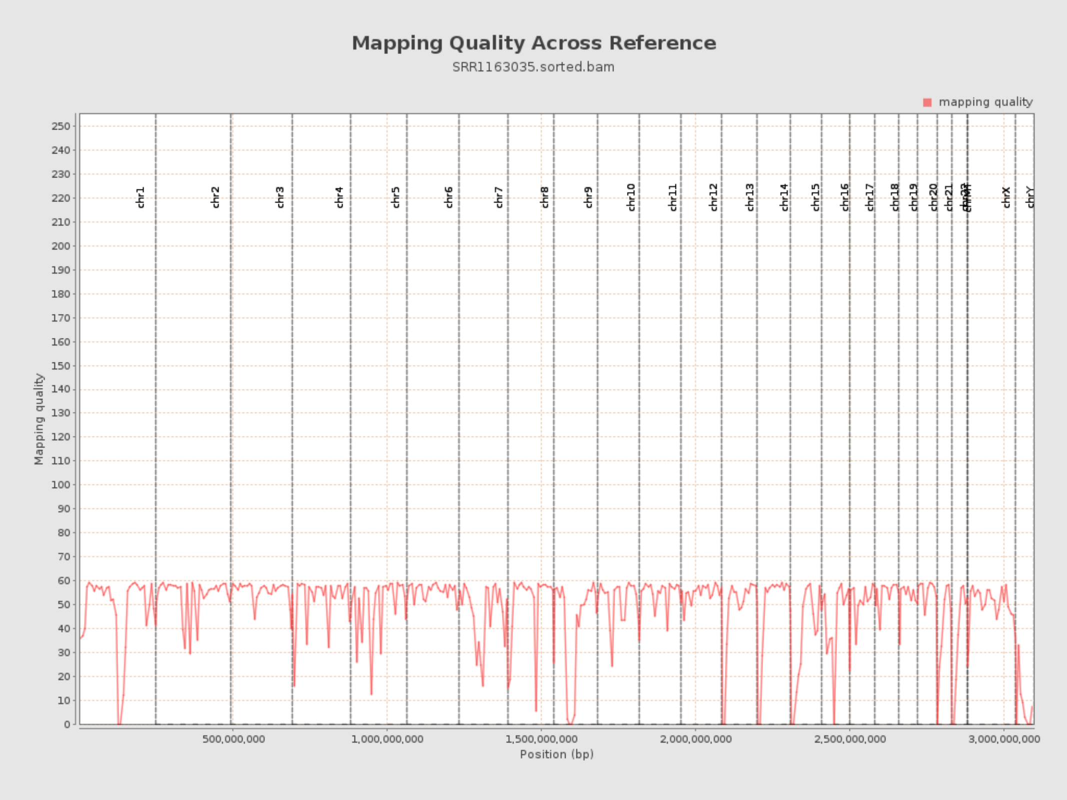
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram