Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 06:42:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163083.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_SRR1163083 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163083.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 06:42:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163083.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,393,580
Mapped reads	74,498,351 / 98.81%
Unmapped reads	895,229 / 1.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	476,925 / 0.63%
Read min/max/mean length	30 / 100 / 100.26
Duplicated reads (estimated)	43,889,160 / 58.21%
Duplication rate	45.74%
Clipped reads	10,778,219 / 14.3%

2.2. ACGT Content

Number/percentage of A's	1,750,662,238 / 24.13%
Number/percentage of C's	1,878,799,660 / 25.89%
Number/percentage of T's	1,738,337,194 / 23.96%
Number/percentage of G's	1,888,199,038 / 26.02%
Number/percentage of N's	525,408 / 0.01%
GC Percentage	51.91%

2.3. Coverage

Mean	2.3444

Standard Deviation	34.3332

2.4. Mapping Quality

Mean Mapping Quality	49.33

2.5. Mismatches and indels

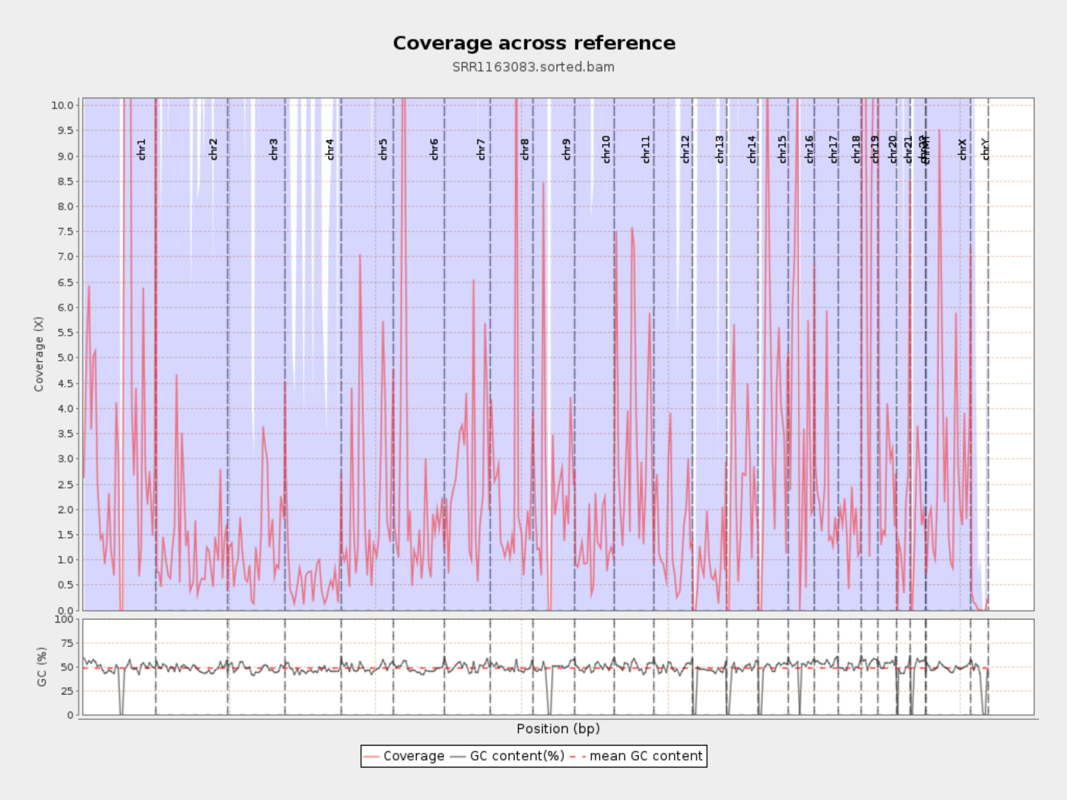
General error rate	0.37%
Mismatches	25,907,230
Insertions	494,459
Mapped reads with at least one insertion	0.66%
Deletions	397,418
Mapped reads with at least one deletion	0.53%
Homopolymer indels	46.26%

2.6. Chromosome stats

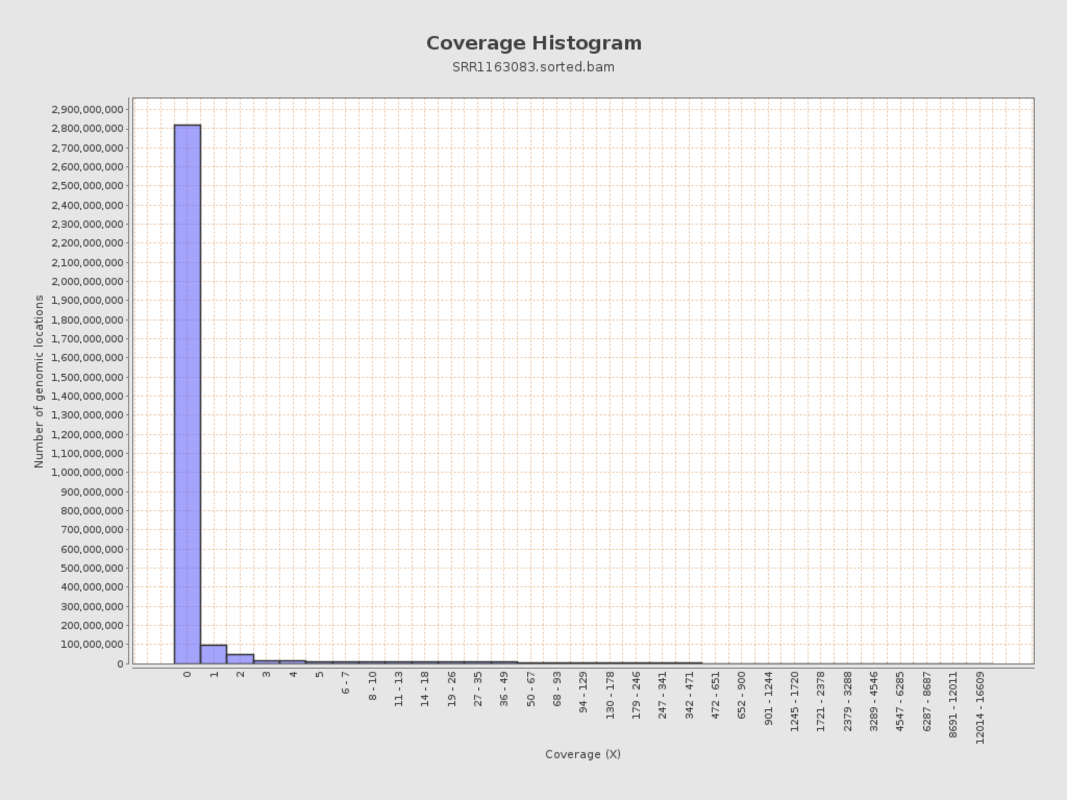
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1015260776	4.0733	49.4356
chr2	243199373	305981040	1.2581	18.4154
chr3	198022430	265112143	1.3388	20.8983
chr4	191154276	121722416	0.6368	11.3062
chr5	180915260	405460520	2.2412	39.0195
chr6	171115067	403711135	2.3593	32.178
chr7	159138663	427546690	2.6866	37.6579

chr8	146364022	350433905	2.3943	42.7284
chr9	141213431	328039296	2.323	31.6988
chr10	135534747	170242715	1.2561	17.4869
chr11	135006516	476063225	3.5262	41.4106
chr12	133851895	210150934	1.57	20.0872
chr13	115169878	100295672	0.8708	21.357
chr14	107349540	255009686	2.3755	30.6125
chr15	102531392	392865212	3.8317	46.3592
chr16	90354753	347028467	3.8407	38.3895
chr17	81195210	184421465	2.2713	27.8032
chr18	78077248	128217725	1.6422	24.9056
chr19	59128983	571446426	9.6644	79.7042
chr20	63025520	159874385	2.5367	27.9706
chr21	48129895	101875545	2.1167	54.083
chr22	51304566	90988612	1.7735	21.4838
chrMT	16571	11774	0.7105	1.1922
chrX	155270560	439676046	2.8317	37.3241
chrY	59373566	5961640	0.1004	6.0183

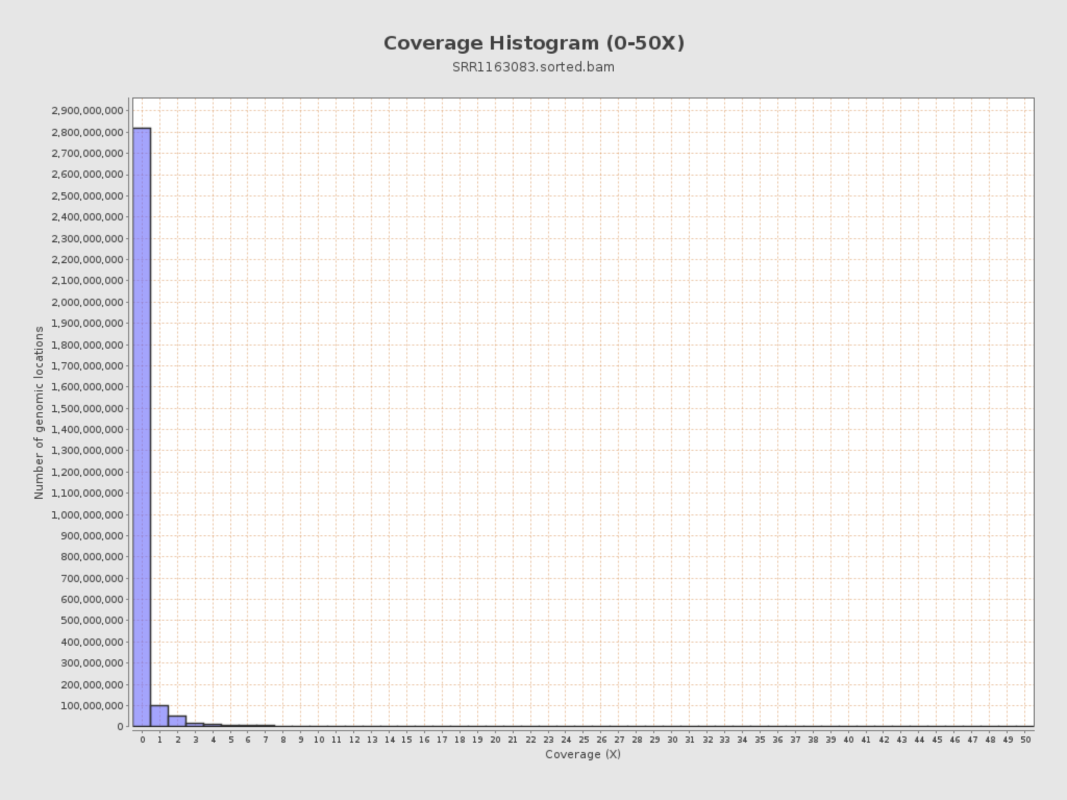
3. Results : Coverage across reference



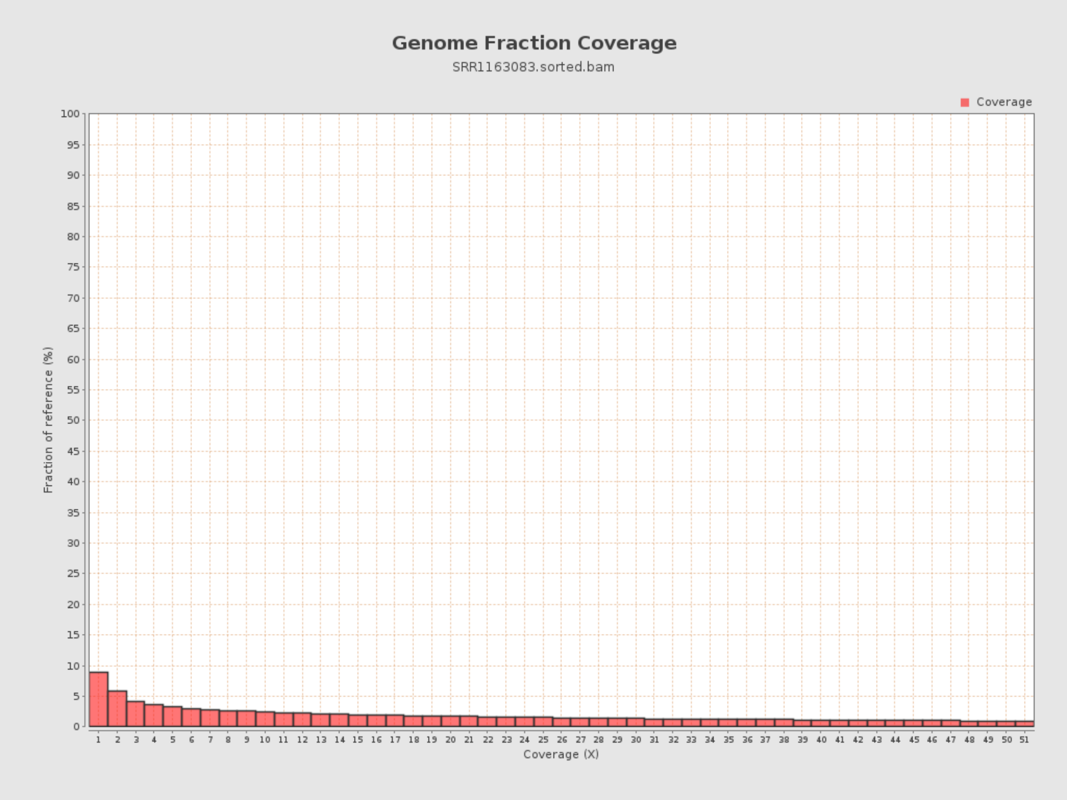
4. Results : Coverage Histogram



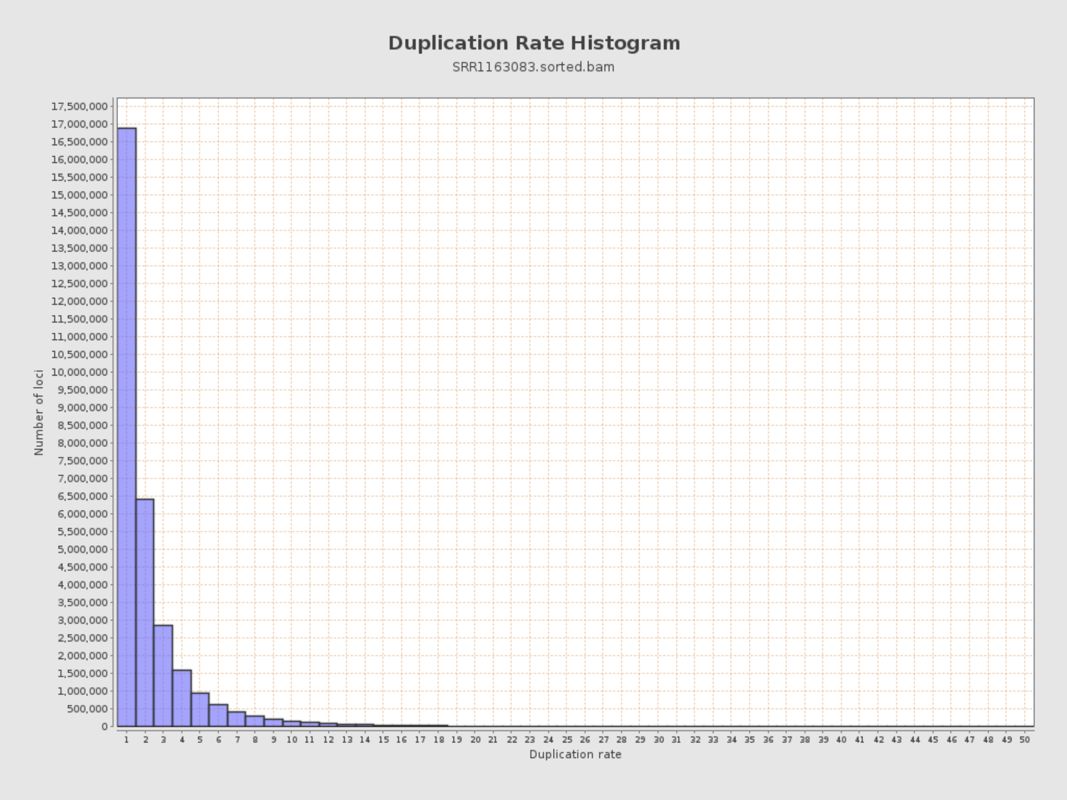
5. Results : Coverage Histogram (0-50X)



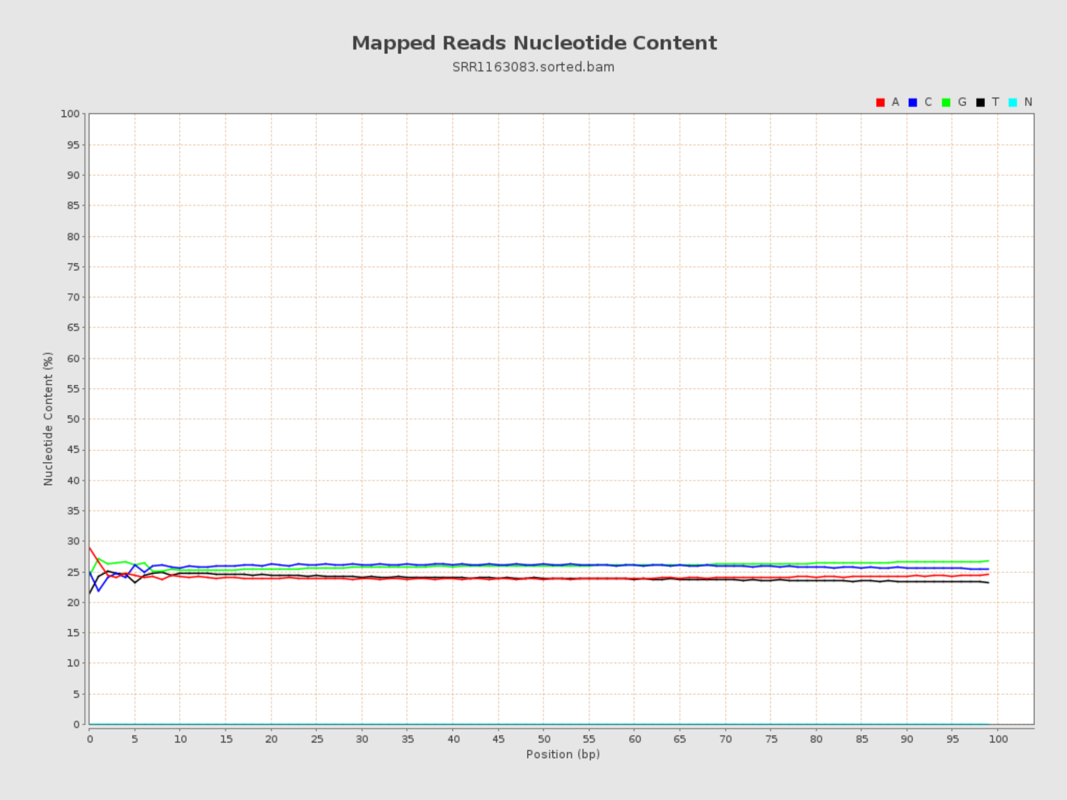
6. Results : Genome Fraction Coverage



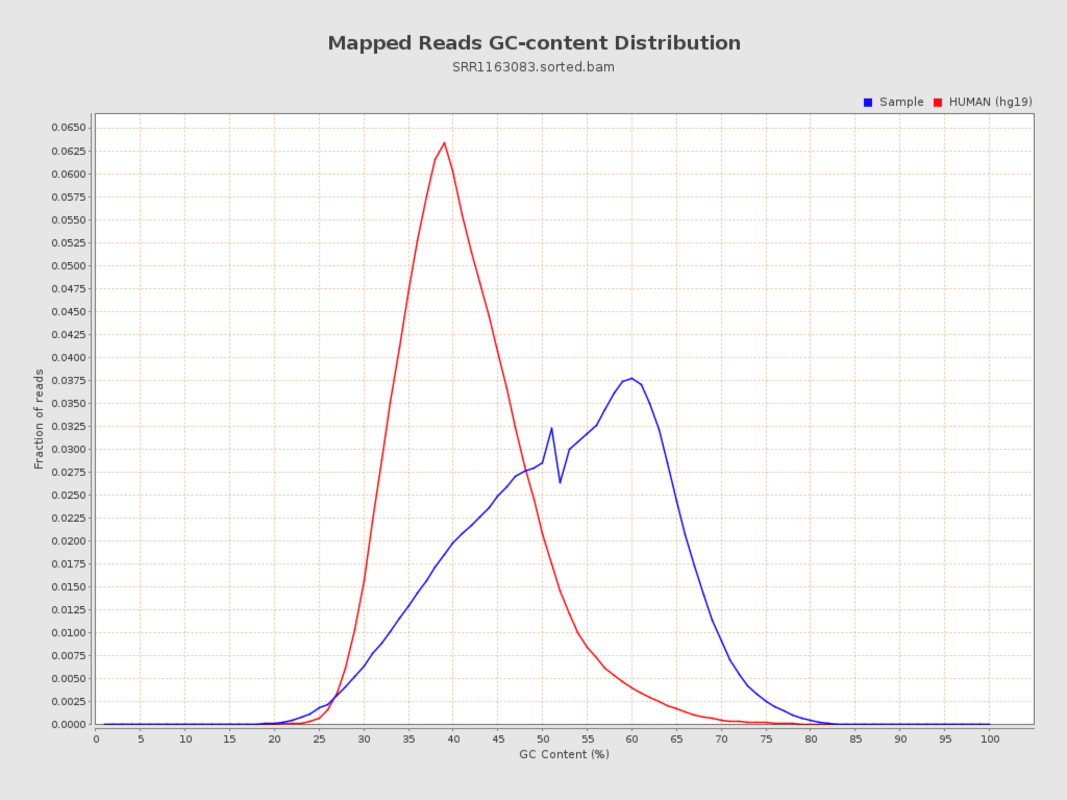
7. Results : Duplication Rate Histogram



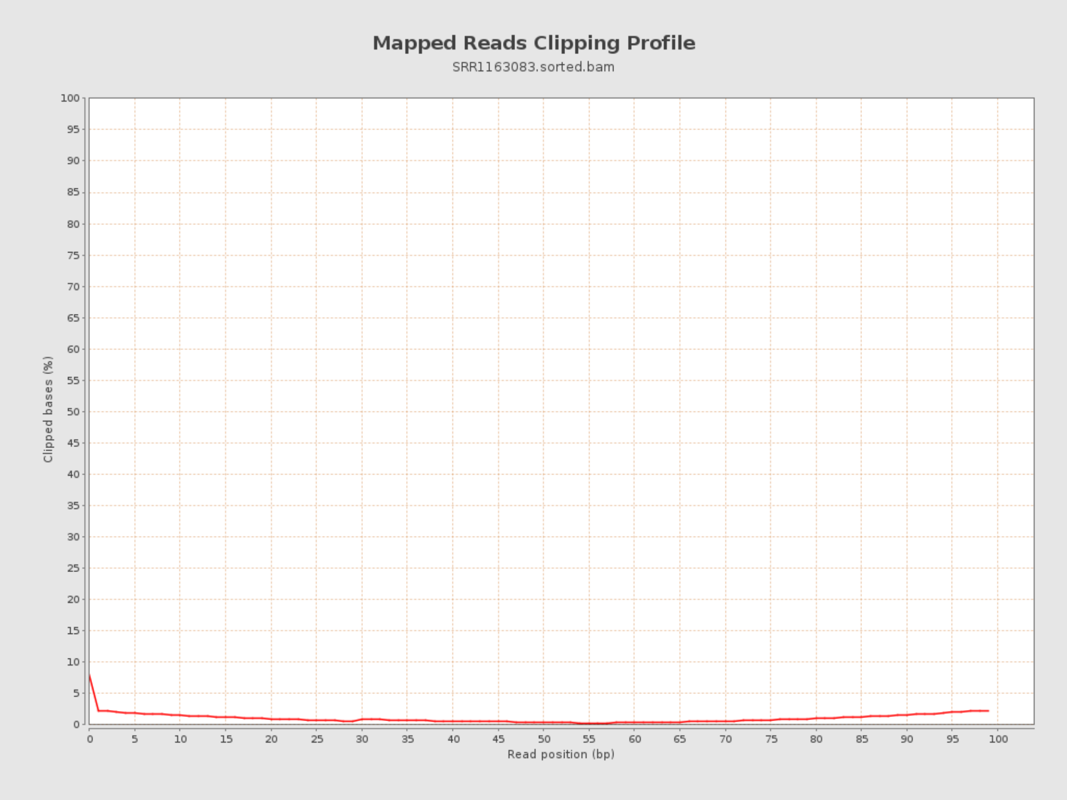
8. Results : Mapped Reads Nucleotide Content



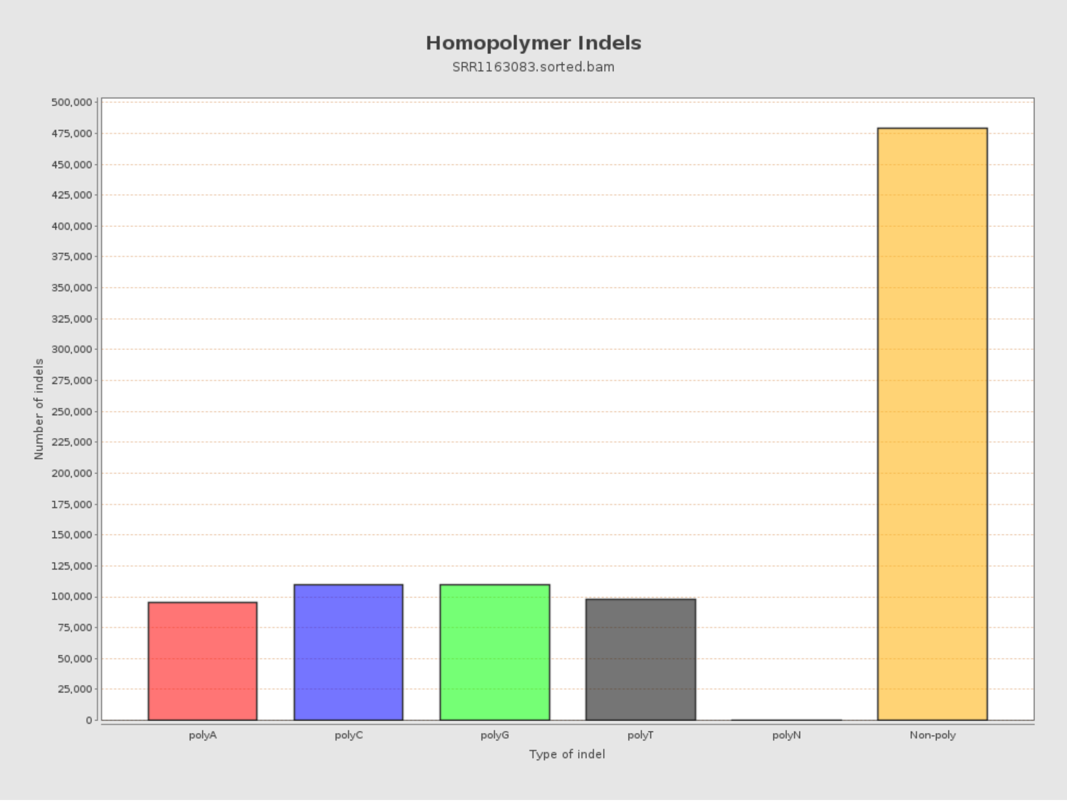
9. Results : Mapped Reads GC-content Distribution



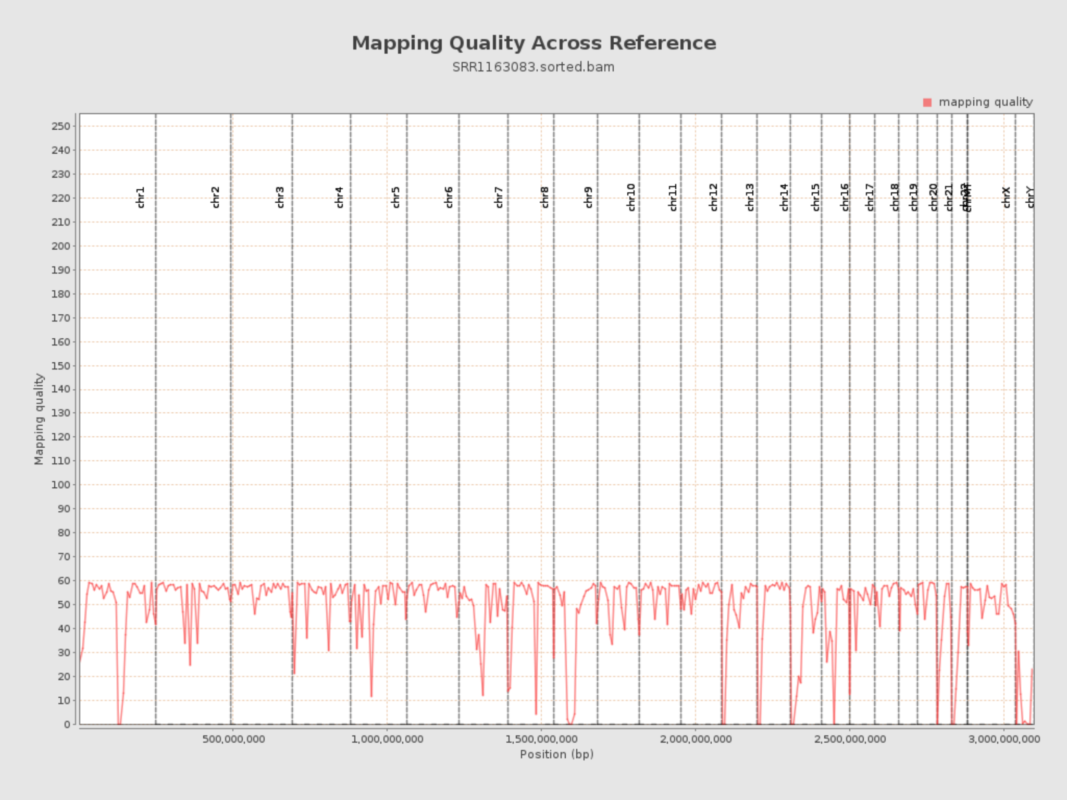
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram