Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 05:39:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163074.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_SRR1163074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 05:39:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	93,070,840
Mapped reads	91,956,368 / 98.8%
Unmapped reads	1,114,472 / 1.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	546,441 / 0.59%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	52,224,073 / 56.11%
Duplication rate	45.2%
Clipped reads	9,806,728 / 10.54%

2.2. ACGT Content

Number/percentage of A's	2,221,944,697 / 24.59%
Number/percentage of C's	2,295,380,066 / 25.4%
Number/percentage of T's	2,214,225,077 / 24.51%
Number/percentage of G's	2,303,109,187 / 25.49%
Number/percentage of N's	658,029 / 0.01%
GC Percentage	50.89%

2.3. Coverage

Mean	2.9191

Standard Deviation	35.6636

2.4. Mapping Quality

Mean Mapping Quality	48.92

2.5. Mismatches and indels

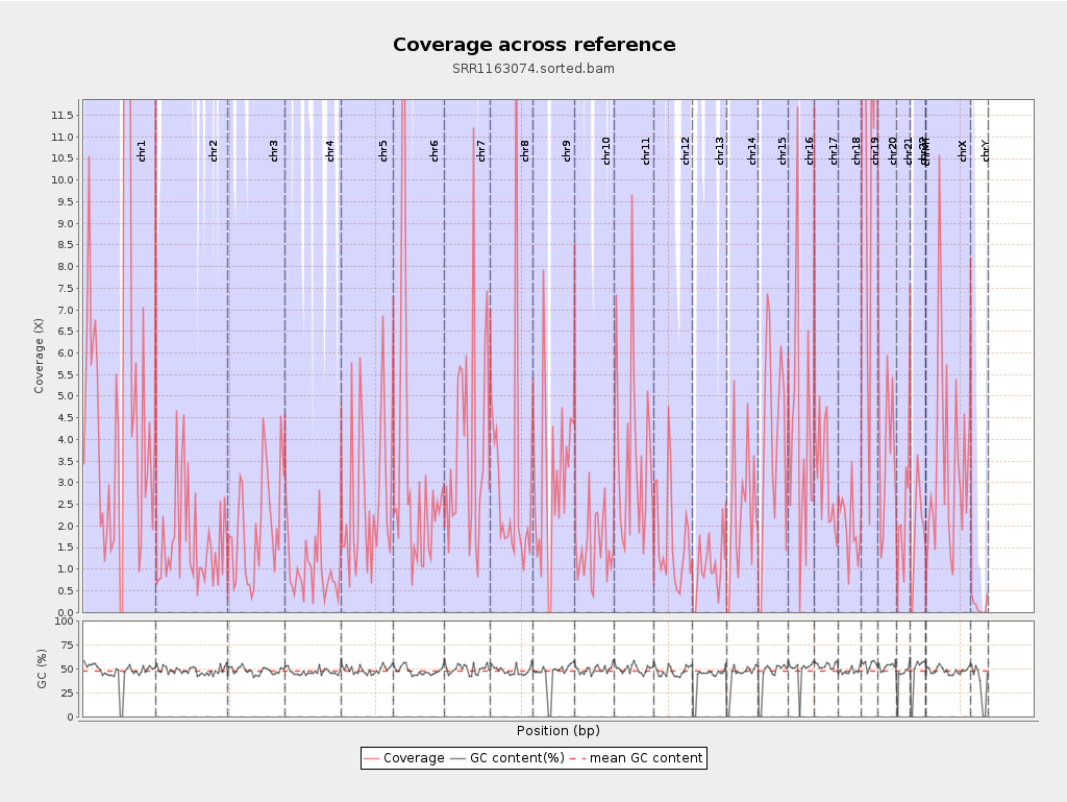
General error rate	0.37%
Mismatches	32,381,724
Insertions	614,094
Mapped reads with at least one insertion	0.66%
Deletions	551,795
Mapped reads with at least one deletion	0.59%
Homopolymer indels	47%

2.6. Chromosome stats

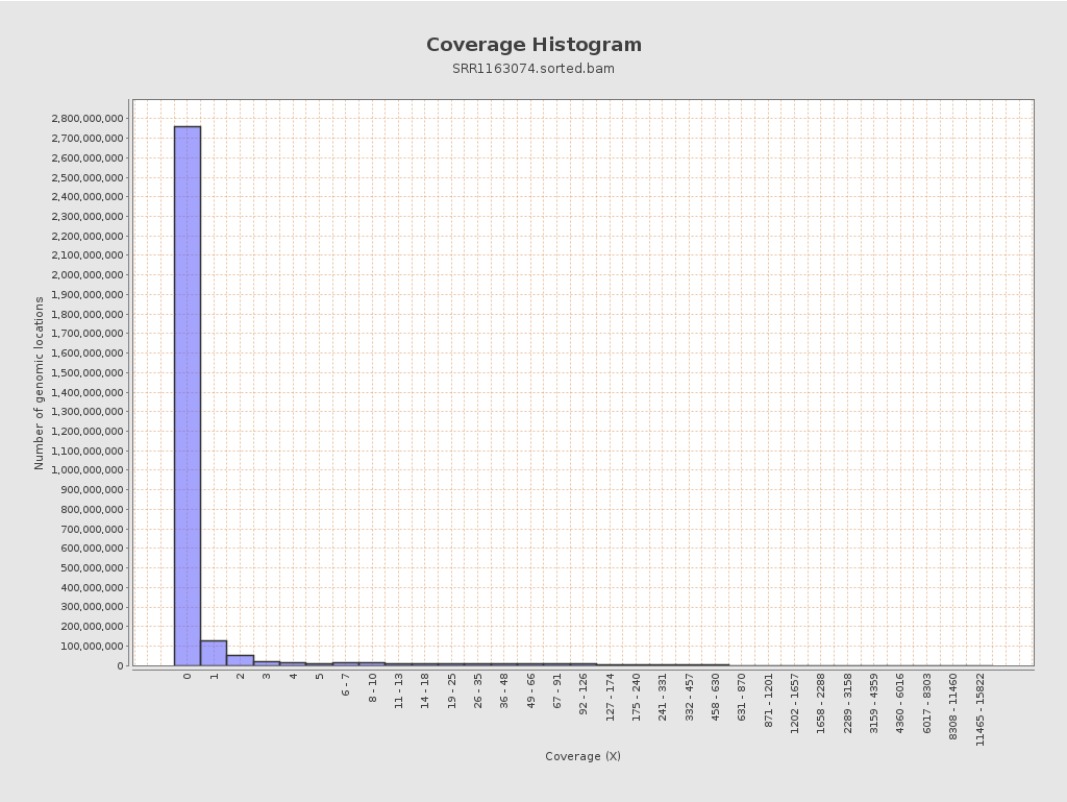
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1333157168	5.3487	52.173
chr2	243199373	402603644	1.6554	18.7534
chr3	198022430	393450410	1.9869	23.4174
chr4	191154276	191705177	1.0029	21.267
chr5	180915260	496834662	2.7462	39.1252
chr6	171115067	535909242	3.1319	35.308
chr7	159138663	615930261	3.8704	53.8809

chr8	146364022	442293497	3.0219	49.0708
chr9	141213431	431375197	3.0548	32.1584
chr10	135534747	204100744	1.5059	17.7821
chr11	135006516	486653212	3.6047	32.1814
chr12	133851895	230553039	1.7224	19.3339
chr13	115169878	123635275	1.0735	14.5342
chr14	107349540	256897999	2.3931	24.6905
chr15	102531392	393506934	3.8379	35.0519
chr16	90354753	361637340	4.0024	32.8725
chr17	81195210	254024140	3.1286	27.7179
chr18	78077248	156022115	1.9983	22.7766
chr19	59128983	727179822	12.2982	86.2352
chr20	63025520	230165171	3.6519	35.2468
chr21	48129895	121531891	2.5251	44.3701
chr22	51304566	98434867	1.9186	17.3894
chrMT	16571	749	0.0452	0.2396
chrX	155270560	539816400	3.4766	39.1036
chrY	59373566	9124493	0.1537	7.1471

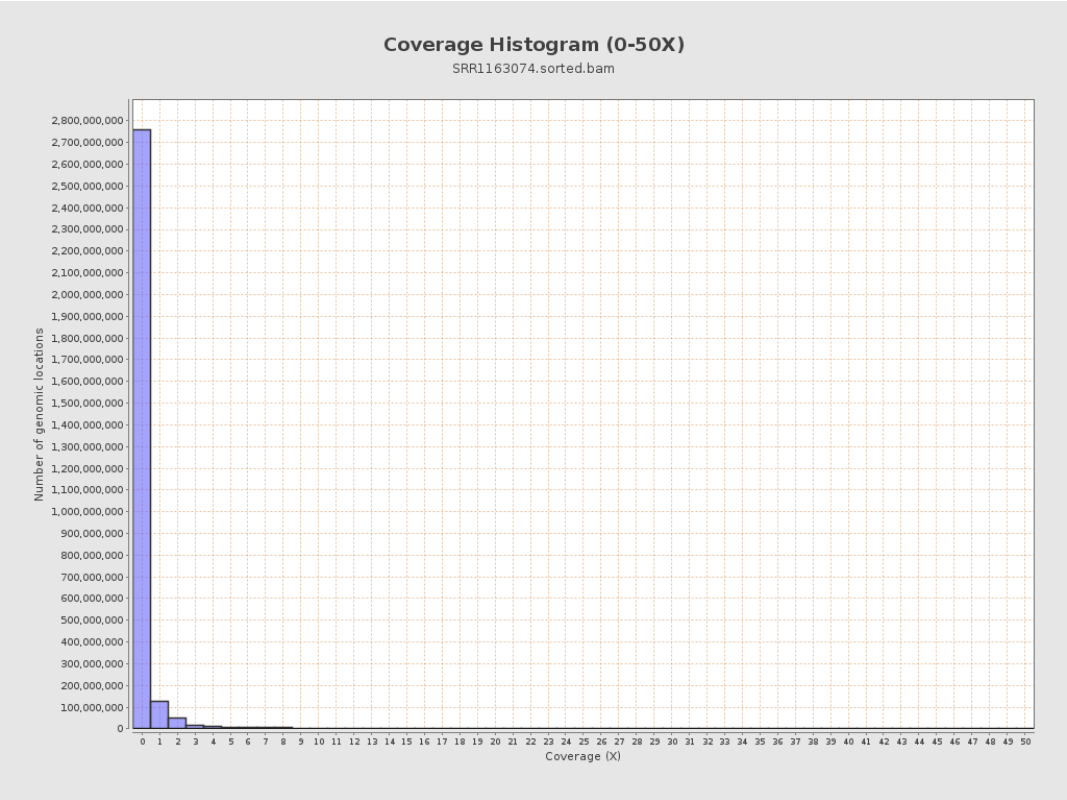
3. Results : Coverage across reference



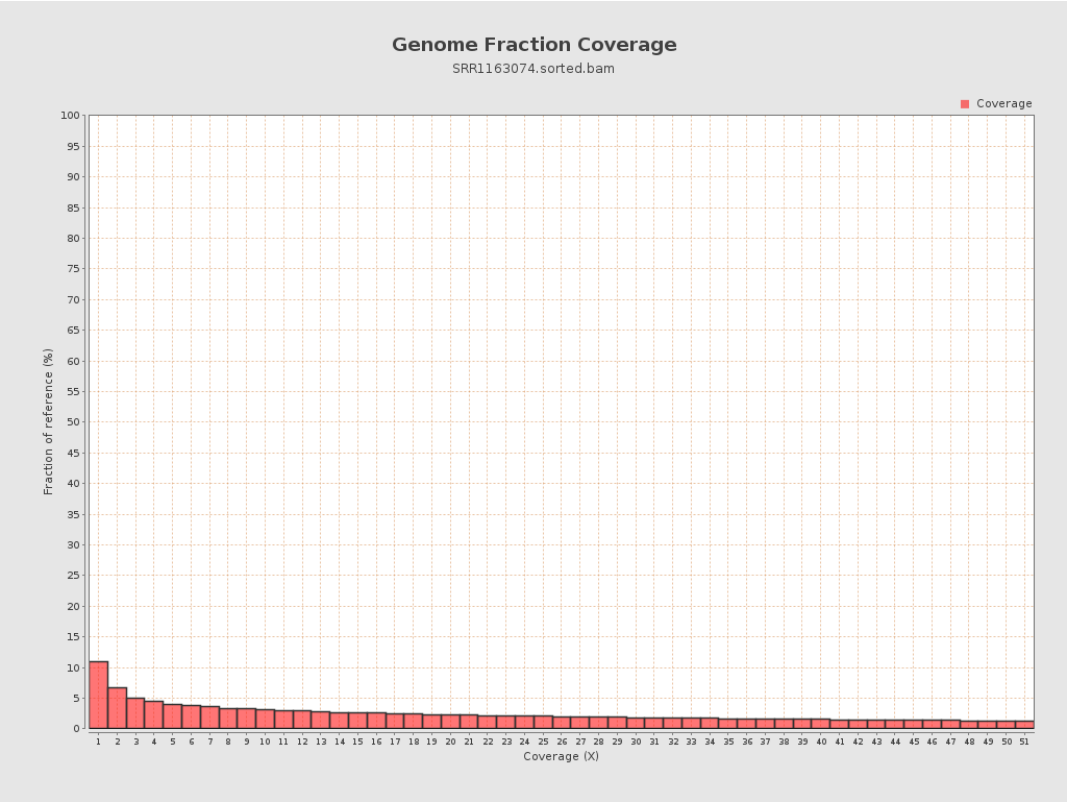
4. Results : Coverage Histogram



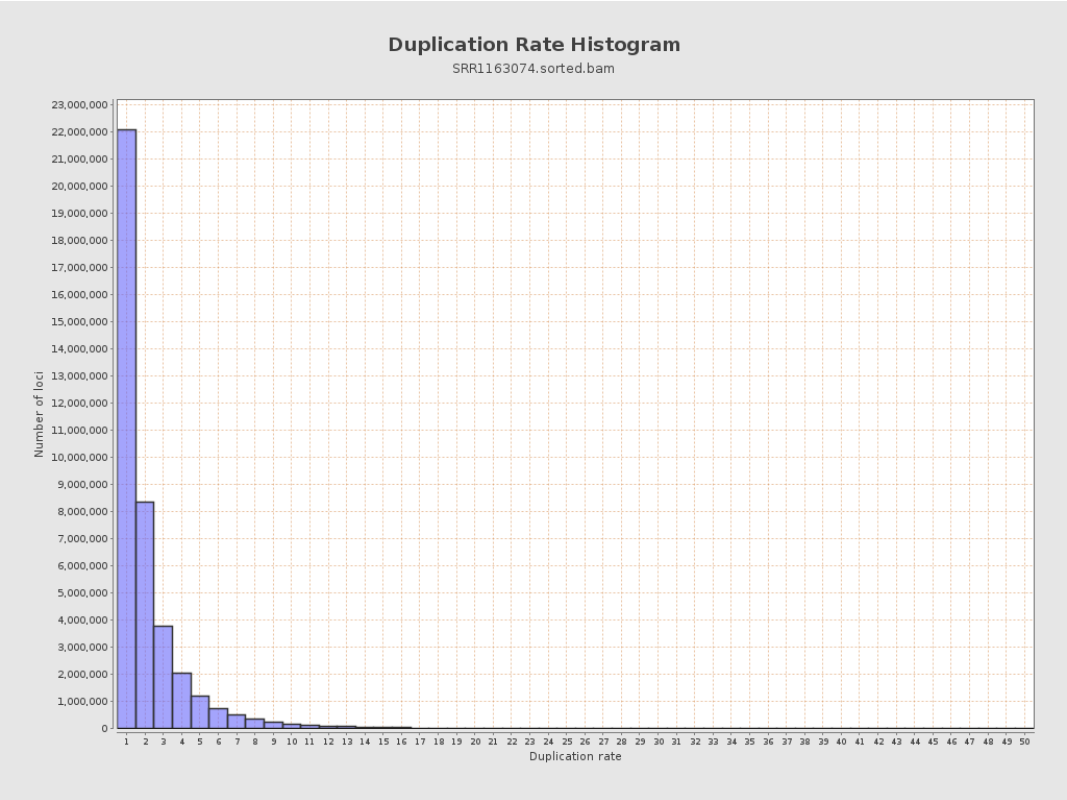
5. Results : Coverage Histogram (0-50X)



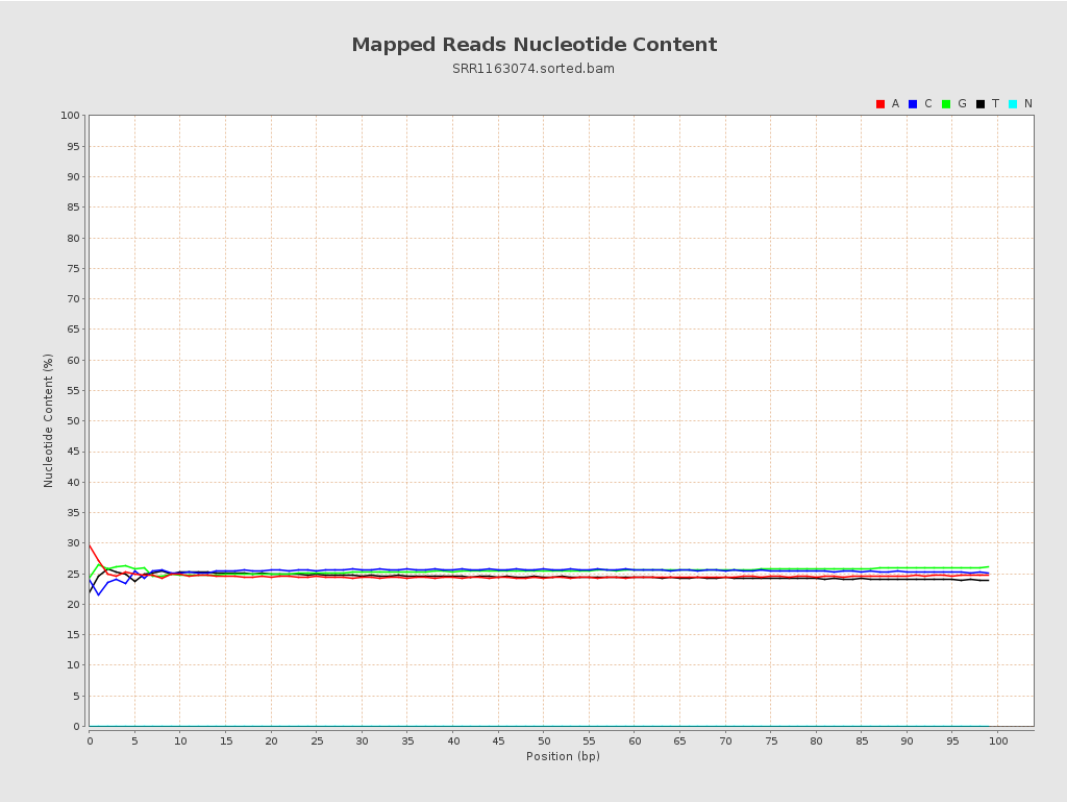
6. Results : Genome Fraction Coverage



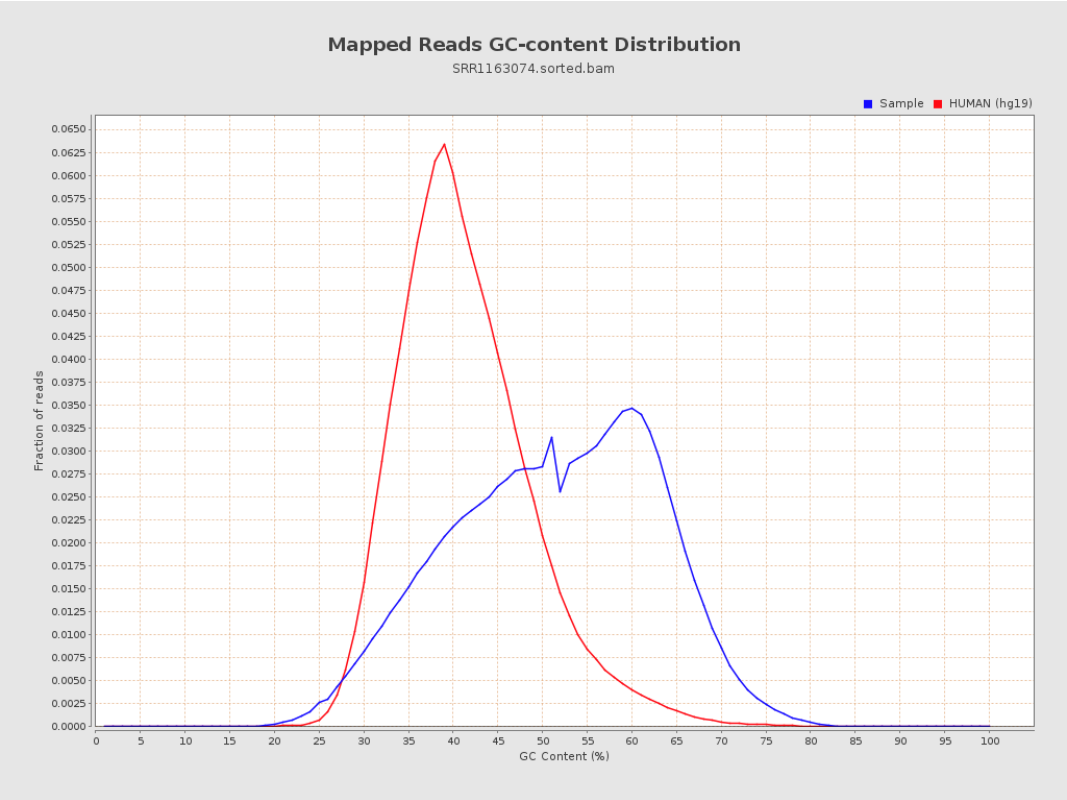
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

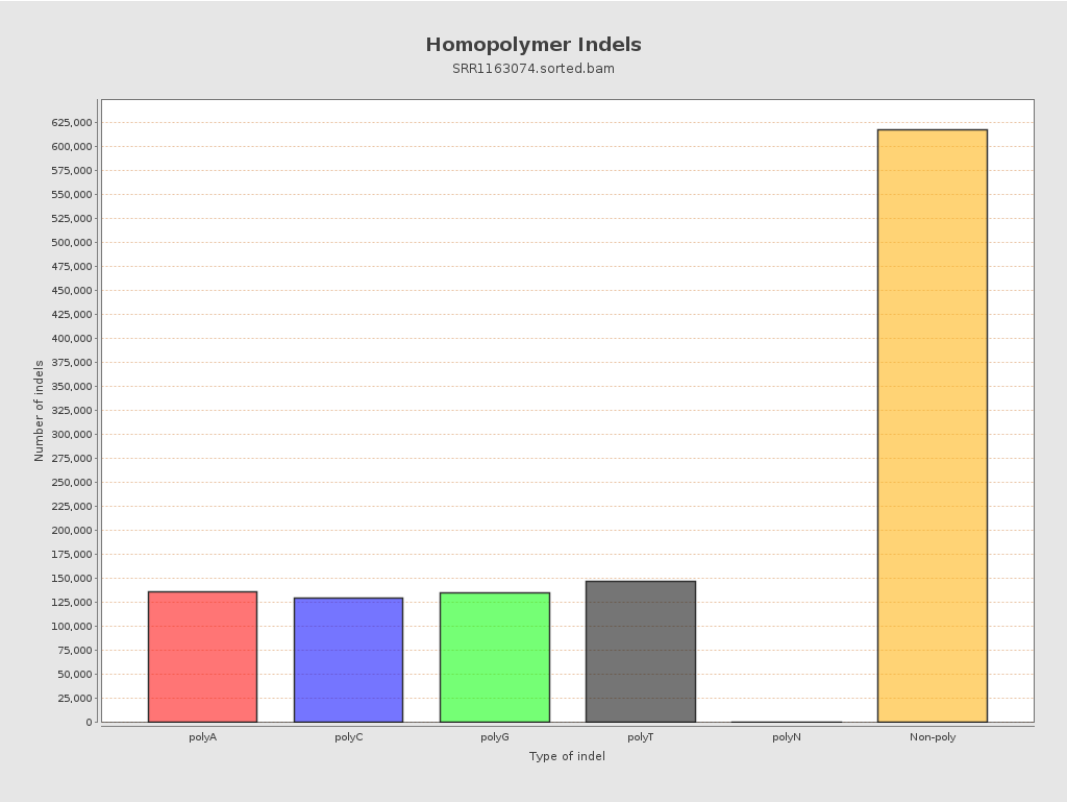


9. Results : Mapped Reads GC-content Distribution

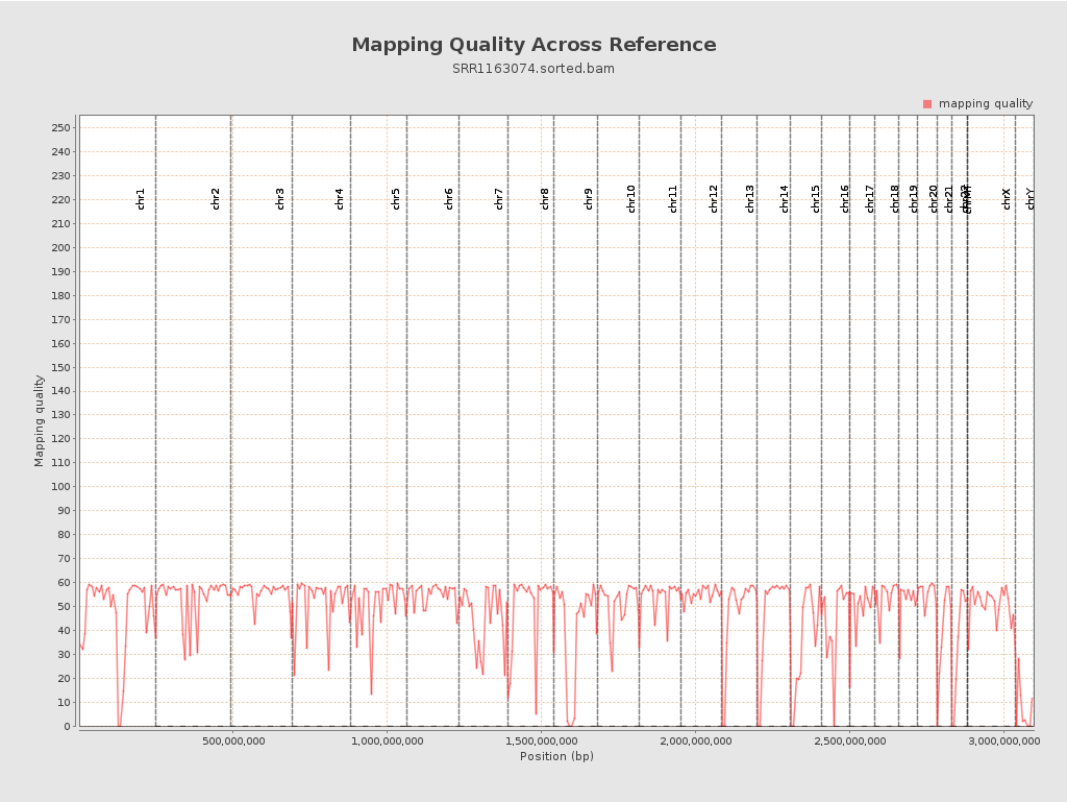


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram