Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 03:46:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163053.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_SRR1163053 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163053.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 03:46:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163053.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	69,617,632
Mapped reads	68,832,134 / 98.87%
Unmapped reads	785,498 / 1.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	357,362 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	40,919,861 / 58.78%
Duplication rate	46.64%
Clipped reads	9,247,676 / 13.28%

2.2. ACGT Content

Number/percentage of A's	1,621,566,300 / 24.16%
Number/percentage of C's	1,733,784,155 / 25.83%
Number/percentage of T's	1,617,316,515 / 24.1%
Number/percentage of G's	1,738,889,857 / 25.91%
Number/percentage of N's	484,384 / 0.01%
GC Percentage	51.74%

2.3. Coverage

Mean	2.1685

Standard Deviation	33.587

2.4. Mapping Quality

Mean Mapping Quality	49.06

2.5. Mismatches and indels

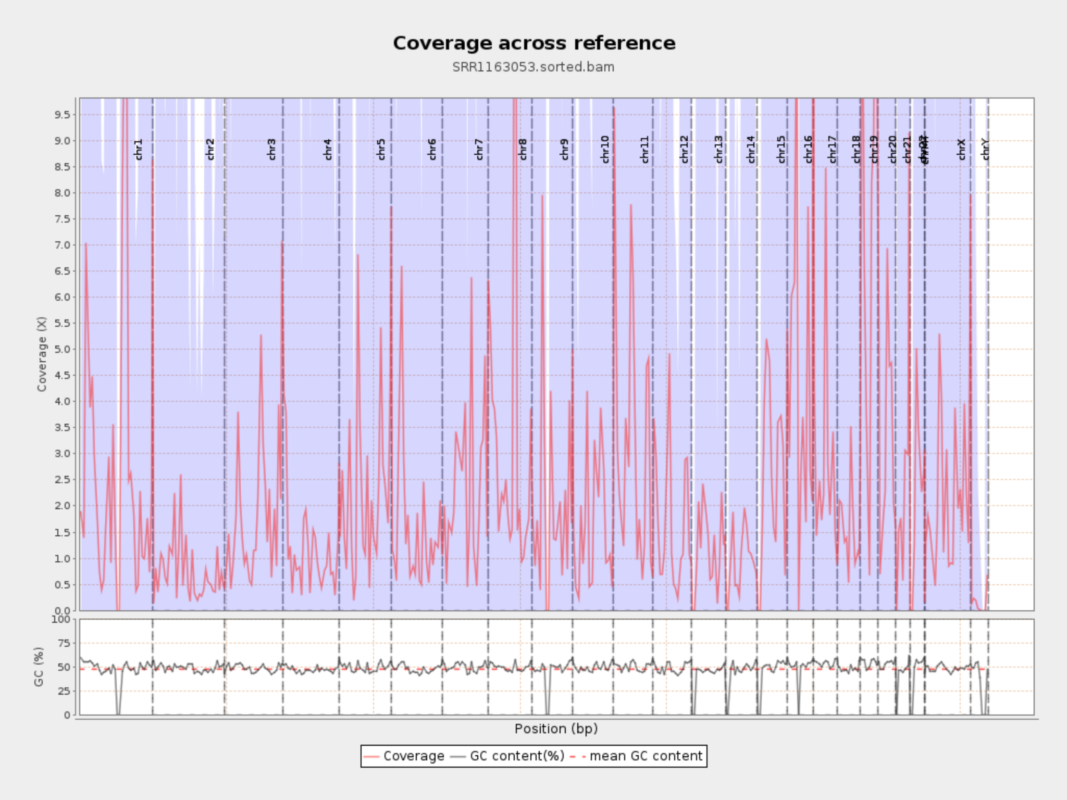
General error rate	0.38%
Mismatches	24,958,056
Insertions	454,405
Mapped reads with at least one insertion	0.65%
Deletions	378,423
Mapped reads with at least one deletion	0.54%
Homopolymer indels	47%

2.6. Chromosome stats

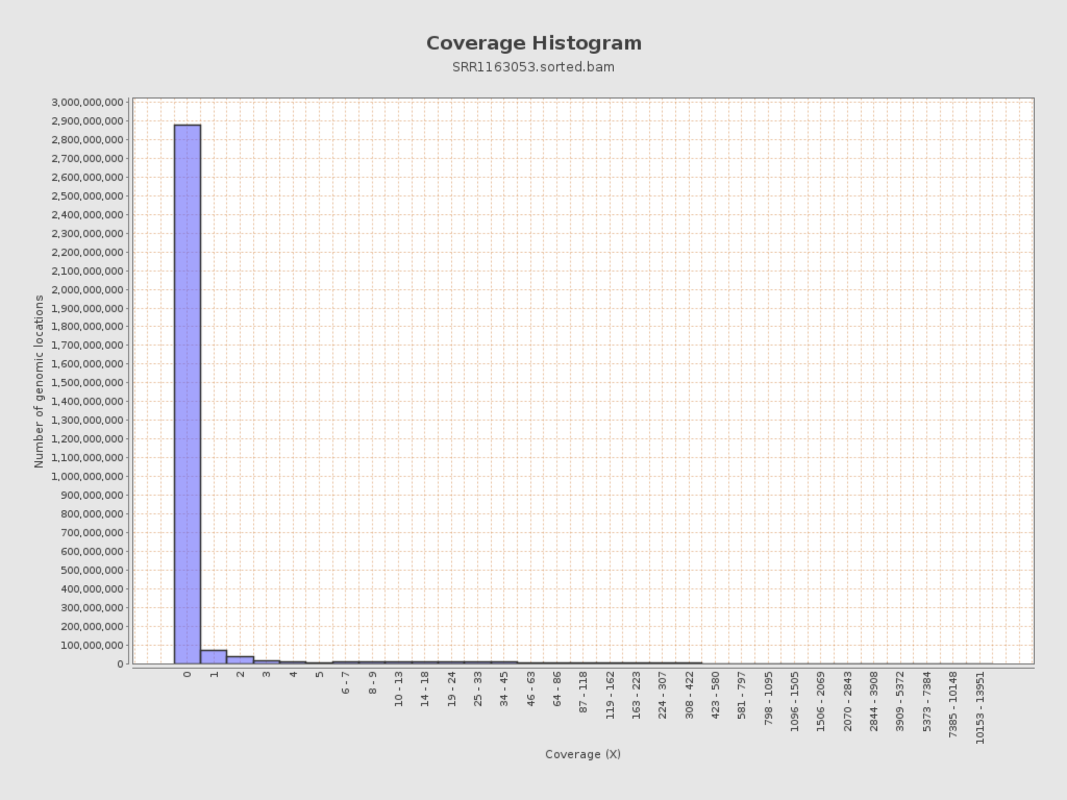
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	704159988	2.8251	38.6389
chr2	243199373	181451835	0.7461	14.1364
chr3	198022430	355633645	1.7959	25.256
chr4	191154276	224656201	1.1753	19.677
chr5	180915260	418535169	2.3134	38.8669
chr6	171115067	267958723	1.566	26.7346
chr7	159138663	378012659	2.3754	42.6491

chr8	146364022	461138338	3.1506	59.6001
chr9	141213431	285564716	2.0222	31.8906
chr10	135534747	229944187	1.6966	22.7256
chr11	135006516	446279808	3.3056	35.4636
chr12	133851895	233922329	1.7476	23.2675
chr13	115169878	135145369	1.1734	19.0832
chr14	107349540	100545435	0.9366	16.1488
chr15	102531392	253252004	2.47	27.8745
chr16	90354753	401500660	4.4436	42.7182
chr17	81195210	235368266	2.8988	32.8254
chr18	78077248	124938234	1.6002	23.7169
chr19	59128983	473567141	8.0091	68.7041
chr20	63025520	214352170	3.401	36.6338
chr21	48129895	121829891	2.5313	47.9631
chr22	51304566	119668971	2.3325	30.0097
chrMT	16571	2482	0.1498	0.4766
chrX	155270560	335743685	2.1623	38.7952
chrY	59373566	9699355	0.1634	9.7766

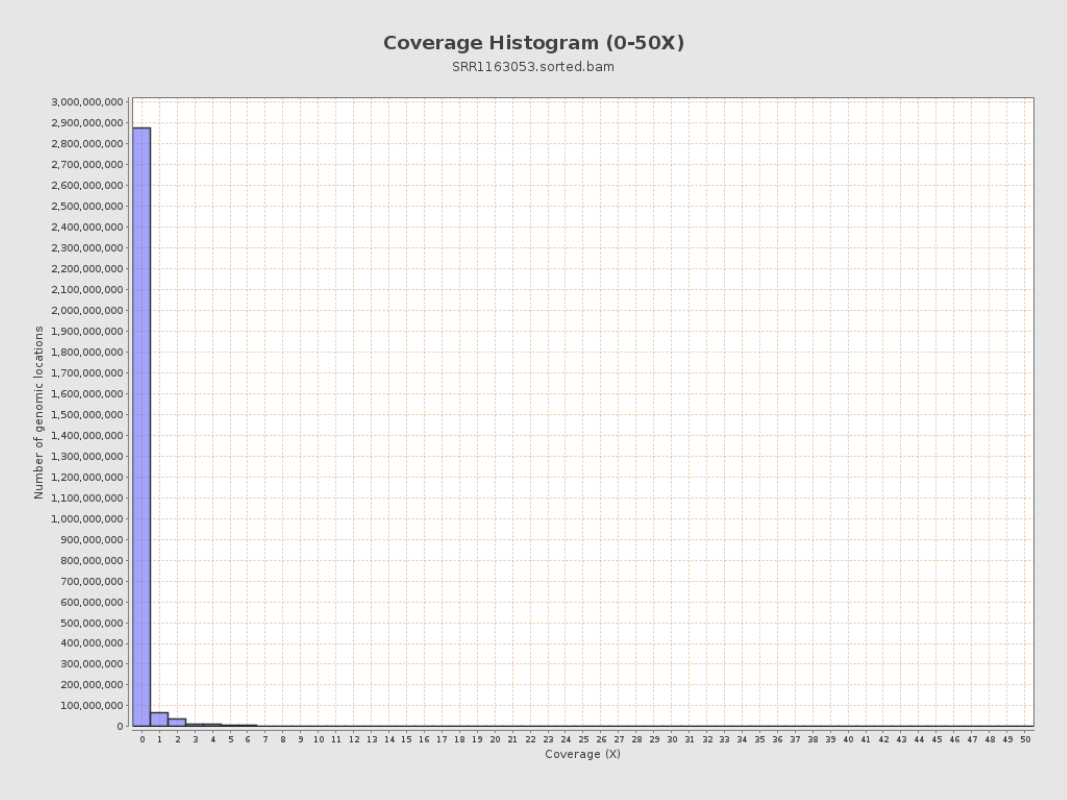
3. Results : Coverage across reference



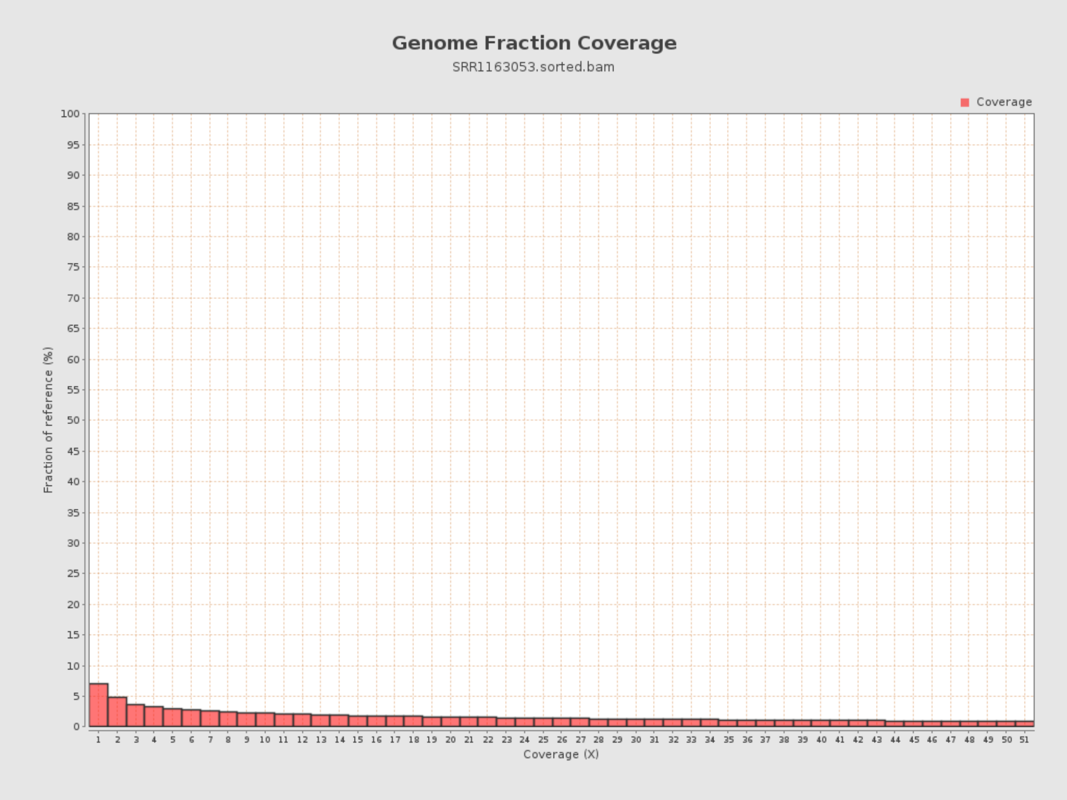
4. Results : Coverage Histogram



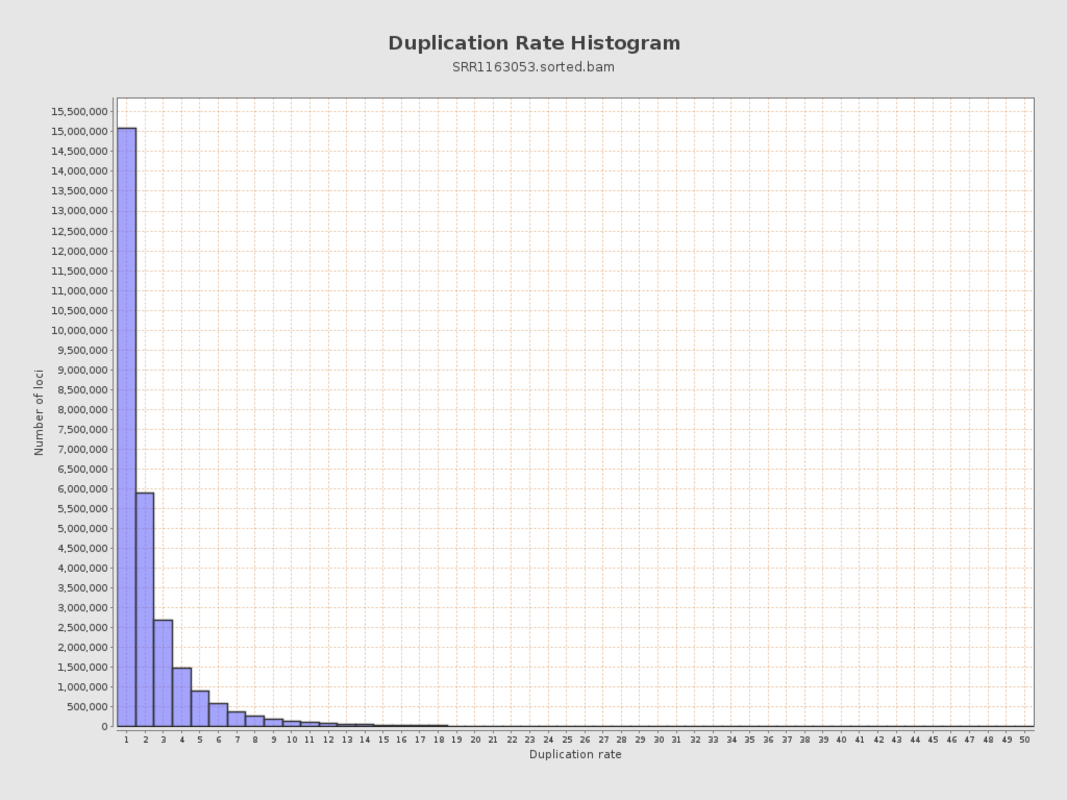
5. Results : Coverage Histogram (0-50X)



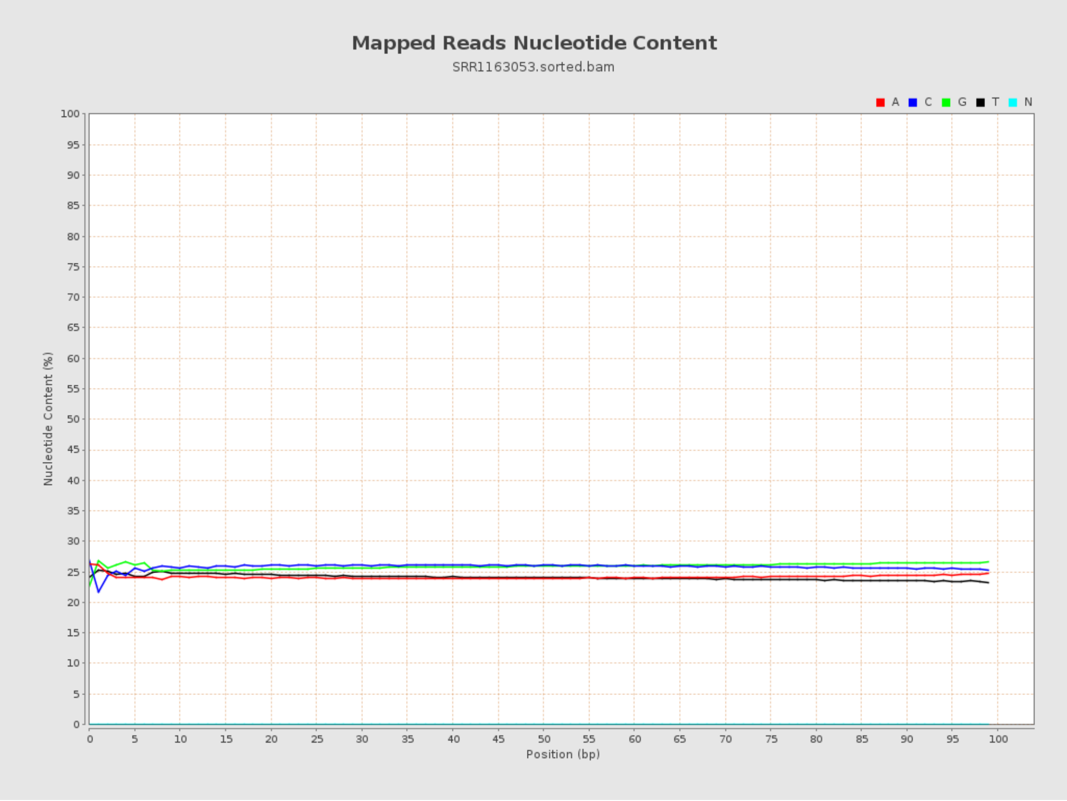
6. Results : Genome Fraction Coverage



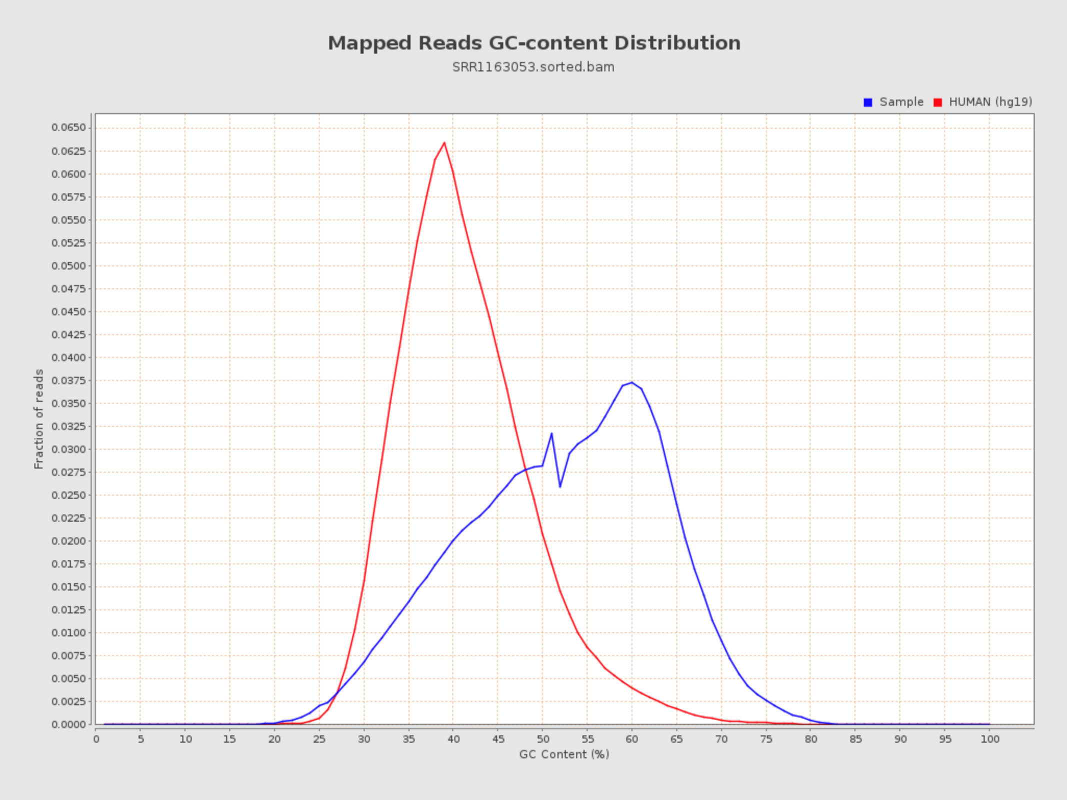
7. Results : Duplication Rate Histogram



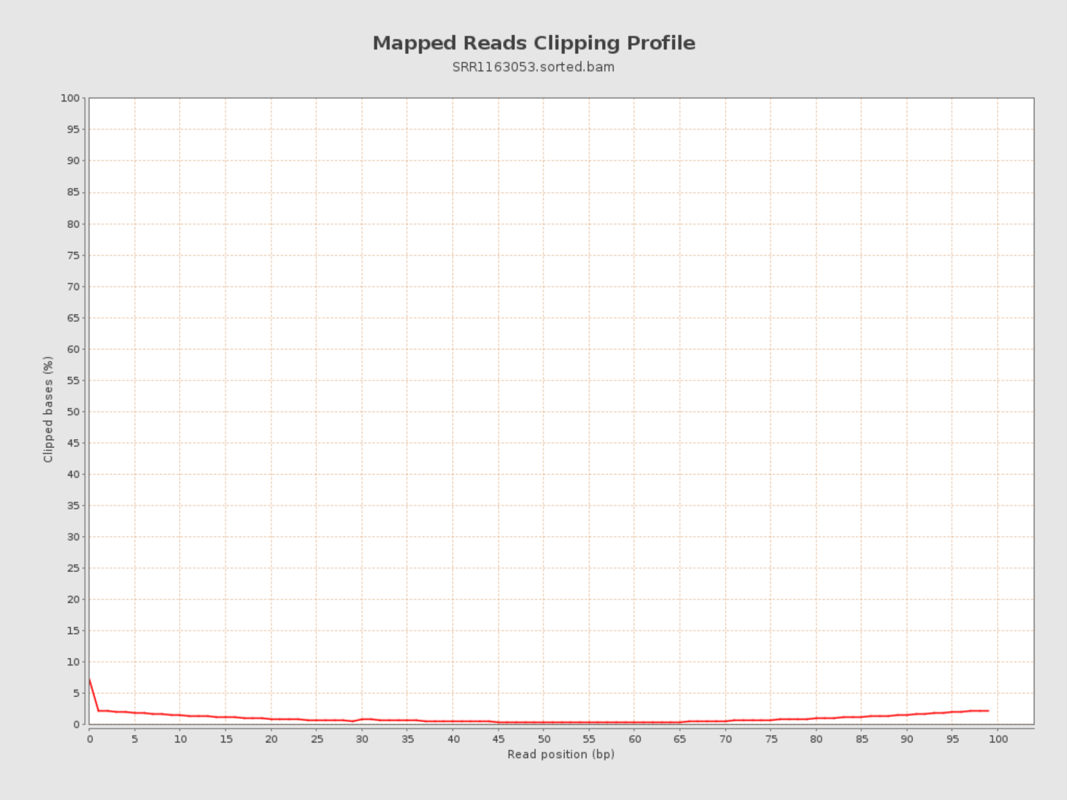
8. Results : Mapped Reads Nucleotide Content



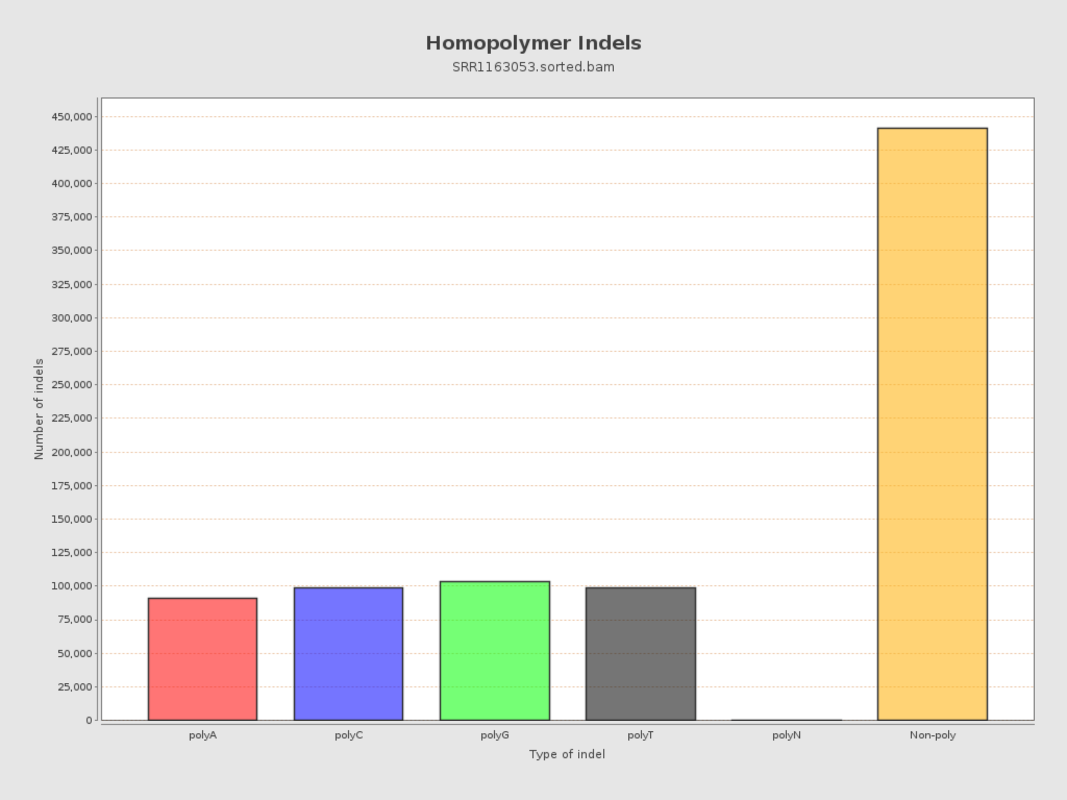
9. Results : Mapped Reads GC-content Distribution



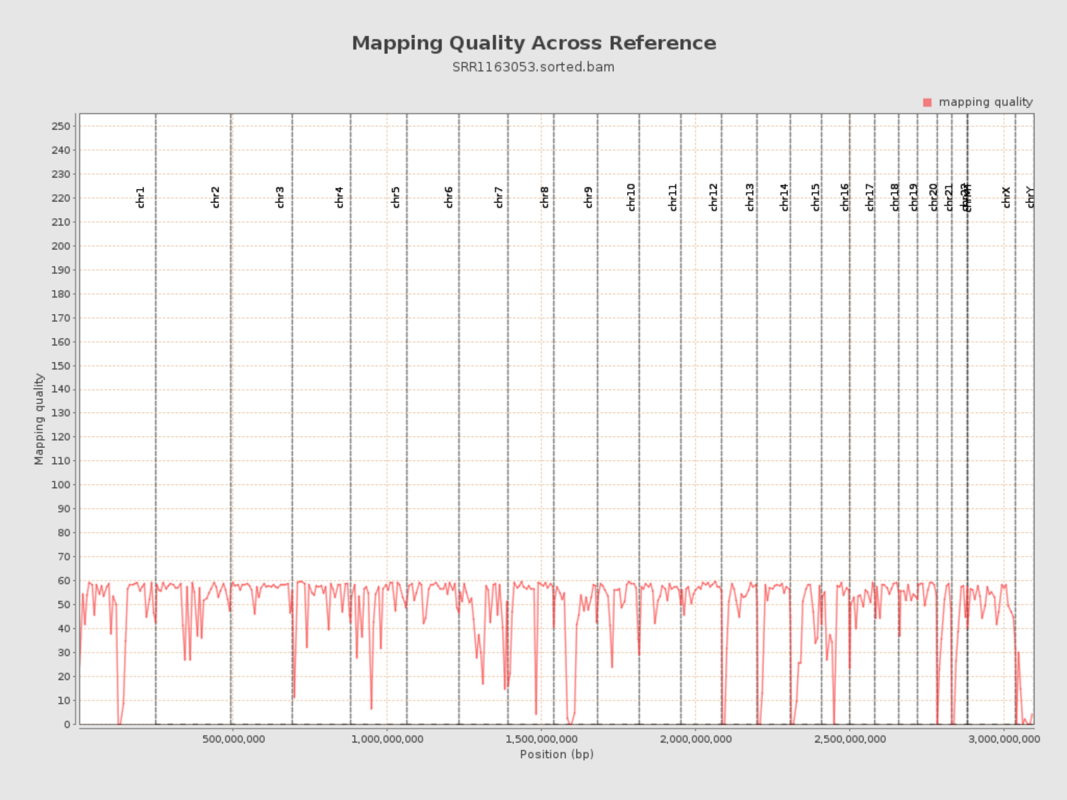
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram