

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/17 20:29:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163012.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_SRR1163012 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163012.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 17 20:29:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163012.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	96,108,720
Mapped reads	94,222,799 / 98.04%
Unmapped reads	1,885,921 / 1.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	662,619 / 0.69%
Read min/max/mean length	30 / 100 / 100.28
Duplicated reads (estimated)	54,682,795 / 56.9%
Duplication rate	47.2%
Clipped reads	13,998,054 / 14.56%

2.2. ACGT Content

Number/percentage of A's	2,190,904,997 / 23.9%
Number/percentage of C's	2,395,466,643 / 26.13%
Number/percentage of T's	2,180,398,161 / 23.78%
Number/percentage of G's	2,399,144,619 / 26.17%
Number/percentage of N's	1,973,592 / 0.02%
GC Percentage	52.3%

2.3. Coverage

Mean	2.9619

Standard Deviation	36.3487
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2.4. Mapping Quality

Mean Mapping Quality	48.86
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2.5. Mismatches and indels

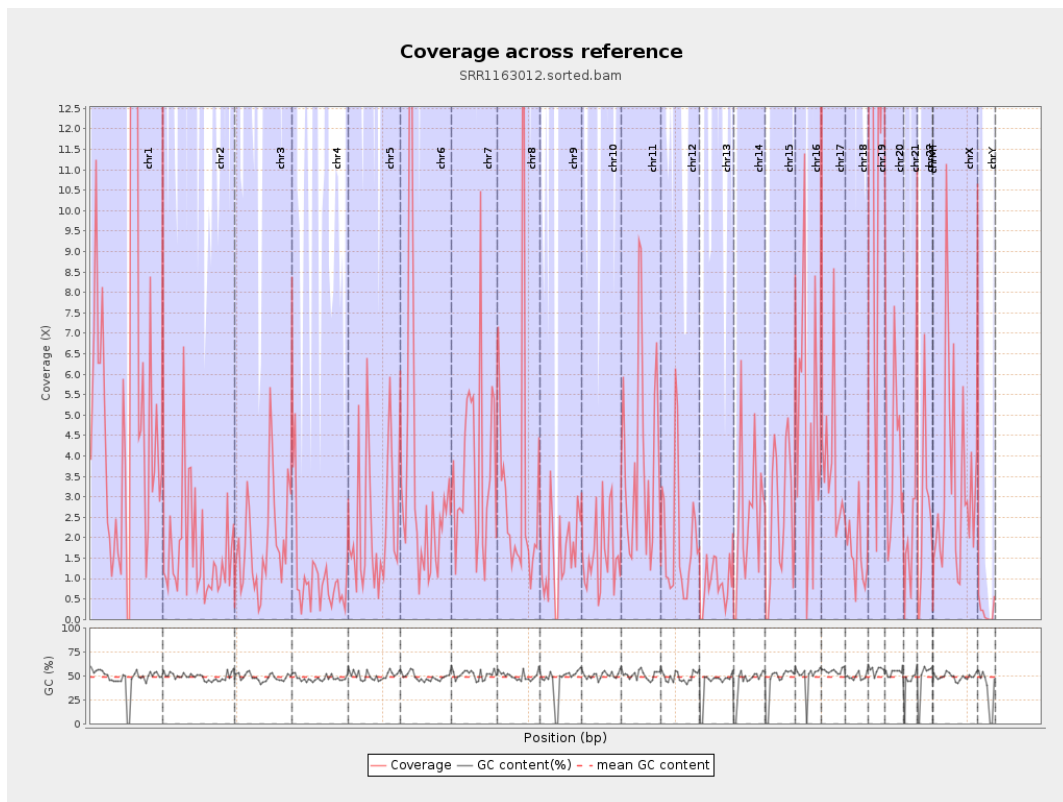
General error rate	0.45%
Mismatches	40,689,381
Insertions	596,696
Mapped reads with at least one insertion	0.63%
Deletions	507,368
Mapped reads with at least one deletion	0.53%
Homopolymer indels	45.78%

2.6. Chromosome stats

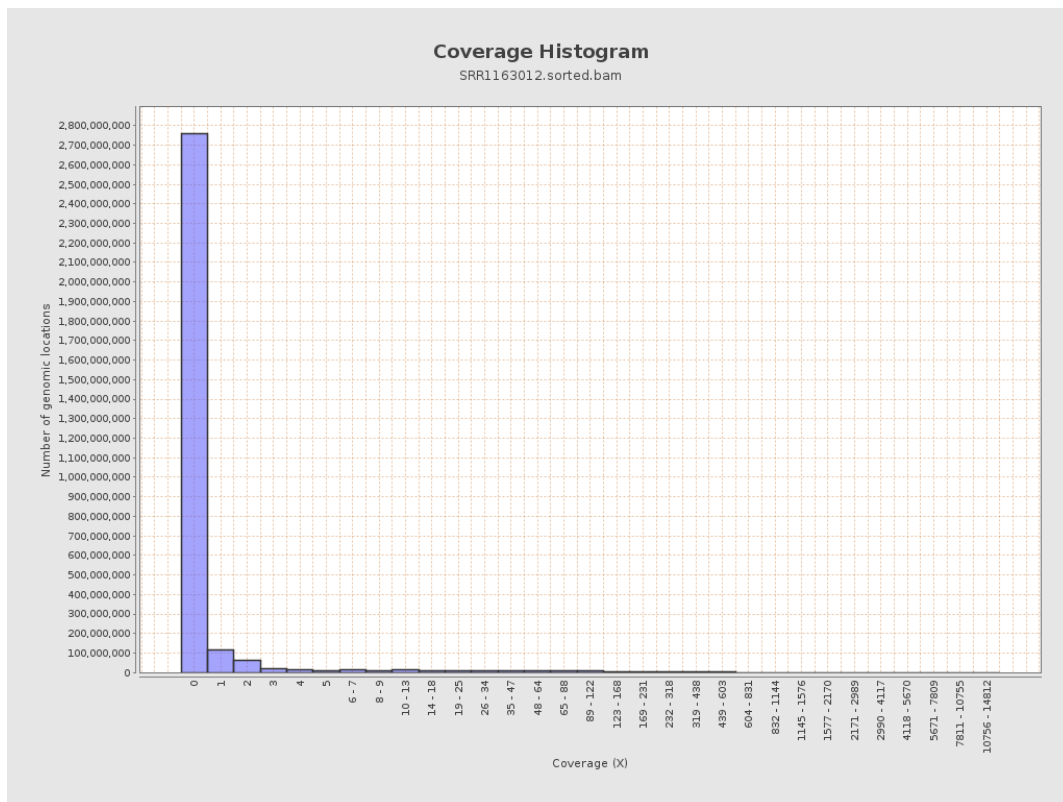
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1520748451	6.1013	58.7661
chr2	243199373	402133461	1.6535	18.5805
chr3	198022430	389150459	1.9652	19.4651
chr4	191154276	199731392	1.0449	17.9979
chr5	180915260	434999147	2.4044	42.3478
chr6	171115067	566472356	3.3105	35.2469
chr7	159138663	594033927	3.7328	37.7533

chr8	146364022	483941245	3.3064	60.4475
chr9	141213431	220315632	1.5602	16.8024
chr10	135534747	216142821	1.5947	16.9254
chr11	135006516	521673328	3.8641	31.4806
chr12	133851895	267224600	1.9964	19.2637
chr13	115169878	101738146	0.8834	13.2307
chr14	107349540	274713377	2.5591	24.3793
chr15	102531392	248069883	2.4195	23.2244
chr16	90354753	431957990	4.7807	37.9845
chr17	81195210	302661496	3.7276	28.4195
chr18	78077248	124912071	1.5999	18.363
chr19	59128983	821140304	13.8873	99.6423
chr20	63025520	247713964	3.9304	32.7041
chr21	48129895	131024350	2.7223	53.0745
chr22	51304566	133912315	2.6101	24.0981
chrMT	16571	3128	0.1888	0.6277
chrX	155270560	523145055	3.3692	39.9127
chrY	59373566	11458375	0.193	9.6407

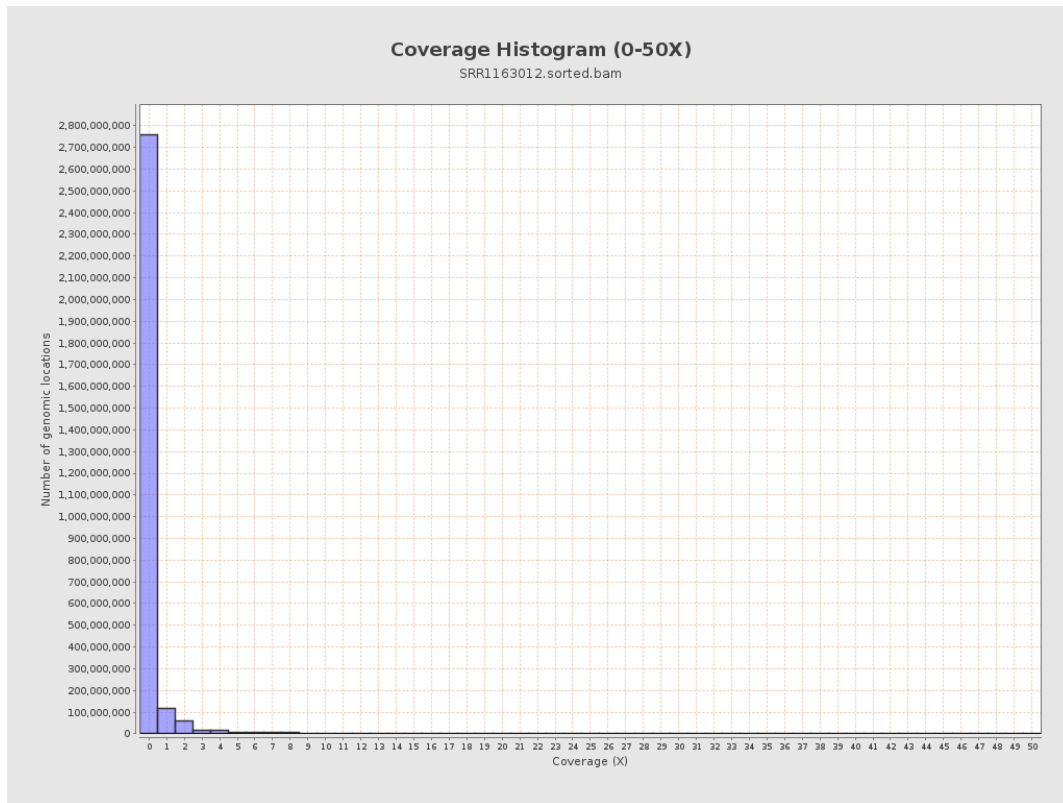
3. Results : Coverage across reference



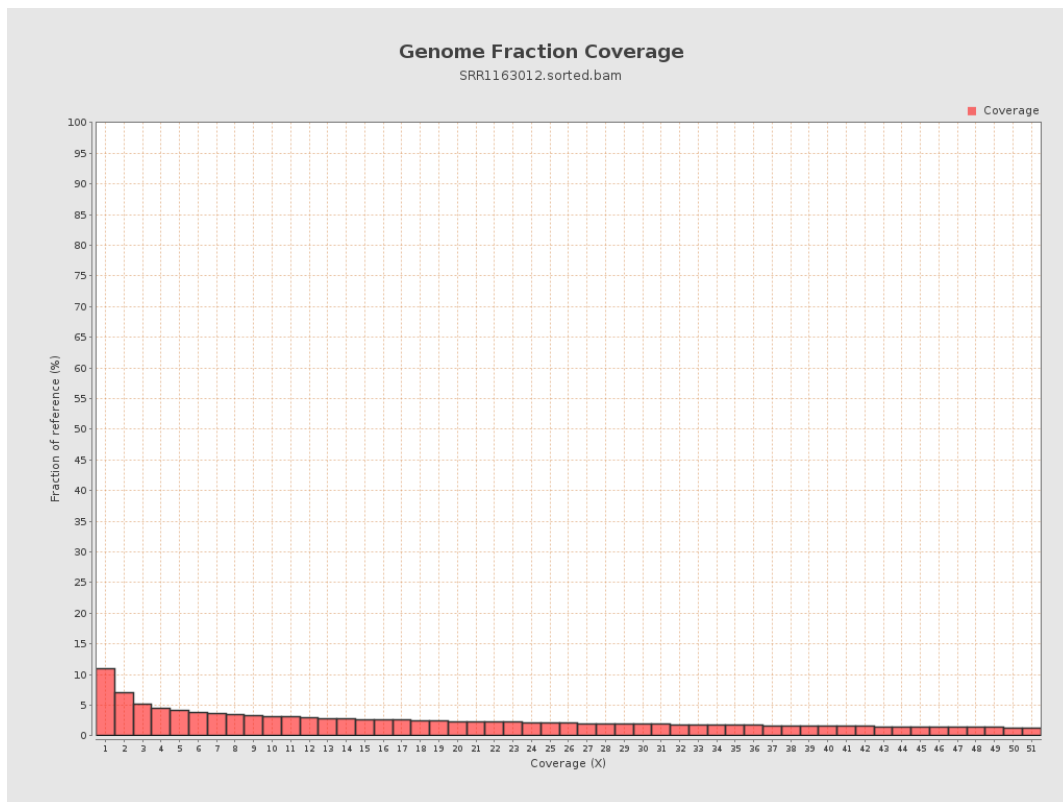
4. Results : Coverage Histogram



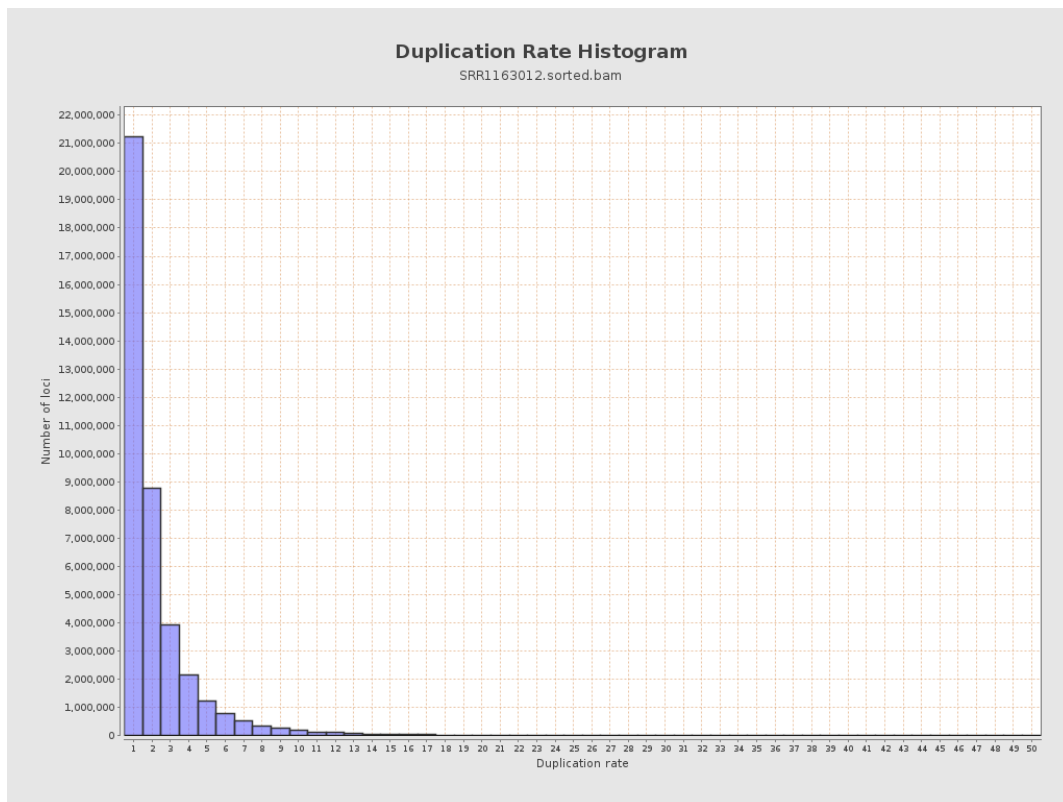
5. Results : Coverage Histogram (0-50X)



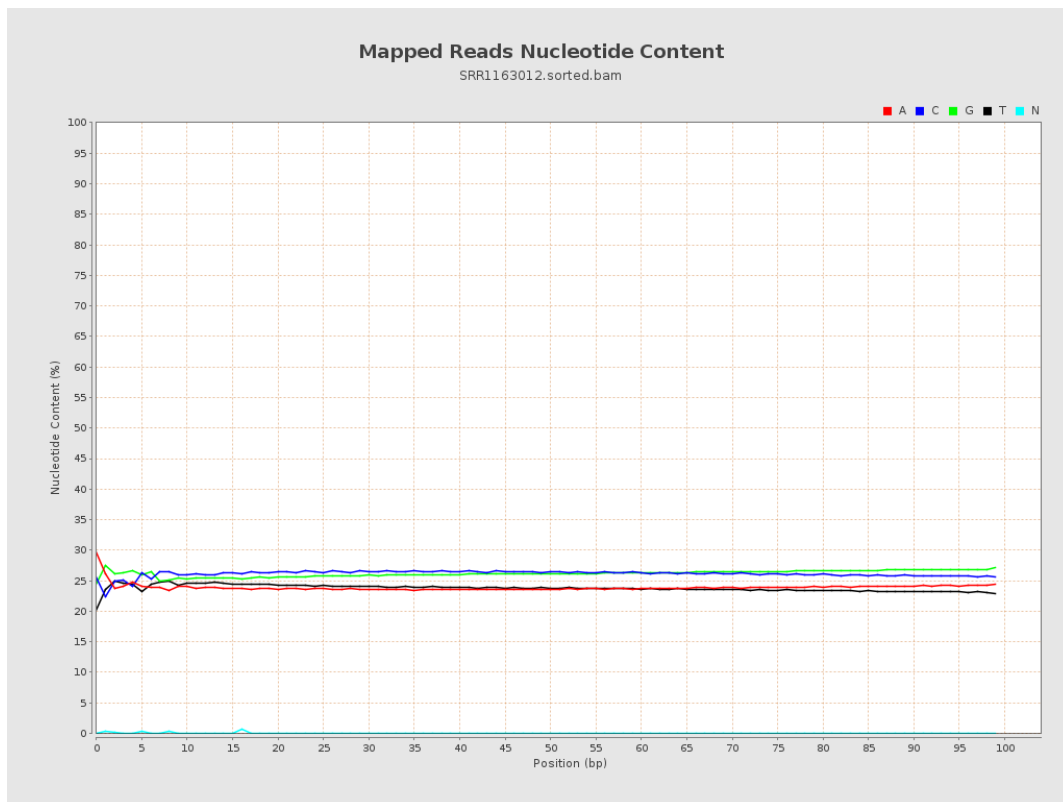
6. Results : Genome Fraction Coverage



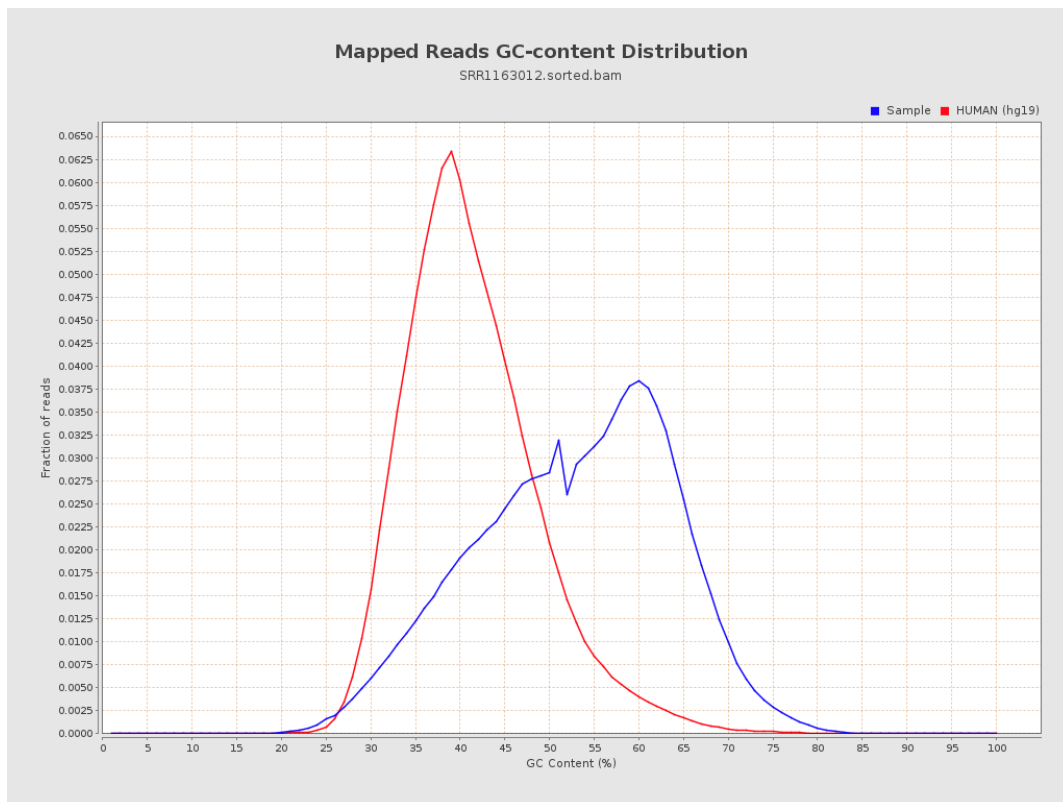
7. Results : Duplication Rate Histogram



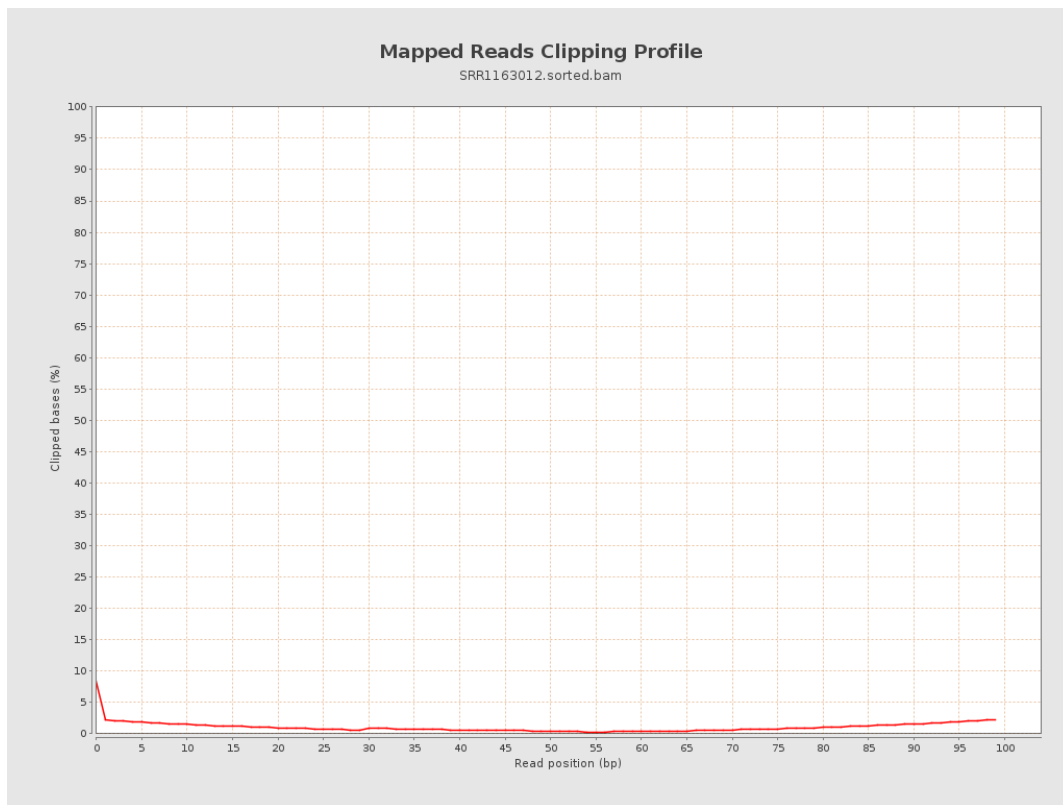
8. Results : Mapped Reads Nucleotide Content



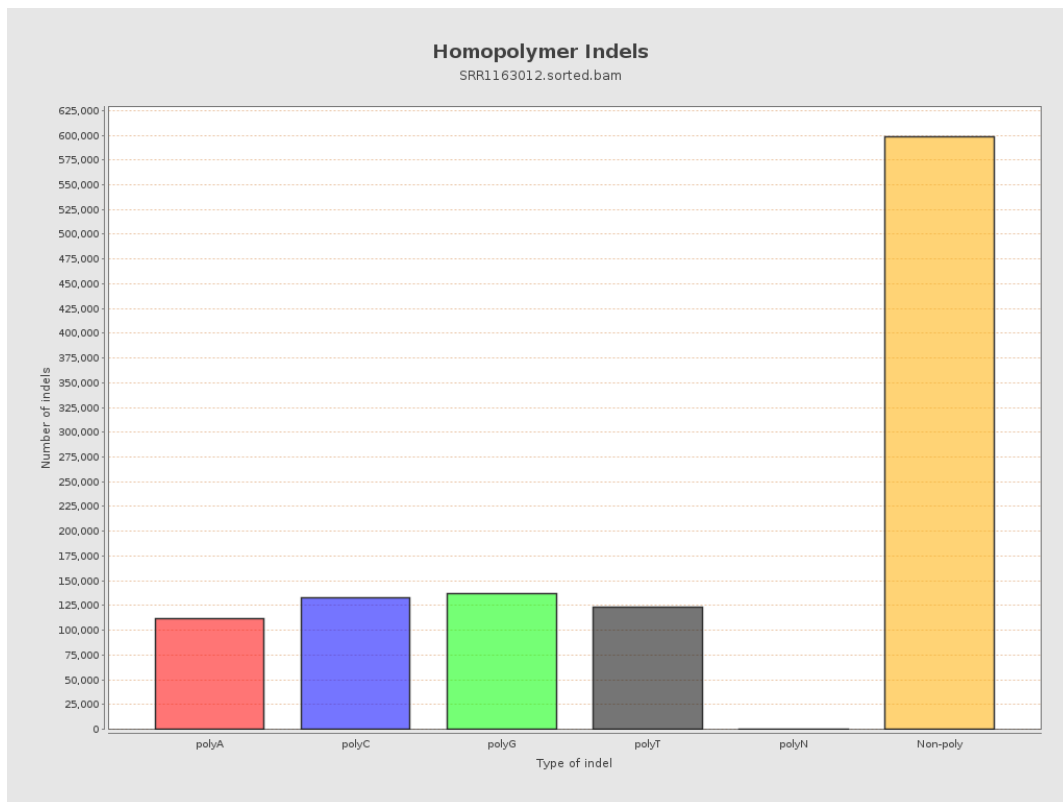
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

