

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/18 17:58:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1163156.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_SRR1163156 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1163156.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 18 17:58:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1163156.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	75,722,878
Mapped reads	73,619,340 / 97.22%
Unmapped reads	2,103,538 / 2.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	345,928 / 0.46%
Read min/max/mean length	30 / 100 / 100.19
Duplicated reads (estimated)	38,214,578 / 50.47%
Duplication rate	41.45%
Clipped reads	9,178,392 / 12.12%

2.2. ACGT Content

Number/percentage of A's	1,790,159,614 / 24.89%
Number/percentage of C's	1,800,992,691 / 25.04%
Number/percentage of T's	1,787,996,596 / 24.86%
Number/percentage of G's	1,802,064,039 / 25.05%
Number/percentage of N's	12,365,262 / 0.17%
GC Percentage	50.09%

2.3. Coverage

Mean	2.324

Standard Deviation	27.5567
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2.4. Mapping Quality

Mean Mapping Quality	49.12
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2.5. Mismatches and indels

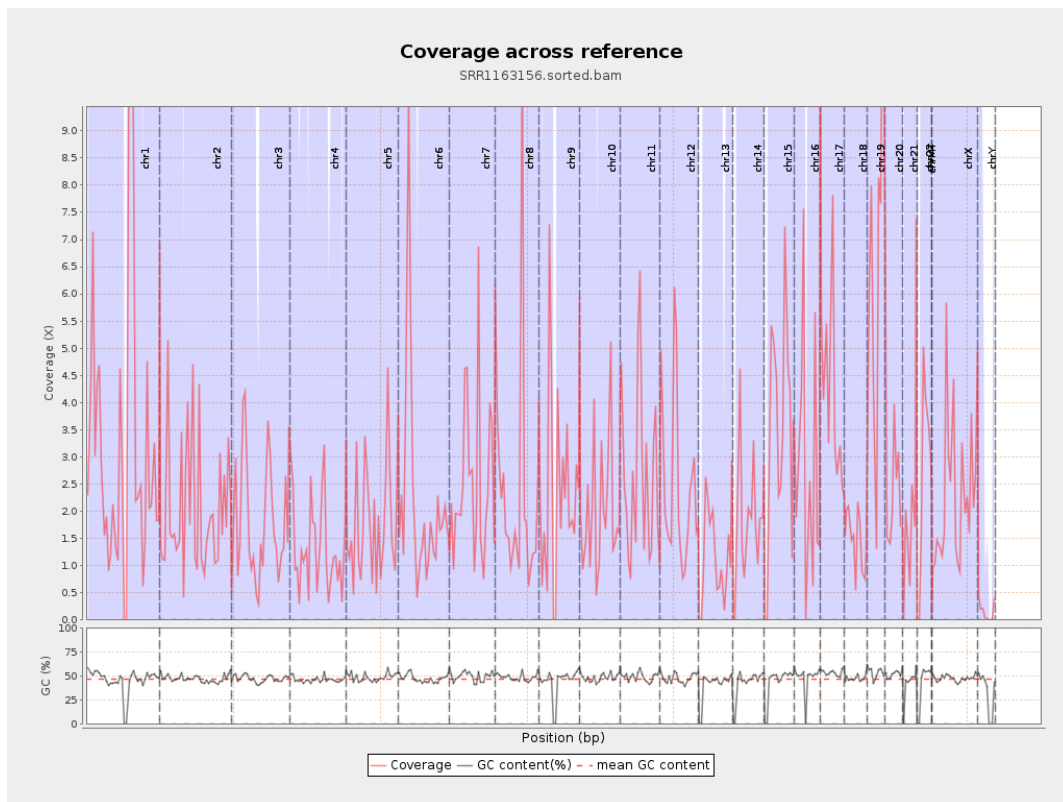
General error rate	0.65%
Mismatches	46,164,768
Insertions	499,283
Mapped reads with at least one insertion	0.67%
Deletions	361,331
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.86%

2.6. Chromosome stats

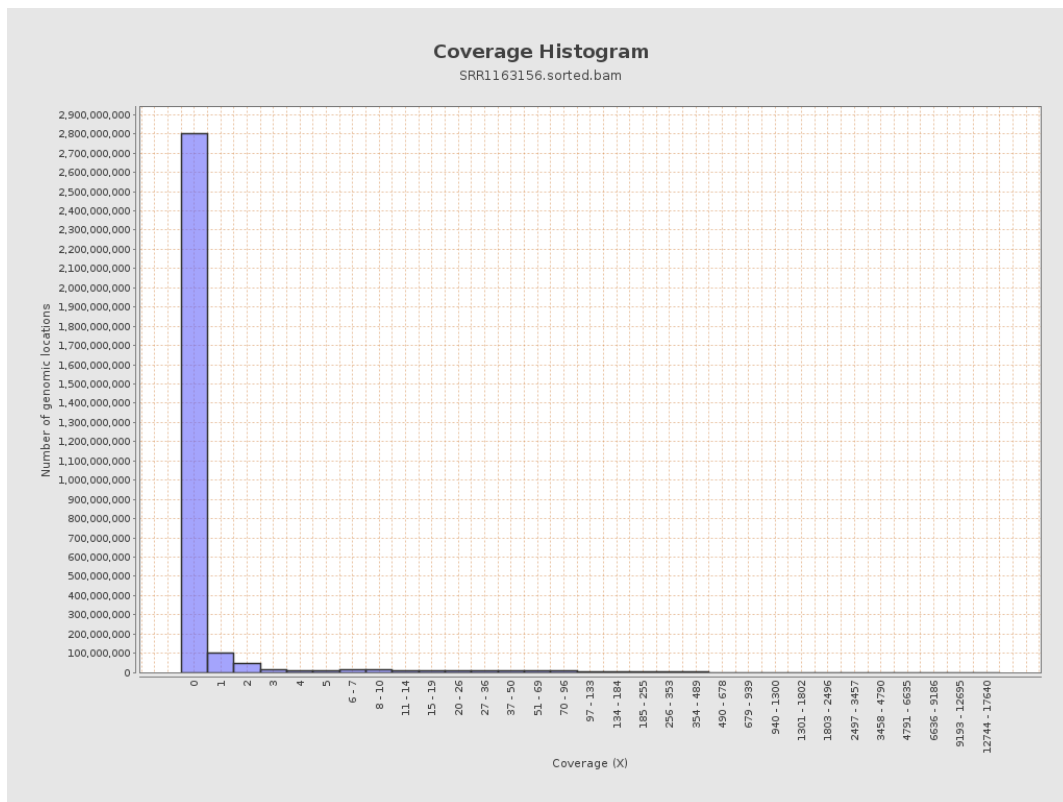
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	822497472	3.2999	38.9245
chr2	243199373	495156034	2.036	22.6163
chr3	198022430	358031888	1.808	20.1882
chr4	191154276	256334846	1.341	22.573
chr5	180915260	329305259	1.8202	26.1122
chr6	171115067	371174592	2.1692	24.263
chr7	159138663	398957262	2.507	32.4101

chr8	146364022	320097857	2.187	34.4535
chr9	141213431	334493862	2.3687	28.4826
chr10	135534747	272852711	2.0132	21.2226
chr11	135006516	366690132	2.7161	26.4095
chr12	133851895	330538195	2.4694	26.4395
chr13	115169878	132232338	1.1482	15.6089
chr14	107349540	190480210	1.7744	18.7207
chr15	102531392	344824154	3.3631	35.3359
chr16	90354753	249226638	2.7583	24.54
chr17	81195210	342295694	4.2157	33.3399
chr18	78077248	114265620	1.4635	17.1413
chr19	59128983	407897915	6.8984	47.7851
chr20	63025520	157775343	2.5034	24.4683
chr21	48129895	99885566	2.0753	36.3858
chr22	51304566	138539199	2.7003	25.0105
chrMT	16571	981	0.0592	0.3383
chrX	155270560	352155825	2.268	26.1699
chrY	59373566	8713340	0.1468	7.4584

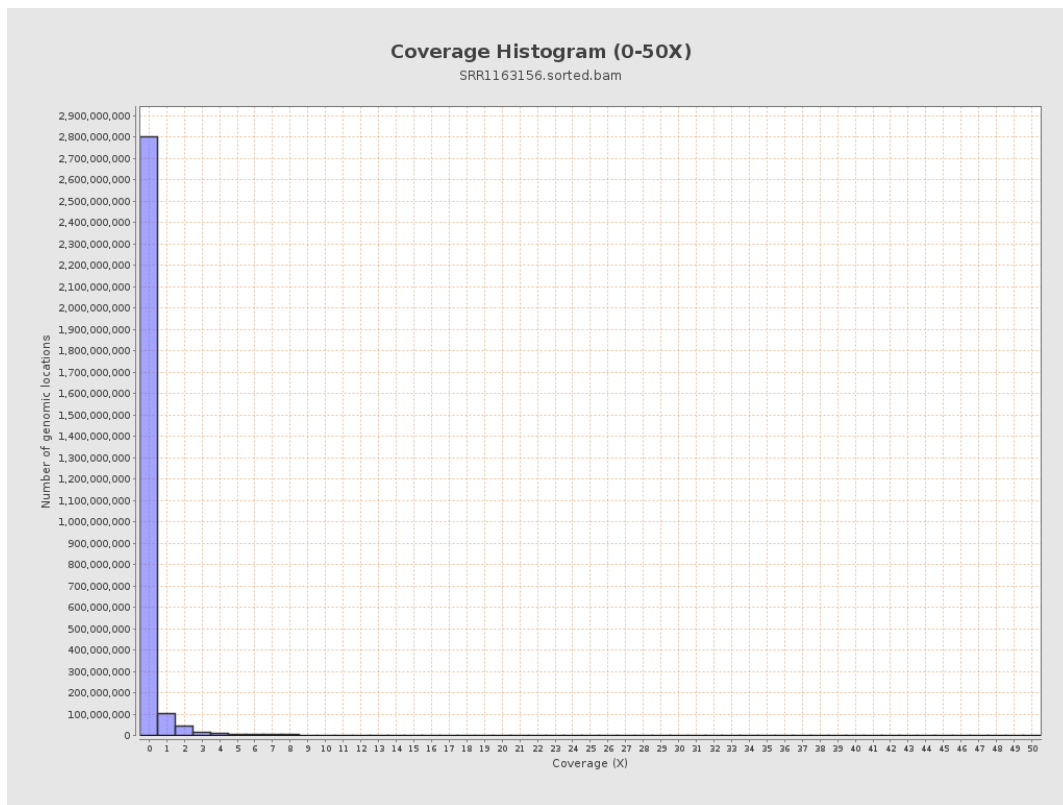
3. Results : Coverage across reference



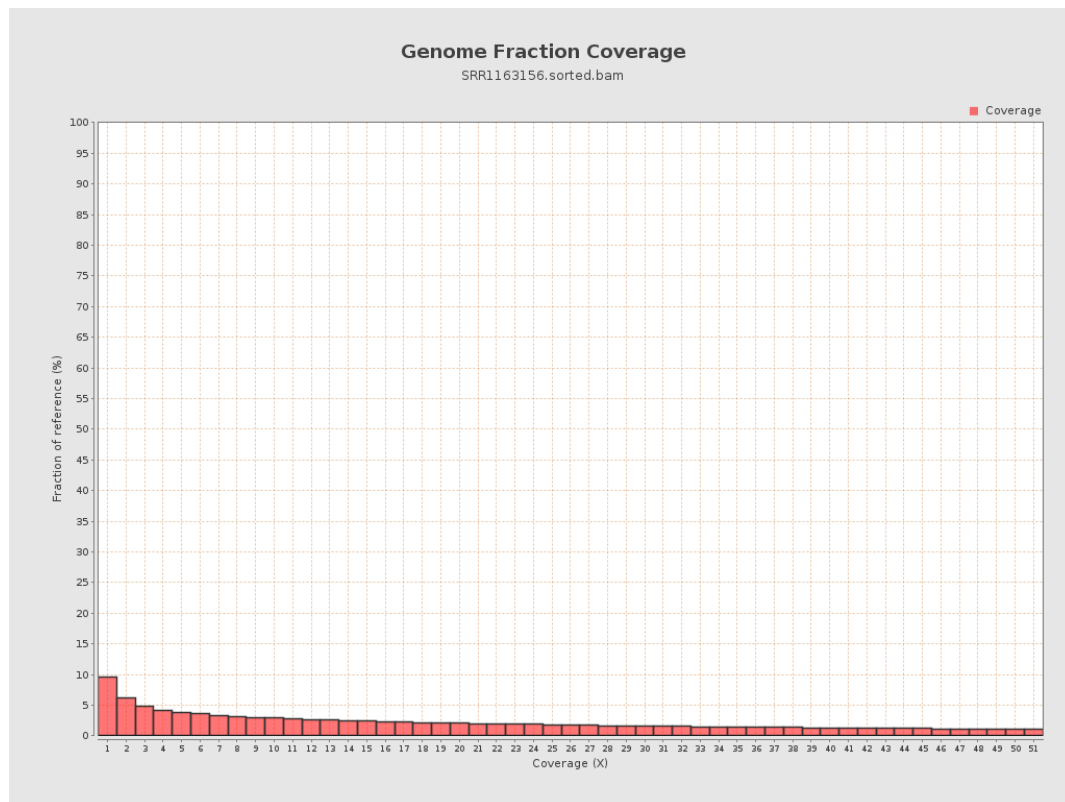
4. Results : Coverage Histogram



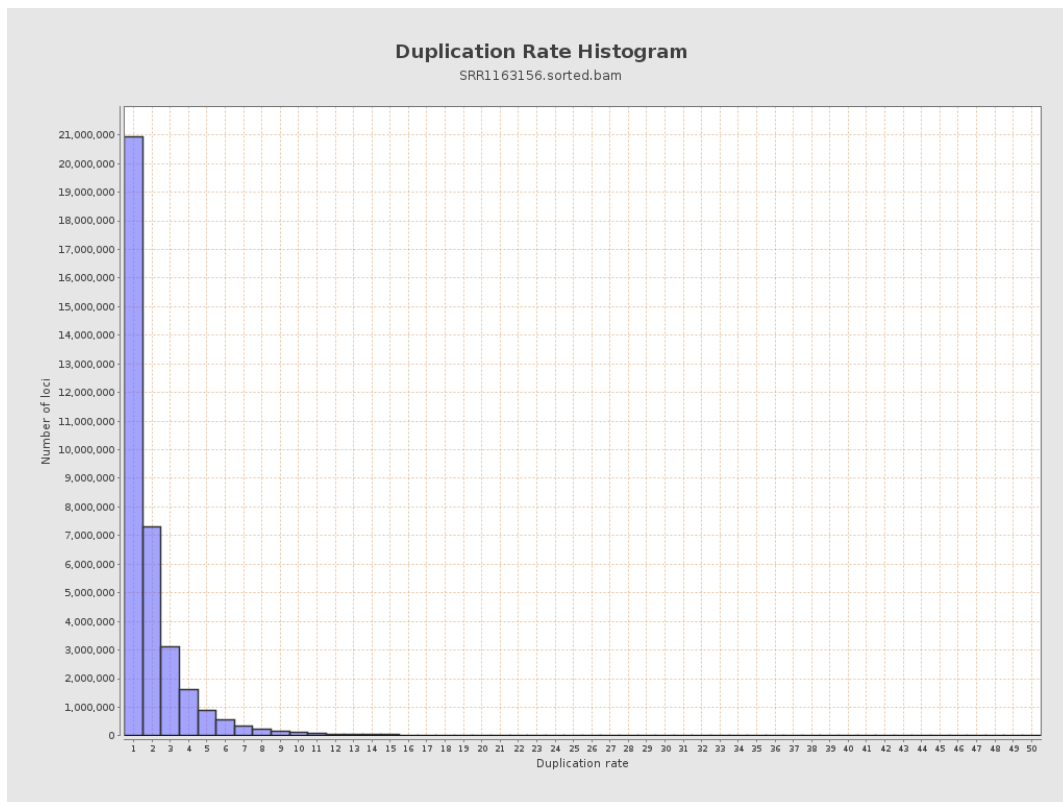
5. Results : Coverage Histogram (0-50X)



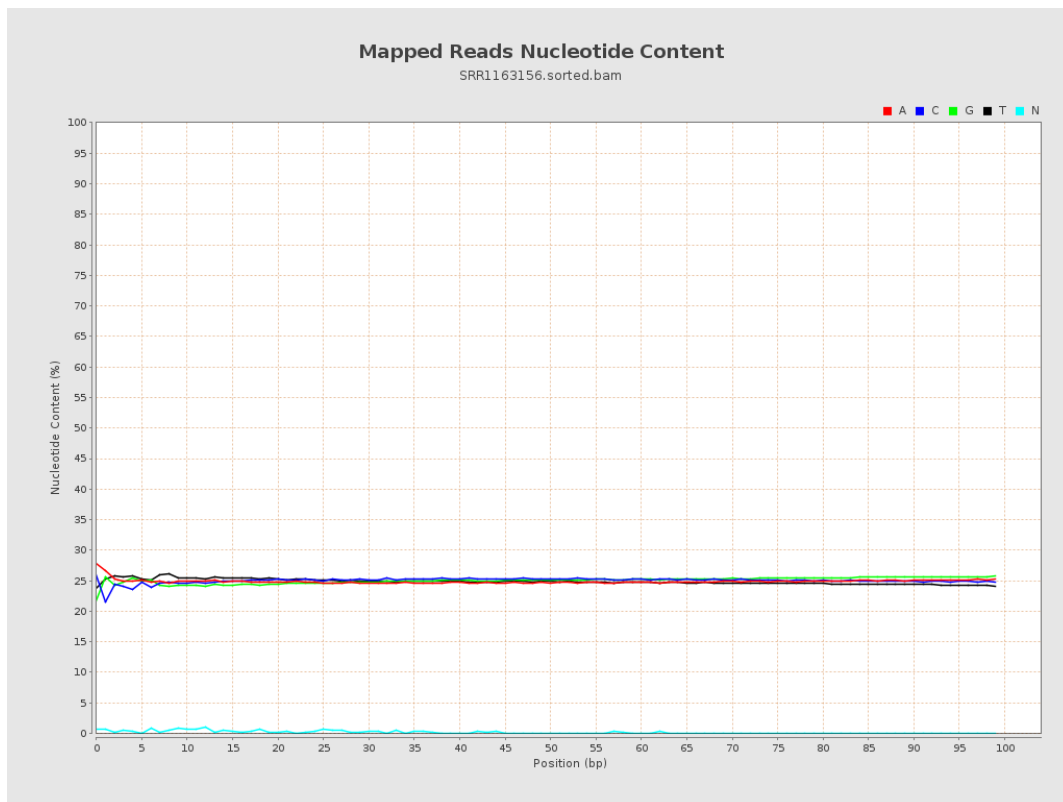
6. Results : Genome Fraction Coverage



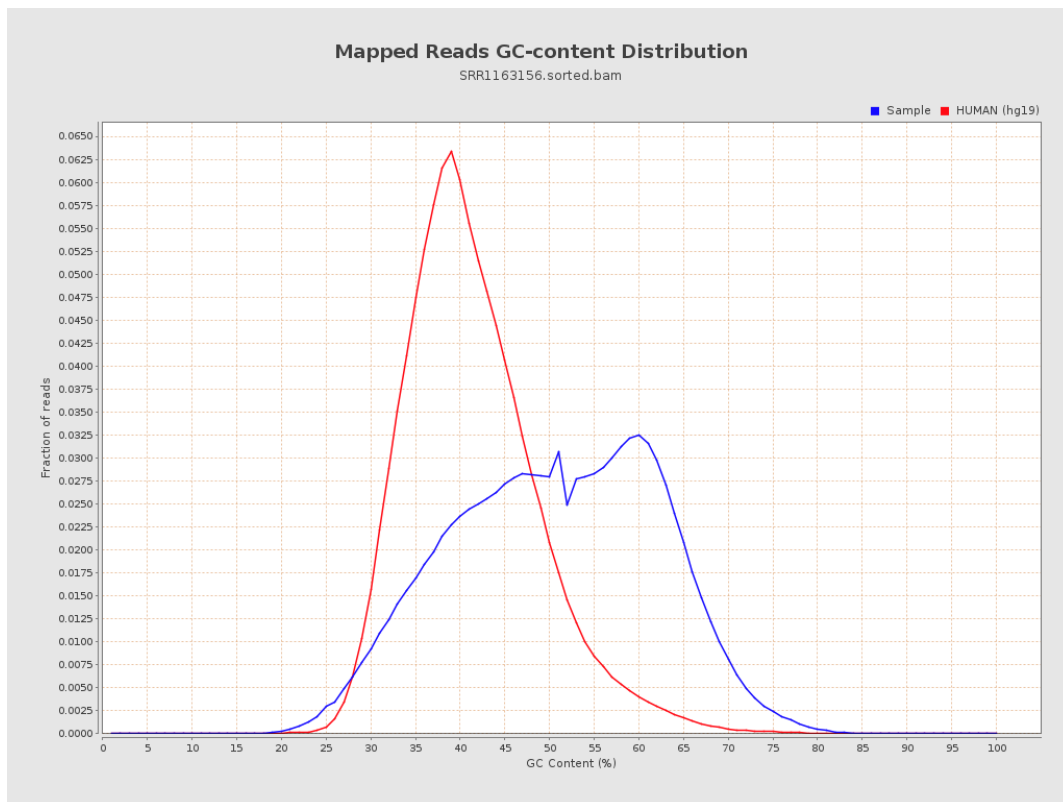
7. Results : Duplication Rate Histogram



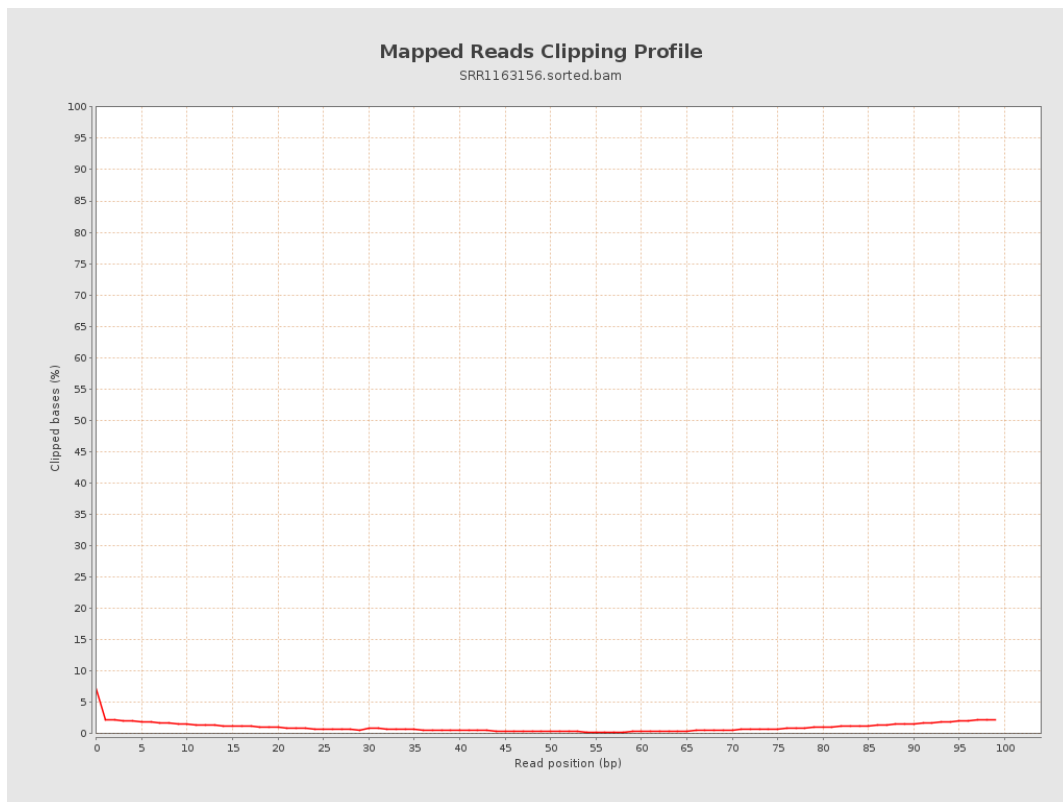
8. Results : Mapped Reads Nucleotide Content



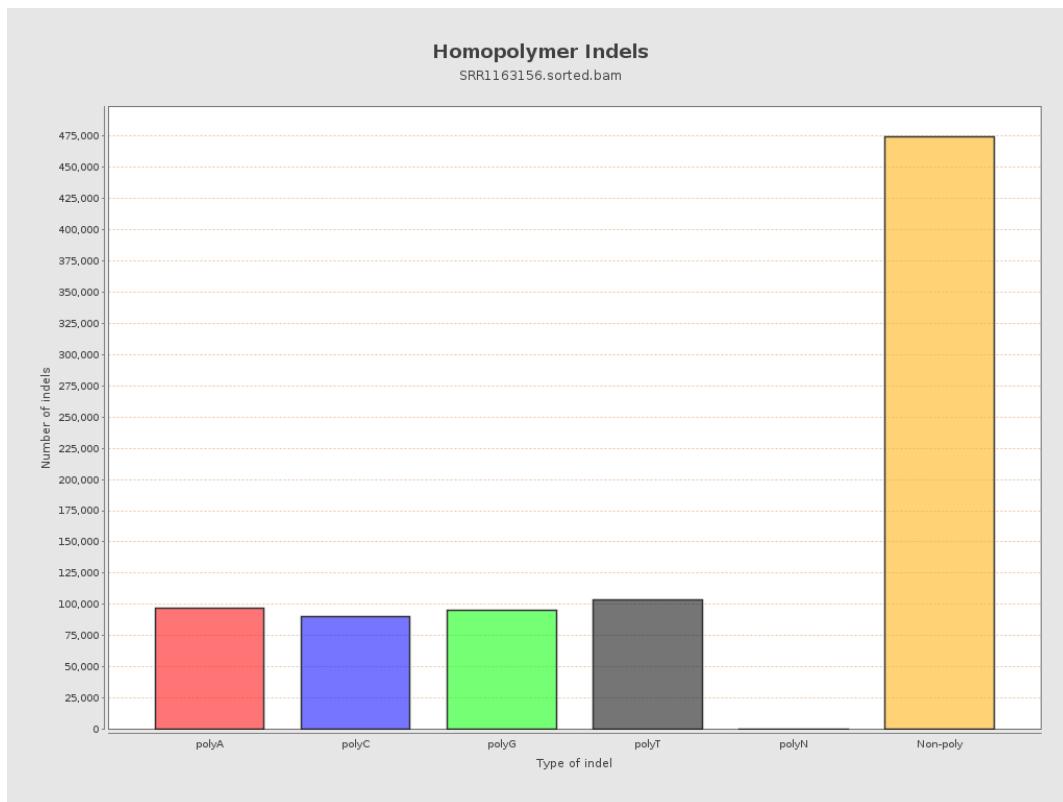
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

