Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 23:24:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751229.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_SRR8751229 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751229.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 23:24:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751229.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,858,806
Mapped reads	4,475,597 / 92.11%
Unmapped reads	383,209 / 7.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	174,417 / 3.59%
Read min/max/mean length	30 / 101 / 102.49
Duplicated reads (estimated)	119,205 / 2.45%
Duplication rate	1.62%
Clipped reads	897,227 / 18.47%

2.2. ACGT Content

Number/percentage of A's	127,851,039 / 29.06%
Number/percentage of C's	92,051,599 / 20.92%
Number/percentage of T's	128,613,982 / 29.23%
Number/percentage of G's	91,485,353 / 20.79%
Number/percentage of N's	2,435 / 0%
GC Percentage	41.71%

2.3. Coverage

Mean	0.1422

Standard Deviation	1.1544

2.4. Mapping Quality

Mean Mapping Quality	51.34

2.5. Mismatches and indels

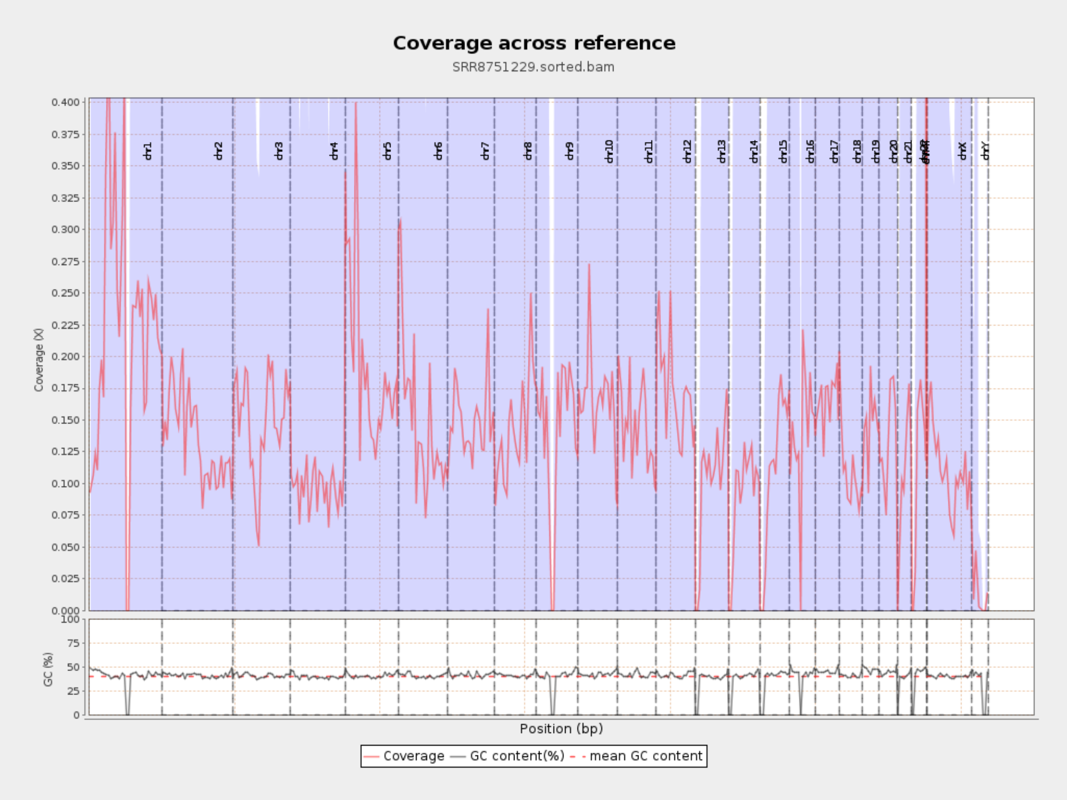
General error rate	0.39%
Mismatches	1,532,618
Insertions	115,622
Mapped reads with at least one insertion	2.53%
Deletions	58,047
Mapped reads with at least one deletion	1.27%
Homopolymer indels	49.25%

2.6. Chromosome stats

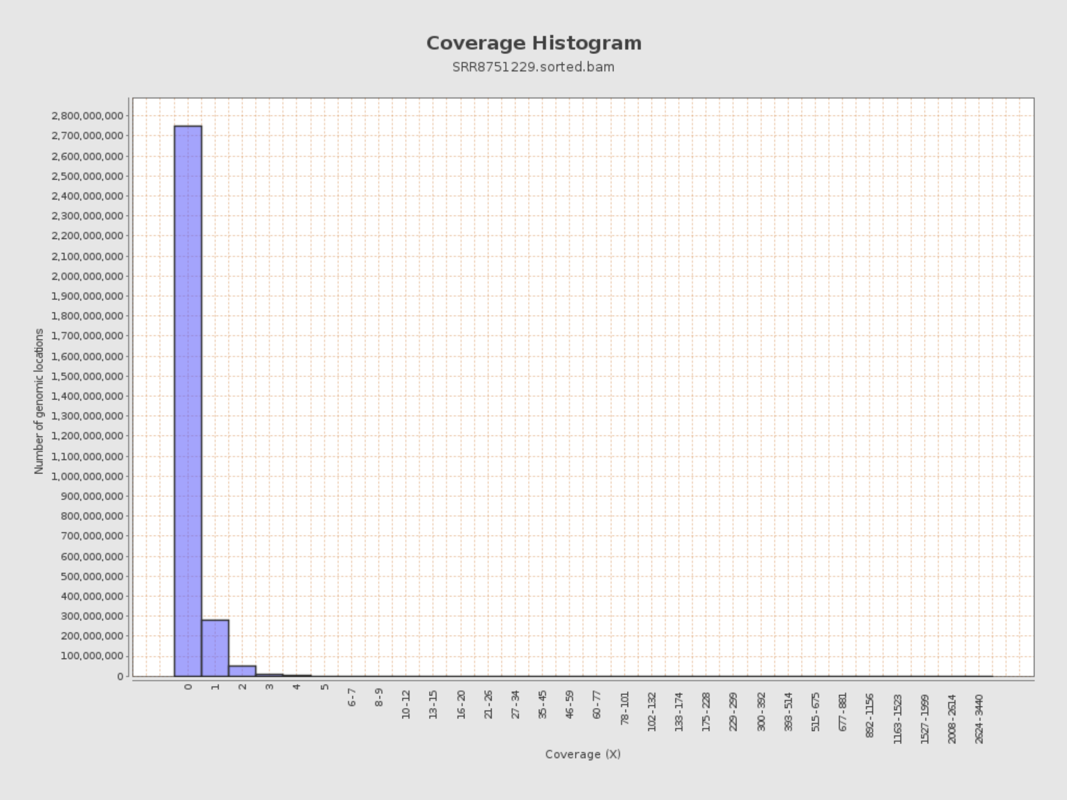
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54973559	0.2206	3.2522
chr2	243199373	32897872	0.1353	0.547
chr3	198022430	29422364	0.1486	0.4792
chr4	191154276	18448319	0.0965	0.3933
chr5	180915260	34820817	0.1925	0.523
chr6	171115067	25618629	0.1497	0.8374
chr7	159138663	23911244	0.1503	0.6535

chr8	146364022	21048782	0.1438	0.5286
chr9	141213431	19710099	0.1396	0.6277
chr10	135534747	22805021	0.1683	1.4323
chr11	135006516	19685998	0.1458	0.6464
chr12	133851895	23404357	0.1749	0.4938
chr13	115169878	11806144	0.1025	0.3729
chr14	107349540	9702887	0.0904	0.3694
chr15	102531392	11350992	0.1107	0.3891
chr16	90354753	12514920	0.1385	0.765
chr17	81195210	13435525	0.1655	0.6362
chr18	78077248	8531468	0.1093	1.0466
chr19	59128983	8613577	0.1457	2.3739
chr20	63025520	8374076	0.1329	0.4349
chr21	48129895	5116594	0.1063	0.4024
chr22	51304566	5463947	0.1065	0.3916
chrMT	16571	476797	28.773	15.0041
chrX	155270560	17204773	0.1108	0.4381
chrY	59373566	793159	0.0134	0.4227

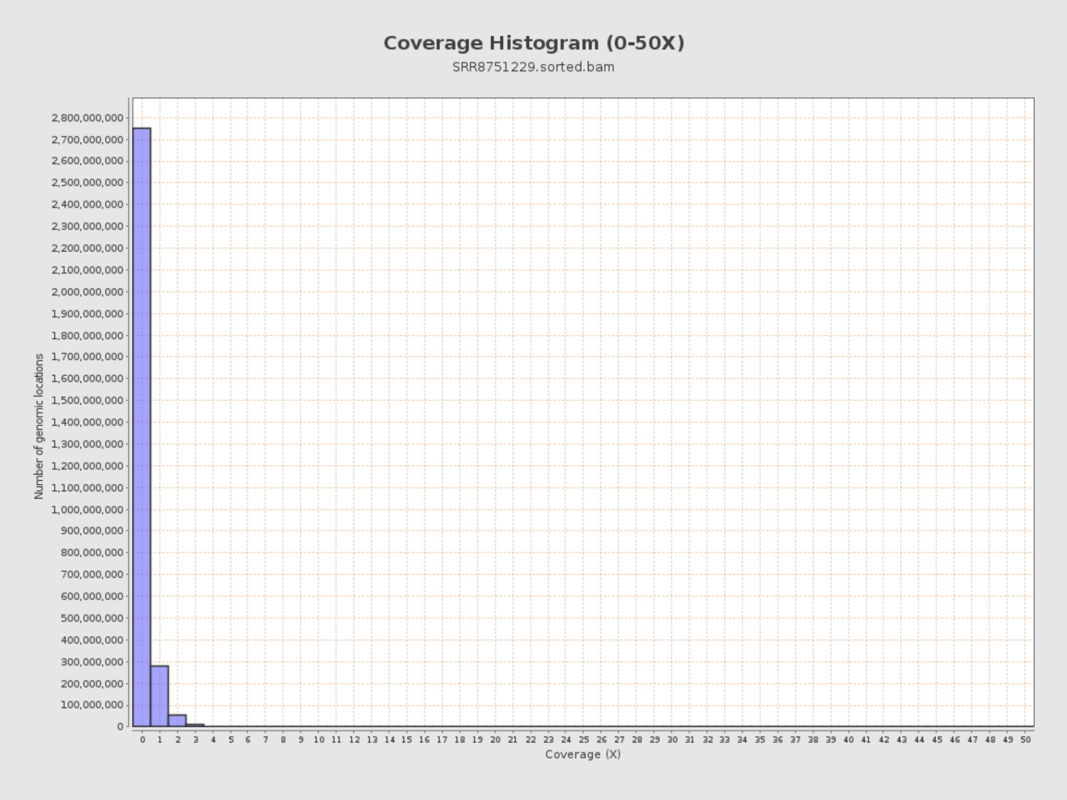
3. Results : Coverage across reference



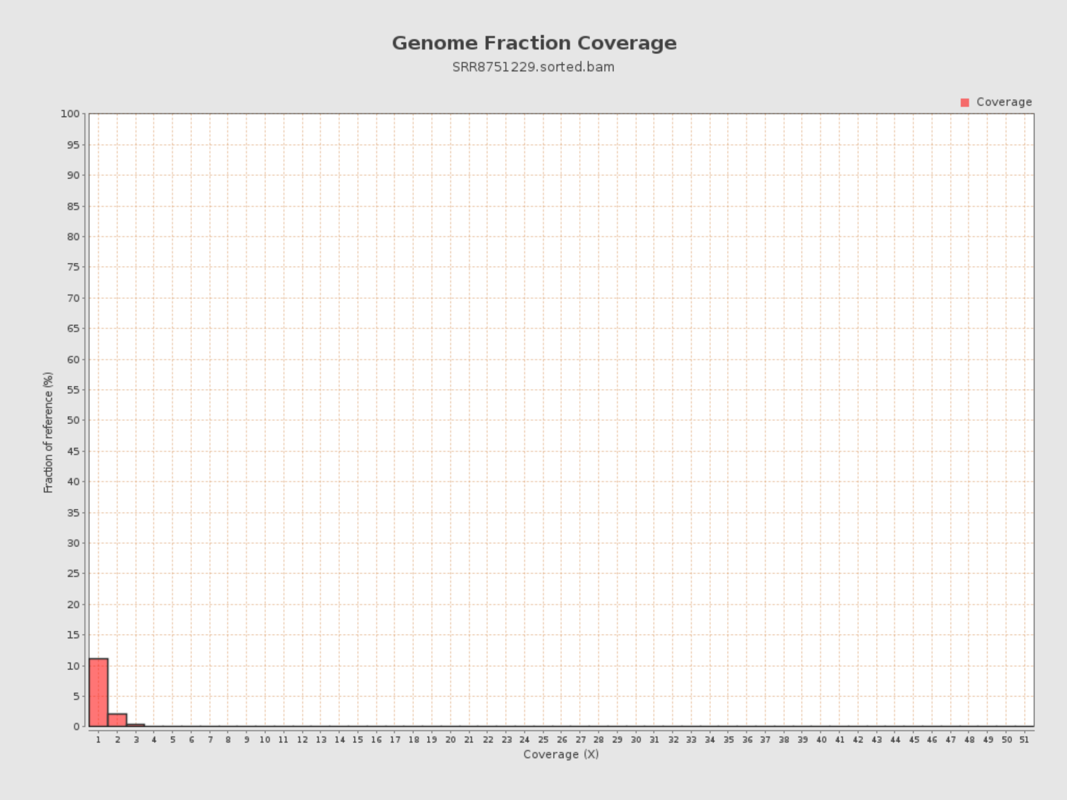
4. Results : Coverage Histogram



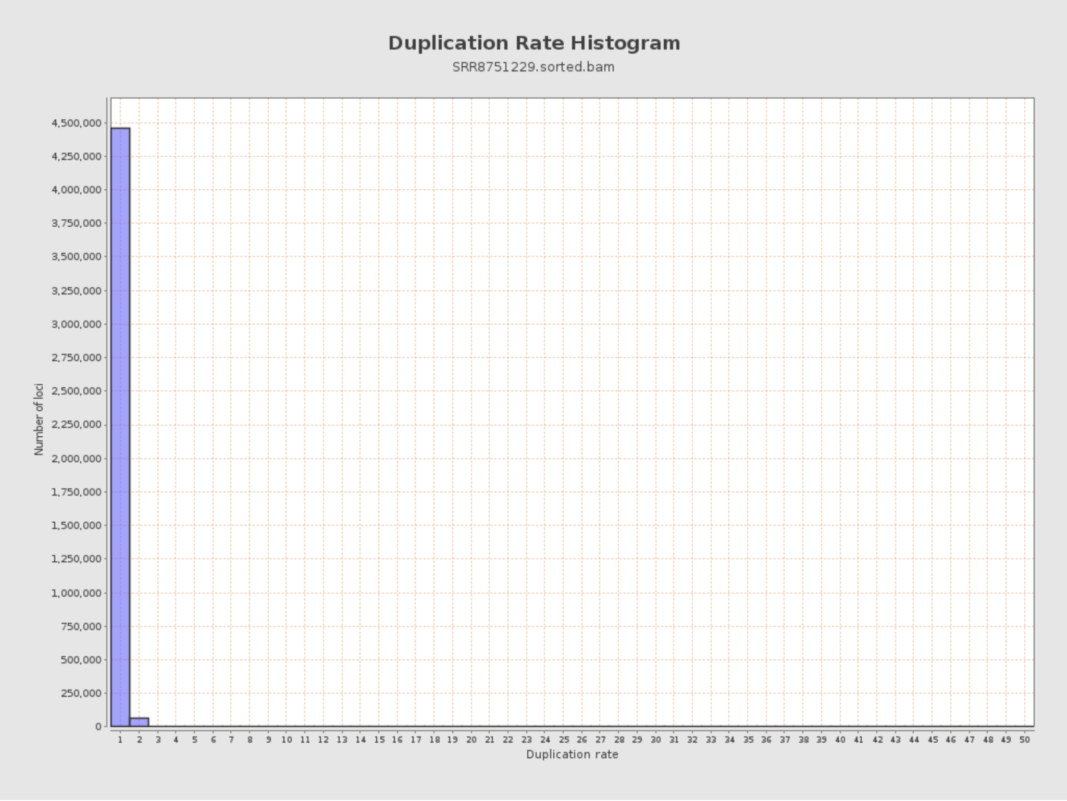
5. Results : Coverage Histogram (0-50X)



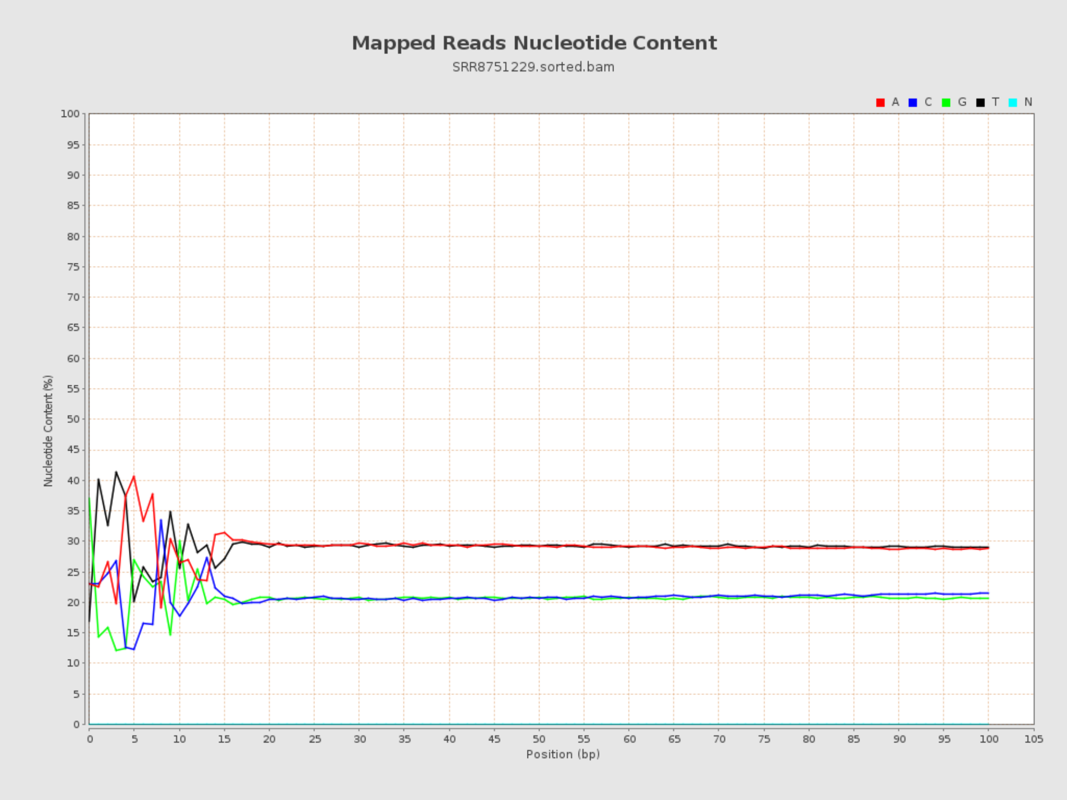
6. Results : Genome Fraction Coverage



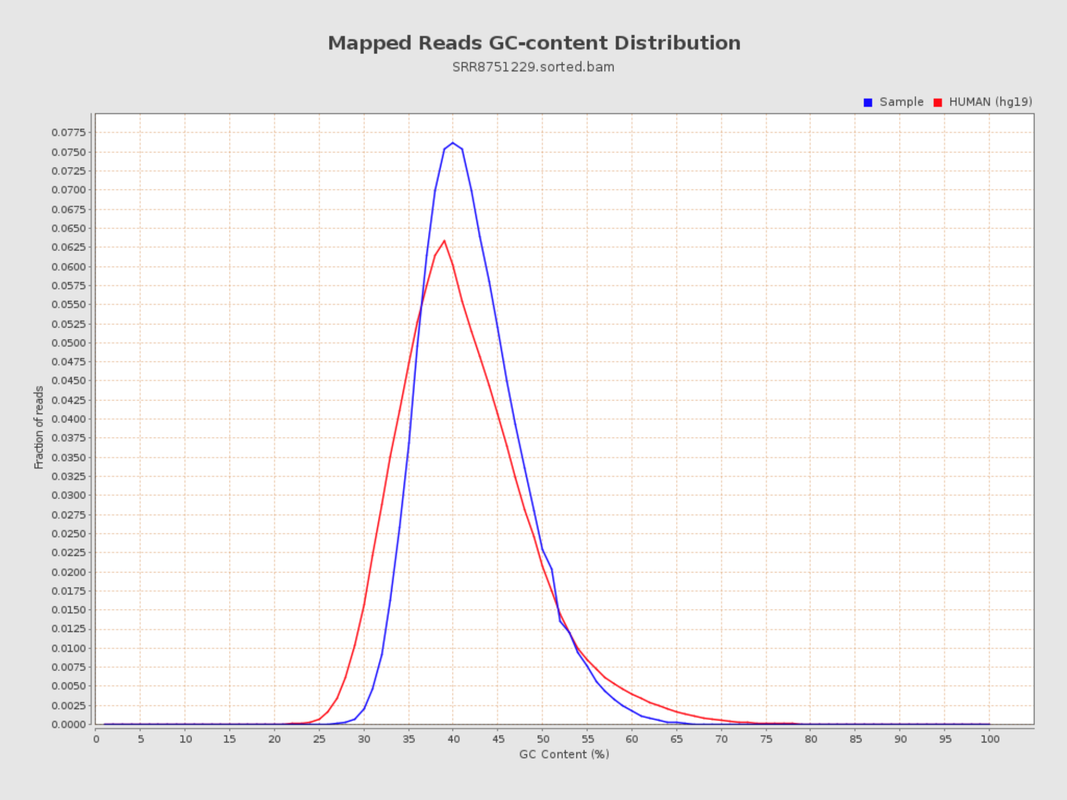
7. Results : Duplication Rate Histogram



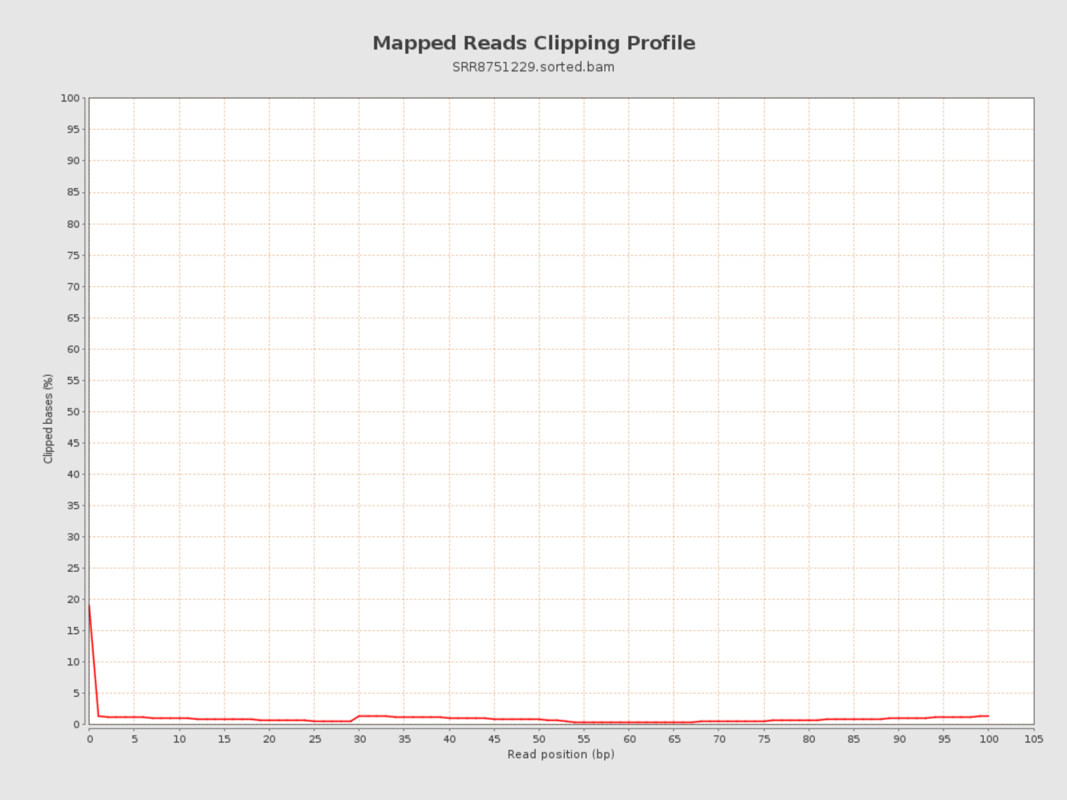
8. Results : Mapped Reads Nucleotide Content



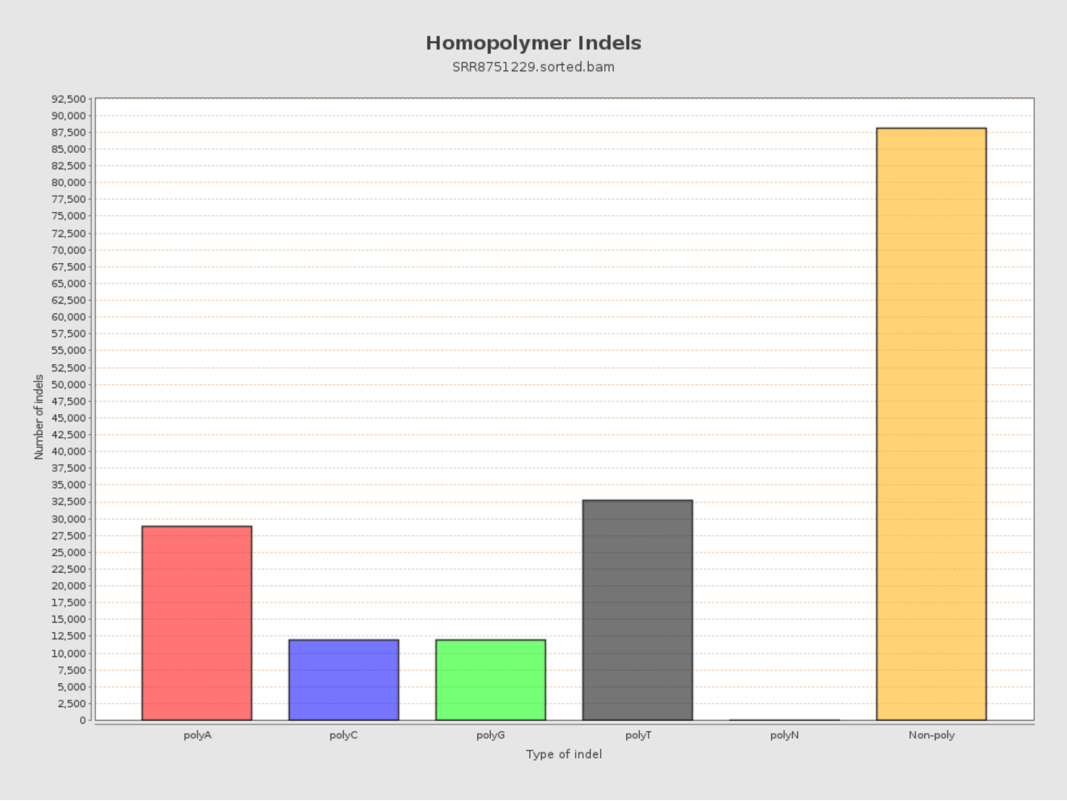
9. Results : Mapped Reads GC-content Distribution



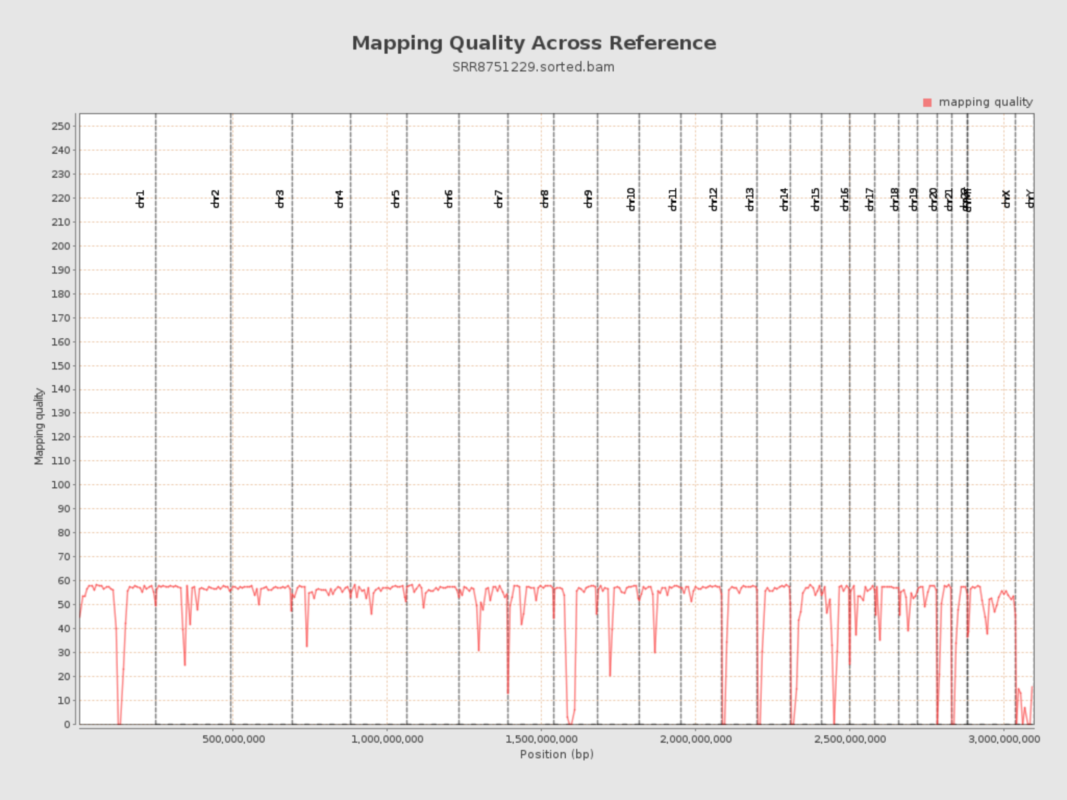
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram