Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 17:29:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751189.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_SRR8751189 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751189.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 17:29:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751189.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,381,905
Mapped reads	4,979,199 / 92.52%
Unmapped reads	402,706 / 7.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	125,034 / 2.32%
Read min/max/mean length	30 / 101 / 101.96
Duplicated reads (estimated)	129,509 / 2.41%
Duplication rate	1.51%
Clipped reads	797,334 / 14.82%

2.2. ACGT Content

Number/percentage of A's	143,426,747 / 29.26%
Number/percentage of C's	101,764,154 / 20.76%
Number/percentage of T's	143,910,207 / 29.36%
Number/percentage of G's	101,006,834 / 20.61%
Number/percentage of N's	2,758 / 0%
GC Percentage	41.37%

2.3. Coverage

Mean	0.1584

Standard Deviation	1.3244

2.4. Mapping Quality

Mean Mapping Quality	51.35

2.5. Mismatches and indels

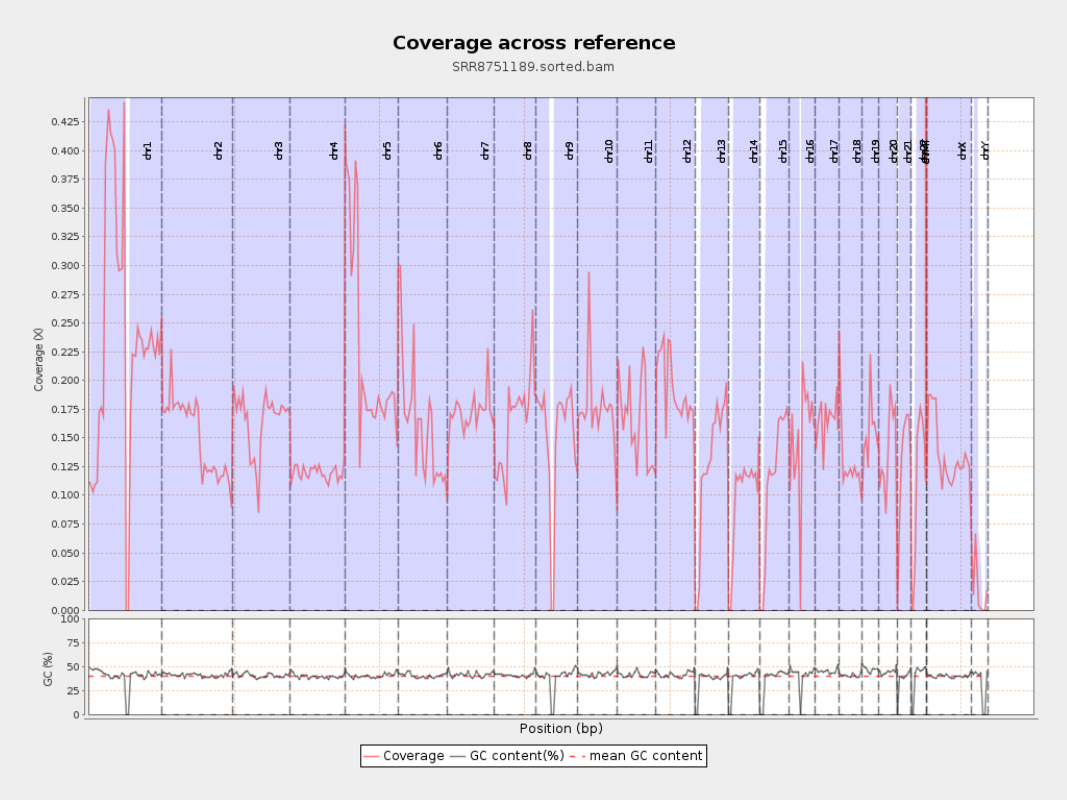
General error rate	0.37%
Mismatches	1,683,792
Insertions	76,174
Mapped reads with at least one insertion	1.51%
Deletions	61,773
Mapped reads with at least one deletion	1.22%
Homopolymer indels	47.04%

2.6. Chromosome stats

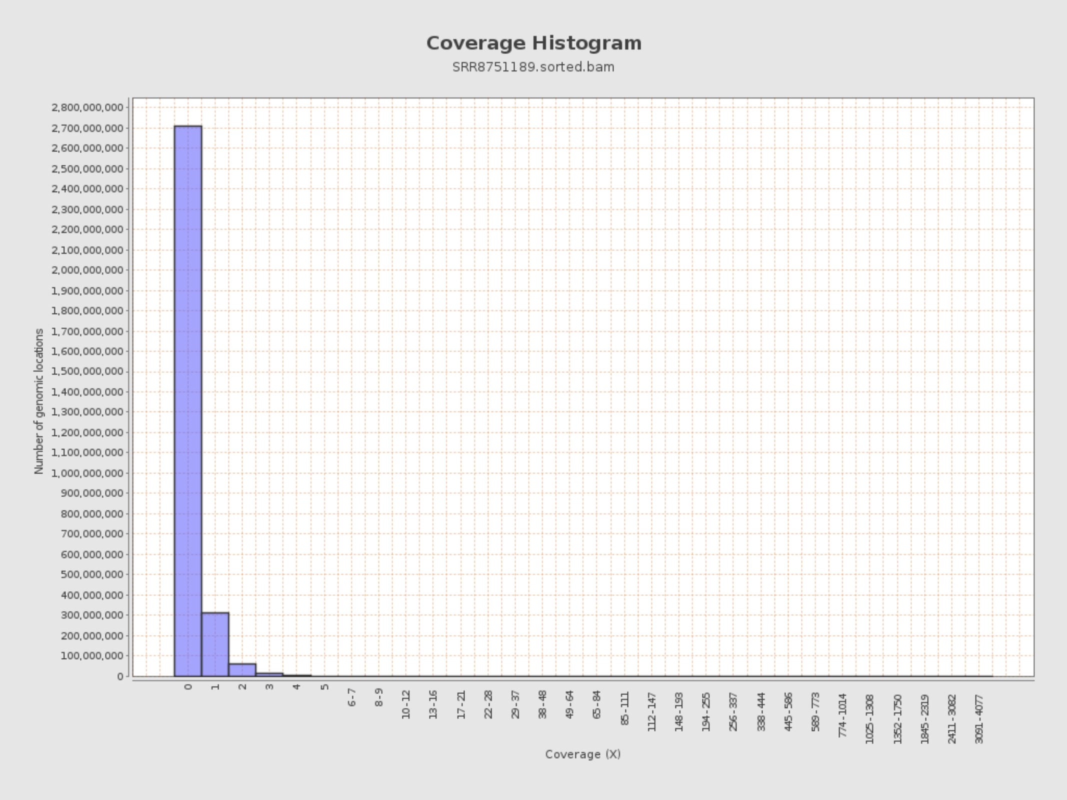
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	58568019	0.235	3.8106
chr2	243199373	36673897	0.1508	0.5463
chr3	198022430	32621077	0.1647	0.4924
chr4	191154276	22831383	0.1194	0.4442
chr5	180915260	40162568	0.222	0.5529
chr6	171115067	27907925	0.1631	0.8911
chr7	159138663	27535205	0.173	0.7106

chr8	146364022	24238649	0.1656	0.523
chr9	141213431	21208496	0.1502	0.63
chr10	135534747	23935149	0.1766	1.5416
chr11	135006516	22165353	0.1642	0.6911
chr12	133851895	25846454	0.1931	0.5107
chr13	115169878	14604557	0.1268	0.4115
chr14	107349540	10332894	0.0963	0.367
chr15	102531392	11785507	0.1149	0.3917
chr16	90354753	13456282	0.1489	0.7541
chr17	81195210	13406371	0.1651	0.6901
chr18	78077248	10060054	0.1288	1.1253
chr19	59128983	9164035	0.155	2.5344
chr20	63025520	8691498	0.1379	0.4383
chr21	48129895	6096047	0.1267	0.4514
chr22	51304566	5553713	0.1082	0.3856
chrMT	16571	1473222	88.9036	37.1478
chrX	155270560	20941504	0.1349	0.4895
chrY	59373566	985480	0.0166	0.5807

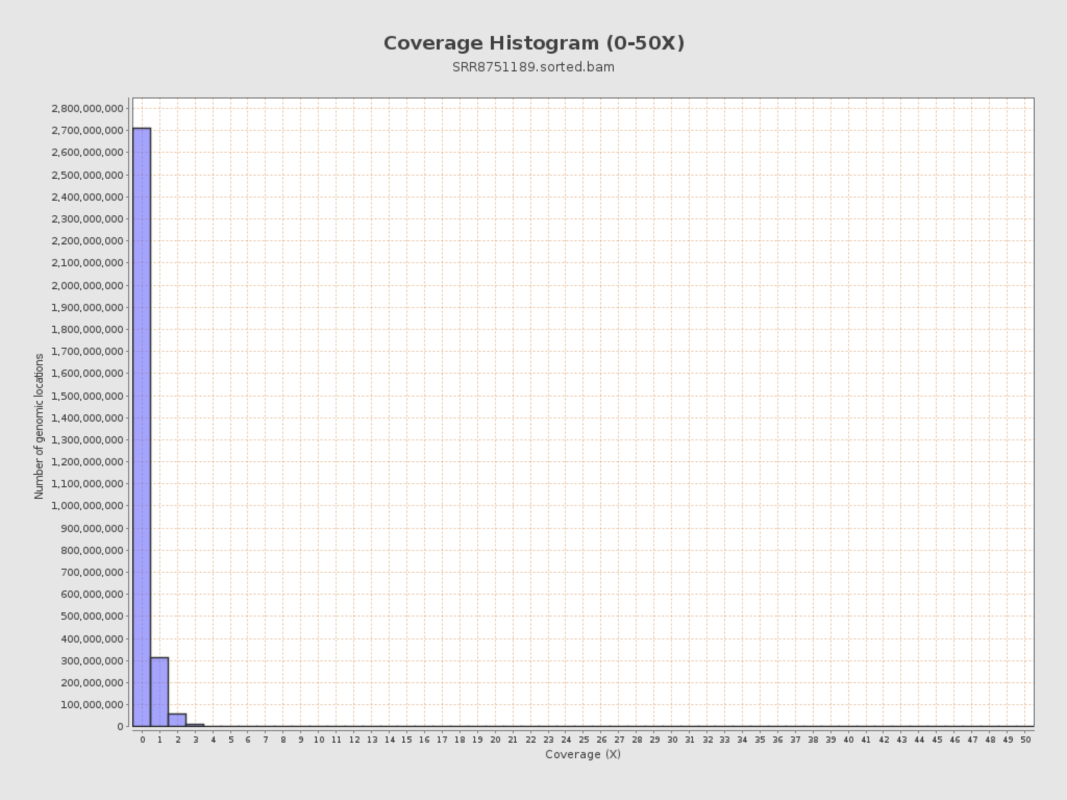
3. Results : Coverage across reference



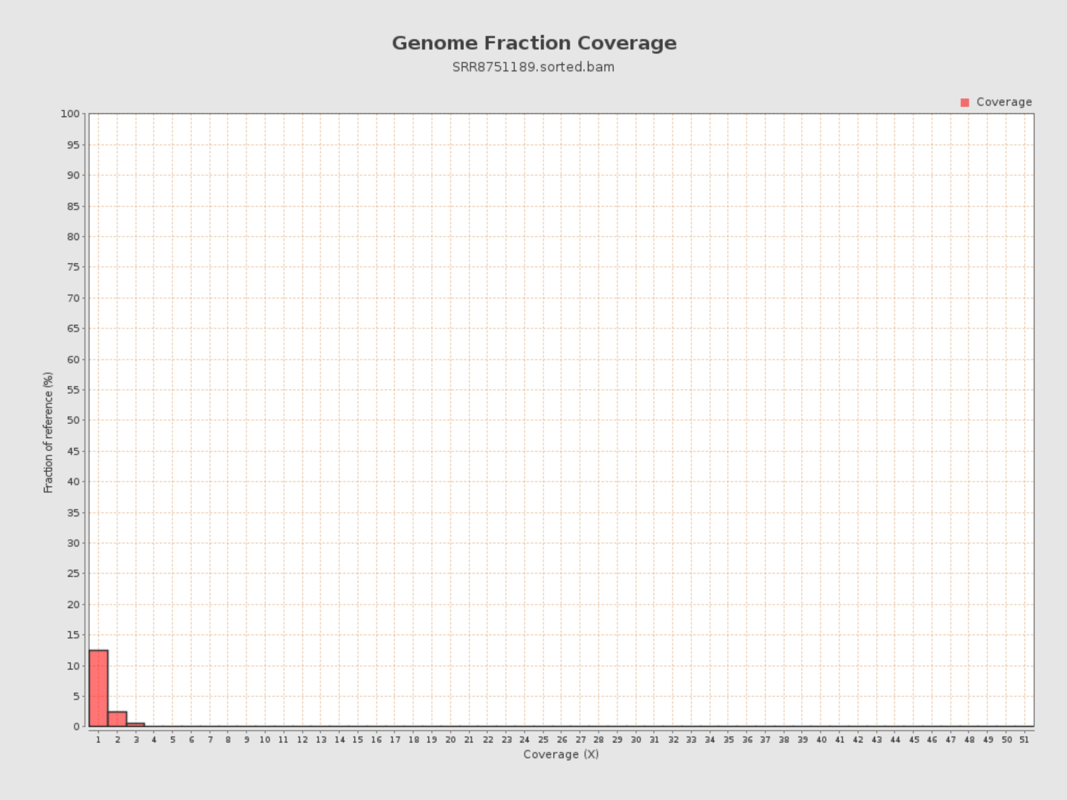
4. Results : Coverage Histogram



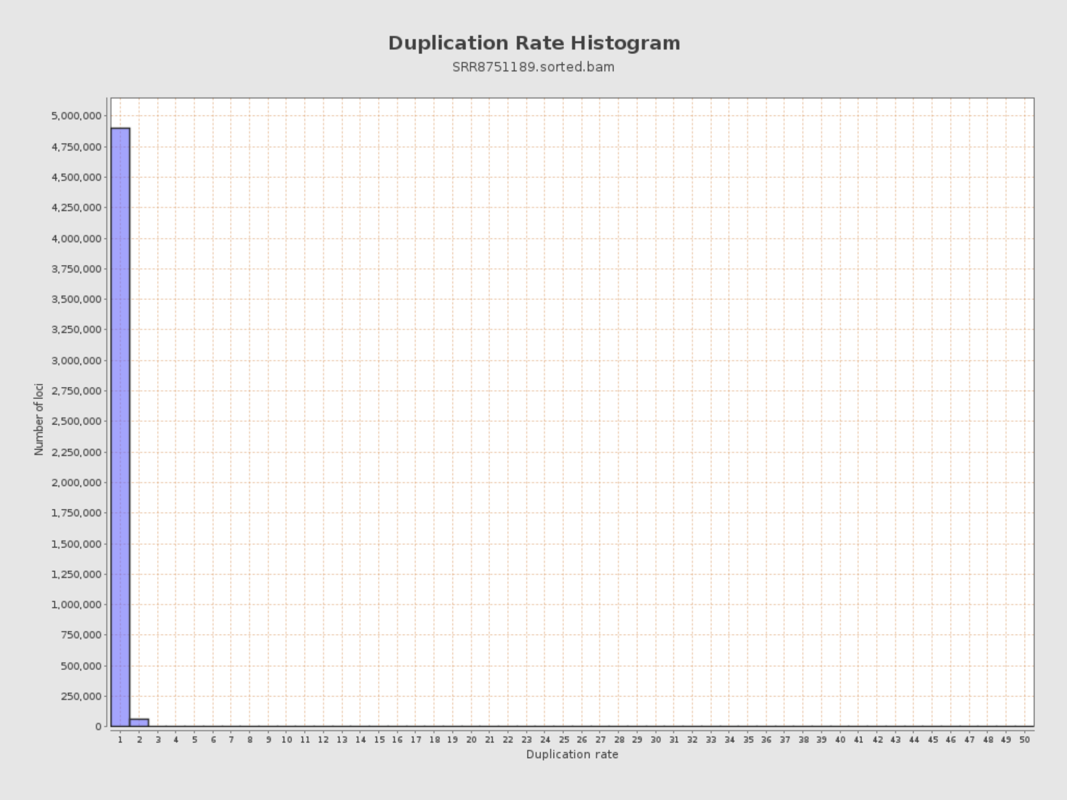
5. Results : Coverage Histogram (0-50X)



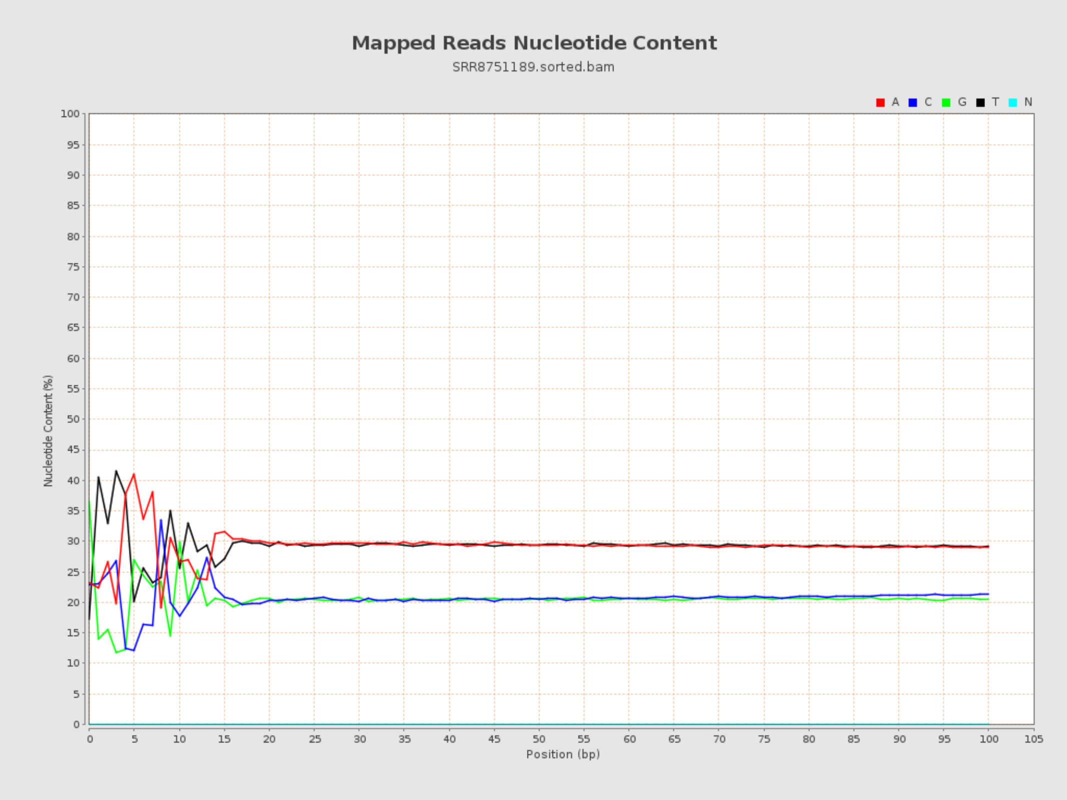
6. Results : Genome Fraction Coverage



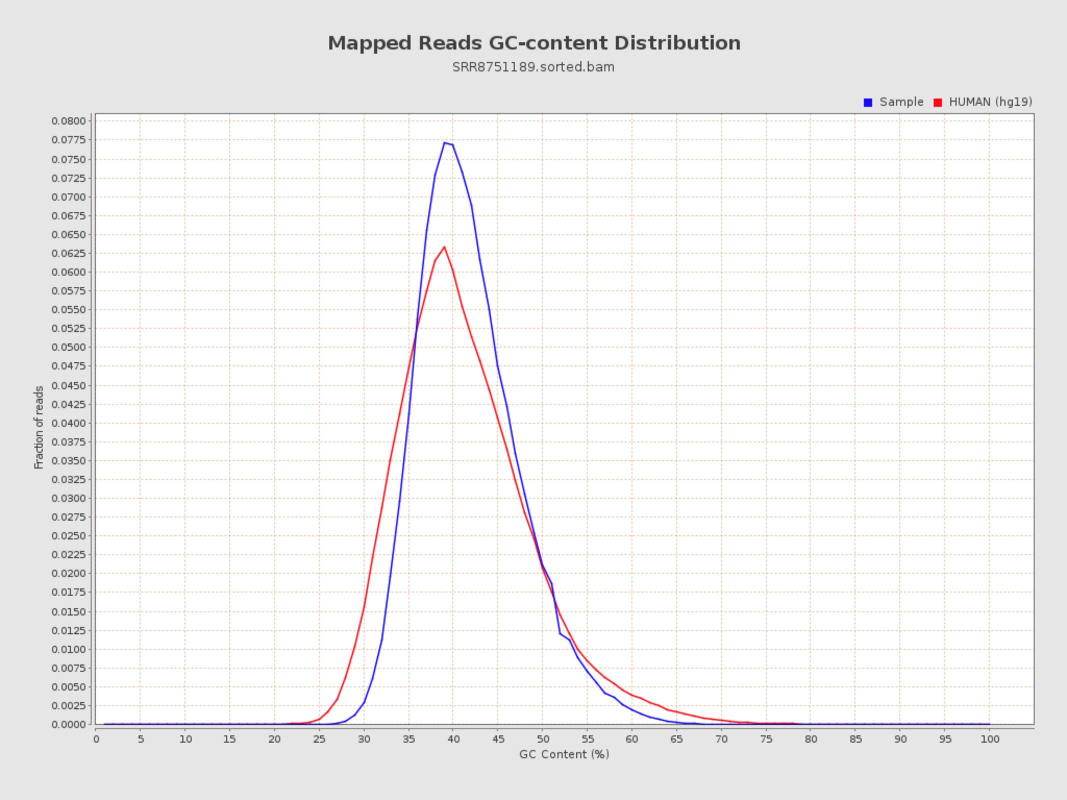
7. Results : Duplication Rate Histogram



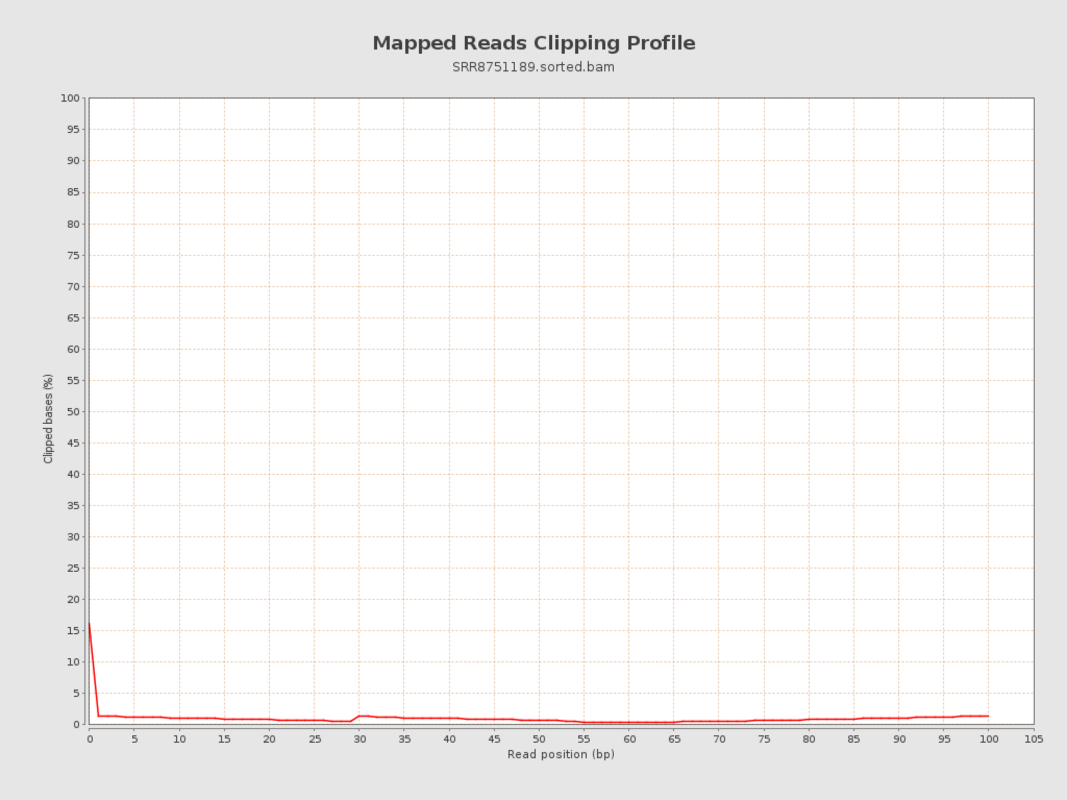
8. Results : Mapped Reads Nucleotide Content



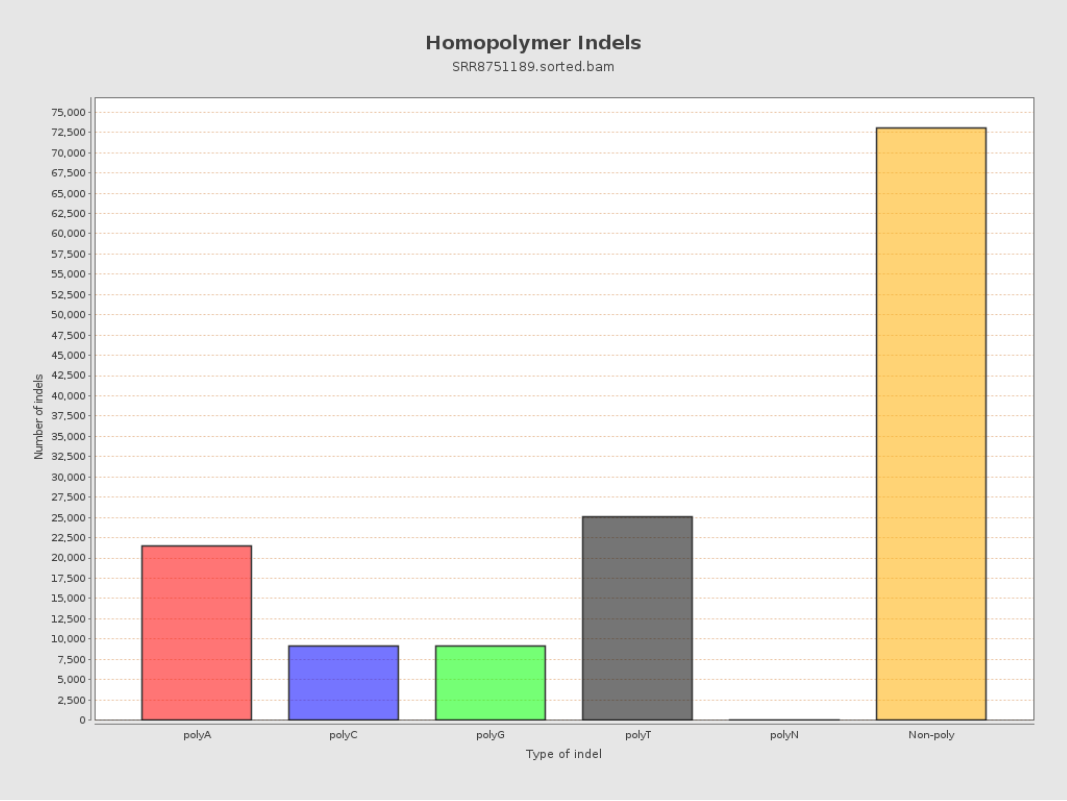
9. Results : Mapped Reads GC-content Distribution



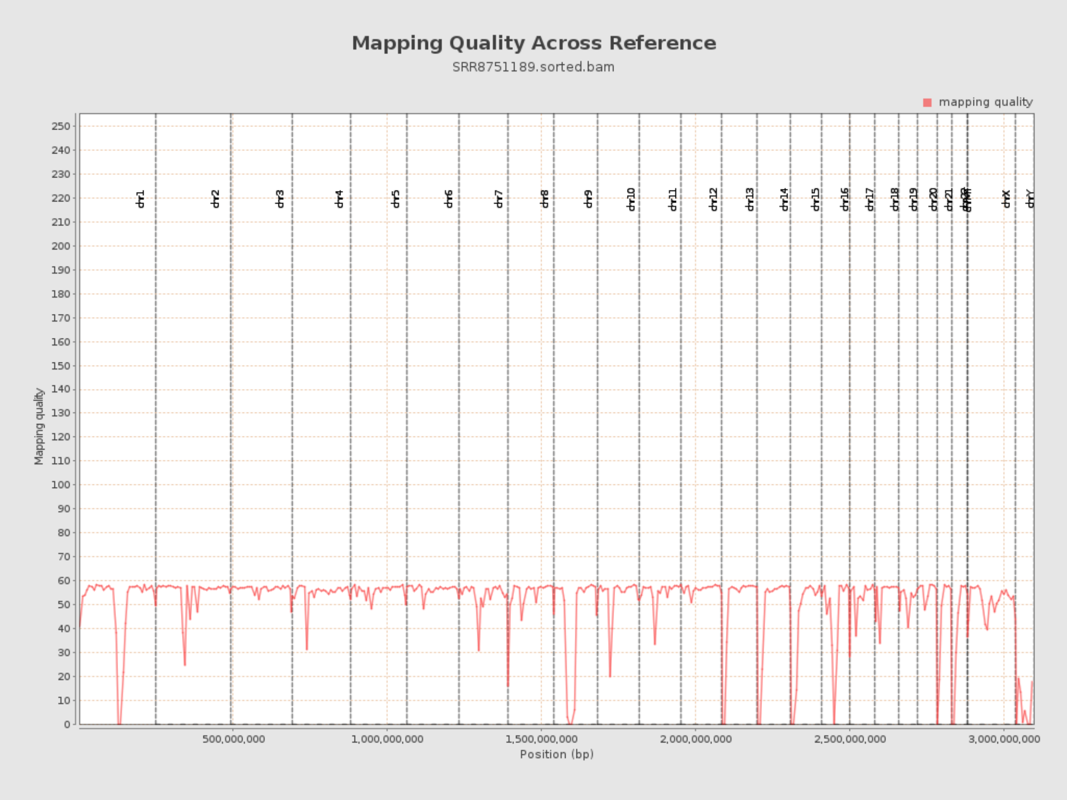
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram