Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 17:53:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751192.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_SRR8751192 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751192.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 17:53:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751192.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,125,124
Mapped reads	6,899,603 / 96.83%
Unmapped reads	225,521 / 3.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	175,341 / 2.46%
Read min/max/mean length	30 / 101 / 102.02
Duplicated reads (estimated)	168,970 / 2.37%
Duplication rate	1.66%
Clipped reads	1,245,110 / 17.47%

2.2. ACGT Content

Number/percentage of A's	196,363,840 / 29.04%
Number/percentage of C's	141,885,324 / 20.98%
Number/percentage of T's	197,496,636 / 29.21%
Number/percentage of G's	140,435,322 / 20.77%
Number/percentage of N's	3,648 / 0%
GC Percentage	41.75%

2.3. Coverage

Mean	0.2185

Standard Deviation	1.326

2.4. Mapping Quality

Mean Mapping Quality	51.5

2.5. Mismatches and indels

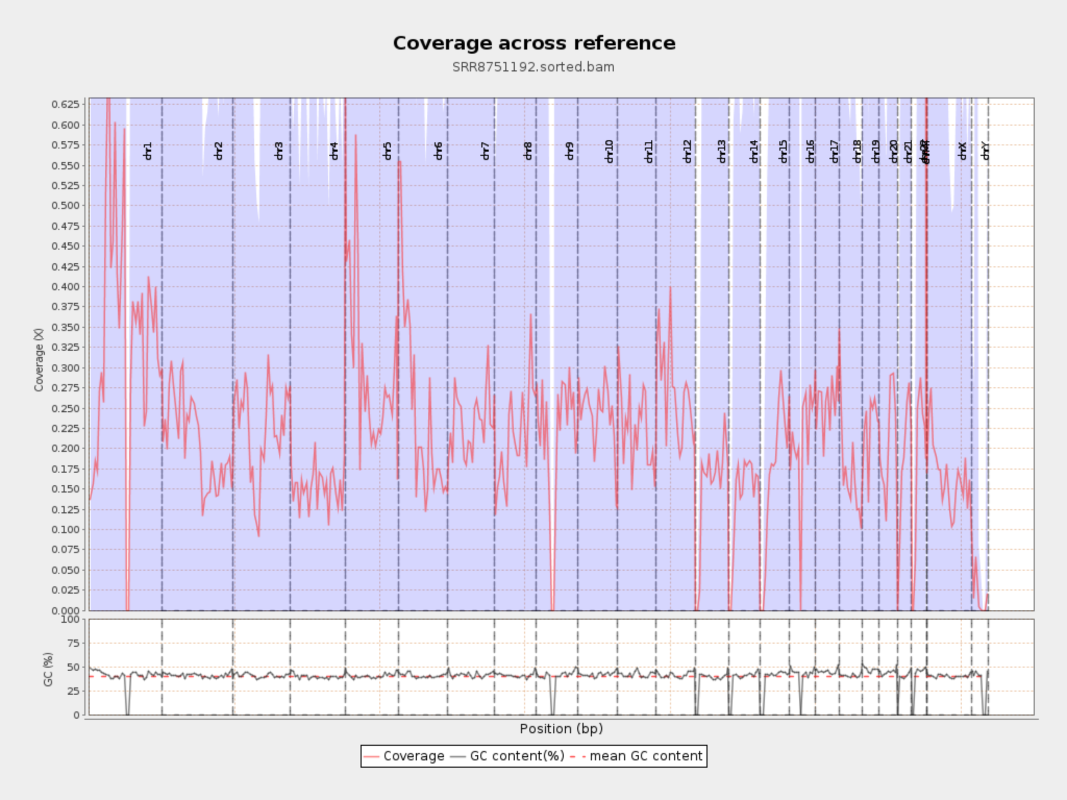
General error rate	0.35%
Mismatches	2,174,178
Insertions	109,905
Mapped reads with at least one insertion	1.57%
Deletions	84,960
Mapped reads with at least one deletion	1.21%
Homopolymer indels	47.26%

2.6. Chromosome stats

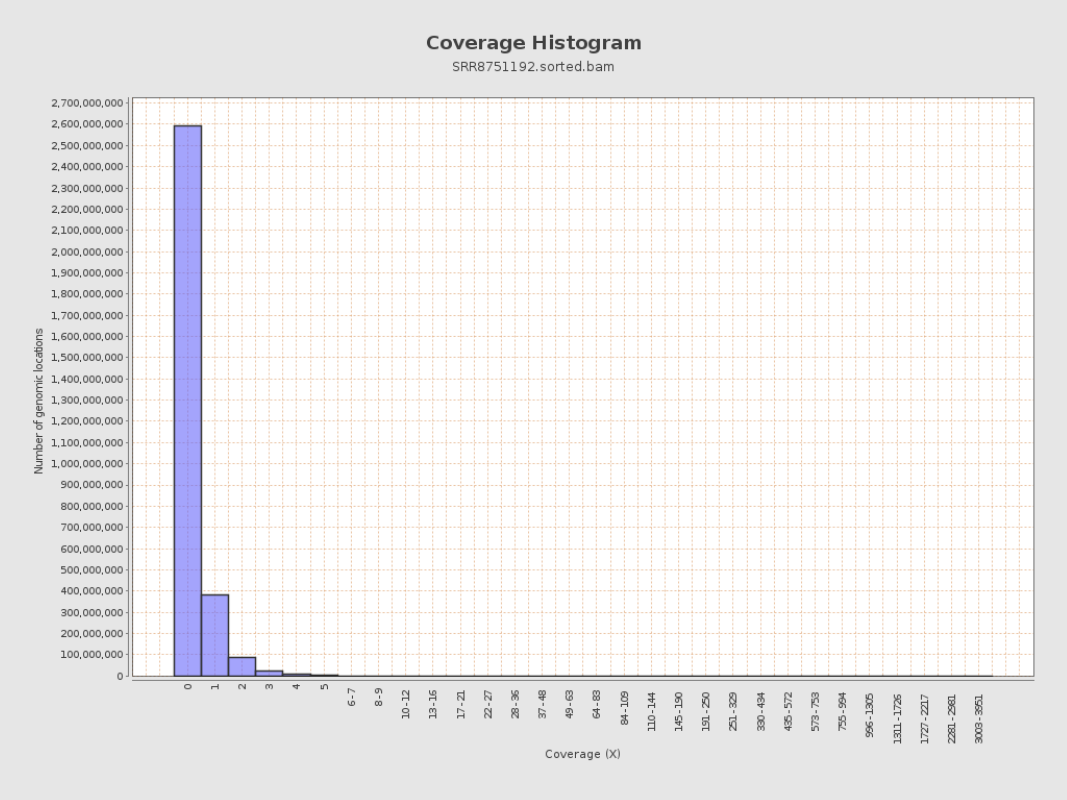
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	83943465	0.3368	3.6979
chr2	243199373	50667024	0.2083	0.6483
chr3	198022430	44364896	0.224	0.5732
chr4	191154276	29069335	0.1521	0.4939
chr5	180915260	53944258	0.2982	0.6671
chr6	171115067	42668369	0.2494	1.1576
chr7	159138663	37008855	0.2326	0.701

chr8	146364022	31491781	0.2152	0.6207
chr9	141213431	29347509	0.2078	0.7354
chr10	135534747	33322236	0.2459	1.2757
chr11	135006516	30267509	0.2242	0.7664
chr12	133851895	36625132	0.2736	0.6309
chr13	115169878	17406791	0.1511	0.4647
chr14	107349540	14713504	0.1371	0.4583
chr15	102531392	17206114	0.1678	0.4919
chr16	90354753	18810928	0.2082	0.7335
chr17	81195210	20685083	0.2548	0.8343
chr18	78077248	13207965	0.1692	1.3376
chr19	59128983	13385979	0.2264	2.6997
chr20	63025520	12851166	0.2039	0.5515
chr21	48129895	8729075	0.1814	0.5441
chr22	51304566	8647377	0.1685	0.5062
chrMT	16571	1008413	60.8541	26.1204
chrX	155270560	25859863	0.1665	0.5408
chrY	59373566	1138114	0.0192	0.6369

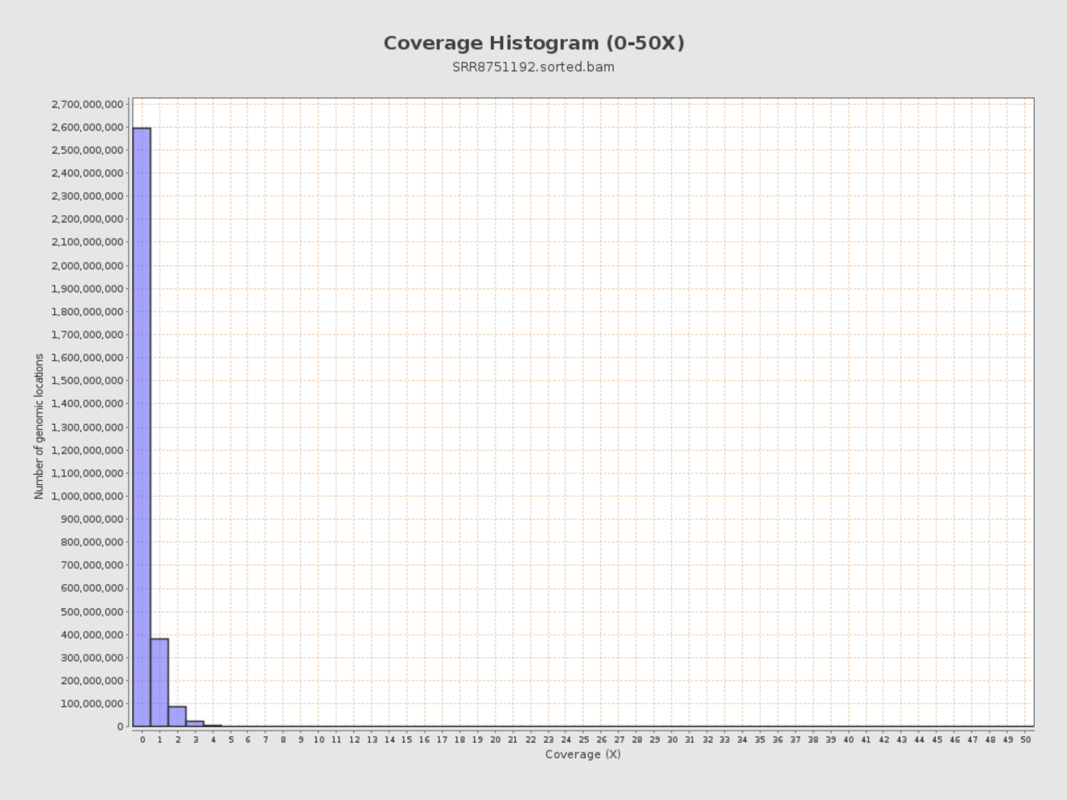
3. Results : Coverage across reference



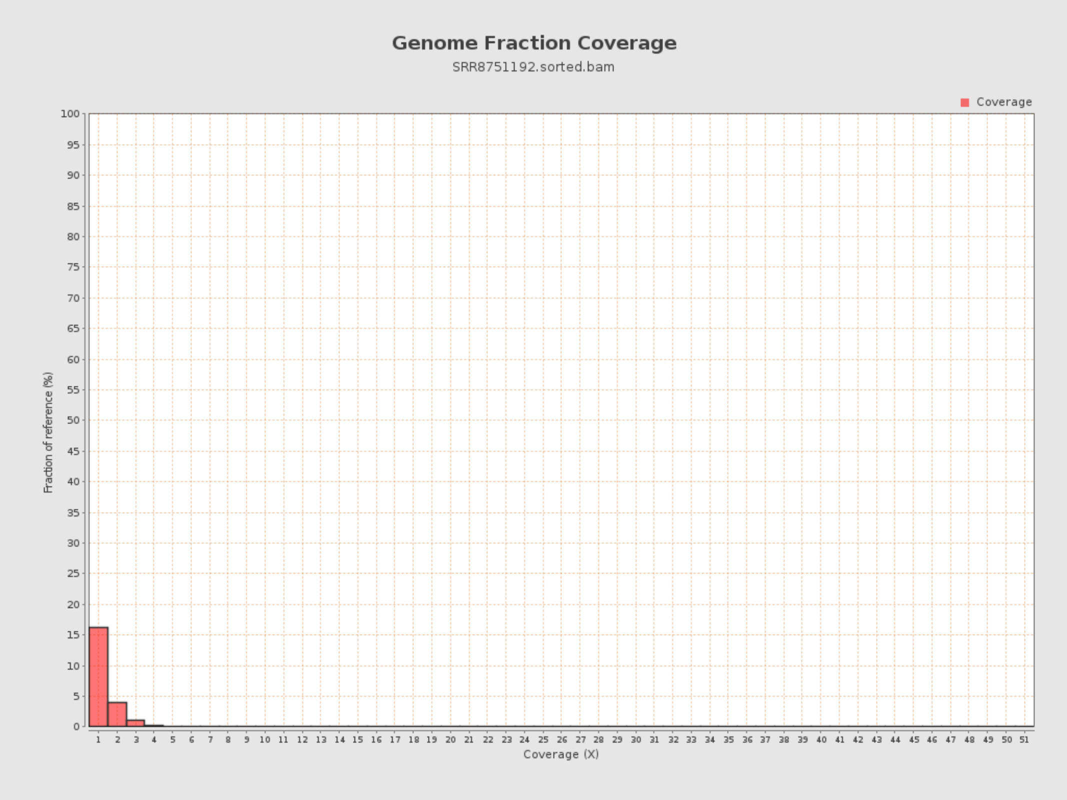
4. Results : Coverage Histogram



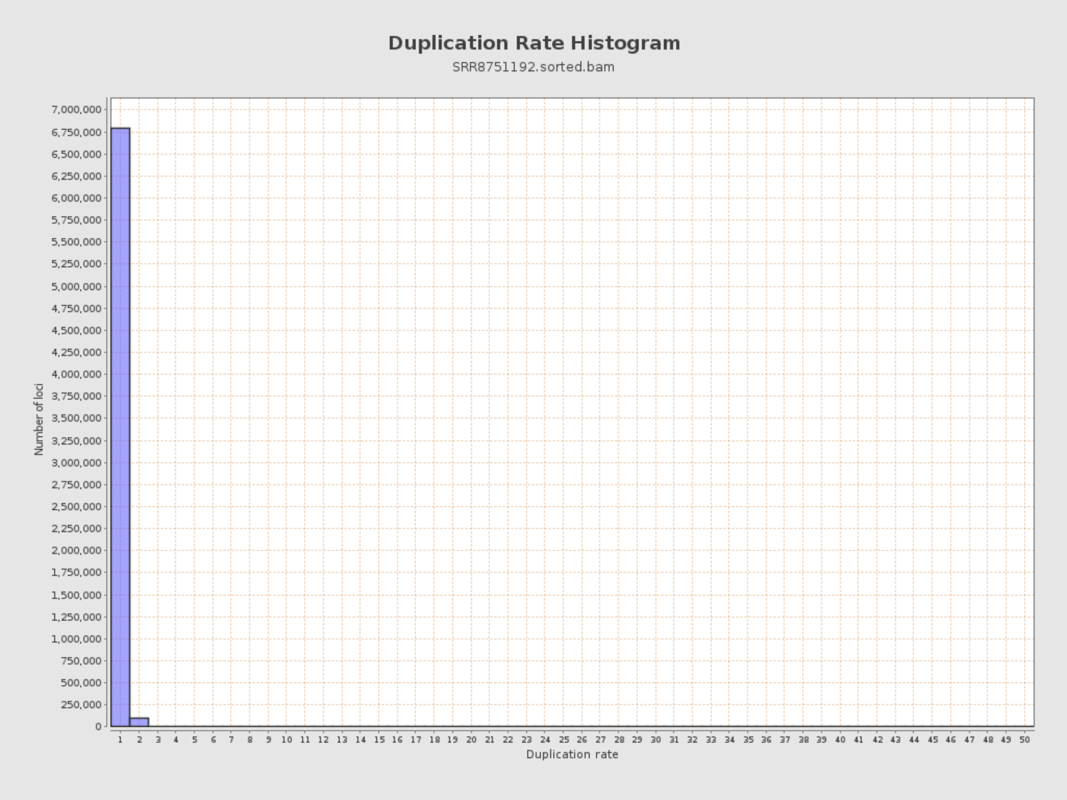
5. Results : Coverage Histogram (0-50X)



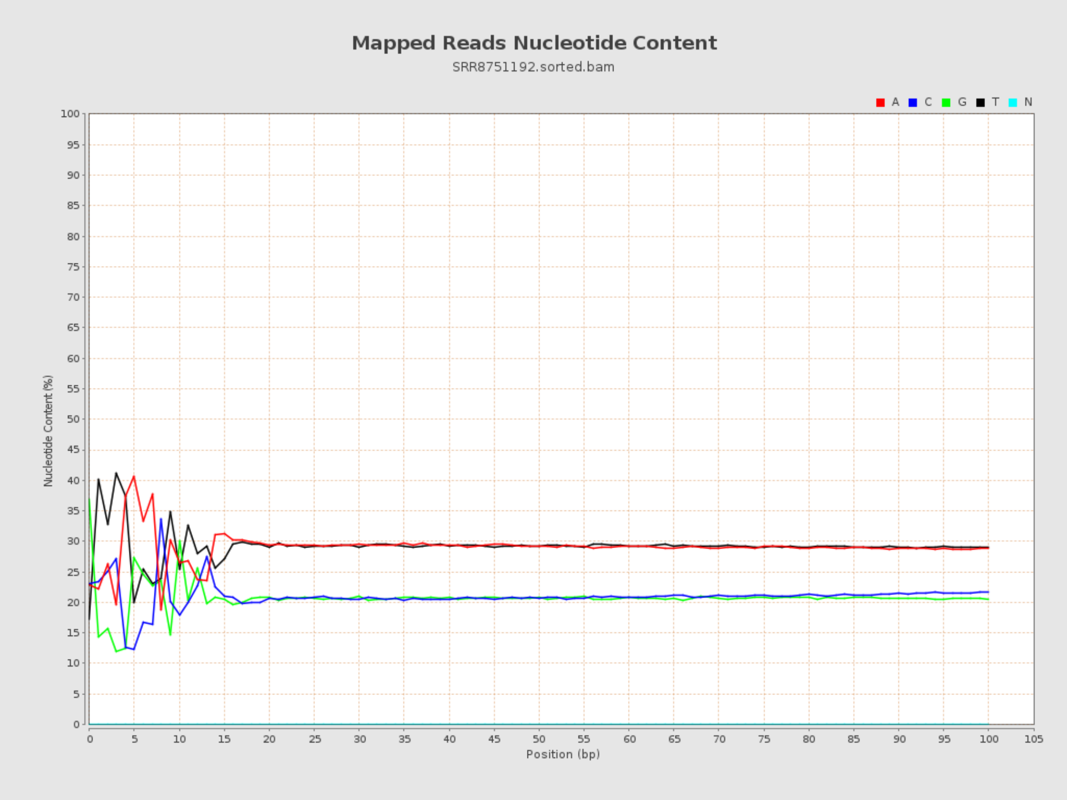
6. Results : Genome Fraction Coverage



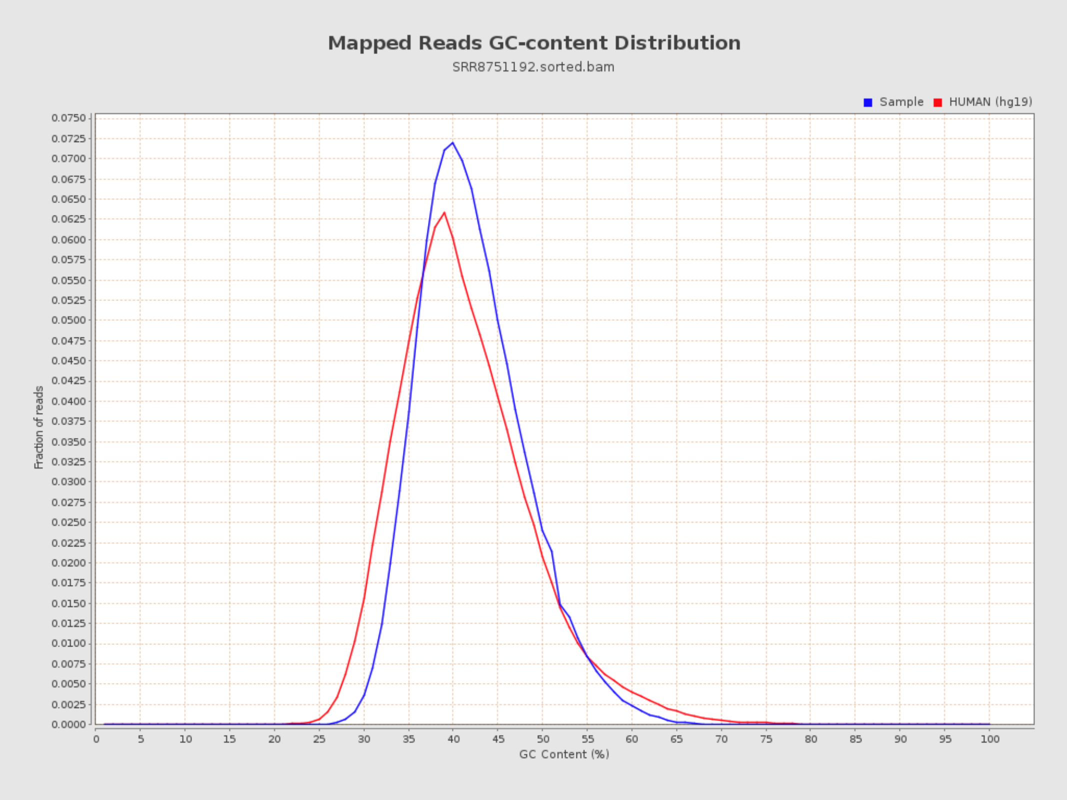
7. Results : Duplication Rate Histogram



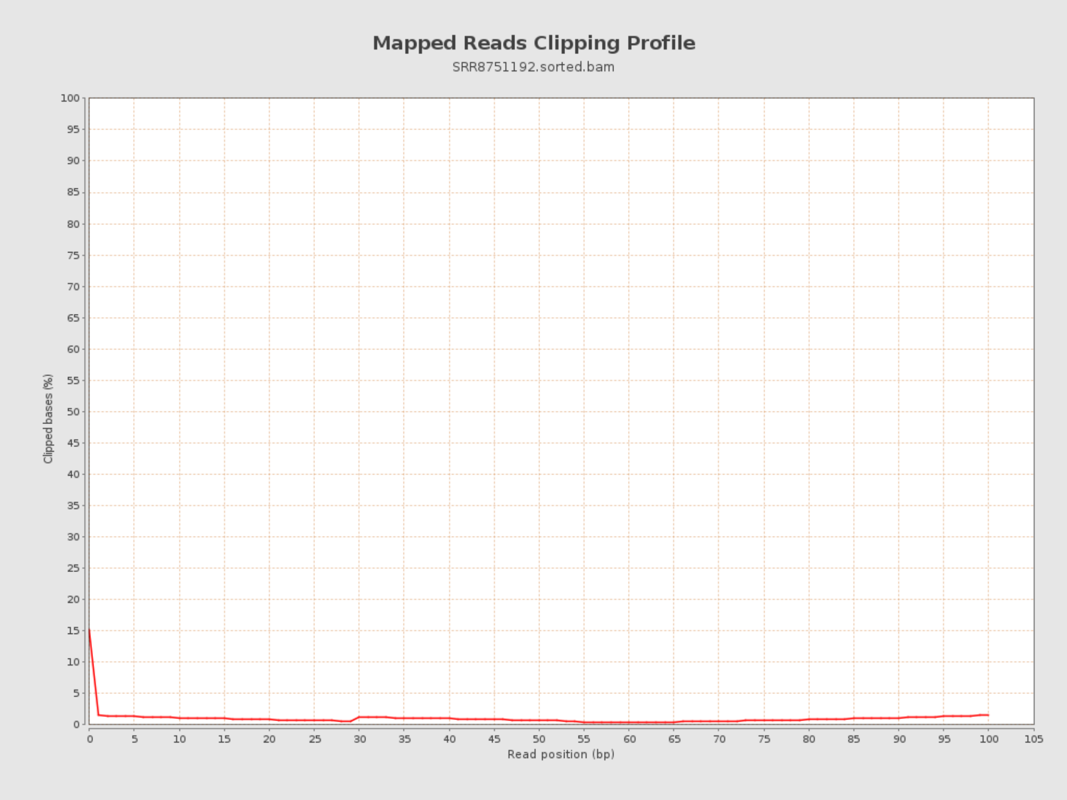
8. Results : Mapped Reads Nucleotide Content



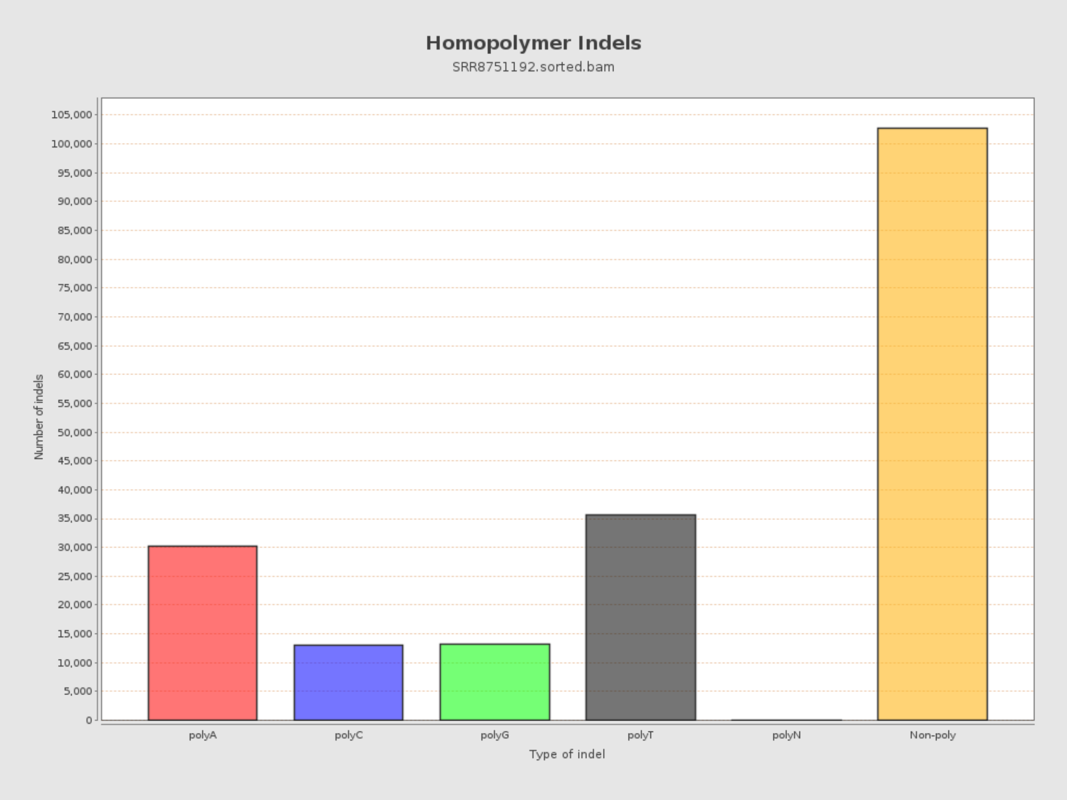
9. Results : Mapped Reads GC-content Distribution



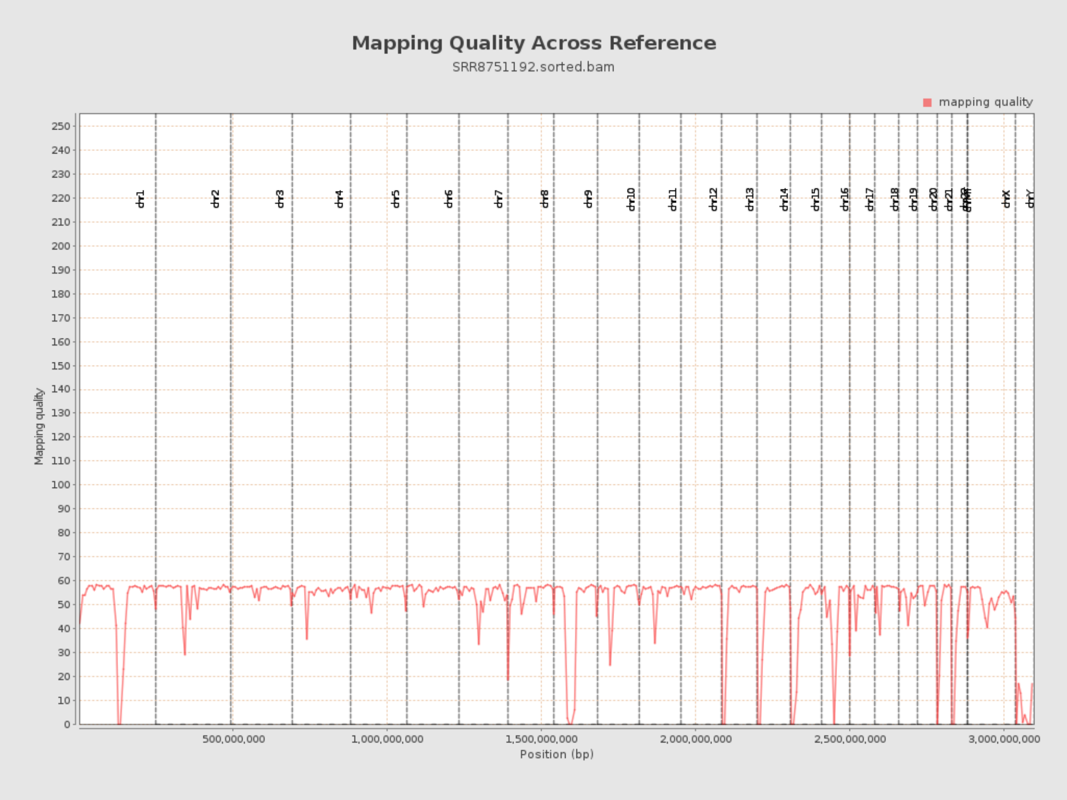
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram