Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 22:54:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505992.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_SRR1505992 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505992.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 22:54:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505992.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,139,615
Mapped reads	3,607,738 / 70.19%
Unmapped reads	1,531,877 / 29.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	202 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	223,664 / 4.35%
Duplication rate	4.74%
Clipped reads	434,554 / 8.45%

2.2. ACGT Content

Number/percentage of A's	50,453,585 / 29.85%
Number/percentage of C's	33,170,186 / 19.62%
Number/percentage of T's	50,794,756 / 30.05%
Number/percentage of G's	34,074,183 / 20.16%
Number/percentage of N's	548,656 / 0.32%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0546

Standard Deviation	0.5472

2.4. Mapping Quality

Mean Mapping Quality	44.83

2.5. Mismatches and indels

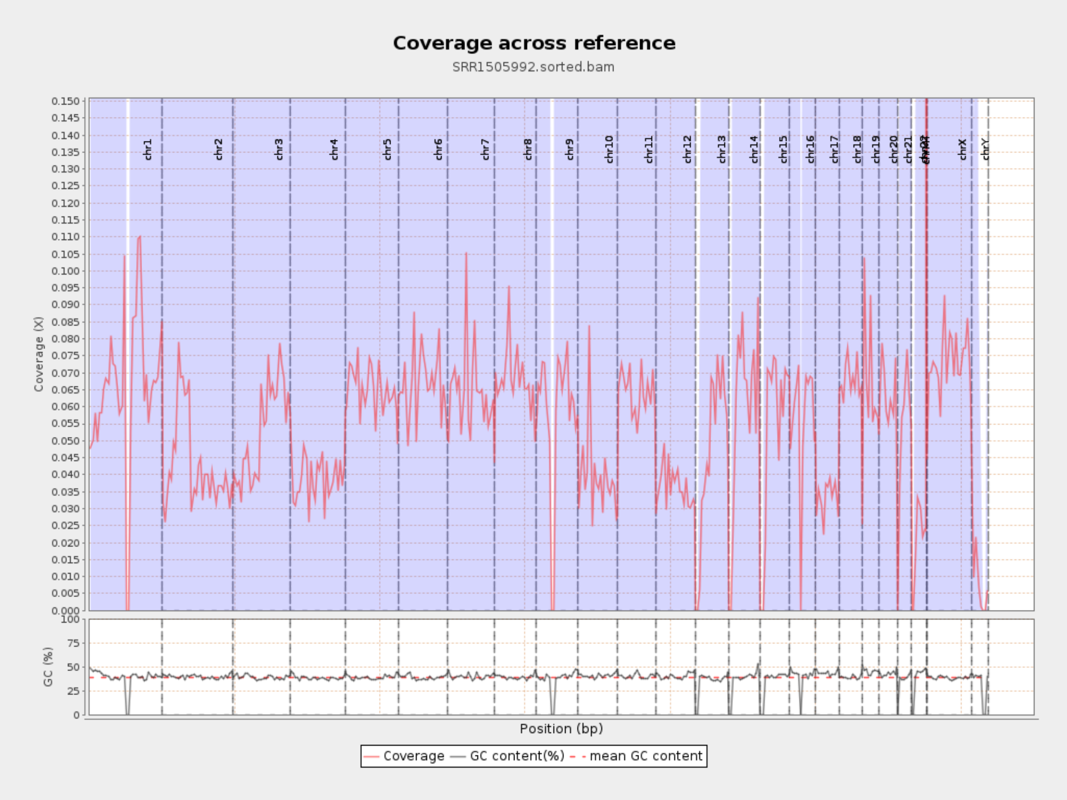
General error rate	0.8%
Mismatches	1,338,170
Insertions	8,066
Mapped reads with at least one insertion	0.22%
Deletions	27,213
Mapped reads with at least one deletion	0.75%
Homopolymer indels	46.34%

2.6. Chromosome stats

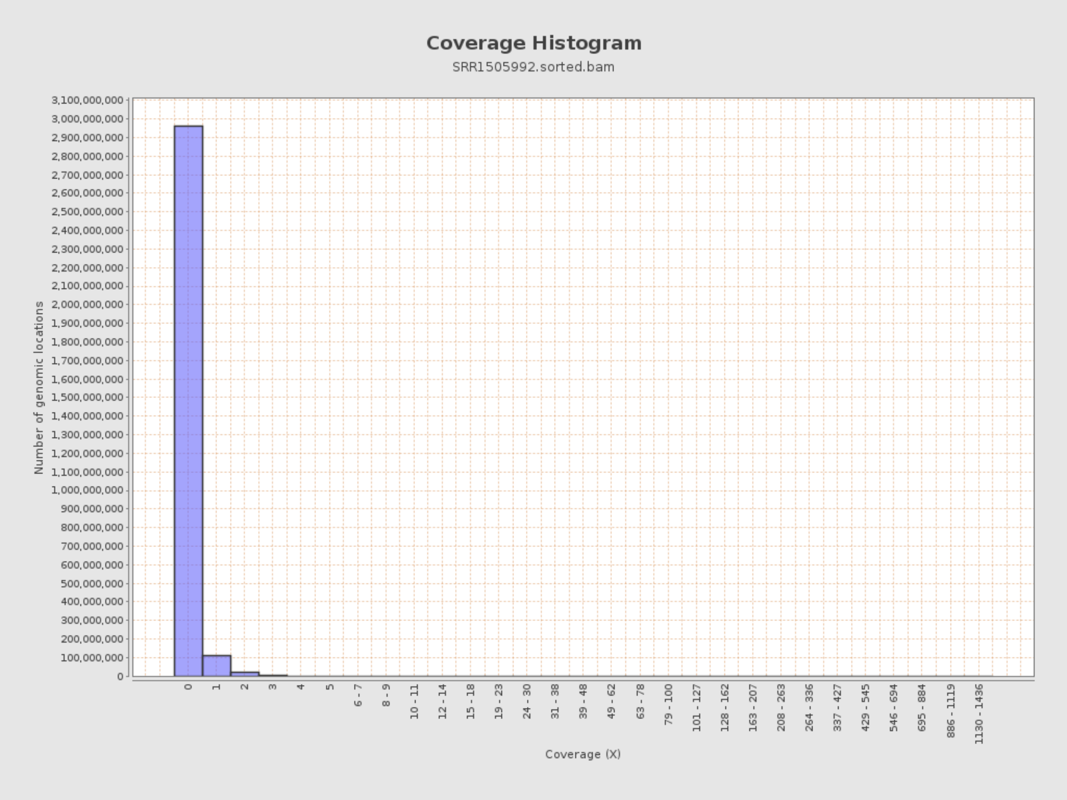
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16404662	0.0658	1.0451
chr2	243199373	10473009	0.0431	0.3586
chr3	198022430	10423960	0.0526	0.2801
chr4	191154276	7366854	0.0385	0.2446
chr5	180915260	11813186	0.0653	0.3154
chr6	171115067	11425001	0.0668	0.3781
chr7	159138663	10373754	0.0652	0.673

chr8	146364022	9997510	0.0683	0.6876
chr9	141213431	8206751	0.0581	0.3909
chr10	135534747	5369325	0.0396	0.4469
chr11	135006516	8574032	0.0635	0.4045
chr12	133851895	4877700	0.0364	0.2549
chr13	115169878	5347947	0.0464	0.2617
chr14	107349540	6341413	0.0591	1.3484
chr15	102531392	5511213	0.0538	0.2816
chr16	90354753	5099828	0.0564	0.3248
chr17	81195210	2683793	0.0331	0.2437
chr18	78077248	5317176	0.0681	0.6577
chr19	59128983	3988787	0.0675	0.7774
chr20	63025520	4044517	0.0642	0.3452
chr21	48129895	2552520	0.053	0.3074
chr22	51304566	1007700	0.0196	0.1644
chrMT	16571	45617	2.7528	2.4337
chrX	155270560	11351193	0.0731	0.3825
chrY	59373566	482053	0.0081	0.1379

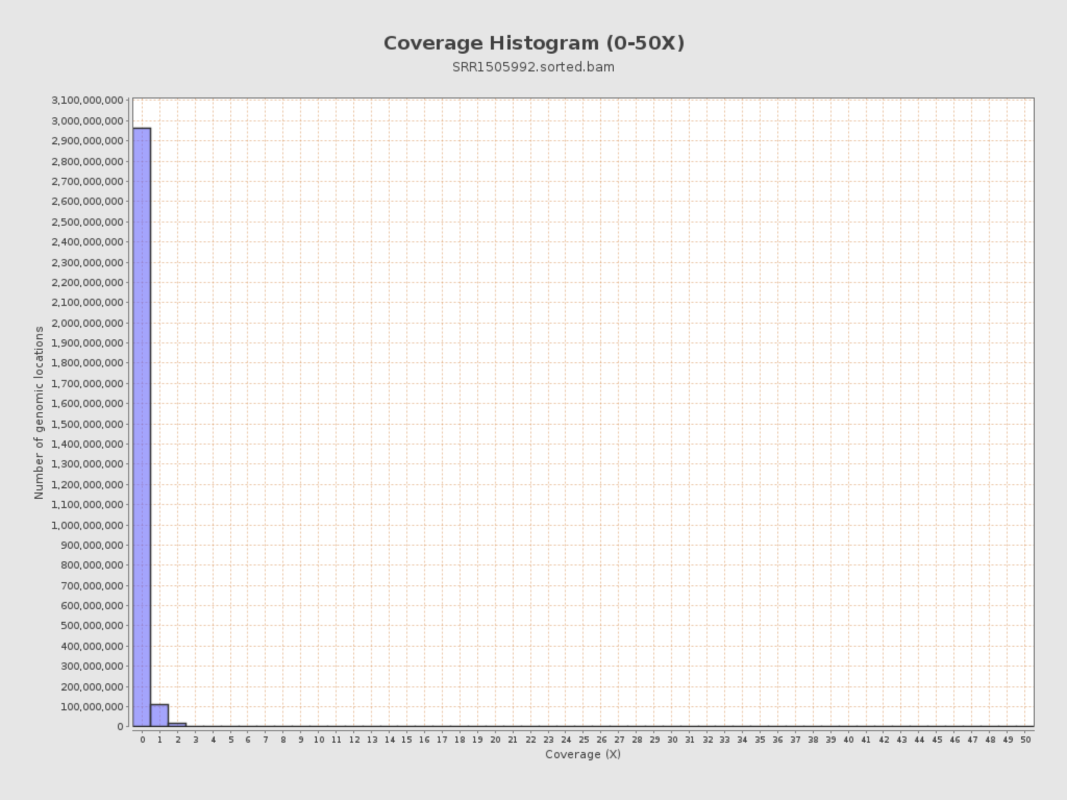
3. Results : Coverage across reference



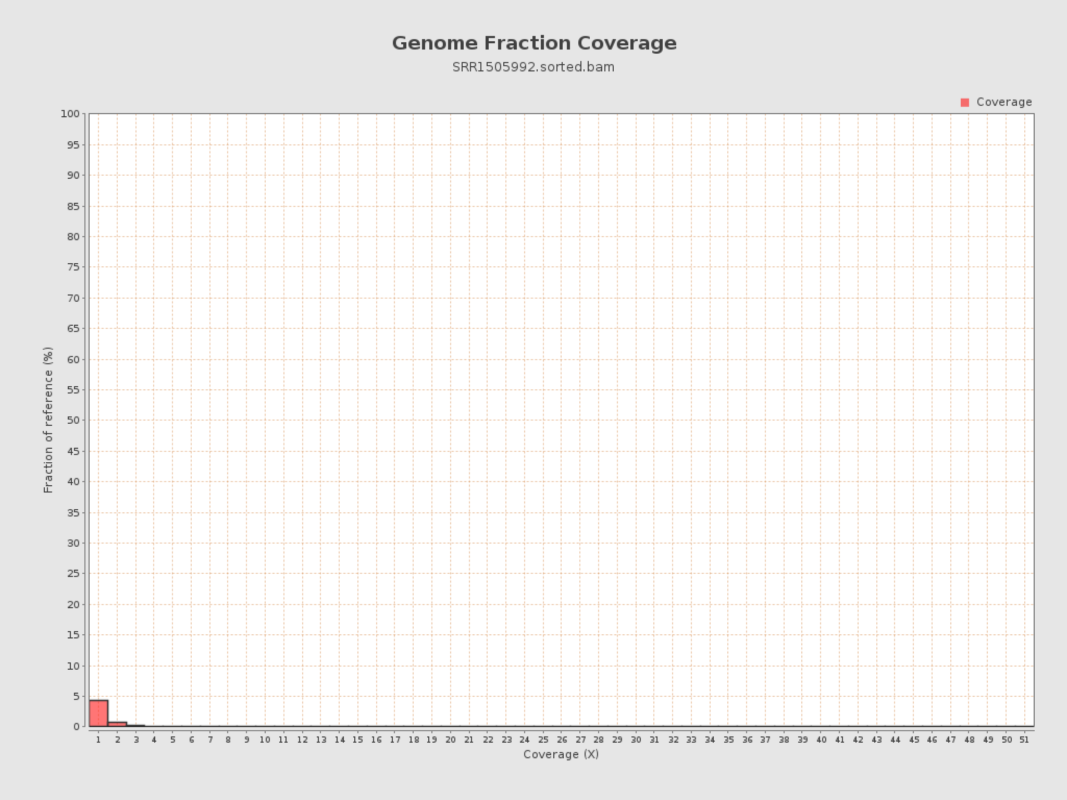
4. Results : Coverage Histogram



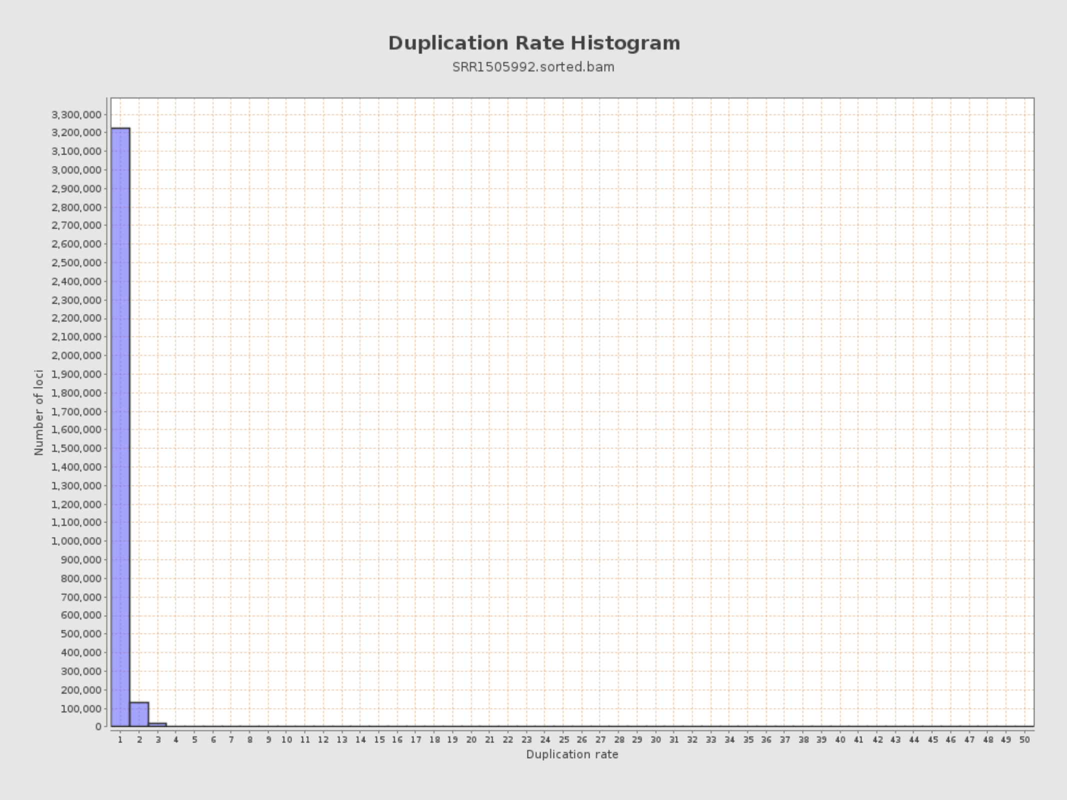
5. Results : Coverage Histogram (0-50X)



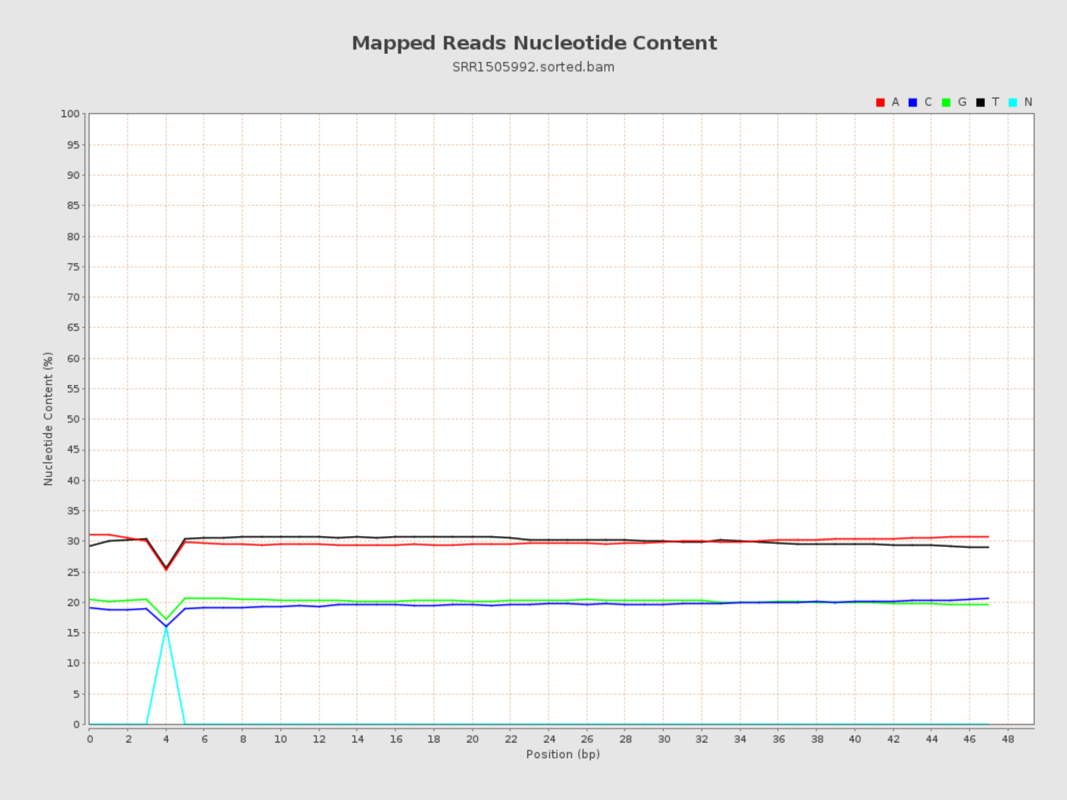
6. Results : Genome Fraction Coverage



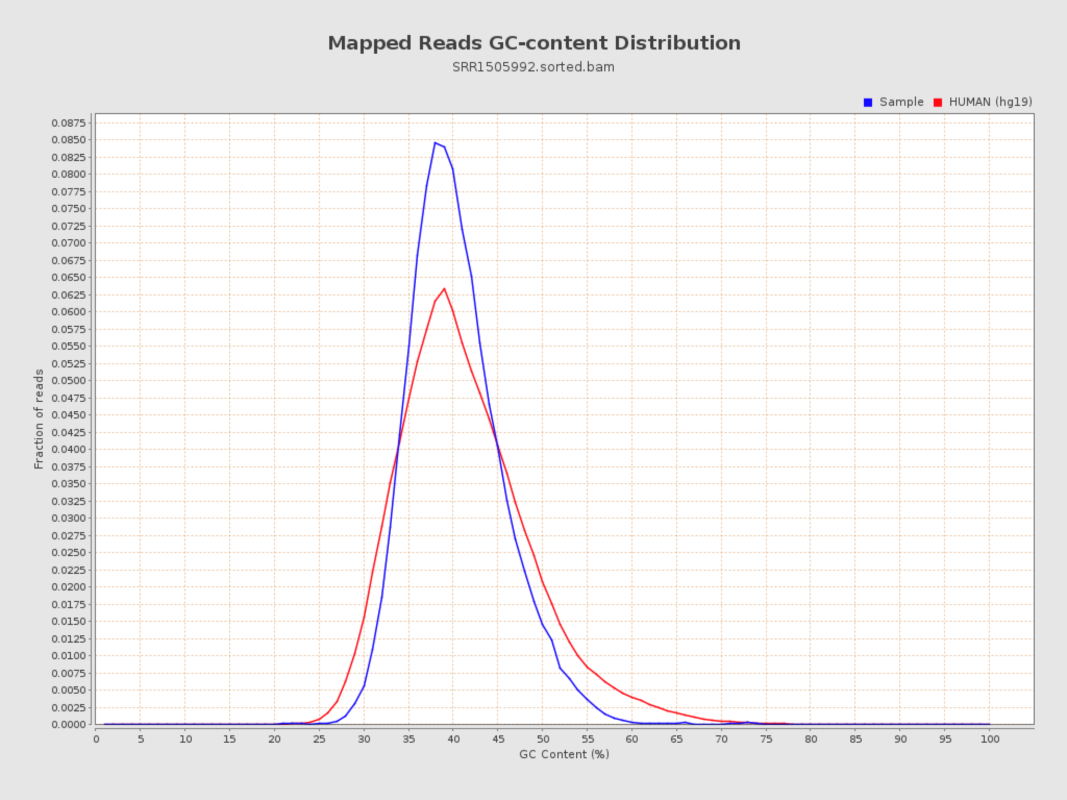
7. Results : Duplication Rate Histogram



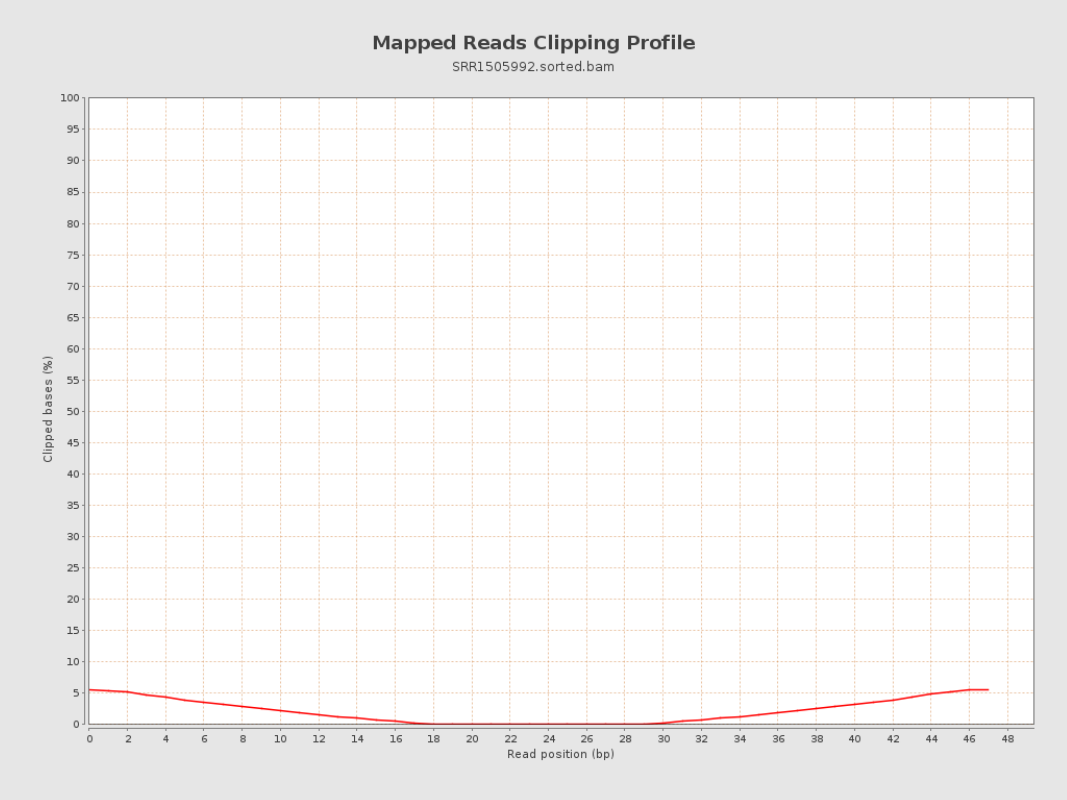
8. Results : Mapped Reads Nucleotide Content



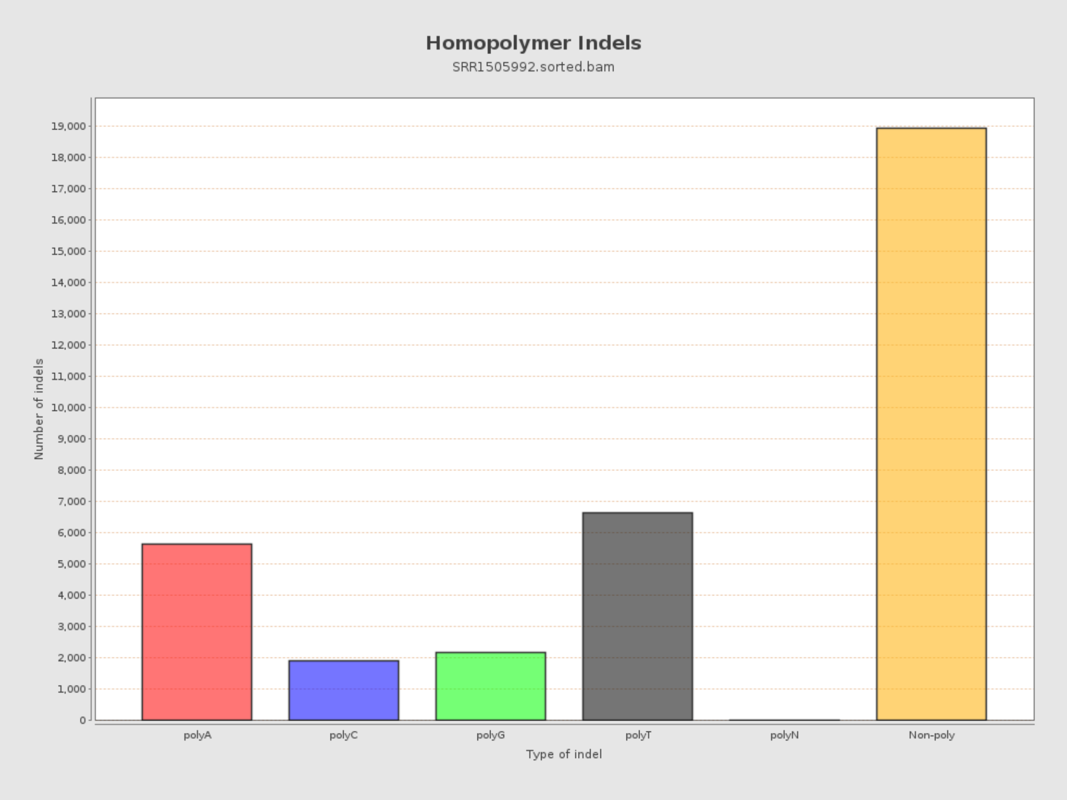
9. Results : Mapped Reads GC-content Distribution



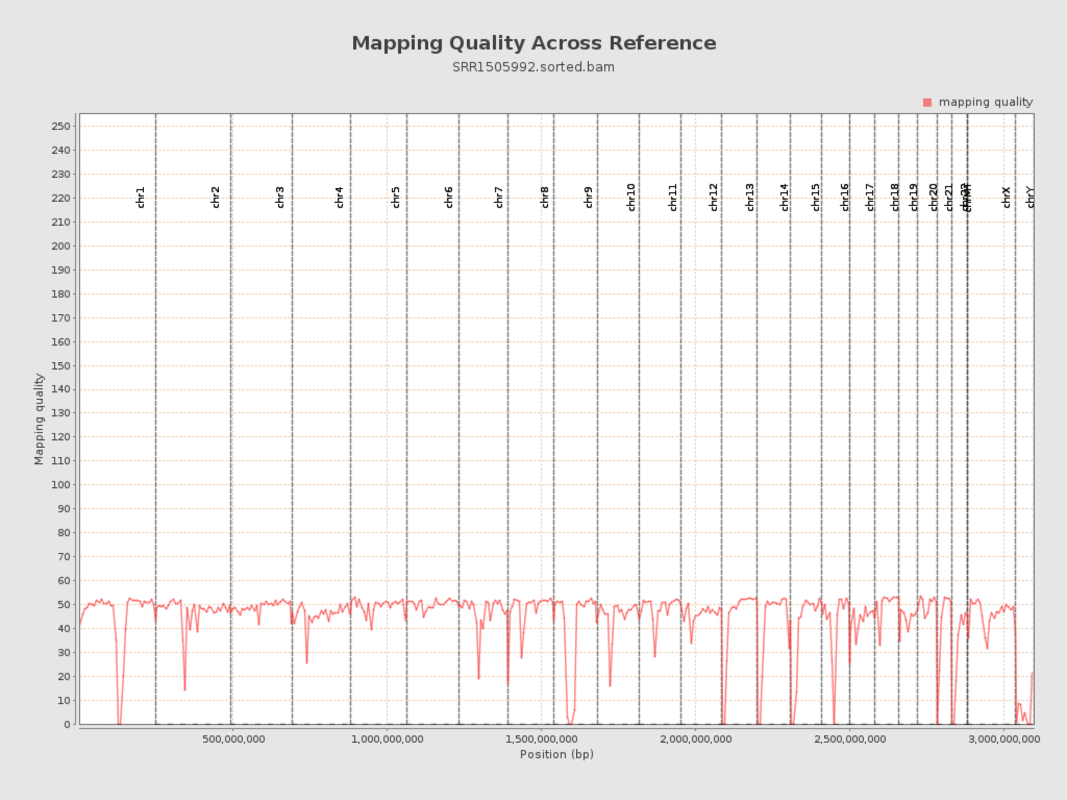
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram