Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/19 21:18:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1505958.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_SRR1505958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1505958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Dec 19 21:18:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1505958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,830,171
Mapped reads	4,460,864 / 76.51%
Unmapped reads	1,369,307 / 23.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	215 / 0%
Read min/max/mean length	30 / 48 / 48
Duplicated reads (estimated)	409,712 / 7.03%
Duplication rate	7.02%
Clipped reads	479,076 / 8.22%

2.2. ACGT Content

Number/percentage of A's	61,492,457 / 29.34%
Number/percentage of C's	43,701,480 / 20.85%
Number/percentage of T's	60,441,107 / 28.84%
Number/percentage of G's	43,939,343 / 20.97%
Number/percentage of N's	945 / 0%
GC Percentage	41.82%

2.3. Coverage

Mean	0.0677

Standard Deviation	0.5788

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

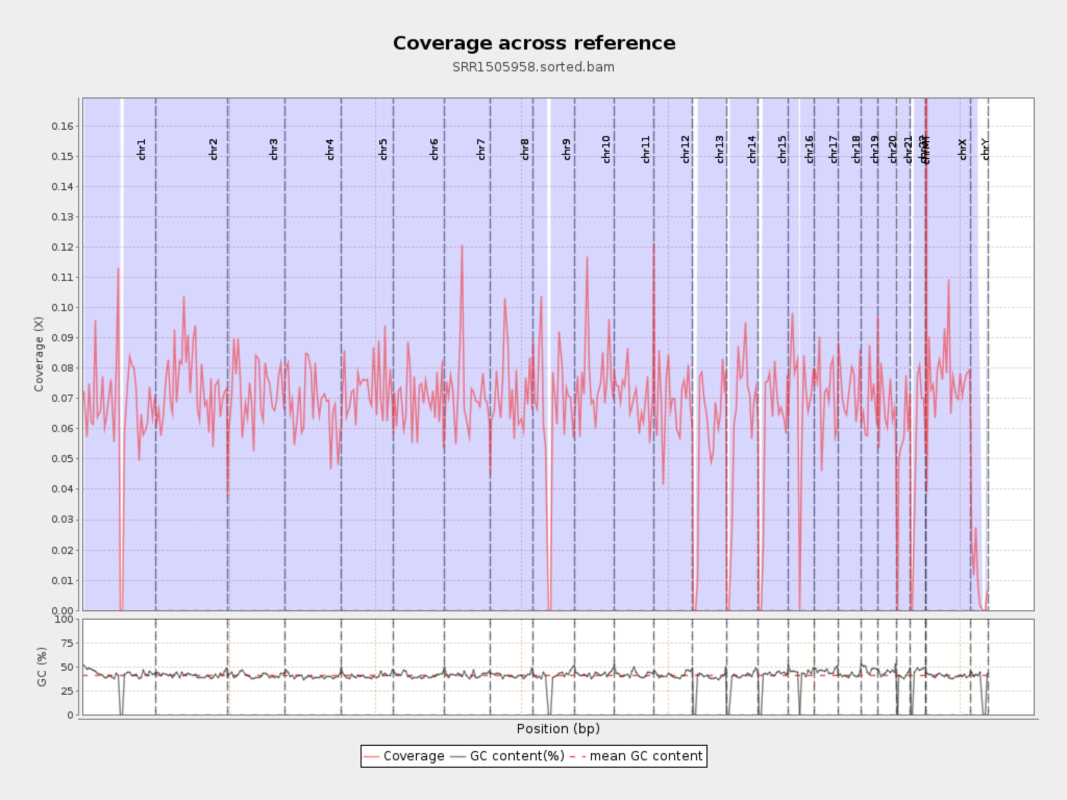
General error rate	0.5%
Mismatches	1,026,568
Insertions	9,342
Mapped reads with at least one insertion	0.21%
Deletions	28,758
Mapped reads with at least one deletion	0.64%
Homopolymer indels	45.91%

2.6. Chromosome stats

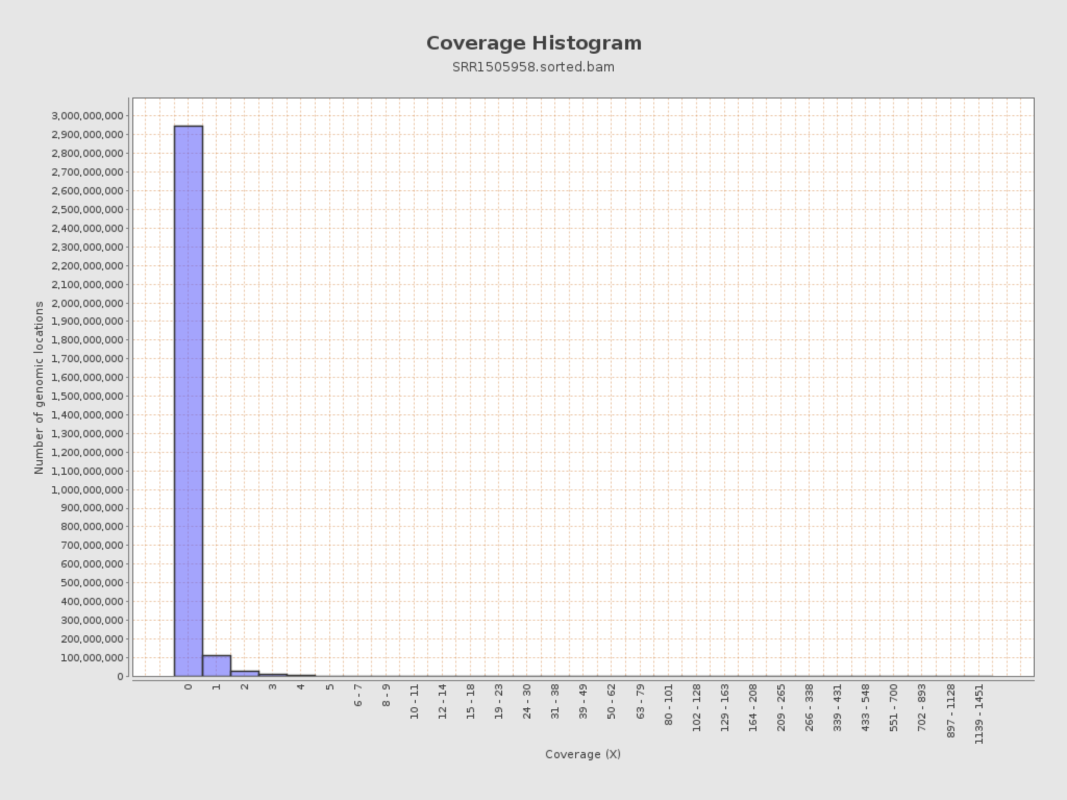
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16390090	0.0658	1.0746
chr2	243199373	18010876	0.0741	0.5211
chr3	198022430	14224735	0.0718	0.3644
chr4	191154276	13027494	0.0682	0.3607
chr5	180915260	13251180	0.0732	0.3688
chr6	171115067	11986928	0.0701	0.3987
chr7	159138663	11468779	0.0721	0.7724

chr8	146364022	10477247	0.0716	0.7768
chr9	141213431	9100252	0.0644	0.4983
chr10	135534747	10323684	0.0762	0.5875
chr11	135006516	9502264	0.0704	0.5751
chr12	133851895	9194782	0.0687	0.374
chr13	115169878	6391858	0.0555	0.3167
chr14	107349540	6541611	0.0609	0.3877
chr15	102531392	5813044	0.0567	0.3192
chr16	90354753	6293483	0.0697	0.3918
chr17	81195210	5840909	0.0719	0.4251
chr18	78077248	5702694	0.073	1.1439
chr19	59128983	4043762	0.0684	0.7614
chr20	63025520	4234668	0.0672	0.3661
chr21	48129895	2651683	0.0551	0.3424
chr22	51304566	2644949	0.0516	0.3107
chrMT	16571	73736	4.4497	3.7196
chrX	155270560	11873115	0.0765	0.4186
chrY	59373566	551238	0.0093	0.1552

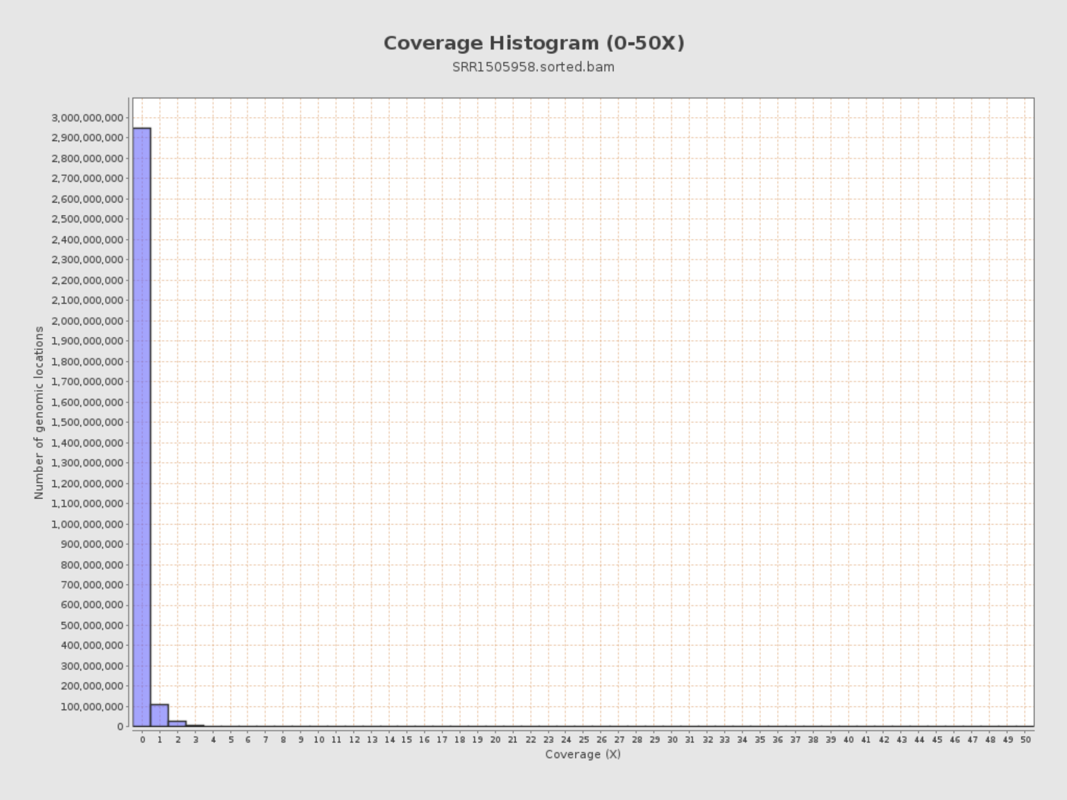
3. Results : Coverage across reference



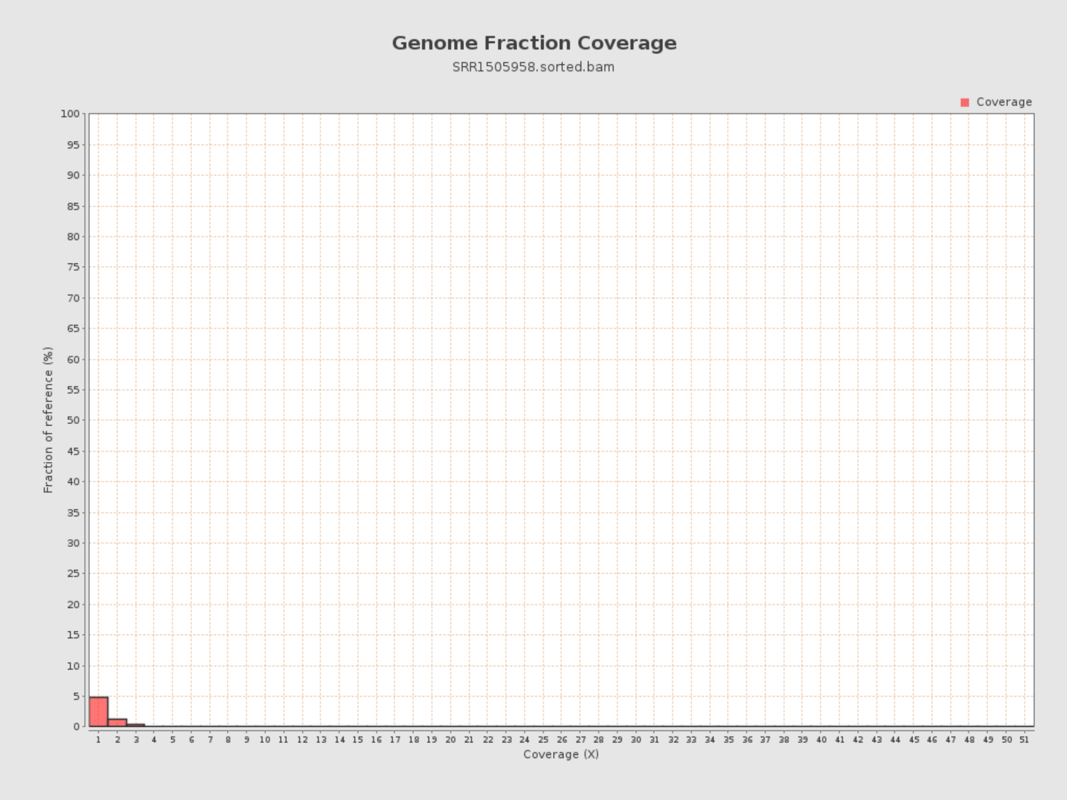
4. Results : Coverage Histogram



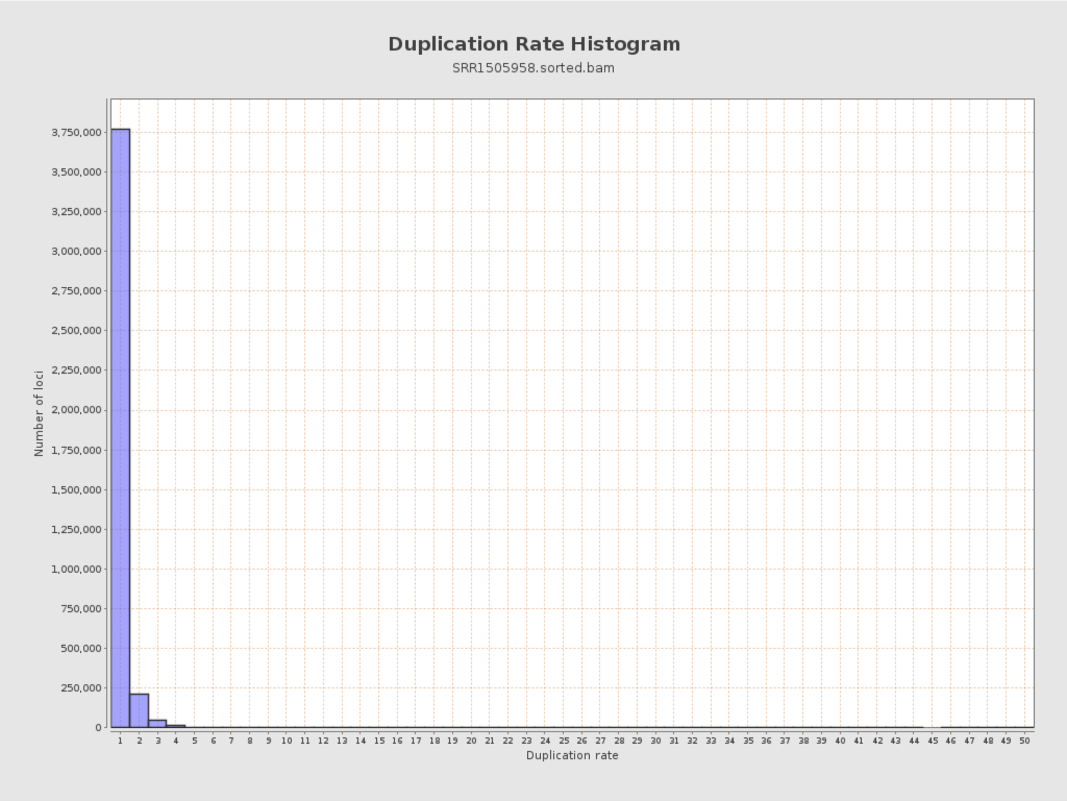
5. Results : Coverage Histogram (0-50X)



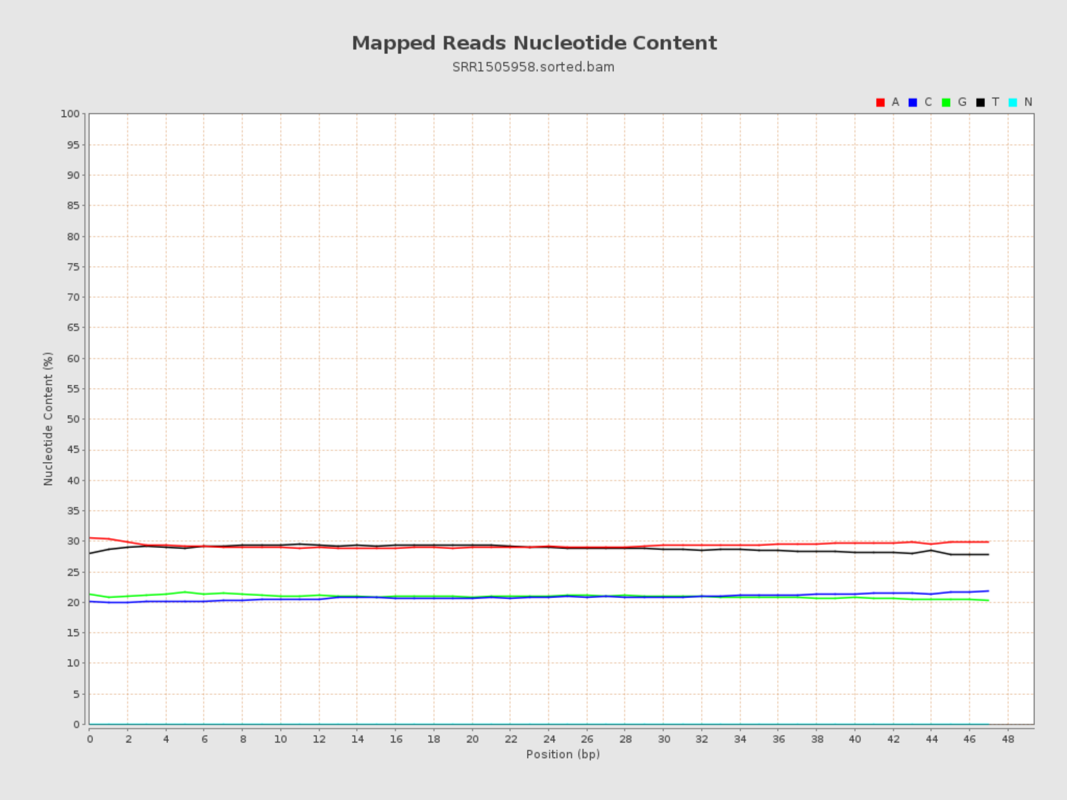
6. Results : Genome Fraction Coverage



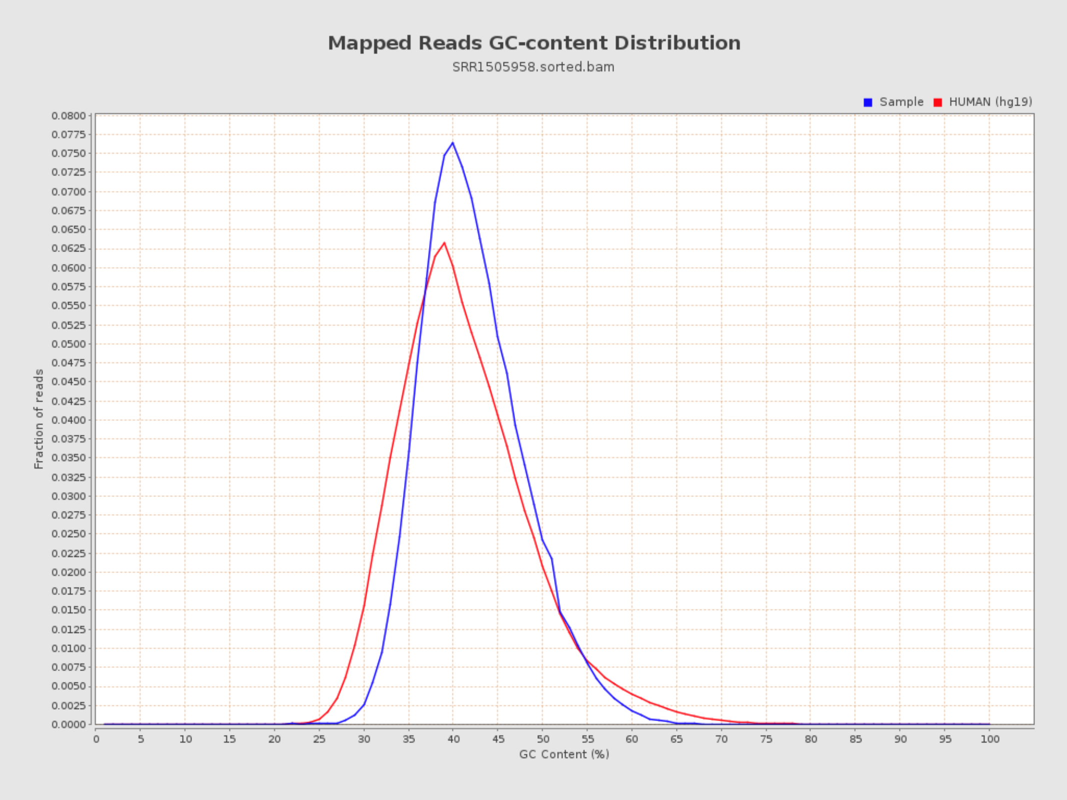
7. Results : Duplication Rate Histogram



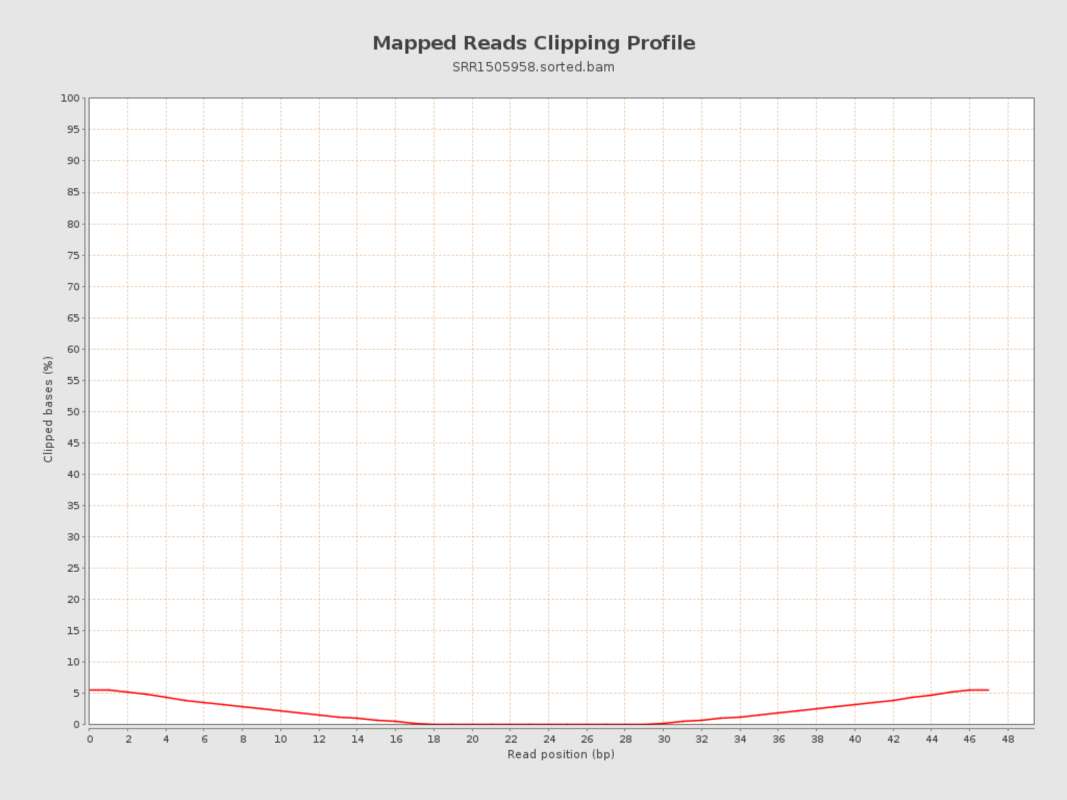
8. Results : Mapped Reads Nucleotide Content



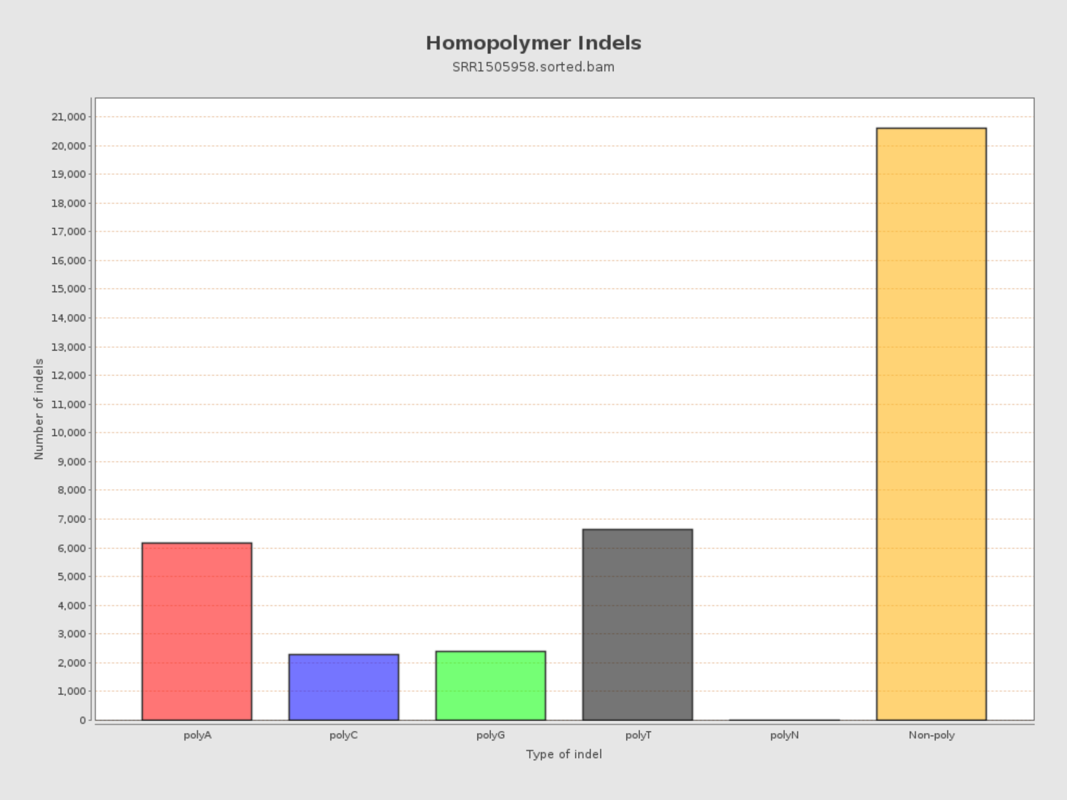
9. Results : Mapped Reads GC-content Distribution



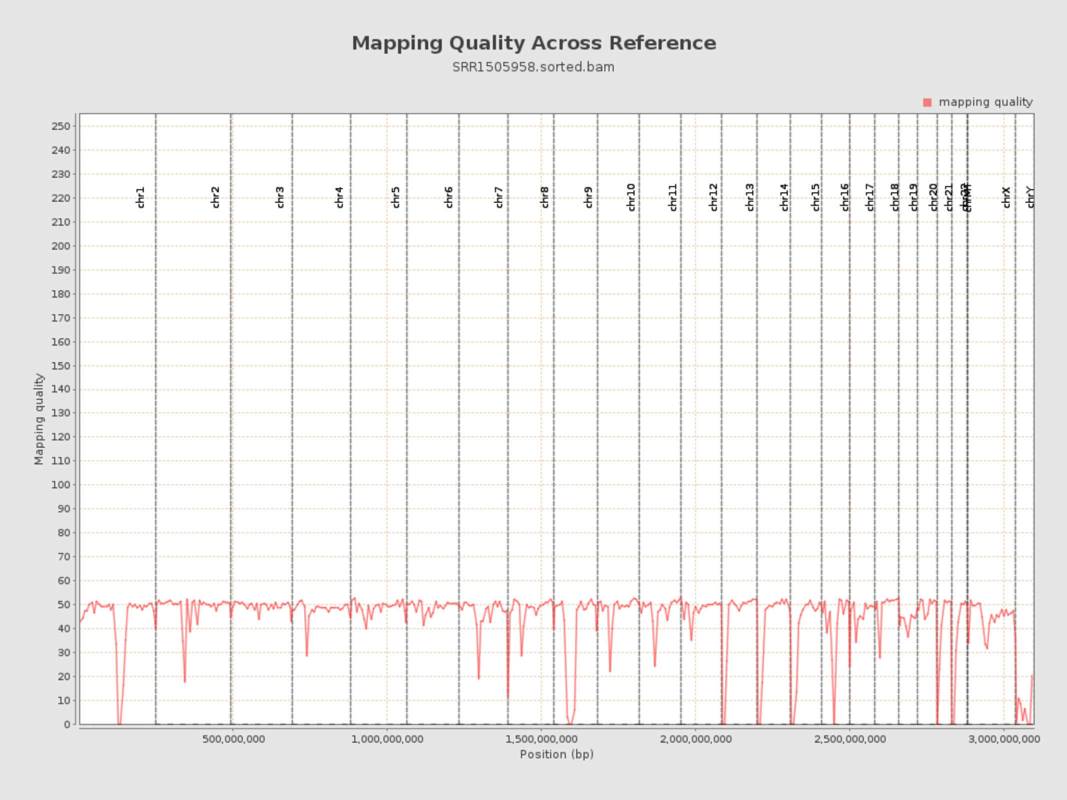
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram