Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 21:50:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751220.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_SRR8751220 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751220.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 21:50:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751220.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,658,674
Mapped reads	4,561,195 / 97.91%
Unmapped reads	97,479 / 2.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	72,244 / 1.55%
Read min/max/mean length	30 / 101 / 101.64
Duplicated reads (estimated)	50,524 / 1.08%
Duplication rate	1.03%
Clipped reads	623,098 / 13.38%

2.2. ACGT Content

Number/percentage of A's	132,624,180 / 29.55%
Number/percentage of C's	92,125,602 / 20.53%
Number/percentage of T's	133,307,703 / 29.7%
Number/percentage of G's	90,758,120 / 20.22%
Number/percentage of N's	2,515 / 0%
GC Percentage	40.75%

2.3. Coverage

Mean	0.145

Standard Deviation	0.4501

2.4. Mapping Quality

Mean Mapping Quality	51.66

2.5. Mismatches and indels

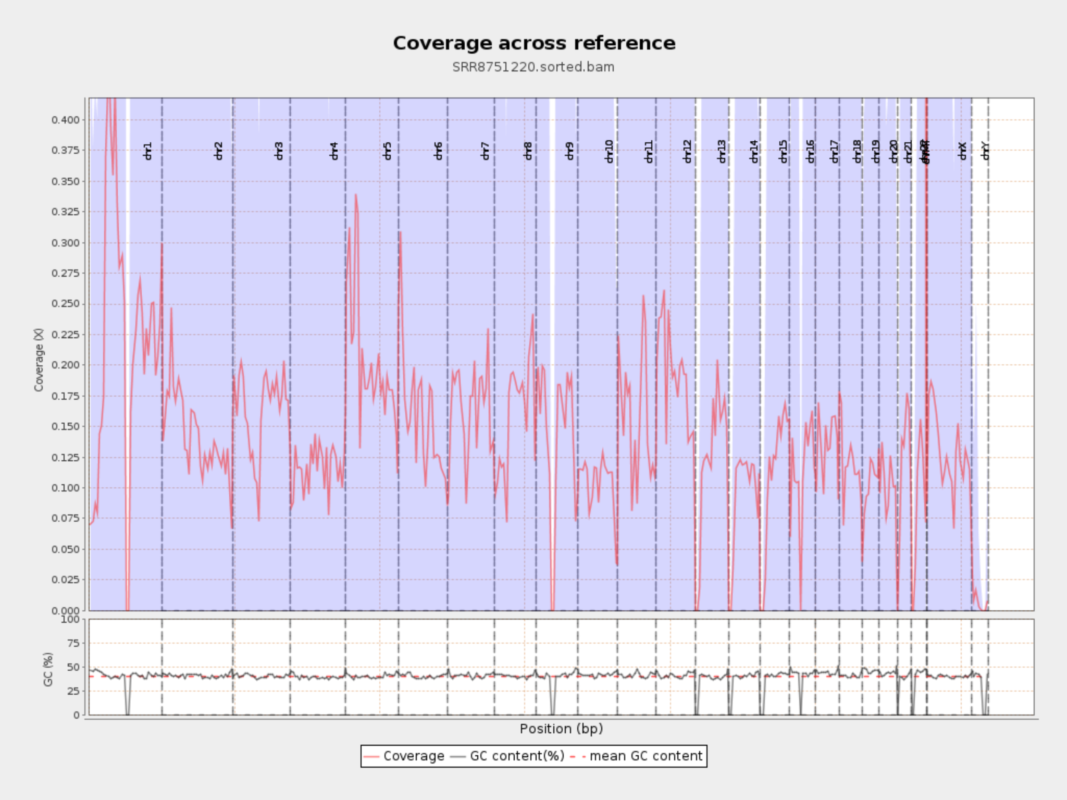
General error rate	0.28%
Mismatches	1,169,781
Insertions	45,568
Mapped reads with at least one insertion	0.99%
Deletions	50,304
Mapped reads with at least one deletion	1.09%
Homopolymer indels	46.84%

2.6. Chromosome stats

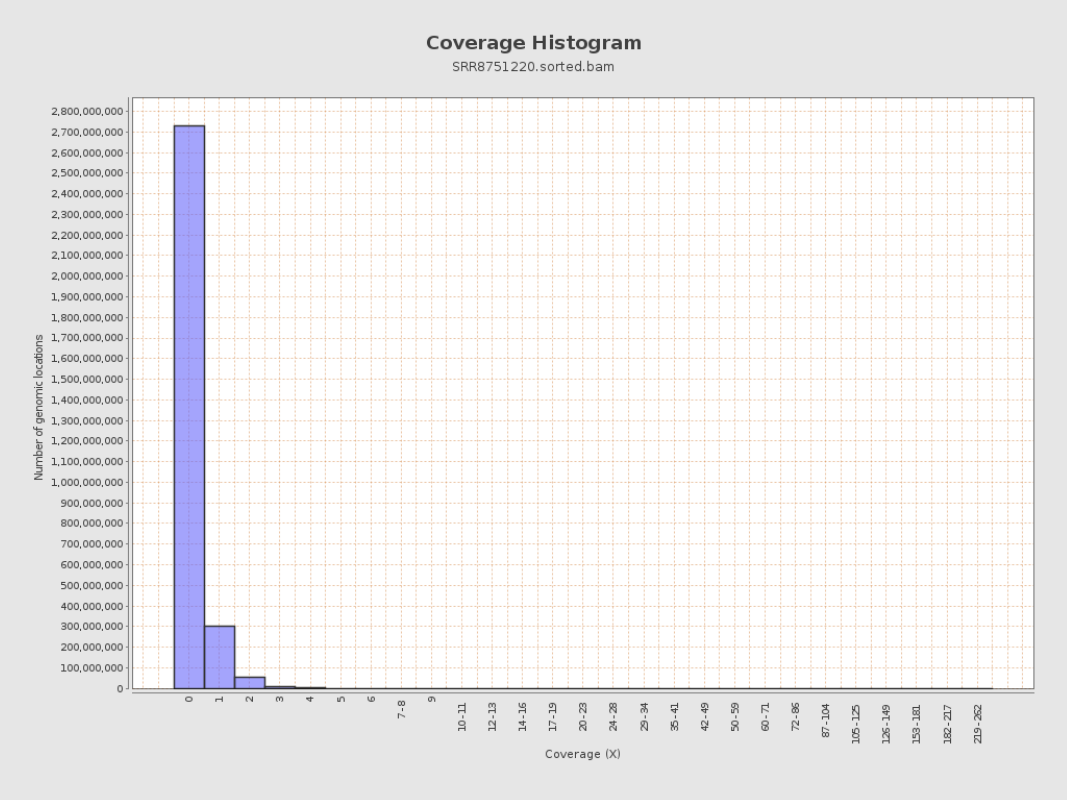
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	55064397	0.2209	0.6005
chr2	243199373	34851721	0.1433	0.426
chr3	198022430	32504043	0.1641	0.4535
chr4	191154276	22126236	0.1158	0.3802
chr5	180915260	36980550	0.2044	0.5128
chr6	171115067	27279523	0.1594	0.4646
chr7	159138663	26479260	0.1664	0.4594

chr8	146364022	23418955	0.16	0.452
chr9	141213431	20247875	0.1434	0.4311
chr10	135534747	14390881	0.1062	0.4038
chr11	135006516	21141388	0.1566	0.4554
chr12	133851895	25778660	0.1926	0.4958
chr13	115169878	13942815	0.1211	0.3929
chr14	107349540	9931409	0.0925	0.3407
chr15	102531392	11153464	0.1088	0.3733
chr16	90354753	10239716	0.1133	0.381
chr17	81195210	10864931	0.1338	0.4229
chr18	78077248	9356547	0.1198	0.4017
chr19	59128983	6051529	0.1023	0.4222
chr20	63025520	6373498	0.1011	0.3577
chr21	48129895	5661681	0.1176	0.3967
chr22	51304566	4263646	0.0831	0.3305
chrMT	16571	506217	30.5484	16.3727
chrX	155270560	19903331	0.1282	0.4025
chrY	59373566	413506	0.007	0.1199

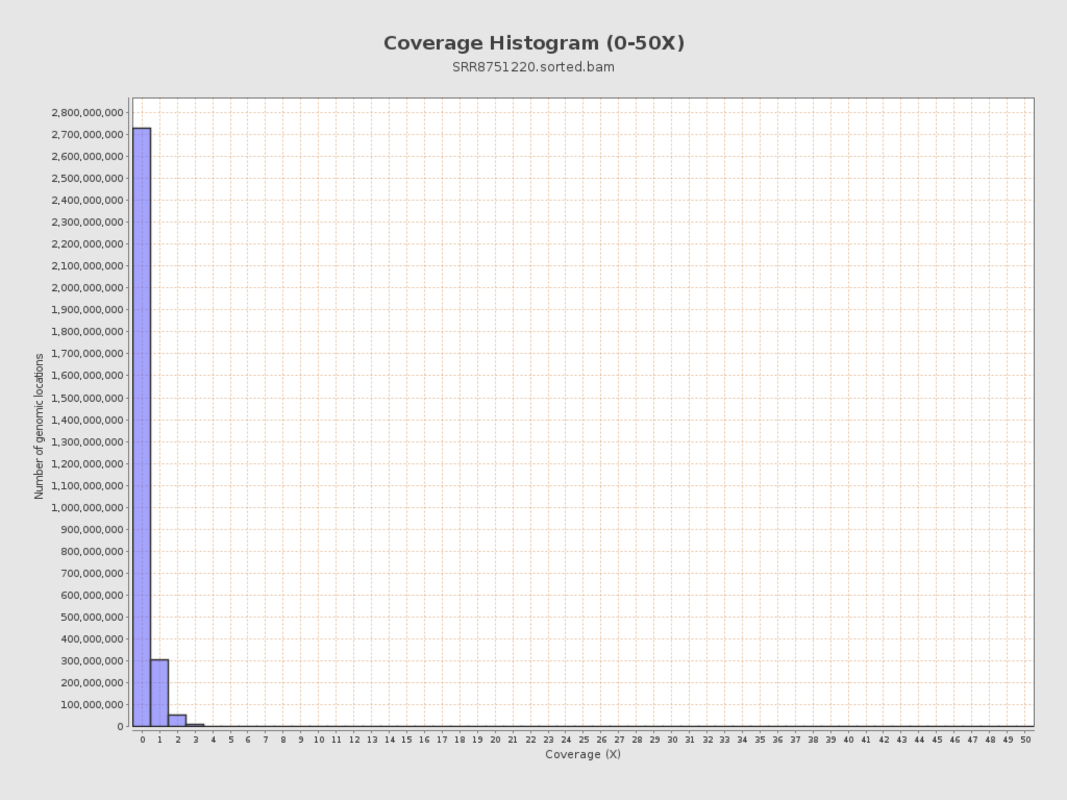
3. Results : Coverage across reference



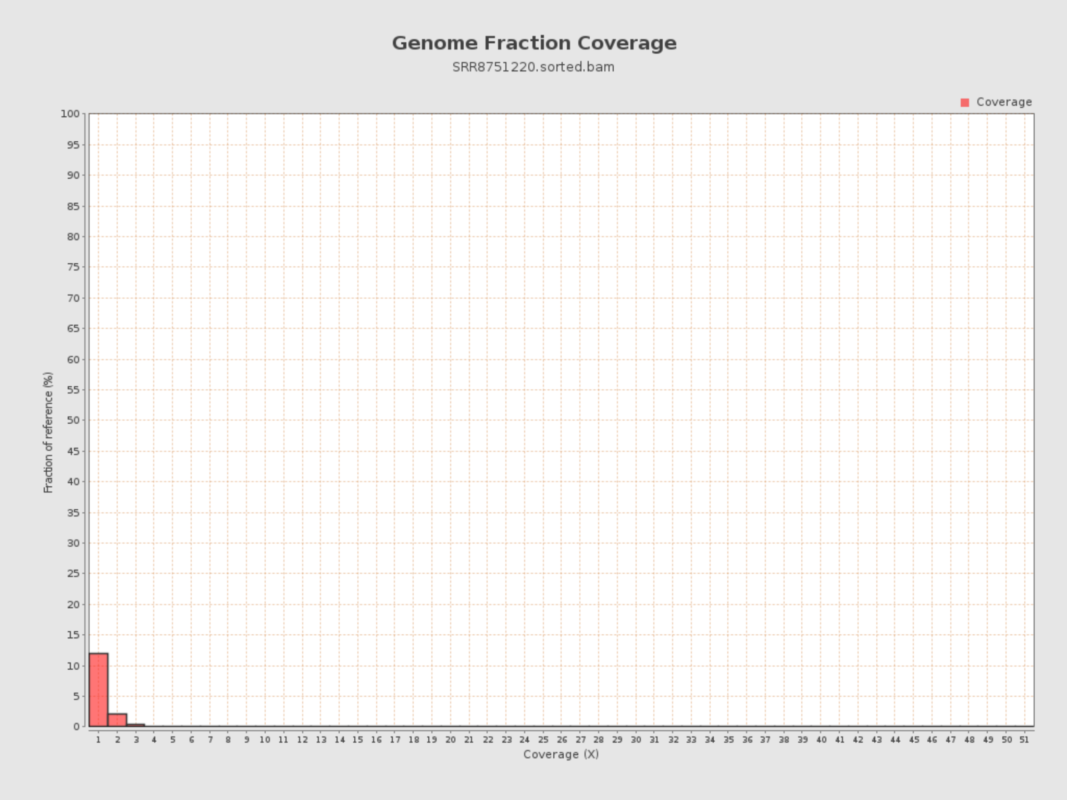
4. Results : Coverage Histogram



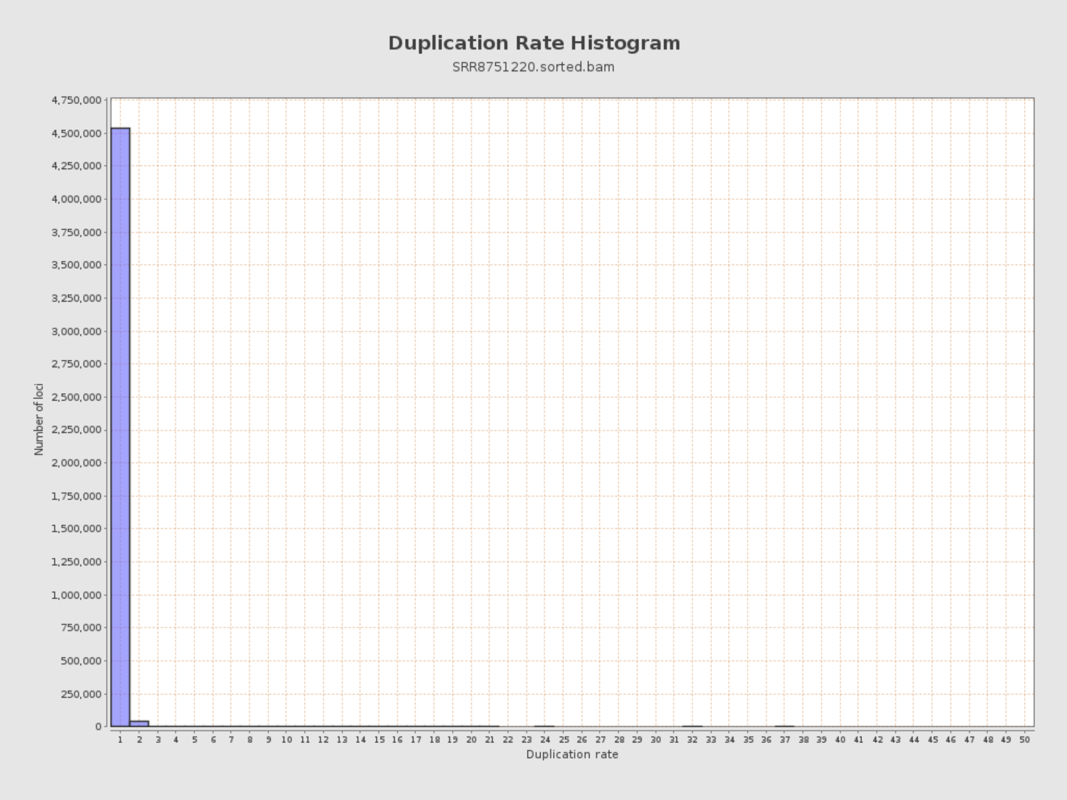
5. Results : Coverage Histogram (0-50X)



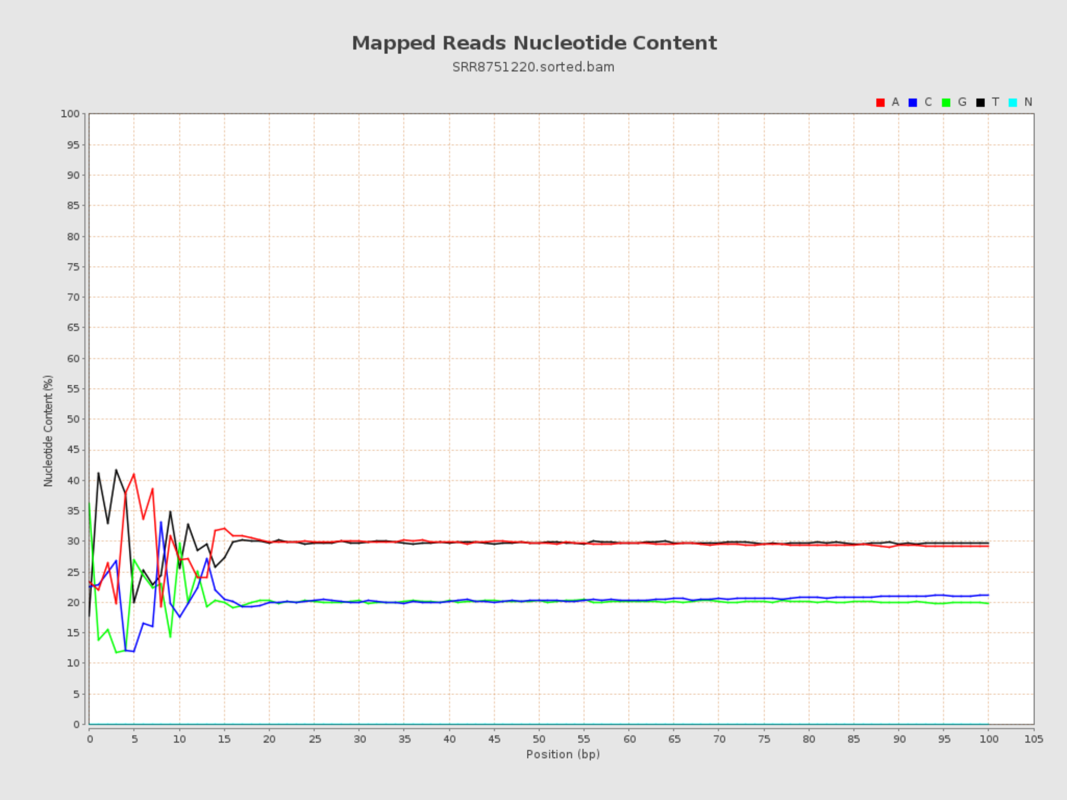
6. Results : Genome Fraction Coverage



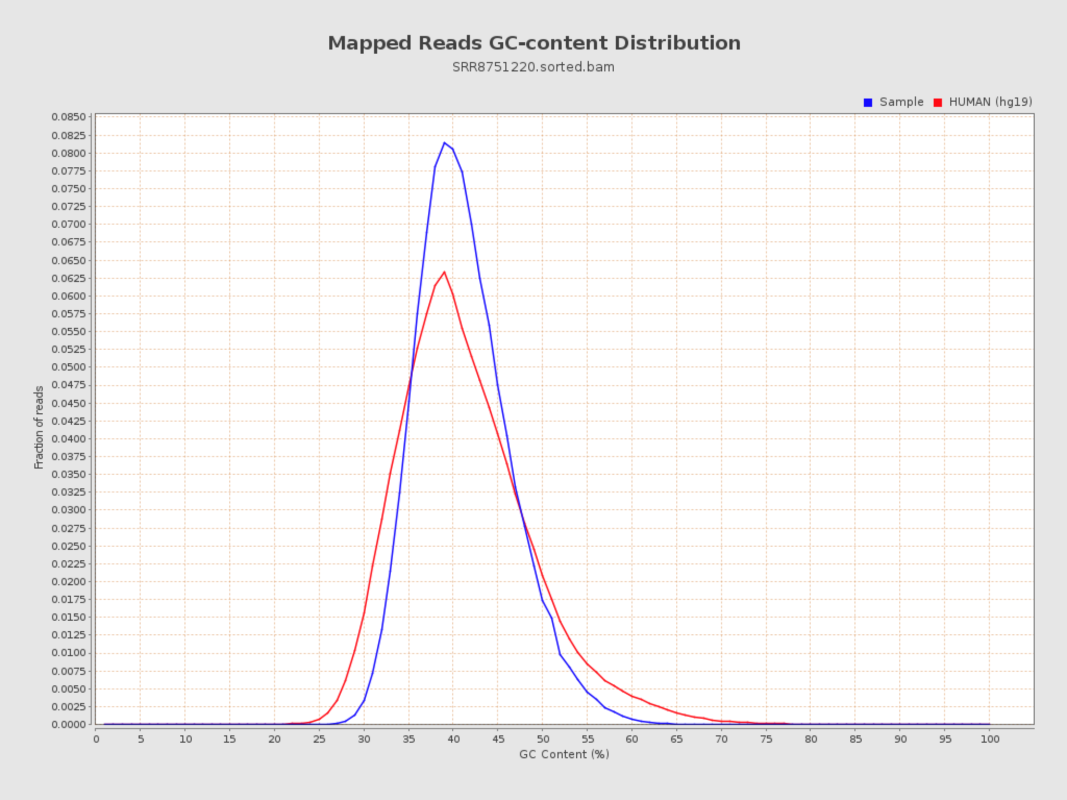
7. Results : Duplication Rate Histogram



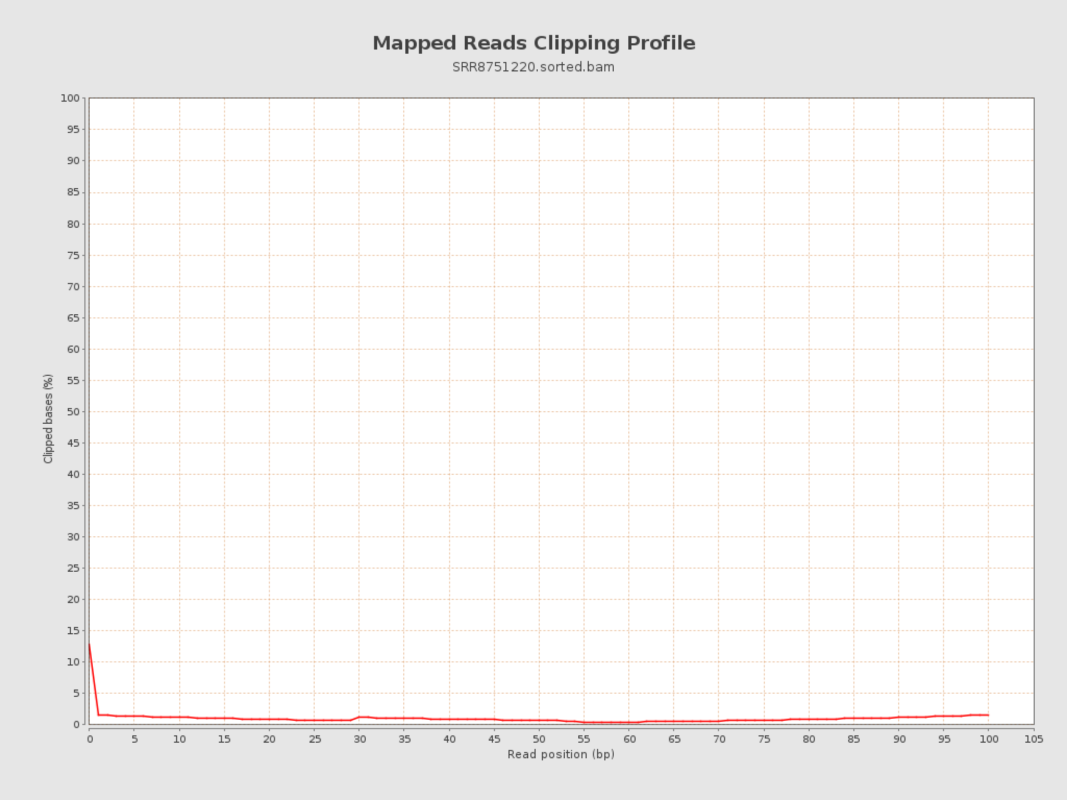
8. Results : Mapped Reads Nucleotide Content



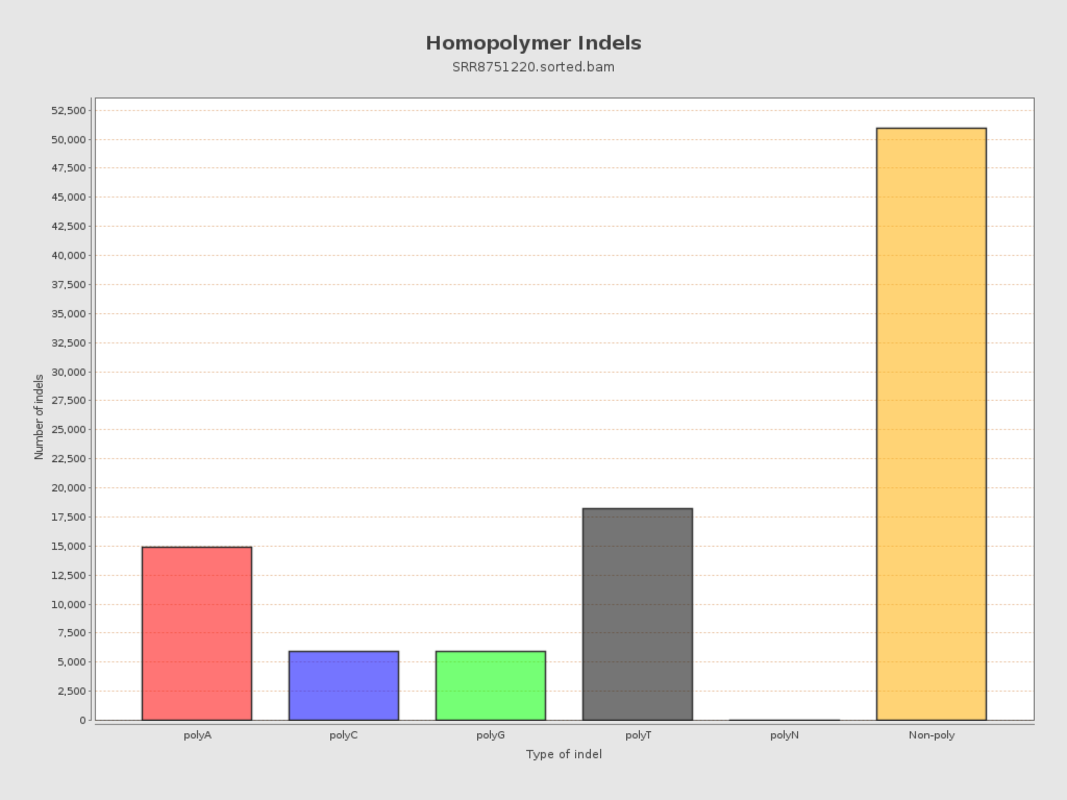
9. Results : Mapped Reads GC-content Distribution



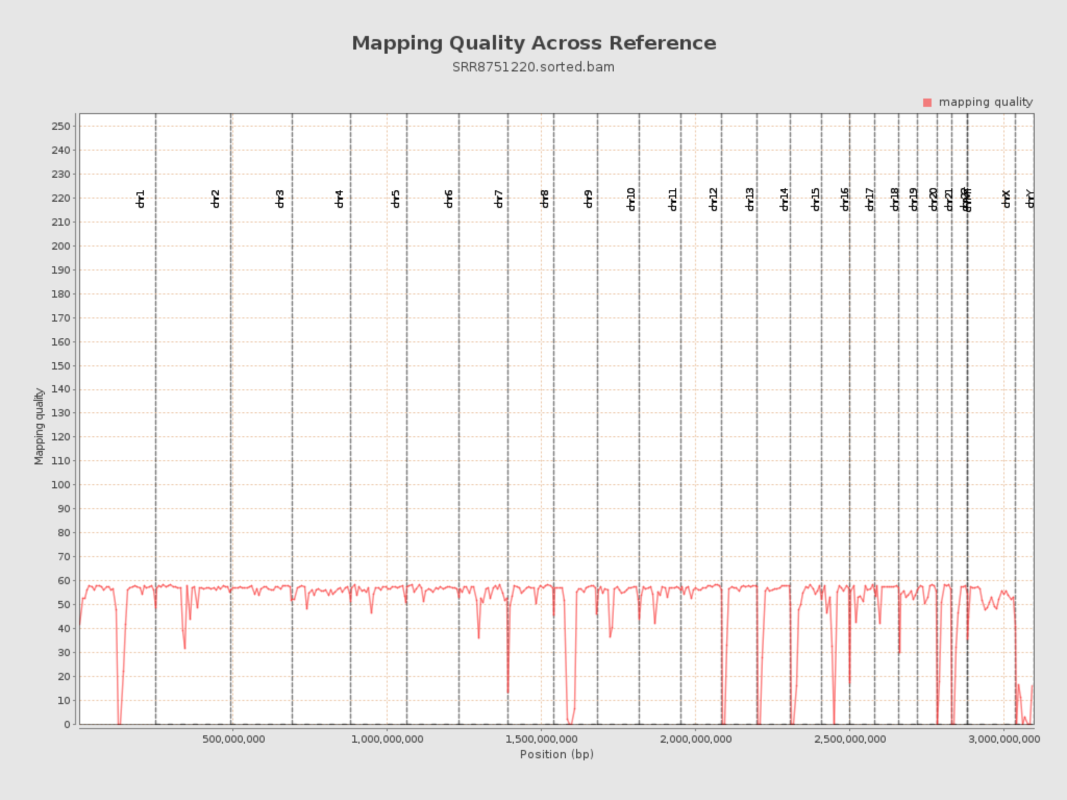
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram