Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 18:47:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971313.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_SRR2971313 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971313.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 18:47:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971313.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	11,531,534
Mapped reads	10,681,774 / 92.63%
Unmapped reads	849,760 / 7.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,044 / 0.02%
Read min/max/mean length	30 / 50 / 50.01
Duplicated reads (estimated)	1,175,303 / 10.19%
Duplication rate	8.94%
Clipped reads	2,503,304 / 21.71%

2.2. ACGT Content

Number/percentage of A's	140,906,131 / 27.59%
Number/percentage of C's	111,413,727 / 21.82%
Number/percentage of T's	144,079,896 / 28.21%
Number/percentage of G's	114,231,662 / 22.37%
Number/percentage of N's	28,462 / 0.01%
GC Percentage	44.19%

2.3. Coverage

Mean	0.165

Standard Deviation	1.4631

2.4. Mapping Quality

Mean Mapping Quality	33.17

2.5. Mismatches and indels

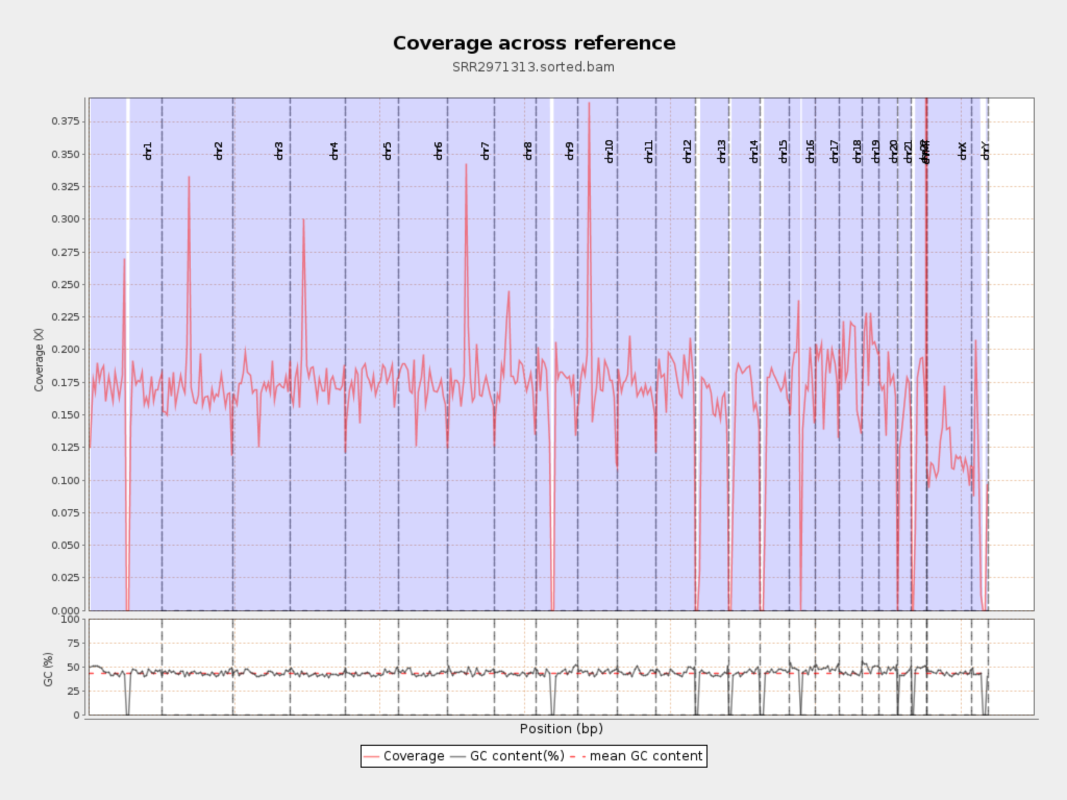
General error rate	0.55%
Mismatches	2,772,481
Insertions	36,732
Mapped reads with at least one insertion	0.34%
Deletions	75,996
Mapped reads with at least one deletion	0.71%
Homopolymer indels	39.26%

2.6. Chromosome stats

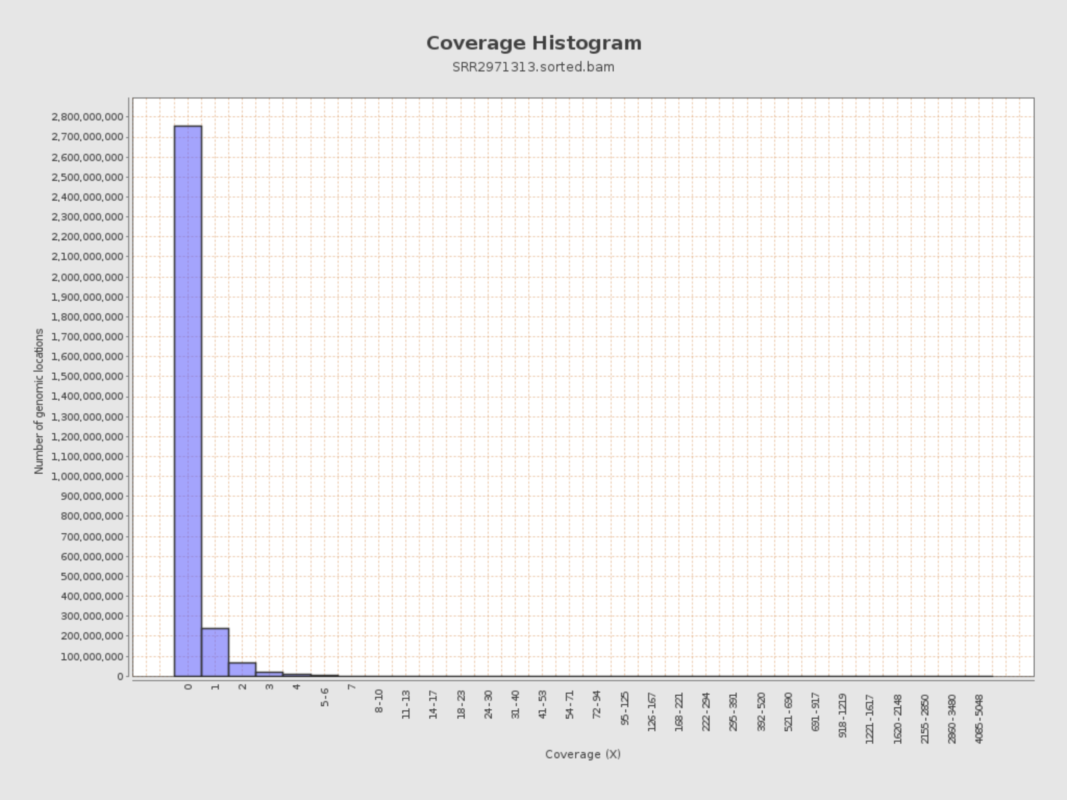
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	40730437	0.1634	2.5375
chr2	243199373	41794261	0.1719	1.4541
chr3	198022430	33944944	0.1714	0.5983
chr4	191154276	34408758	0.18	0.9309
chr5	180915260	31486944	0.174	0.6008
chr6	171115067	29511922	0.1725	0.6504
chr7	159138663	28911211	0.1817	2.0317

chr8	146364022	26289003	0.1796	2.6769
chr9	141213431	22255058	0.1576	1.5451
chr10	135534747	25113245	0.1853	1.7286
chr11	135006516	23137819	0.1714	1.2032
chr12	133851895	24236357	0.1811	0.6631
chr13	115169878	15491050	0.1345	0.5133
chr14	107349540	15715089	0.1464	0.8047
chr15	102531392	14661652	0.143	0.5564
chr16	90354753	14897229	0.1649	0.8071
chr17	81195210	14922740	0.1838	0.8229
chr18	78077248	14592740	0.1869	2.98
chr19	59128983	12092841	0.2045	2.1853
chr20	63025520	10549446	0.1674	0.6646
chr21	48129895	6648707	0.1381	0.908
chr22	51304566	6434650	0.1254	0.6397
chrMT	16571	119388	7.2046	6.2199
chrX	155270560	18322962	0.118	0.6997
chrY	59373566	4500294	0.0758	0.8454

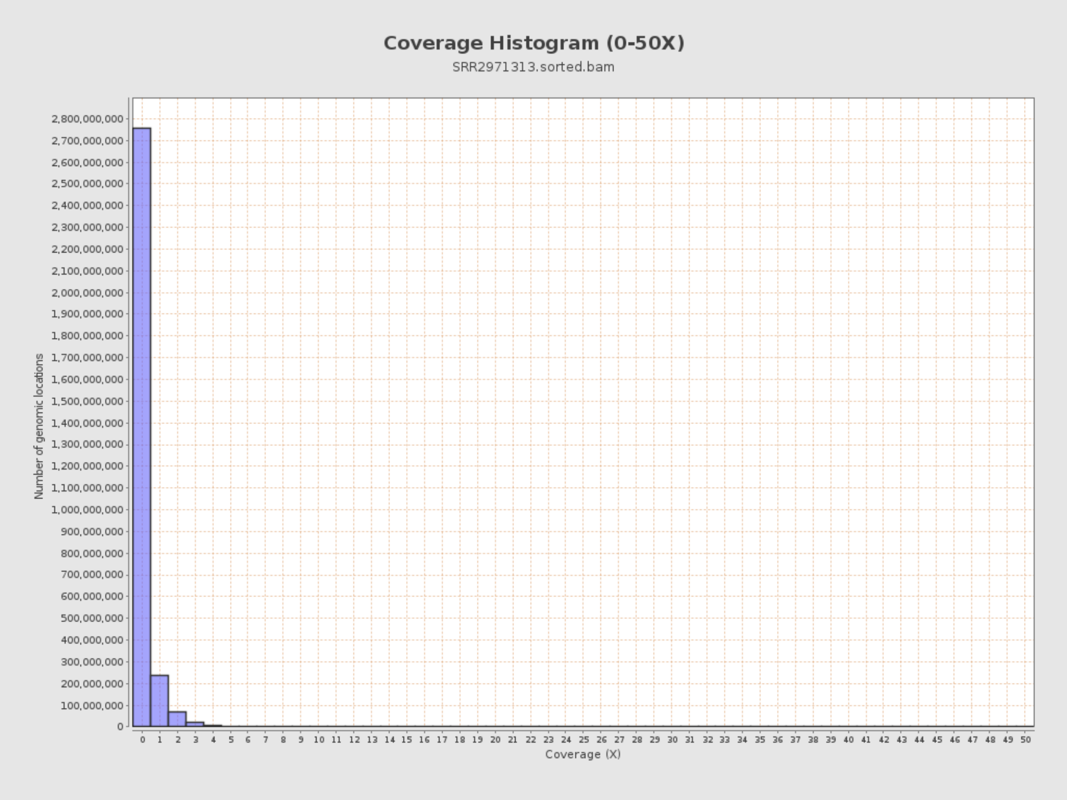
3. Results : Coverage across reference



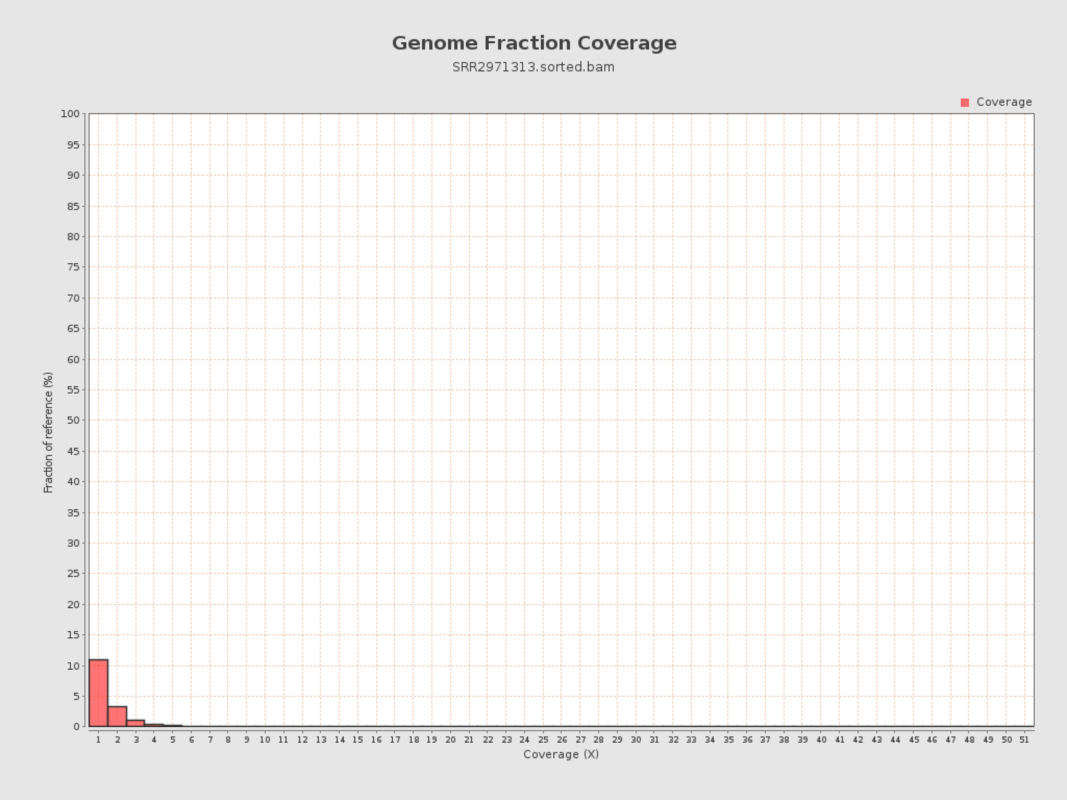
4. Results : Coverage Histogram



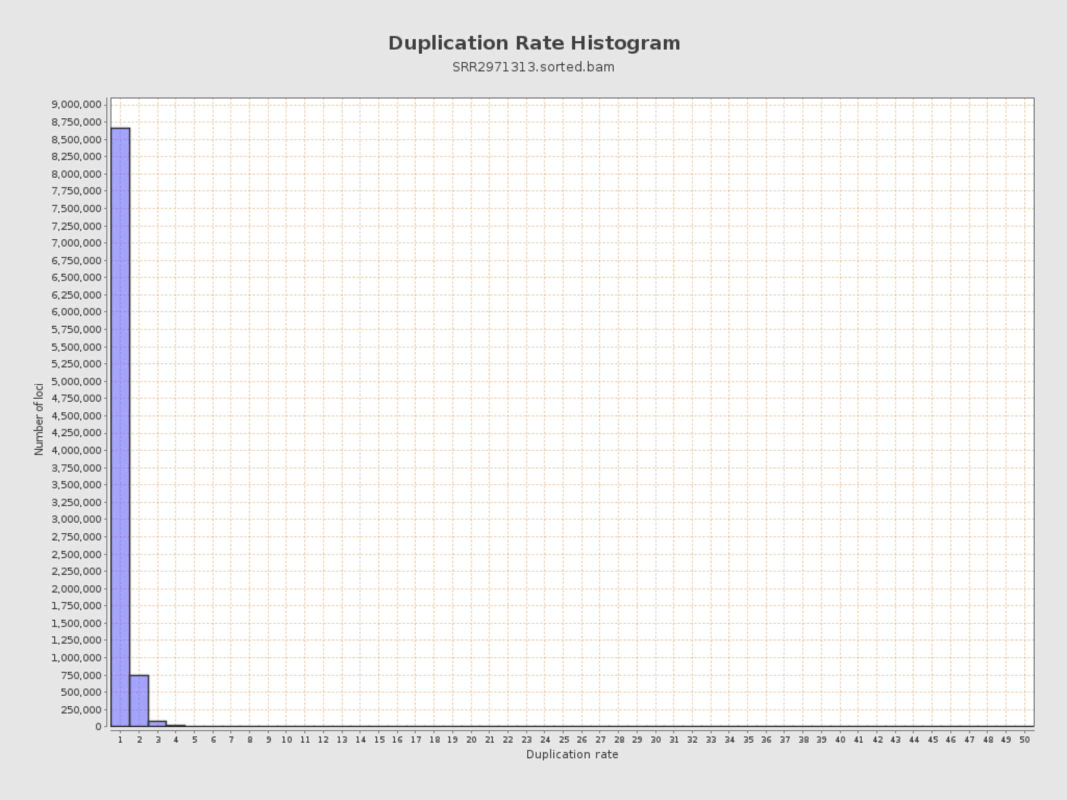
5. Results : Coverage Histogram (0-50X)



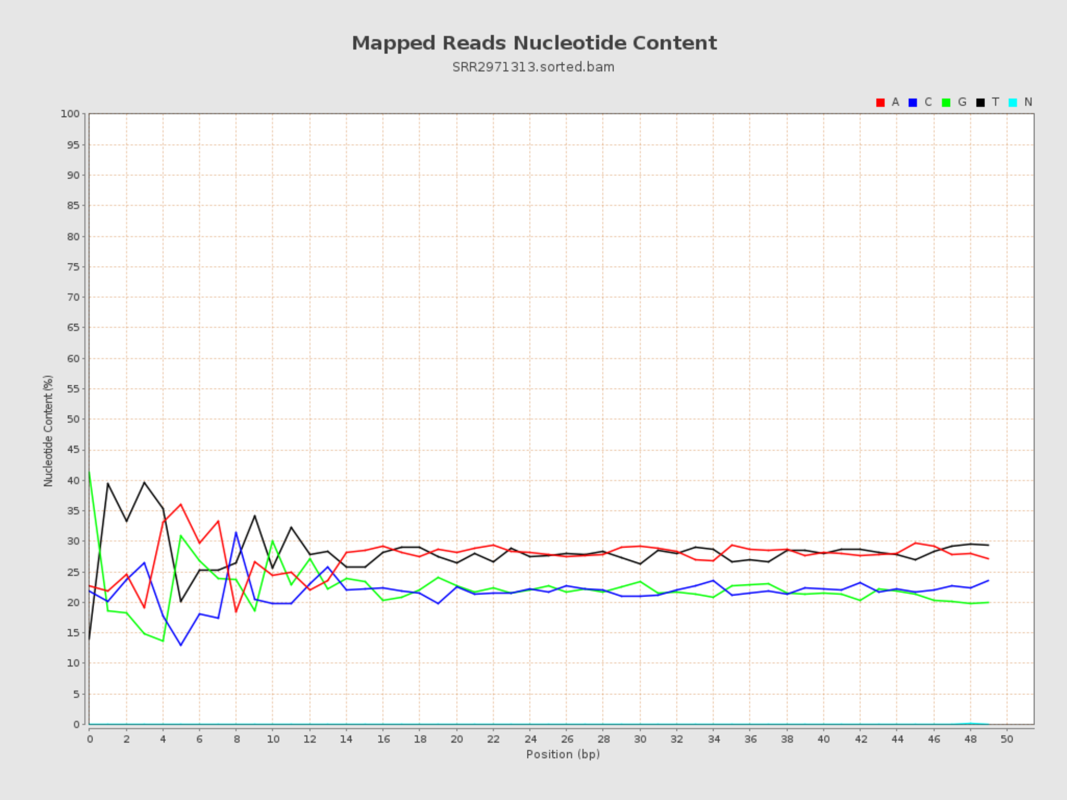
6. Results : Genome Fraction Coverage



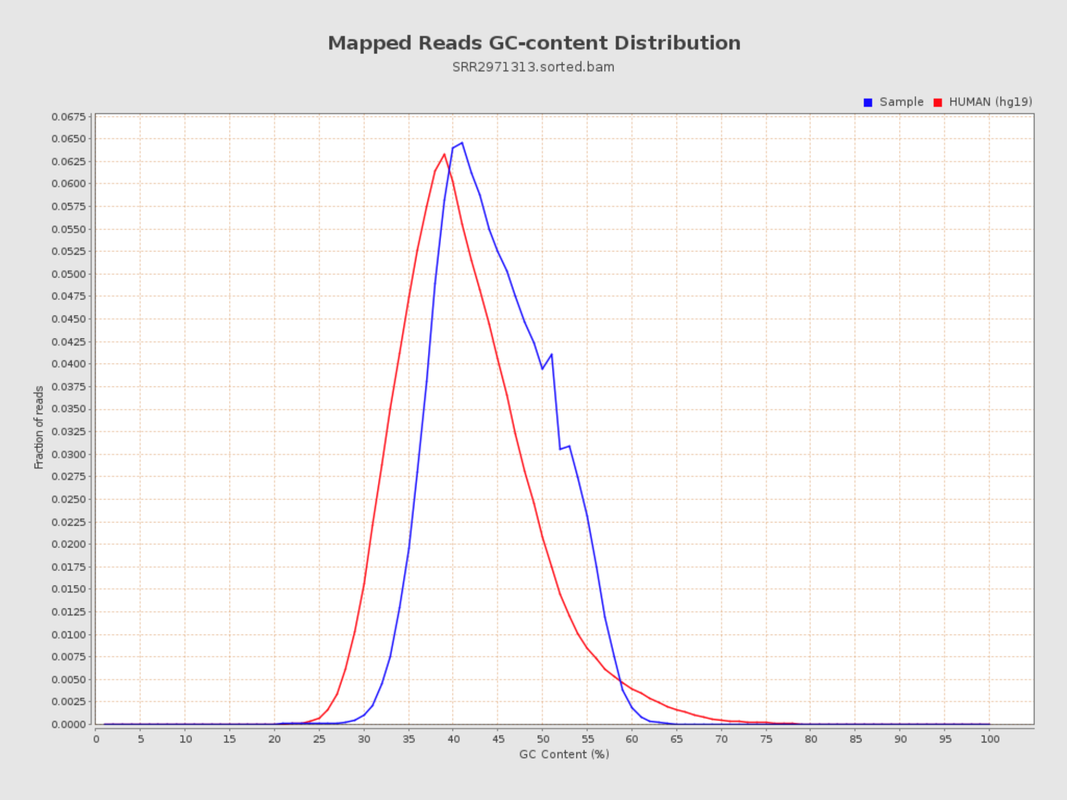
7. Results : Duplication Rate Histogram



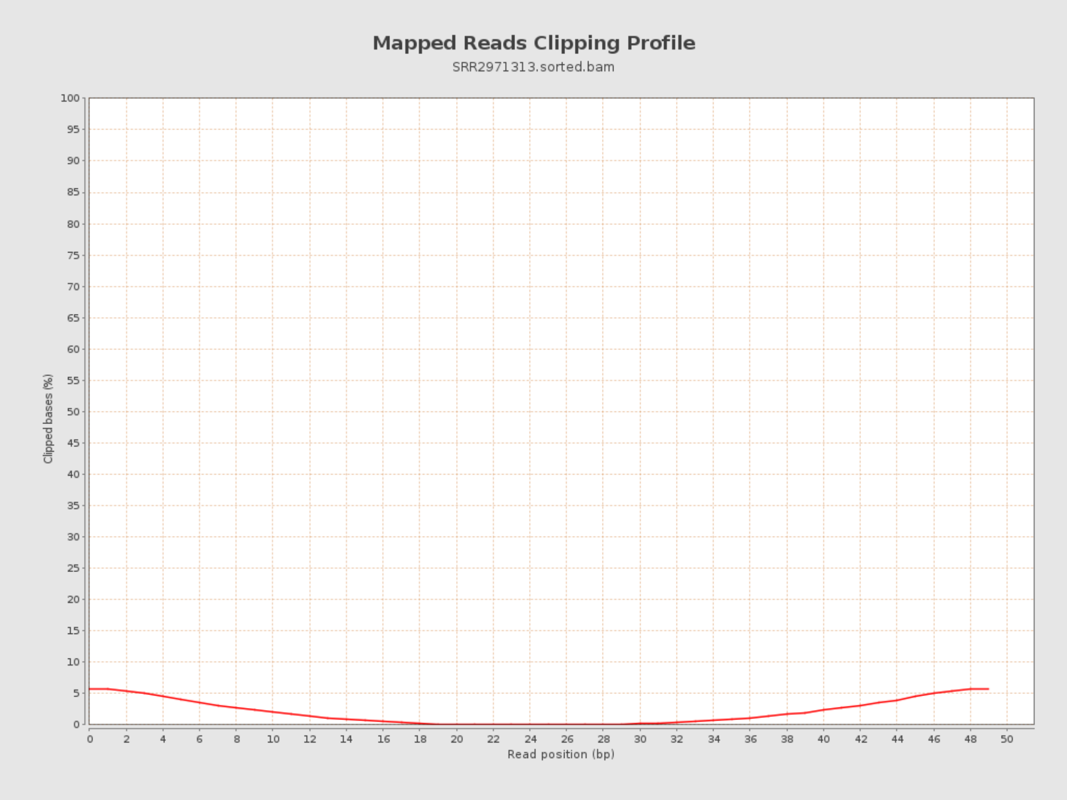
8. Results : Mapped Reads Nucleotide Content



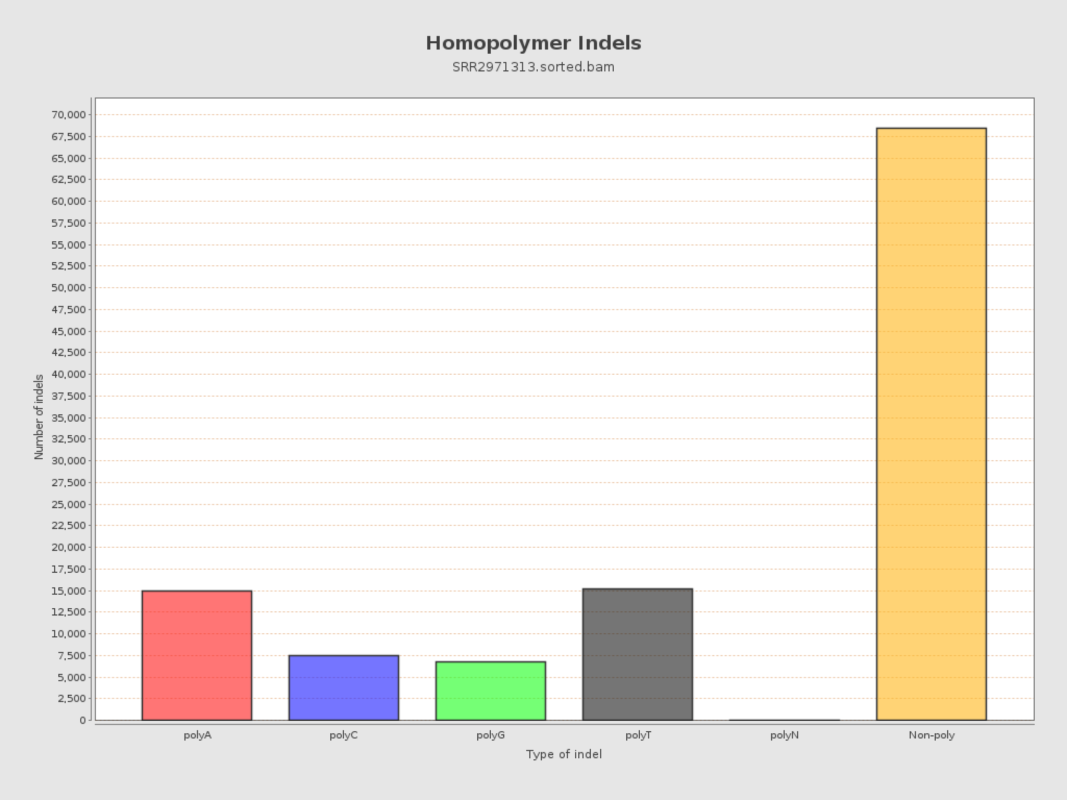
9. Results : Mapped Reads GC-content Distribution



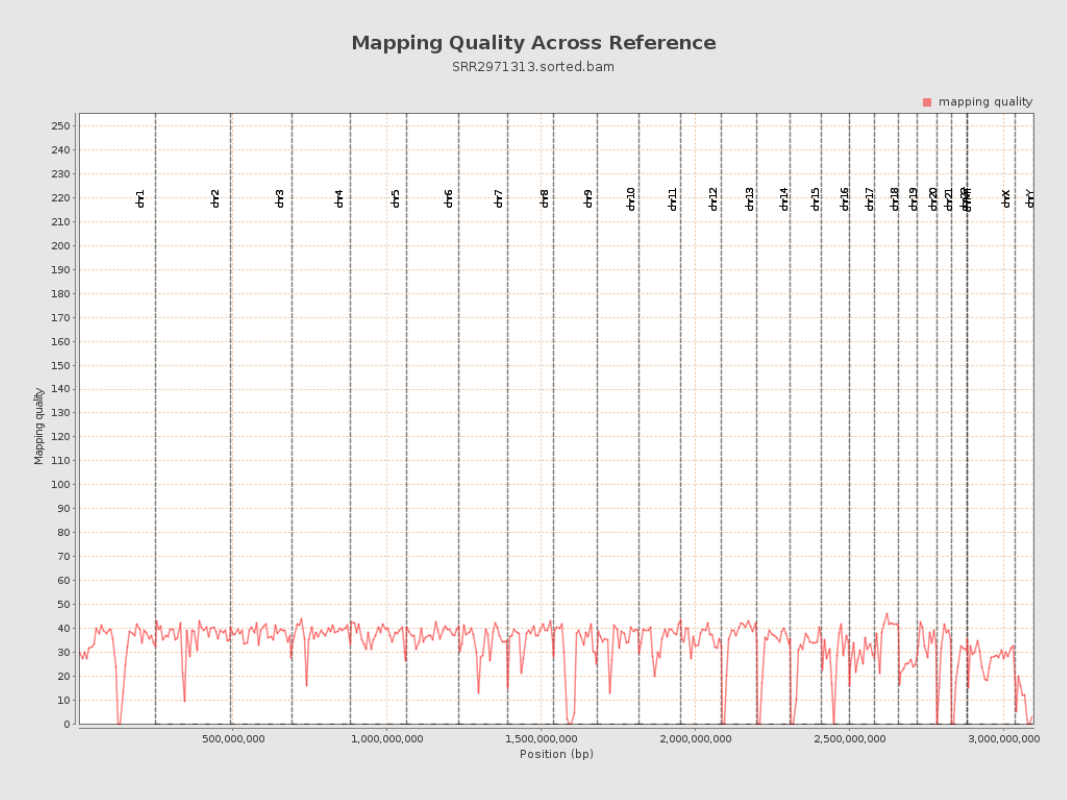
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram