Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 19:00:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2971314.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_SRR2971314 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2971314.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 19:00:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2971314.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,342,920
Mapped reads	12,371,101 / 92.72%
Unmapped reads	971,819 / 7.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,038 / 0.02%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	1,393,225 / 10.44%
Duplication rate	9.16%
Clipped reads	2,728,388 / 20.45%

2.2. ACGT Content

Number/percentage of A's	166,454,273 / 28.09%
Number/percentage of C's	126,222,346 / 21.3%
Number/percentage of T's	169,789,815 / 28.65%
Number/percentage of G's	130,140,183 / 21.96%
Number/percentage of N's	33,363 / 0.01%
GC Percentage	43.26%

2.3. Coverage

Mean	0.1915

Standard Deviation	1.8178

2.4. Mapping Quality

Mean Mapping Quality	35.52

2.5. Mismatches and indels

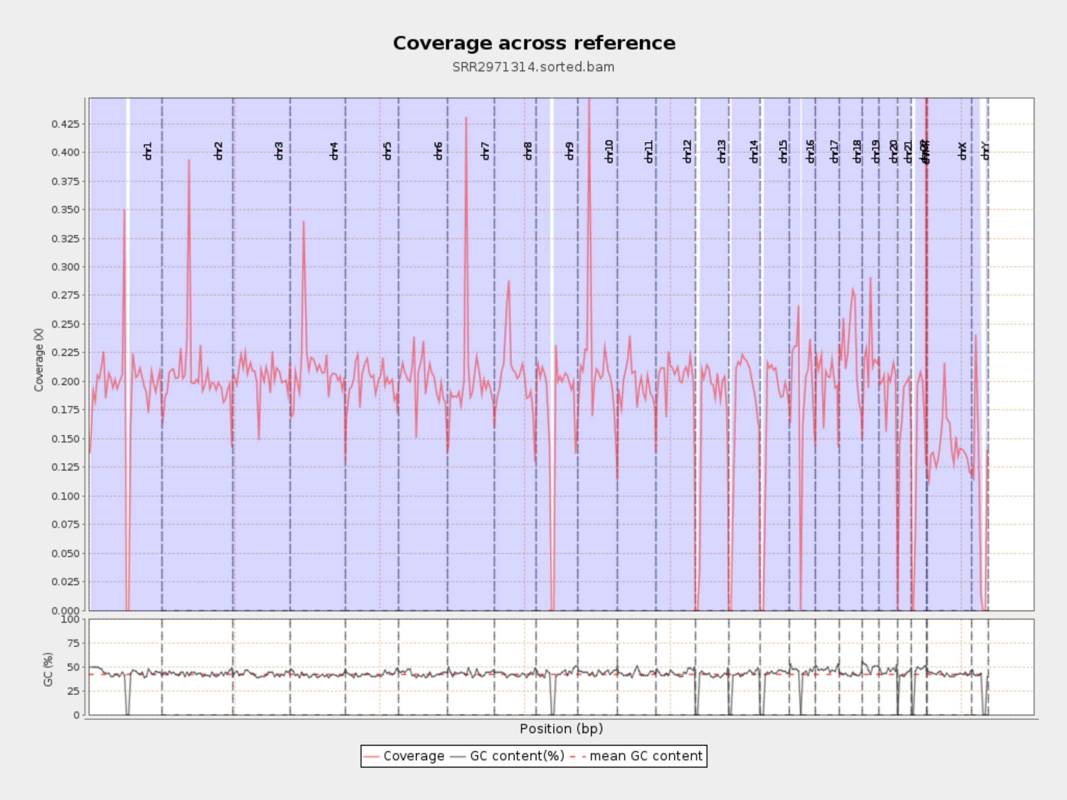
General error rate	0.52%
Mismatches	3,038,964
Insertions	39,721
Mapped reads with at least one insertion	0.32%
Deletions	87,738
Mapped reads with at least one deletion	0.71%
Homopolymer indels	40.68%

2.6. Chromosome stats

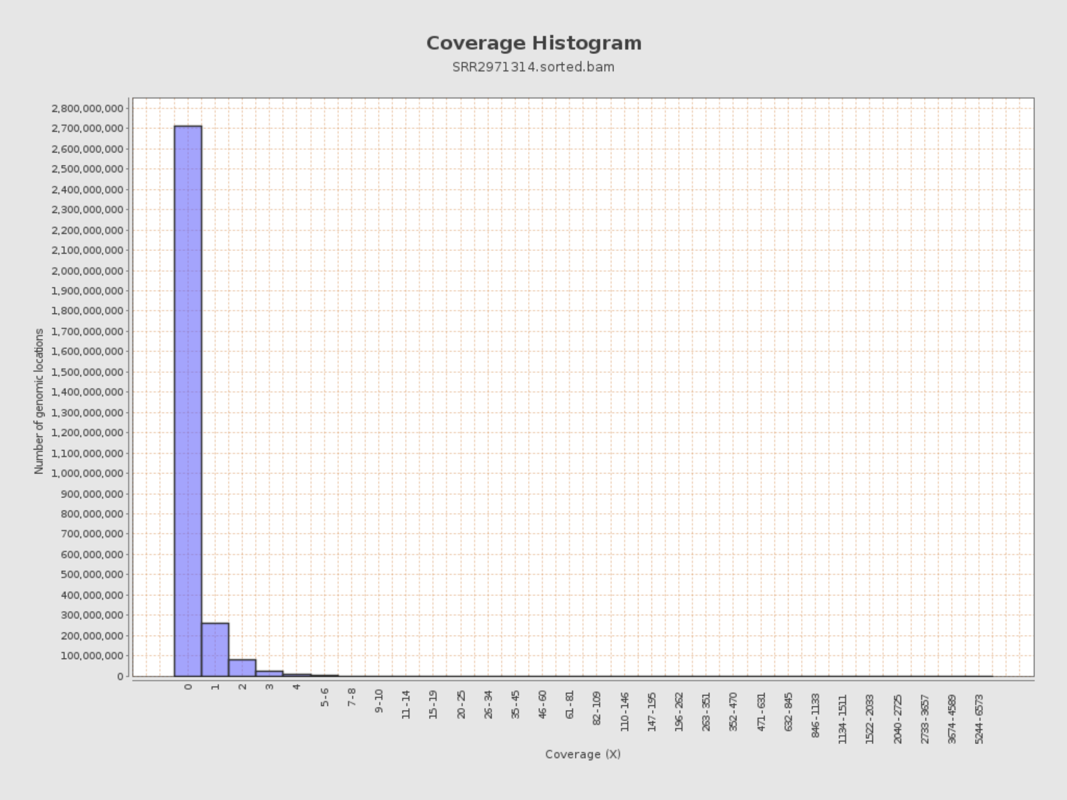
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	47312366	0.1898	3.5272
chr2	243199373	50031422	0.2057	1.595
chr3	198022430	40576952	0.2049	0.6636
chr4	191154276	40271168	0.2107	0.9871
chr5	180915260	36277107	0.2005	0.6664
chr6	171115067	34422349	0.2012	0.7287
chr7	159138663	32627434	0.205	2.8242

chr8	146364022	29834753	0.2038	3.4313
chr9	141213431	24800480	0.1756	1.6369
chr10	135534747	29284940	0.2161	1.9025
chr11	135006516	26447403	0.1959	1.3198
chr12	133851895	27378636	0.2045	0.7159
chr13	115169878	19047393	0.1654	0.5713
chr14	107349540	18292878	0.1704	0.9188
chr15	102531392	16890429	0.1647	0.5988
chr16	90354753	17291008	0.1914	0.8721
chr17	81195210	16329412	0.2011	0.8958
chr18	78077248	17963380	0.2301	3.2264
chr19	59128983	13140459	0.2222	2.9887
chr20	63025520	12251334	0.1944	0.7082
chr21	48129895	7829214	0.1627	0.9782
chr22	51304566	6701303	0.1306	0.6634
chrMT	16571	65077	3.9272	3.6419
chrX	155270560	22126556	0.1425	0.8068
chrY	59373566	5573973	0.0939	0.9708

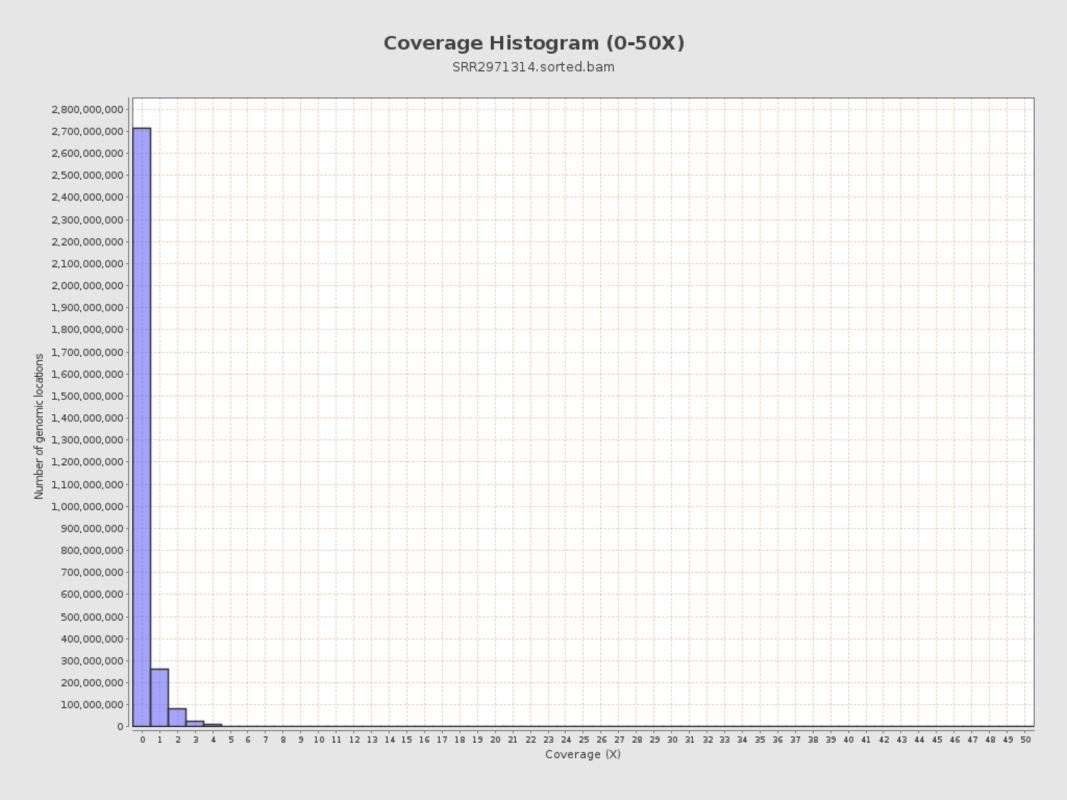
3. Results : Coverage across reference



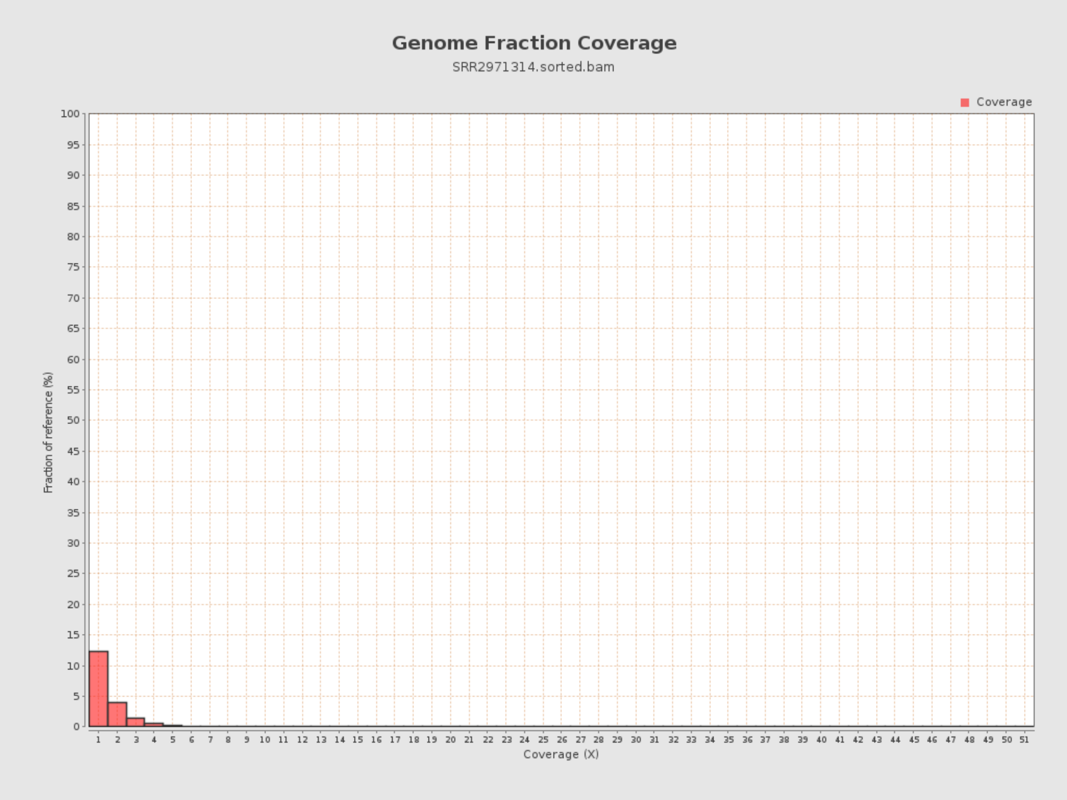
4. Results : Coverage Histogram



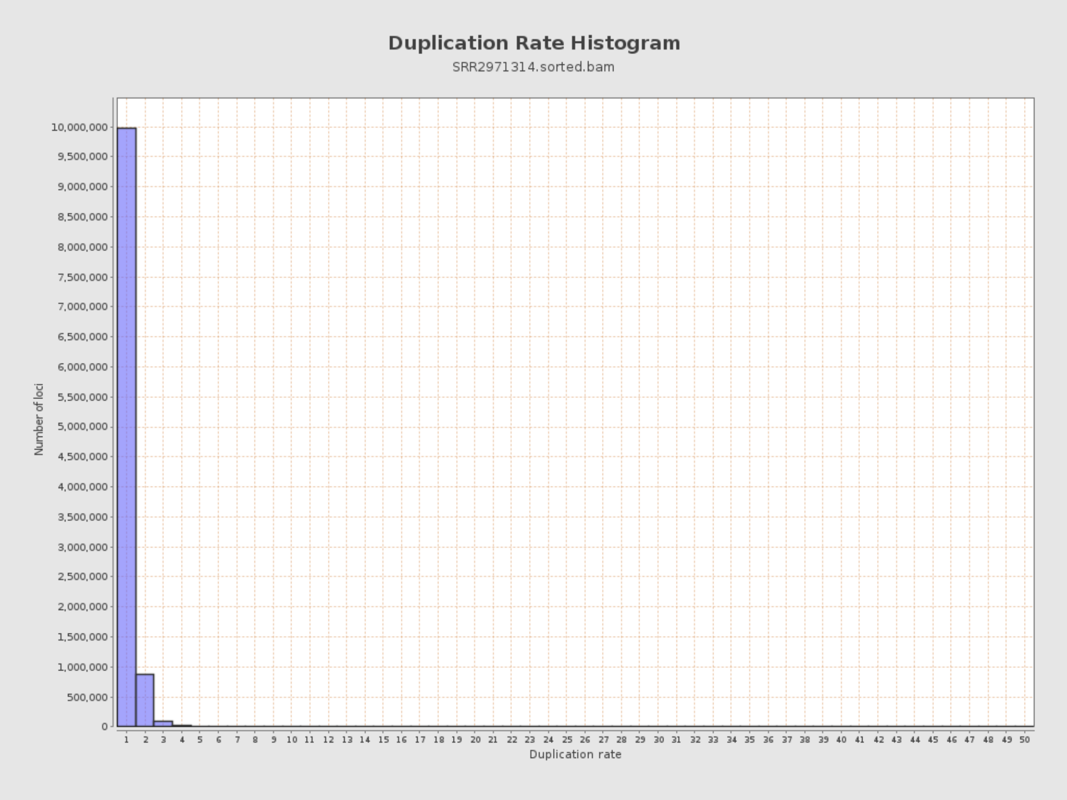
5. Results : Coverage Histogram (0-50X)



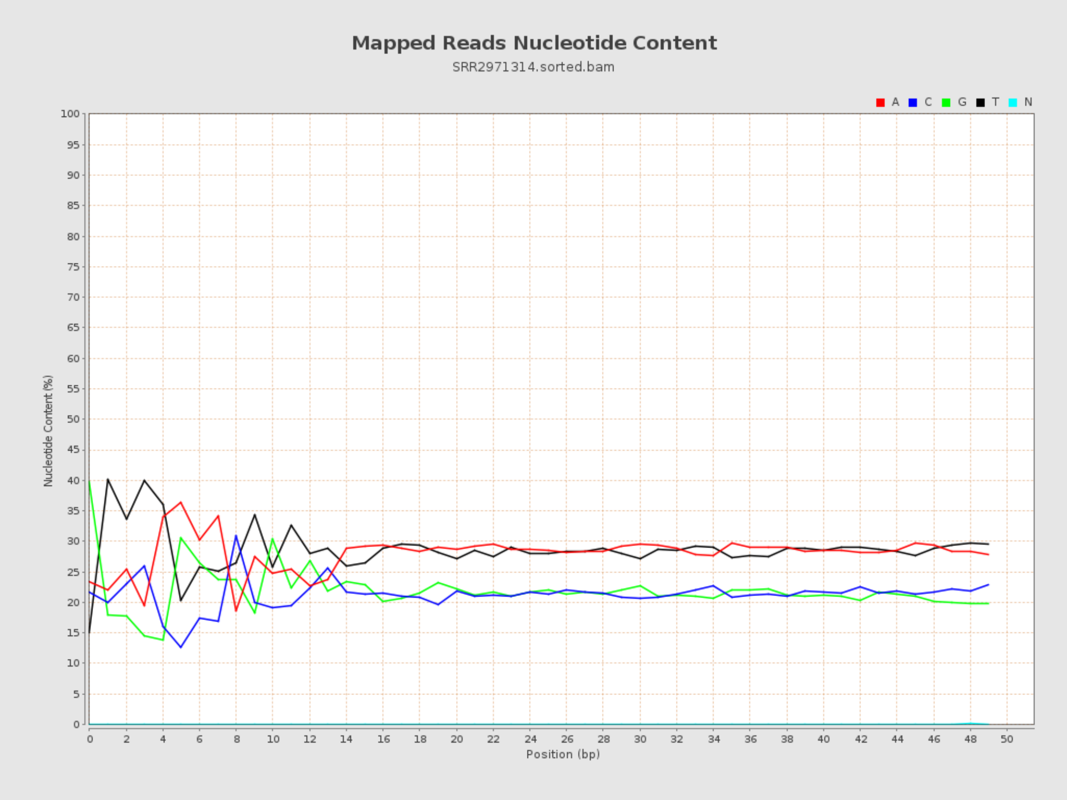
6. Results : Genome Fraction Coverage



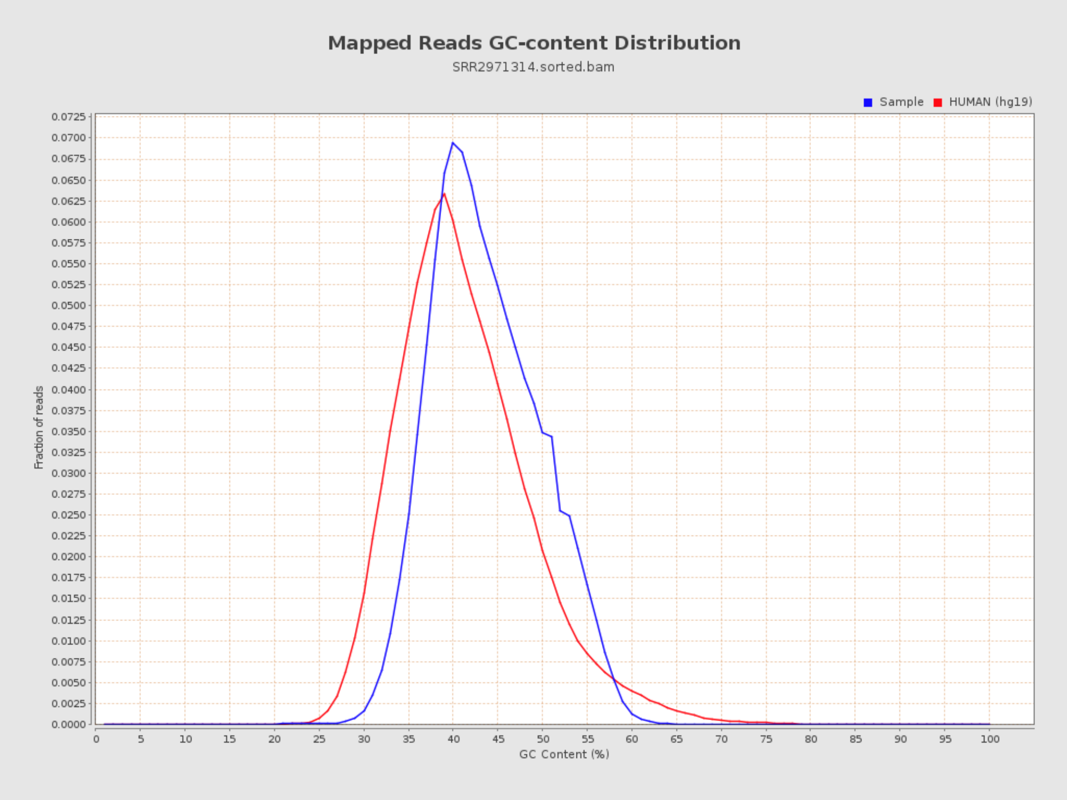
7. Results : Duplication Rate Histogram



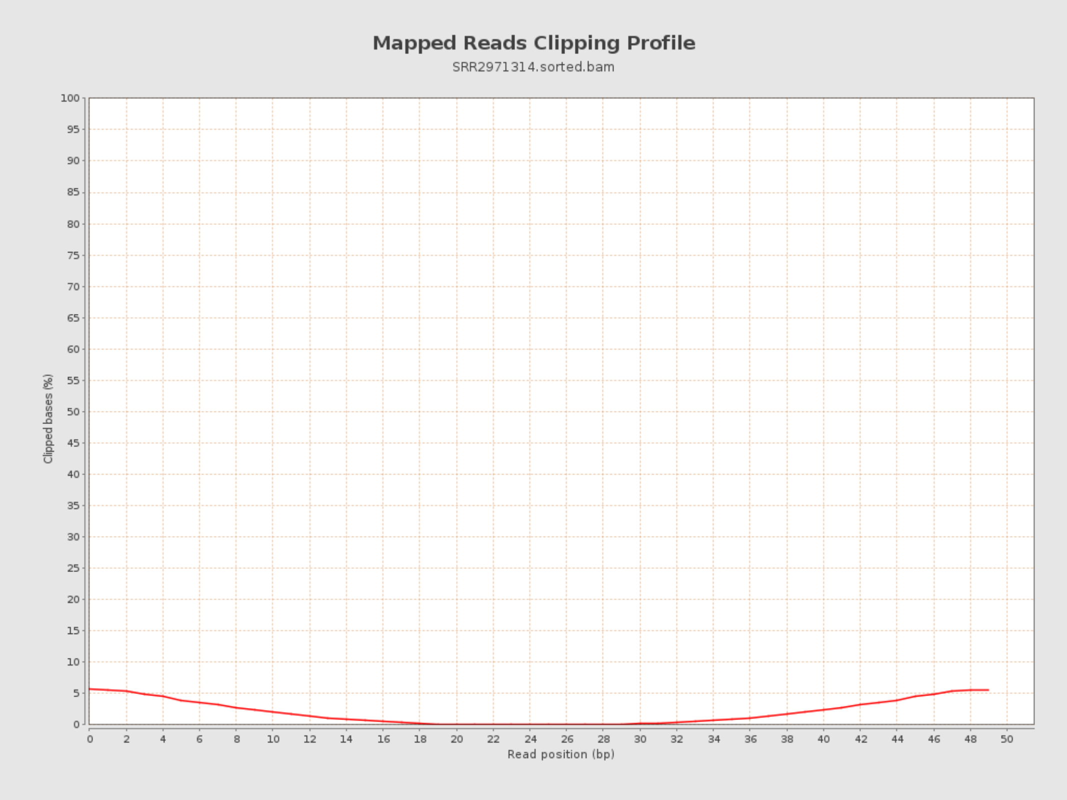
8. Results : Mapped Reads Nucleotide Content



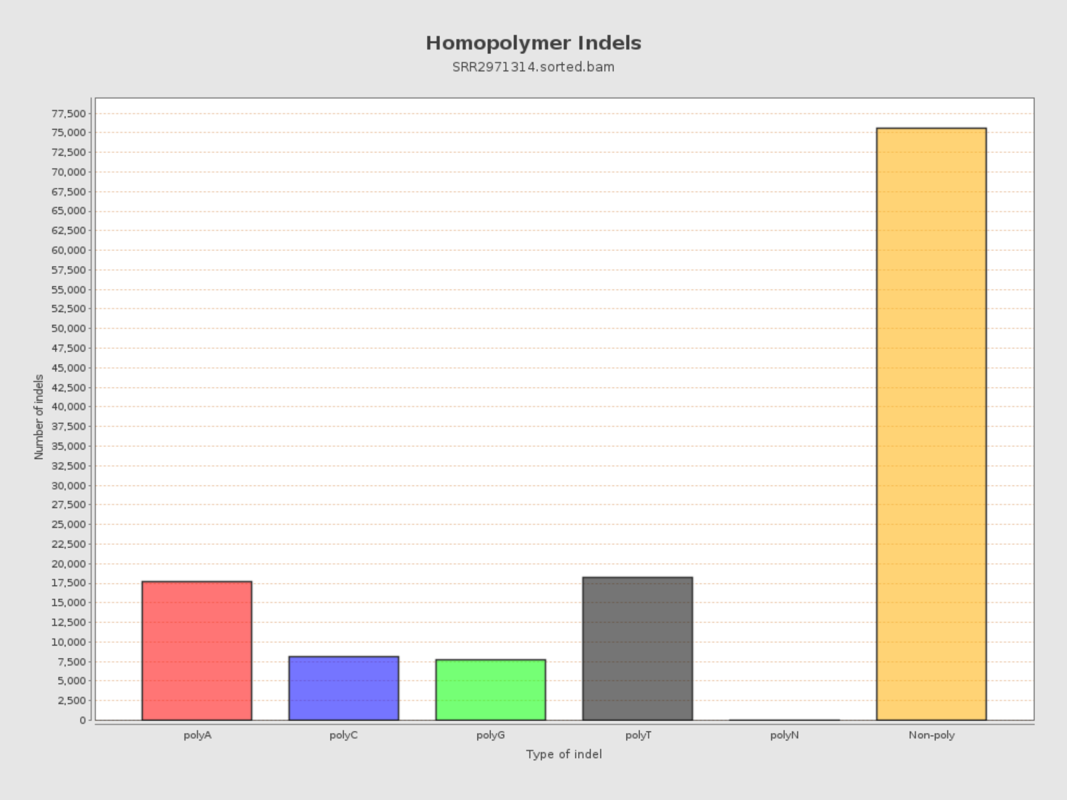
9. Results : Mapped Reads GC-content Distribution



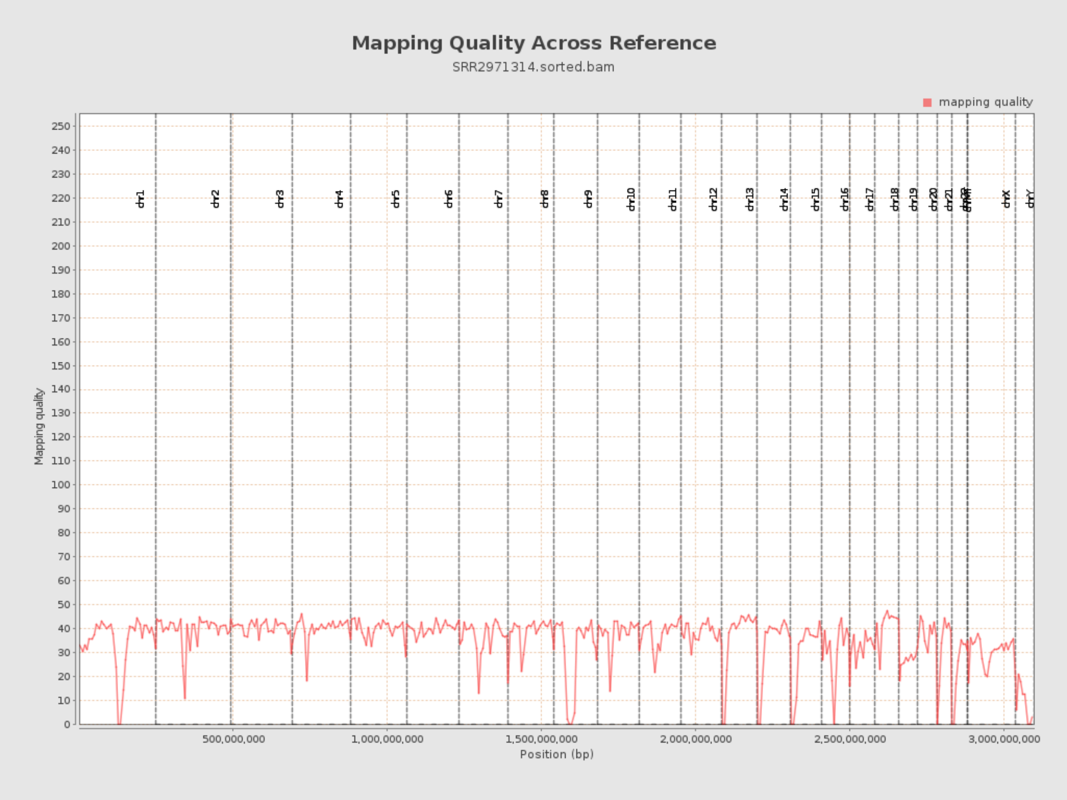
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram