Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 19:04:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013274.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_SRR6013274 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013274.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 19:04:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013274.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,334,117
Mapped reads	1,111,936 / 83.35%
Unmapped reads	222,181 / 16.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,314 / 1.15%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	79,076 / 5.93%
Duplication rate	5.84%
Clipped reads	625,803 / 46.91%

2.2. ACGT Content

Number/percentage of A's	20,353,629 / 28.54%
Number/percentage of C's	12,460,796 / 17.47%
Number/percentage of T's	23,515,137 / 32.97%
Number/percentage of G's	14,977,793 / 21%
Number/percentage of N's	16,431 / 0.02%
GC Percentage	38.47%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2997

2.4. Mapping Quality

Mean Mapping Quality	44.51

2.5. Mismatches and indels

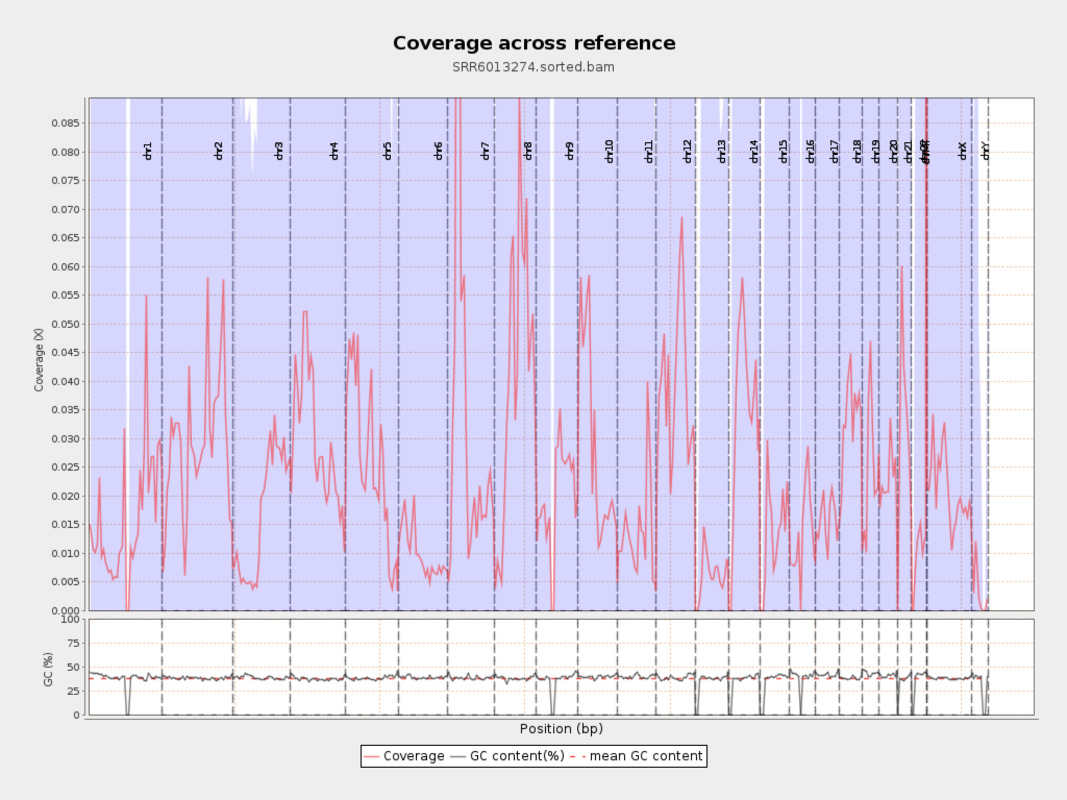
General error rate	1.03%
Mismatches	722,856
Insertions	5,615
Mapped reads with at least one insertion	0.5%
Deletions	38,658
Mapped reads with at least one deletion	3.41%
Homopolymer indels	42.1%

2.6. Chromosome stats

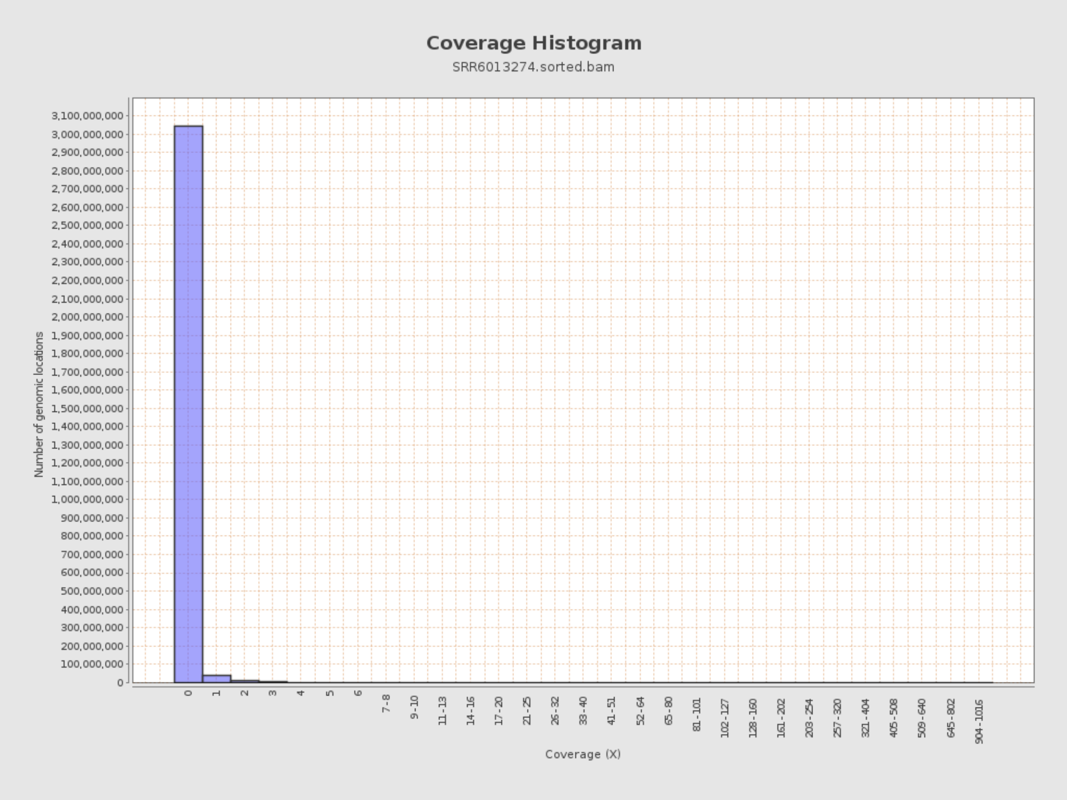
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3920349	0.0157	0.5444
chr2	243199373	7027795	0.0289	0.2942
chr3	198022430	3297511	0.0167	0.1663
chr4	191154276	5685927	0.0297	0.2368
chr5	180915260	4824402	0.0267	0.2176
chr6	171115067	1719788	0.0101	0.1417
chr7	159138663	5578322	0.0351	0.3018

chr8	146364022	5977939	0.0408	0.6321
chr9	141213431	2832825	0.0201	0.2287
chr10	135534747	3986386	0.0294	0.2913
chr11	135006516	1808237	0.0134	0.1648
chr12	133851895	5278343	0.0394	0.2649
chr13	115169878	705836	0.0061	0.099
chr14	107349540	3765218	0.0351	0.252
chr15	102531392	1403840	0.0137	0.1479
chr16	90354753	1217308	0.0135	0.1633
chr17	81195210	1272820	0.0157	0.1611
chr18	78077248	2603941	0.0334	0.4315
chr19	59128983	1489354	0.0252	0.3528
chr20	63025520	1449116	0.023	0.2065
chr21	48129895	1575726	0.0327	0.2429
chr22	51304566	468542	0.0091	0.119
chrMT	16571	11761	0.7097	1.0157
chrX	155270560	3293030	0.0212	0.2001
chrY	59373566	196946	0.0033	0.104

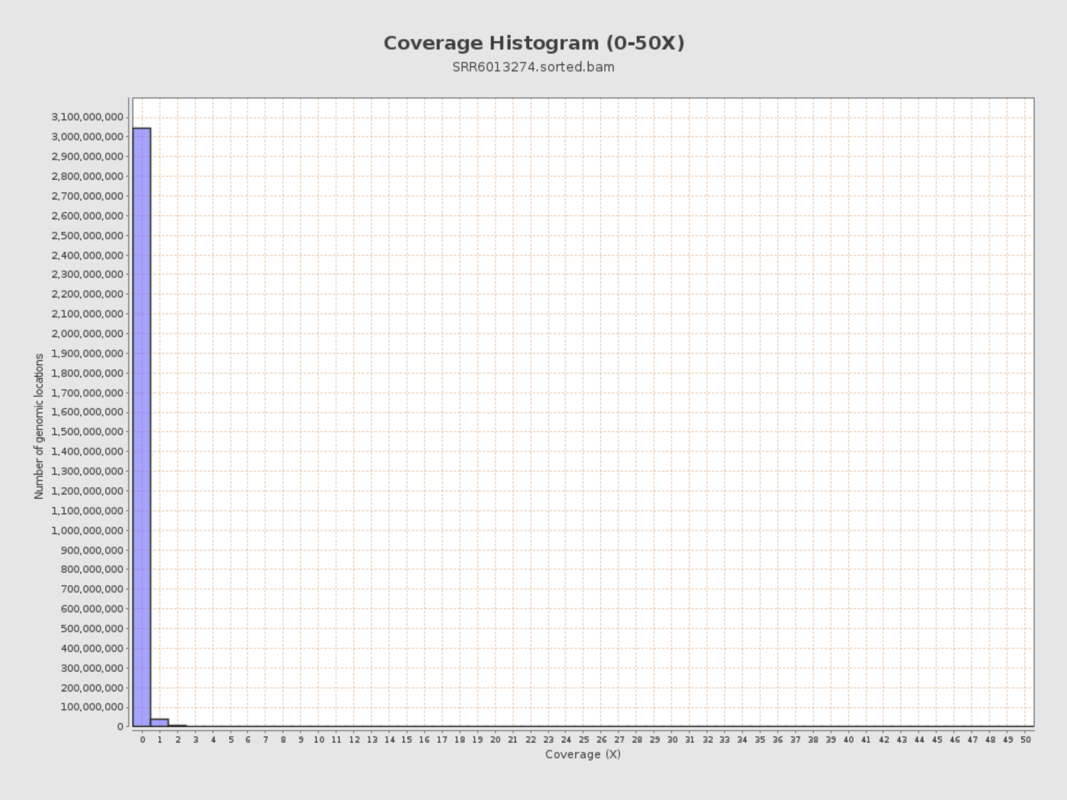
3. Results : Coverage across reference



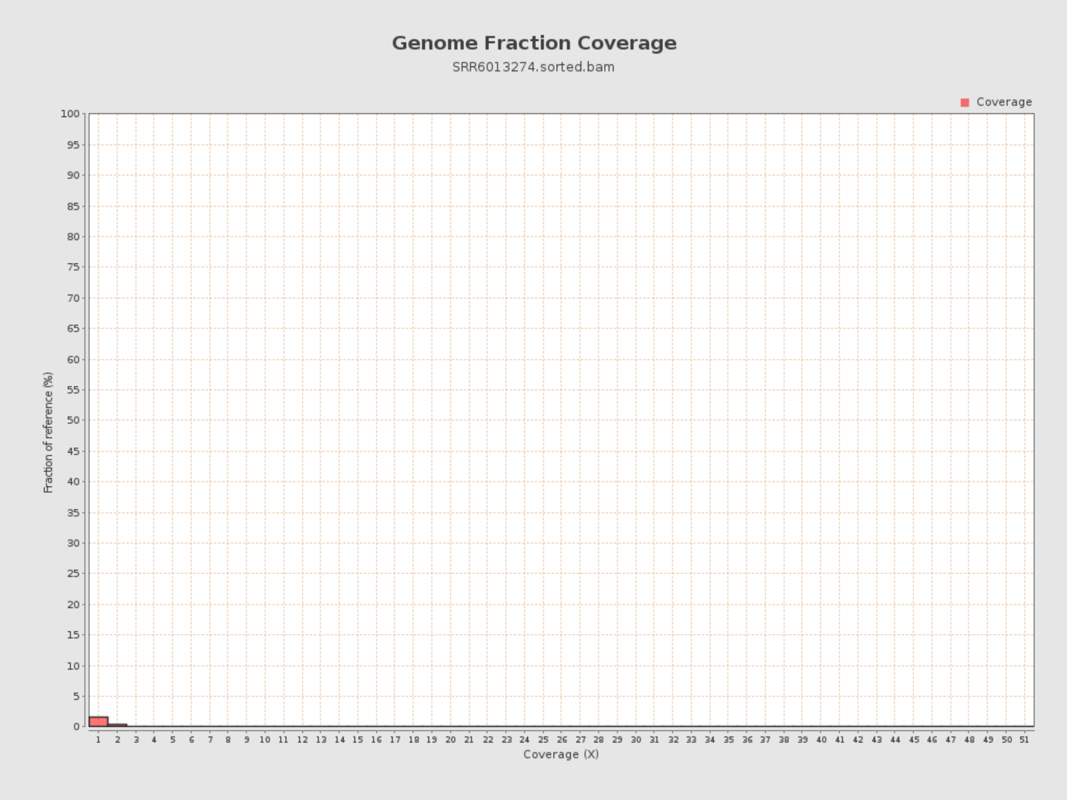
4. Results : Coverage Histogram



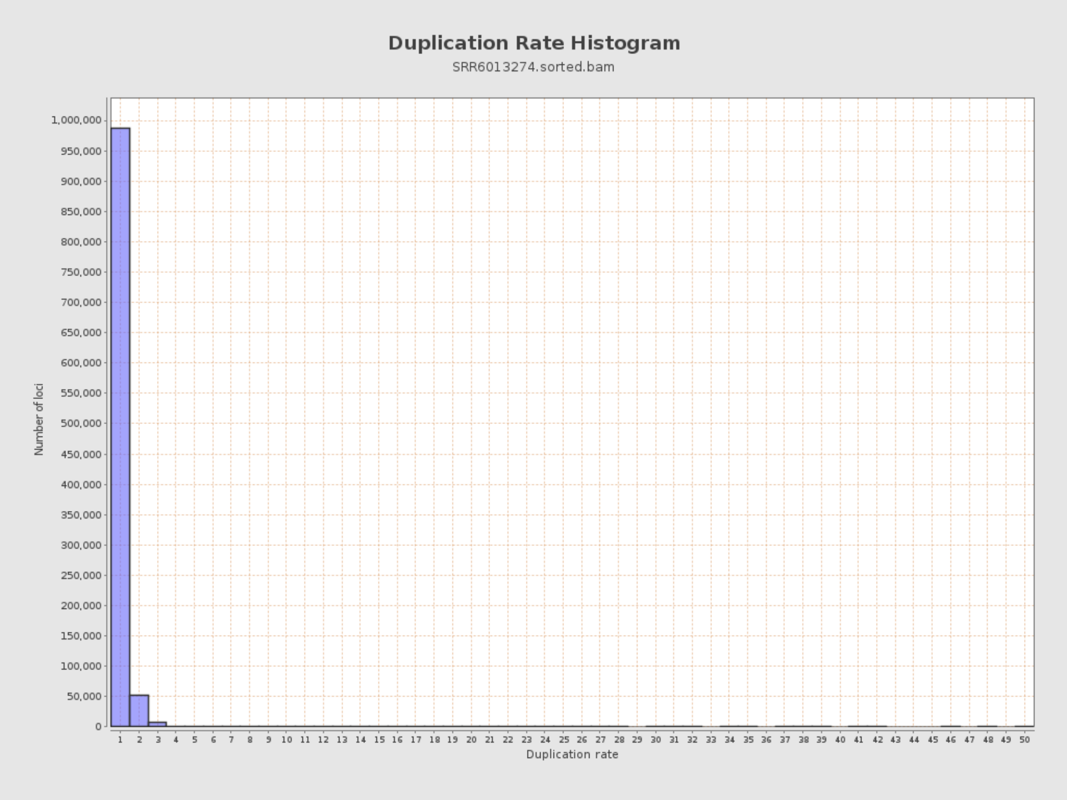
5. Results : Coverage Histogram (0-50X)



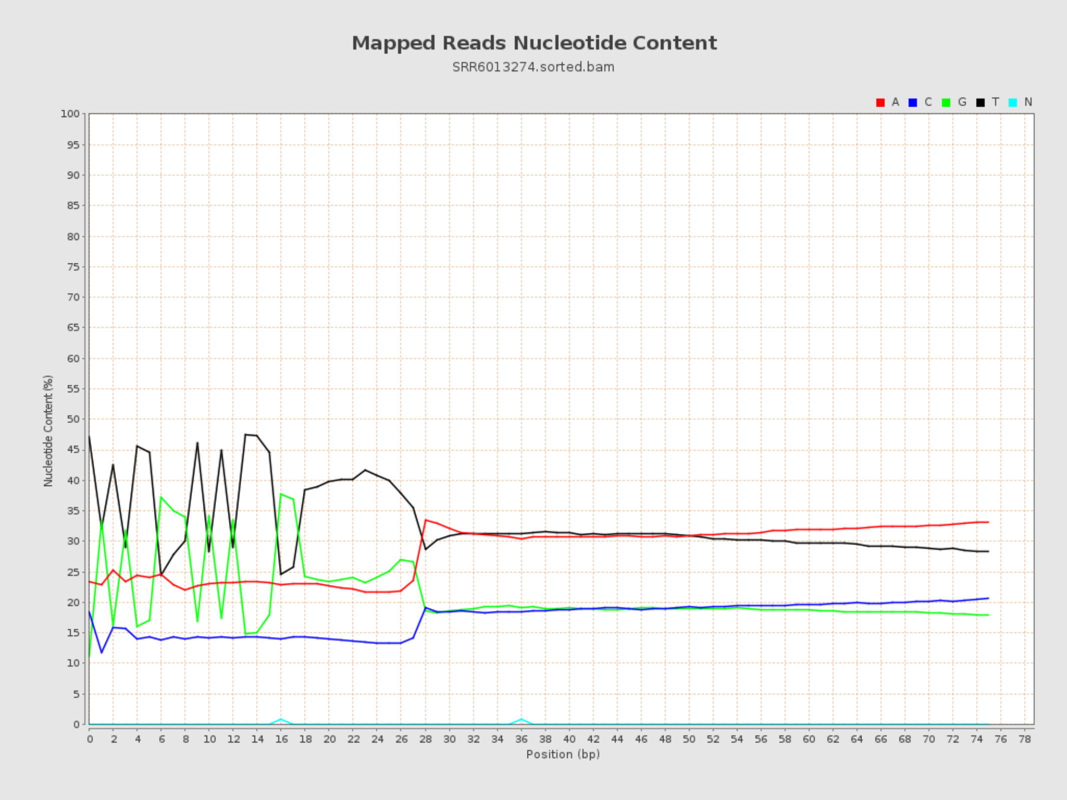
6. Results : Genome Fraction Coverage



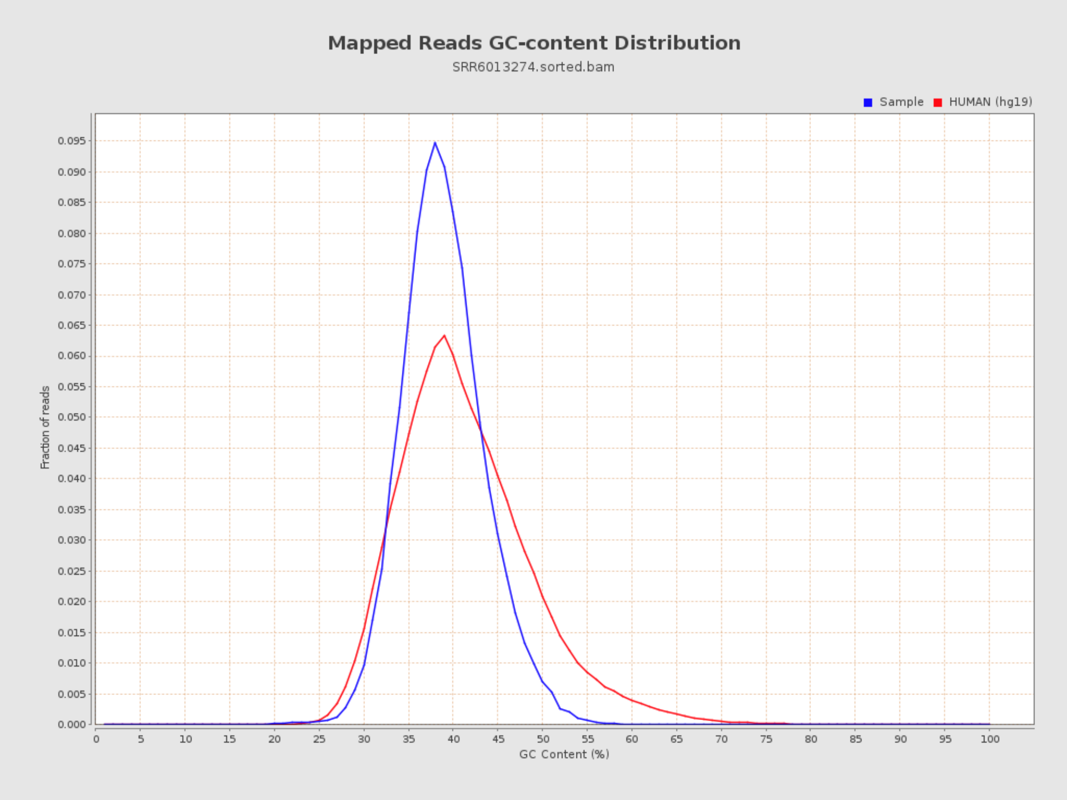
7. Results : Duplication Rate Histogram



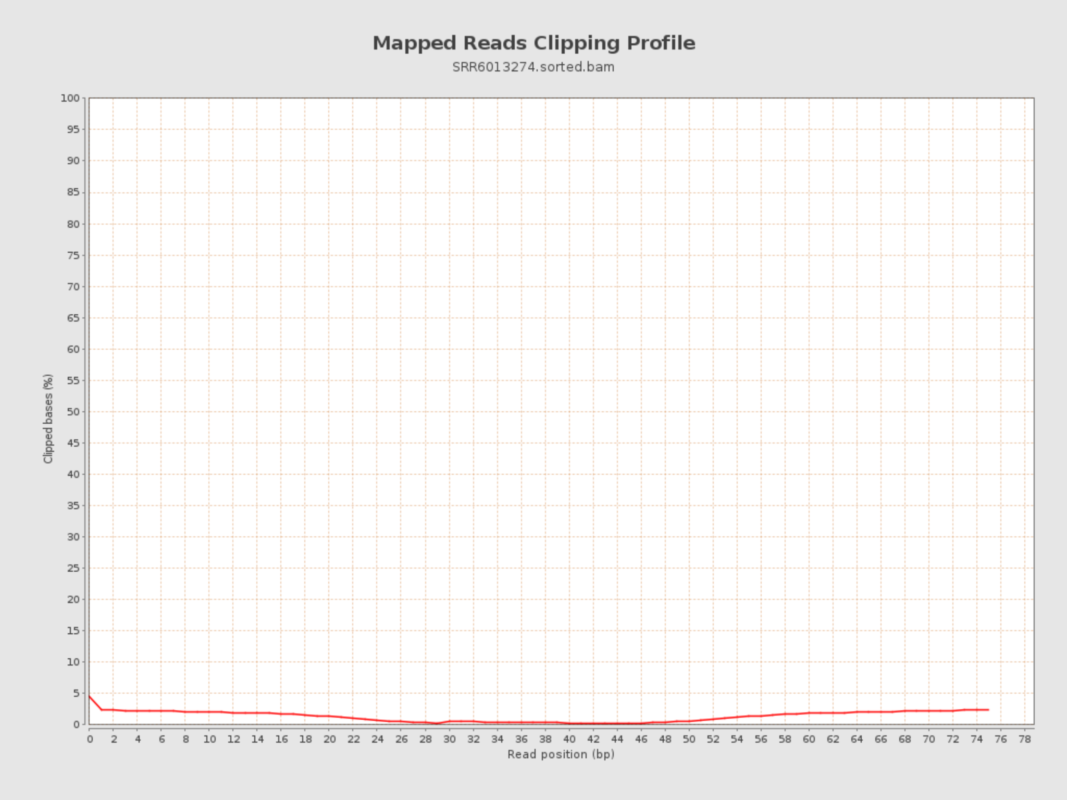
8. Results : Mapped Reads Nucleotide Content



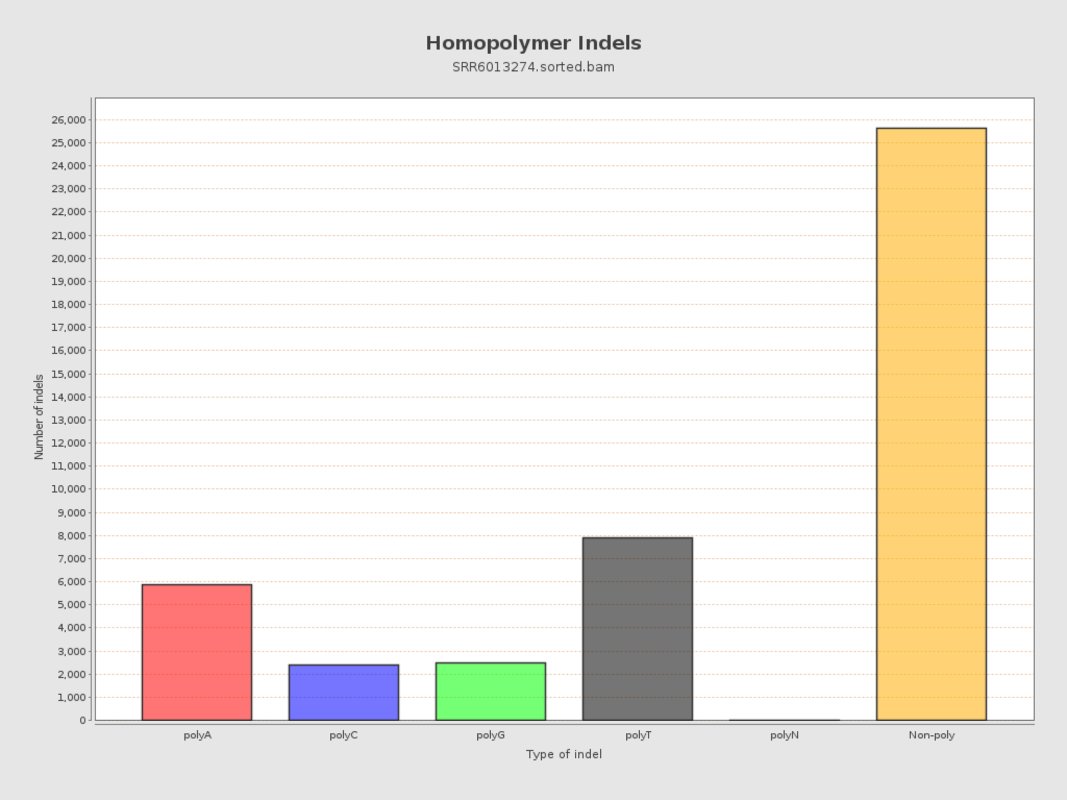
9. Results : Mapped Reads GC-content Distribution



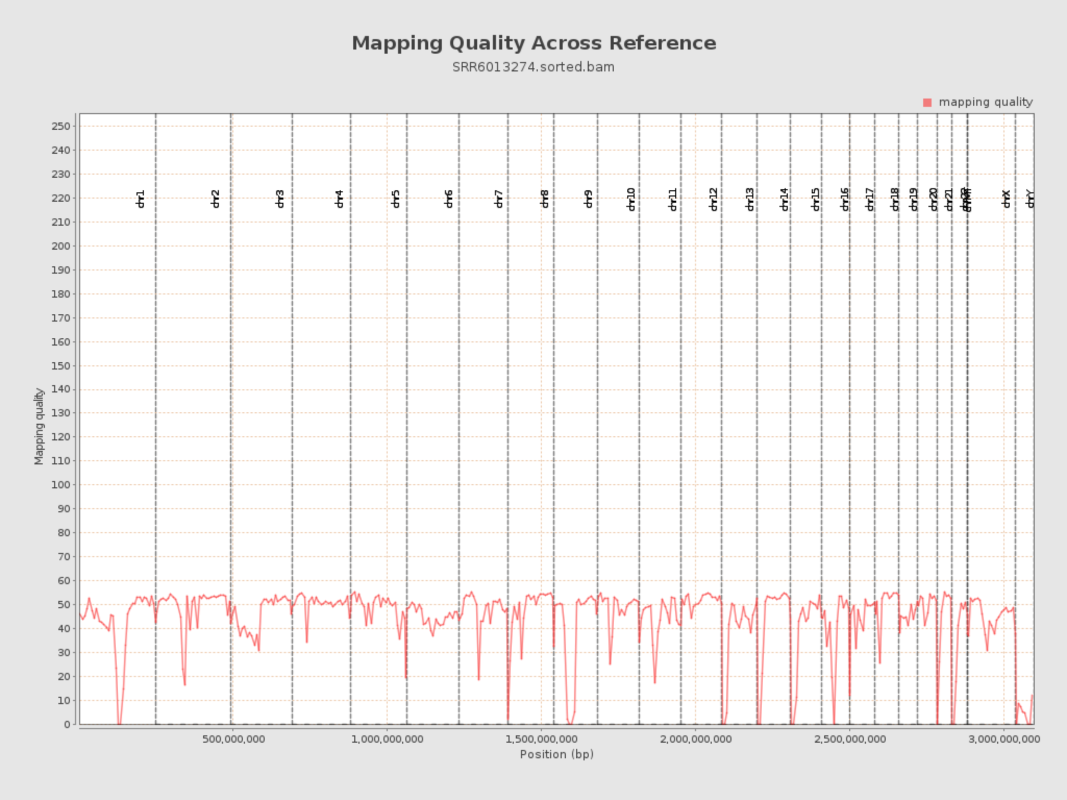
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram