Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 02:29:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240015.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_SRR6240015 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240015.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 02:29:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240015.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,369,500
Mapped reads	1,000,596 / 73.06%
Unmapped reads	368,904 / 26.94%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,910 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	227,002 / 16.58%
Duplication rate	13.78%
Clipped reads	691,321 / 50.48%

2.2. ACGT Content

Number/percentage of A's	16,200,108 / 26.7%
Number/percentage of C's	10,185,177 / 16.79%
Number/percentage of T's	19,425,401 / 32.01%
Number/percentage of G's	14,831,010 / 24.44%
Number/percentage of N's	38,017 / 0.06%
GC Percentage	41.23%

2.3. Coverage

Mean	0.0196

Standard Deviation	0.3414

2.4. Mapping Quality

Mean Mapping Quality	42.18

2.5. Mismatches and indels

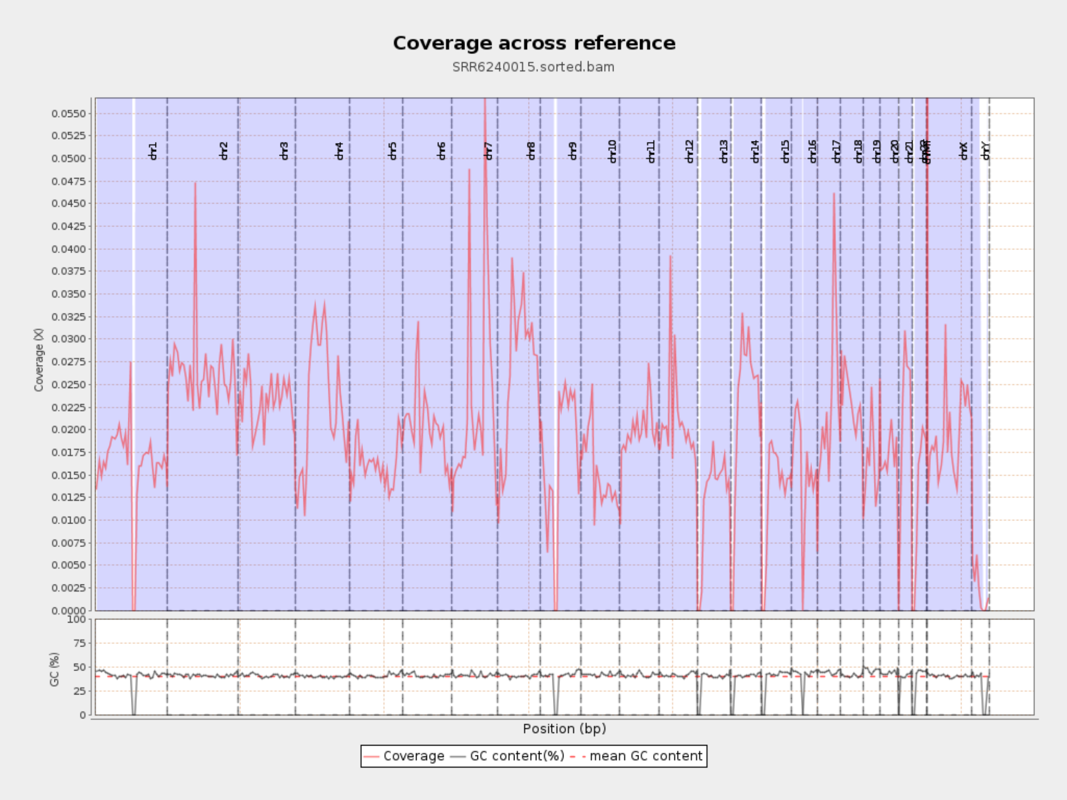
General error rate	1.07%
Mismatches	640,801
Insertions	4,450
Mapped reads with at least one insertion	0.44%
Deletions	20,119
Mapped reads with at least one deletion	1.99%
Homopolymer indels	49.52%

2.6. Chromosome stats

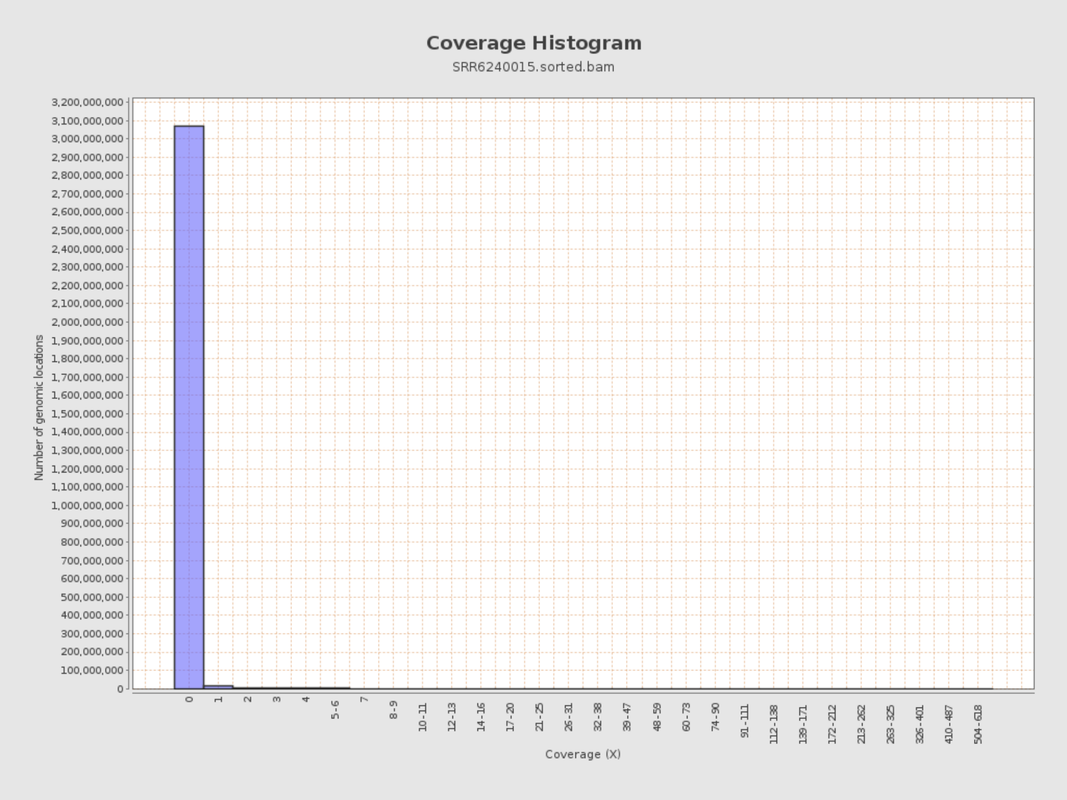
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4028468	0.0162	0.3608
chr2	243199373	6422252	0.0264	0.4138
chr3	198022430	4623796	0.0233	0.3266
chr4	191154276	4402059	0.023	0.3271
chr5	180915260	2941610	0.0163	0.2549
chr6	171115067	3482370	0.0204	0.3176
chr7	159138663	3675763	0.0231	0.6001

chr8	146364022	3946870	0.027	0.4415
chr9	141213431	2392007	0.0169	0.3014
chr10	135534747	2068243	0.0153	0.2678
chr11	135006516	2701942	0.02	0.3077
chr12	133851895	2805868	0.021	0.3047
chr13	115169878	1431012	0.0124	0.2273
chr14	107349540	2412220	0.0225	0.3184
chr15	102531392	1322921	0.0129	0.2352
chr16	90354753	1391615	0.0154	0.2476
chr17	81195210	1887178	0.0232	0.3227
chr18	78077248	1803420	0.0231	0.4216
chr19	59128983	988499	0.0167	0.3172
chr20	63025520	1068843	0.017	0.2602
chr21	48129895	1028525	0.0214	0.3143
chr22	51304566	648258	0.0126	0.2294
chrMT	16571	63737	3.8463	4.1259
chrX	155270560	3045930	0.0196	0.2963
chrY	59373566	132436	0.0022	0.0725

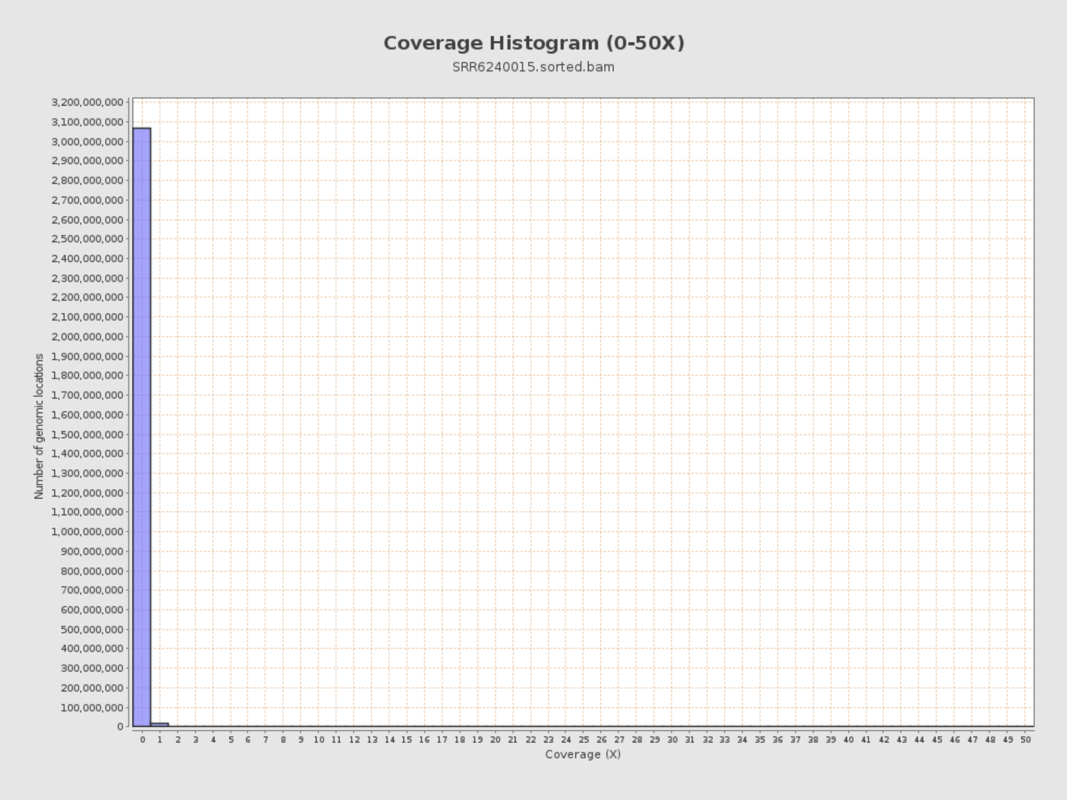
3. Results : Coverage across reference



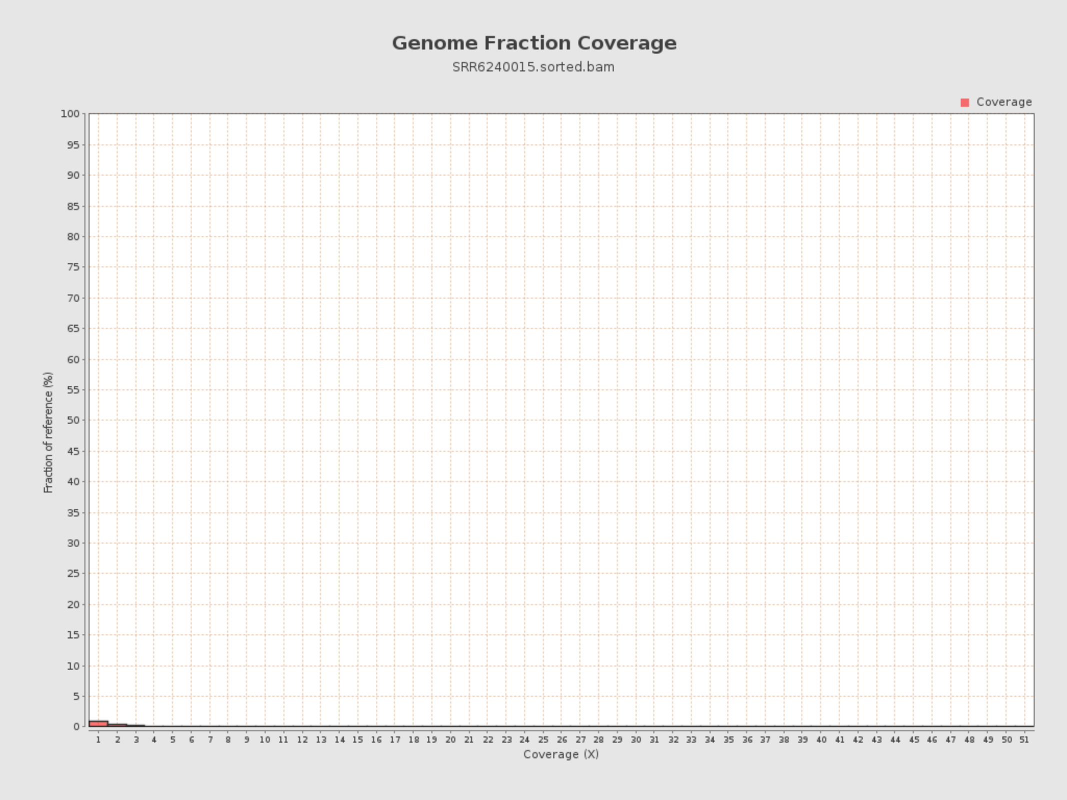
4. Results : Coverage Histogram



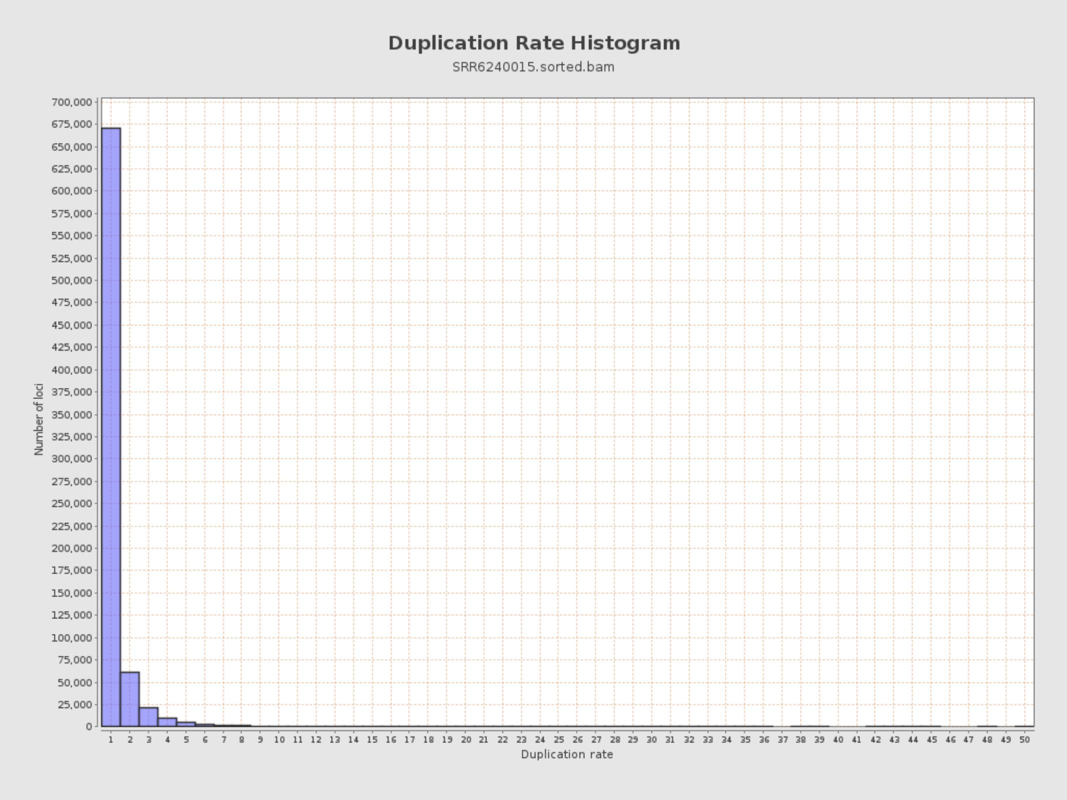
5. Results : Coverage Histogram (0-50X)



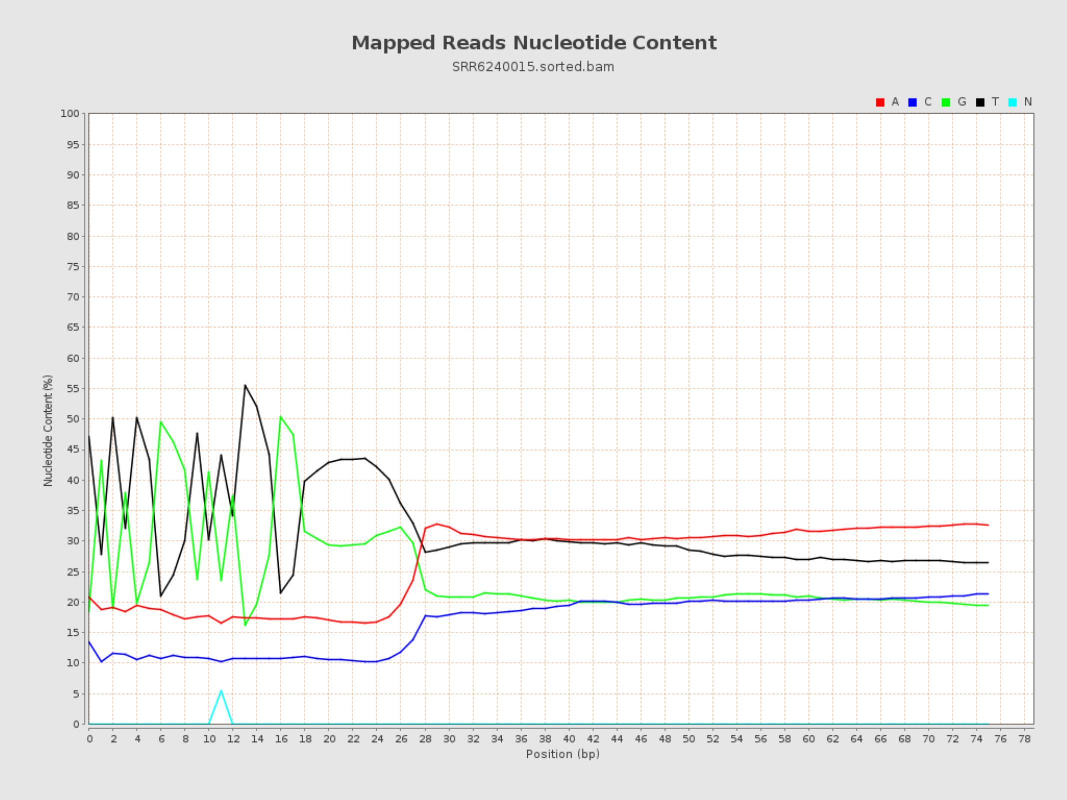
6. Results : Genome Fraction Coverage



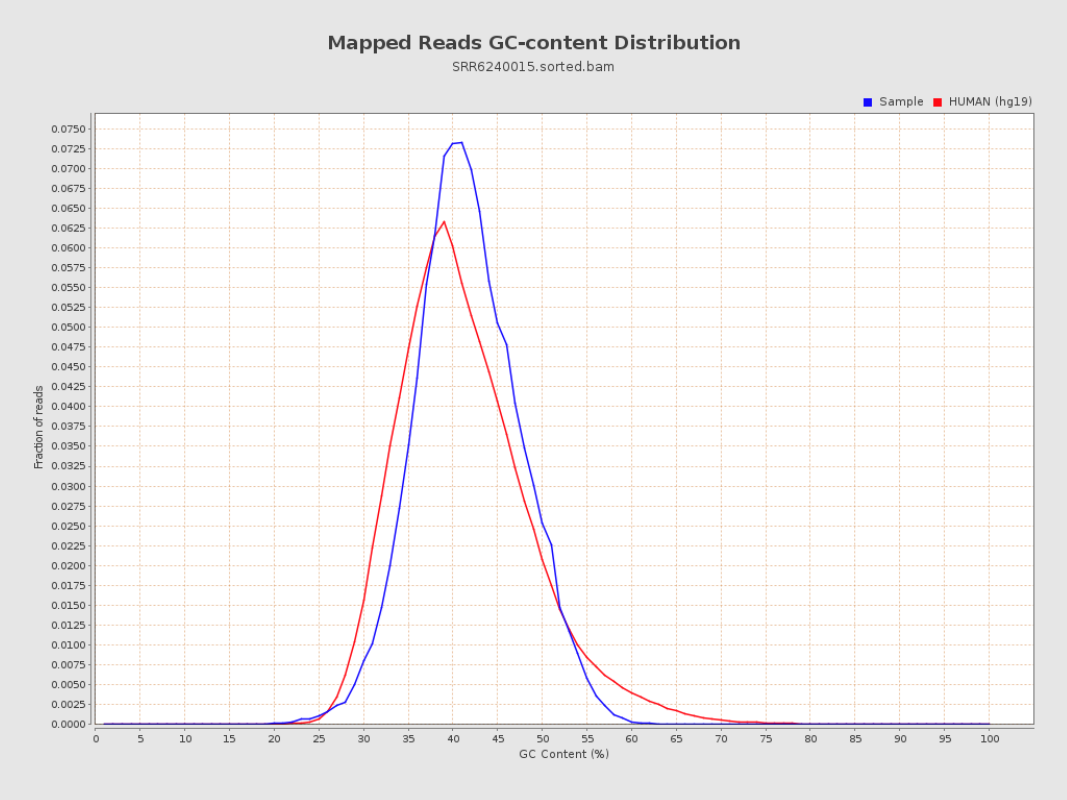
7. Results : Duplication Rate Histogram



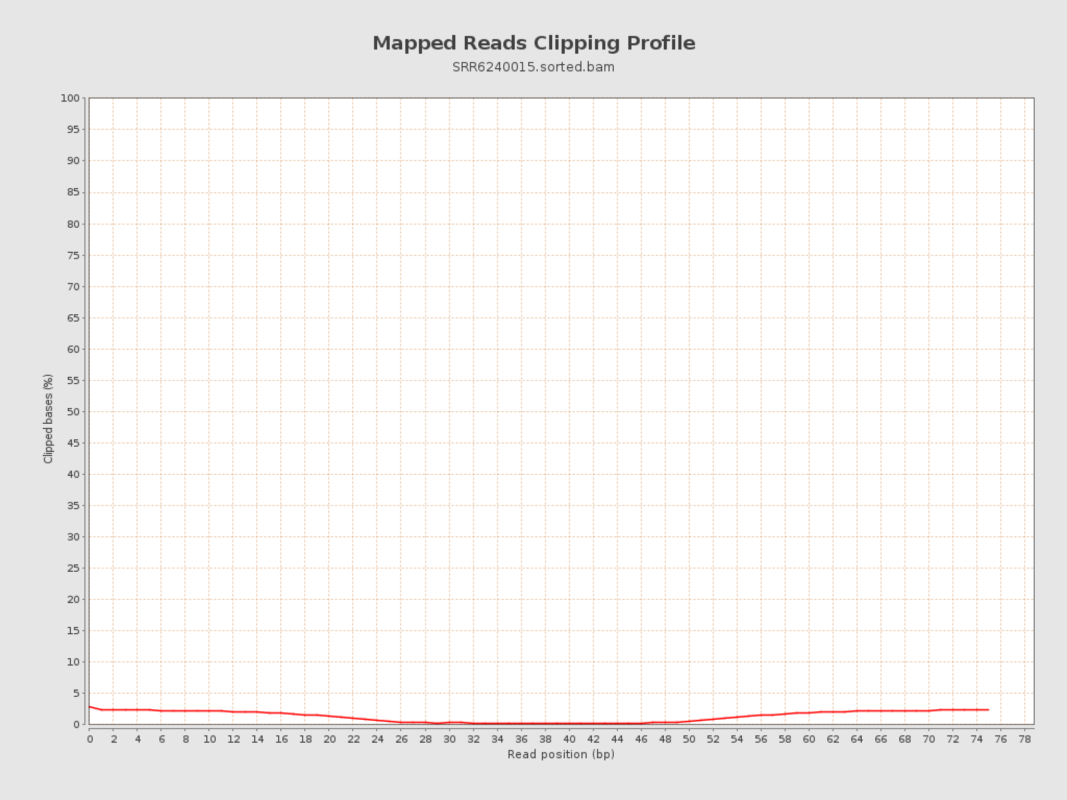
8. Results : Mapped Reads Nucleotide Content



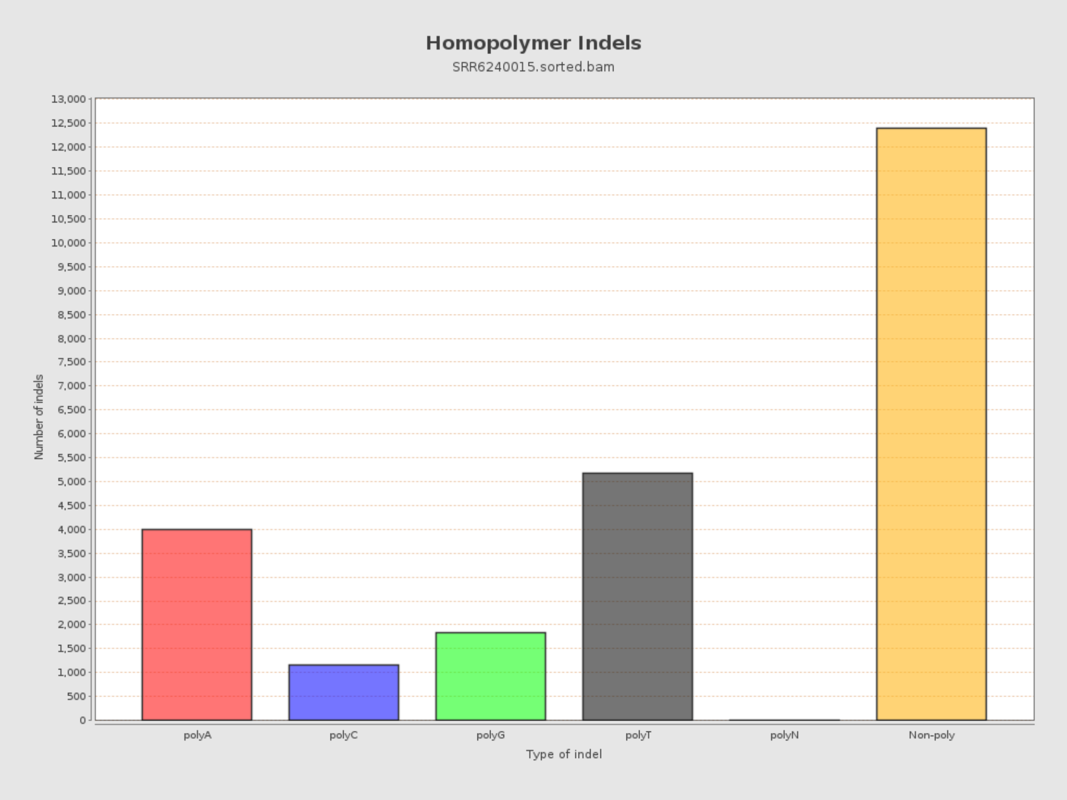
9. Results : Mapped Reads GC-content Distribution



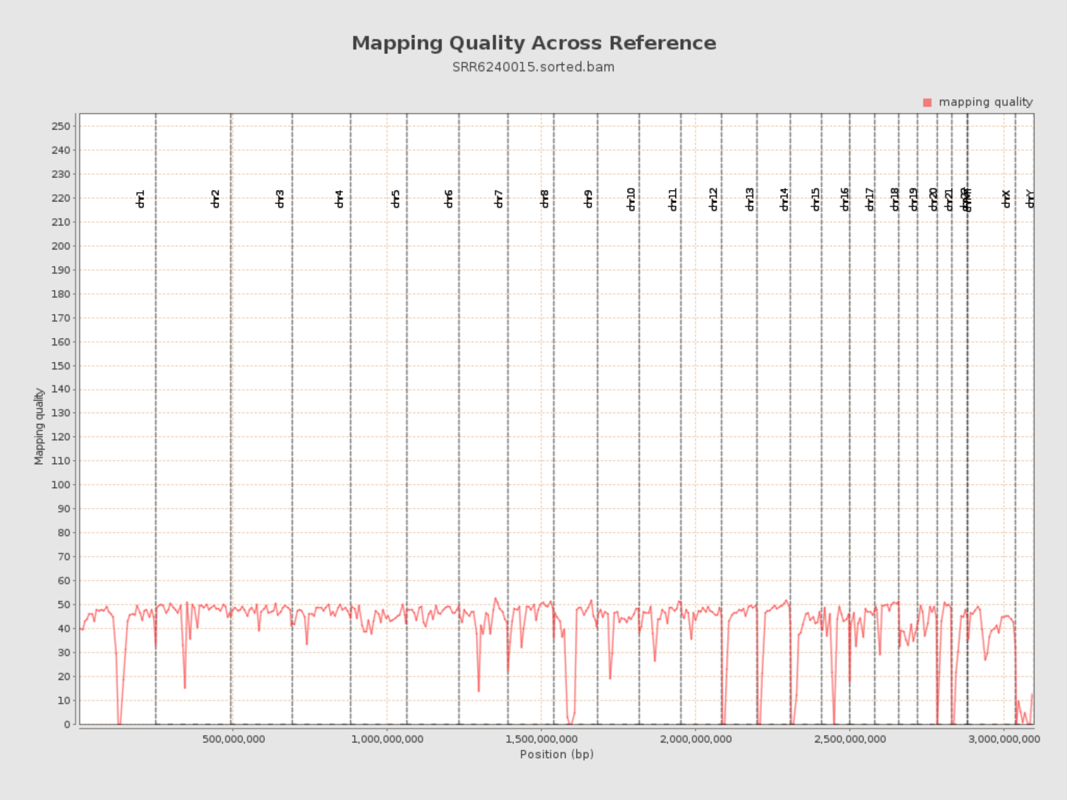
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram