Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:20:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240034.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_SRR6240034 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240034.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:20:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240034.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,341,476
Mapped reads	1,031,201 / 76.87%
Unmapped reads	310,275 / 23.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,349 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	146,518 / 10.92%
Duplication rate	11.01%
Clipped reads	530,751 / 39.56%

2.2. ACGT Content

Number/percentage of A's	18,177,746 / 27.21%
Number/percentage of C's	11,847,780 / 17.73%
Number/percentage of T's	21,885,795 / 32.76%
Number/percentage of G's	14,898,500 / 22.3%
Number/percentage of N's	5,983 / 0.01%
GC Percentage	40.03%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2829

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

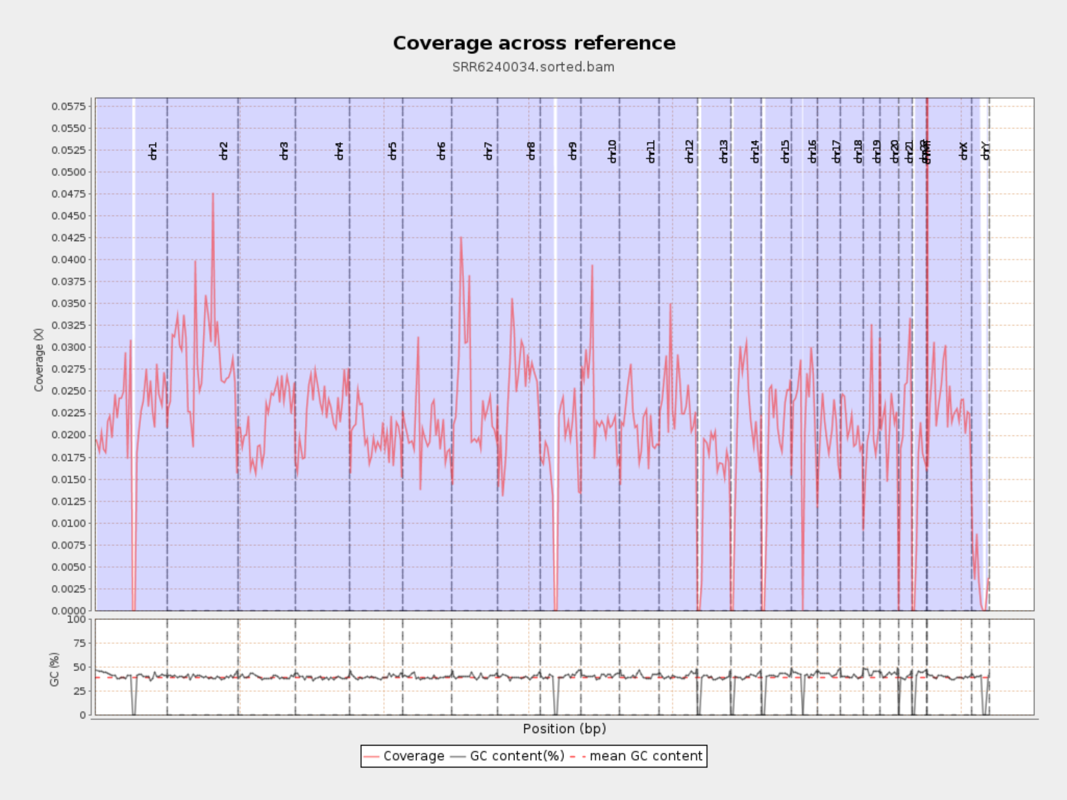
General error rate	0.85%
Mismatches	562,104
Insertions	4,900
Mapped reads with at least one insertion	0.47%
Deletions	18,354
Mapped reads with at least one deletion	1.76%
Homopolymer indels	48.86%

2.6. Chromosome stats

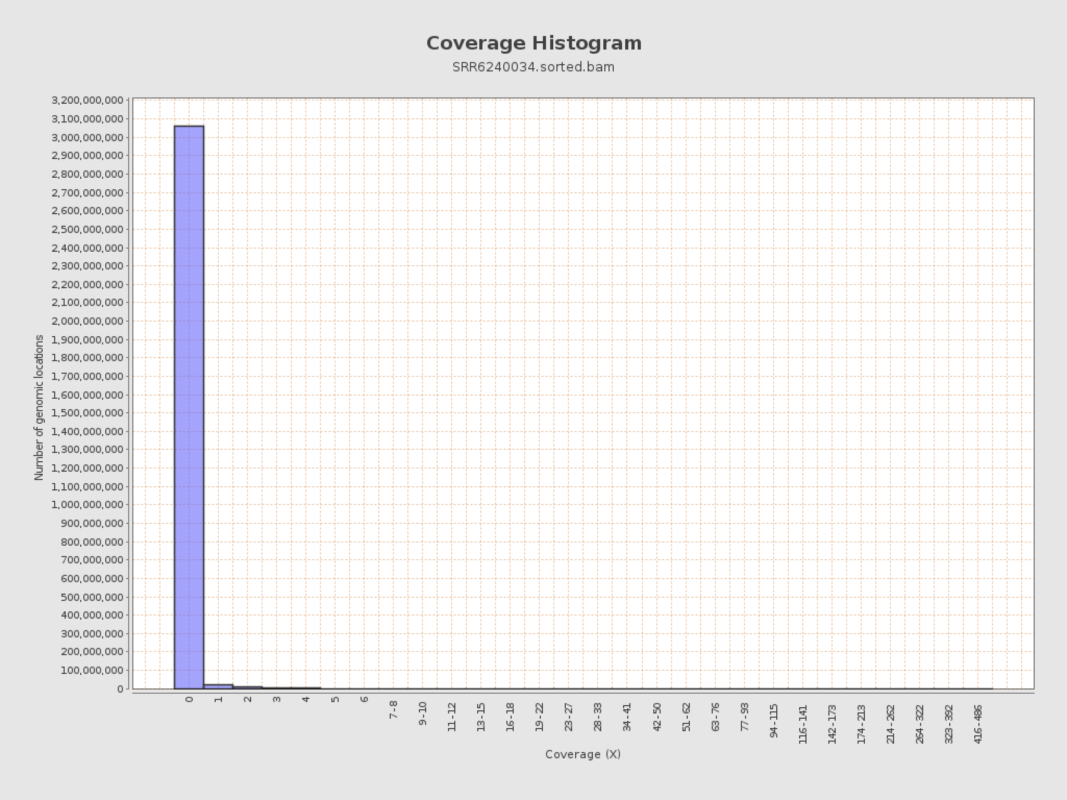
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5372843	0.0216	0.3822
chr2	243199373	7079098	0.0291	0.3354
chr3	198022430	4316437	0.0218	0.245
chr4	191154276	4382340	0.0229	0.2527
chr5	180915260	3614002	0.02	0.2321
chr6	171115067	3498905	0.0204	0.2511
chr7	159138663	3952515	0.0248	0.3533

chr8	146364022	3713462	0.0254	0.3873
chr9	141213431	2458110	0.0174	0.2429
chr10	135534747	3195516	0.0236	0.2882
chr11	135006516	2833530	0.021	0.2634
chr12	133851895	3230573	0.0241	0.2573
chr13	115169878	1725279	0.015	0.2027
chr14	107349540	2149551	0.02	0.2339
chr15	102531392	1924151	0.0188	0.2252
chr16	90354753	1986572	0.022	0.2426
chr17	81195210	1630607	0.0201	0.2405
chr18	78077248	1640122	0.021	0.3454
chr19	59128983	1220504	0.0206	0.2953
chr20	63025520	1313468	0.0208	0.2361
chr21	48129895	1067804	0.0222	0.2459
chr22	51304566	658052	0.0128	0.1832
chrMT	16571	17042	1.0284	1.9451
chrX	155270560	3674963	0.0237	0.2619
chrY	59373566	192444	0.0032	0.0857

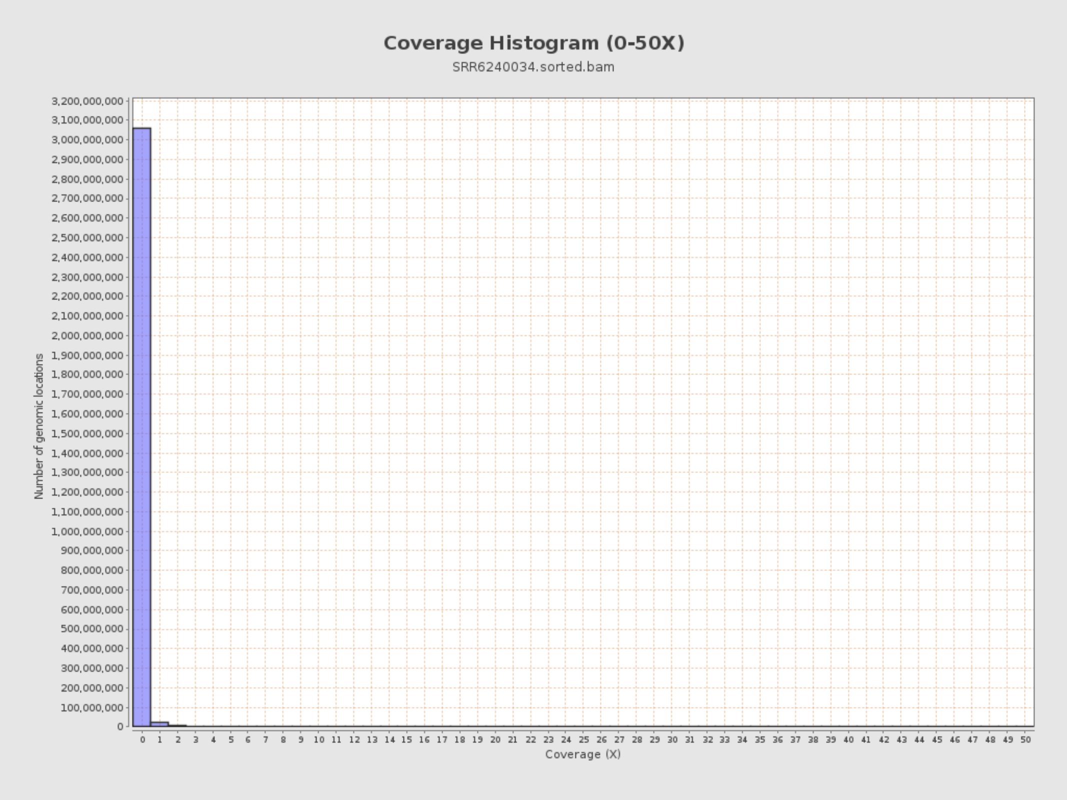
3. Results : Coverage across reference



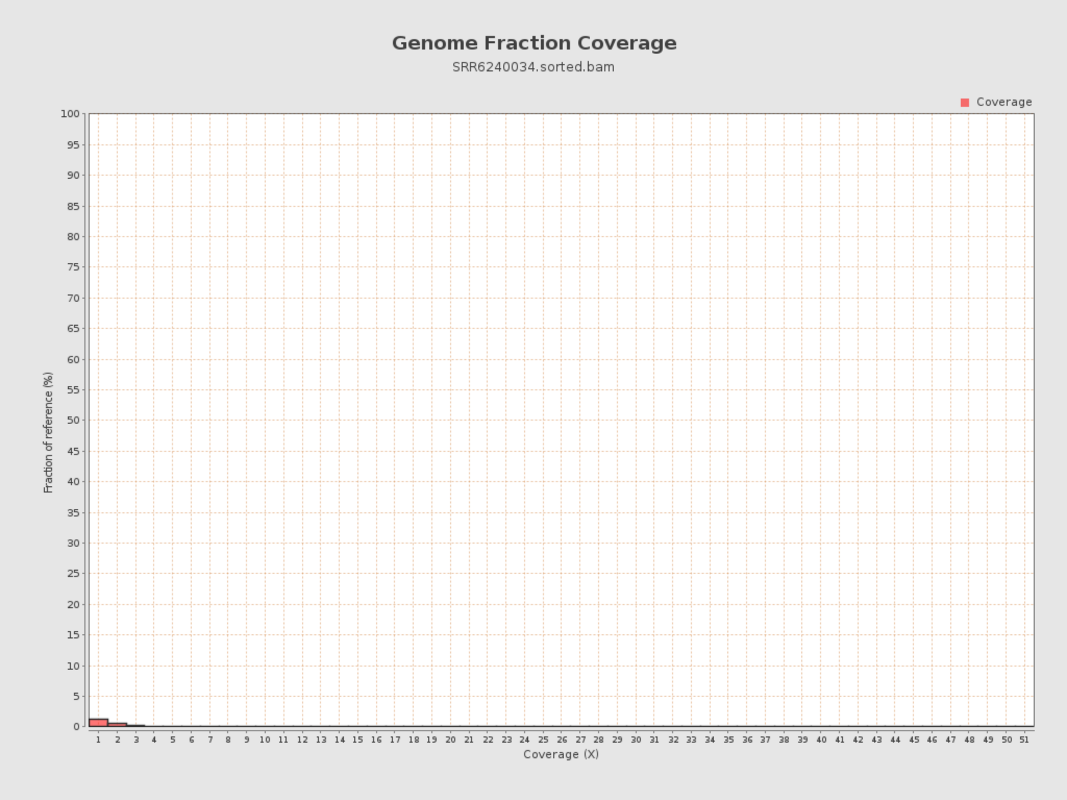
4. Results : Coverage Histogram



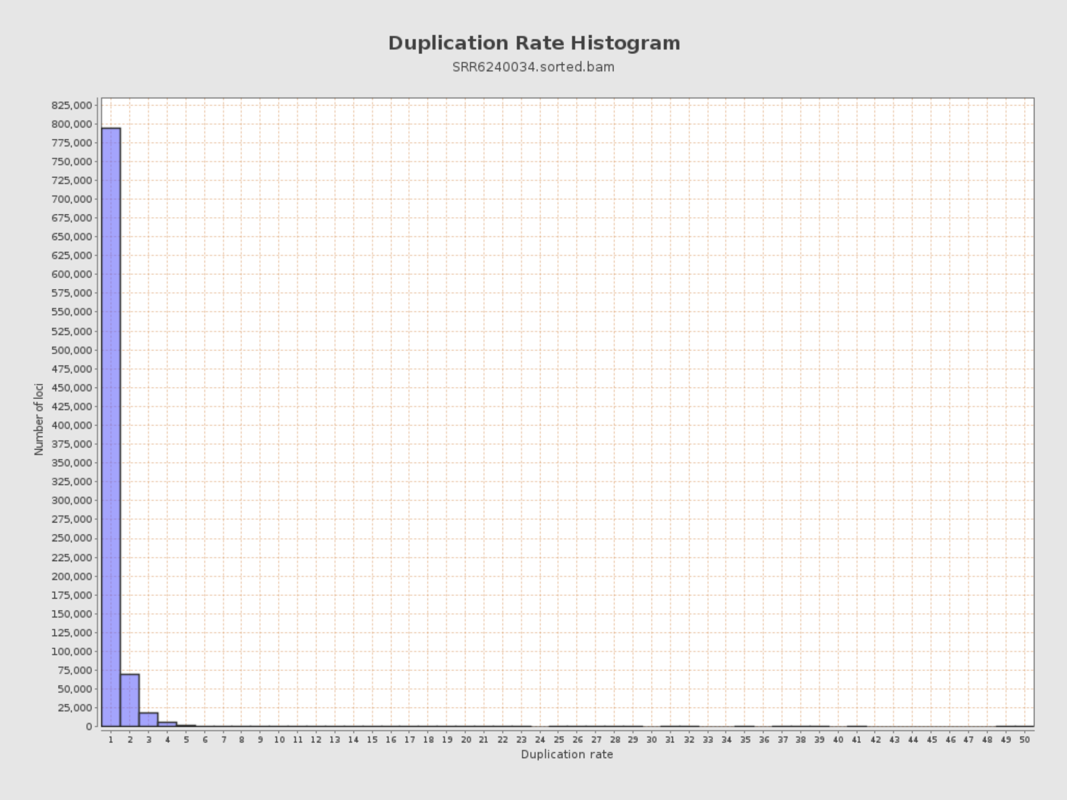
5. Results : Coverage Histogram (0-50X)



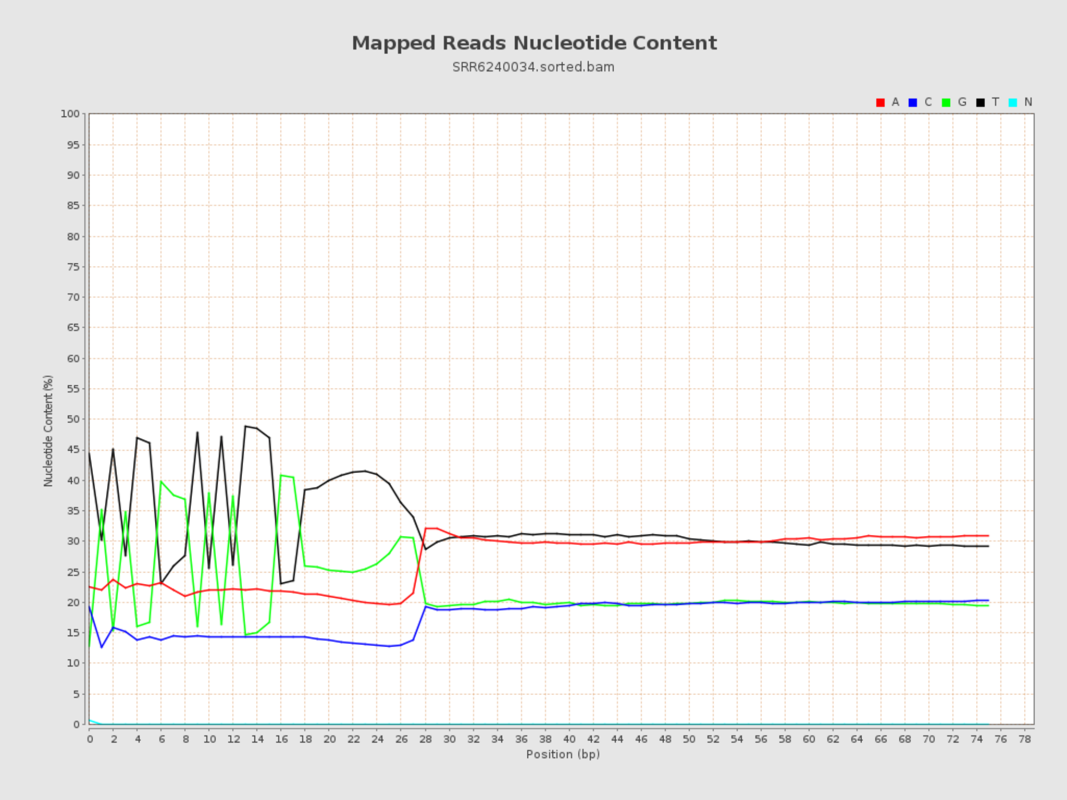
6. Results : Genome Fraction Coverage



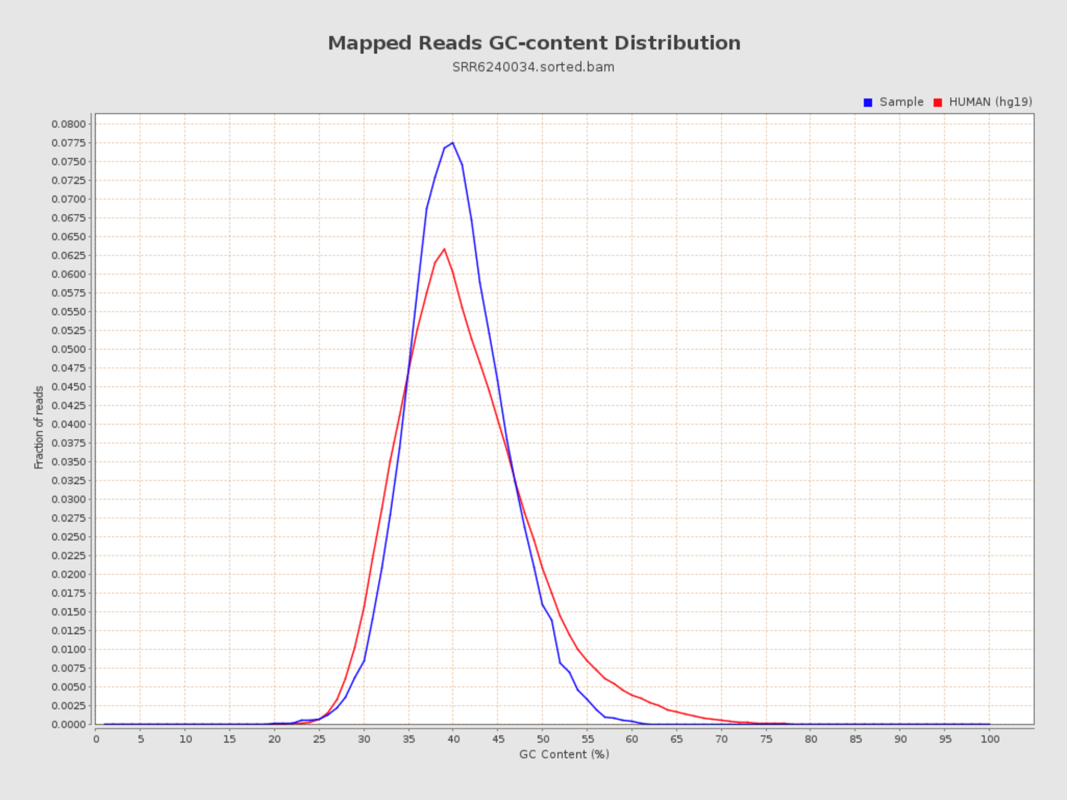
7. Results : Duplication Rate Histogram



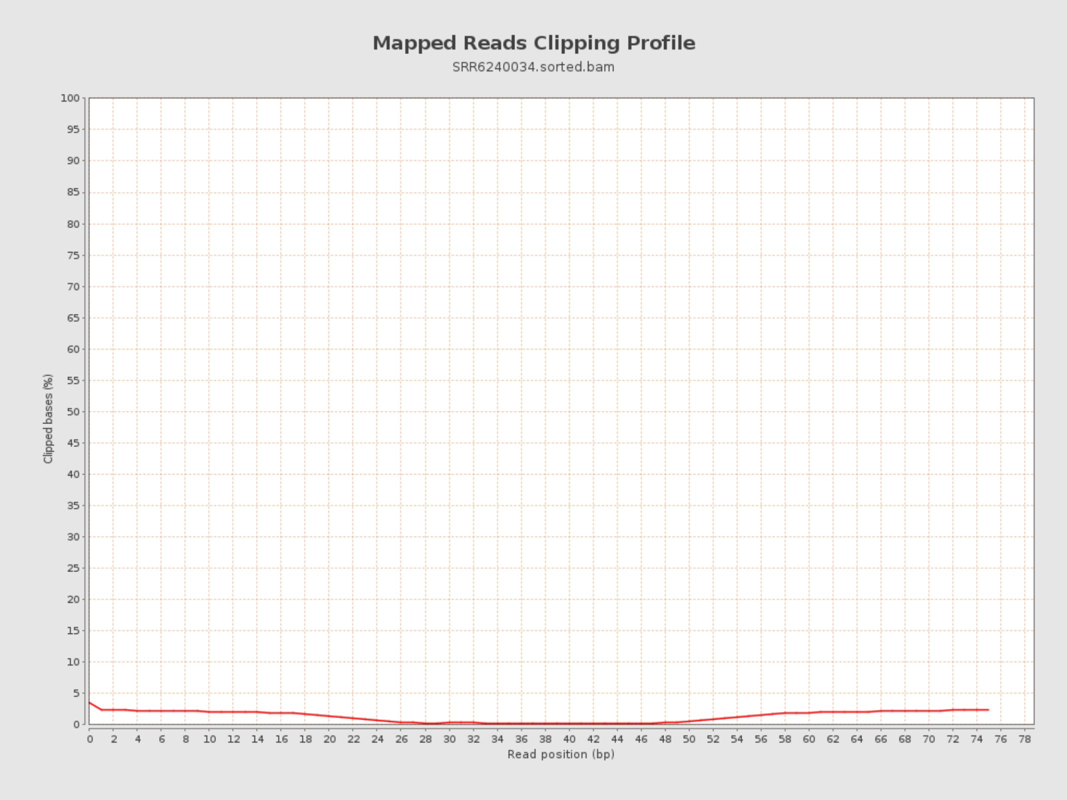
8. Results : Mapped Reads Nucleotide Content



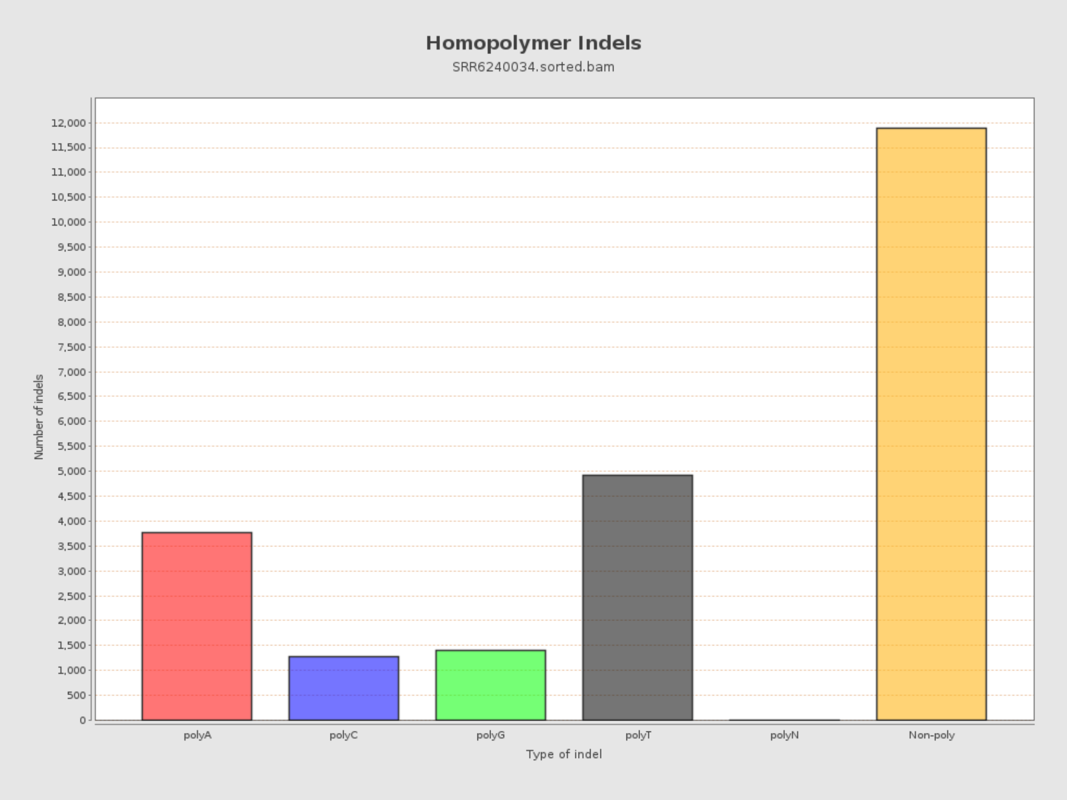
9. Results : Mapped Reads GC-content Distribution



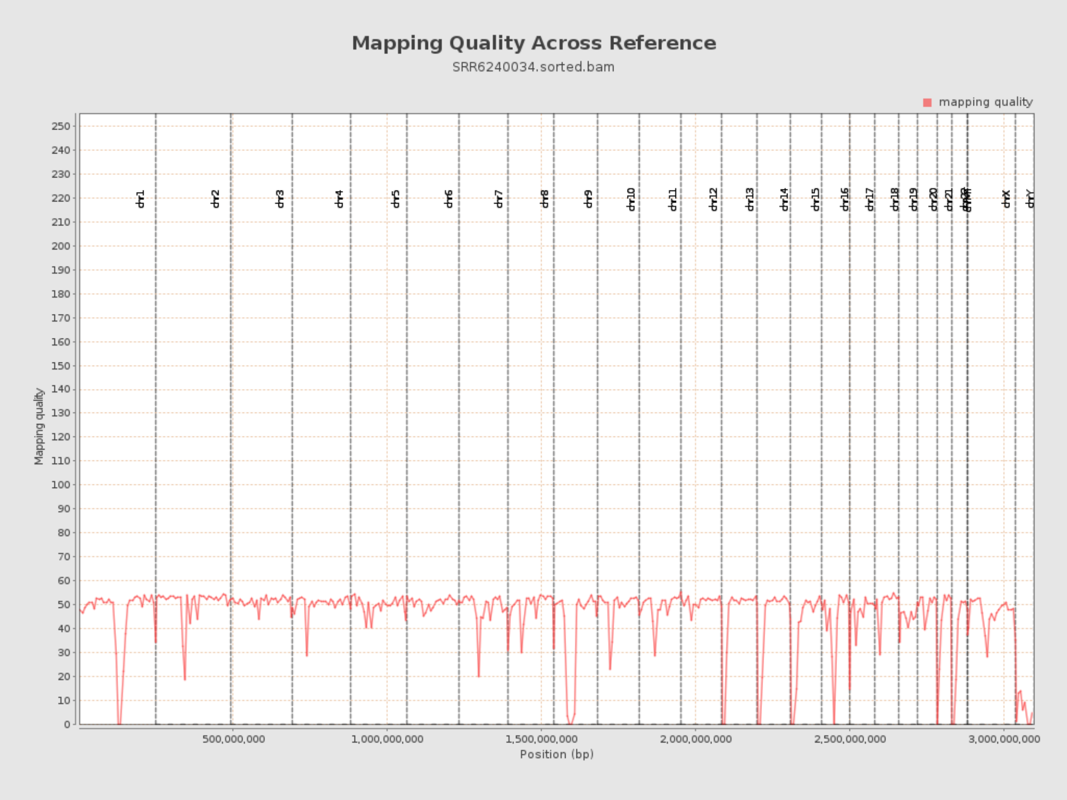
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram