Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 03:25:44

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240036.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_SRR6240036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 03:25:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,699,314
Mapped reads	1,287,538 / 75.77%
Unmapped reads	411,776 / 24.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,623 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	164,427 / 9.68%
Duplication rate	9.98%
Clipped reads	797,555 / 46.93%

2.2. ACGT Content

Number/percentage of A's	21,735,400 / 27.09%
Number/percentage of C's	14,373,694 / 17.91%
Number/percentage of T's	25,693,270 / 32.02%
Number/percentage of G's	18,380,323 / 22.91%
Number/percentage of N's	51,492 / 0.06%
GC Percentage	40.82%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.368

2.4. Mapping Quality

Mean Mapping Quality	44.46

2.5. Mismatches and indels

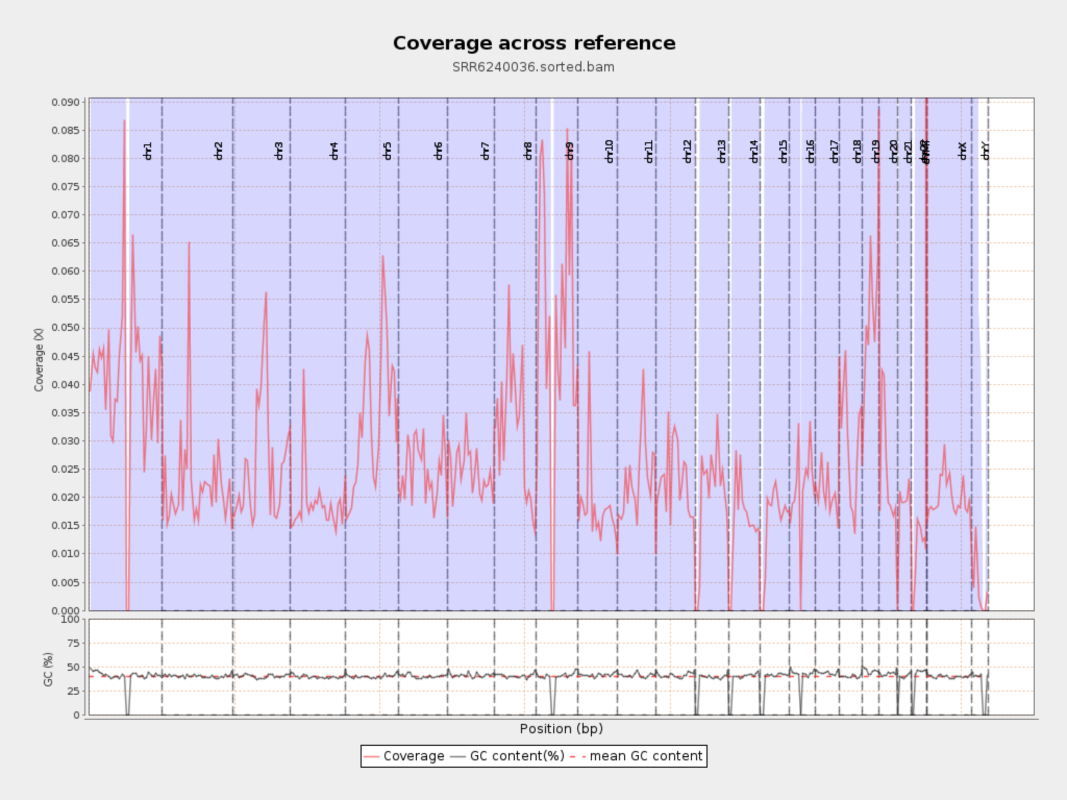
General error rate	0.94%
Mismatches	738,248
Insertions	6,496
Mapped reads with at least one insertion	0.5%
Deletions	19,930
Mapped reads with at least one deletion	1.53%
Homopolymer indels	46.37%

2.6. Chromosome stats

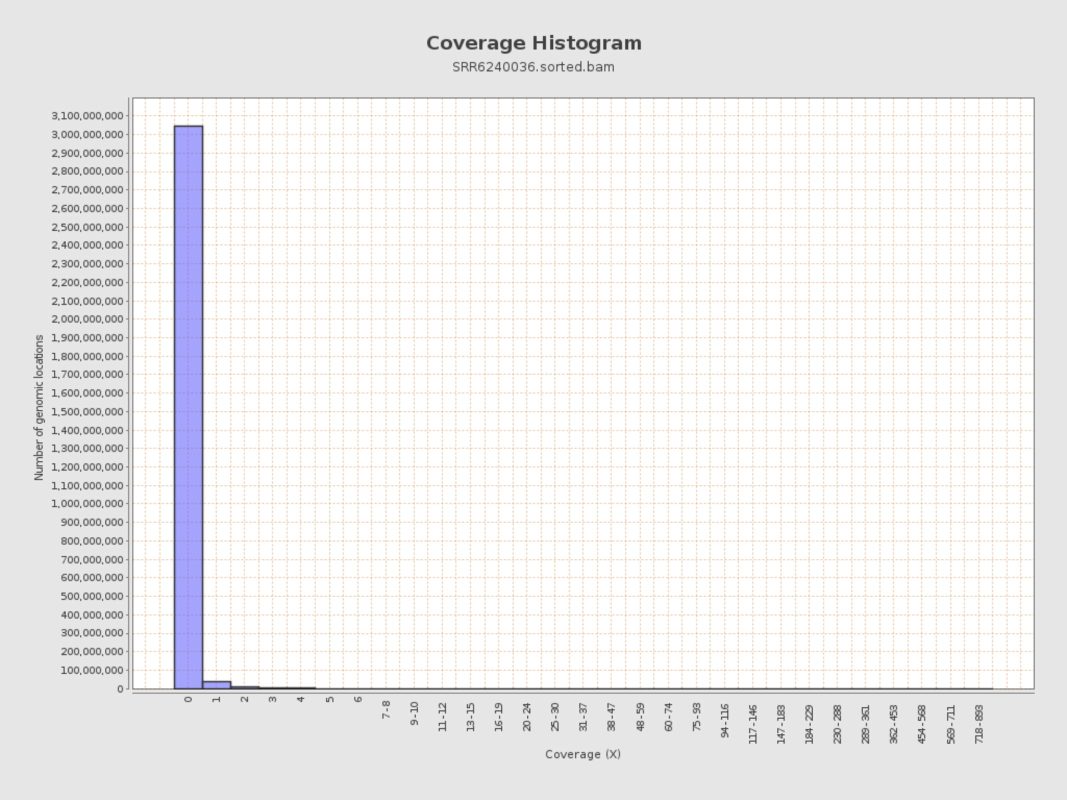
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10094539	0.0405	0.7818
chr2	243199373	5469024	0.0225	0.4503
chr3	198022430	5195549	0.0262	0.2326
chr4	191154276	3557882	0.0186	0.2334
chr5	180915260	6249423	0.0345	0.2689
chr6	171115067	4263049	0.0249	0.2483
chr7	159138663	3928503	0.0247	0.2687

chr8	146364022	4692670	0.0321	0.3982
chr9	141213431	7206453	0.051	0.4433
chr10	135534747	2466598	0.0182	0.2973
chr11	135006516	3192772	0.0236	0.2555
chr12	133851895	3071244	0.0229	0.2339
chr13	115169878	2306328	0.02	0.2044
chr14	107349540	1665853	0.0155	0.2203
chr15	102531392	1559785	0.0152	0.1852
chr16	90354753	1960893	0.0217	0.2371
chr17	81195210	1670525	0.0206	0.2285
chr18	78077248	2345981	0.03	0.5237
chr19	59128983	3093691	0.0523	0.5966
chr20	63025520	1547750	0.0246	0.2323
chr21	48129895	863086	0.0179	0.2263
chr22	51304566	503751	0.0098	0.135
chrMT	16571	26506	1.5995	2.1012
chrX	155270560	3110304	0.02	0.2325
chrY	59373566	225881	0.0038	0.1428

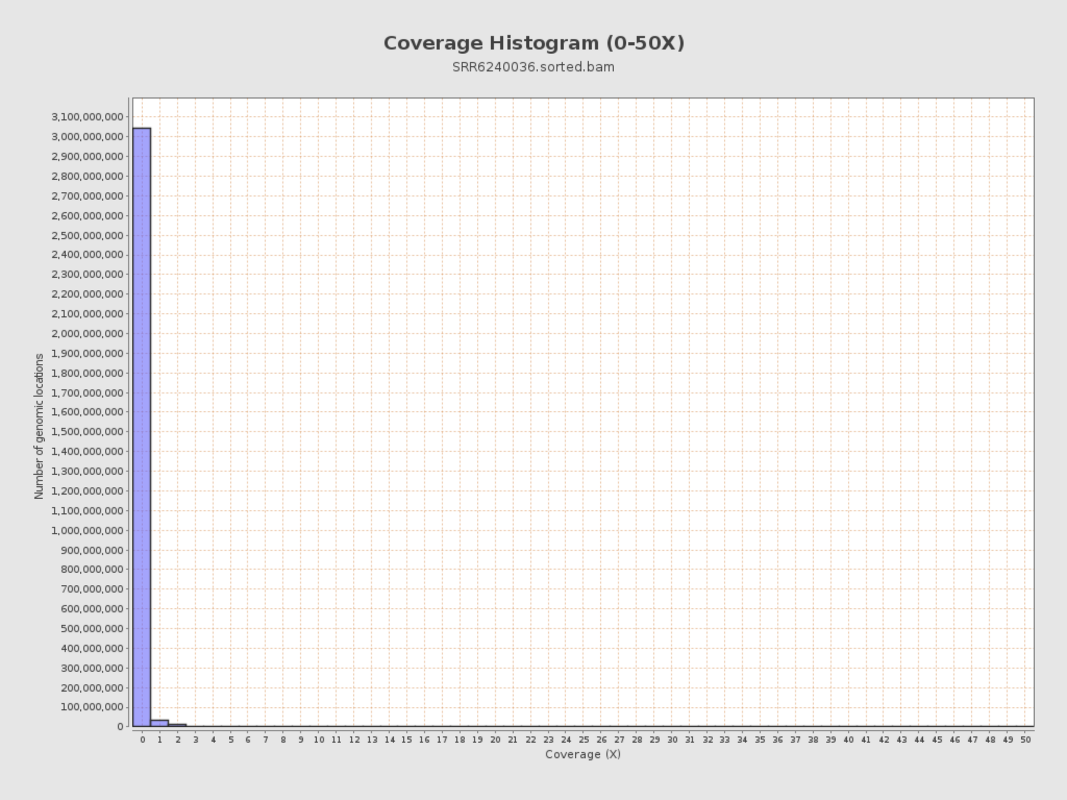
3. Results : Coverage across reference



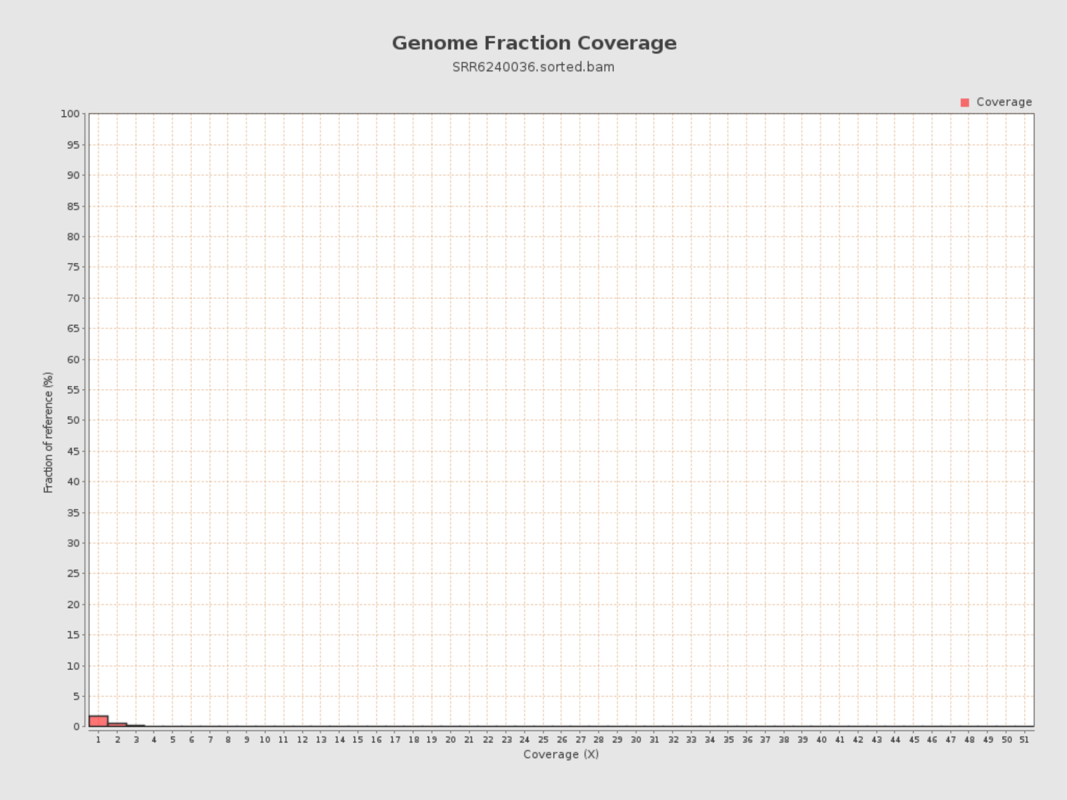
4. Results : Coverage Histogram



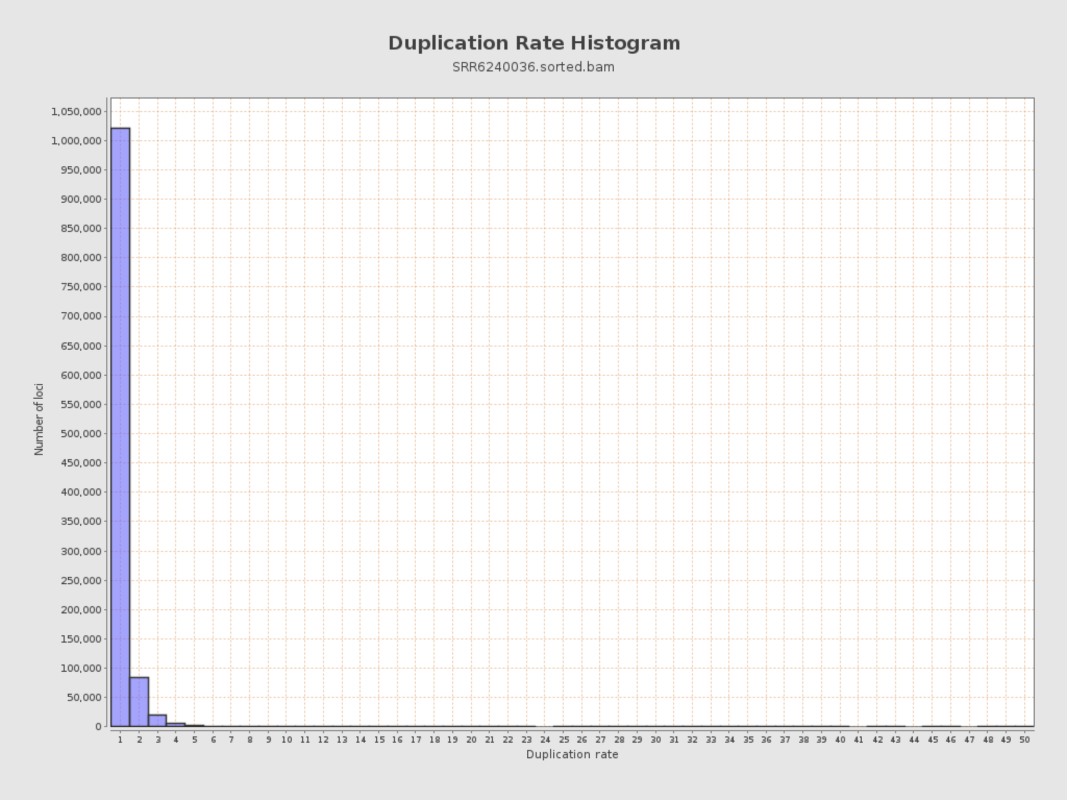
5. Results : Coverage Histogram (0-50X)



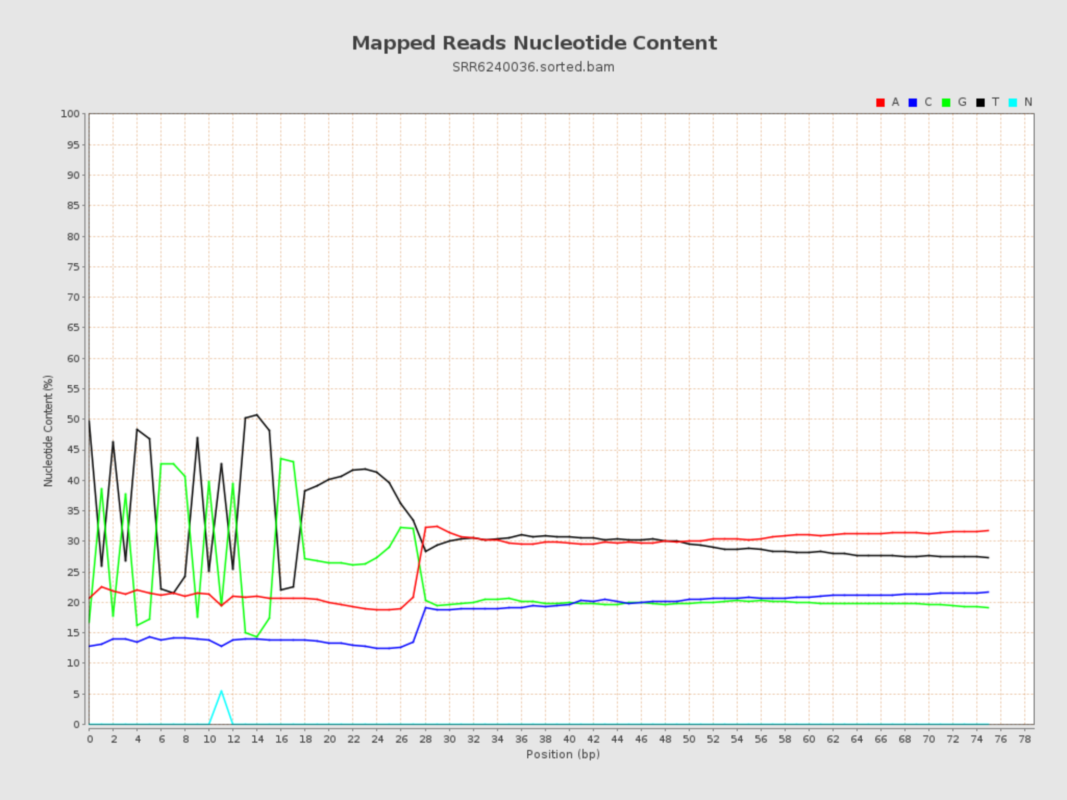
6. Results : Genome Fraction Coverage



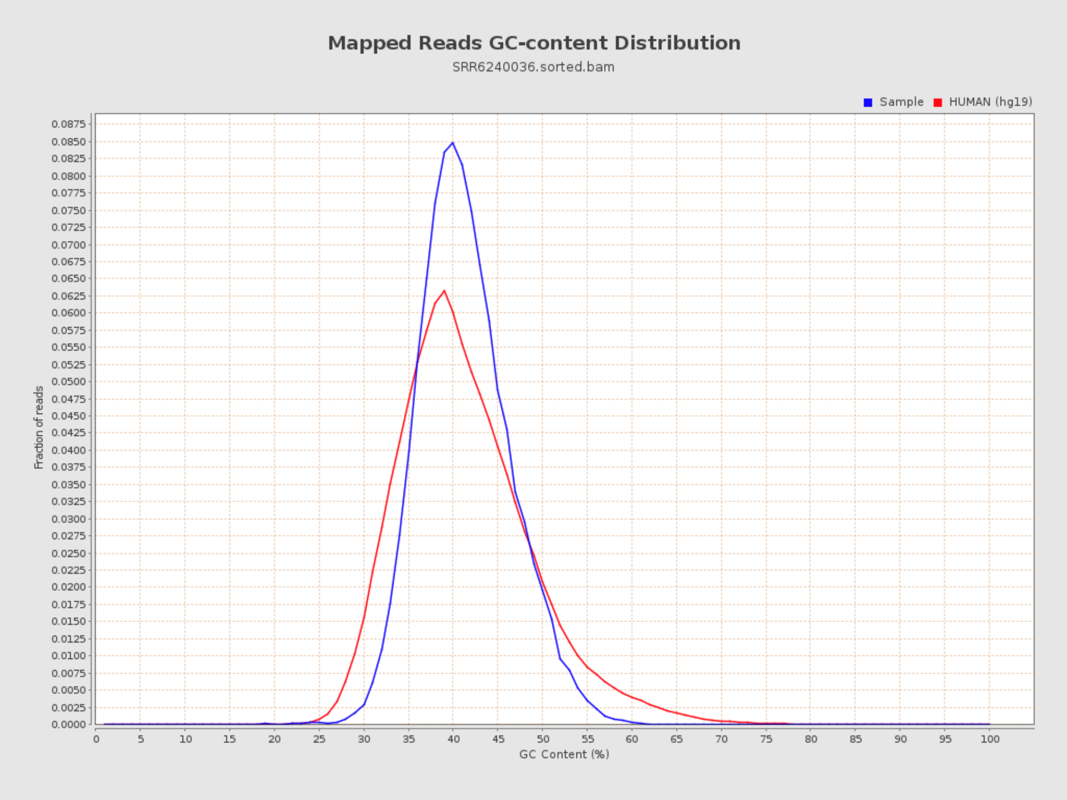
7. Results : Duplication Rate Histogram



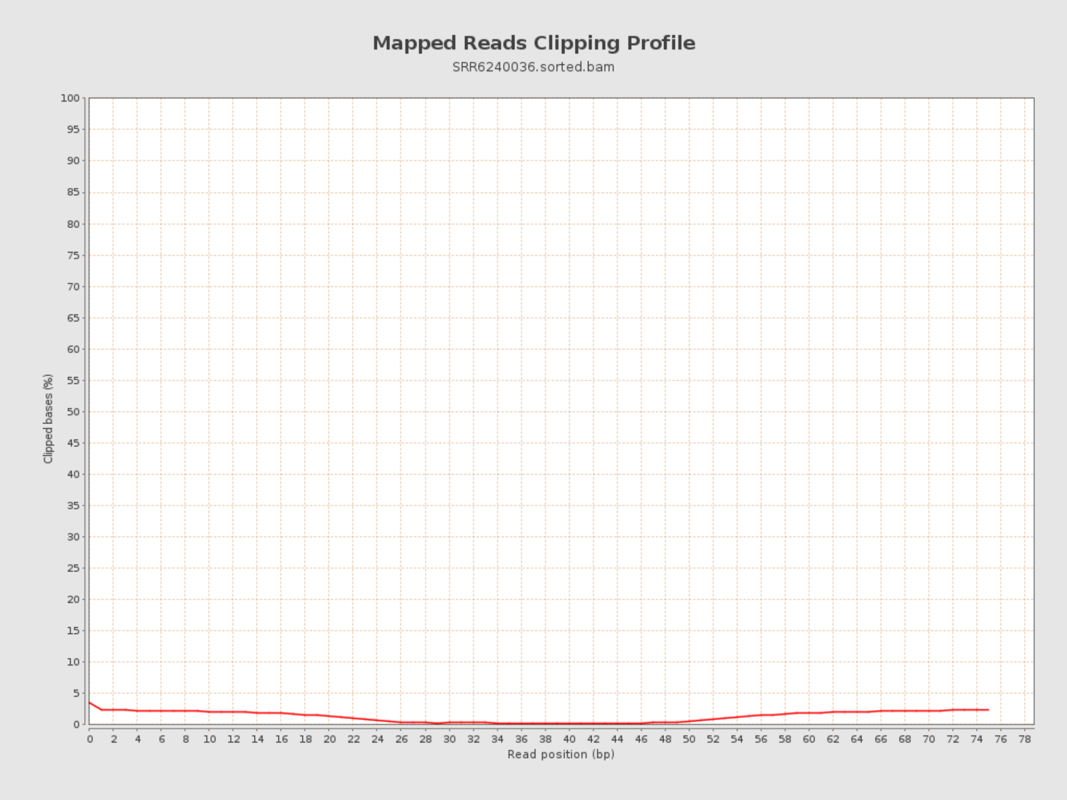
8. Results : Mapped Reads Nucleotide Content



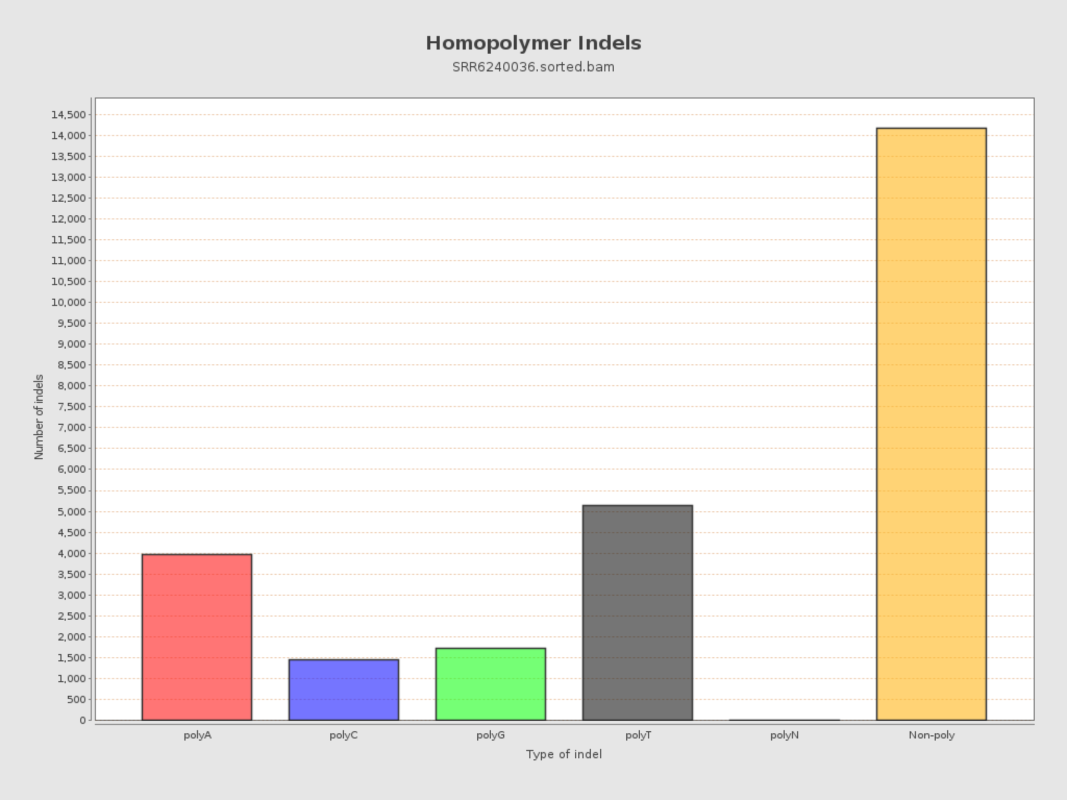
9. Results : Mapped Reads GC-content Distribution



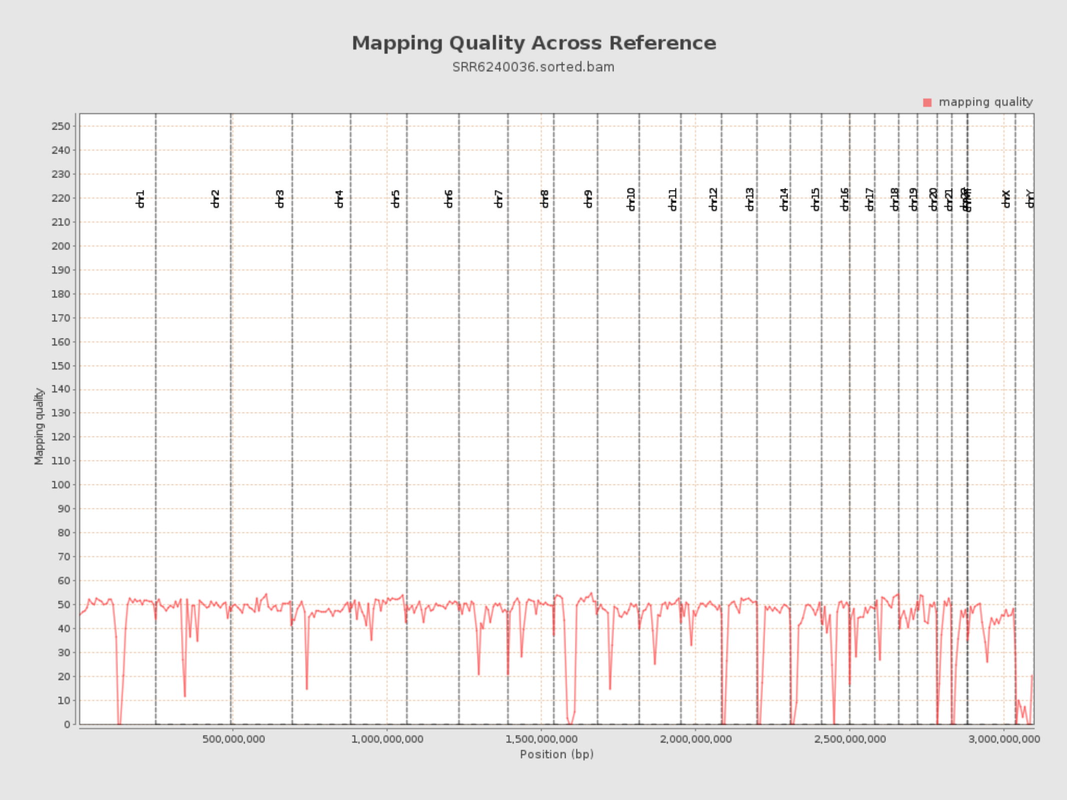
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram