Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:21:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231725.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_SRR6231725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231725.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:21:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,612,960
Mapped reads	1,223,625 / 75.86%
Unmapped reads	389,335 / 24.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,542 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	41,010 / 2.54%
Duplication rate	2.54%
Clipped reads	743,638 / 46.1%

2.2. ACGT Content

Number/percentage of A's	20,163,326 / 26.15%
Number/percentage of C's	14,562,907 / 18.89%
Number/percentage of T's	23,702,085 / 30.74%
Number/percentage of G's	18,661,955 / 24.2%
Number/percentage of N's	12,455 / 0.02%
GC Percentage	43.09%

2.3. Coverage

Mean	0.0249

Standard Deviation	0.2488

2.4. Mapping Quality

Mean Mapping Quality	42

2.5. Mismatches and indels

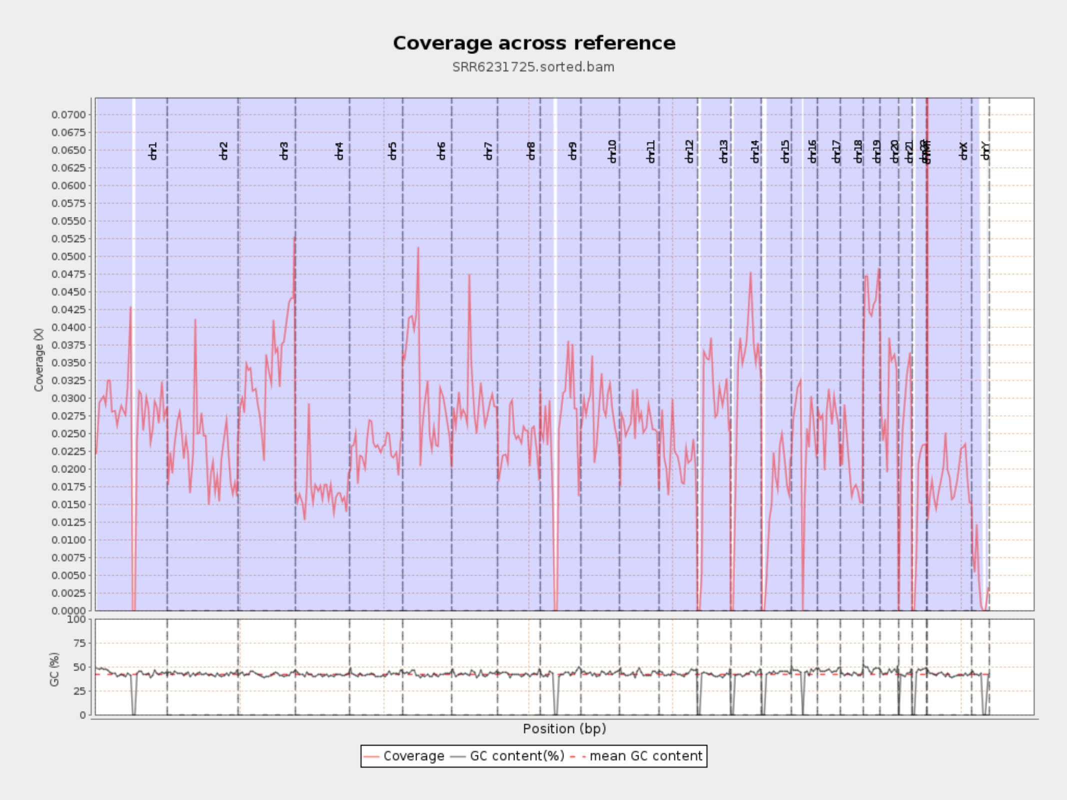
General error rate	0.88%
Mismatches	669,061
Insertions	6,347
Mapped reads with at least one insertion	0.51%
Deletions	26,669
Mapped reads with at least one deletion	2.15%
Homopolymer indels	45.51%

2.6. Chromosome stats

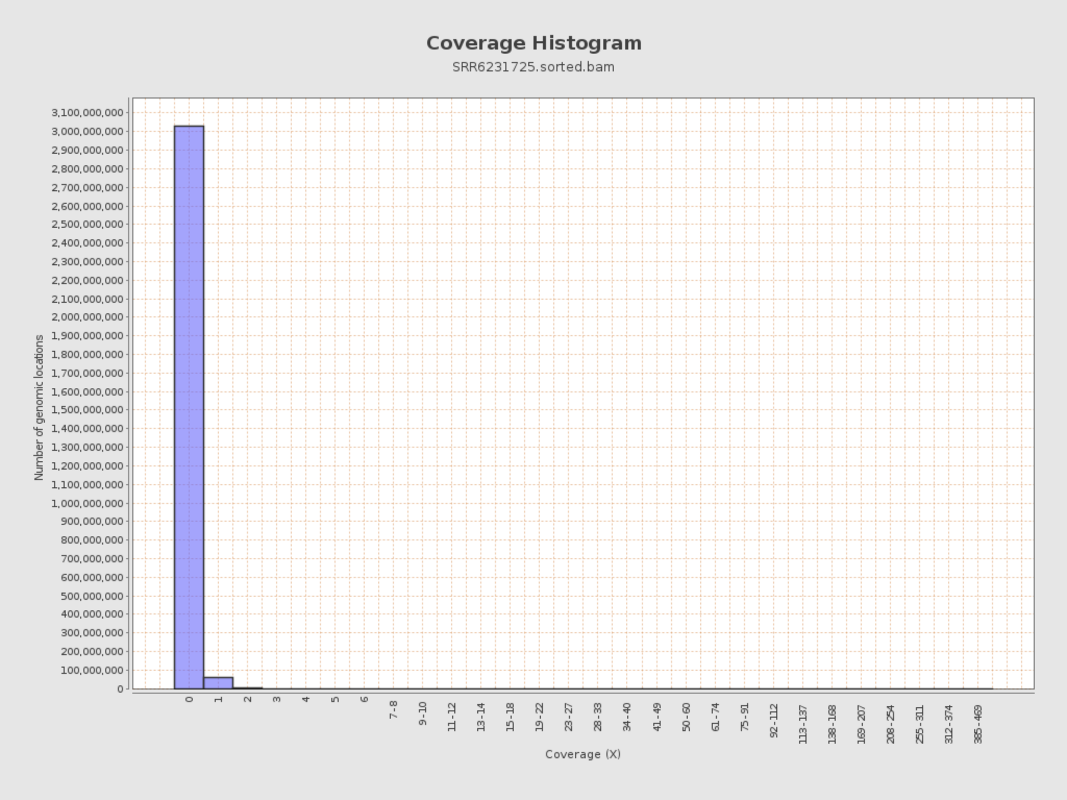
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6750102	0.0271	0.4021
chr2	243199373	5408527	0.0222	0.2909
chr3	198022430	6749077	0.0341	0.2052
chr4	191154276	3216730	0.0168	0.1566
chr5	180915260	4165725	0.023	0.1703
chr6	171115067	5353700	0.0313	0.2427
chr7	159138663	4677057	0.0294	0.372

chr8	146364022	3462222	0.0237	0.2837
chr9	141213431	3476199	0.0246	0.219
chr10	135534747	3825153	0.0282	0.2225
chr11	135006516	3594102	0.0266	0.2406
chr12	133851895	2907157	0.0217	0.166
chr13	115169878	3056168	0.0265	0.1863
chr14	107349540	3368051	0.0314	0.2072
chr15	102531392	1554797	0.0152	0.1471
chr16	90354753	2166006	0.024	0.1841
chr17	81195210	2189713	0.027	0.2019
chr18	78077248	1518755	0.0195	0.3615
chr19	59128983	2616287	0.0442	0.322
chr20	63025520	1885014	0.0299	0.2003
chr21	48129895	1259677	0.0262	0.1852
chr22	51304566	786128	0.0153	0.1369
chrMT	16571	42625	2.5723	2.6278
chrX	155270560	2877572	0.0185	0.1643
chrY	59373566	243444	0.0041	0.0859

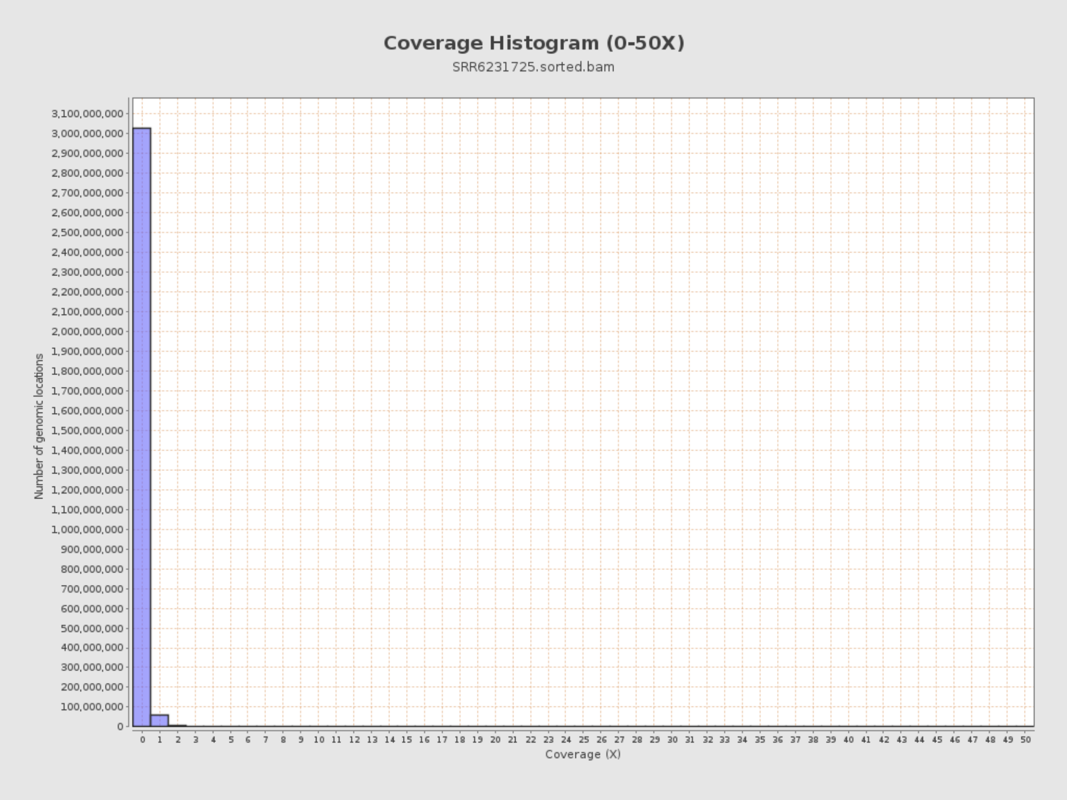
3. Results : Coverage across reference



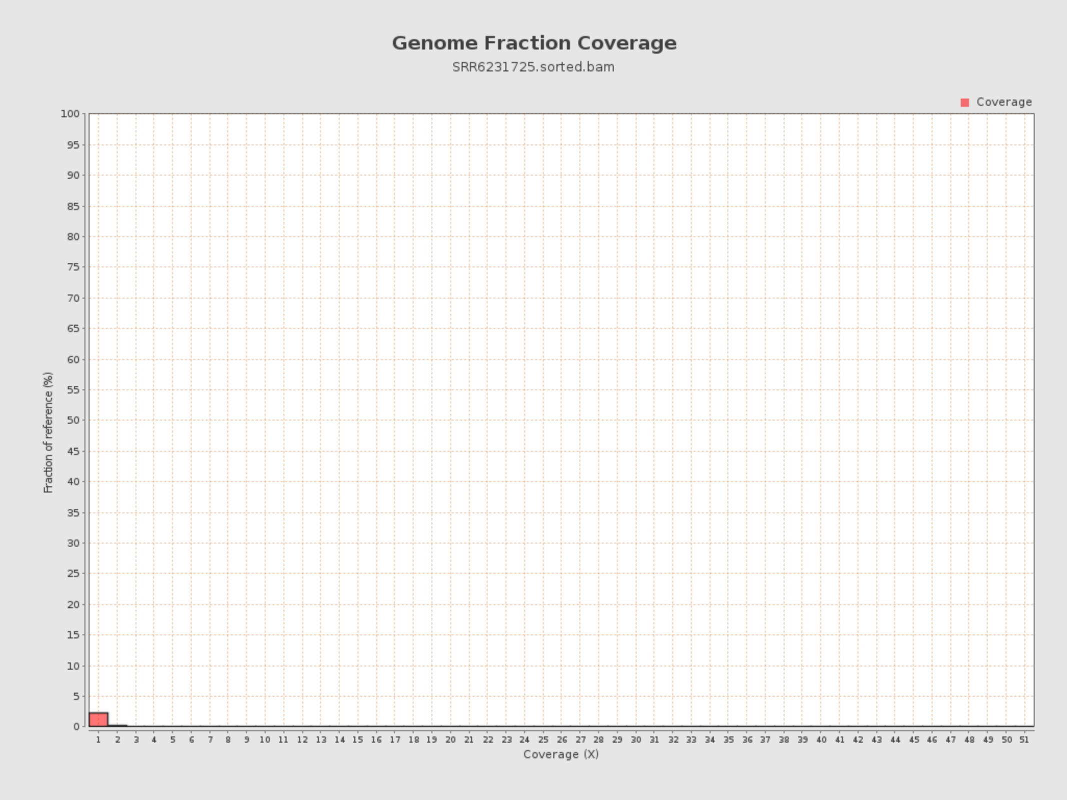
4. Results : Coverage Histogram



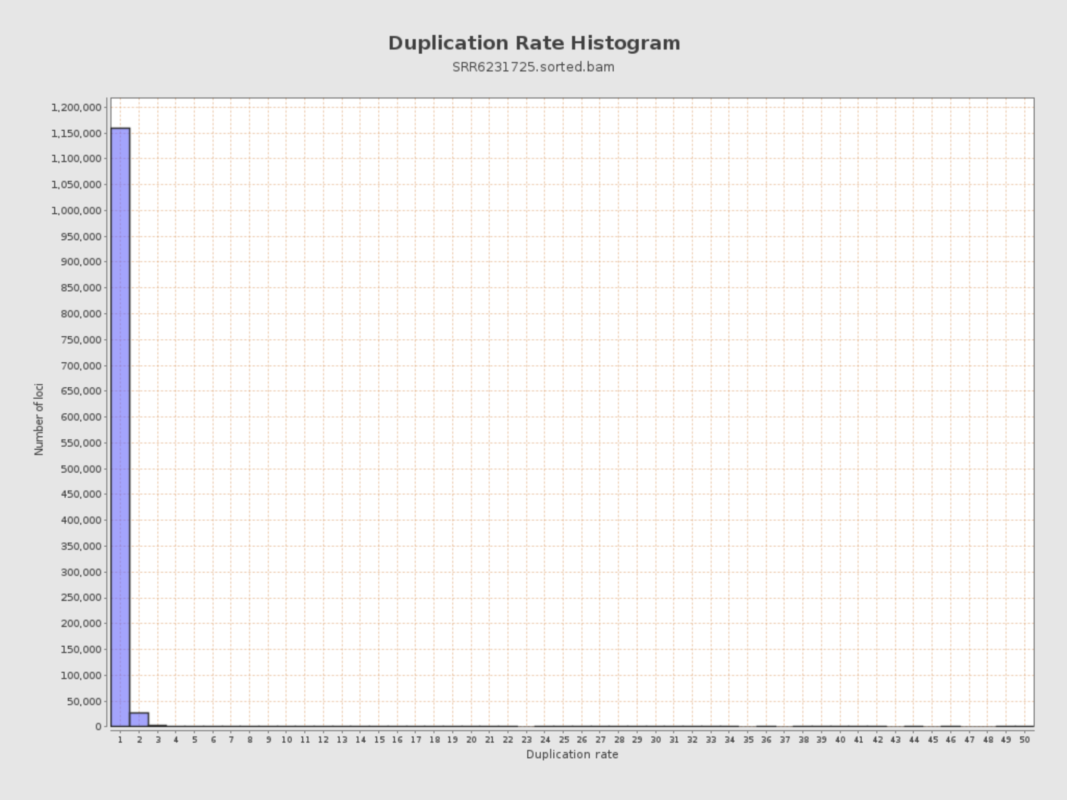
5. Results : Coverage Histogram (0-50X)



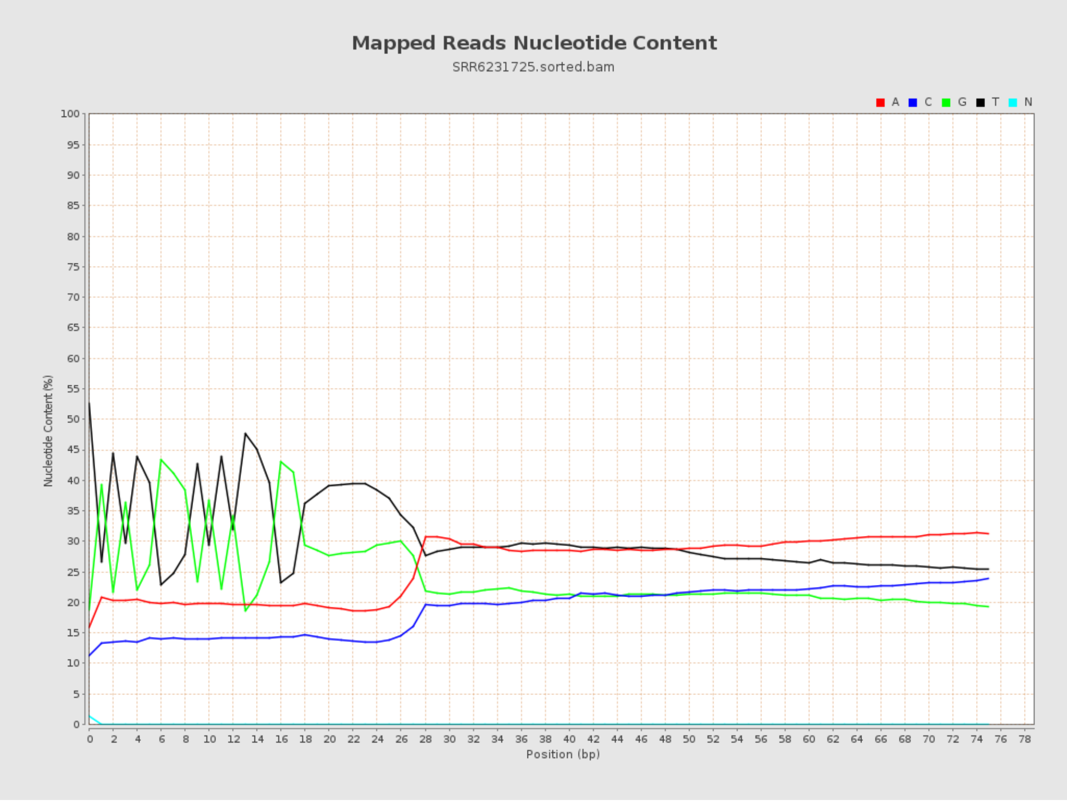
6. Results : Genome Fraction Coverage



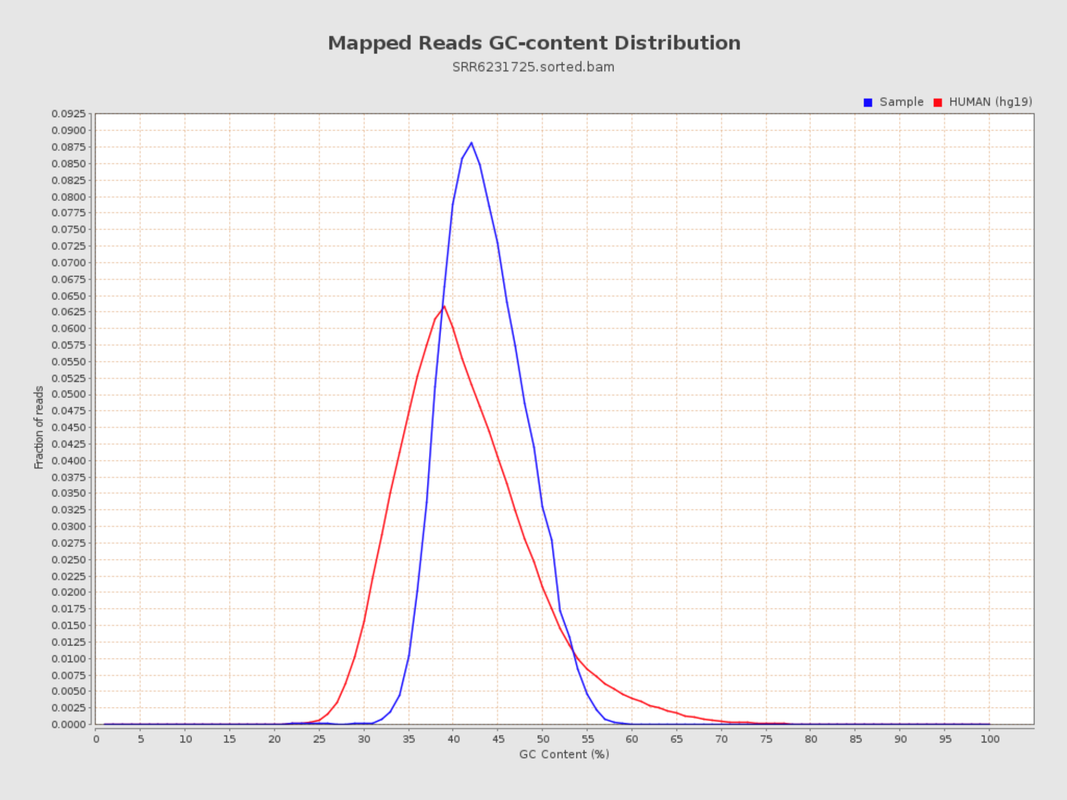
7. Results : Duplication Rate Histogram



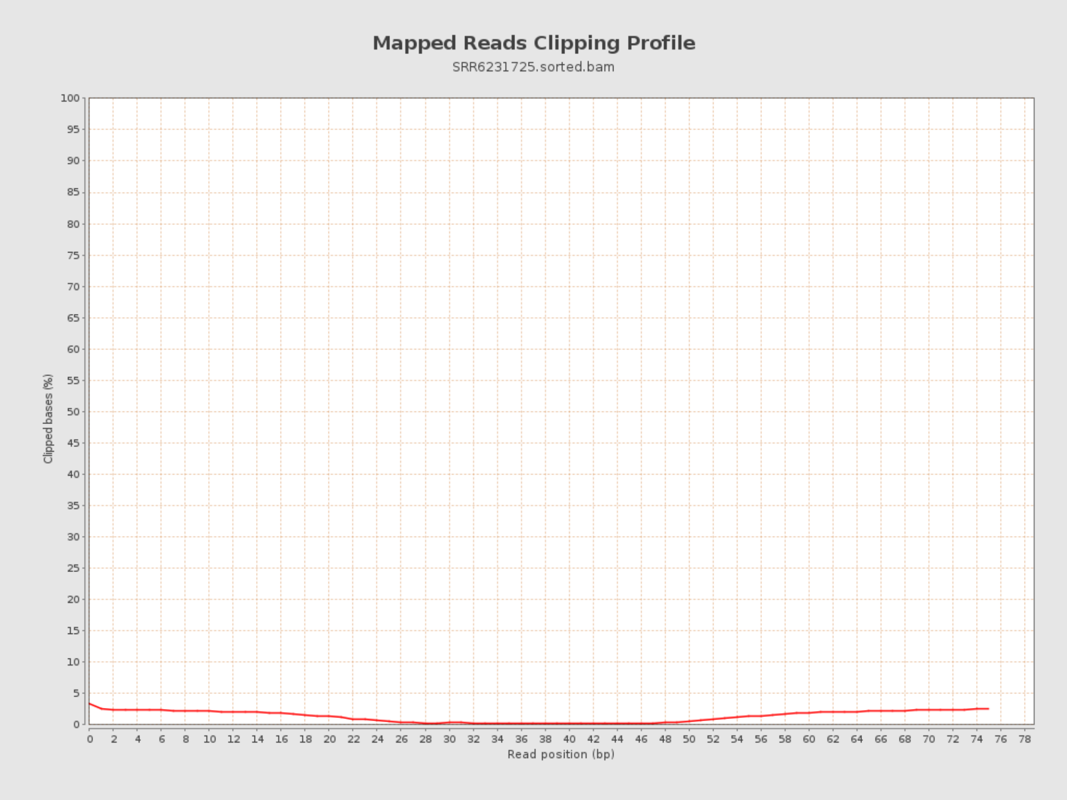
8. Results : Mapped Reads Nucleotide Content



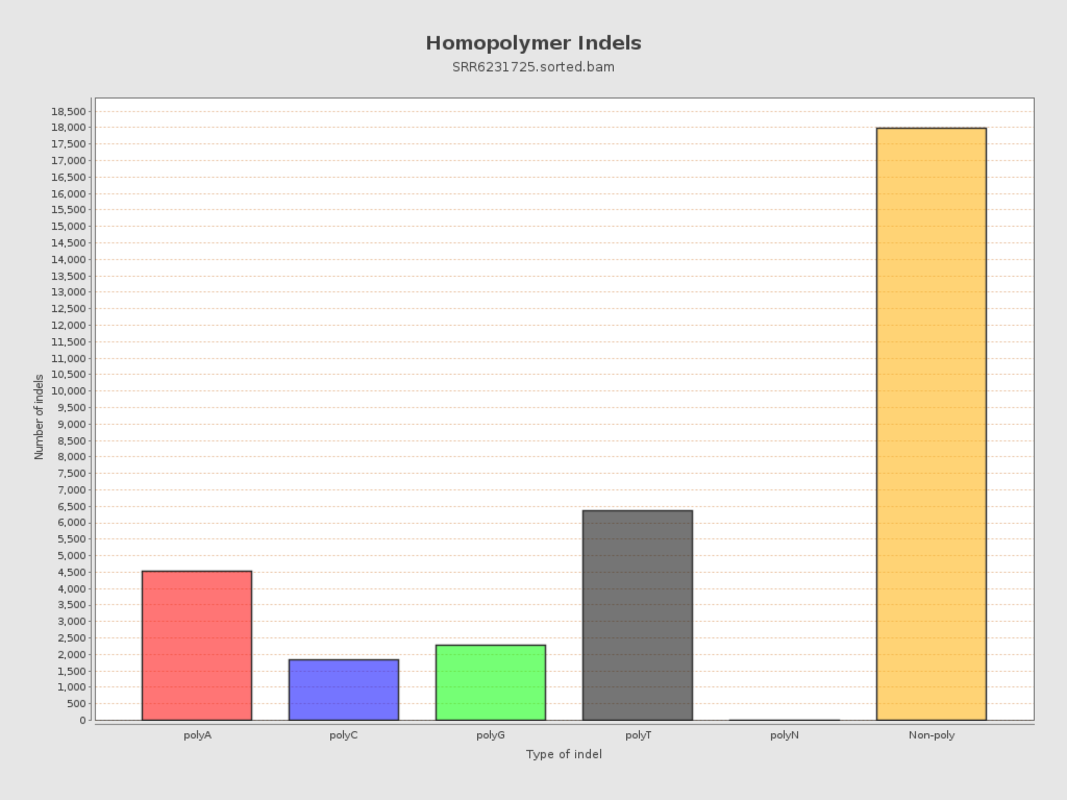
9. Results : Mapped Reads GC-content Distribution



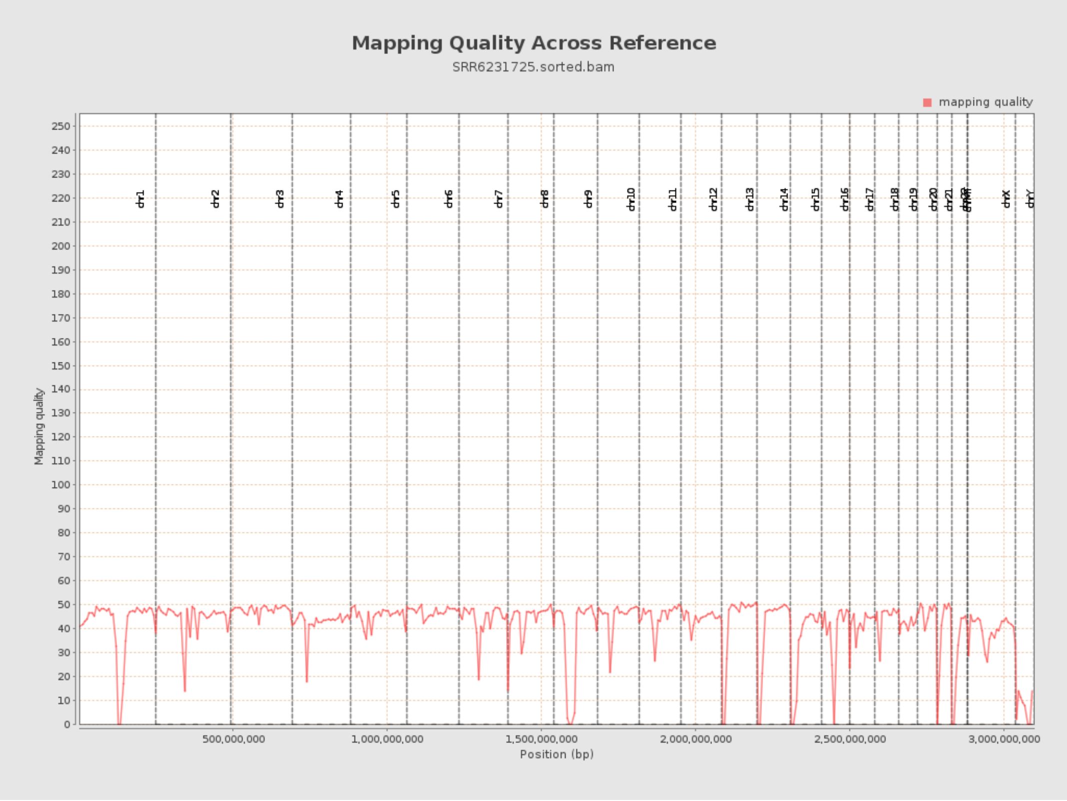
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram