Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:12:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237605.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_SRR6237605 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237605.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:12:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237605.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,783,615
Mapped reads	1,552,710 / 87.05%
Unmapped reads	230,905 / 12.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,988 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	75,651 / 4.24%
Duplication rate	4.03%
Clipped reads	800,683 / 44.89%

2.2. ACGT Content

Number/percentage of A's	27,240,068 / 27.15%
Number/percentage of C's	17,476,249 / 17.42%
Number/percentage of T's	32,886,397 / 32.78%
Number/percentage of G's	22,541,857 / 22.47%
Number/percentage of N's	185,291 / 0.18%
GC Percentage	39.89%

2.3. Coverage

Mean	0.0324

Standard Deviation	0.2965

2.4. Mapping Quality

Mean Mapping Quality	45.86

2.5. Mismatches and indels

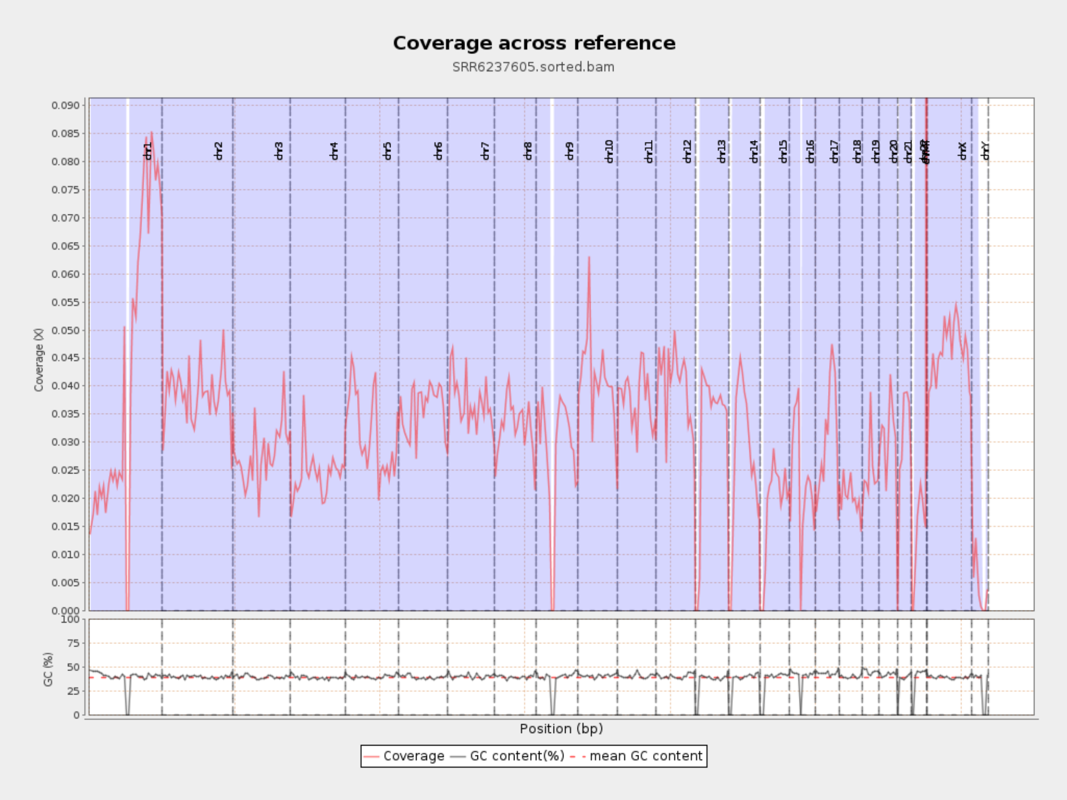
General error rate	0.92%
Mismatches	910,508
Insertions	8,288
Mapped reads with at least one insertion	0.53%
Deletions	37,061
Mapped reads with at least one deletion	2.35%
Homopolymer indels	45.54%

2.6. Chromosome stats

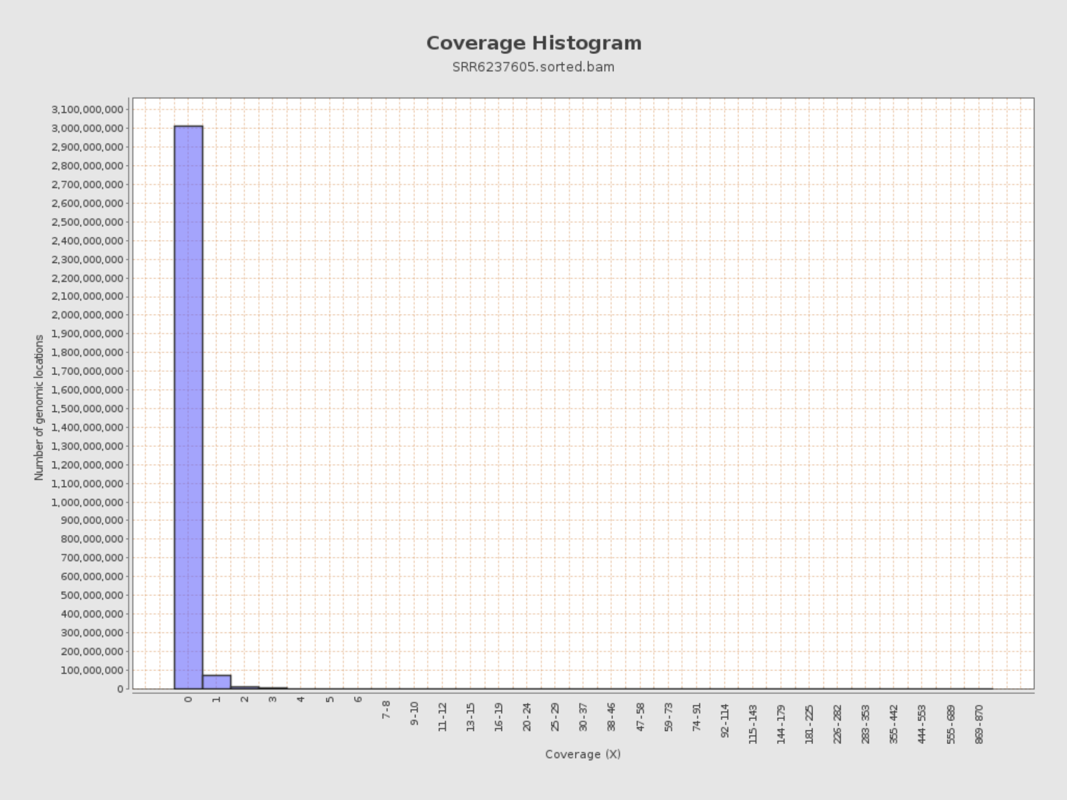
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10543188	0.0423	0.4993
chr2	243199373	9450262	0.0389	0.4346
chr3	198022430	5534851	0.028	0.1941
chr4	191154276	4608267	0.0241	0.1917
chr5	180915260	5684102	0.0314	0.2036
chr6	171115067	6160767	0.036	0.2691
chr7	159138663	5935330	0.0373	0.3294

chr8	146364022	4776998	0.0326	0.3944
chr9	141213431	4029469	0.0285	0.2273
chr10	135534747	5665982	0.0418	0.3297
chr11	135006516	5073666	0.0376	0.2565
chr12	133851895	5379101	0.0402	0.2308
chr13	115169878	3652329	0.0317	0.2095
chr14	107349540	2933412	0.0273	0.1981
chr15	102531392	1882496	0.0184	0.1566
chr16	90354753	2110213	0.0234	0.1912
chr17	81195210	2496404	0.0307	0.2153
chr18	78077248	1583579	0.0203	0.3422
chr19	59128983	1478862	0.025	0.343
chr20	63025520	1953977	0.031	0.2044
chr21	48129895	1417247	0.0294	0.2039
chr22	51304566	672605	0.0131	0.1288
chrMT	16571	12466	0.7523	1.2012
chrX	155270560	7084852	0.0456	0.2564
chrY	59373566	270519	0.0046	0.1086

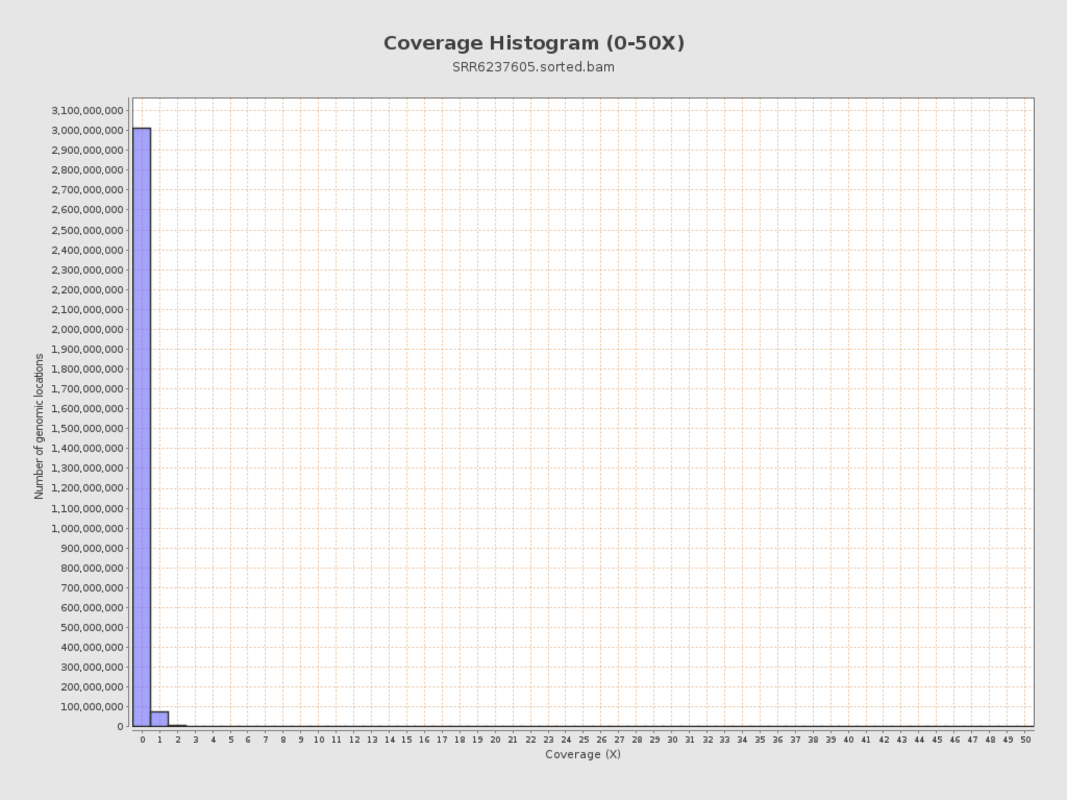
3. Results : Coverage across reference



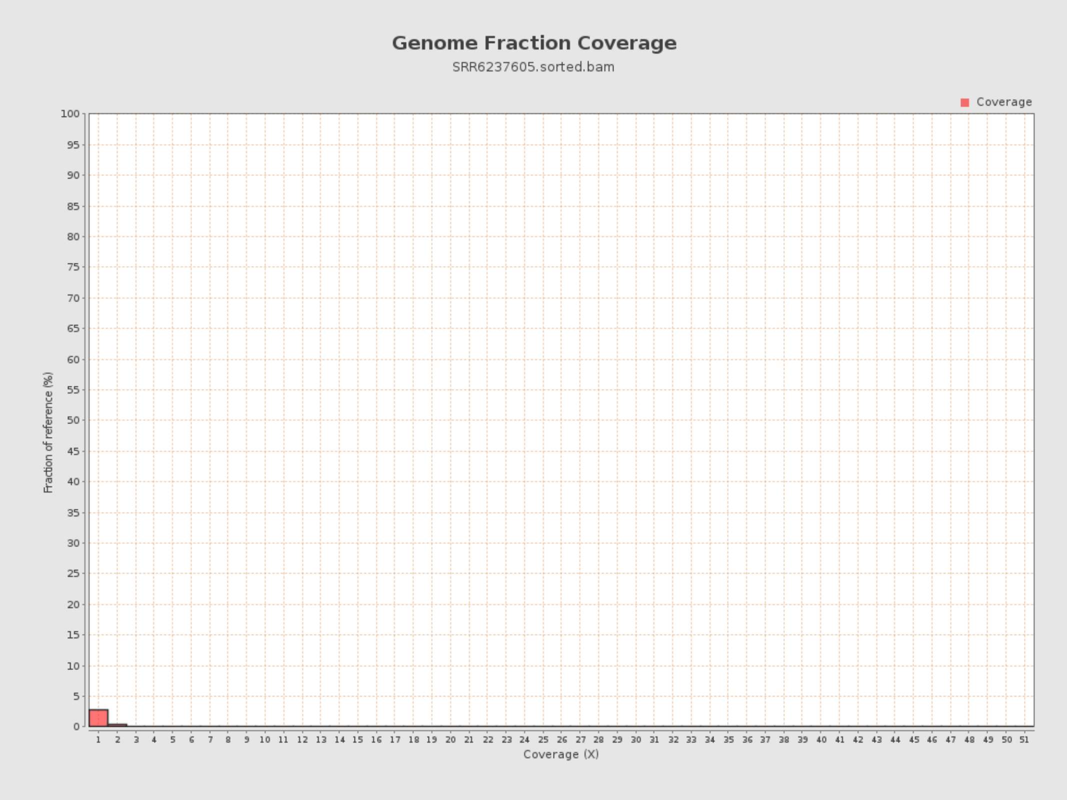
4. Results : Coverage Histogram



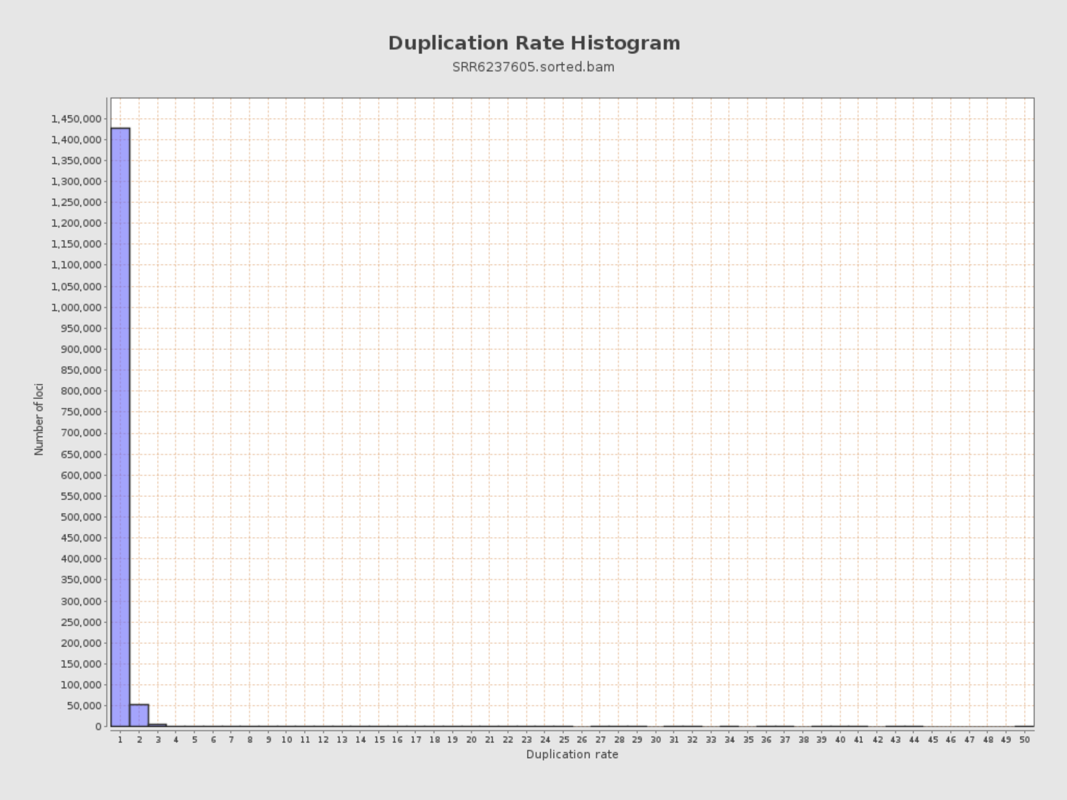
5. Results : Coverage Histogram (0-50X)



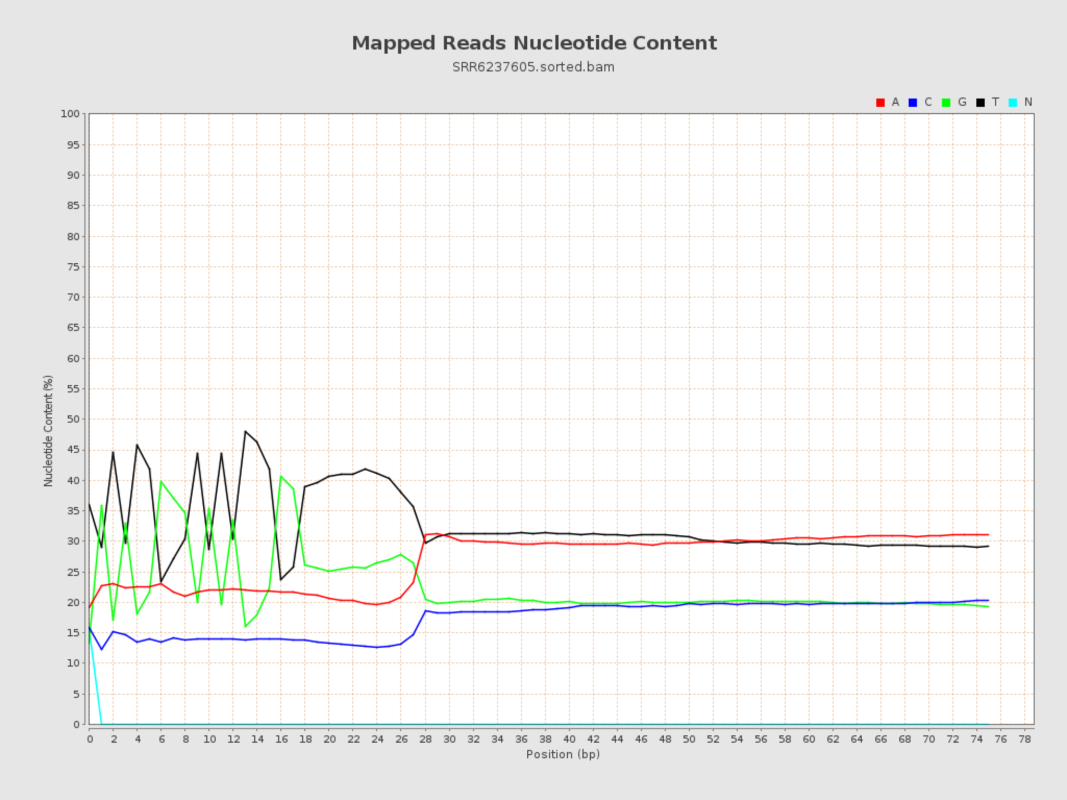
6. Results : Genome Fraction Coverage



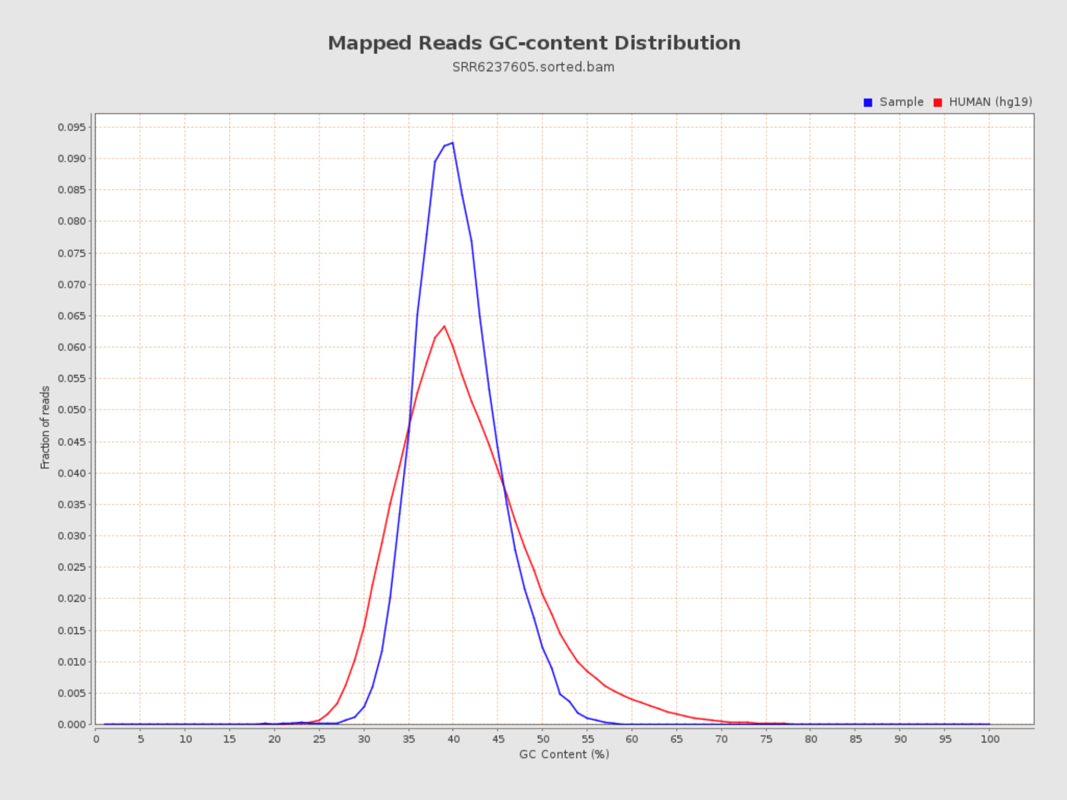
7. Results : Duplication Rate Histogram



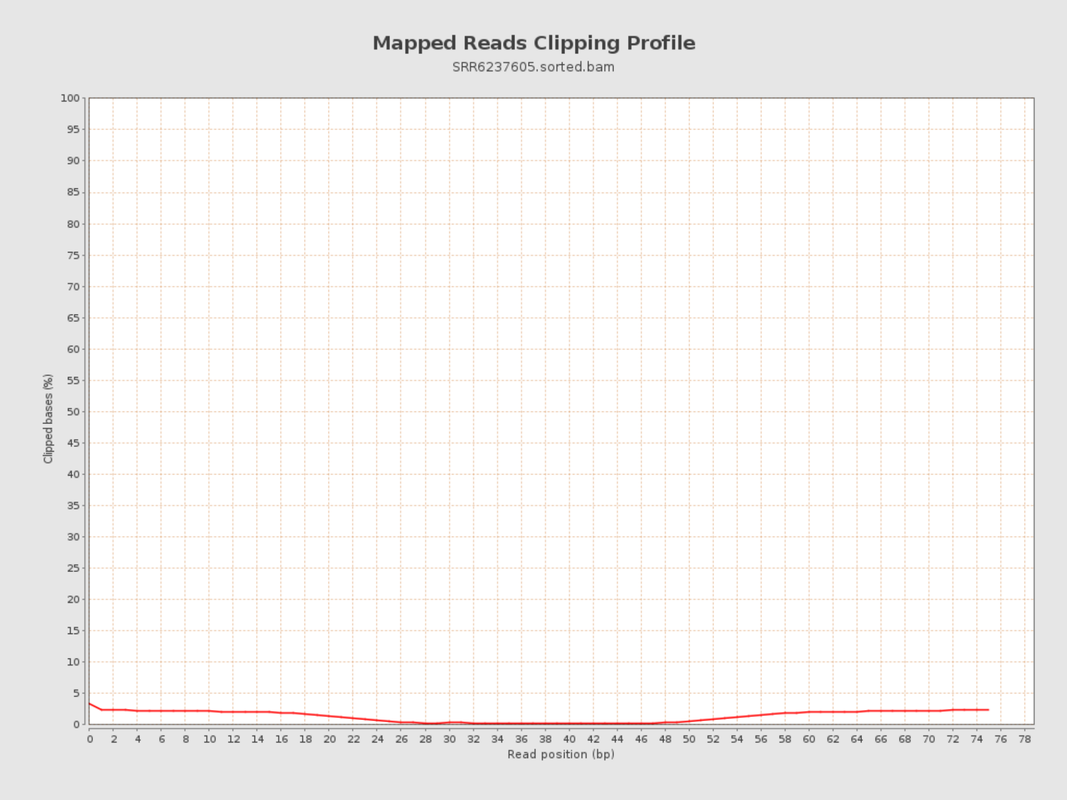
8. Results : Mapped Reads Nucleotide Content



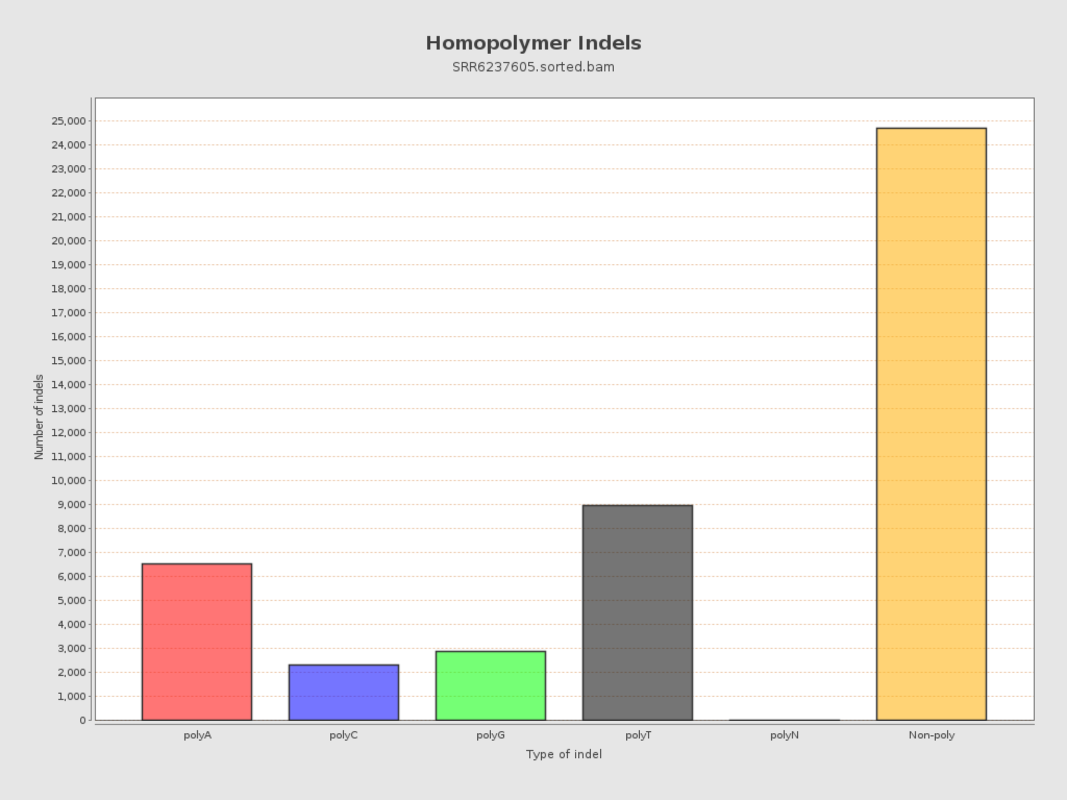
9. Results : Mapped Reads GC-content Distribution



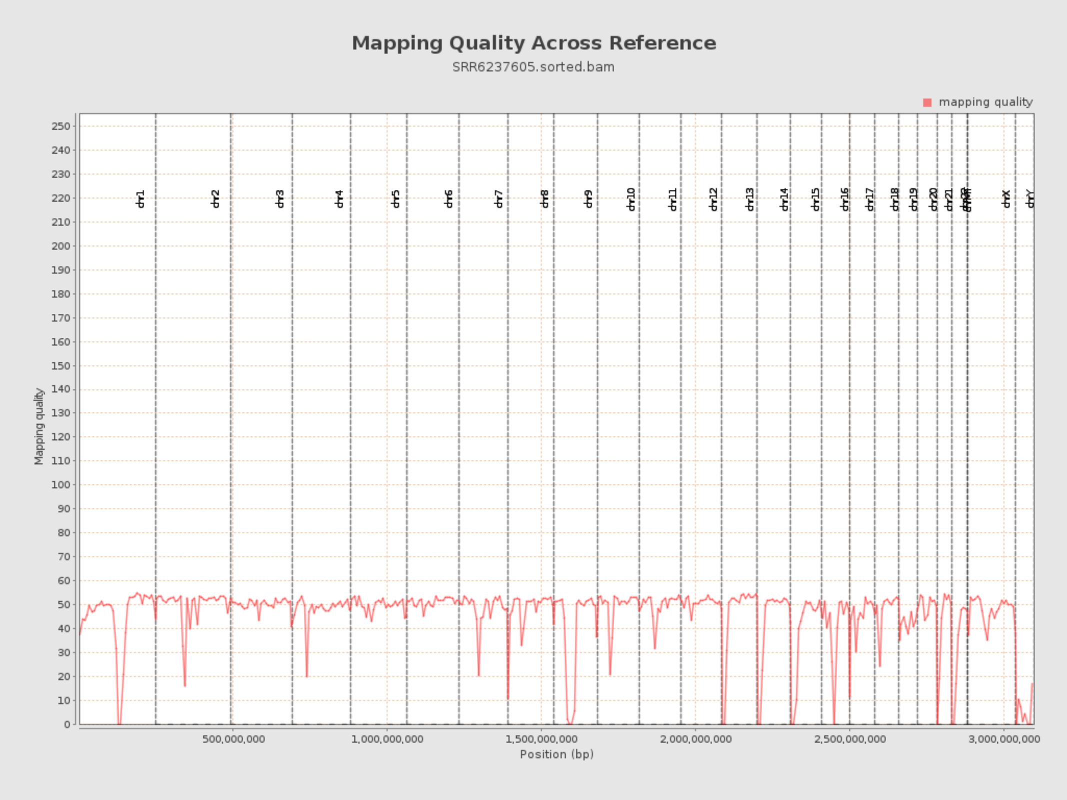
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram