Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 03:38:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237570.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_SRR6237570 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237570.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 03:38:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237570.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,621,451
Mapped reads	1,294,769 / 79.85%
Unmapped reads	326,682 / 20.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,465 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	72,673 / 4.48%
Duplication rate	3.86%
Clipped reads	872,605 / 53.82%

2.2. ACGT Content

Number/percentage of A's	20,685,678 / 25.79%
Number/percentage of C's	14,286,513 / 17.81%
Number/percentage of T's	25,611,713 / 31.93%
Number/percentage of G's	19,615,497 / 24.45%
Number/percentage of N's	13,416 / 0.02%
GC Percentage	42.27%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.2778

2.4. Mapping Quality

Mean Mapping Quality	42.14

2.5. Mismatches and indels

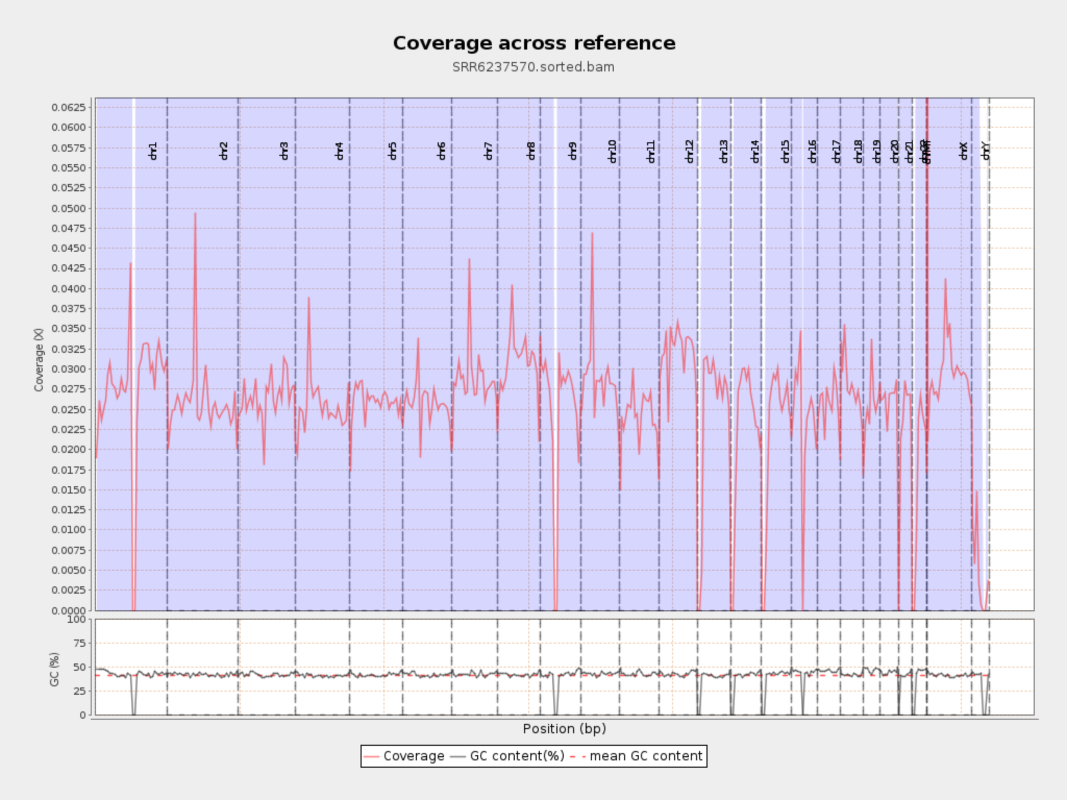
General error rate	0.98%
Mismatches	770,394
Insertions	7,509
Mapped reads with at least one insertion	0.57%
Deletions	29,295
Mapped reads with at least one deletion	2.23%
Homopolymer indels	46.69%

2.6. Chromosome stats

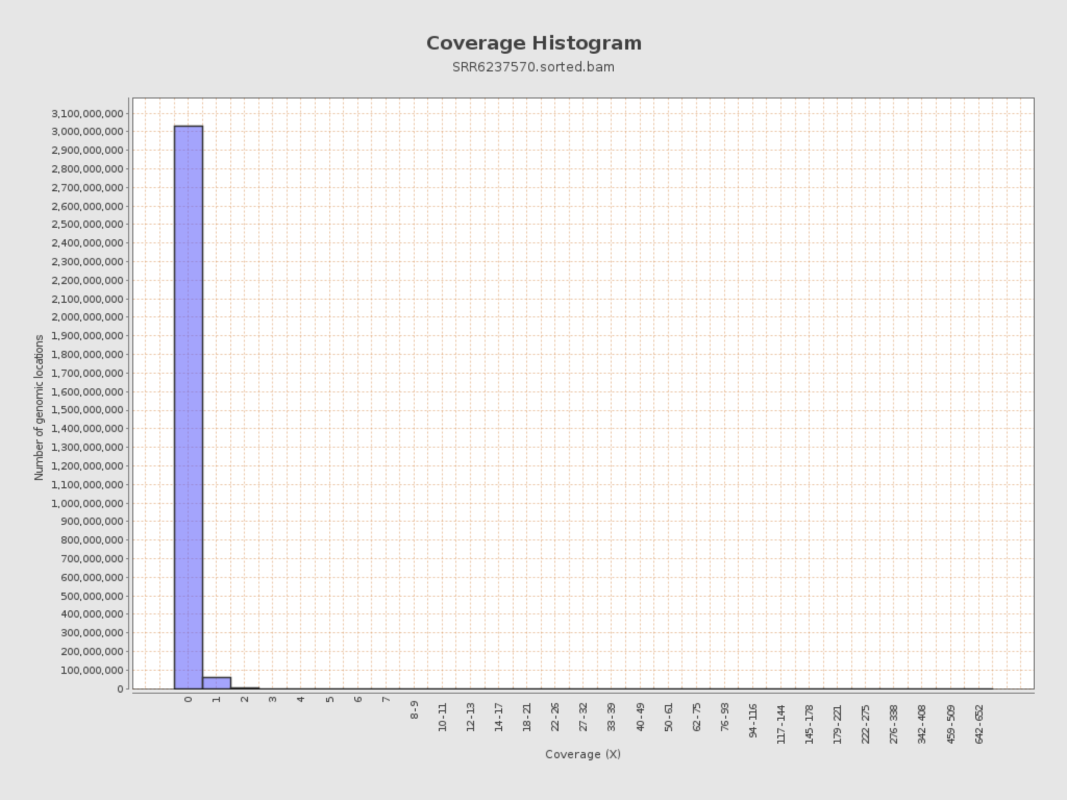
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6808718	0.0273	0.4433
chr2	243199373	6297326	0.0259	0.3831
chr3	198022430	5237895	0.0265	0.2017
chr4	191154276	4847506	0.0254	0.2049
chr5	180915260	4732504	0.0262	0.1976
chr6	171115067	4406180	0.0257	0.2226
chr7	159138663	4607368	0.029	0.3217

chr8	146364022	4531200	0.031	0.3332
chr9	141213431	3476402	0.0246	0.2598
chr10	135534747	3917069	0.0289	0.2607
chr11	135006516	3293598	0.0244	0.2329
chr12	133851895	4304618	0.0322	0.2217
chr13	115169878	2754937	0.0239	0.1927
chr14	107349540	2380231	0.0222	0.2068
chr15	102531392	2245647	0.0219	0.1871
chr16	90354753	2105169	0.0233	0.2046
chr17	81195210	2092656	0.0258	0.2007
chr18	78077248	2190469	0.0281	0.4368
chr19	59128983	1523029	0.0258	0.3222
chr20	63025520	1636896	0.026	0.2125
chr21	48129895	1091256	0.0227	0.1991
chr22	51304566	857484	0.0167	0.1542
chrMT	16571	43424	2.6205	3.2827
chrX	155270560	4601548	0.0296	0.2469
chrY	59373566	276715	0.0047	0.1203

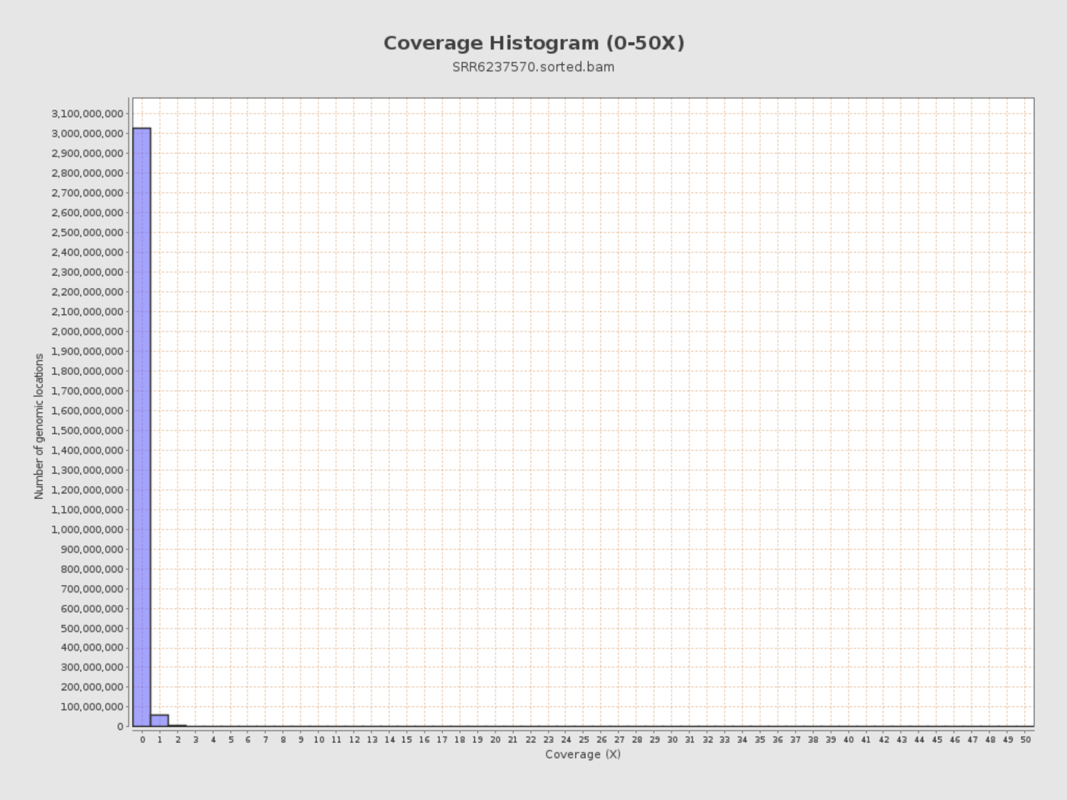
3. Results : Coverage across reference



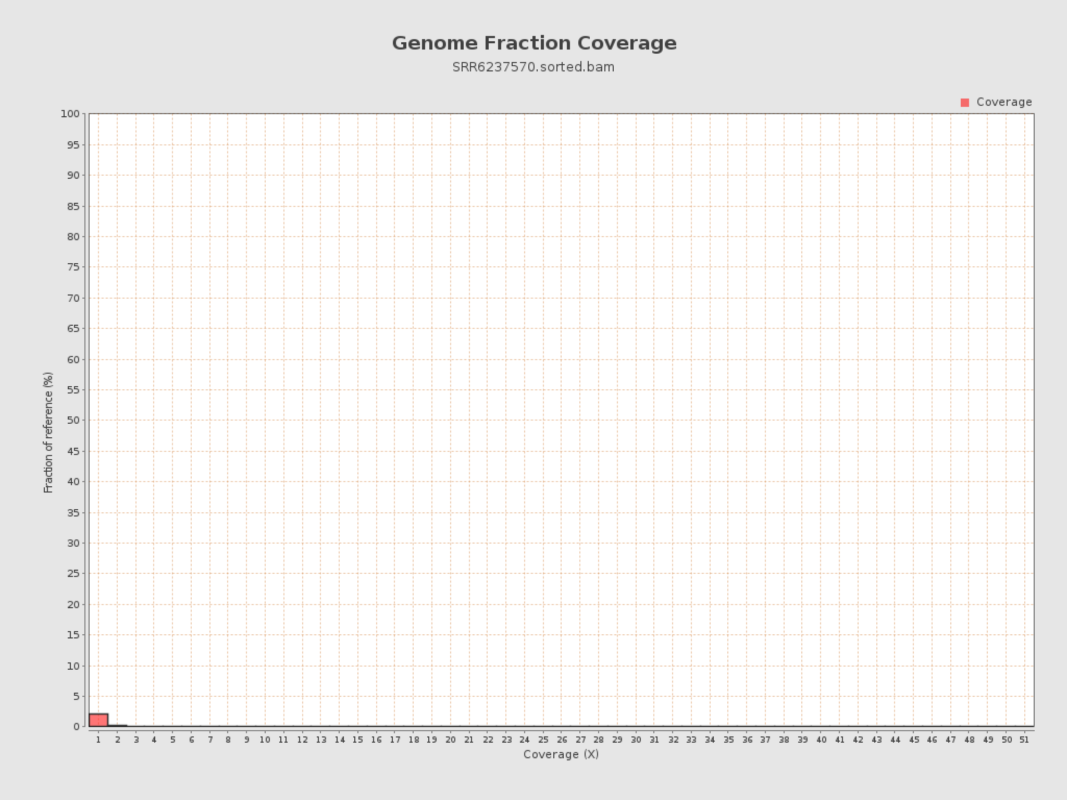
4. Results : Coverage Histogram



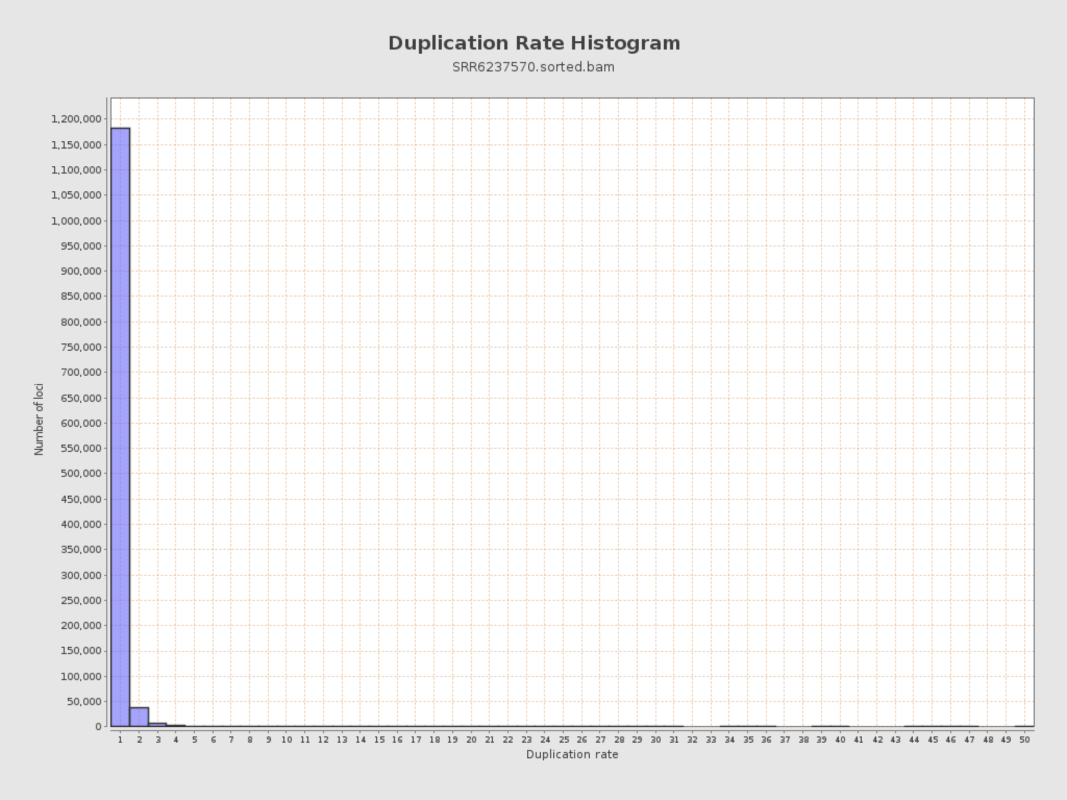
5. Results : Coverage Histogram (0-50X)



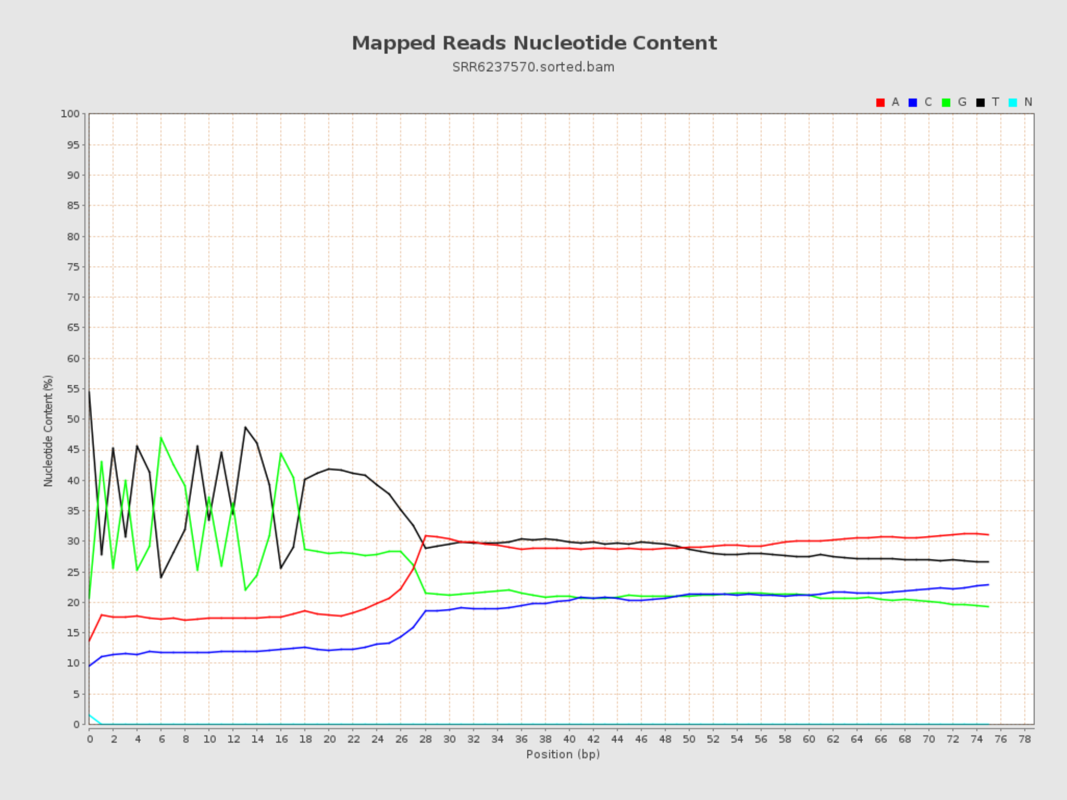
6. Results : Genome Fraction Coverage



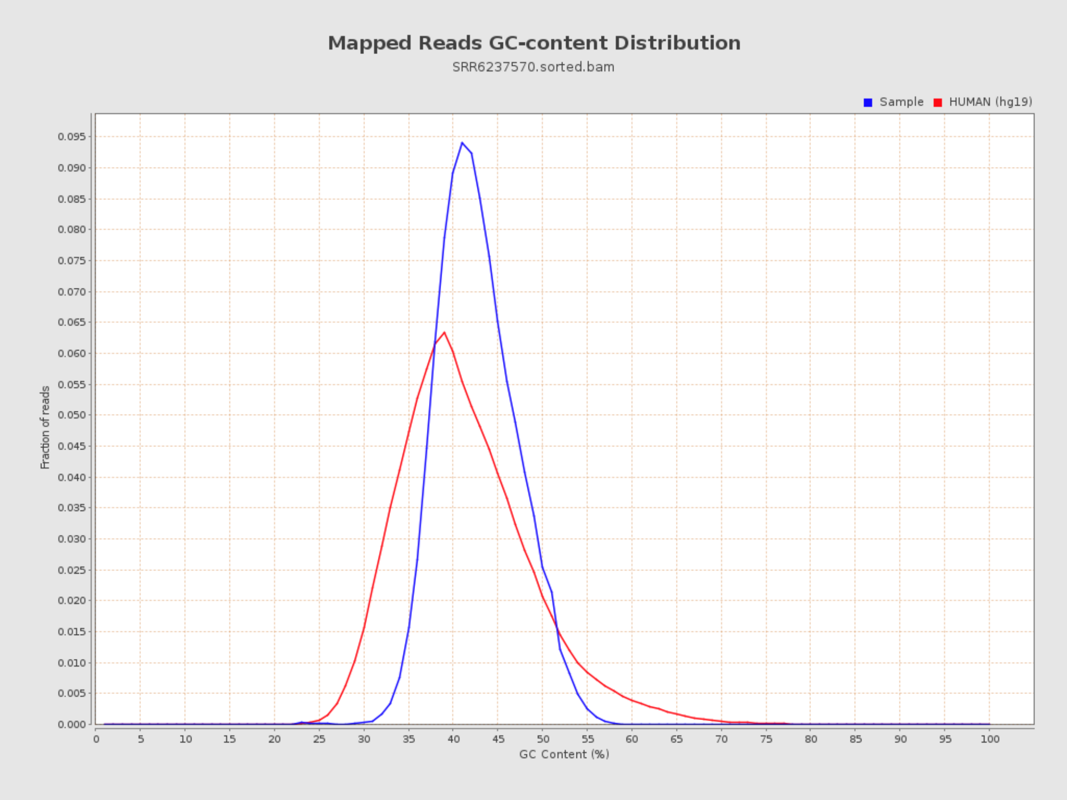
7. Results : Duplication Rate Histogram



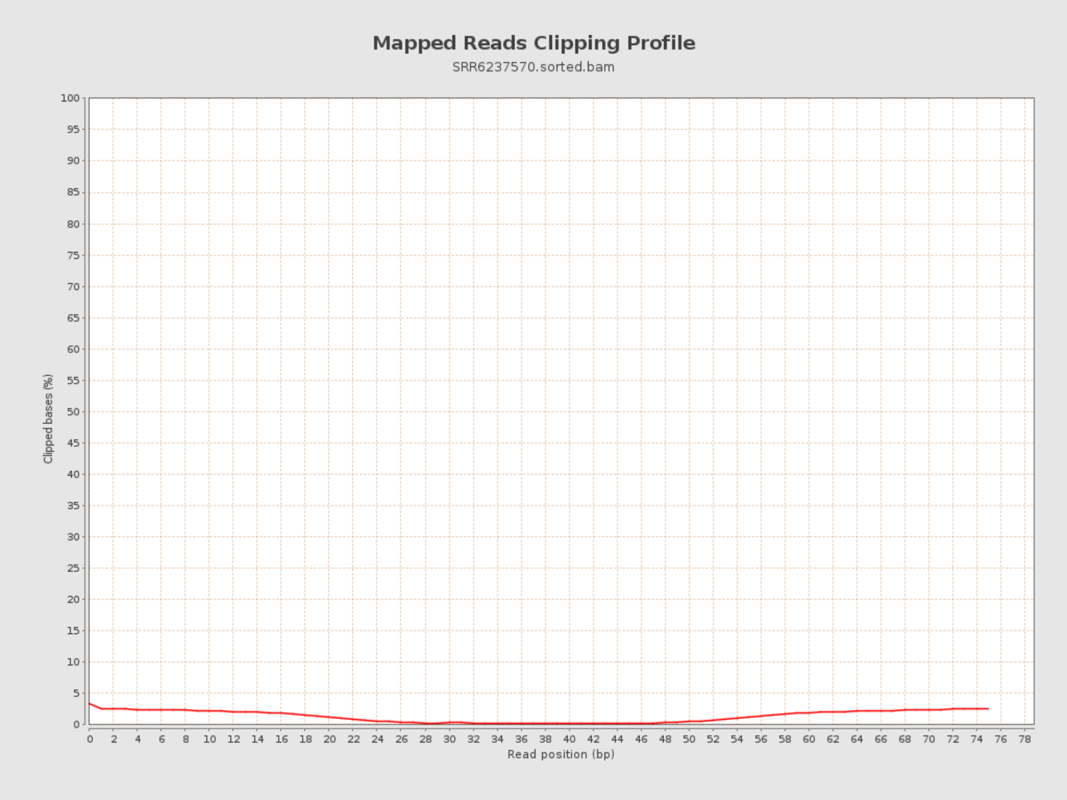
8. Results : Mapped Reads Nucleotide Content



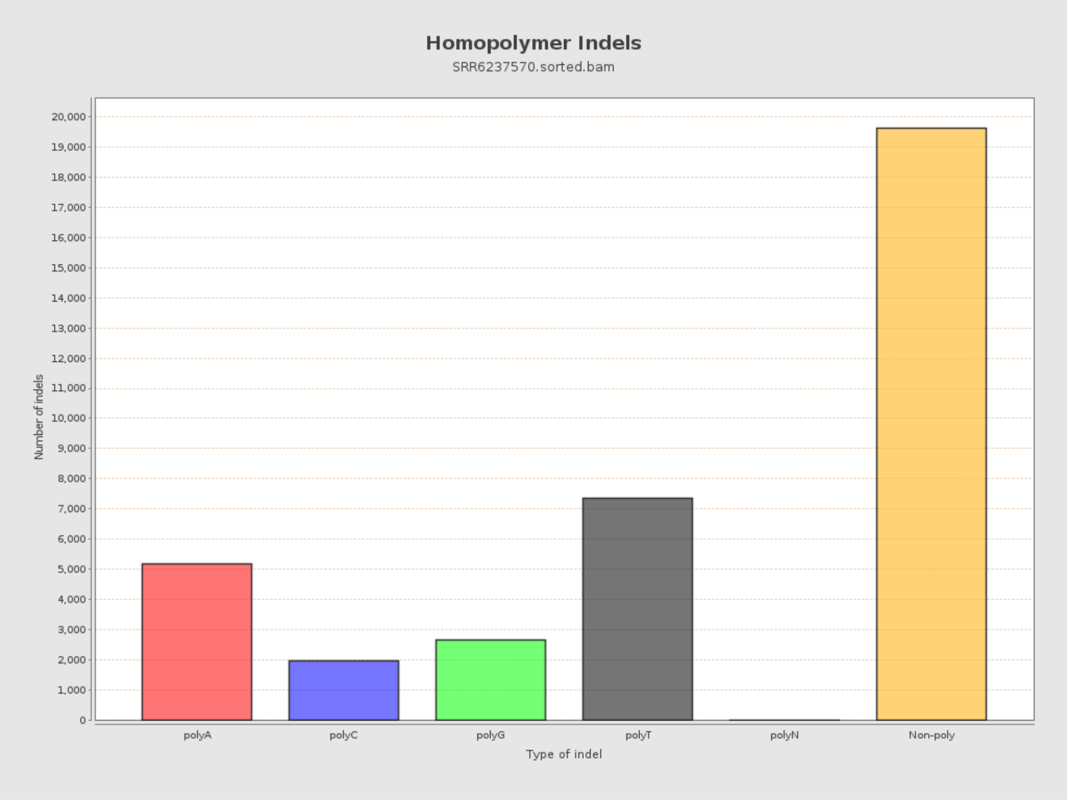
9. Results : Mapped Reads GC-content Distribution



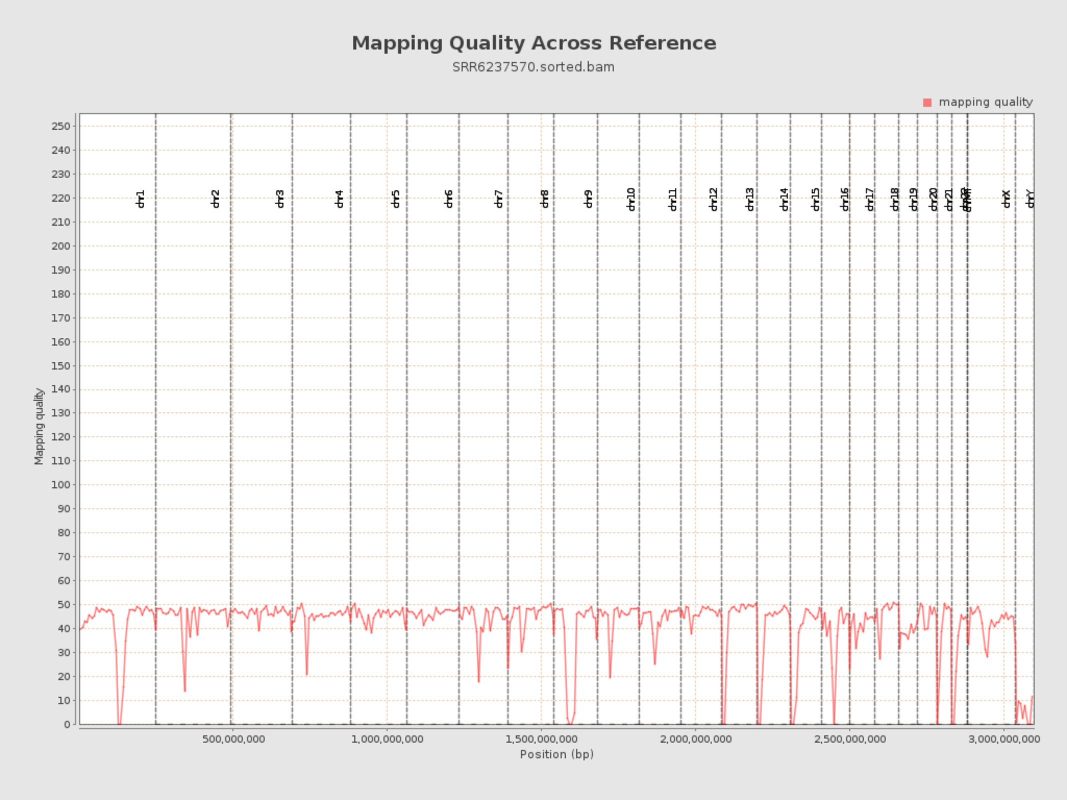
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram