Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 09:15:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237856.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_SRR6237856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237856.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 09:15:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,227,569
Mapped reads	2,696,636 / 83.55%
Unmapped reads	530,933 / 16.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,710 / 0.73%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	205,456 / 6.37%
Duplication rate	6%
Clipped reads	506,015 / 15.68%

2.2. ACGT Content

Number/percentage of A's	58,345,558 / 29.65%
Number/percentage of C's	39,454,868 / 20.05%
Number/percentage of T's	58,883,961 / 29.92%
Number/percentage of G's	39,748,371 / 20.2%
Number/percentage of N's	355,986 / 0.18%
GC Percentage	40.25%

2.3. Coverage

Mean	0.0636

Standard Deviation	0.7889

2.4. Mapping Quality

Mean Mapping Quality	46.95

2.5. Mismatches and indels

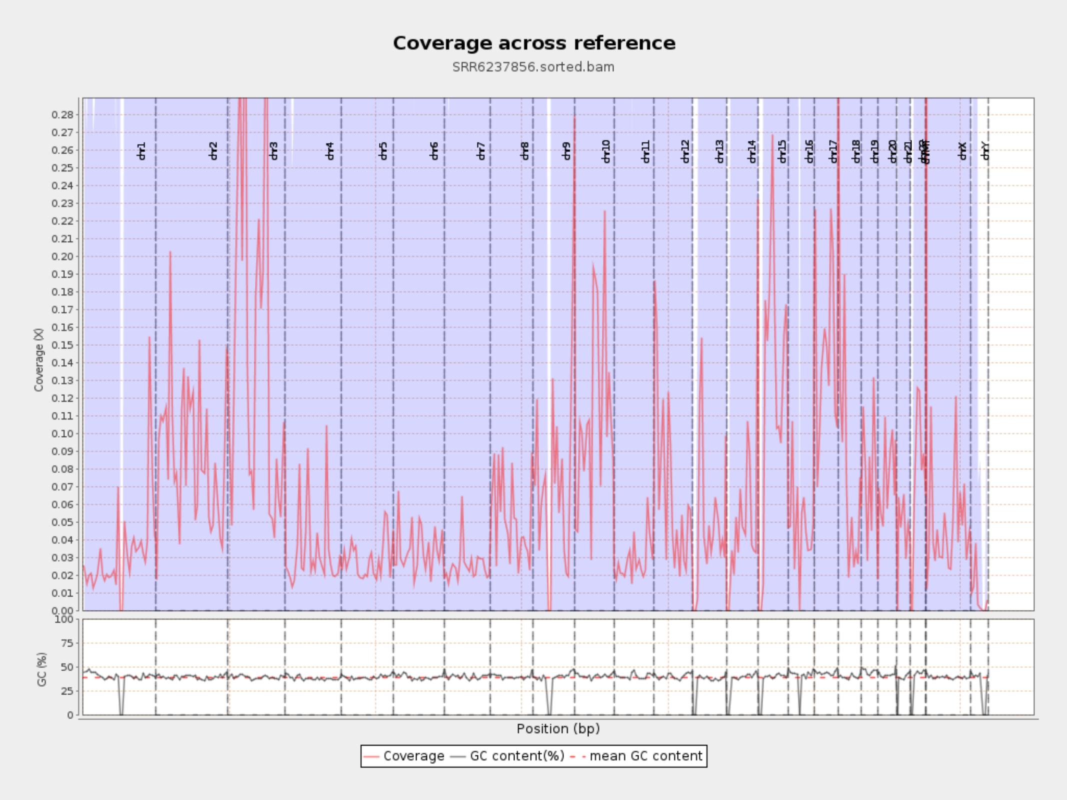
General error rate	0.88%
Mismatches	1,690,129
Insertions	16,103
Mapped reads with at least one insertion	0.59%
Deletions	46,513
Mapped reads with at least one deletion	1.7%
Homopolymer indels	48.01%

2.6. Chromosome stats

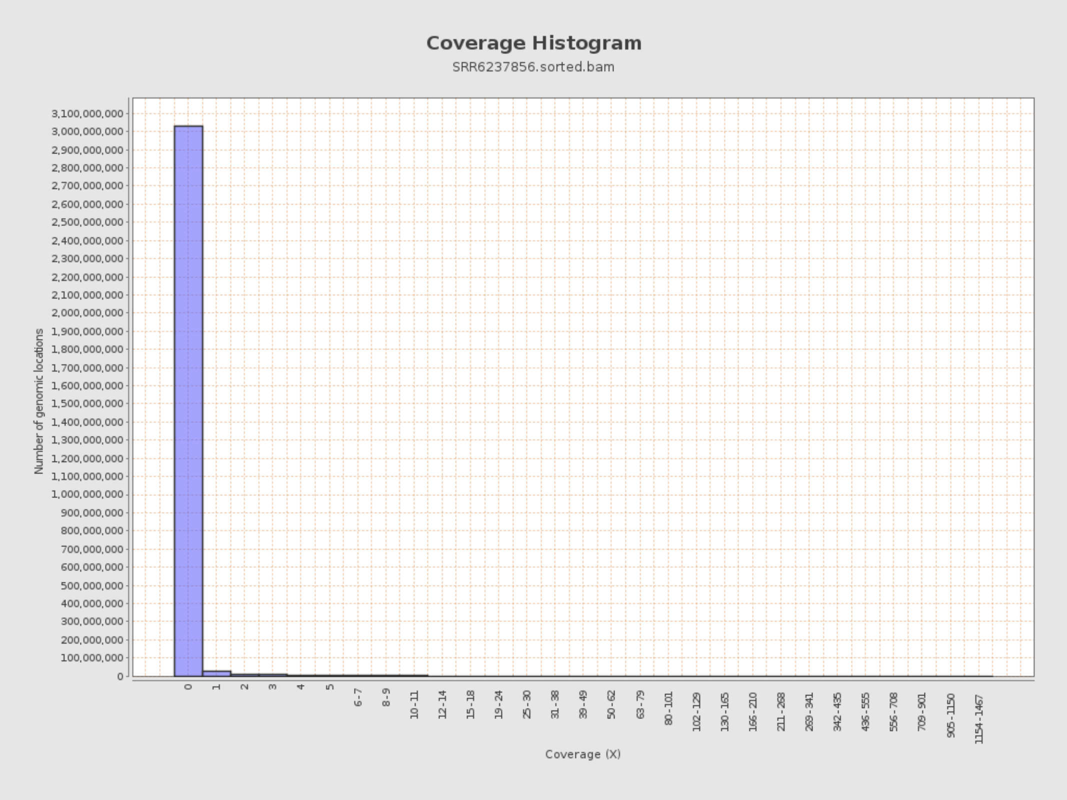
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8003820	0.0321	1.2183
chr2	243199373	21533092	0.0885	1
chr3	198022430	29919056	0.1511	0.9592
chr4	191154276	6505607	0.034	0.4766
chr5	180915260	5276479	0.0292	0.405
chr6	171115067	5918759	0.0346	0.4477
chr7	159138663	4042076	0.0254	0.5103

chr8	146364022	7673272	0.0524	0.8539
chr9	141213431	10159768	0.0719	0.8325
chr10	135534747	15519503	0.1145	1.0203
chr11	135006516	3830189	0.0284	0.4233
chr12	133851895	9326102	0.0697	0.6487
chr13	115169878	5502024	0.0478	0.5276
chr14	107349540	4858106	0.0453	0.5158
chr15	102531392	12736248	0.1242	0.849
chr16	90354753	4400985	0.0487	0.5571
chr17	81195210	12024659	0.1481	0.9154
chr18	78077248	6421226	0.0822	1.458
chr19	59128983	4388718	0.0742	0.8111
chr20	63025520	4775663	0.0758	0.6697
chr21	48129895	2172555	0.0451	0.5335
chr22	51304566	3853567	0.0751	0.6268
chrMT	16571	109965	6.636	6.1259
chrX	155270560	7386184	0.0476	0.5462
chrY	59373566	536884	0.009	0.3345

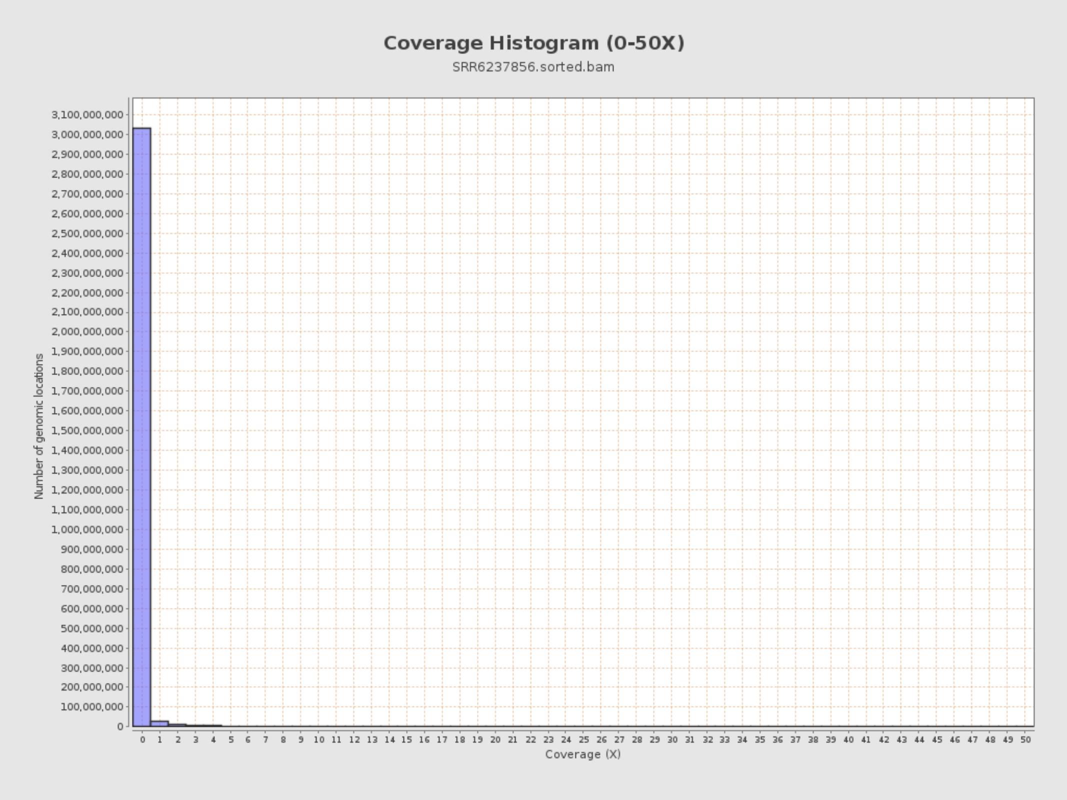
3. Results : Coverage across reference



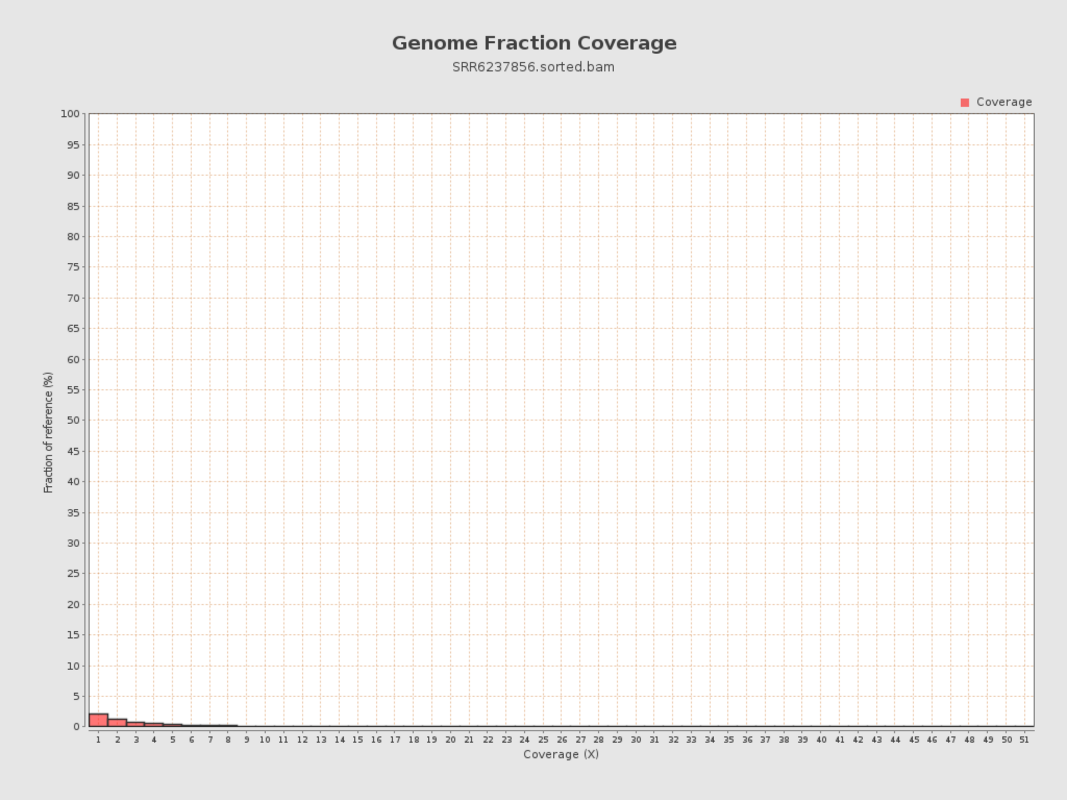
4. Results : Coverage Histogram



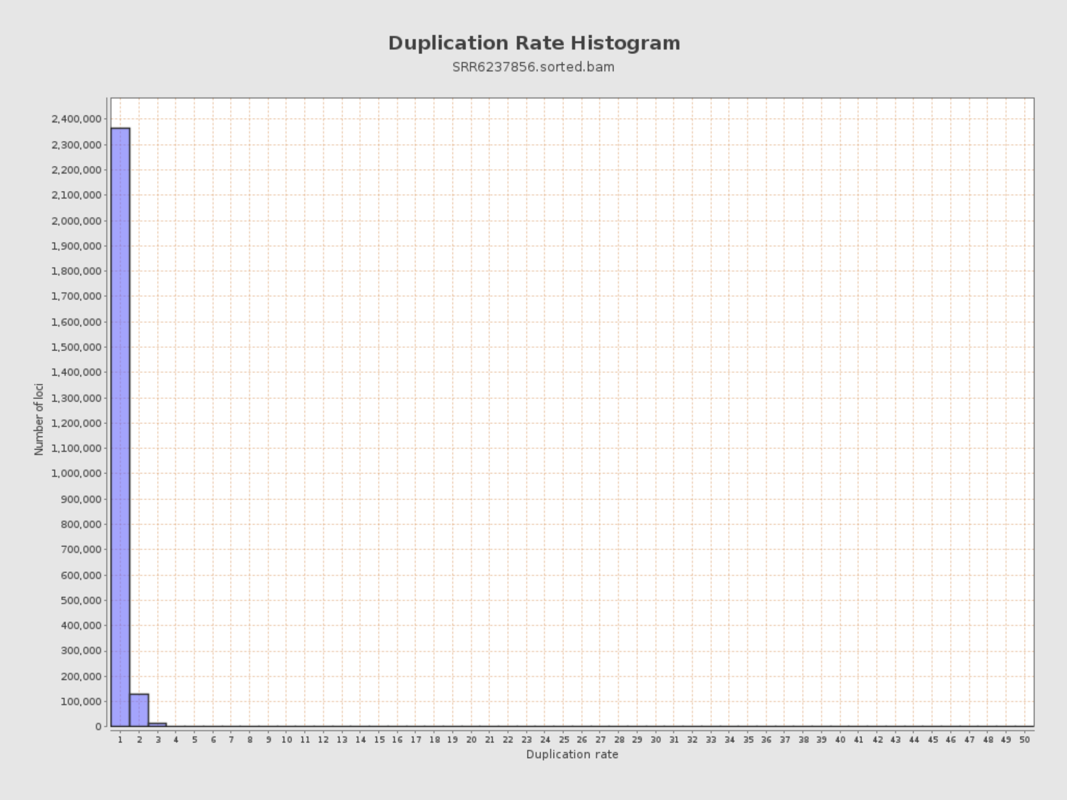
5. Results : Coverage Histogram (0-50X)



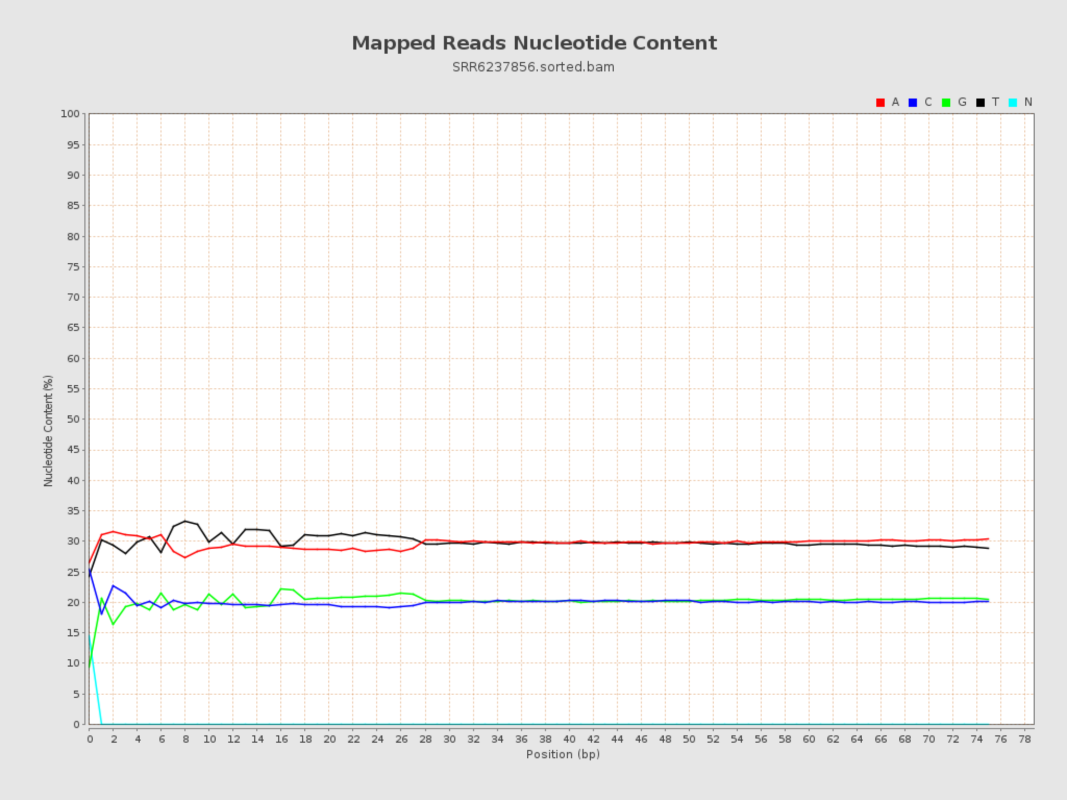
6. Results : Genome Fraction Coverage



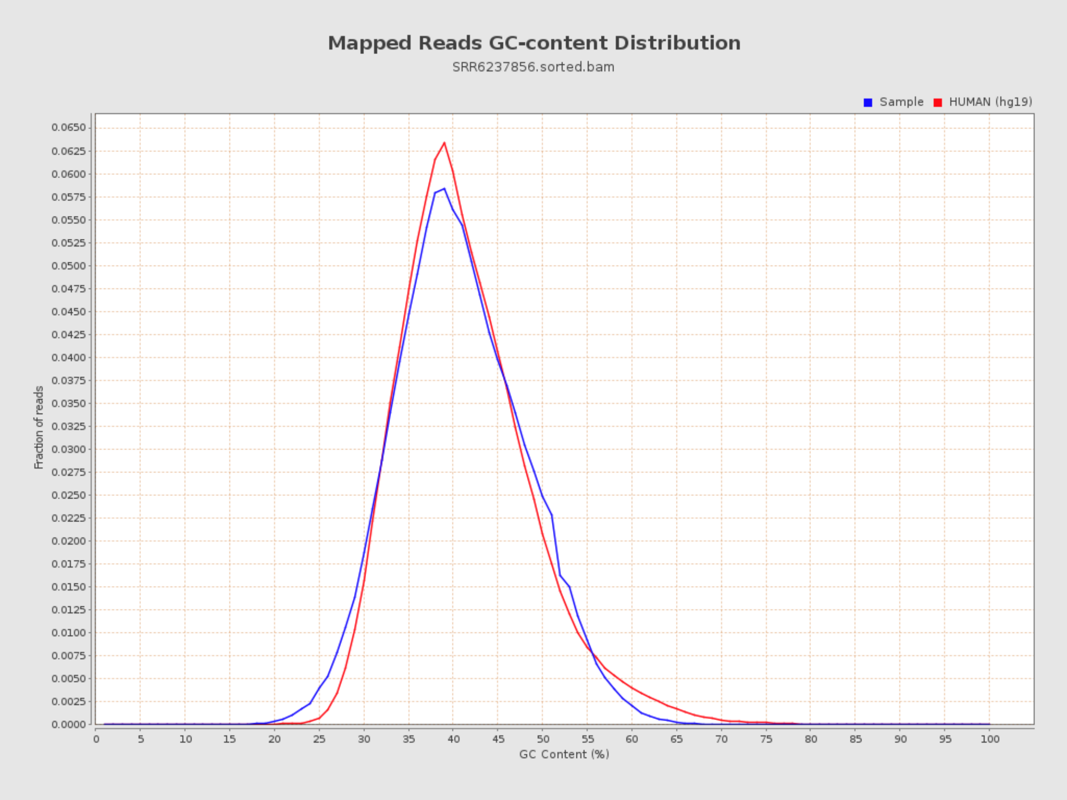
7. Results : Duplication Rate Histogram



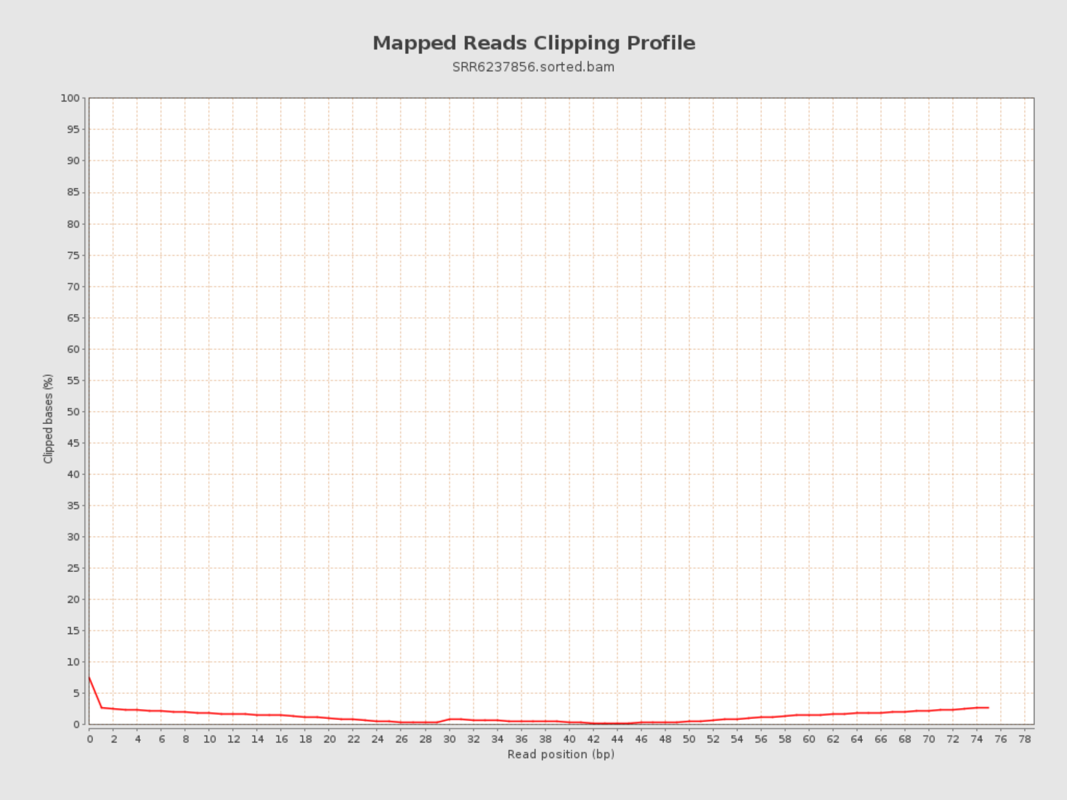
8. Results : Mapped Reads Nucleotide Content



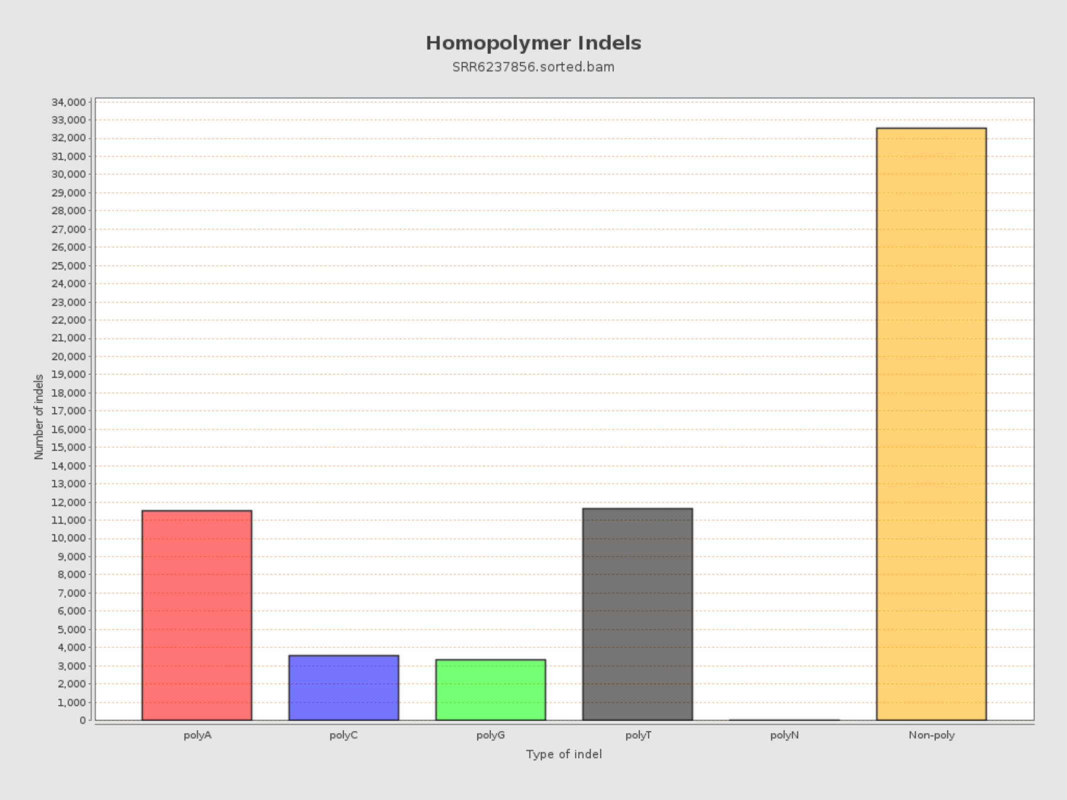
9. Results : Mapped Reads GC-content Distribution



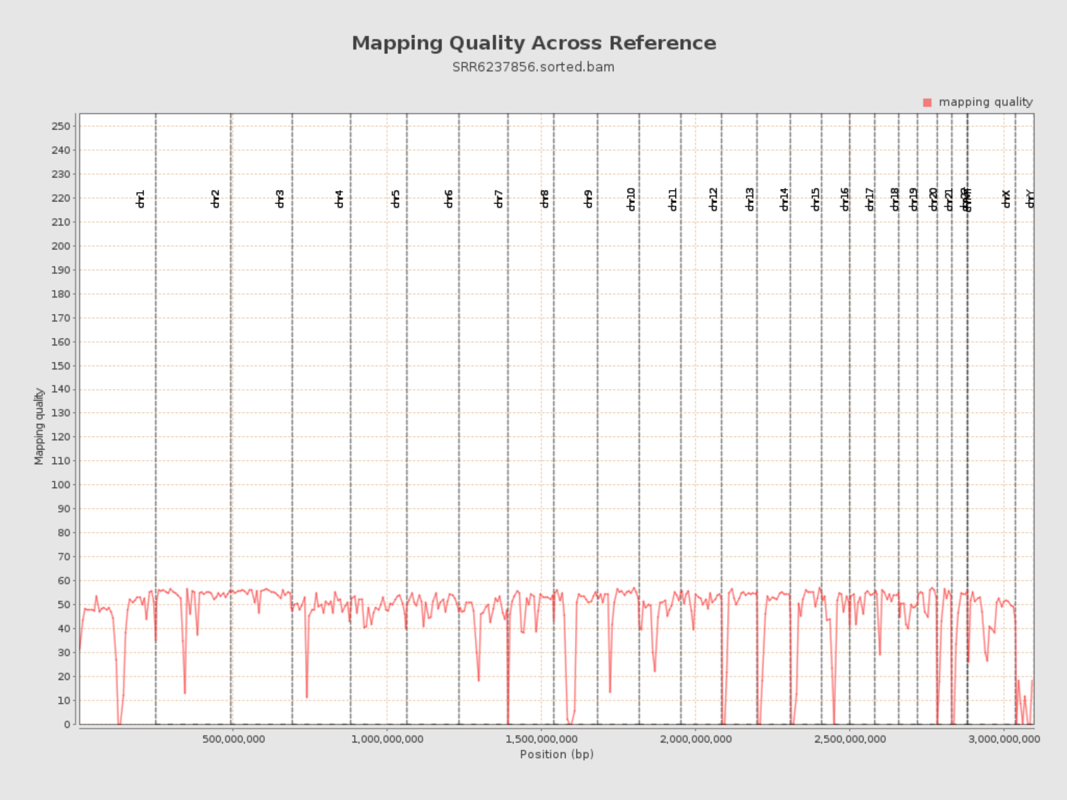
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram