Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 05:17:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237607.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_SRR6237607 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237607.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 05:17:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237607.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,600,051
Mapped reads	1,370,671 / 85.66%
Unmapped reads	229,380 / 14.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,977 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	45,435 / 2.84%
Duplication rate	2.21%
Clipped reads	738,215 / 46.14%

2.2. ACGT Content

Number/percentage of A's	23,143,868 / 26.4%
Number/percentage of C's	15,769,657 / 17.99%
Number/percentage of T's	27,662,374 / 31.56%
Number/percentage of G's	20,930,869 / 23.88%
Number/percentage of N's	147,109 / 0.17%
GC Percentage	41.87%

2.3. Coverage

Mean	0.0283

Standard Deviation	0.2972

2.4. Mapping Quality

Mean Mapping Quality	43.1

2.5. Mismatches and indels

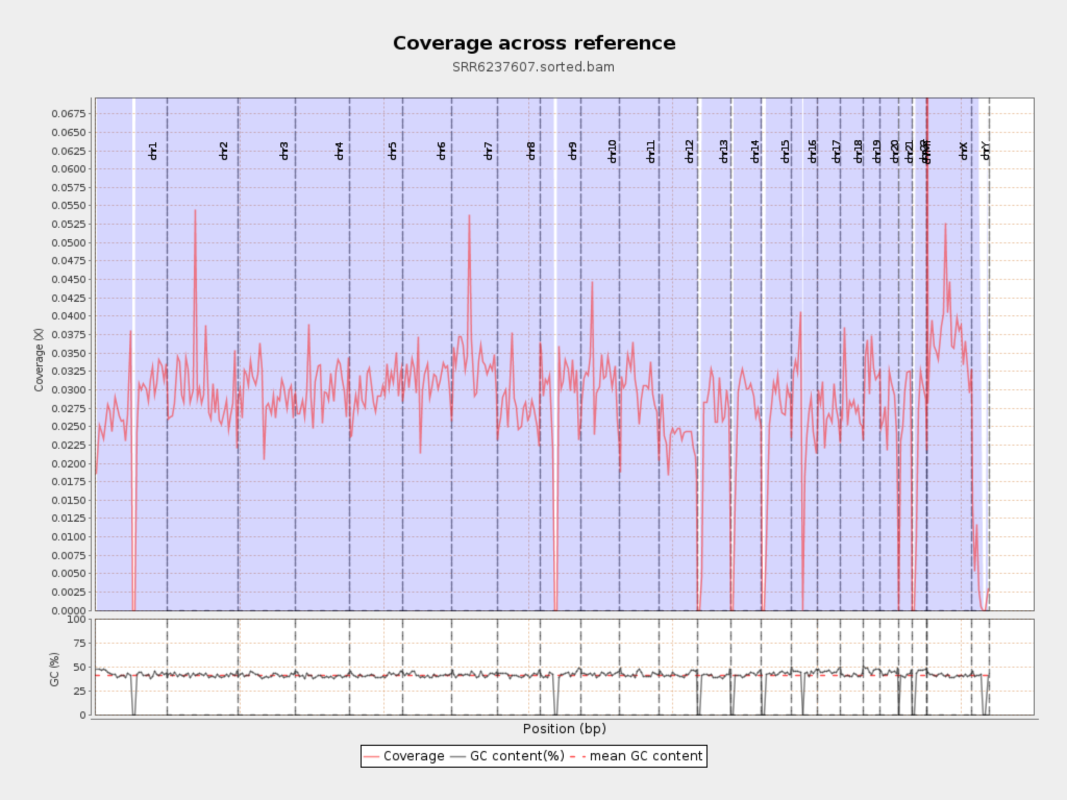
General error rate	0.87%
Mismatches	751,158
Insertions	8,058
Mapped reads with at least one insertion	0.58%
Deletions	26,314
Mapped reads with at least one deletion	1.9%
Homopolymer indels	45.62%

2.6. Chromosome stats

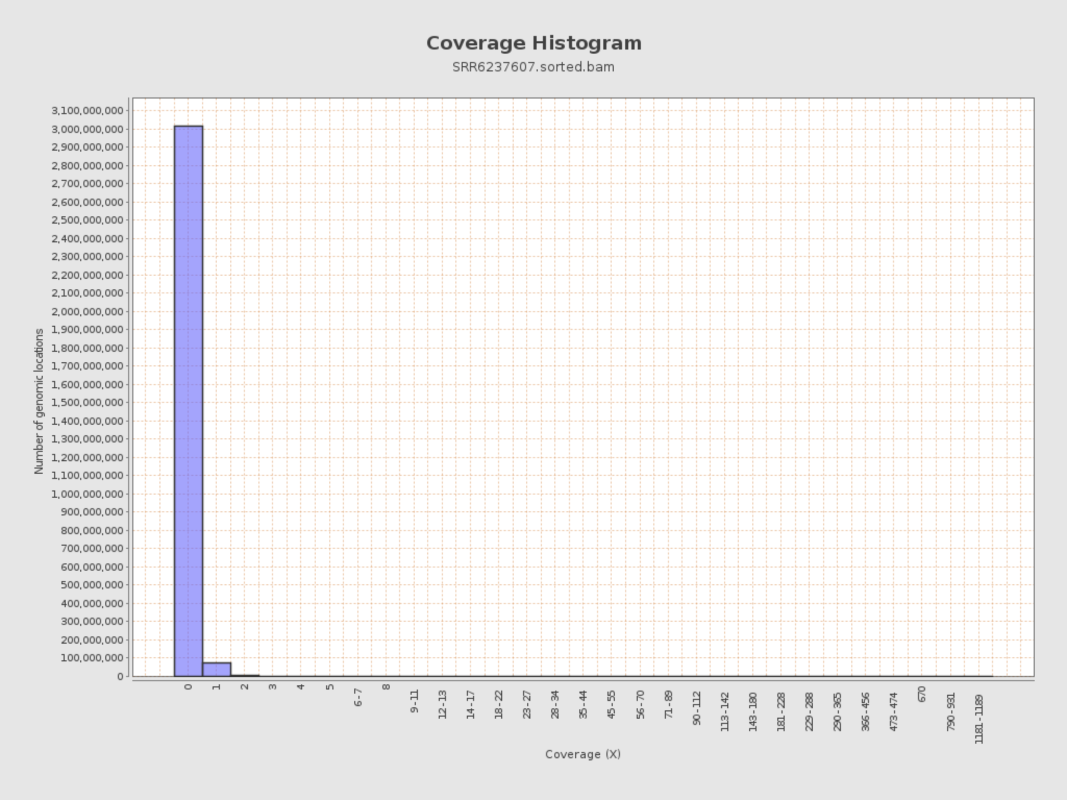
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6631118	0.0266	0.3572
chr2	243199373	7269918	0.0299	0.561
chr3	198022430	5870273	0.0296	0.186
chr4	191154276	5765093	0.0302	0.1958
chr5	180915260	5418785	0.03	0.1884
chr6	171115067	5344282	0.0312	0.2853
chr7	159138663	5510770	0.0346	0.375

chr8	146364022	4019109	0.0275	0.2882
chr9	141213431	3886004	0.0275	0.3022
chr10	135534747	4280799	0.0316	0.2485
chr11	135006516	4101881	0.0304	0.2671
chr12	133851895	3172391	0.0237	0.1763
chr13	115169878	2729603	0.0237	0.1749
chr14	107349540	2654849	0.0247	0.1934
chr15	102531392	2378790	0.0232	0.1712
chr16	90354753	2313787	0.0256	0.2226
chr17	81195210	2204795	0.0272	0.1977
chr18	78077248	2188214	0.028	0.5347
chr19	59128983	1949221	0.033	0.3043
chr20	63025520	1676912	0.0266	0.1817
chr21	48129895	1224642	0.0254	0.1881
chr22	51304566	1043654	0.0203	0.1532
chrMT	16571	9225	0.5567	0.9143
chrX	155270560	5799008	0.0373	0.2443
chrY	59373566	254876	0.0043	0.0988

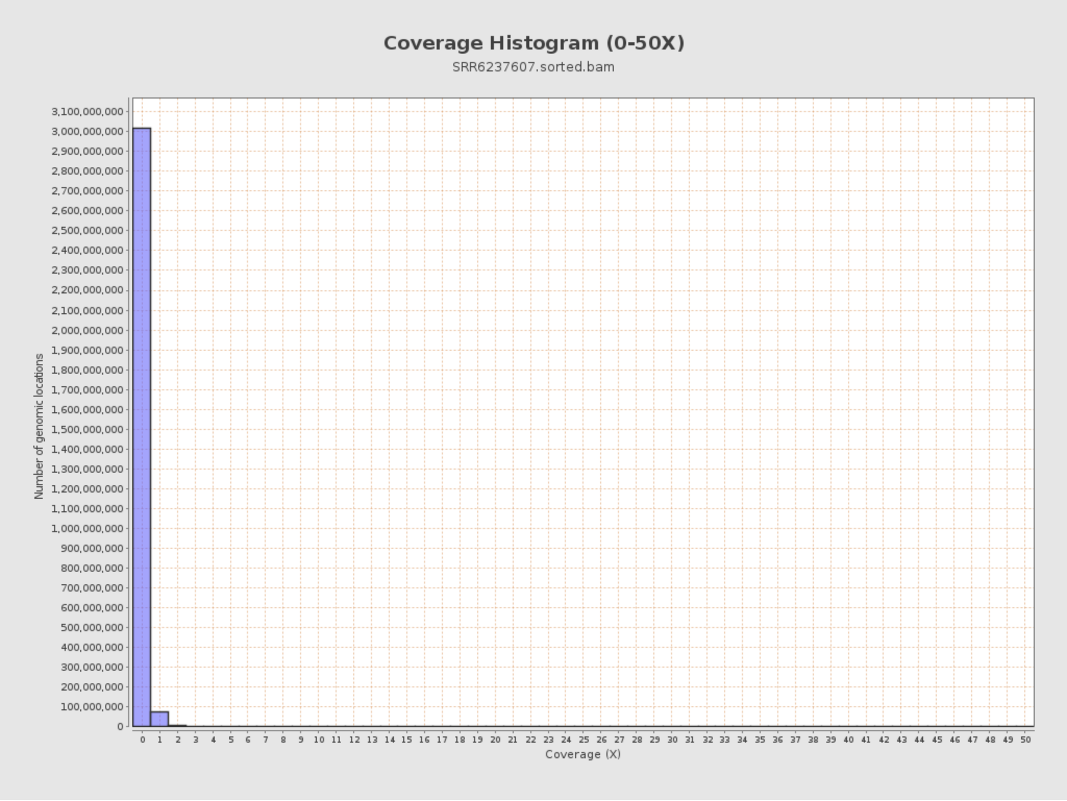
3. Results : Coverage across reference



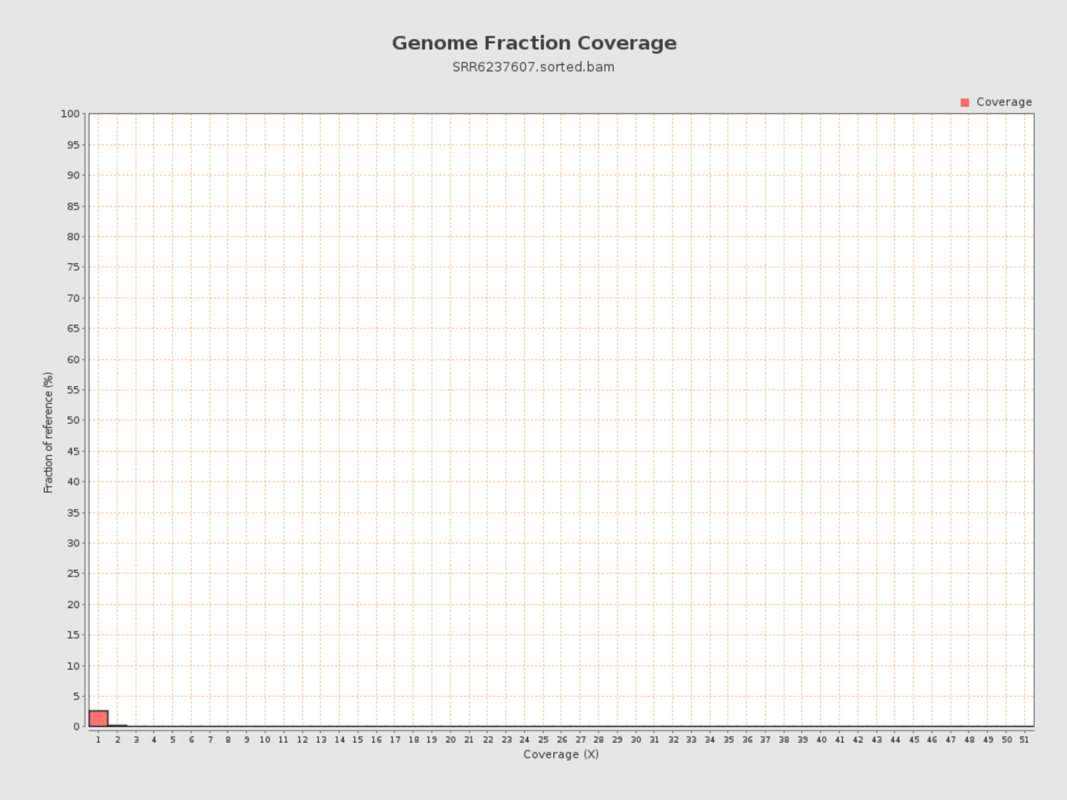
4. Results : Coverage Histogram



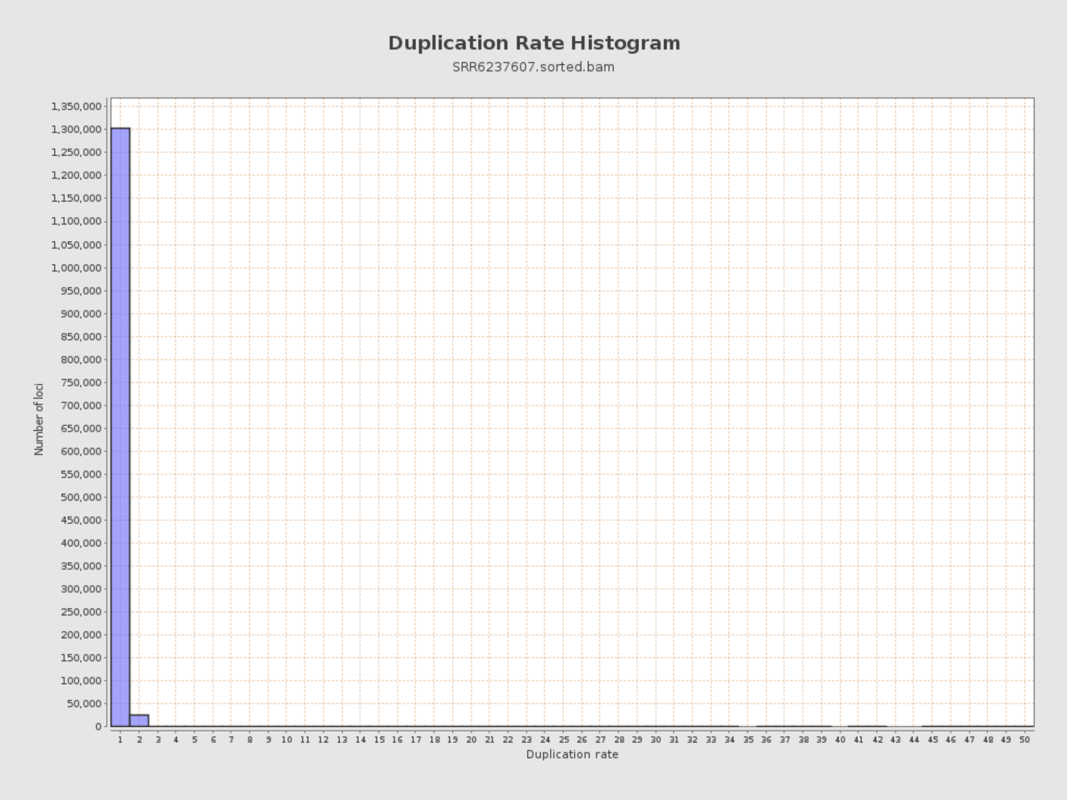
5. Results : Coverage Histogram (0-50X)



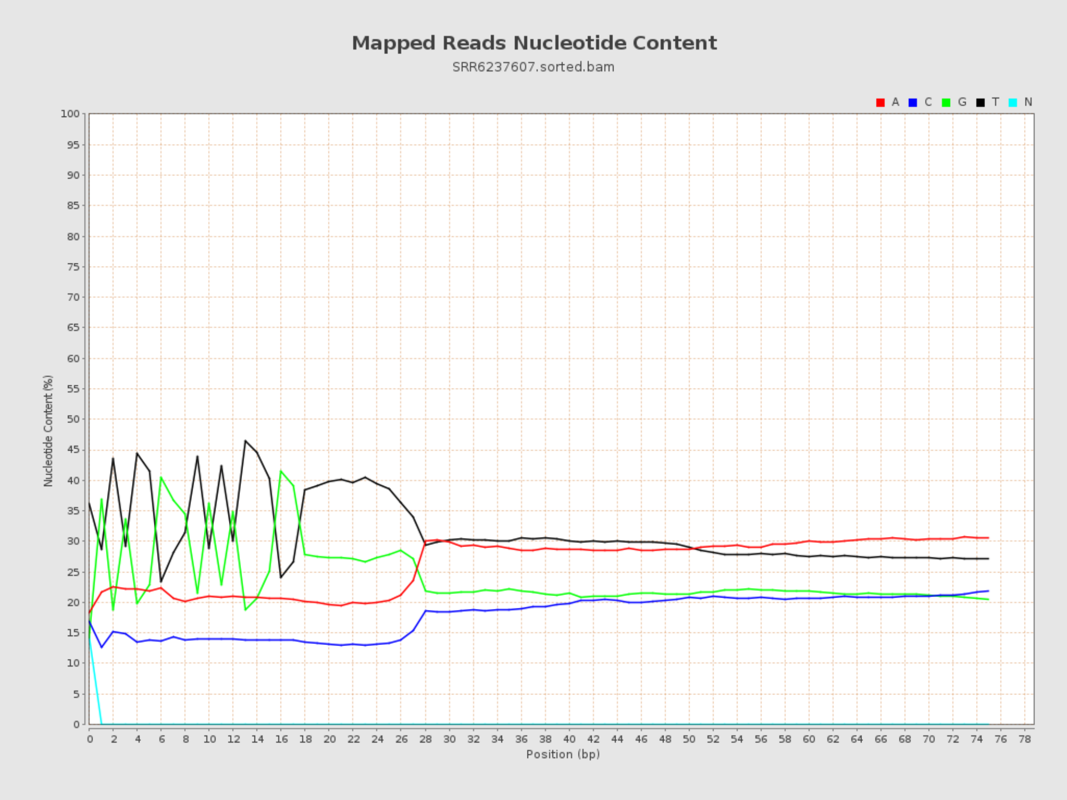
6. Results : Genome Fraction Coverage



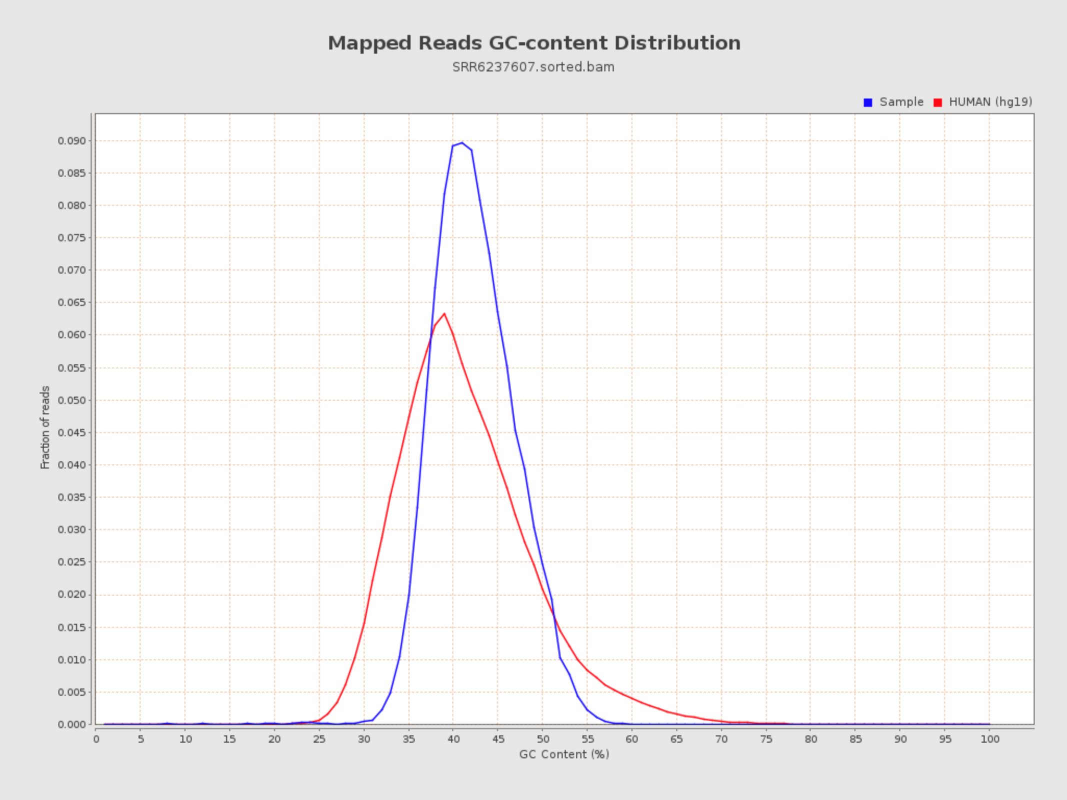
7. Results : Duplication Rate Histogram



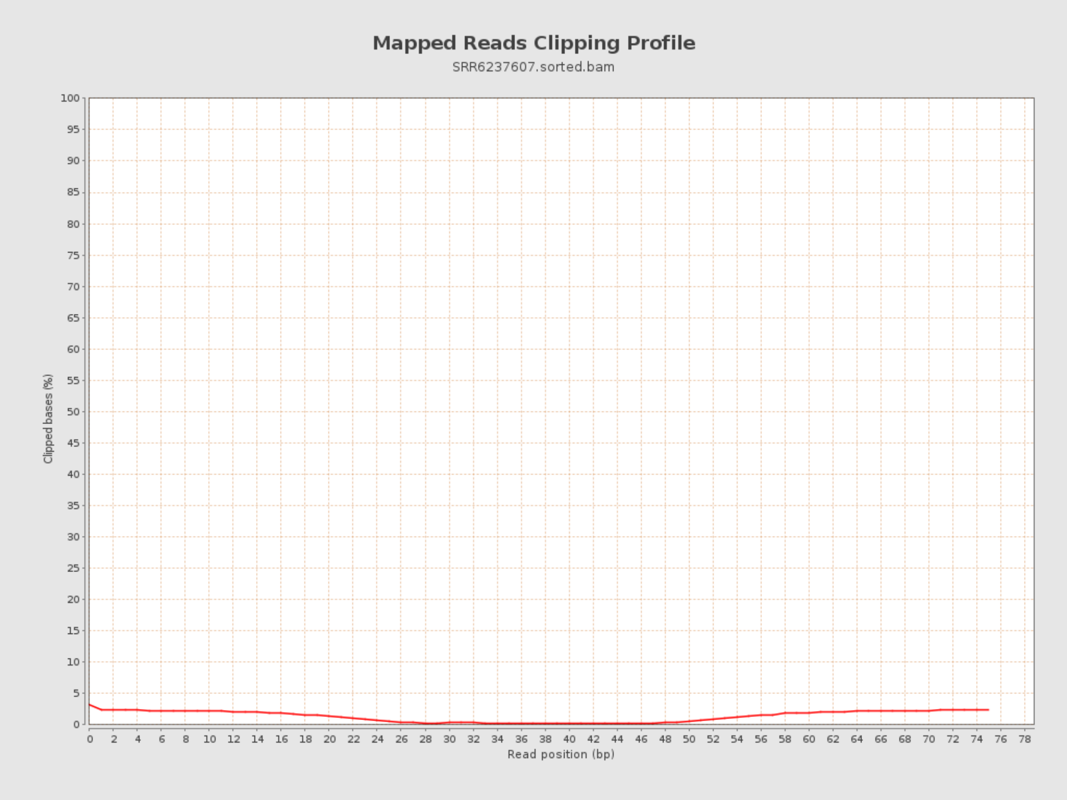
8. Results : Mapped Reads Nucleotide Content



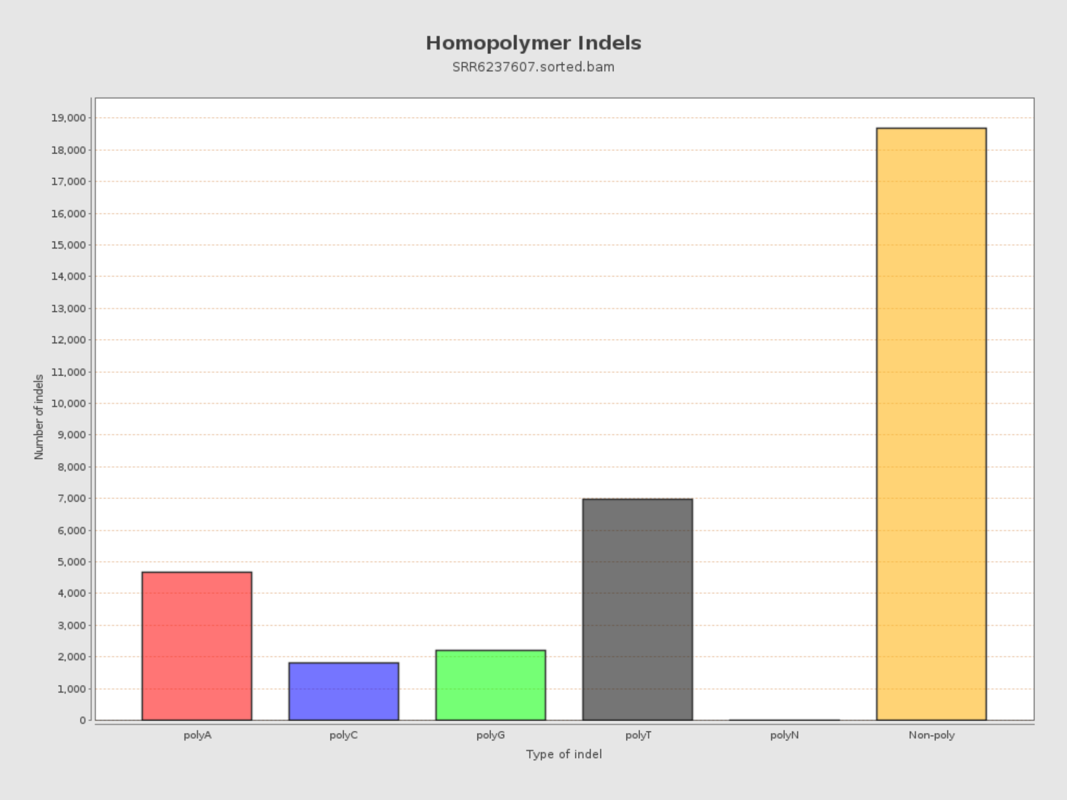
9. Results : Mapped Reads GC-content Distribution



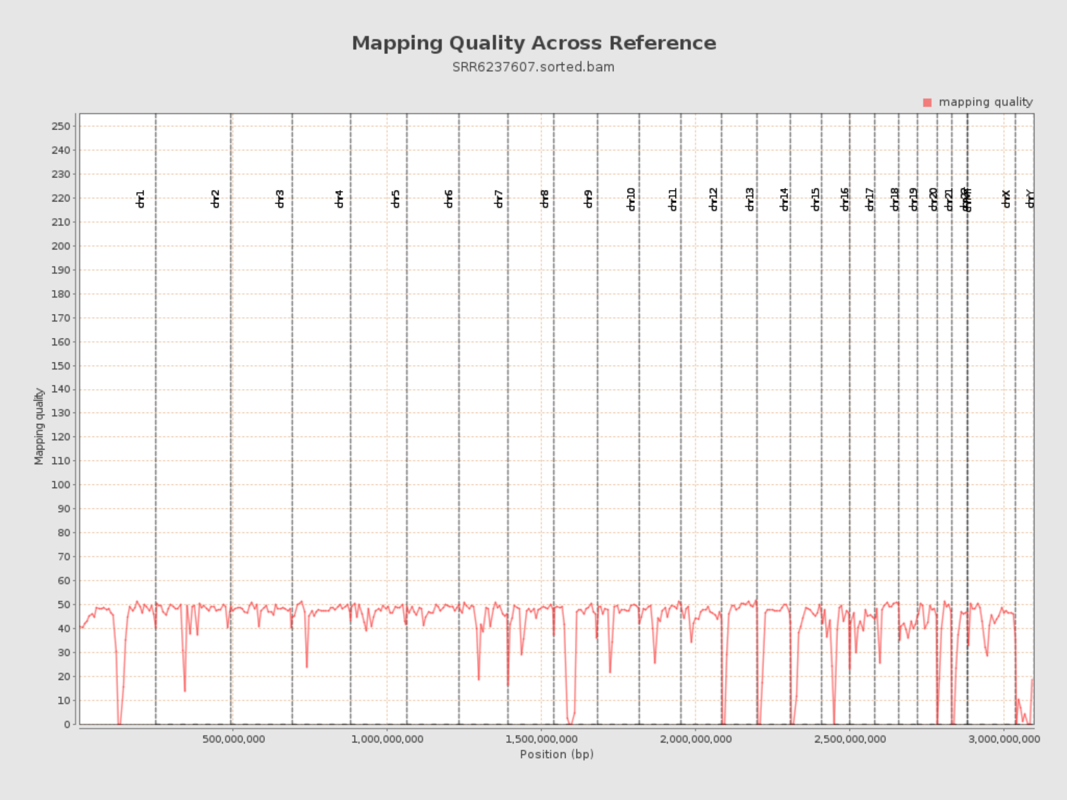
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram