Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 07:41:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6237825.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_SRR6237825 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6237825.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 07:41:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6237825.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,902,620
Mapped reads	3,629,682 / 93.01%
Unmapped reads	272,938 / 6.99%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	38,598 / 0.99%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	278,835 / 7.14%
Duplication rate	6.17%
Clipped reads	967,204 / 24.78%

2.2. ACGT Content

Number/percentage of A's	78,768,860 / 30.24%
Number/percentage of C's	50,663,175 / 19.45%
Number/percentage of T's	78,608,624 / 30.17%
Number/percentage of G's	52,020,020 / 19.97%
Number/percentage of N's	457,387 / 0.18%
GC Percentage	39.41%

2.3. Coverage

Mean	0.0842

Standard Deviation	0.9143

2.4. Mapping Quality

Mean Mapping Quality	46.91

2.5. Mismatches and indels

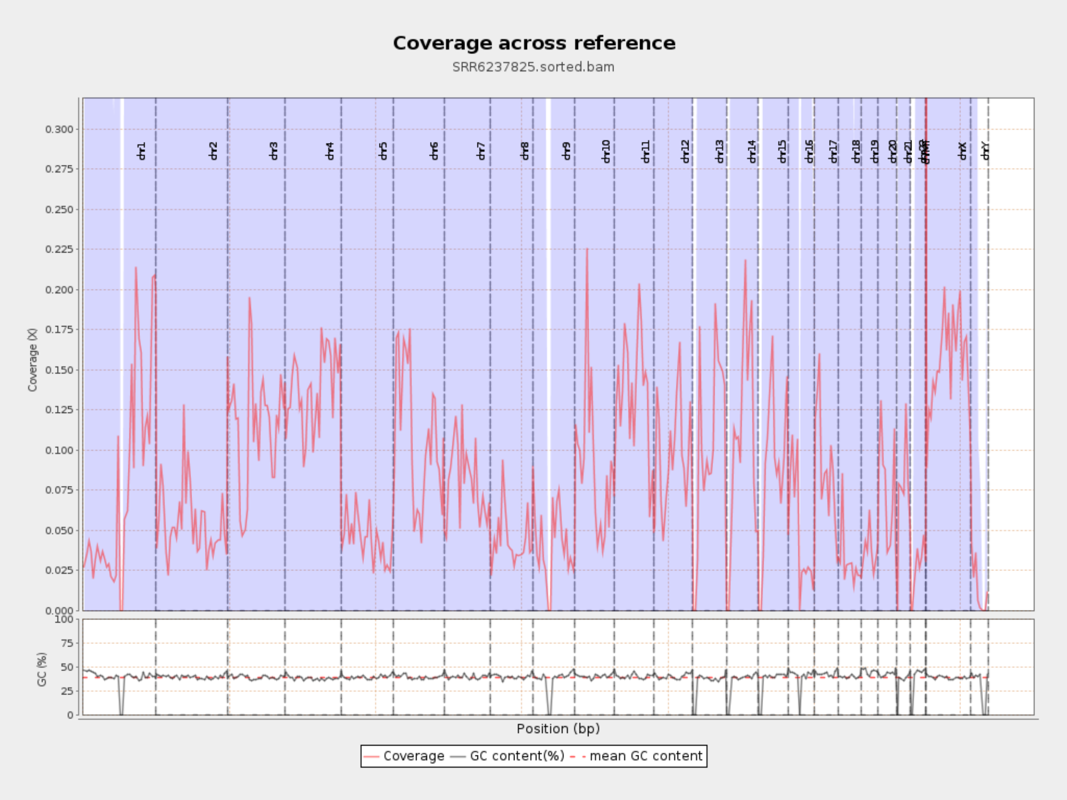
General error rate	0.97%
Mismatches	2,487,735
Insertions	19,116
Mapped reads with at least one insertion	0.52%
Deletions	118,003
Mapped reads with at least one deletion	3.2%
Homopolymer indels	43.65%

2.6. Chromosome stats

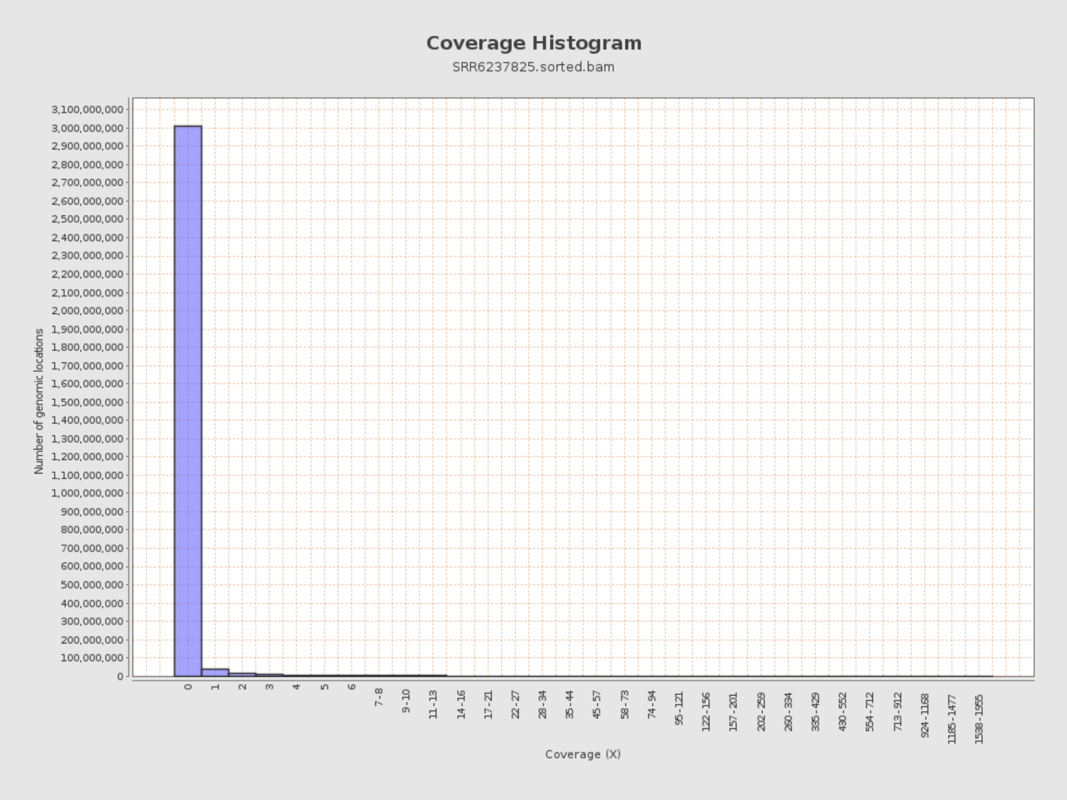
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19002681	0.0762	1.2001
chr2	243199373	13332605	0.0548	0.7401
chr3	198022430	23030050	0.1163	0.8524
chr4	191154276	26275825	0.1375	0.9517
chr5	180915260	8191884	0.0453	0.5213
chr6	171115067	18635221	0.1089	0.9271
chr7	159138663	12727339	0.08	0.9009

chr8	146364022	6437957	0.044	1.2564
chr9	141213431	5581866	0.0395	0.6627
chr10	135534747	12318668	0.0909	1.0236
chr11	135006516	18255952	0.1352	1.0971
chr12	133851895	13040725	0.0974	0.7946
chr13	115169878	11988466	0.1041	0.8148
chr14	107349540	11627614	0.1083	0.8641
chr15	102531392	8974382	0.0875	0.7438
chr16	90354753	4195683	0.0464	0.5842
chr17	81195210	7550332	0.093	0.9848
chr18	78077248	2433445	0.0312	1.4215
chr19	59128983	2239159	0.0379	0.8614
chr20	63025520	4985495	0.0791	0.7426
chr21	48129895	3631478	0.0755	0.6961
chr22	51304566	1314619	0.0256	0.3722
chrMT	16571	16811	1.0145	2.4107
chrX	155270560	24134409	0.1554	1.0449
chrY	59373566	802710	0.0135	0.3542

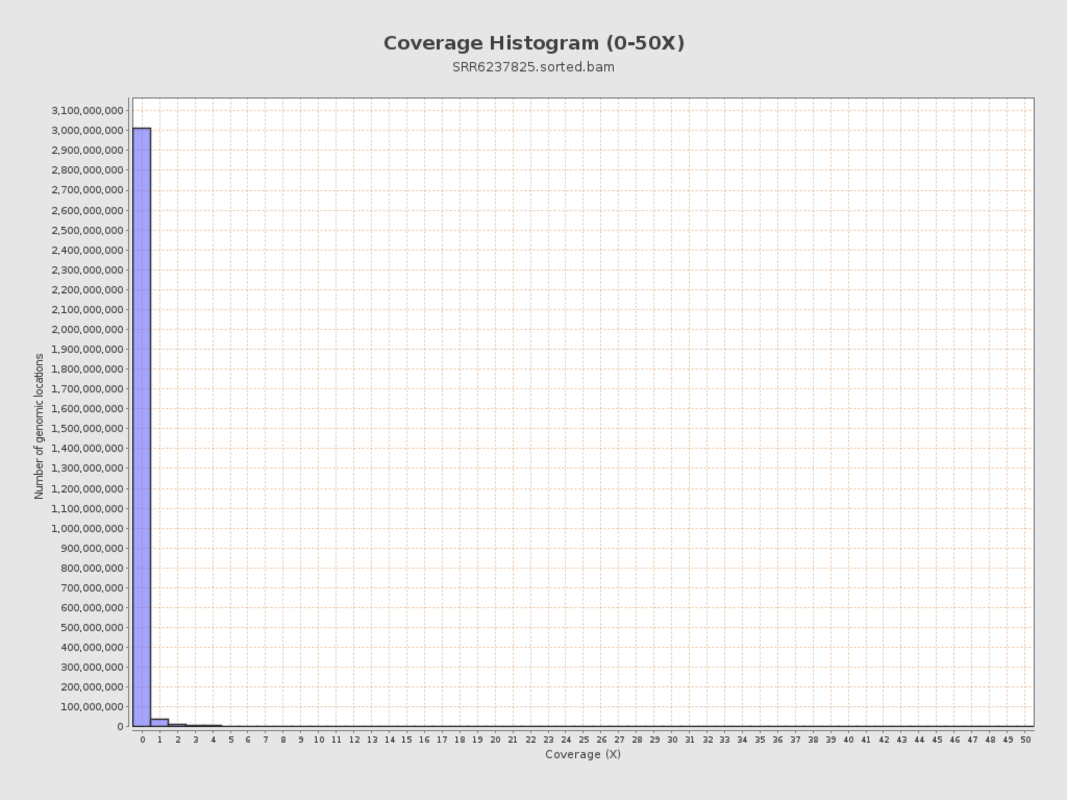
3. Results : Coverage across reference



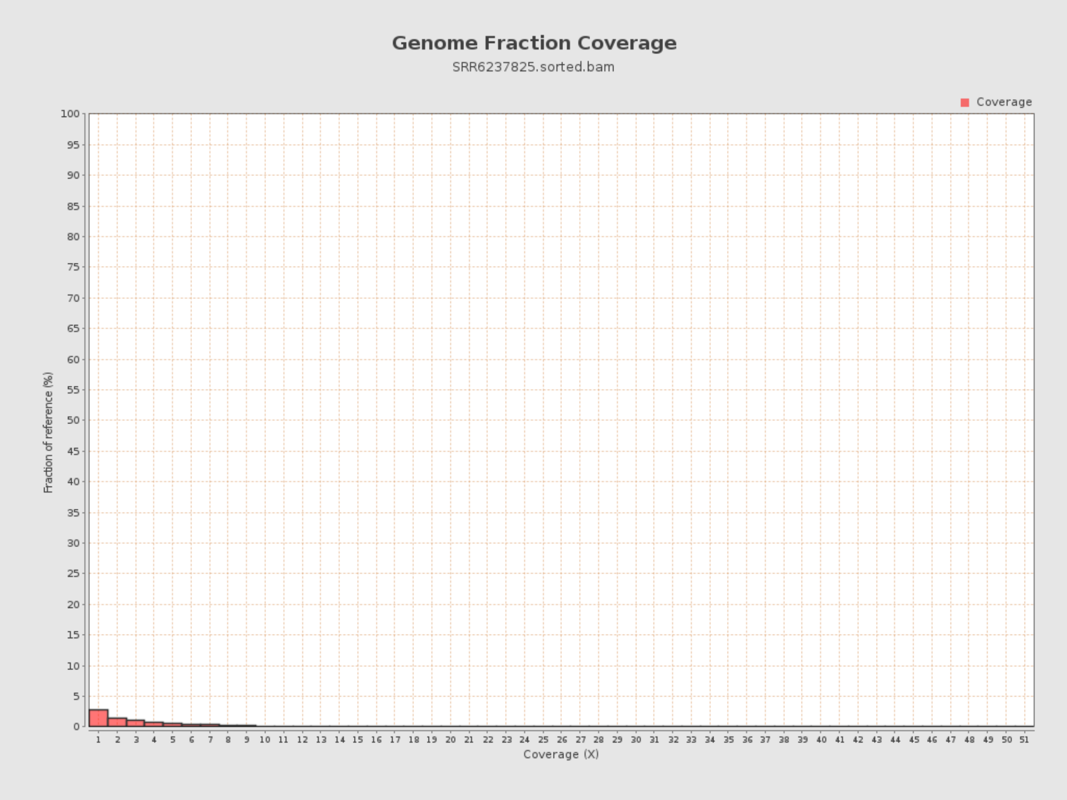
4. Results : Coverage Histogram



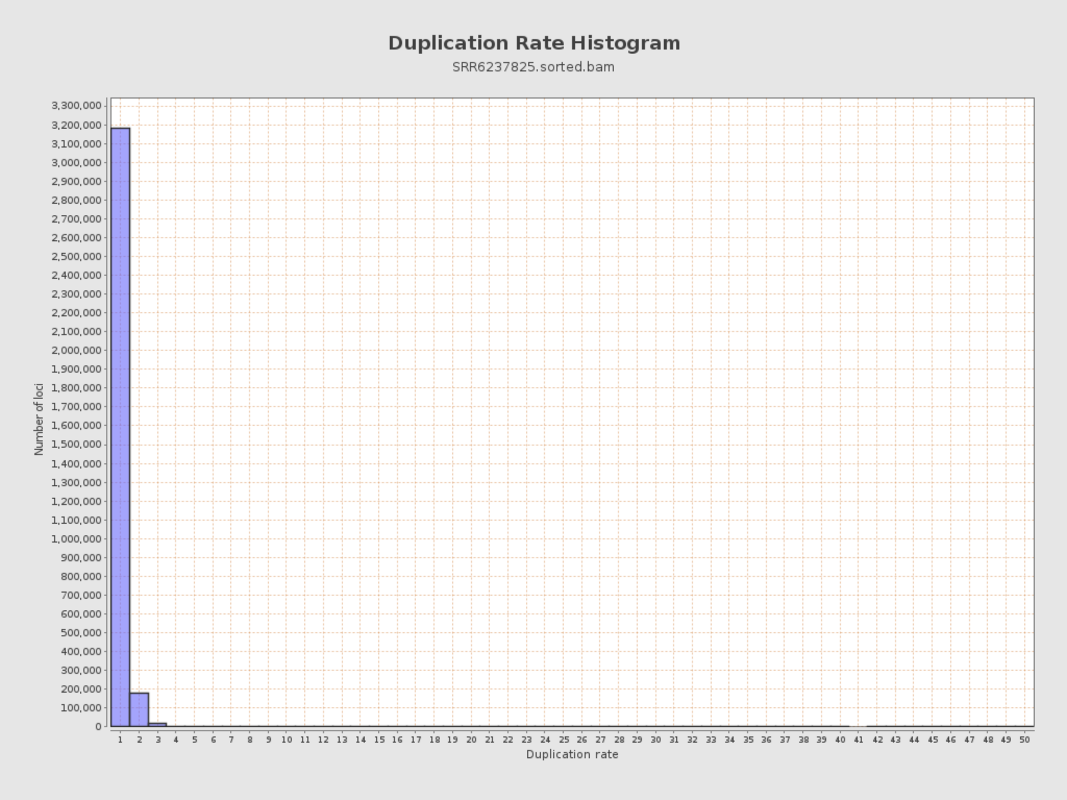
5. Results : Coverage Histogram (0-50X)



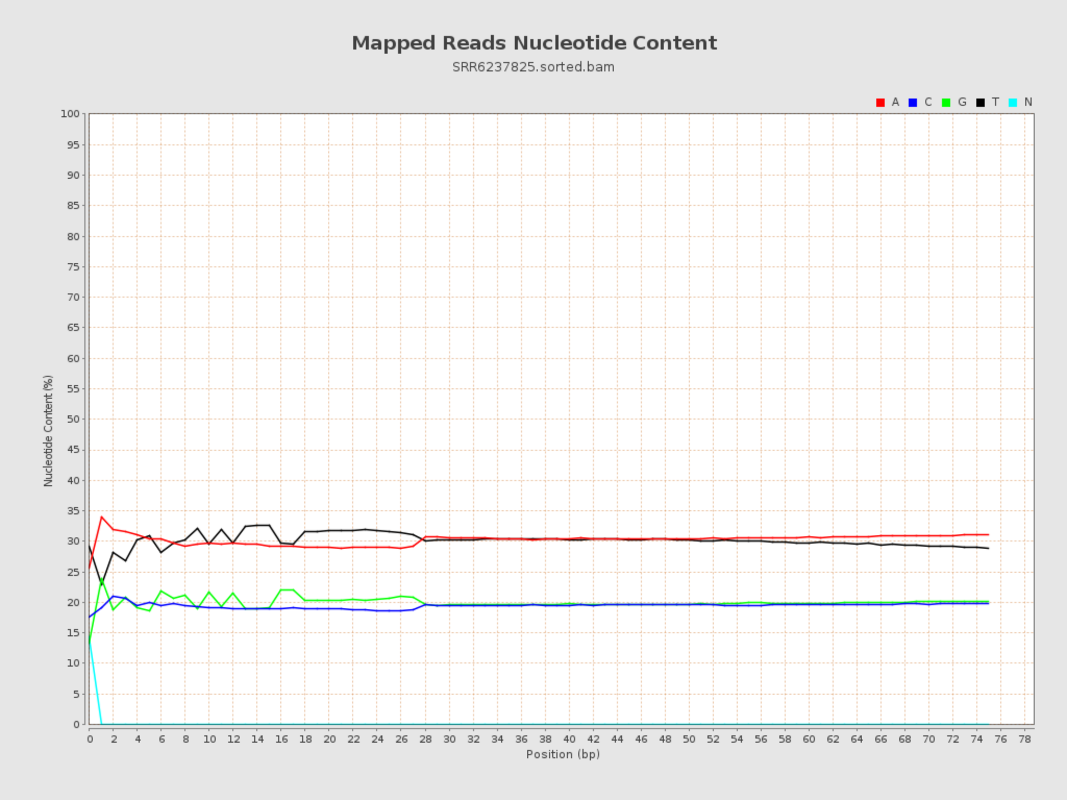
6. Results : Genome Fraction Coverage



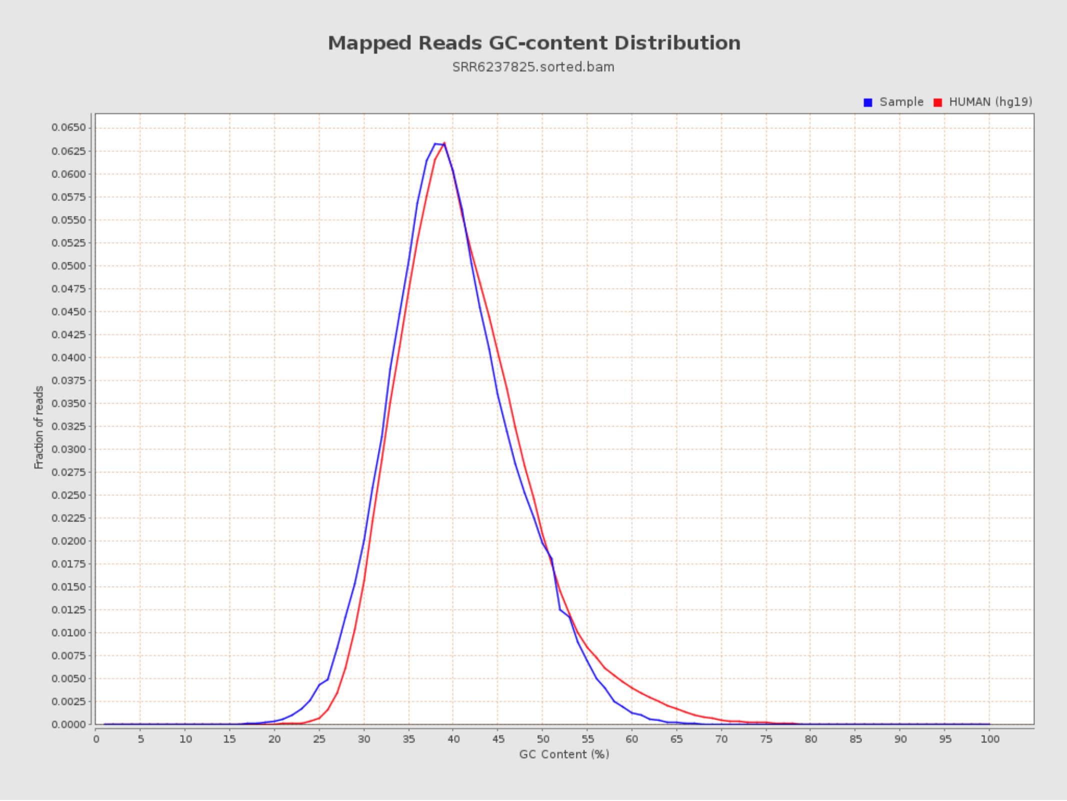
7. Results : Duplication Rate Histogram



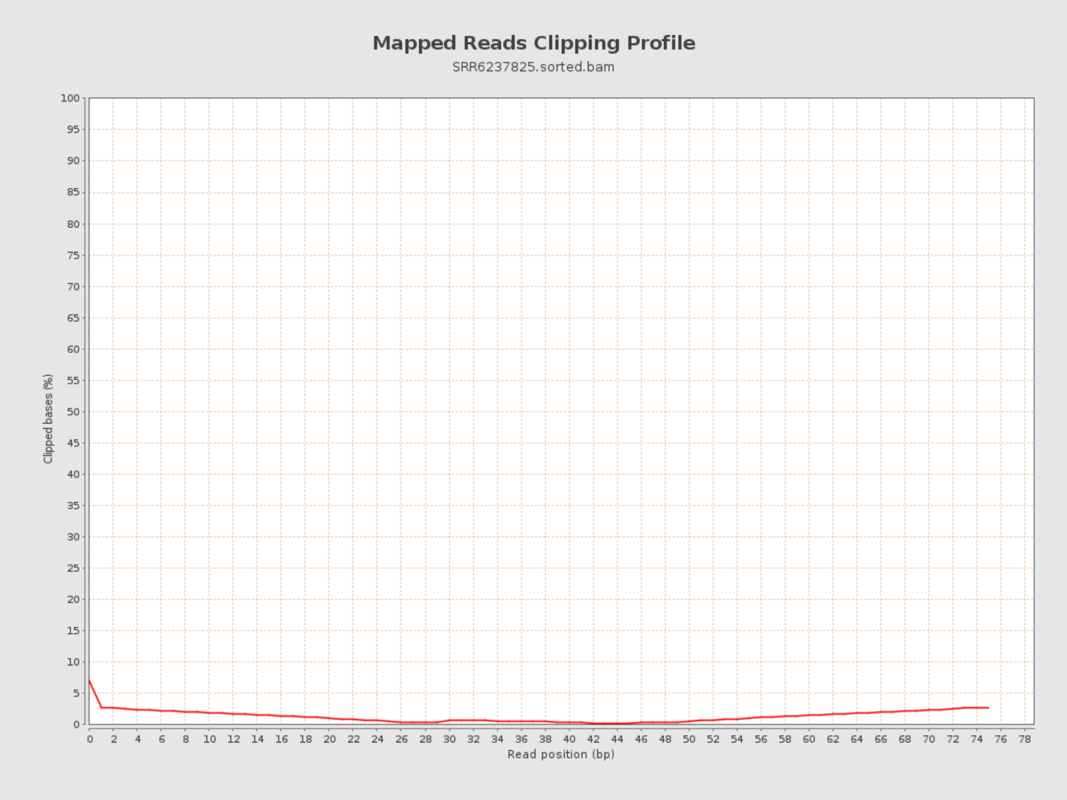
8. Results : Mapped Reads Nucleotide Content



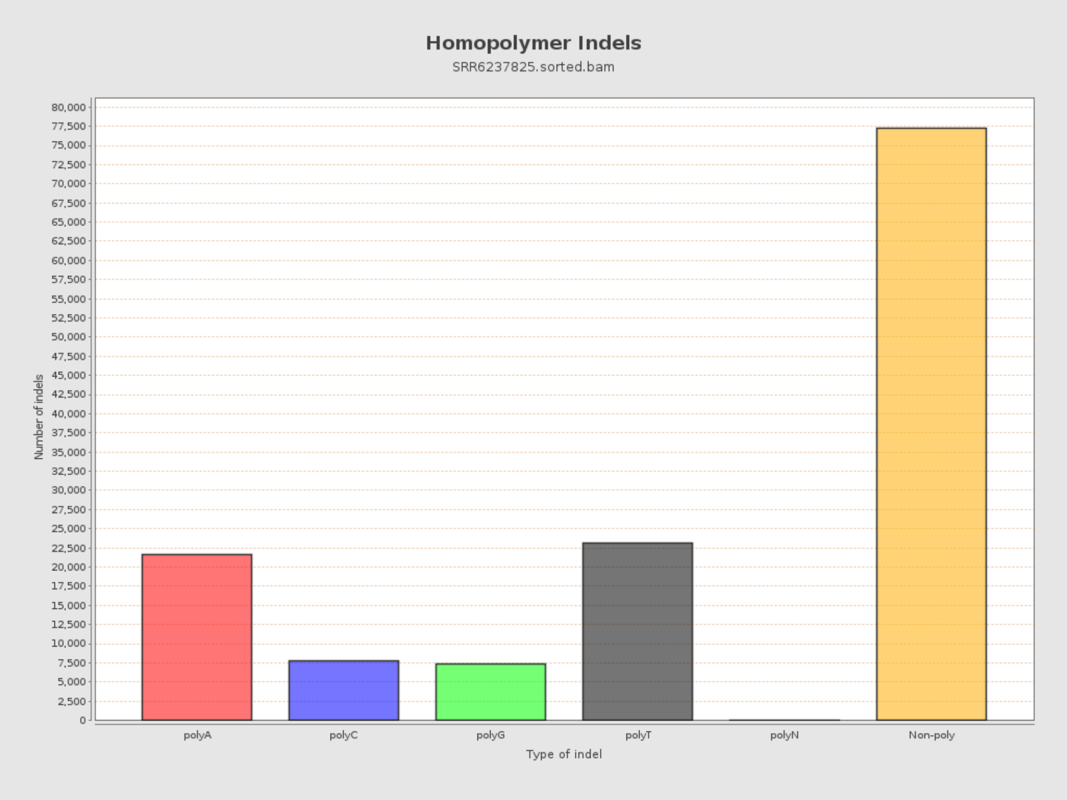
9. Results : Mapped Reads GC-content Distribution



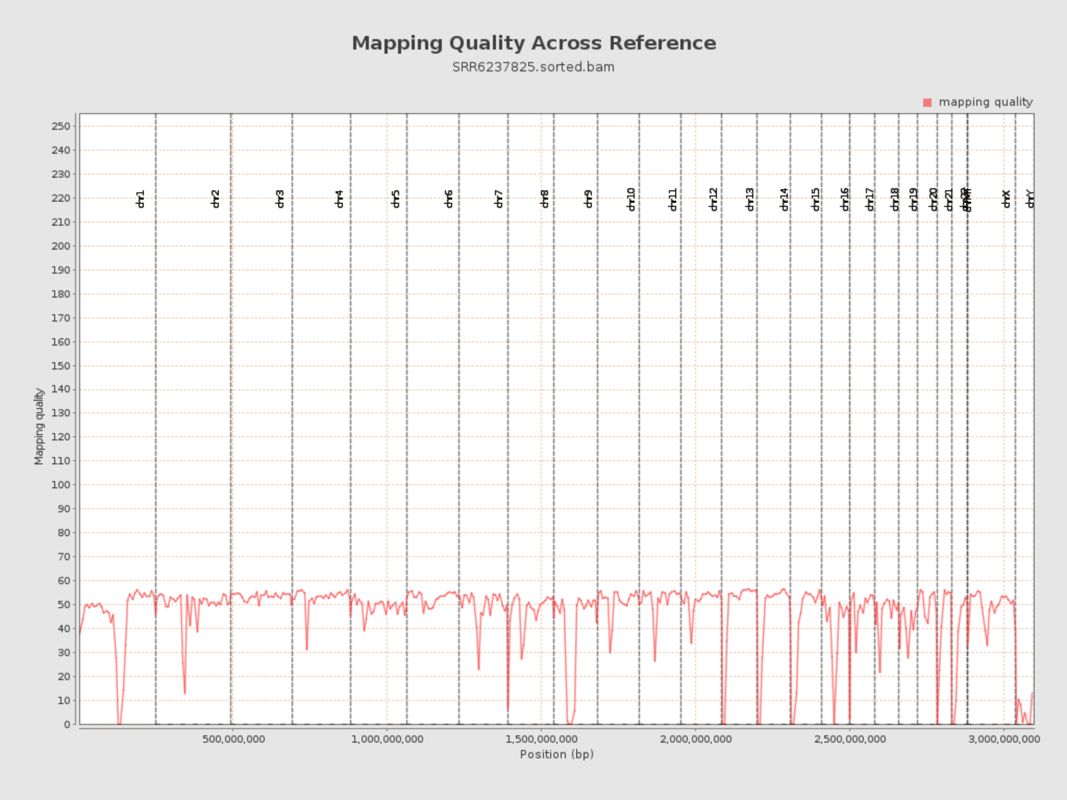
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram