Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:16:16

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819137.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_SRR1819137 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819137.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:16:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819137.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,727,584
Mapped reads	1,593,533 / 92.24%
Unmapped reads	134,051 / 7.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,684 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	113,244 / 6.56%
Duplication rate	5.6%
Clipped reads	1,597,045 / 92.44%

2.2. ACGT Content

Number/percentage of A's	23,108,055 / 24.76%
Number/percentage of C's	17,567,414 / 18.83%
Number/percentage of T's	29,920,021 / 32.06%
Number/percentage of G's	22,715,039 / 24.34%
Number/percentage of N's	1,363 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0302

Standard Deviation	0.2858

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

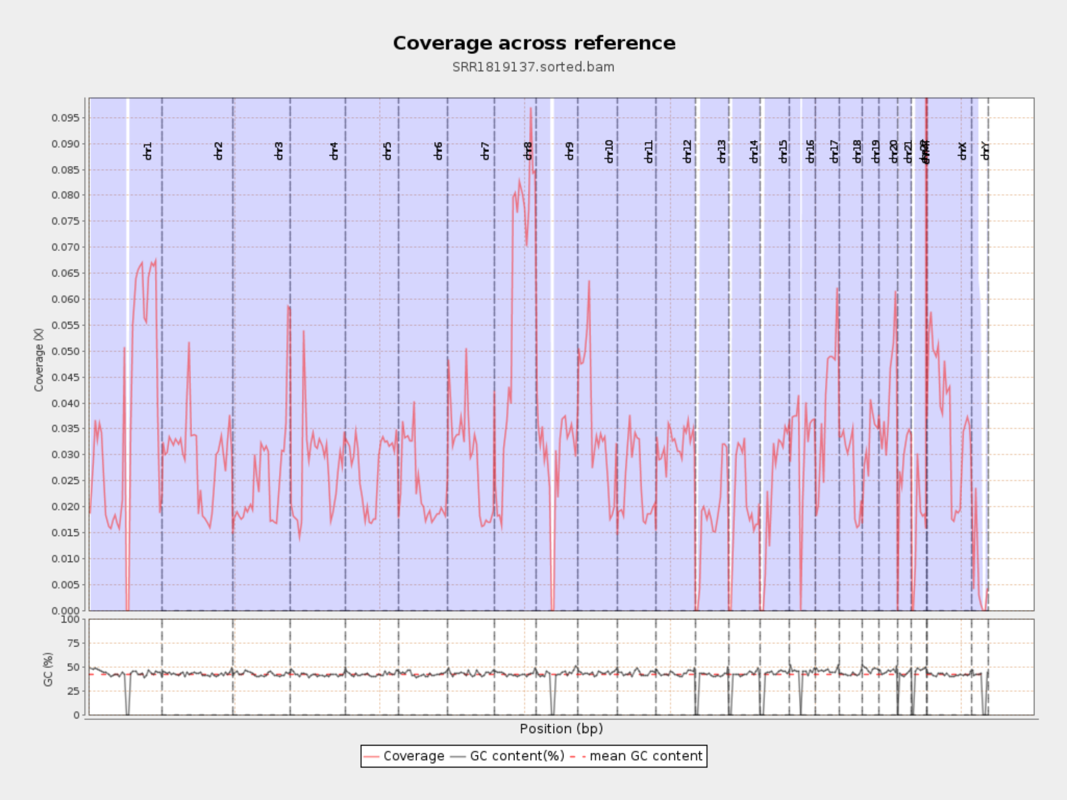
General error rate	0.51%
Mismatches	466,608
Insertions	6,298
Mapped reads with at least one insertion	0.39%
Deletions	16,630
Mapped reads with at least one deletion	1.04%
Homopolymer indels	43.73%

2.6. Chromosome stats

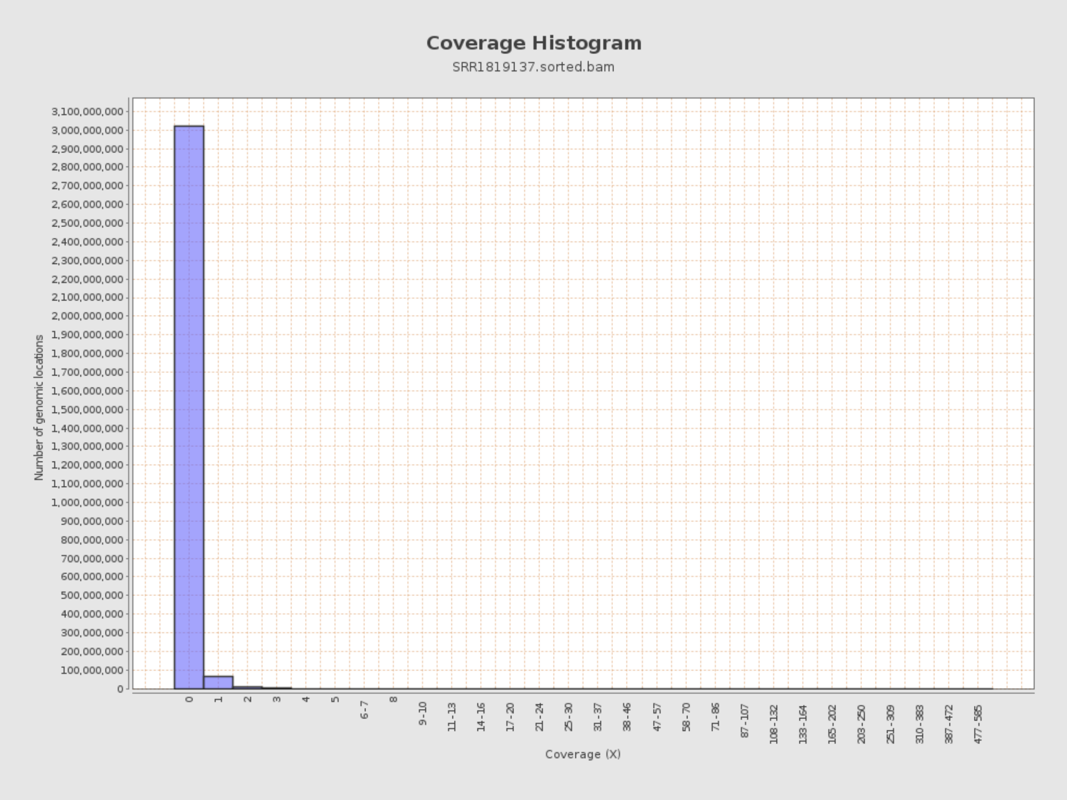
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9251999	0.0371	0.4889
chr2	243199373	7207215	0.0296	0.3477
chr3	198022430	4965054	0.0251	0.186
chr4	191154276	5216066	0.0273	0.2408
chr5	180915260	4977025	0.0275	0.1947
chr6	171115067	4080265	0.0238	0.2163
chr7	159138663	4698987	0.0295	0.3423

chr8	146364022	8587905	0.0587	0.3554
chr9	141213431	4053808	0.0287	0.2343
chr10	135534747	4894642	0.0361	0.3315
chr11	135006516	3290834	0.0244	0.2423
chr12	133851895	4328567	0.0323	0.2116
chr13	115169878	2089147	0.0181	0.1569
chr14	107349540	2145432	0.02	0.1696
chr15	102531392	2366477	0.0231	0.1786
chr16	90354753	2917581	0.0323	0.2226
chr17	81195210	3297557	0.0406	0.2486
chr18	78077248	2142559	0.0274	0.3946
chr19	59128983	1940118	0.0328	0.3556
chr20	63025520	2640696	0.0419	0.249
chr21	48129895	1325775	0.0275	0.2264
chr22	51304566	765053	0.0149	0.1431
chrMT	16571	31307	1.8893	1.8418
chrX	155270560	5766134	0.0371	0.2403
chrY	59373566	359644	0.0061	0.1963

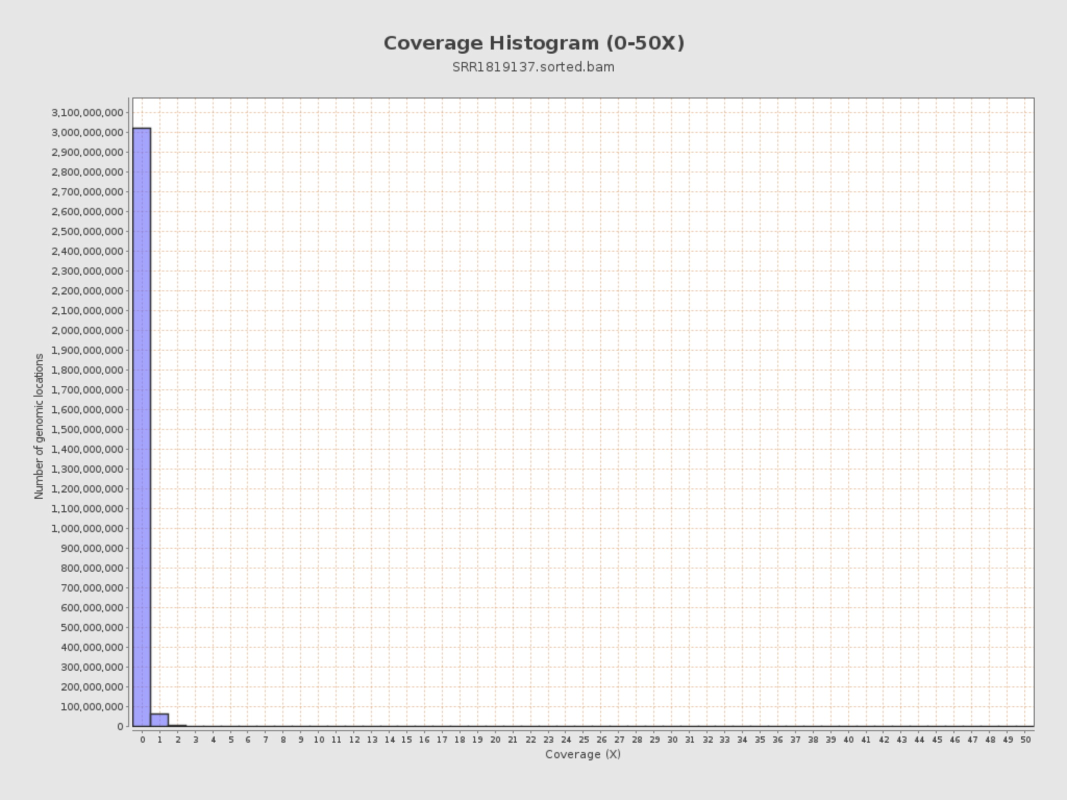
3. Results : Coverage across reference



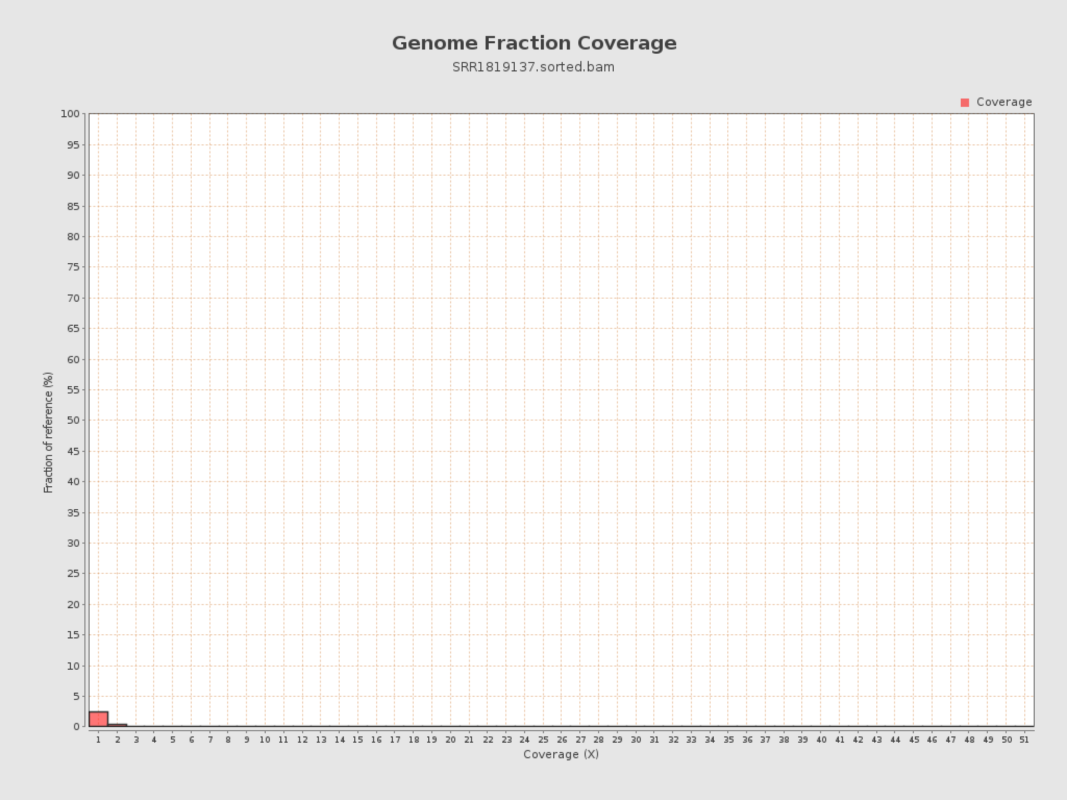
4. Results : Coverage Histogram



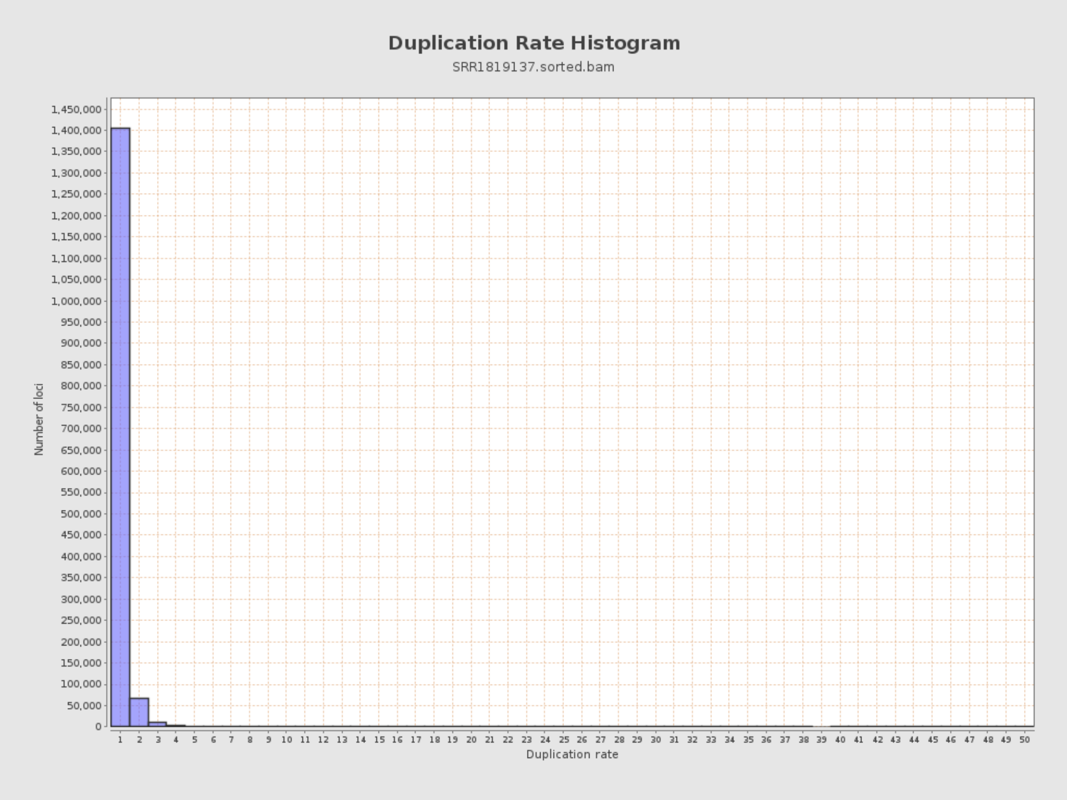
5. Results : Coverage Histogram (0-50X)



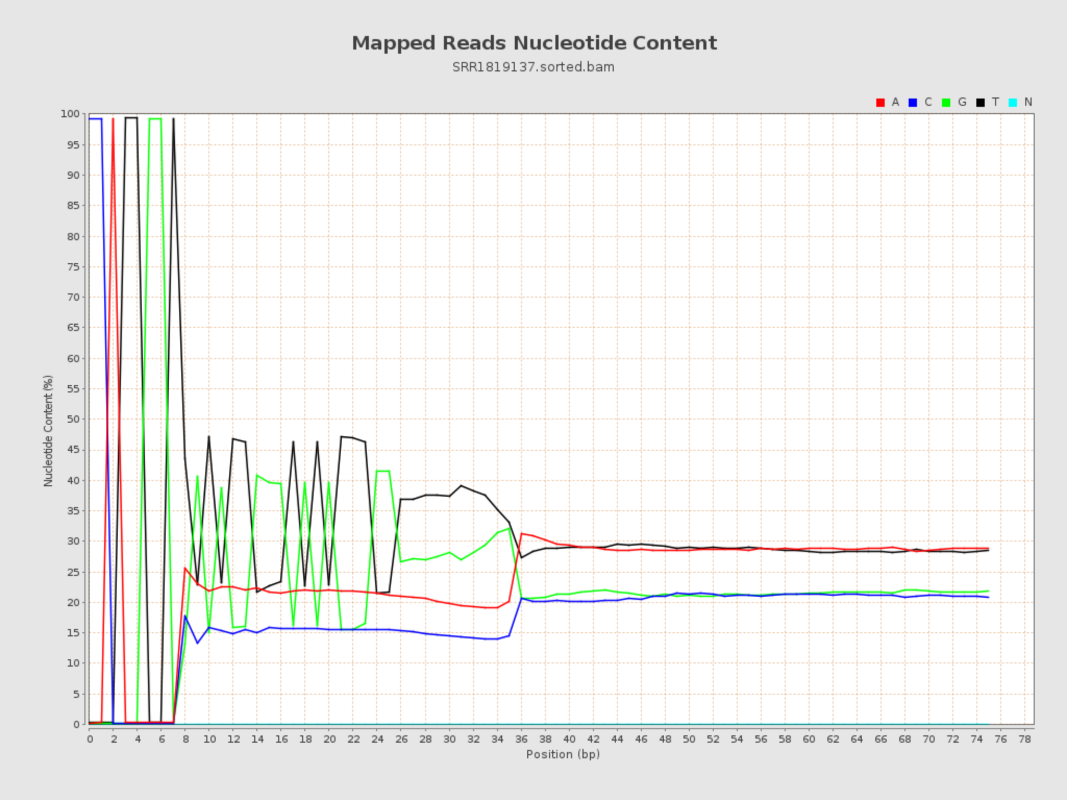
6. Results : Genome Fraction Coverage



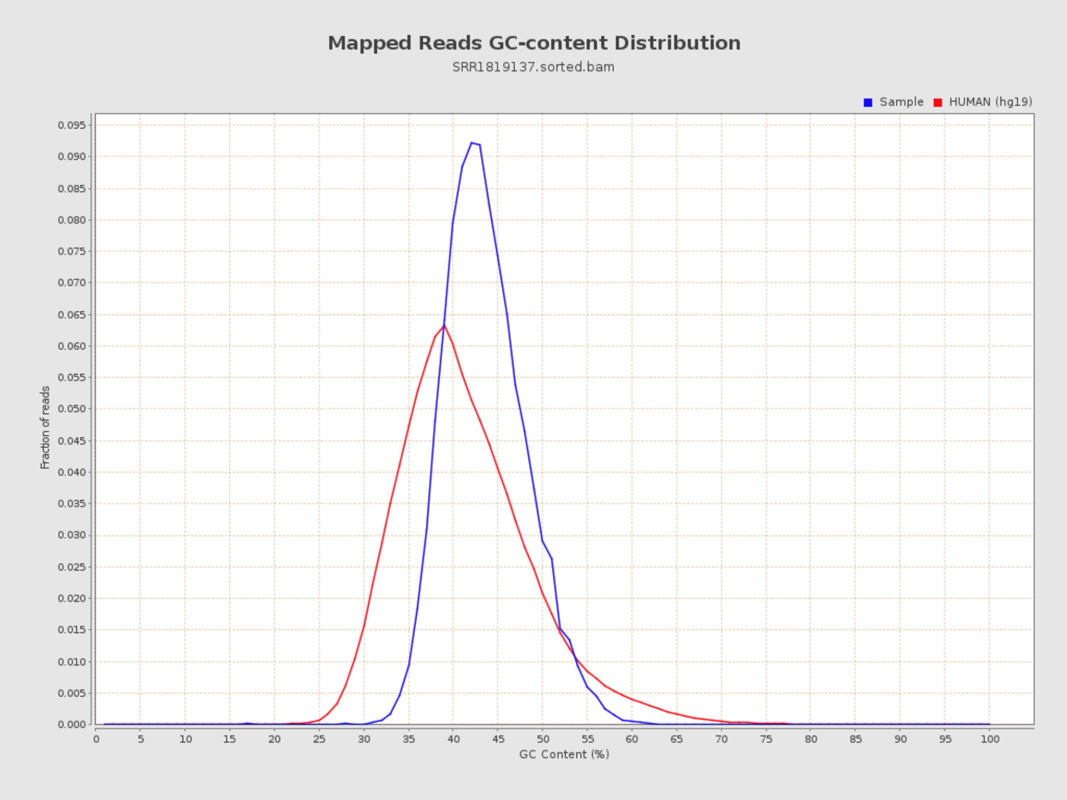
7. Results : Duplication Rate Histogram



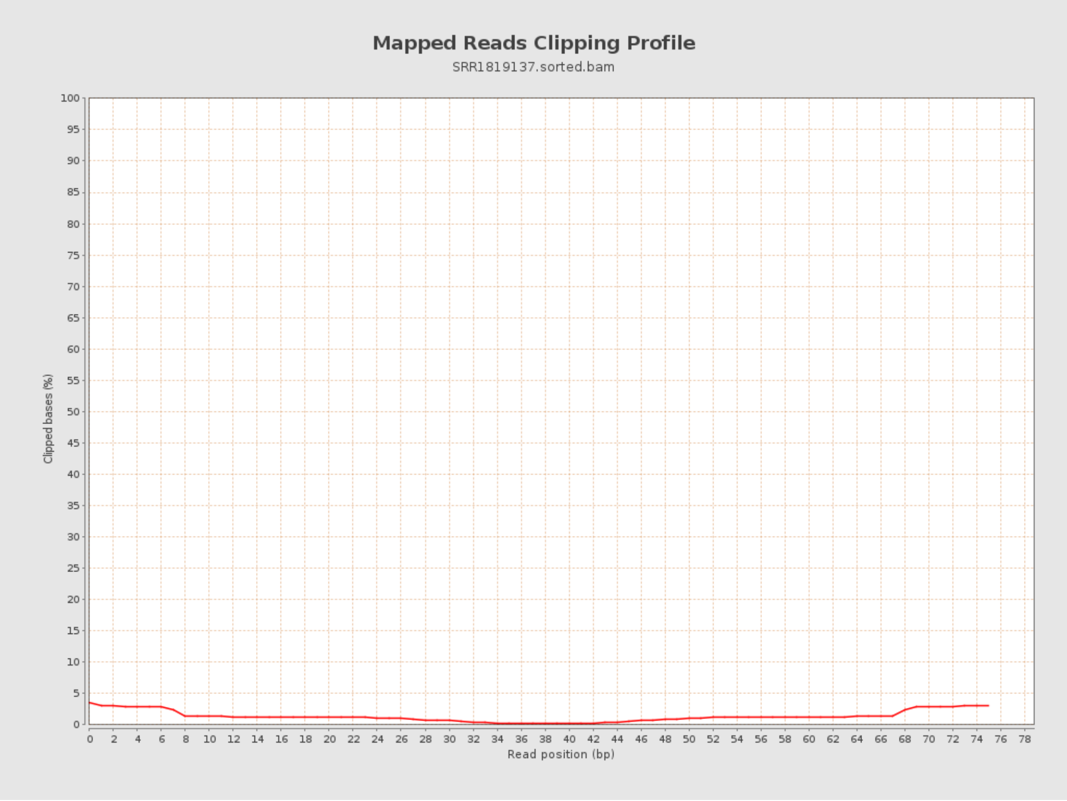
8. Results : Mapped Reads Nucleotide Content



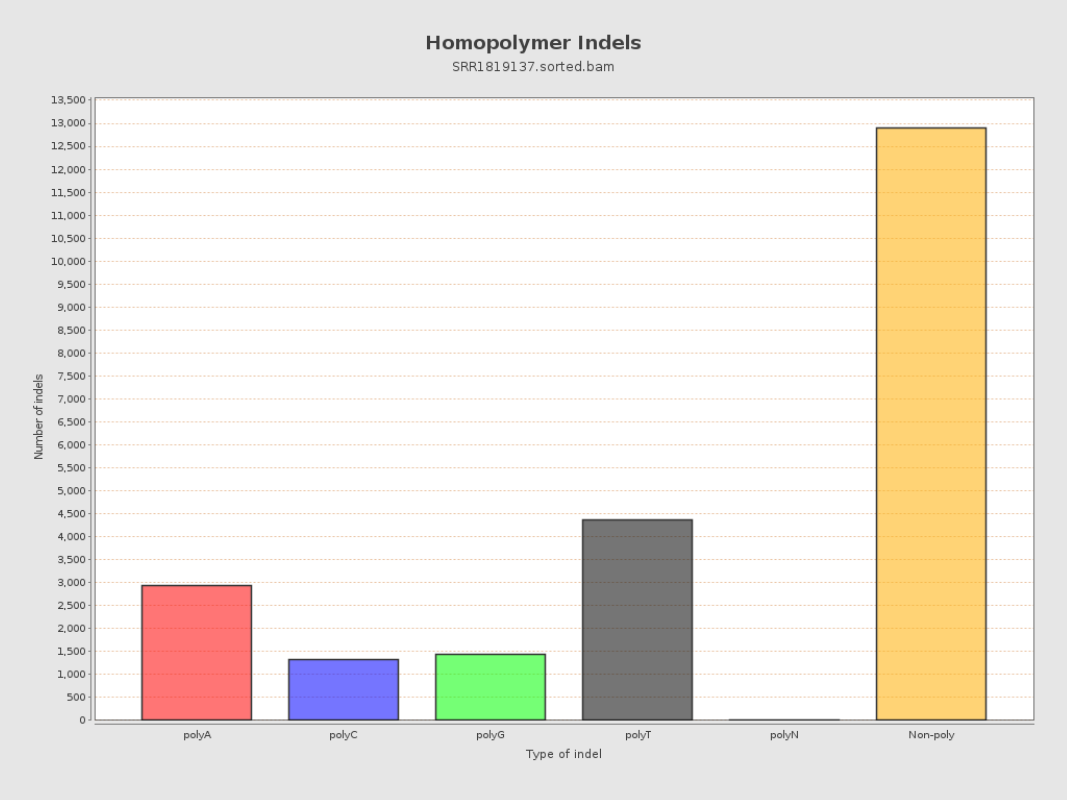
9. Results : Mapped Reads GC-content Distribution



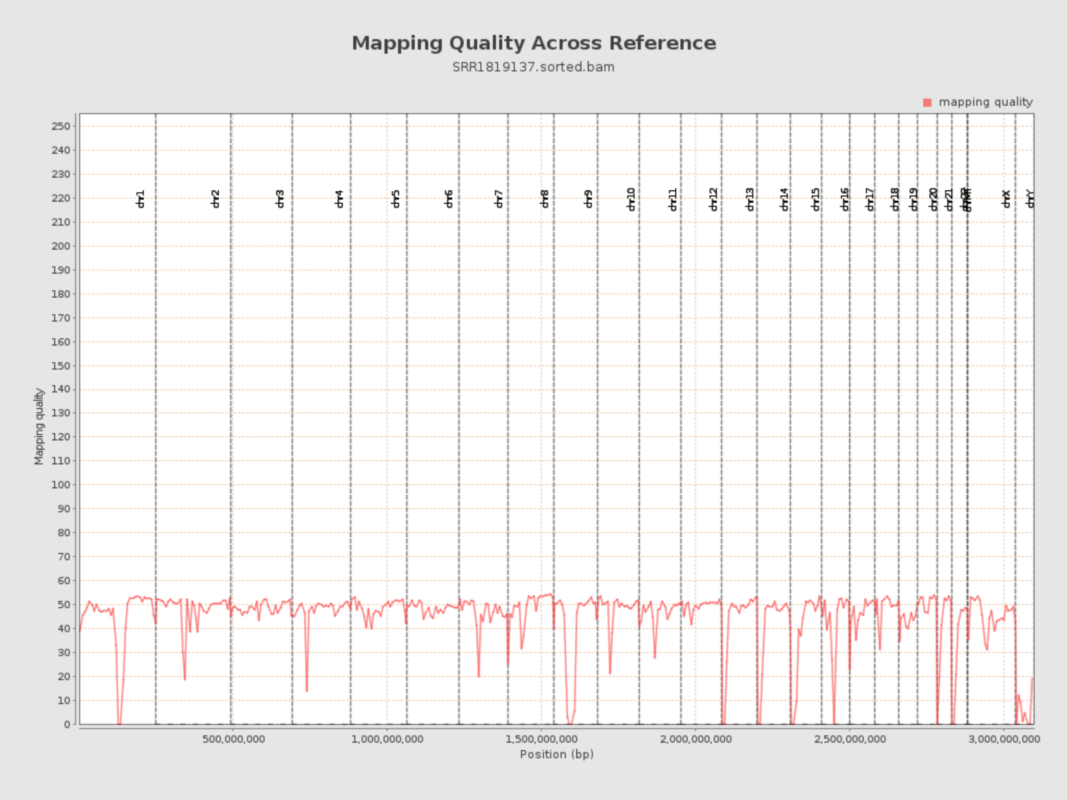
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram