Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 22:10:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525187.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_SRR10525187 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525187.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 22:10:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525187.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,452,653
Mapped reads	1,351,689 / 93.05%
Unmapped reads	100,964 / 6.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,299 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	37,573 / 2.59%
Duplication rate	1.93%
Clipped reads	1,351,772 / 93.06%

2.2. ACGT Content

Number/percentage of A's	21,342,258 / 26.35%
Number/percentage of C's	16,220,780 / 20.03%
Number/percentage of T's	24,781,743 / 30.6%
Number/percentage of G's	18,639,320 / 23.02%
Number/percentage of N's	1,917 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.2642

2.4. Mapping Quality

Mean Mapping Quality	45.52

2.5. Mismatches and indels

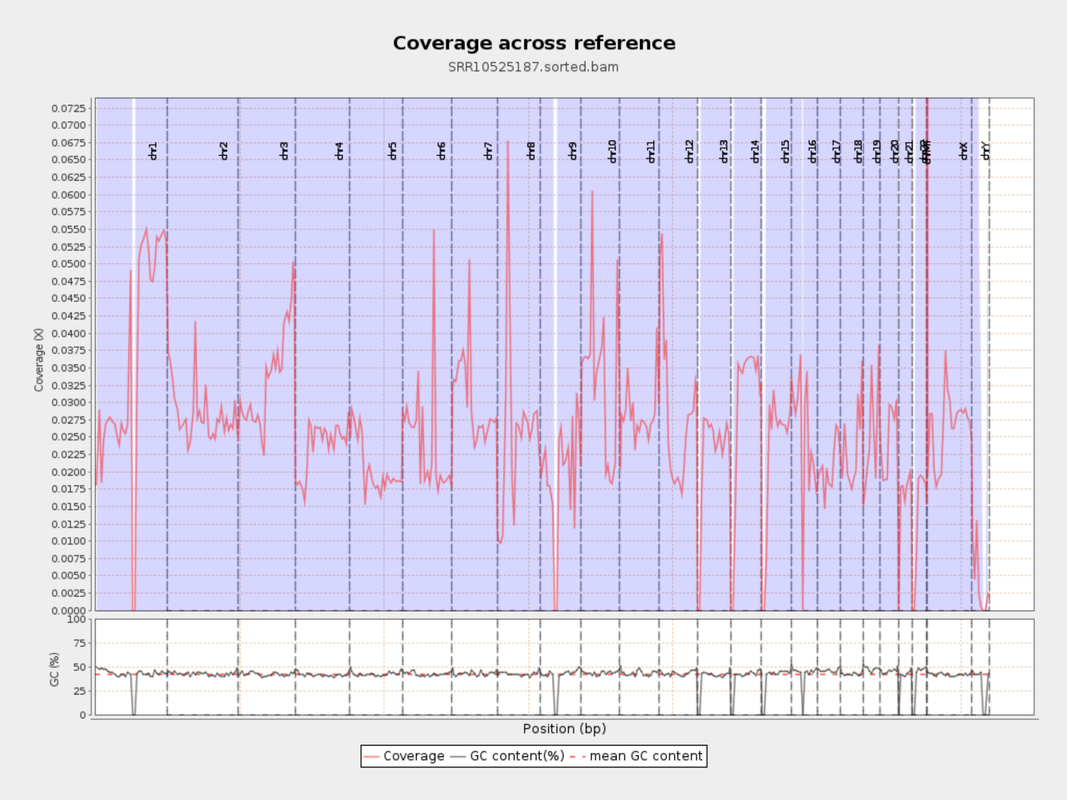
General error rate	0.51%
Mismatches	405,939
Insertions	5,271
Mapped reads with at least one insertion	0.39%
Deletions	17,501
Mapped reads with at least one deletion	1.29%
Homopolymer indels	43.65%

2.6. Chromosome stats

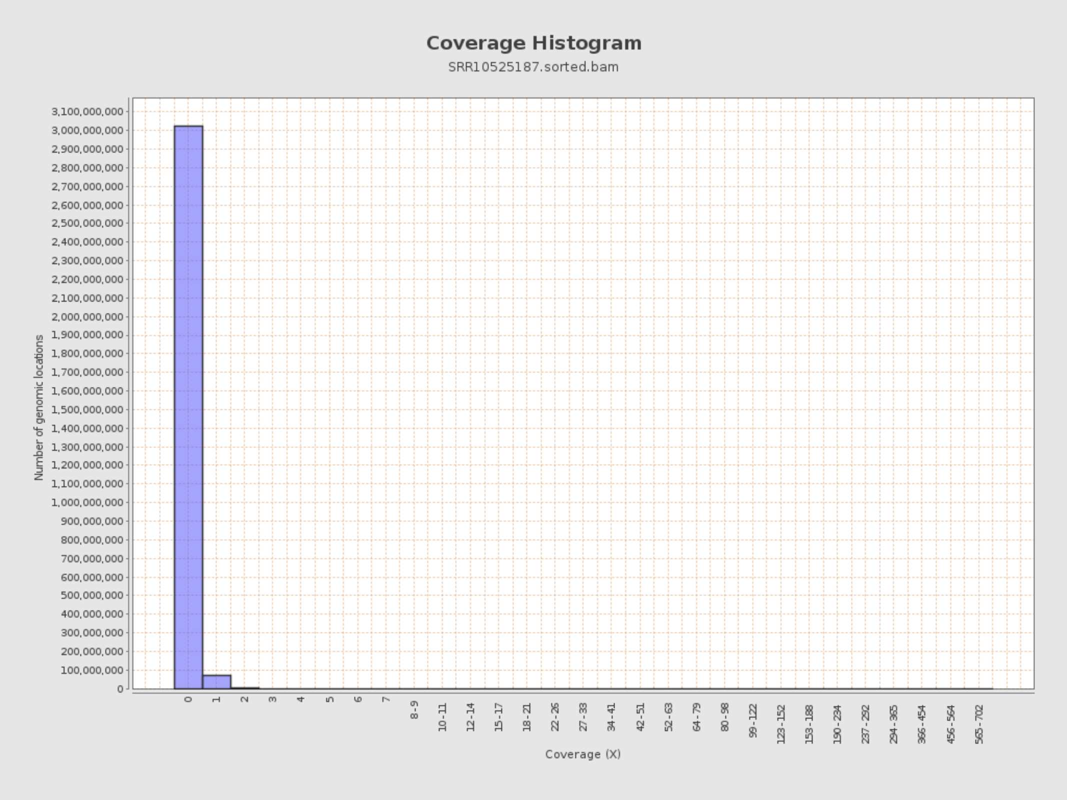
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8904258	0.0357	0.5304
chr2	243199373	6895358	0.0284	0.3046
chr3	198022430	6592333	0.0333	0.1958
chr4	191154276	4550861	0.0238	0.1705
chr5	180915260	3741653	0.0207	0.1529
chr6	171115067	4175290	0.0244	0.1917
chr7	159138663	4845499	0.0304	0.3881

chr8	146364022	3823355	0.0261	0.2101
chr9	141213431	2723825	0.0193	0.1923
chr10	135534747	4568431	0.0337	0.3038
chr11	135006516	3804290	0.0282	0.2188
chr12	133851895	3788189	0.0283	0.1814
chr13	115169878	2550291	0.0221	0.1595
chr14	107349540	3140218	0.0293	0.1863
chr15	102531392	2282384	0.0223	0.1585
chr16	90354753	2255694	0.025	0.185
chr17	81195210	1697689	0.0209	0.1597
chr18	78077248	1783137	0.0228	0.3339
chr19	59128983	1500235	0.0254	0.3594
chr20	63025520	1541088	0.0245	0.1677
chr21	48129895	781560	0.0162	0.1461
chr22	51304566	679480	0.0132	0.1213
chrMT	16571	11634	0.7021	1.0003
chrX	155270560	4144258	0.0267	0.187
chrY	59373566	233064	0.0039	0.1239

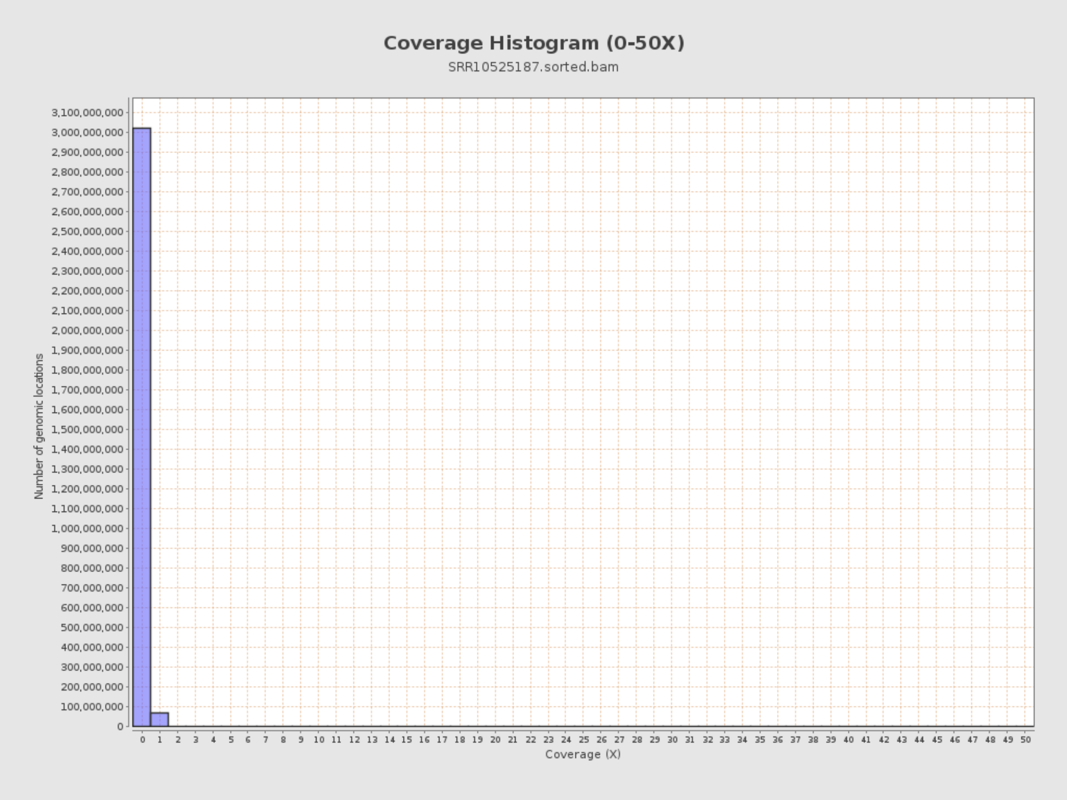
3. Results : Coverage across reference



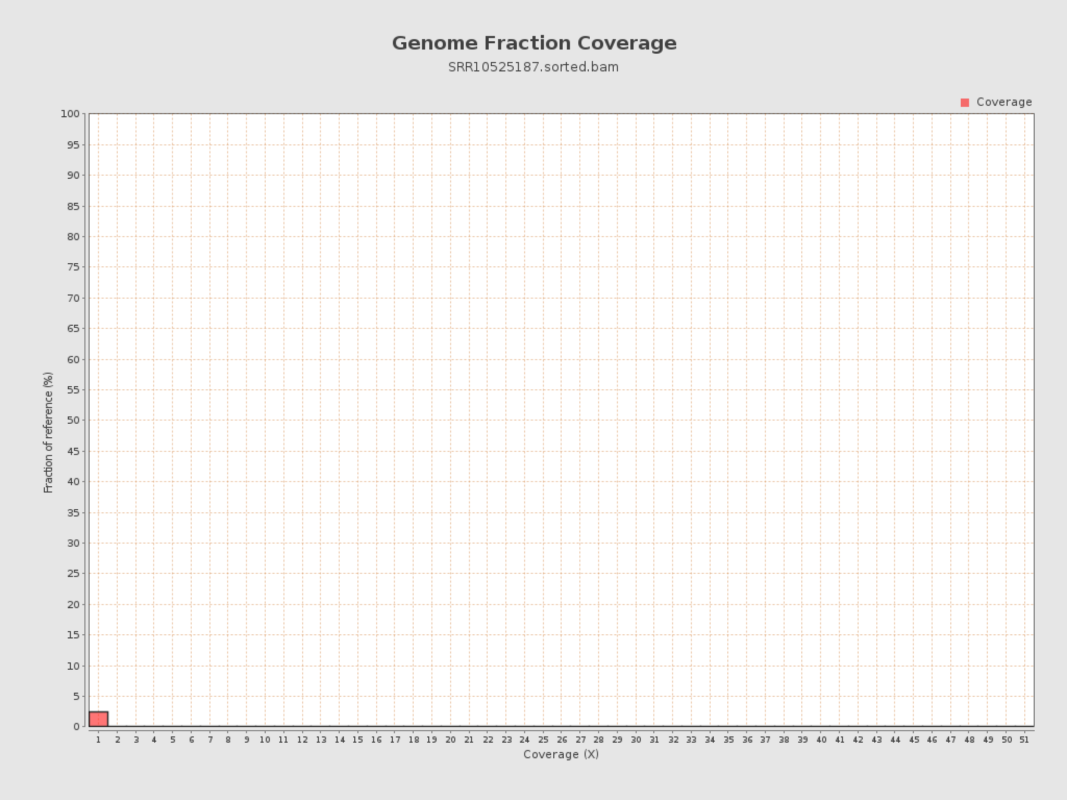
4. Results : Coverage Histogram



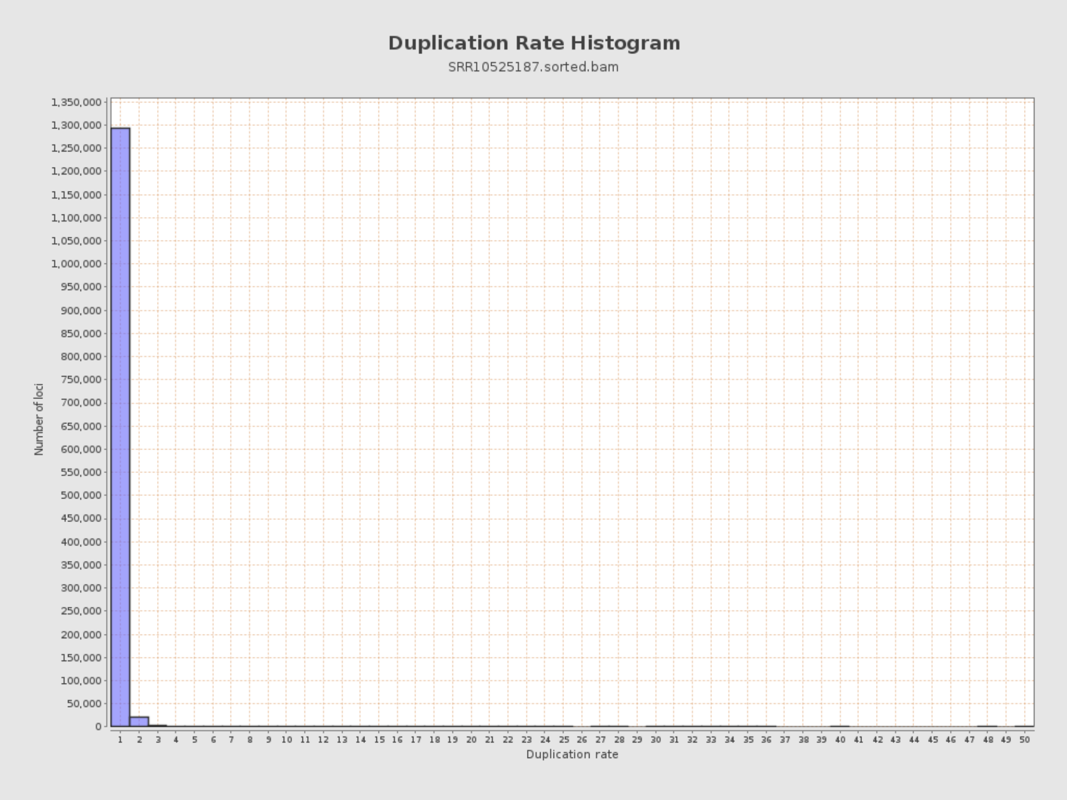
5. Results : Coverage Histogram (0-50X)



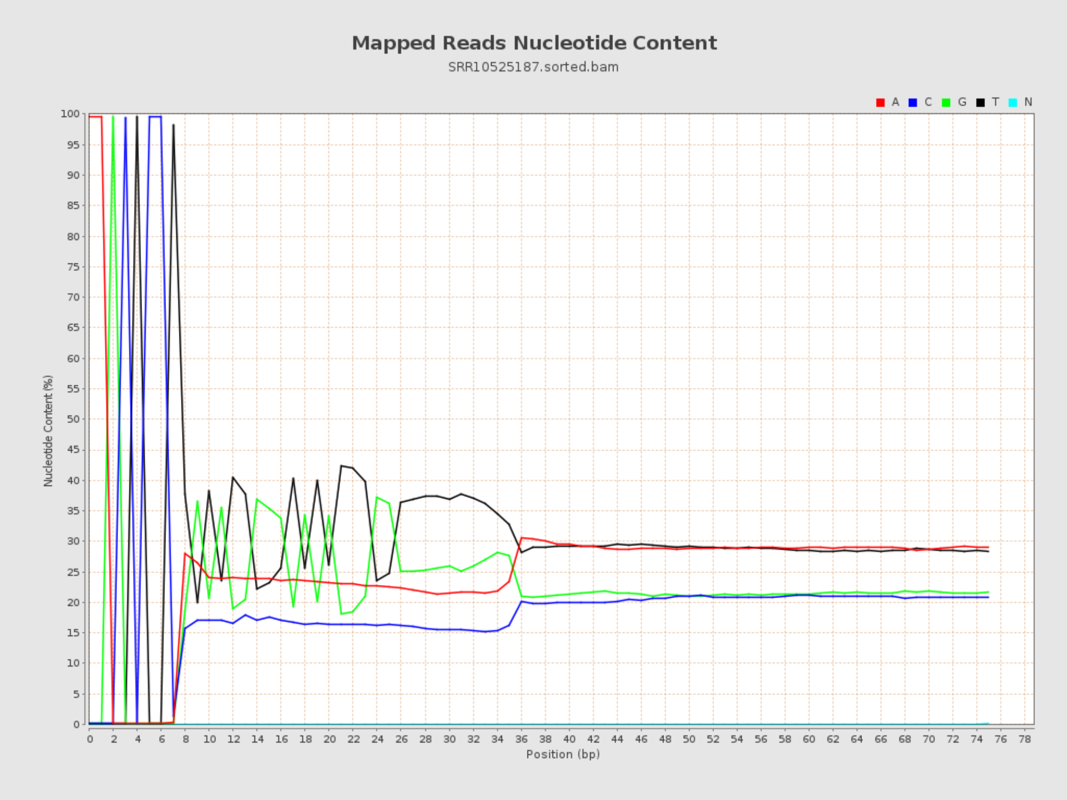
6. Results : Genome Fraction Coverage



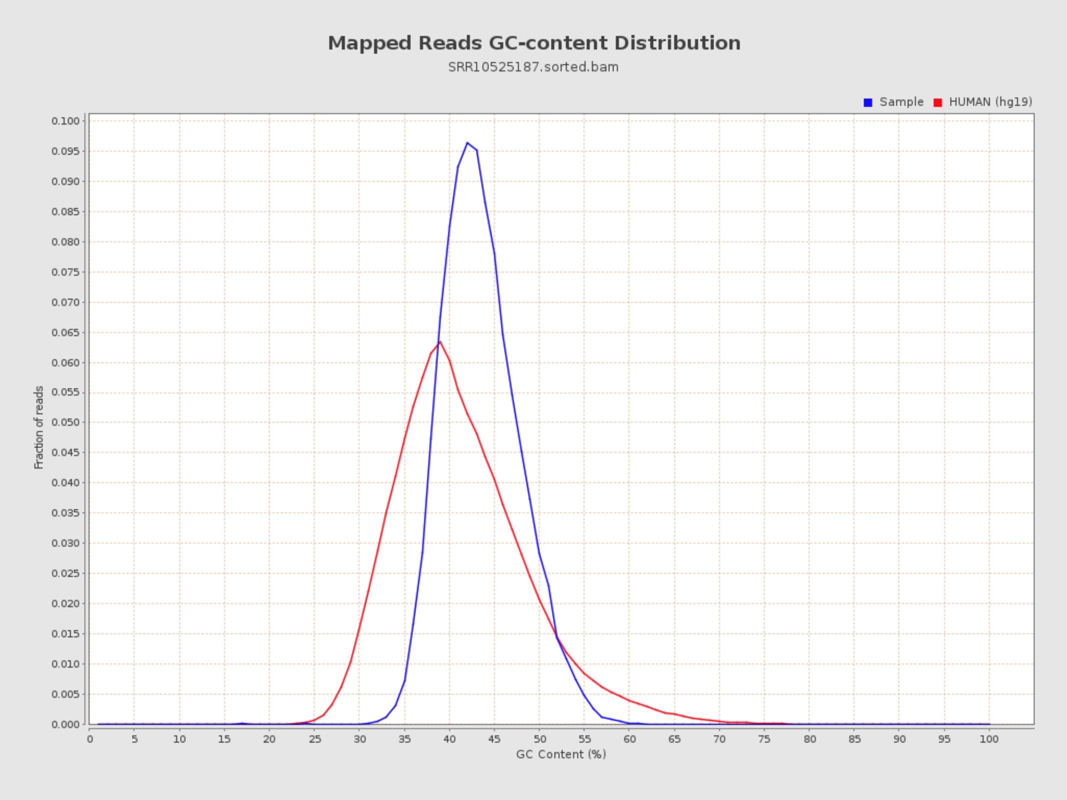
7. Results : Duplication Rate Histogram



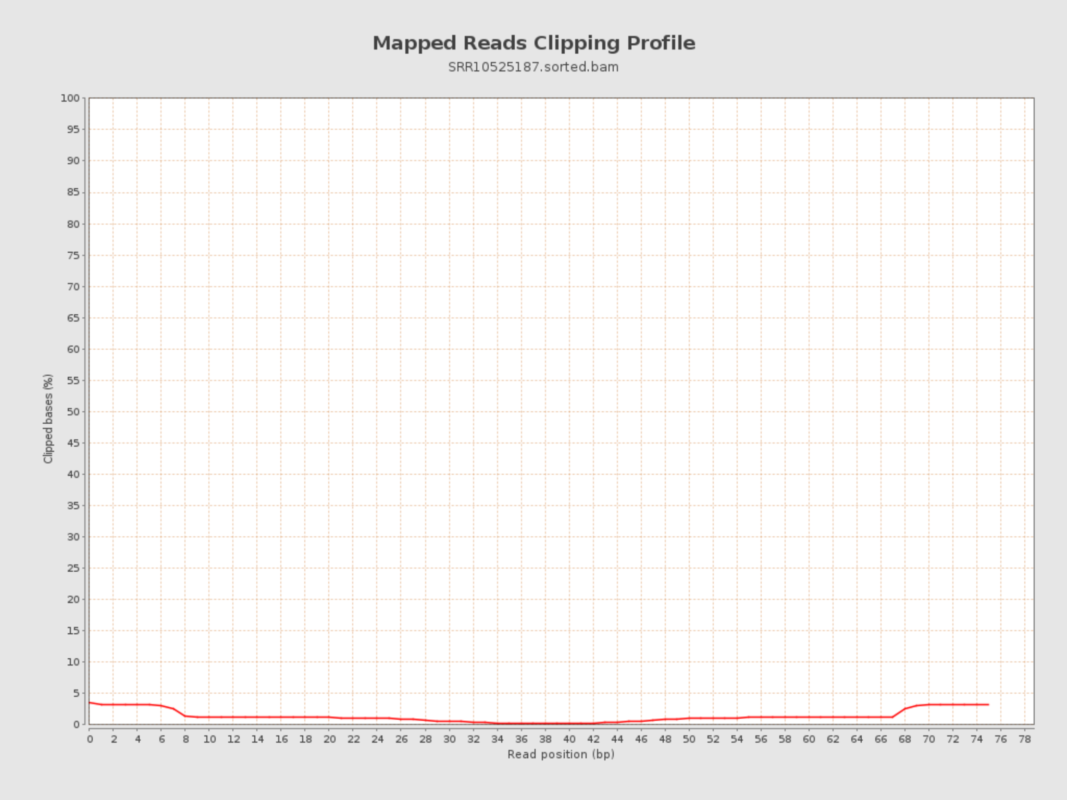
8. Results : Mapped Reads Nucleotide Content



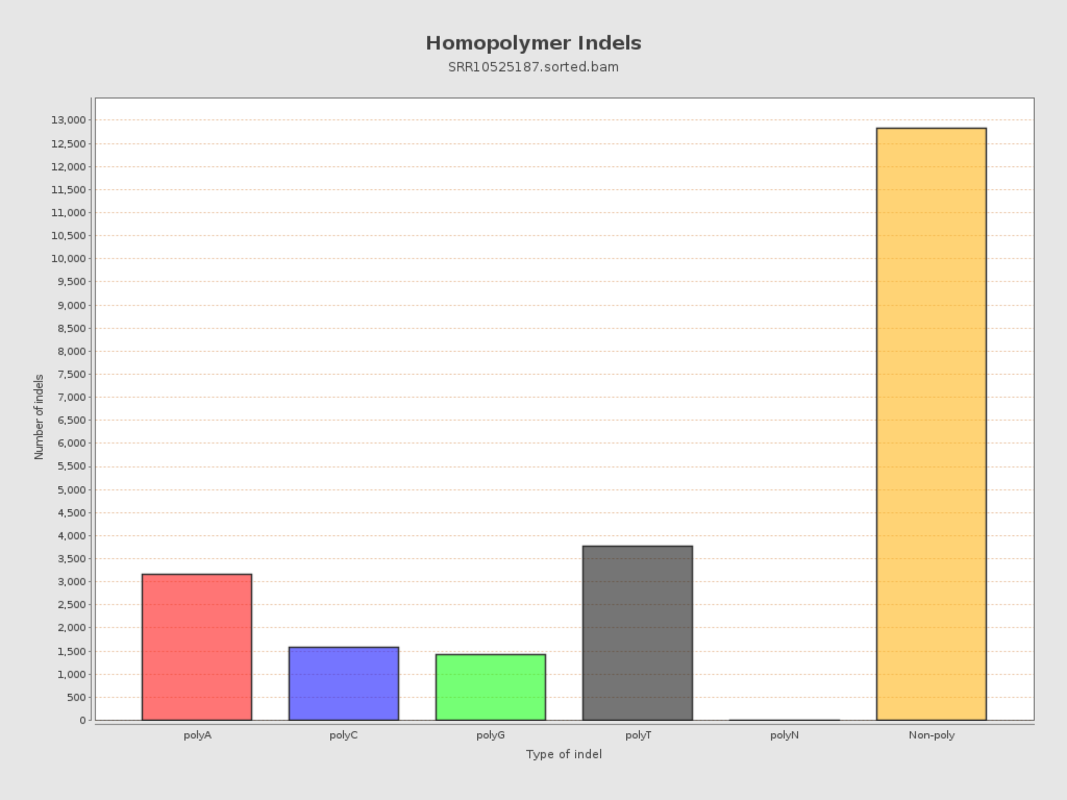
9. Results : Mapped Reads GC-content Distribution



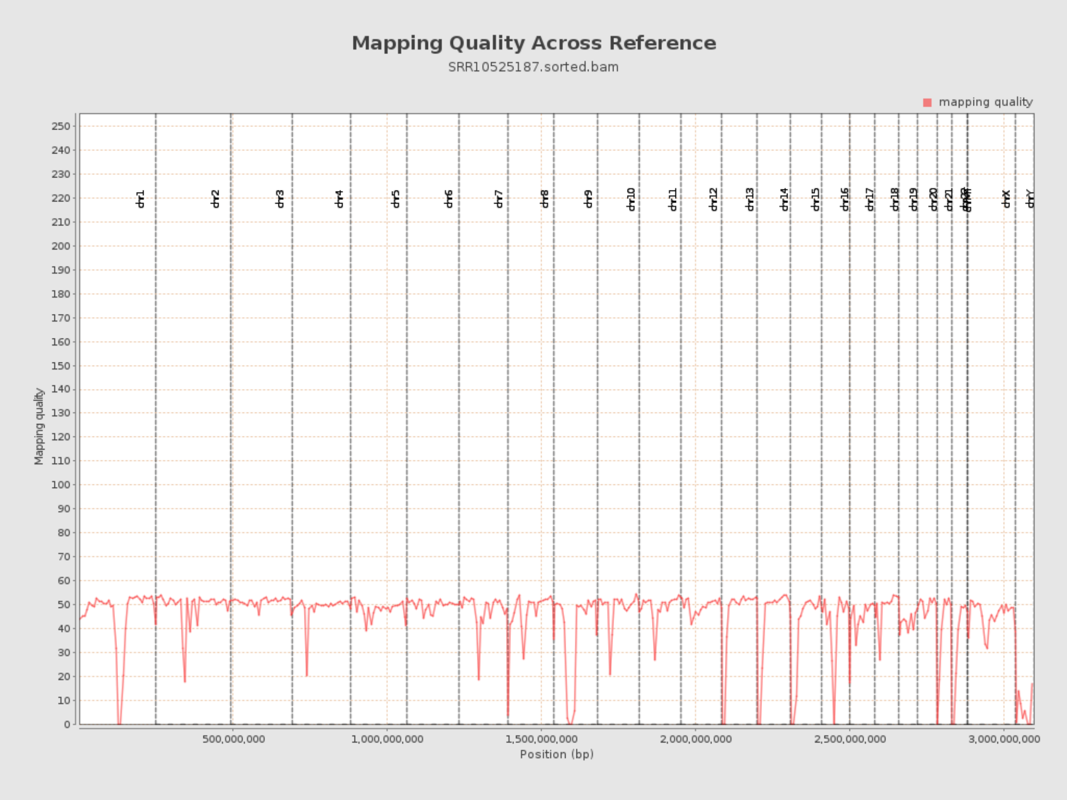
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram