Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:31:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524687.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_SRR10524687 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524687.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:31:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524687.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,940,036
Mapped reads	1,791,290 / 92.33%
Unmapped reads	148,746 / 7.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,549 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	73,471 / 3.79%
Duplication rate	2.95%
Clipped reads	1,793,257 / 92.43%

2.2. ACGT Content

Number/percentage of A's	28,244,395 / 26.48%
Number/percentage of C's	19,150,509 / 17.96%
Number/percentage of T's	33,150,022 / 31.08%
Number/percentage of G's	26,095,695 / 24.47%
Number/percentage of N's	15,625 / 0.01%
GC Percentage	42.42%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.3272

2.4. Mapping Quality

Mean Mapping Quality	45.99

2.5. Mismatches and indels

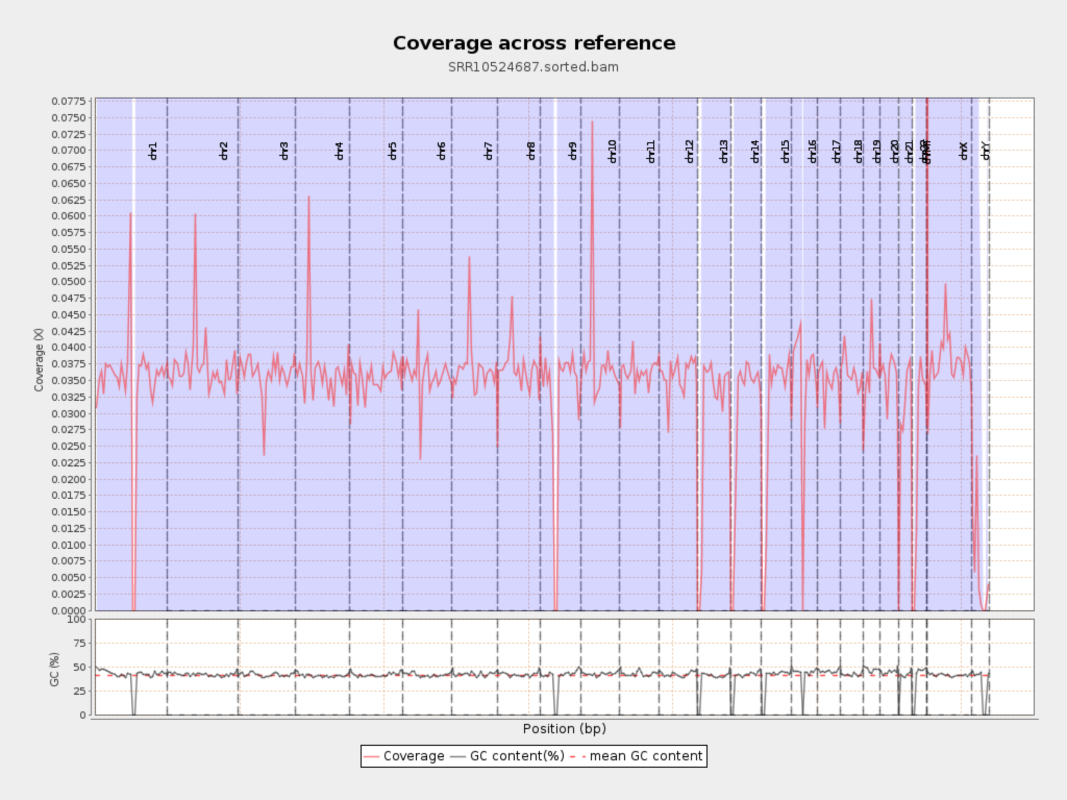
General error rate	0.52%
Mismatches	535,843
Insertions	7,562
Mapped reads with at least one insertion	0.42%
Deletions	20,997
Mapped reads with at least one deletion	1.16%
Homopolymer indels	43.37%

2.6. Chromosome stats

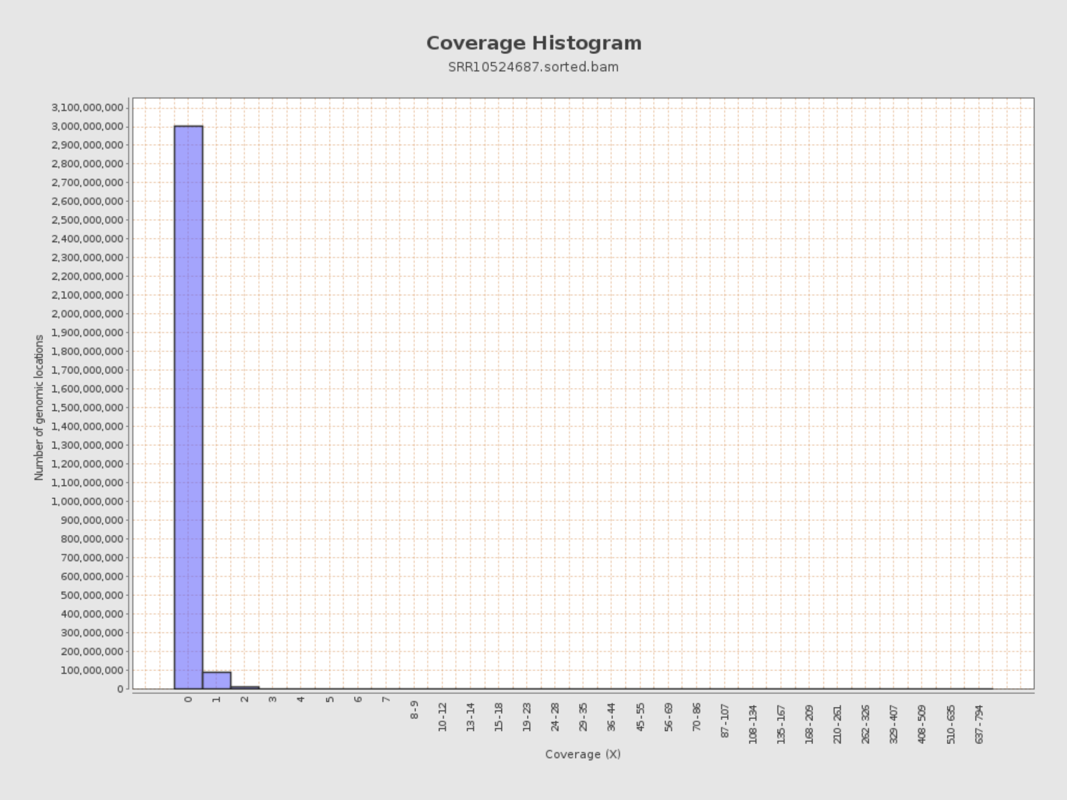
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8550968	0.0343	0.6167
chr2	243199373	9038685	0.0372	0.4242
chr3	198022430	7133238	0.036	0.2094
chr4	191154276	7011330	0.0367	0.2511
chr5	180915260	6449335	0.0356	0.2086
chr6	171115067	6141432	0.0359	0.2355
chr7	159138663	5890510	0.037	0.3511

chr8	146364022	5411877	0.037	0.3893
chr9	141213431	4488906	0.0318	0.2665
chr10	135534747	5210474	0.0384	0.3533
chr11	135006516	4891421	0.0362	0.2724
chr12	133851895	4786553	0.0358	0.2105
chr13	115169878	3363755	0.0292	0.1871
chr14	107349540	3174895	0.0296	0.197
chr15	102531392	3029296	0.0295	0.1888
chr16	90354753	3089321	0.0342	0.2266
chr17	81195210	2827891	0.0348	0.2178
chr18	78077248	2830317	0.0363	0.4943
chr19	59128983	2160702	0.0365	0.4552
chr20	63025520	2245526	0.0356	0.2128
chr21	48129895	1412705	0.0294	0.2225
chr22	51304566	1246010	0.0243	0.1712
chrMT	16571	11480	0.6928	0.9842
chrX	155270560	5927813	0.0382	0.2343
chrY	59373566	365370	0.0062	0.2256

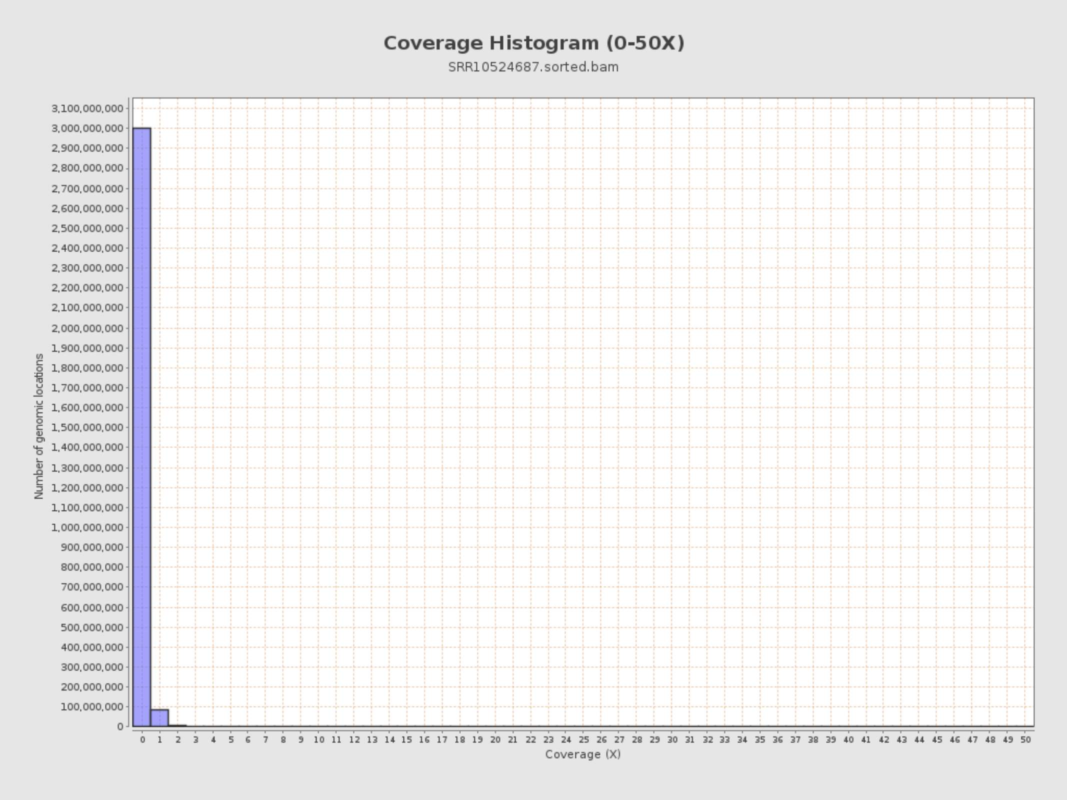
3. Results : Coverage across reference



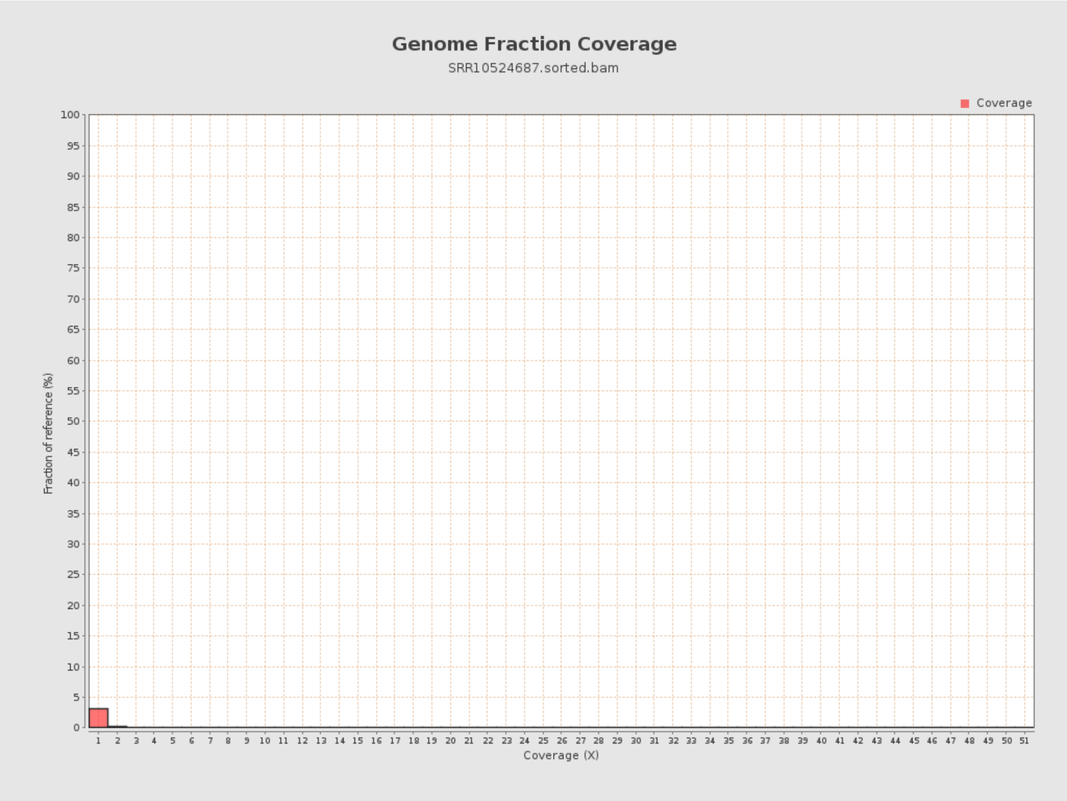
4. Results : Coverage Histogram



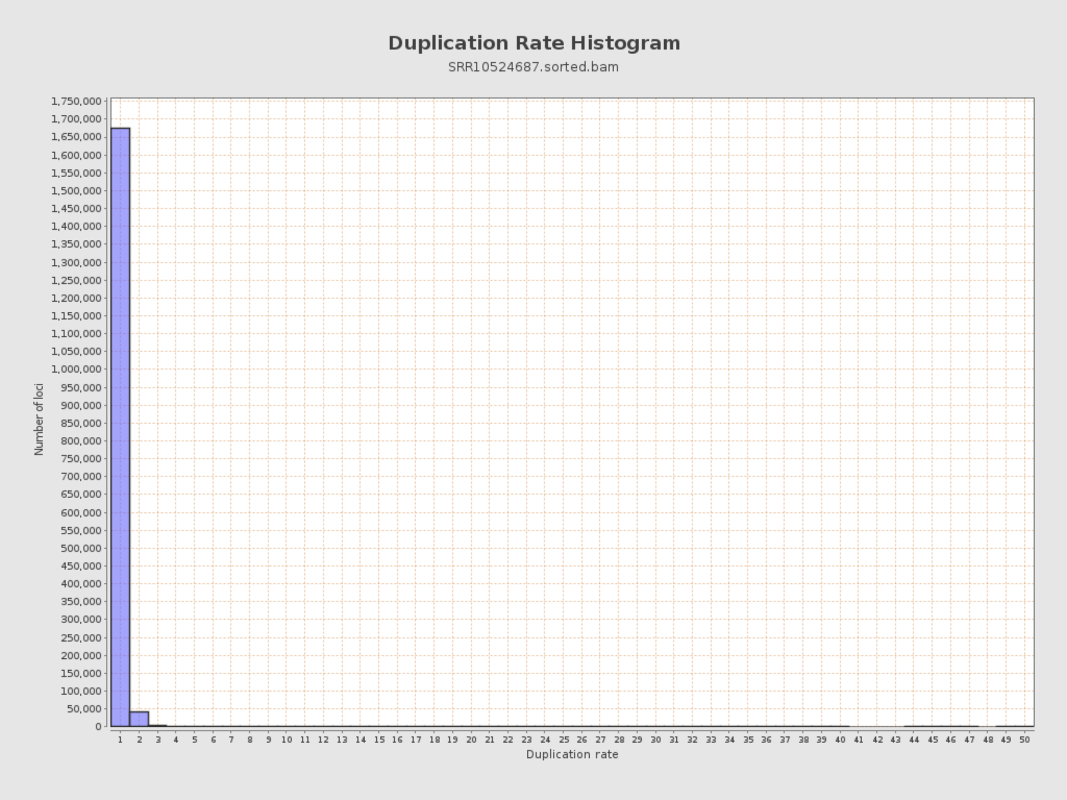
5. Results : Coverage Histogram (0-50X)



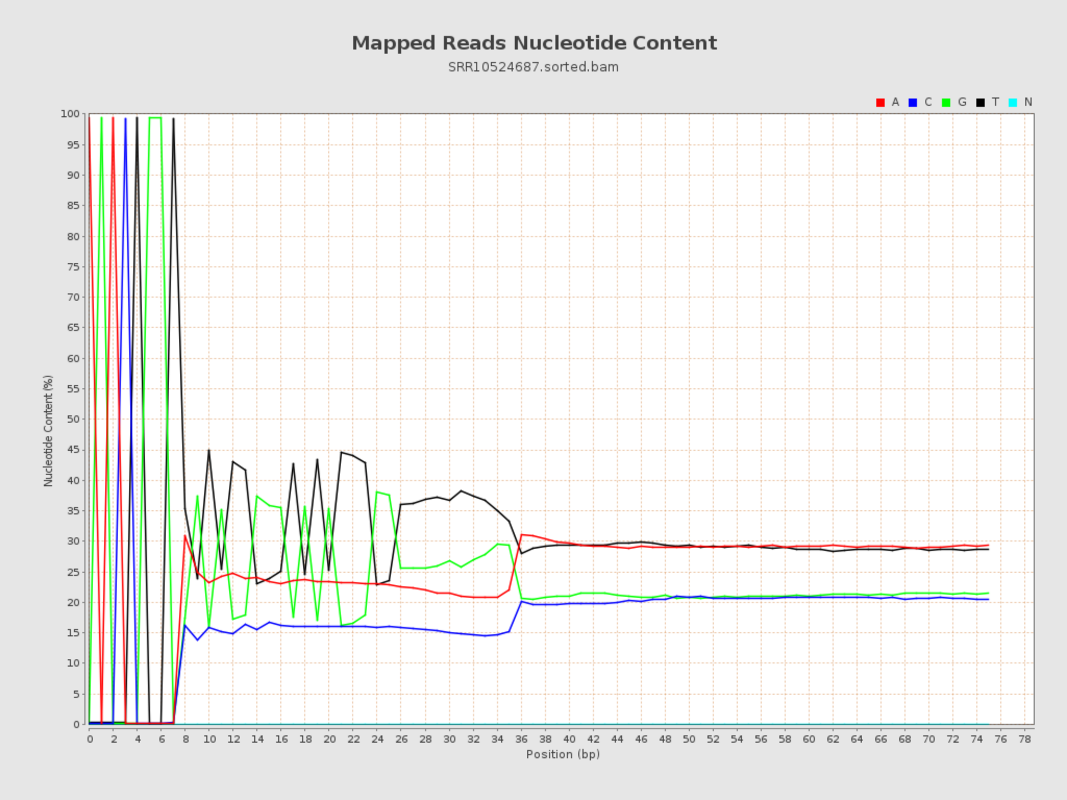
6. Results : Genome Fraction Coverage



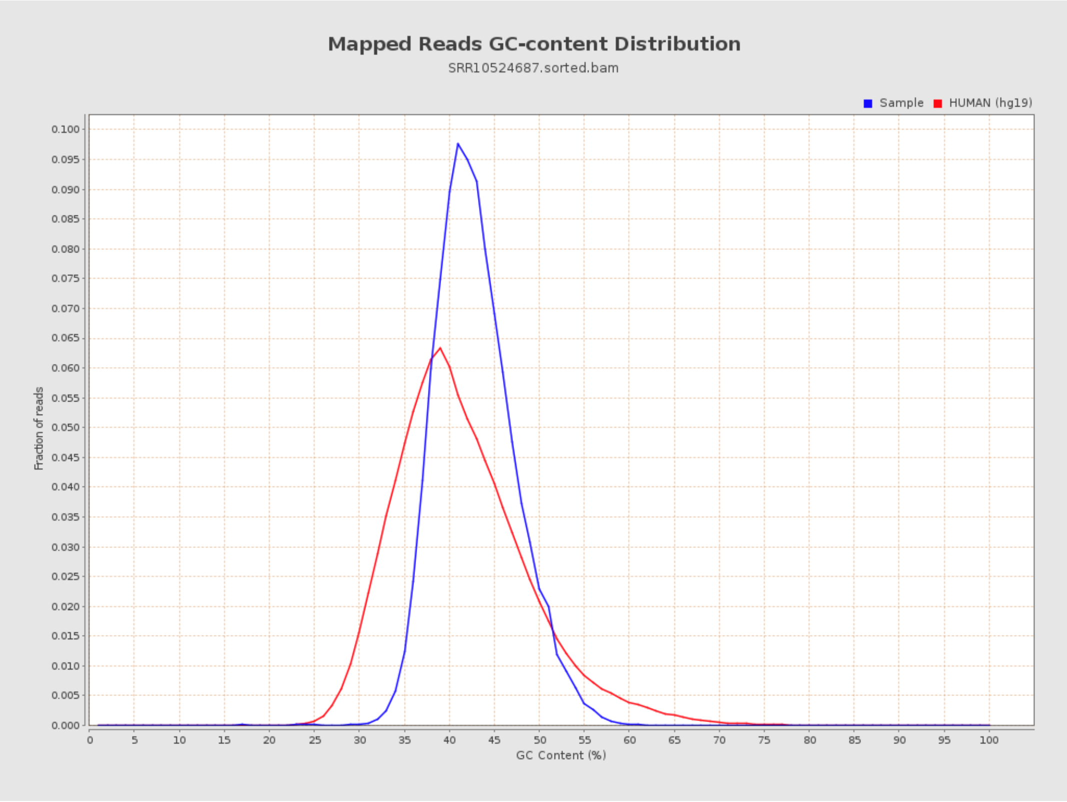
7. Results : Duplication Rate Histogram



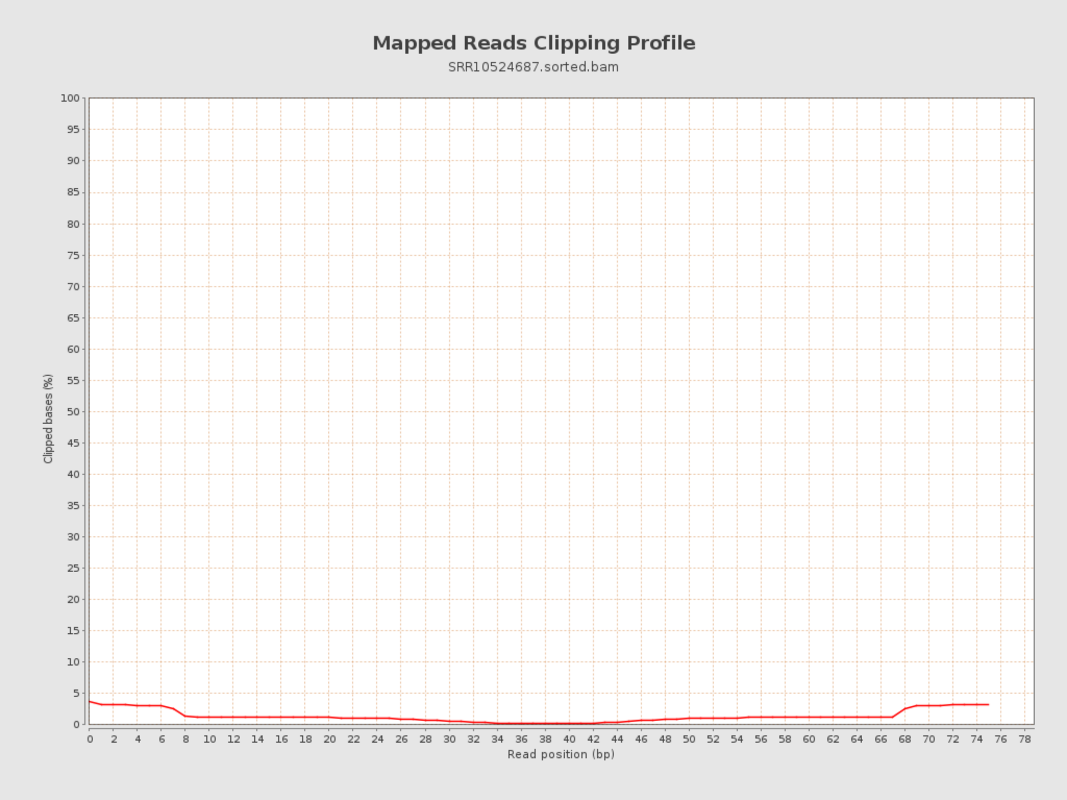
8. Results : Mapped Reads Nucleotide Content



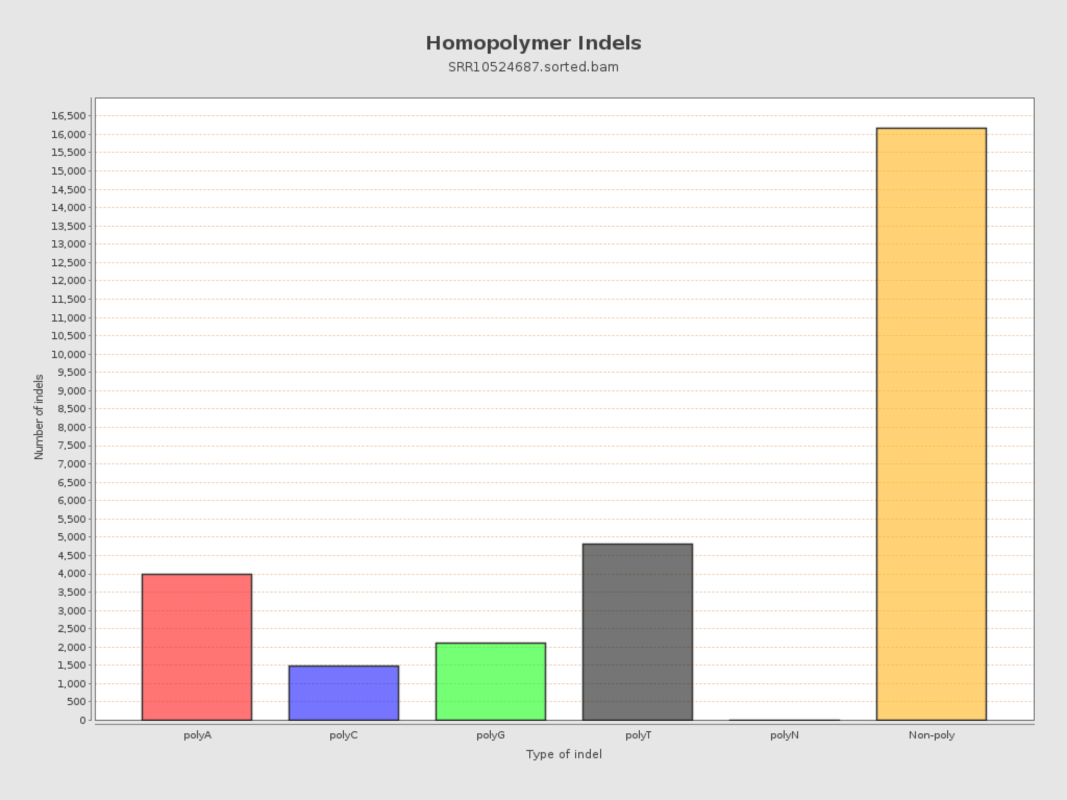
9. Results : Mapped Reads GC-content Distribution



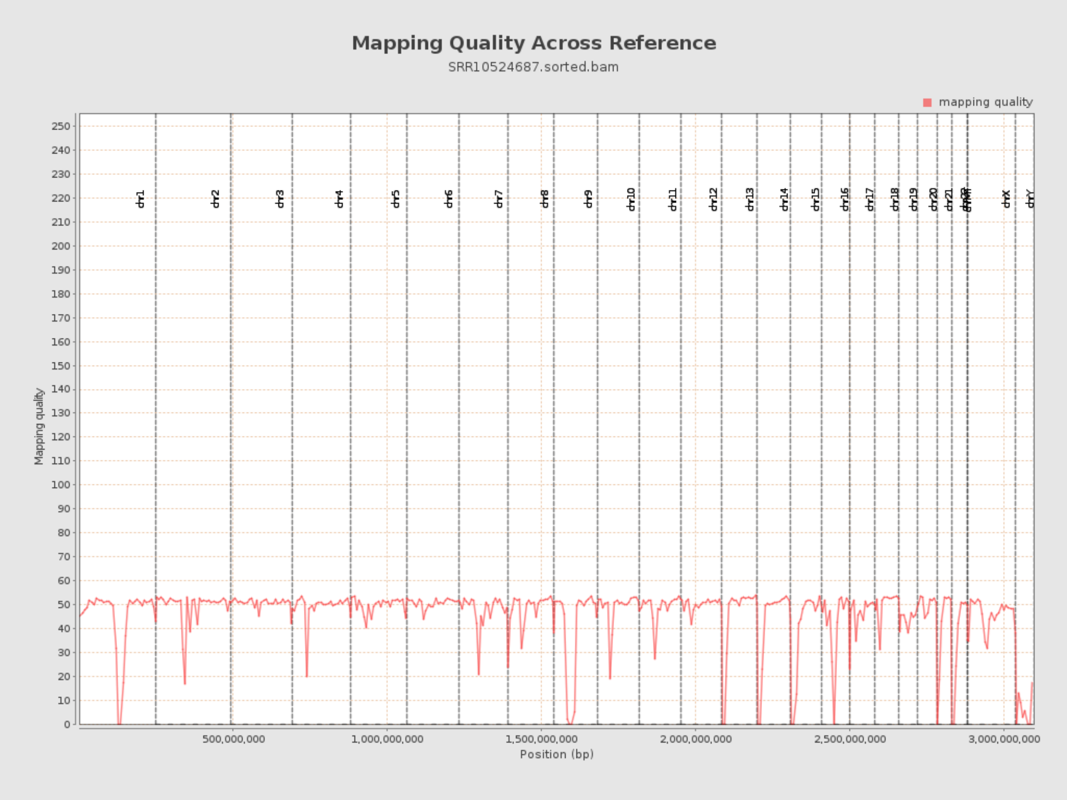
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram