Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 17:37:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818824.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_SRR1818824 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818824.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 17:37:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818824.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,697,510
Mapped reads	1,655,465 / 97.52%
Unmapped reads	42,045 / 2.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,055 / 0.71%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	715,834 / 42.17%
Duplication rate	36.41%
Clipped reads	1,663,558 / 98%

2.2. ACGT Content

Number/percentage of A's	30,722,121 / 27.33%
Number/percentage of C's	25,833,010 / 22.98%
Number/percentage of T's	32,006,829 / 28.47%
Number/percentage of G's	23,850,011 / 21.22%
Number/percentage of N's	7,040 / 0.01%
GC Percentage	44.19%

2.3. Coverage

Mean	0.0363

Standard Deviation	0.4631

2.4. Mapping Quality

Mean Mapping Quality	47.75

2.5. Mismatches and indels

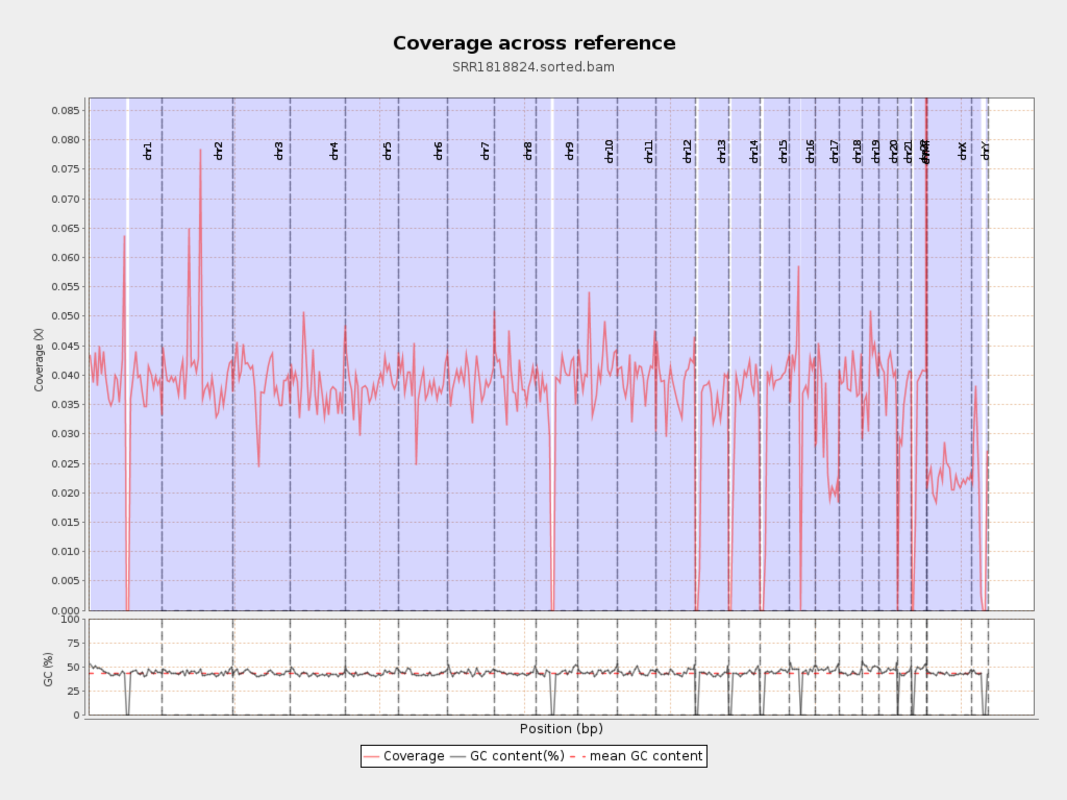
General error rate	0.53%
Mismatches	569,710
Insertions	11,405
Mapped reads with at least one insertion	0.68%
Deletions	28,172
Mapped reads with at least one deletion	1.69%
Homopolymer indels	42.2%

2.6. Chromosome stats

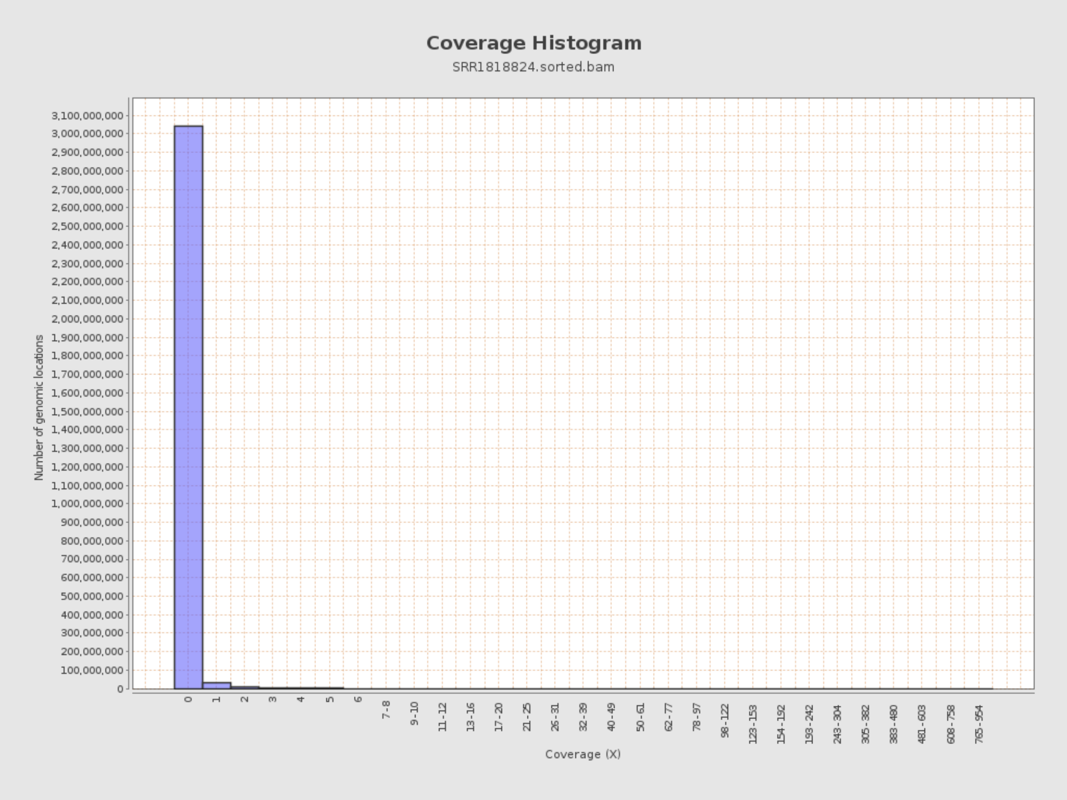
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9361102	0.0376	0.6337
chr2	243199373	9999421	0.0411	0.735
chr3	198022430	7724844	0.039	0.3525
chr4	191154276	7259168	0.038	0.3932
chr5	180915260	6929111	0.0383	0.3613
chr6	171115067	6593884	0.0385	0.3809
chr7	159138663	6164570	0.0387	0.4144

chr8	146364022	5752623	0.0393	0.3892
chr9	141213431	4897263	0.0347	0.3828
chr10	135534747	5588934	0.0412	0.5049
chr11	135006516	5386448	0.0399	0.3958
chr12	133851895	5203861	0.0389	0.369
chr13	115169878	3534487	0.0307	0.3105
chr14	107349540	3511772	0.0327	0.3563
chr15	102531392	3286176	0.0321	0.3241
chr16	90354753	3487564	0.0386	0.5152
chr17	81195210	2252666	0.0277	0.3257
chr18	78077248	3097707	0.0397	0.4822
chr19	59128983	2360264	0.0399	0.5889
chr20	63025520	2526957	0.0401	0.3788
chr21	48129895	1533972	0.0319	0.3296
chr22	51304566	1436171	0.028	0.3439
chrMT	16571	60938	3.6774	4.7661
chrX	155270560	3479899	0.0224	0.2977
chrY	59373566	1034527	0.0174	0.8637

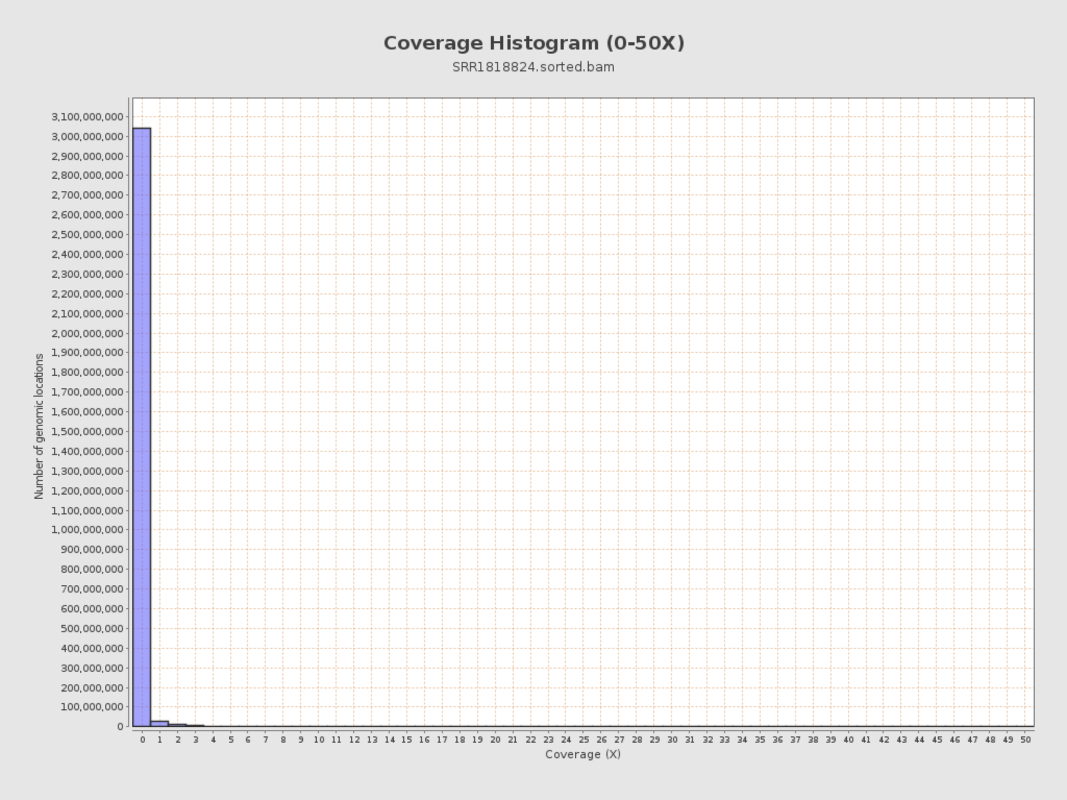
3. Results : Coverage across reference



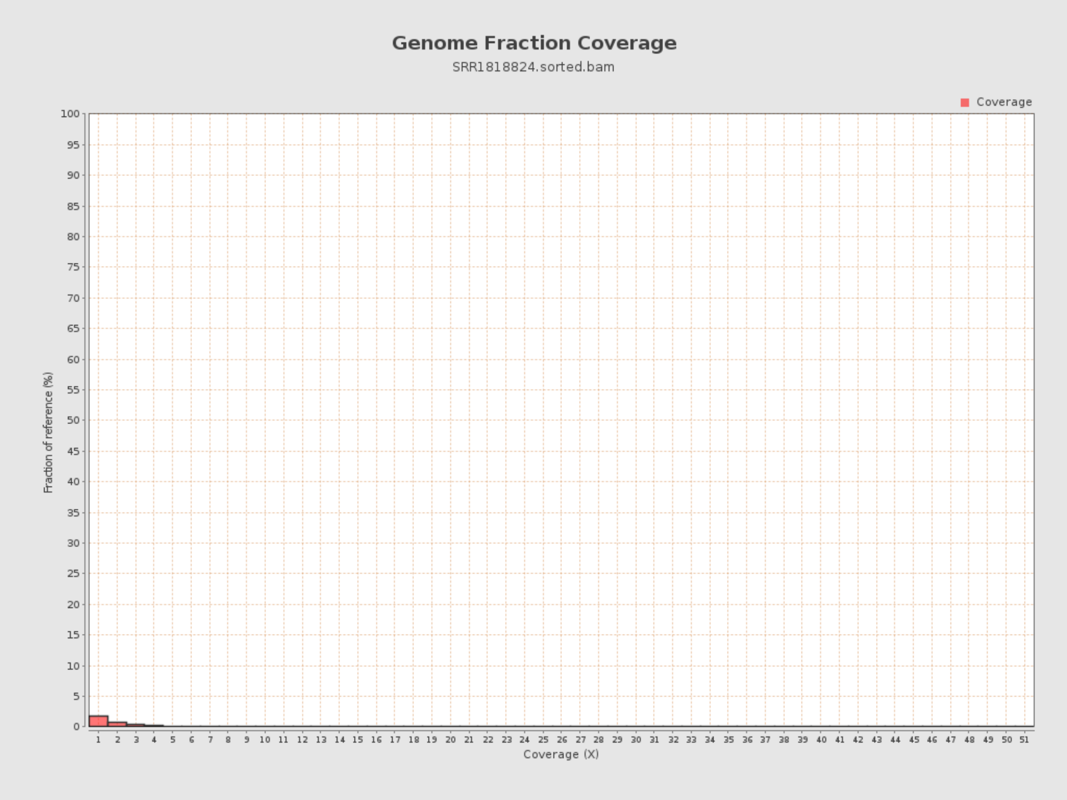
4. Results : Coverage Histogram



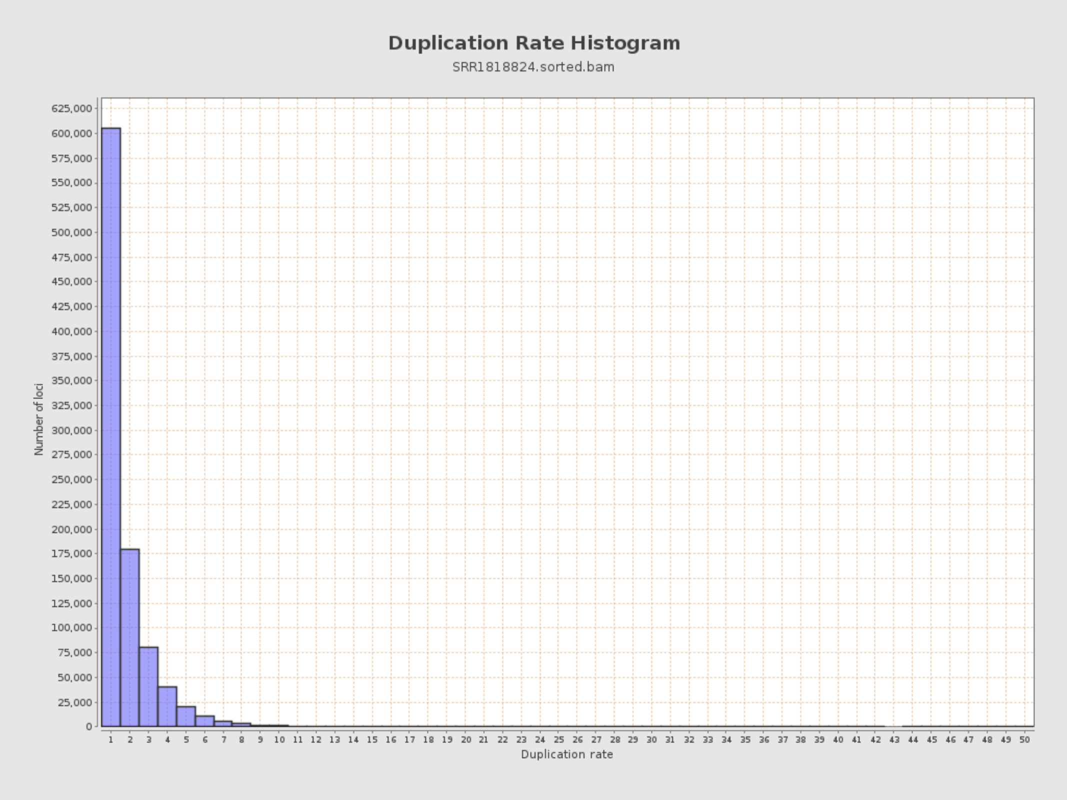
5. Results : Coverage Histogram (0-50X)



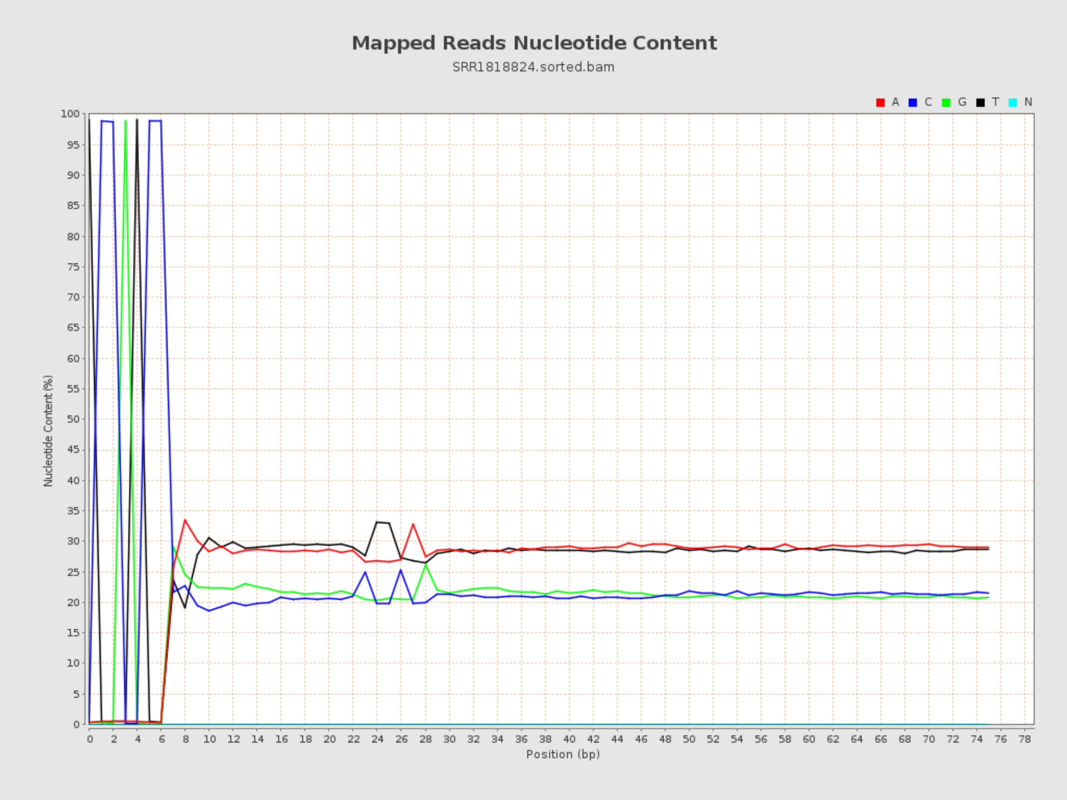
6. Results : Genome Fraction Coverage



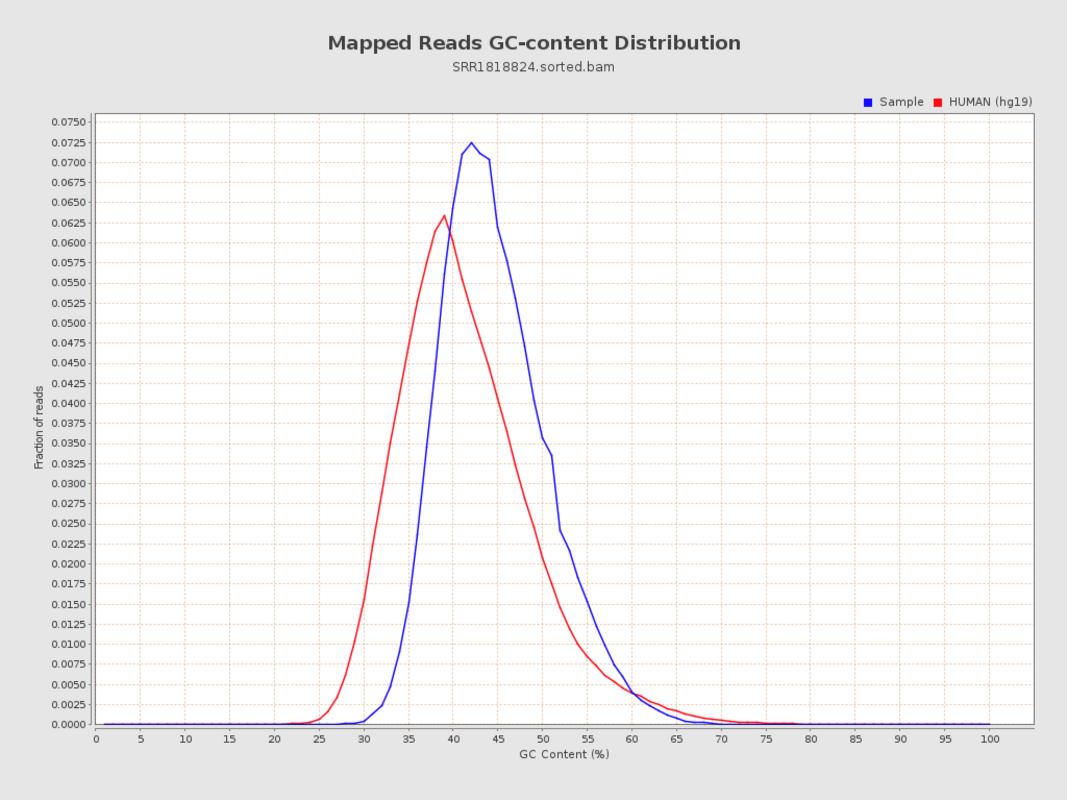
7. Results : Duplication Rate Histogram



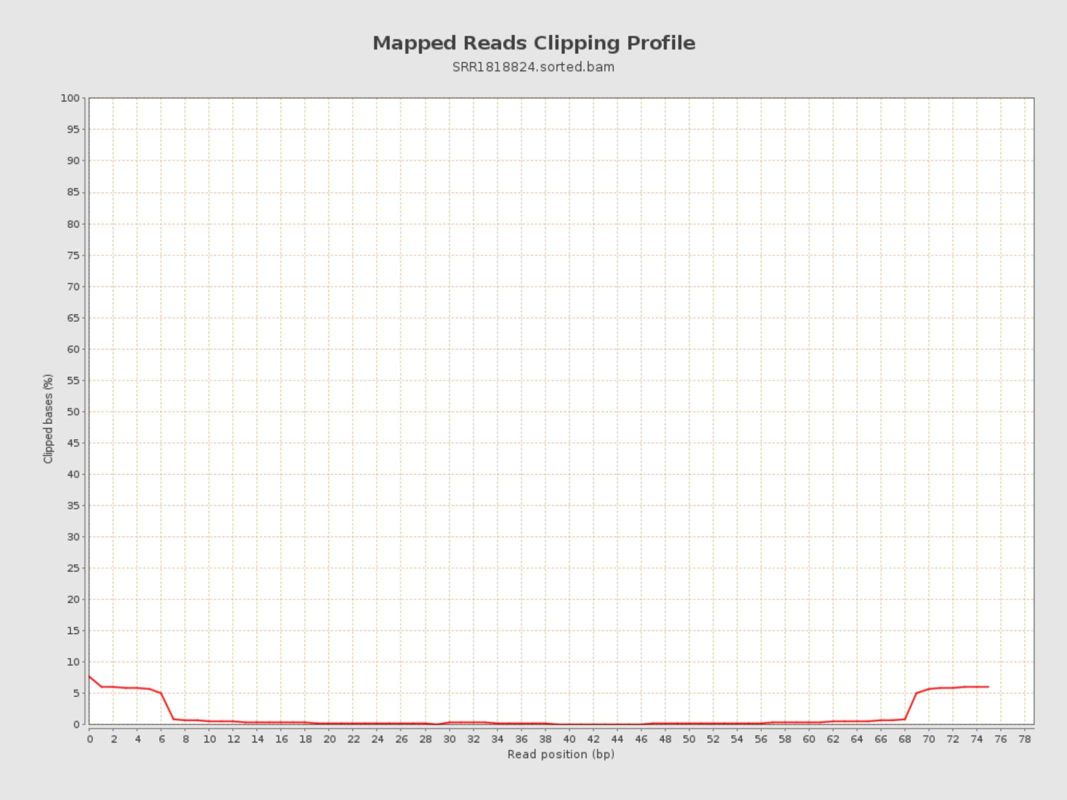
8. Results : Mapped Reads Nucleotide Content



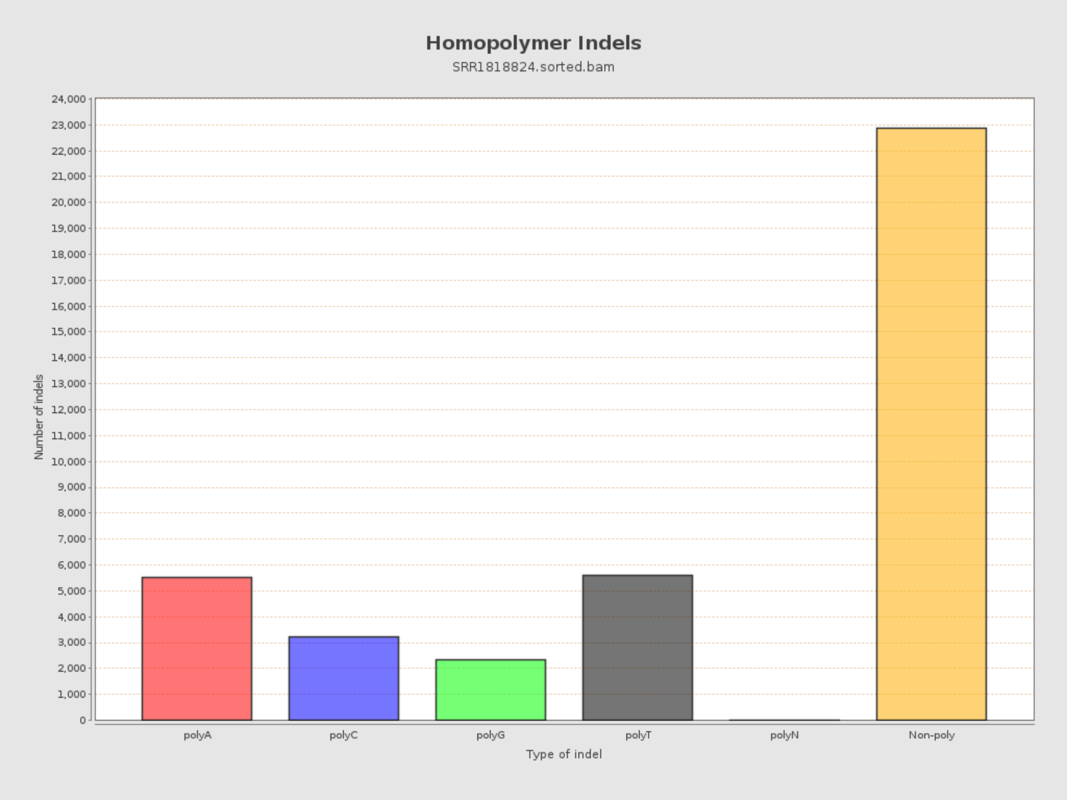
9. Results : Mapped Reads GC-content Distribution



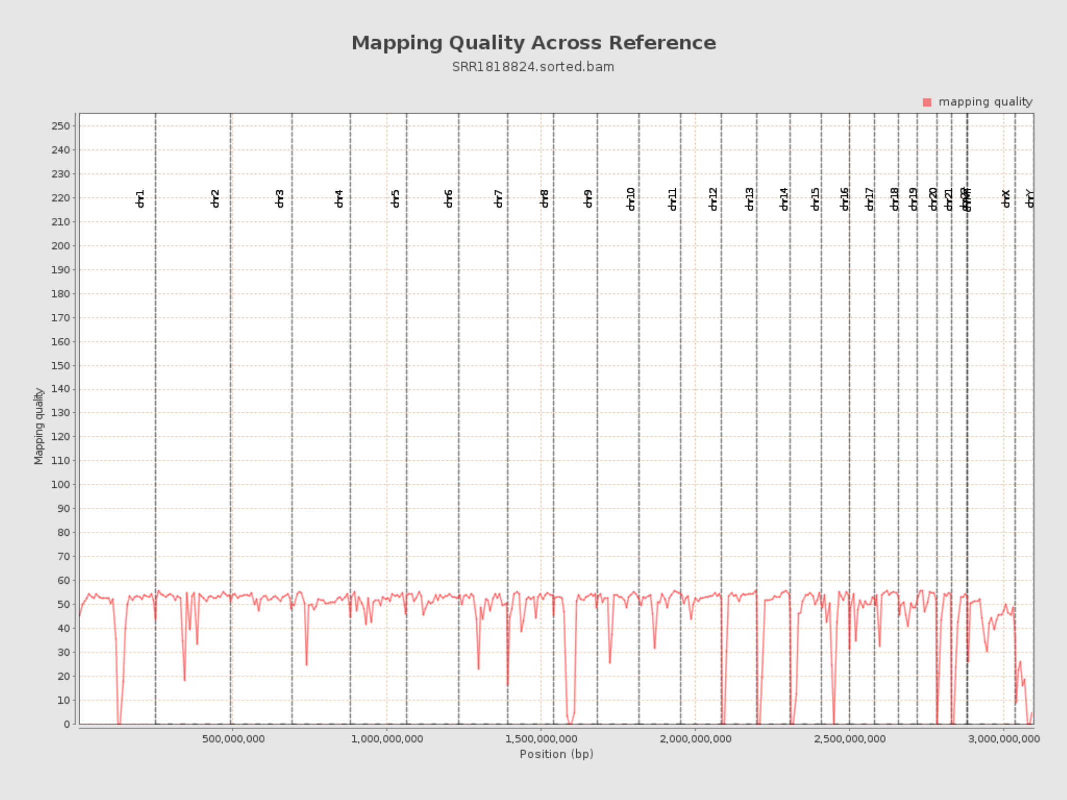
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram