Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 07:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818915.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_SRR1818915 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818915.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 07:51:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818915.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,027,851
Mapped reads	1,998,425 / 98.55%
Unmapped reads	29,426 / 1.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,855 / 1.37%
Read min/max/mean length	30 / 101 / 101.53
Duplicated reads (estimated)	486,461 / 23.99%
Duplication rate	20.05%
Clipped reads	2,003,589 / 98.8%

2.2. ACGT Content

Number/percentage of A's	51,537,799 / 27.85%
Number/percentage of C's	37,968,563 / 20.52%
Number/percentage of T's	54,165,827 / 29.27%
Number/percentage of G's	41,385,106 / 22.36%
Number/percentage of N's	2,720 / 0%
GC Percentage	42.88%

2.3. Coverage

Mean	0.0598

Standard Deviation	0.7644

2.4. Mapping Quality

Mean Mapping Quality	49.26

2.5. Mismatches and indels

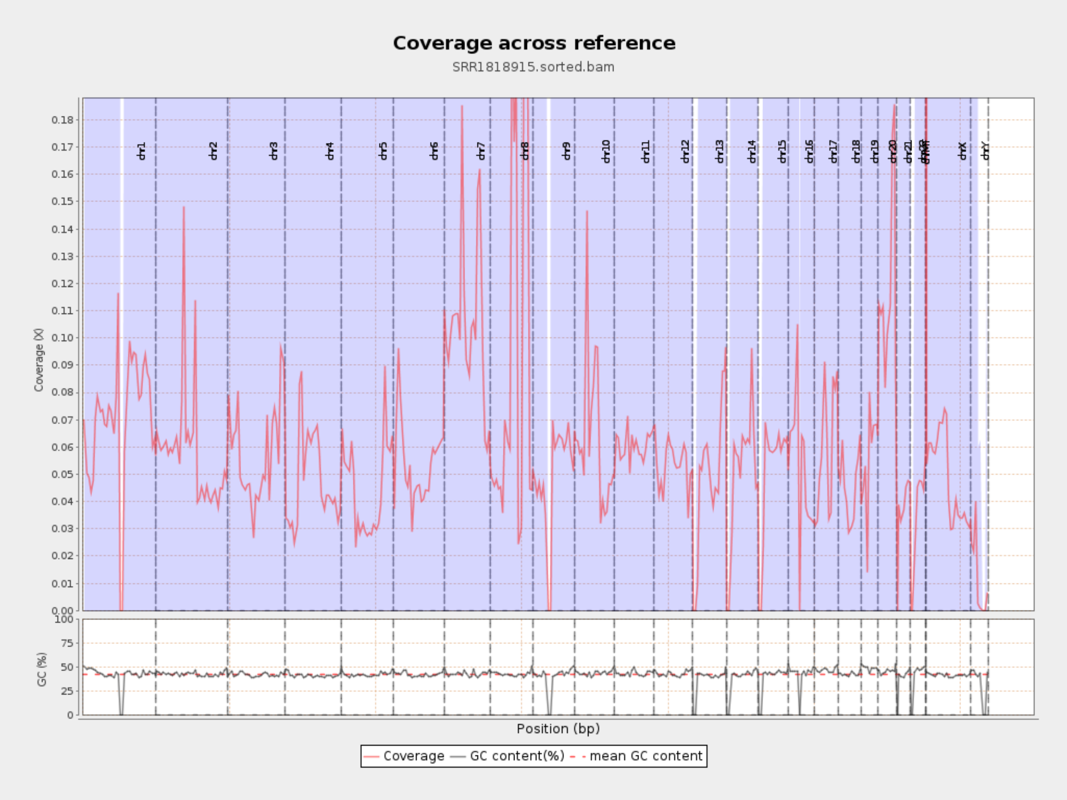
General error rate	0.65%
Mismatches	1,130,699
Insertions	26,511
Mapped reads with at least one insertion	1.29%
Deletions	59,740
Mapped reads with at least one deletion	2.92%
Homopolymer indels	40.8%

2.6. Chromosome stats

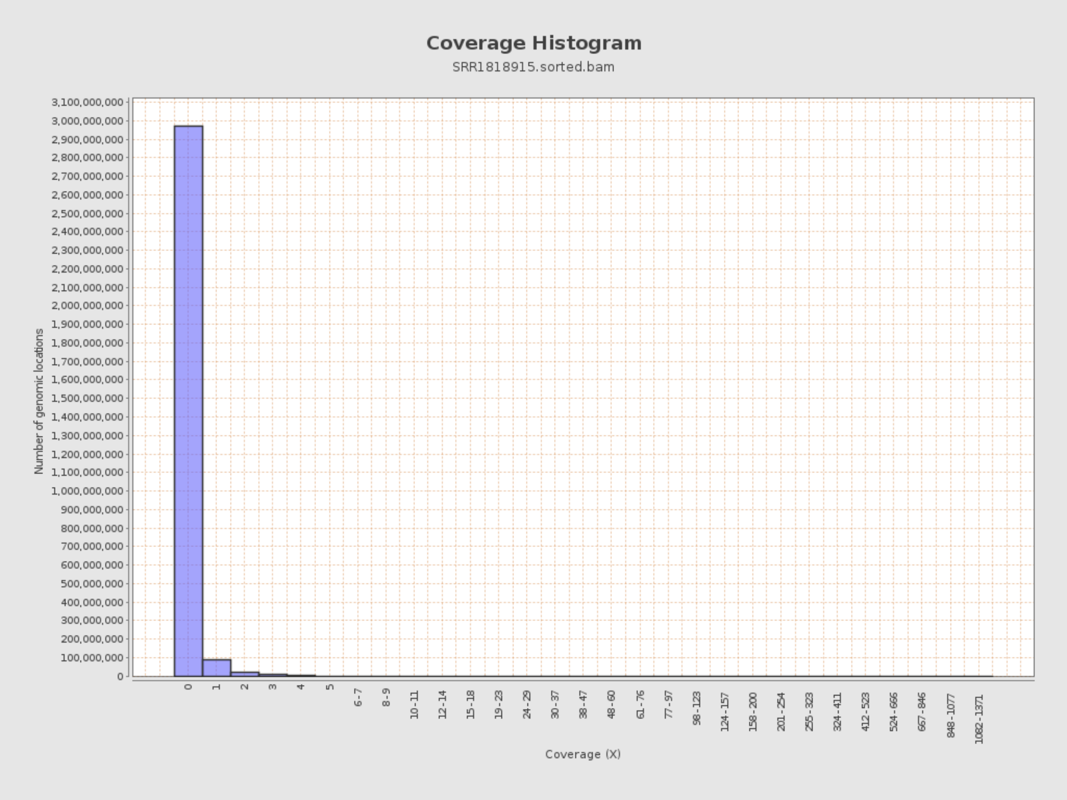
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17543970	0.0704	1.1157
chr2	243199373	14154333	0.0582	1.1384
chr3	198022430	11403874	0.0576	0.3347
chr4	191154276	9224995	0.0483	0.4162
chr5	180915260	8154992	0.0451	0.3225
chr6	171115067	9194879	0.0537	0.3642
chr7	159138663	16742618	0.1052	1.7876

chr8	146364022	15993390	0.1093	0.6035
chr9	141213431	6917846	0.049	0.6576
chr10	135534747	8542308	0.063	0.9645
chr11	135006516	8124093	0.0602	0.4388
chr12	133851895	7182021	0.0537	0.3323
chr13	115169878	5618809	0.0488	0.3029
chr14	107349540	5532904	0.0515	0.3516
chr15	102531392	5136727	0.0501	0.3201
chr16	90354753	4676128	0.0518	0.7651
chr17	81195210	4726103	0.0582	0.4647
chr18	78077248	3563050	0.0456	0.7373
chr19	59128983	3262919	0.0552	0.9549
chr20	63025520	7700495	0.1222	0.5311
chr21	48129895	1792196	0.0372	0.3414
chr22	51304566	1681918	0.0328	0.2769
chrMT	16571	53040	3.2008	2.905
chrX	155270560	7572365	0.0488	0.3746
chrY	59373566	681093	0.0115	0.8702

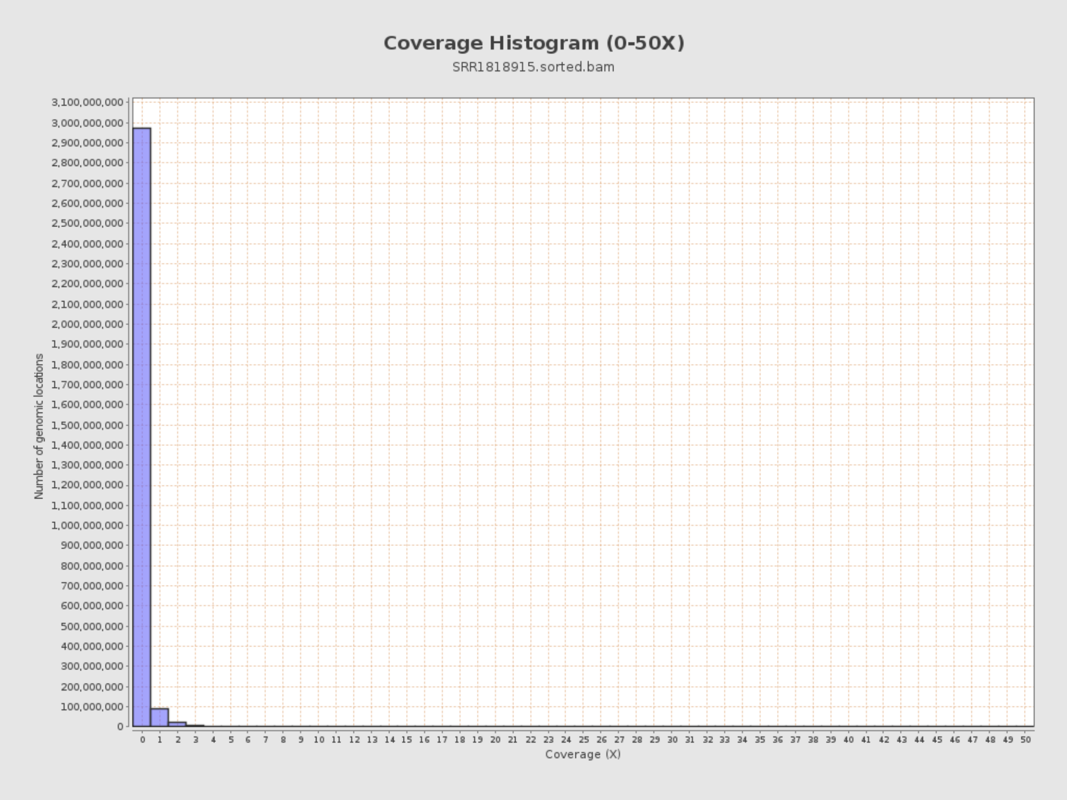
3. Results : Coverage across reference



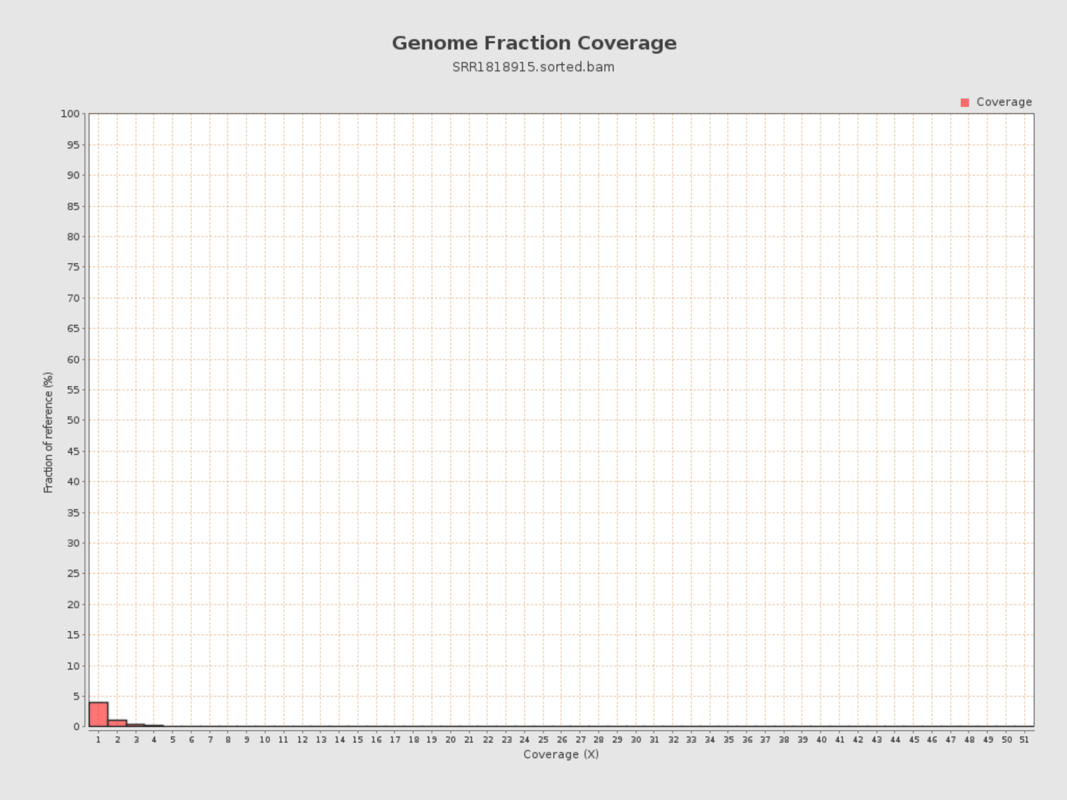
4. Results : Coverage Histogram



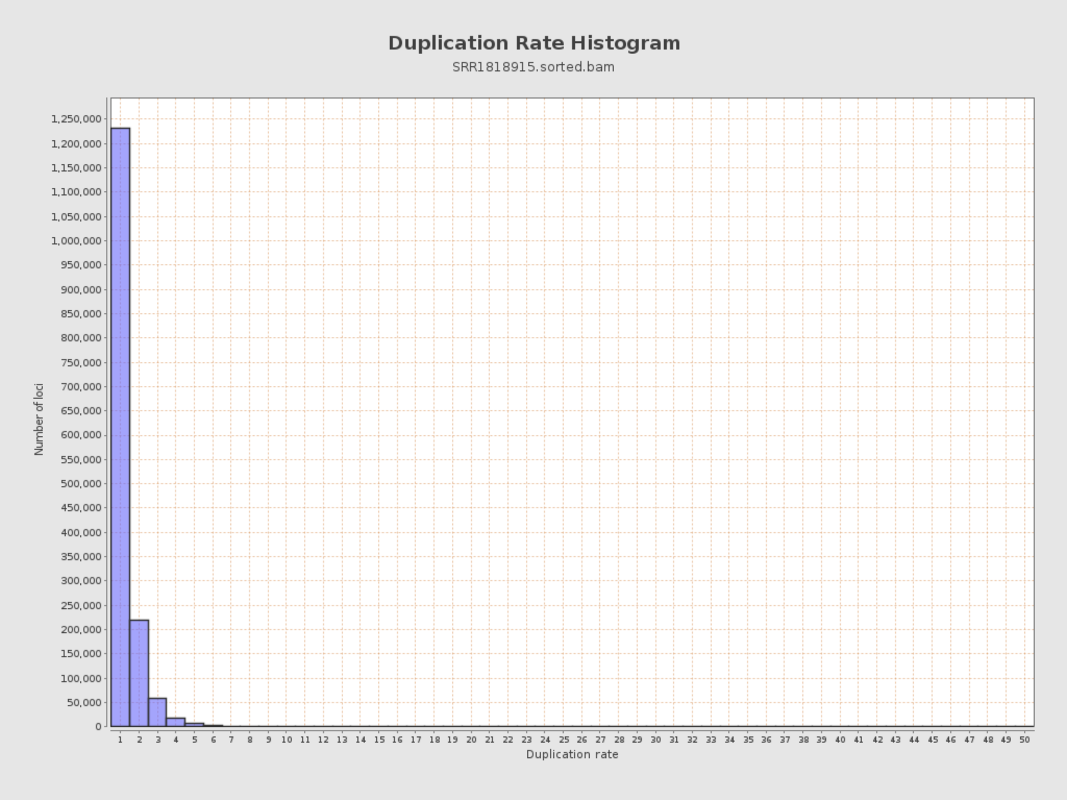
5. Results : Coverage Histogram (0-50X)



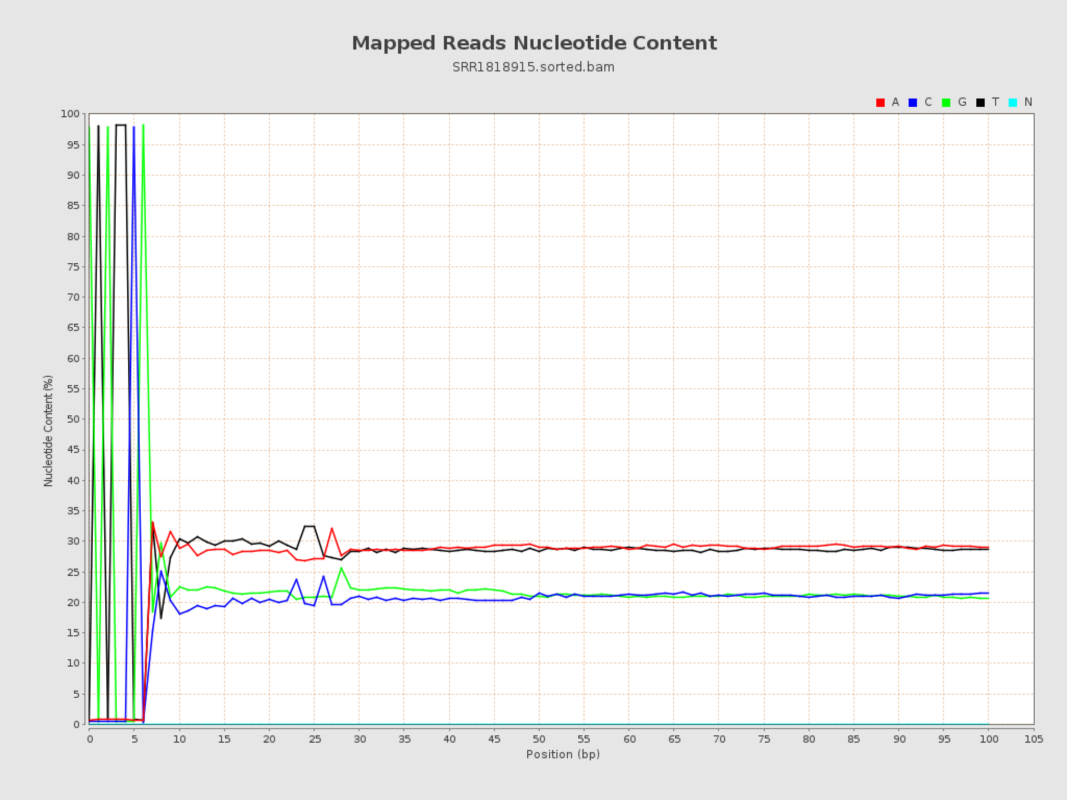
6. Results : Genome Fraction Coverage



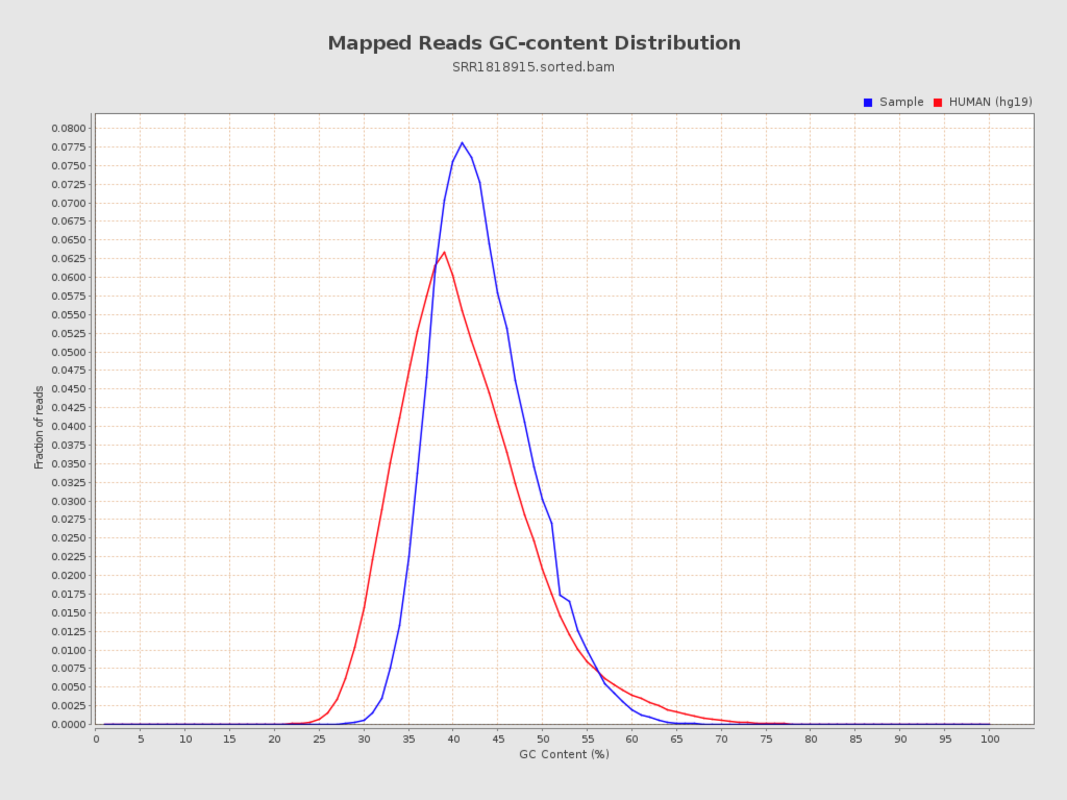
7. Results : Duplication Rate Histogram



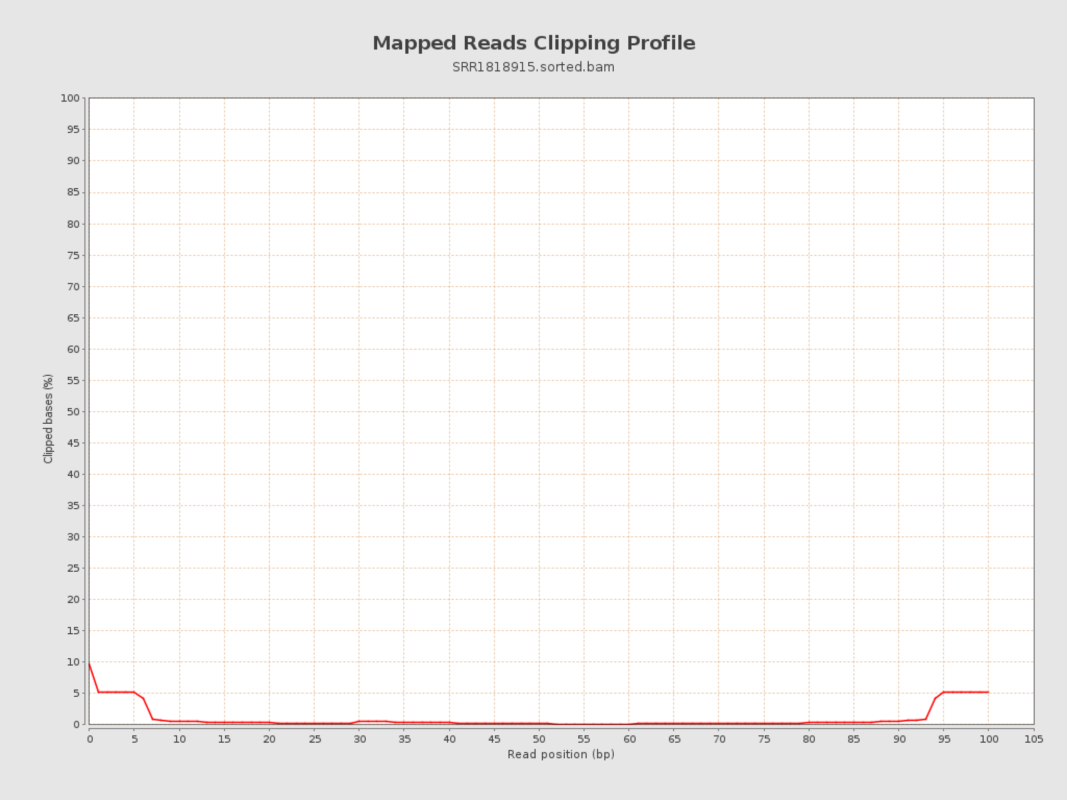
8. Results : Mapped Reads Nucleotide Content



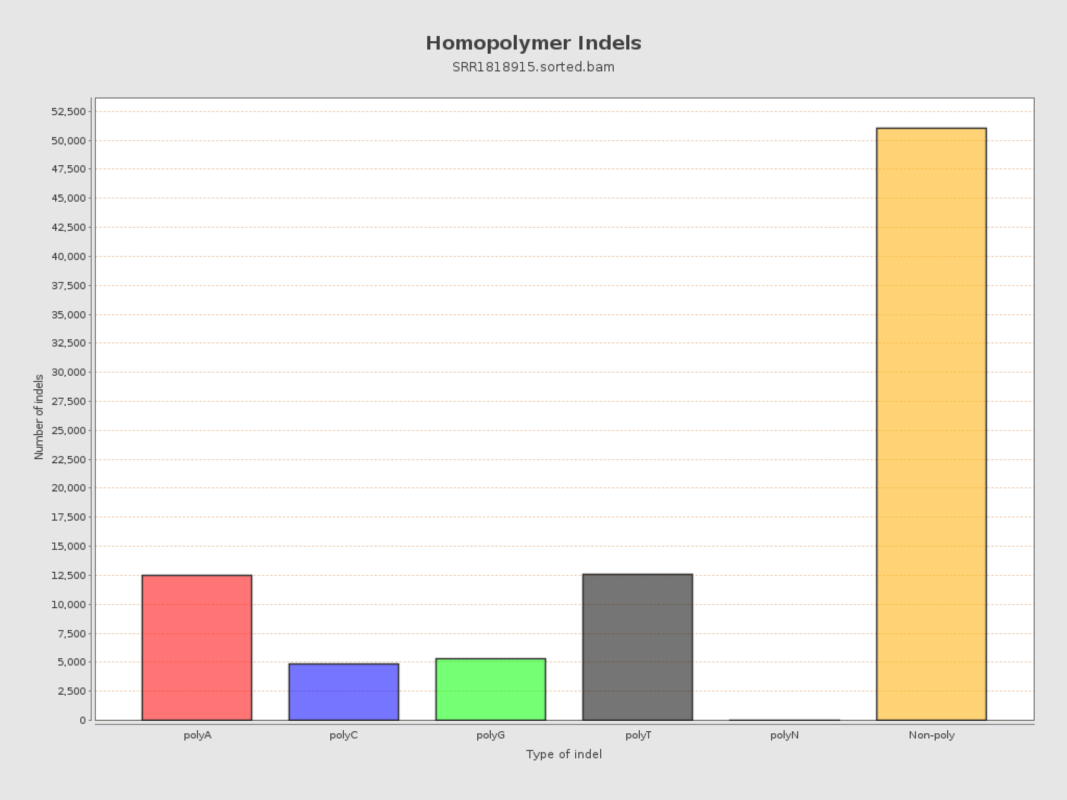
9. Results : Mapped Reads GC-content Distribution



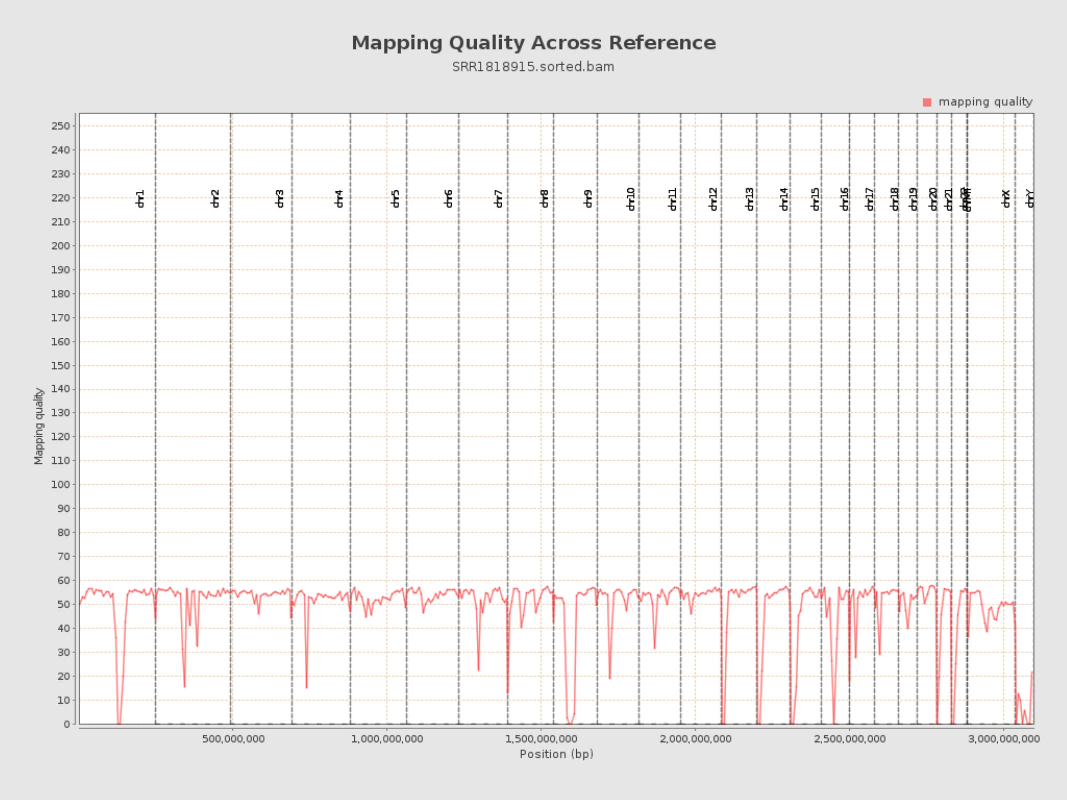
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram