Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 12:08:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514725.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_SRR5514725 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514725.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 12:08:42 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514725.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	69,055,952
Mapped reads	67,549,475 / 97.82%
Unmapped reads	1,506,477 / 2.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,491,324 / 3.61%
Read min/max/mean length	30 / 100 / 99.36
Duplicated reads (estimated)	47,119,713 / 68.23%
Duplication rate	45.12%
Clipped reads	14,195,743 / 20.56%

2.2. ACGT Content

Number/percentage of A's	1,683,933,082 / 26.47%
Number/percentage of C's	1,461,077,390 / 22.97%
Number/percentage of T's	1,702,091,687 / 26.76%
Number/percentage of G's	1,464,281,895 / 23.02%
Number/percentage of N's	49,625,489 / 0.78%
GC Percentage	45.99%

2.3. Coverage

Mean	2.0559

Standard Deviation	45.4515

2.4. Mapping Quality

Mean Mapping Quality	39.62

2.5. Mismatches and indels

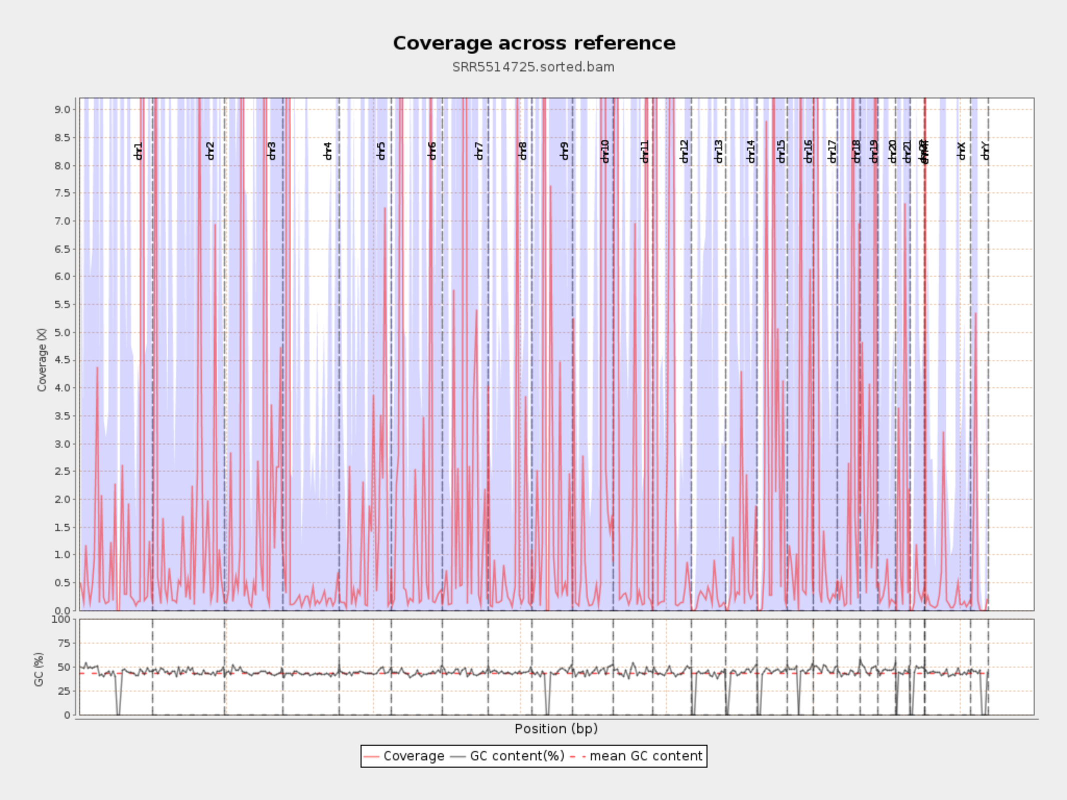
General error rate	0.94%
Mismatches	56,302,247
Insertions	2,271,935
Mapped reads with at least one insertion	3.25%
Deletions	1,785,534
Mapped reads with at least one deletion	2.54%
Homopolymer indels	45.46%

2.6. Chromosome stats

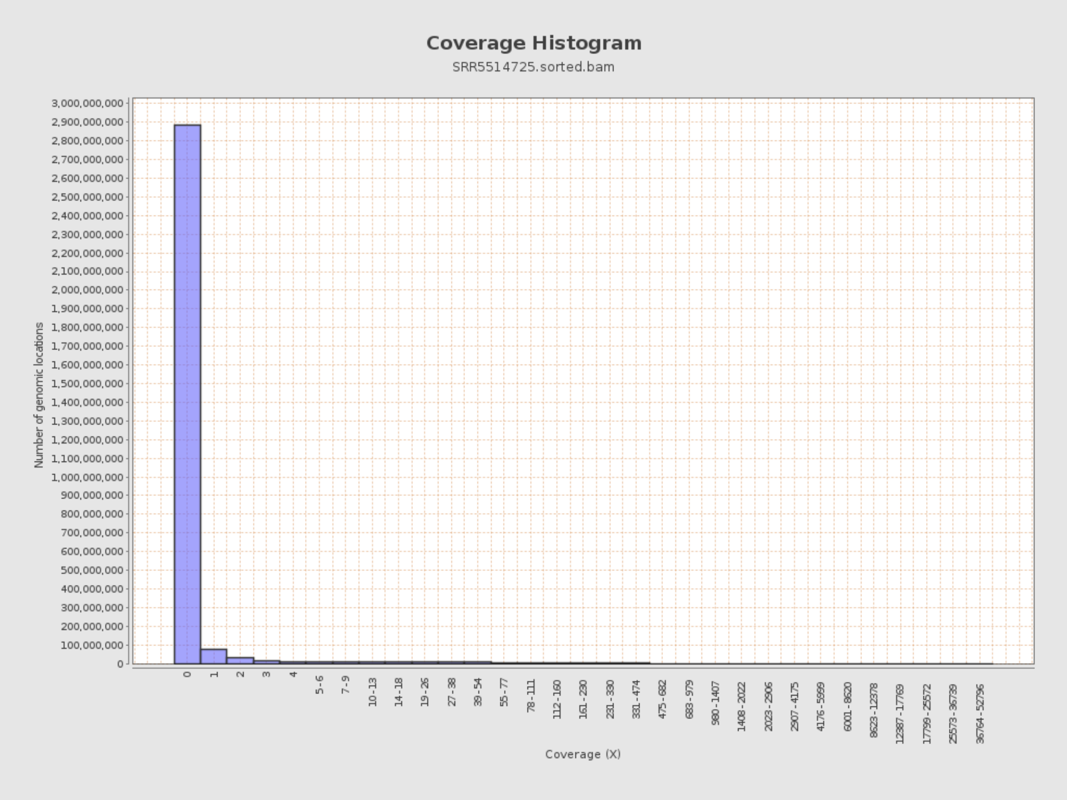
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	424610662	1.7035	53.2082
chr2	243199373	404477485	1.6632	37.5505
chr3	198022430	530788923	2.6804	27.8092
chr4	191154276	580669745	3.0377	59.7196
chr5	180915260	226464588	1.2518	22.0686
chr6	171115067	333034100	1.9463	82.0809
chr7	159138663	419179866	2.6341	43.7875

chr8	146364022	141013338	0.9634	21.2595
chr9	141213431	299310223	2.1196	92.183
chr10	135534747	551724774	4.0707	58.3987
chr11	135006516	373380734	2.7656	30.069
chr12	133851895	544928871	4.0711	37.5882
chr13	115169878	26802080	0.2327	7.5956
chr14	107349540	94049803	0.8761	15.1075
chr15	102531392	266003897	2.5944	28.9841
chr16	90354753	189225897	2.0943	33.6755
chr17	81195210	281009663	3.4609	27.0516
chr18	78077248	181996191	2.331	21.3365
chr19	59128983	243558239	4.1191	91.4552
chr20	63025520	20628684	0.3273	8.6963
chr21	48129895	103985297	2.1605	37.5096
chr22	51304566	17818042	0.3473	4.5226
chrMT	16571	1031304	62.2355	48.1924
chrX	155270560	50676437	0.3264	11.0968
chrY	59373566	58197554	0.9802	18.5381

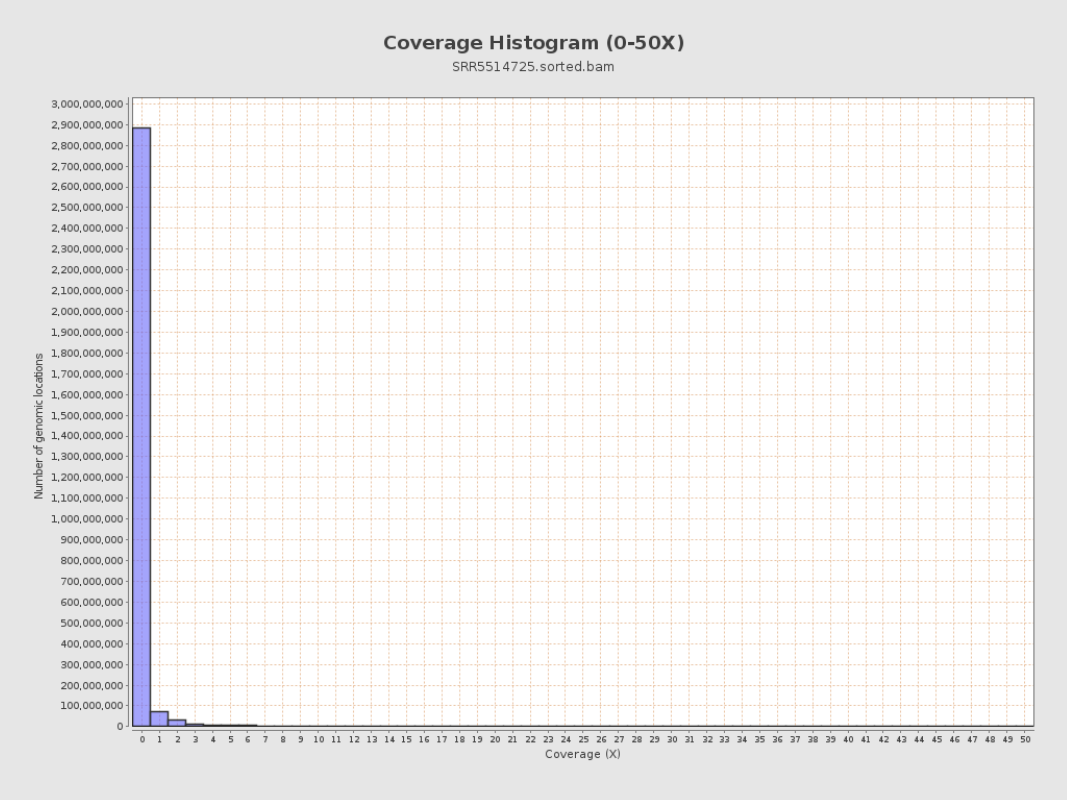
3. Results : Coverage across reference



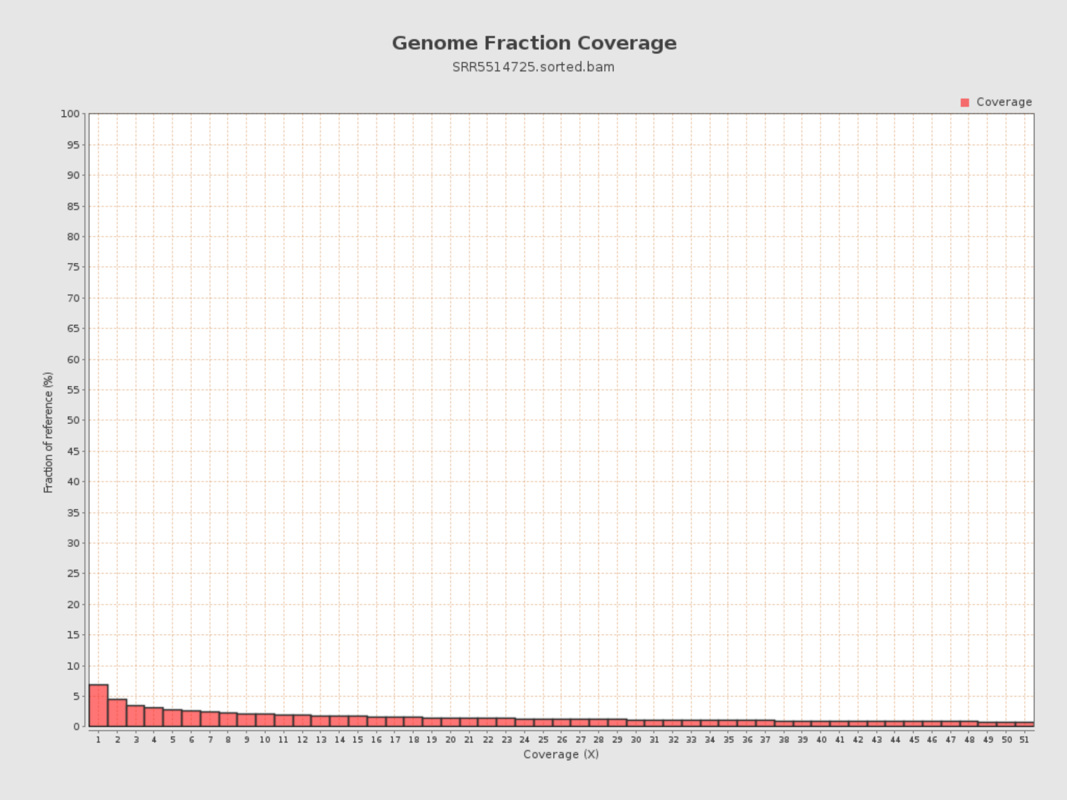
4. Results : Coverage Histogram



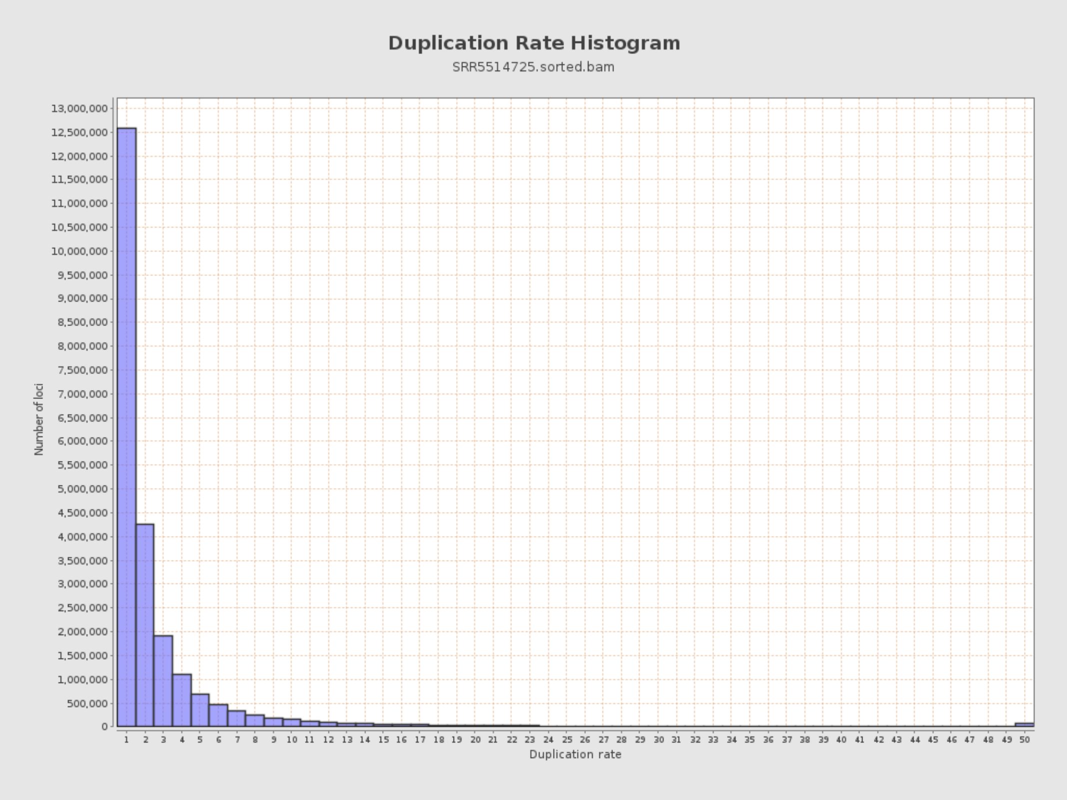
5. Results : Coverage Histogram (0-50X)



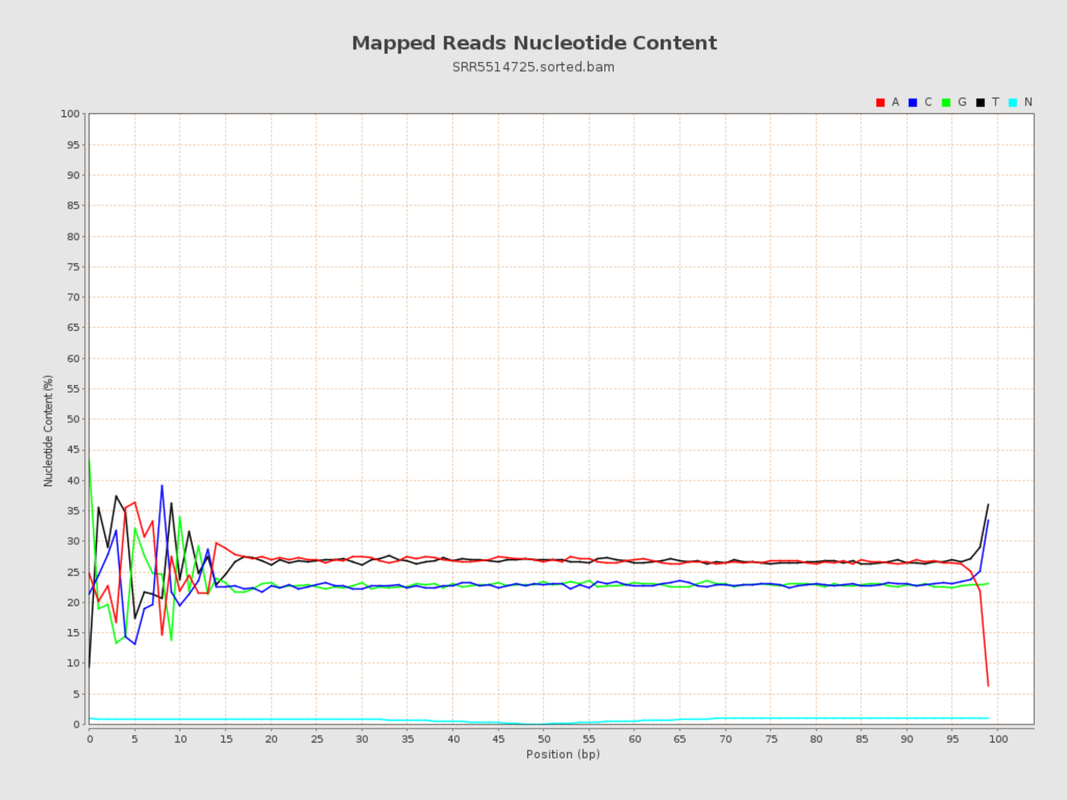
6. Results : Genome Fraction Coverage



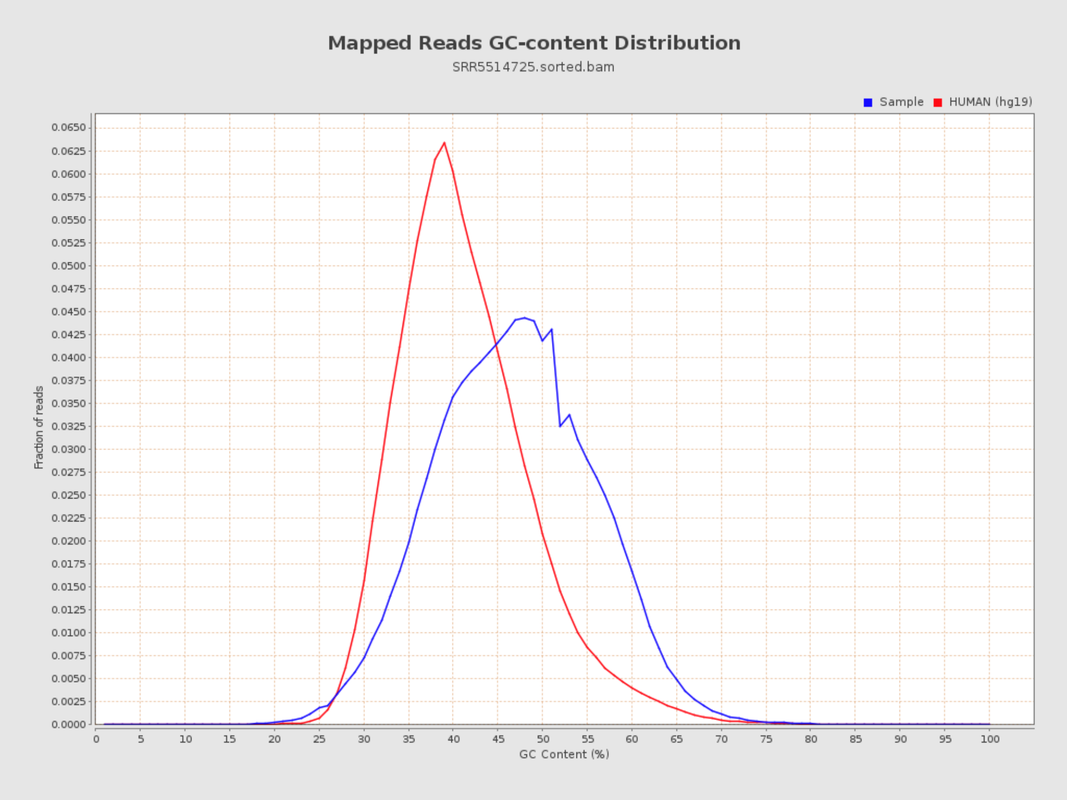
7. Results : Duplication Rate Histogram



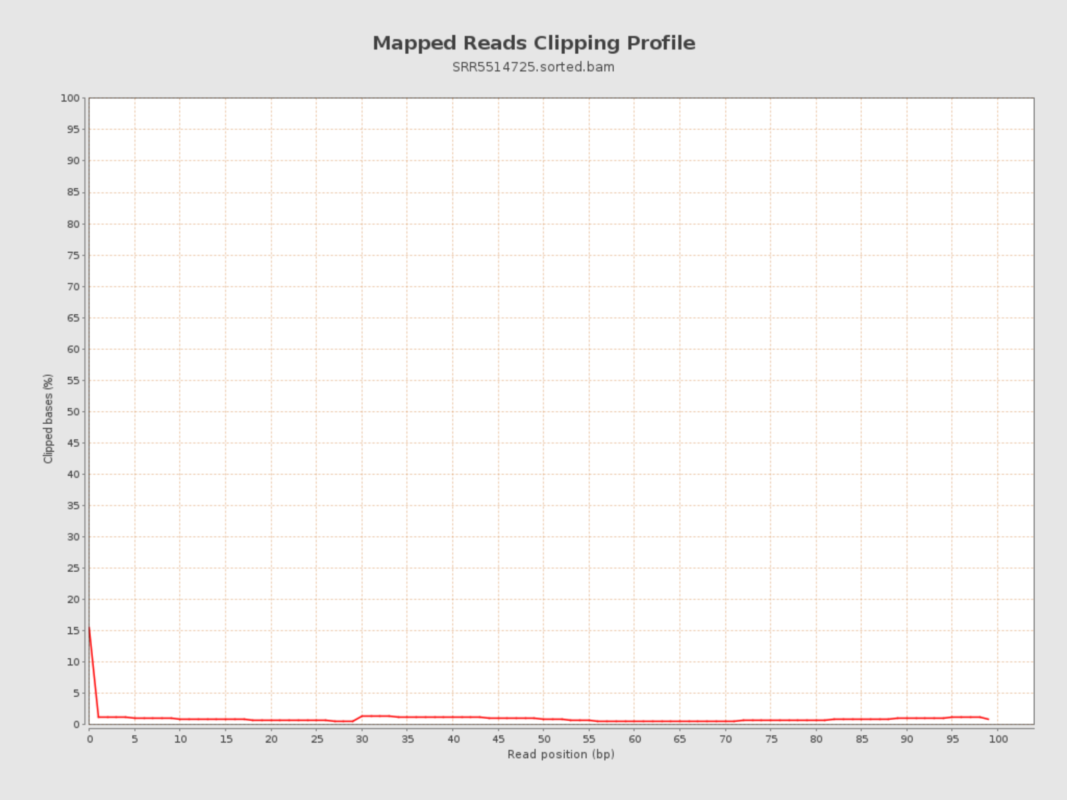
8. Results : Mapped Reads Nucleotide Content



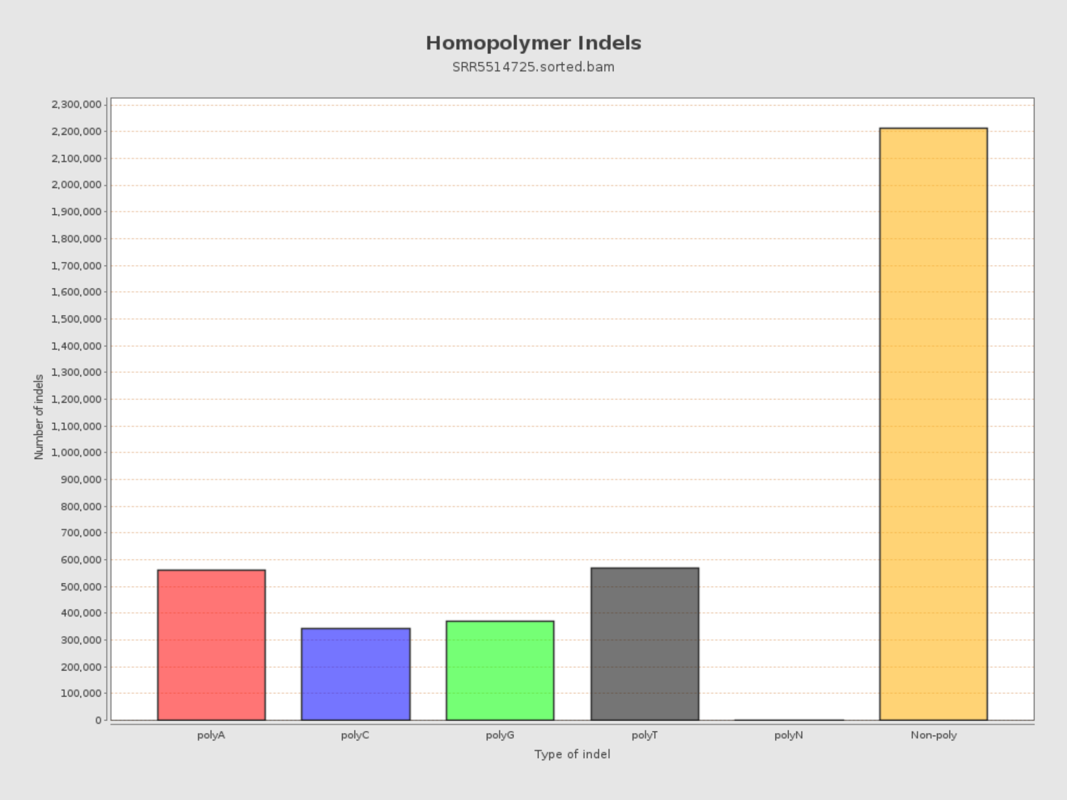
9. Results : Mapped Reads GC-content Distribution



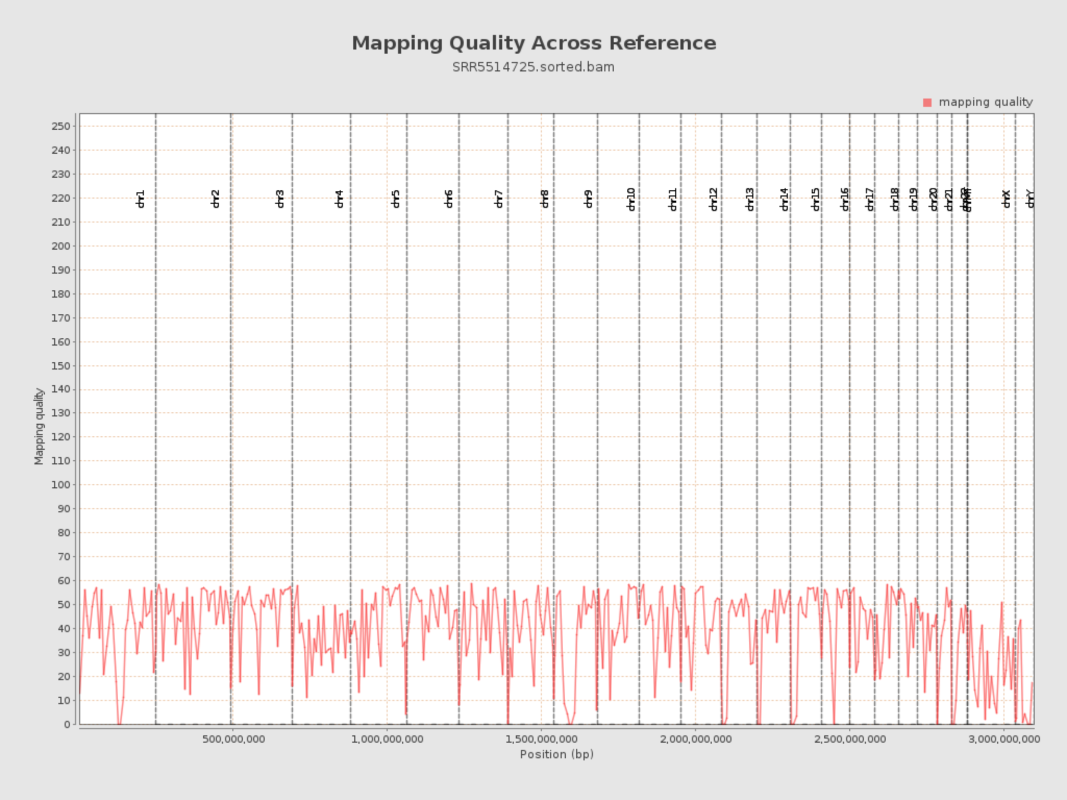
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram