Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/11 12:58:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514727.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_SRR5514727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514727.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Apr 11 12:58:36 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	42,865,081
Mapped reads	41,958,639 / 97.89%
Unmapped reads	906,442 / 2.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,125,122 / 2.62%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	29,651,707 / 69.17%
Duplication rate	43.7%
Clipped reads	6,961,605 / 16.24%

2.2. ACGT Content

Number/percentage of A's	1,077,989,815 / 26.79%
Number/percentage of C's	917,532,557 / 22.8%
Number/percentage of T's	1,087,558,941 / 27.03%
Number/percentage of G's	919,053,424 / 22.84%
Number/percentage of N's	22,049,257 / 0.55%
GC Percentage	45.64%

2.3. Coverage

Mean	1.3005

Standard Deviation	34.0651

2.4. Mapping Quality

Mean Mapping Quality	42.6

2.5. Mismatches and indels

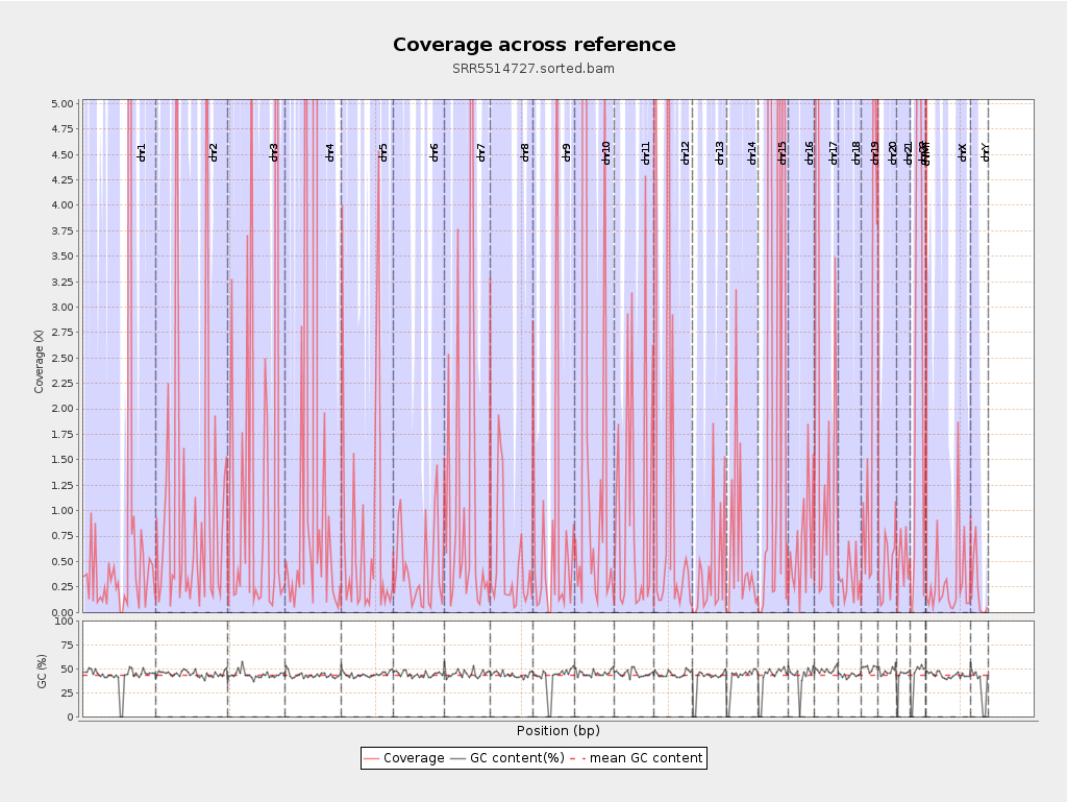
General error rate	0.97%
Mismatches	37,140,289
Insertions	1,405,285
Mapped reads with at least one insertion	3.24%
Deletions	1,020,075
Mapped reads with at least one deletion	2.37%
Homopolymer indels	46.84%

2.6. Chromosome stats

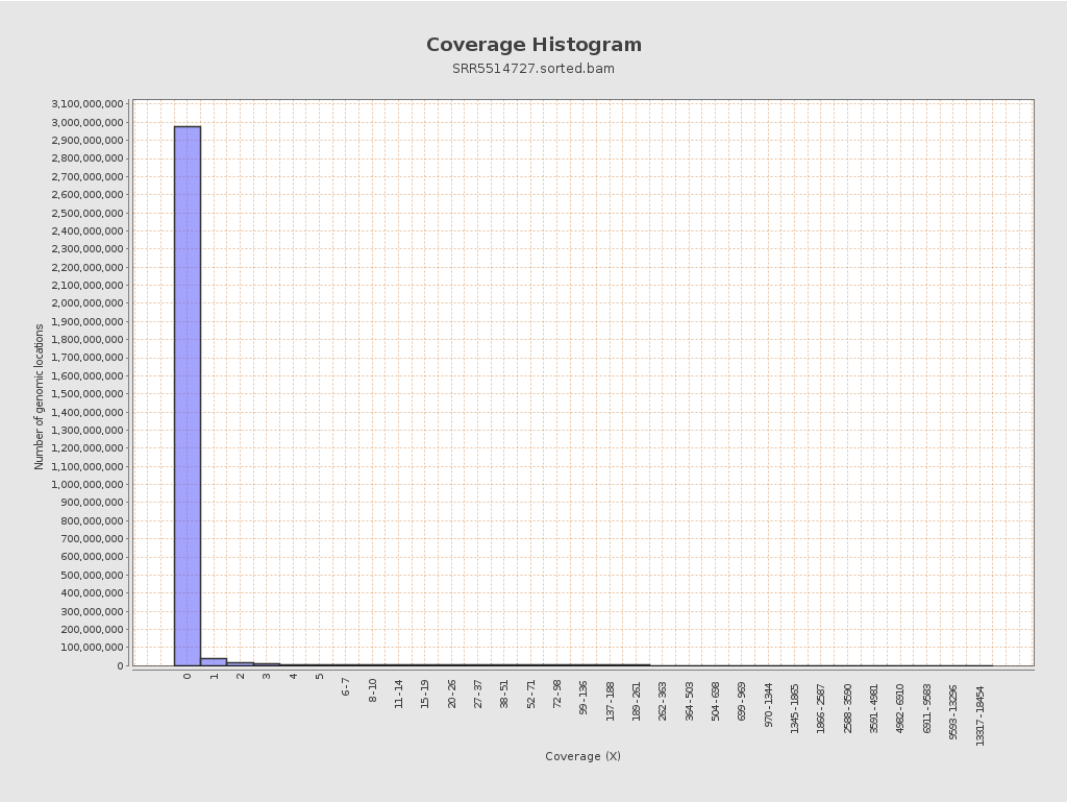
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	197417574	0.792	35.9566
chr2	243199373	260016316	1.0691	26.2011
chr3	198022430	282712419	1.4277	42.4796
chr4	191154276	939566903	4.9152	73.597
chr5	180915260	142528608	0.7878	12.4017
chr6	171115067	75201677	0.4395	9.743
chr7	159138663	199461899	1.2534	55.4404

chr8	146364022	70842216	0.484	17.7077
chr9	141213431	102643241	0.7269	17.458
chr10	135534747	273056833	2.0147	46.2646
chr11	135006516	147060770	1.0893	18.747
chr12	133851895	256336628	1.9151	20.749
chr13	115169878	50956883	0.4424	19.1536
chr14	107349540	65965924	0.6145	11.2326
chr15	102531392	302591949	2.9512	46.5484
chr16	90354753	61065296	0.6758	21.0333
chr17	81195210	189137611	2.3294	47.4537
chr18	78077248	25235164	0.3232	8.3658
chr19	59128983	121556943	2.0558	29.2951
chr20	63025520	28102609	0.4459	16.7714
chr21	48129895	23487766	0.488	20.3129
chr22	51304566	144685952	2.8201	28.3654
chrMT	16571	2115372	127.6551	63.1947
chrX	155270560	50287183	0.3239	13.0746
chrY	59373566	13988159	0.2356	21.0481

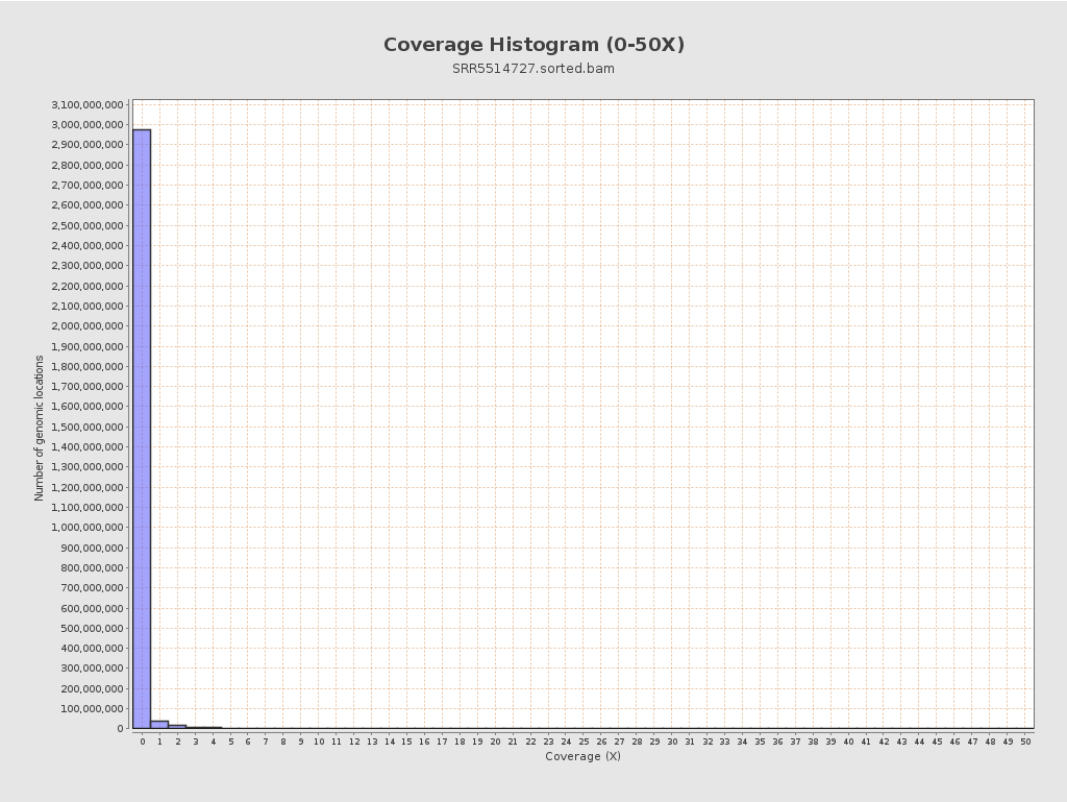
3. Results : Coverage across reference



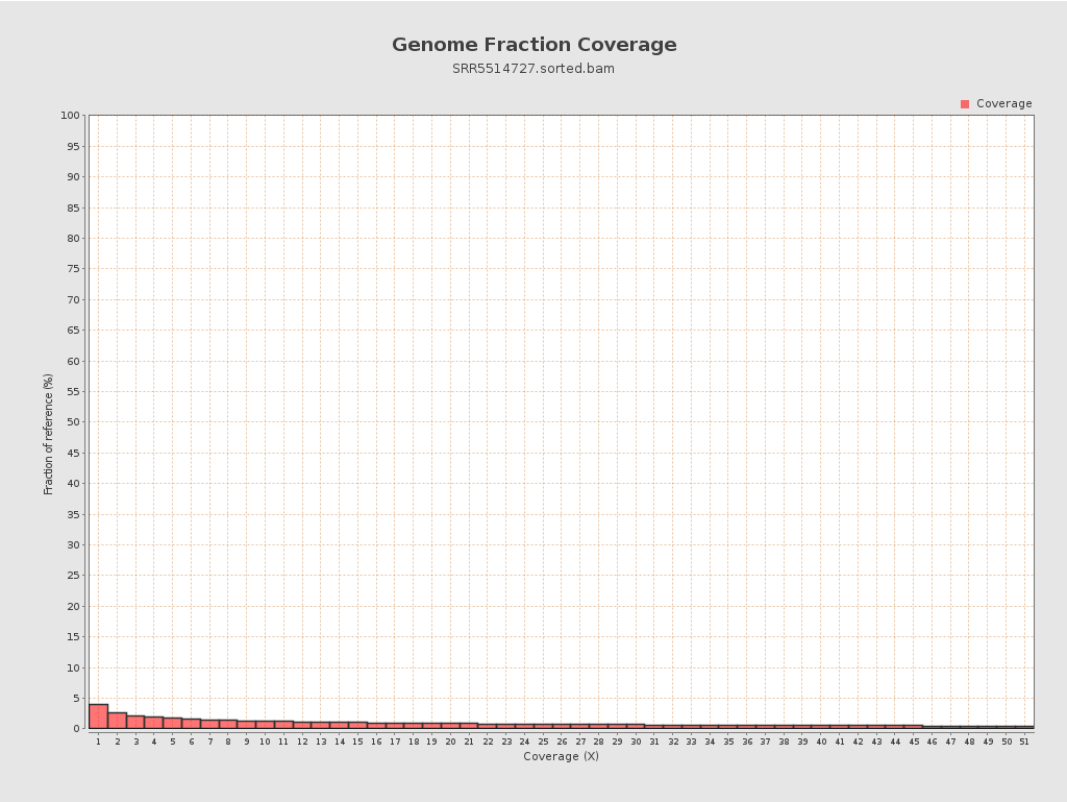
4. Results : Coverage Histogram



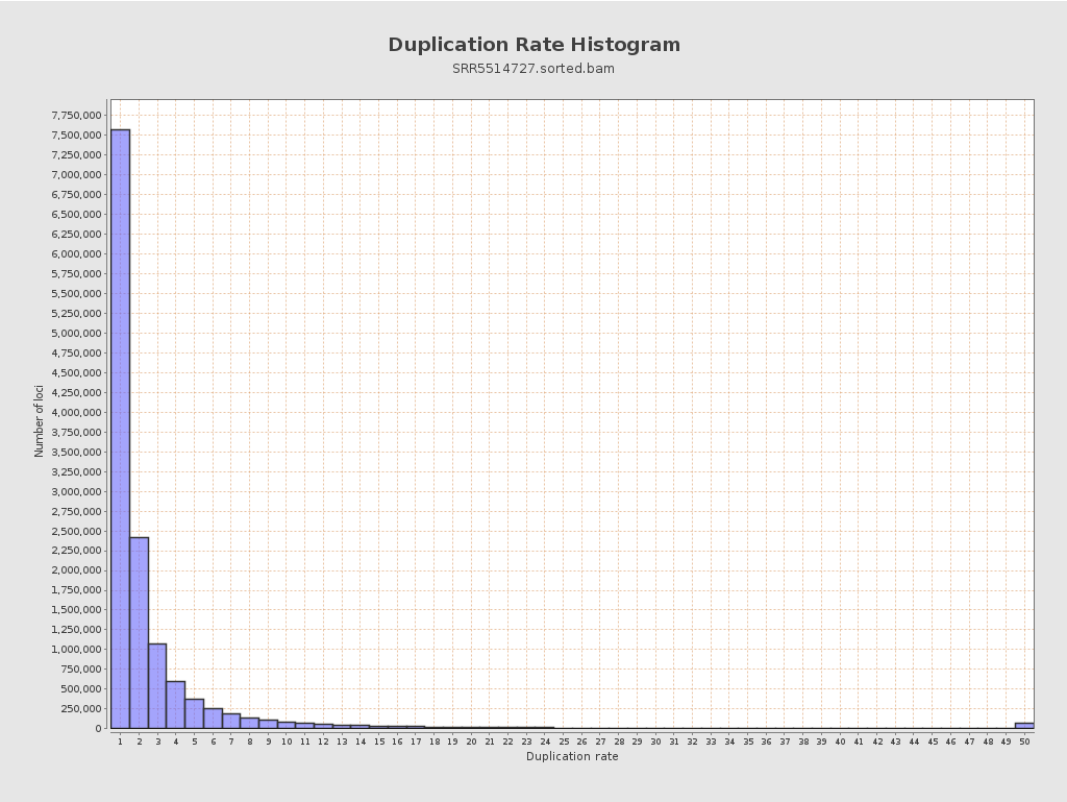
5. Results : Coverage Histogram (0-50X)



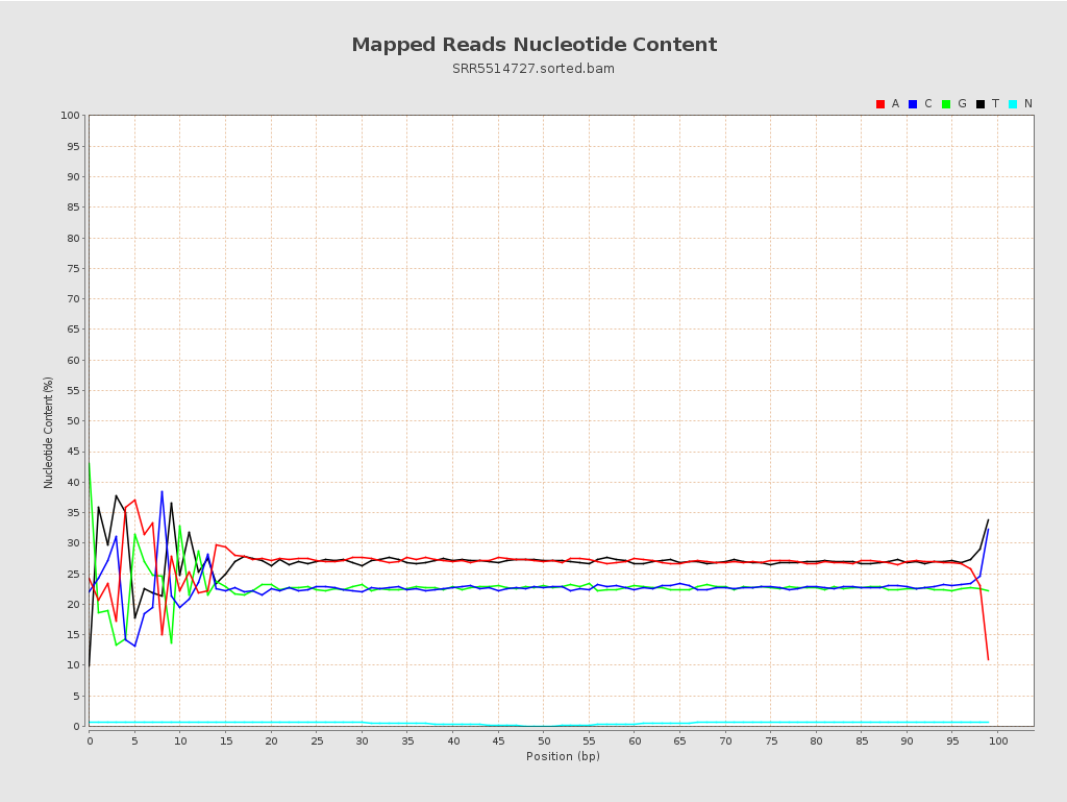
6. Results : Genome Fraction Coverage



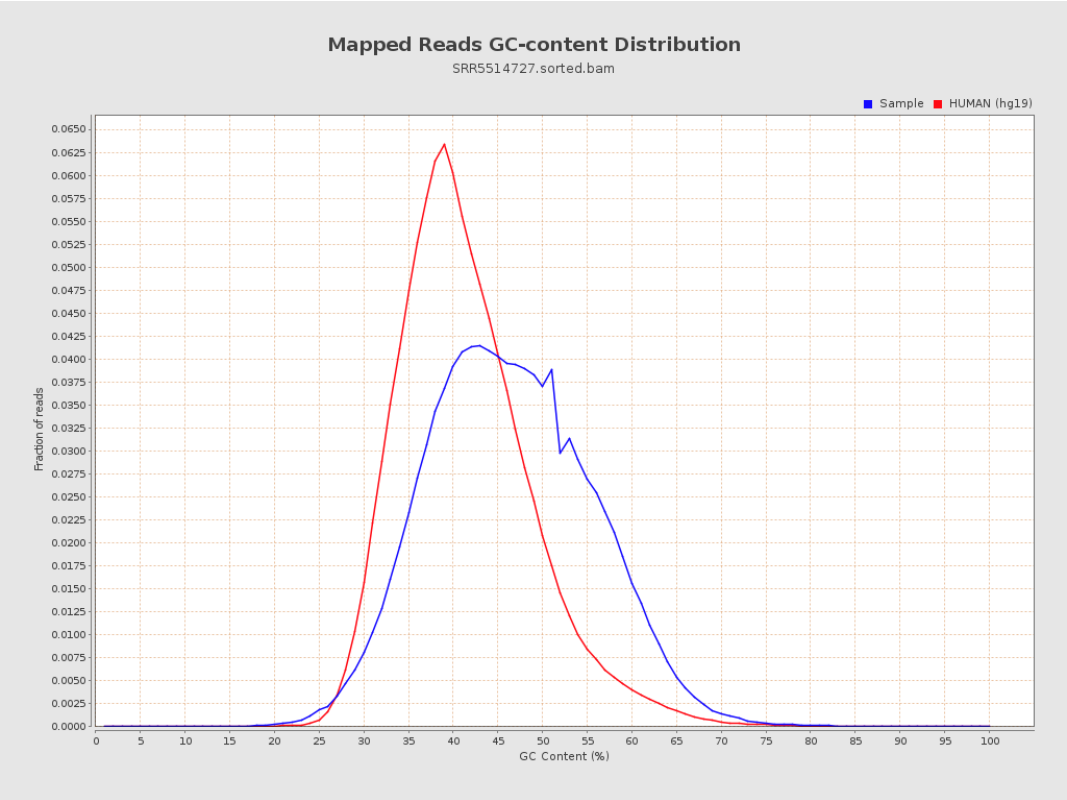
7. Results : Duplication Rate Histogram



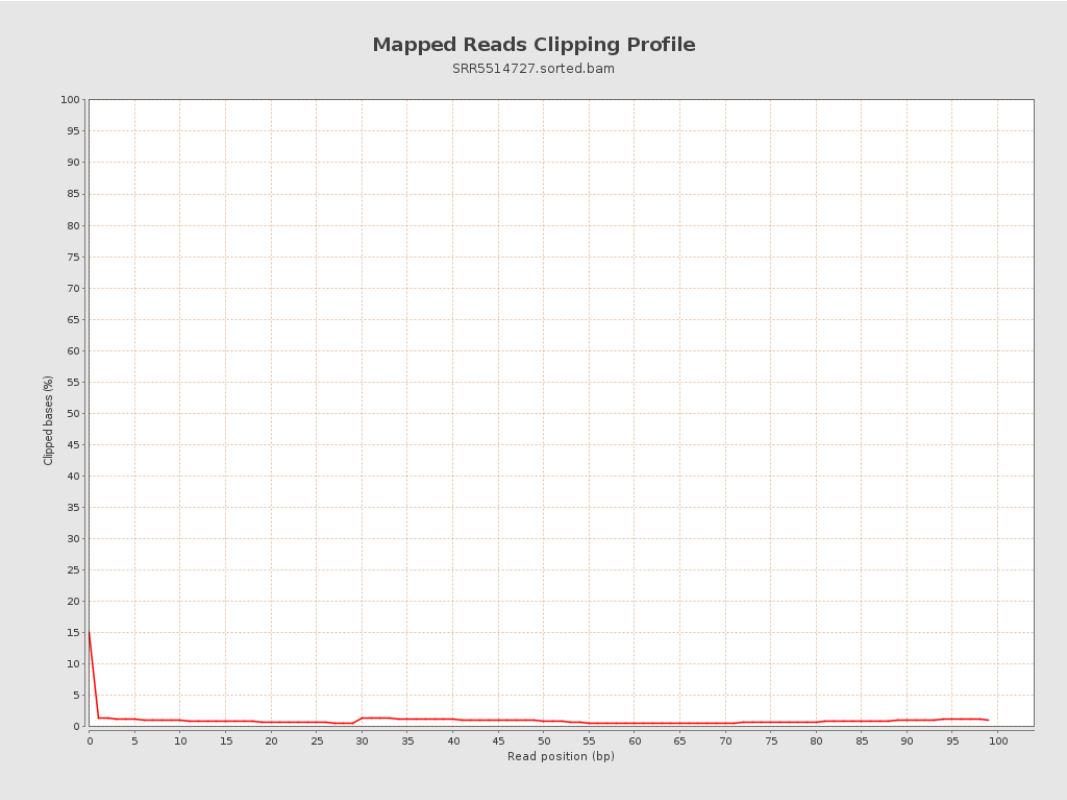
8. Results : Mapped Reads Nucleotide Content



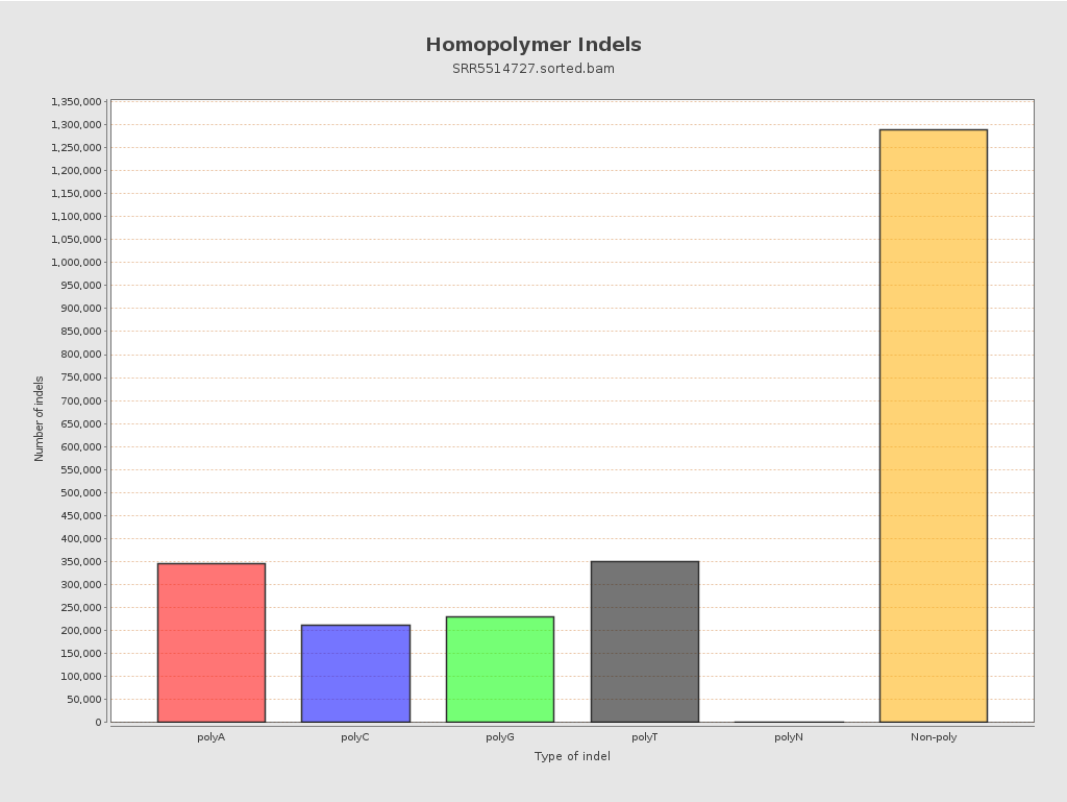
9. Results : Mapped Reads GC-content Distribution



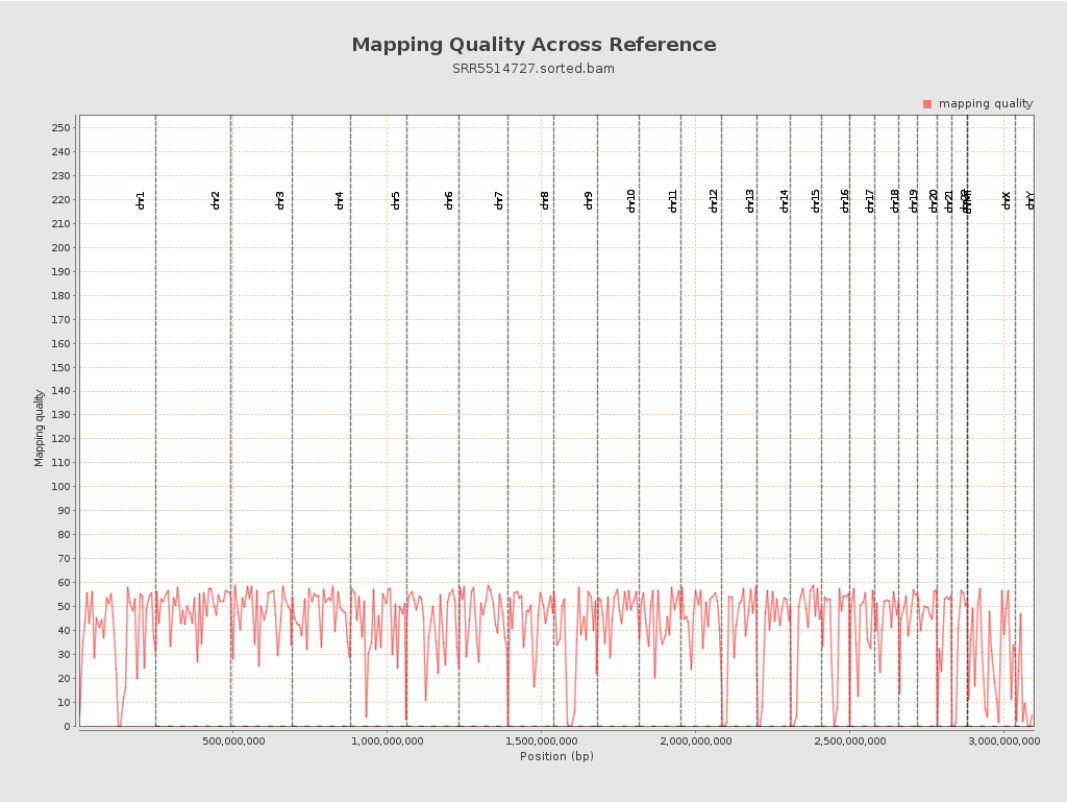
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram