Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/18 19:22:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR536747.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_SRR536747 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR536747.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Mar 18 19:22:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR536747.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	17,356,496
Mapped reads	14,100,743 / 81.24%
Unmapped reads	3,255,753 / 18.76%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	256 / 0%
Read min/max/mean length	30 / 50 / 50
Duplicated reads (estimated)	86,251 / 0.5%
Duplication rate	0.61%
Clipped reads	227,677 / 1.31%

2.2. ACGT Content

Number/percentage of A's	217,459,953 / 30.93%
Number/percentage of C's	133,675,866 / 19.01%
Number/percentage of T's	215,730,546 / 30.68%
Number/percentage of G's	136,291,817 / 19.38%
Number/percentage of N's	15,150 / 0%
GC Percentage	38.39%

2.3. Coverage

Mean	0.2272

Standard Deviation	0.5209

2.4. Mapping Quality

Mean Mapping Quality	47.17

2.5. Mismatches and indels

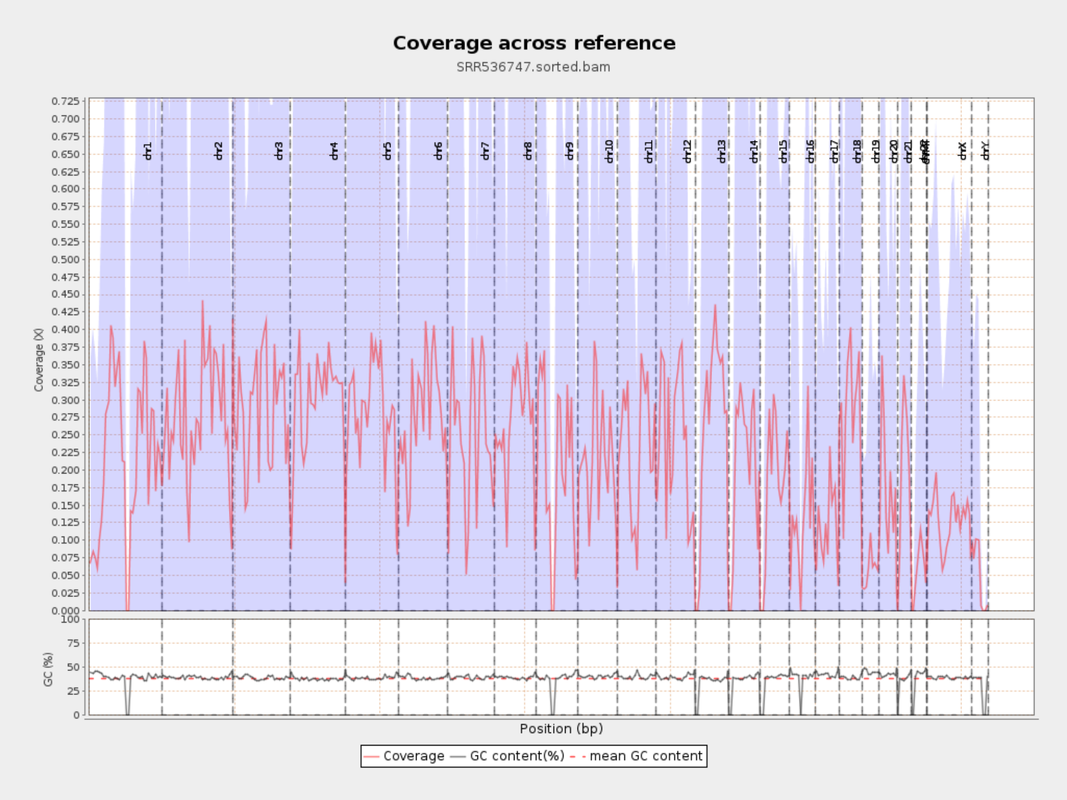
General error rate	0.35%
Mismatches	2,433,864
Insertions	45,368
Mapped reads with at least one insertion	0.32%
Deletions	33,614
Mapped reads with at least one deletion	0.24%
Homopolymer indels	49.46%

2.6. Chromosome stats

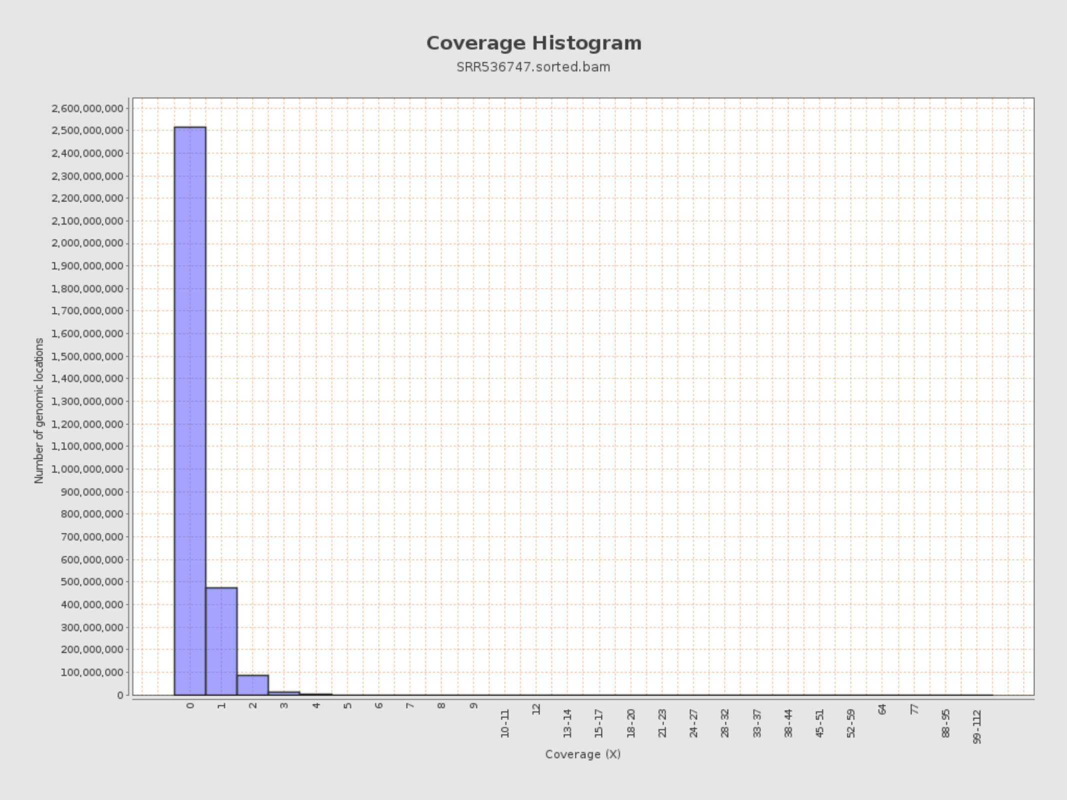
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	54149165	0.2172	0.5143
chr2	243199373	67029111	0.2756	0.567
chr3	198022430	57433240	0.29	0.58
chr4	191154276	57829978	0.3025	0.5896
chr5	180915260	51386746	0.284	0.5731
chr6	171115067	47713040	0.2788	0.5696
chr7	159138663	40598224	0.2551	0.5515

chr8	146364022	39815835	0.272	0.5617
chr9	141213431	29550793	0.2093	0.5054
chr10	135534747	30144101	0.2224	0.5069
chr11	135006516	31872788	0.2361	0.5279
chr12	133851895	32175442	0.2404	0.5335
chr13	115169878	30529892	0.2651	0.5639
chr14	107349540	21907215	0.2041	0.4964
chr15	102531392	18295597	0.1784	0.465
chr16	90354753	11812017	0.1307	0.3934
chr17	81195210	9478314	0.1167	0.3736
chr18	78077248	22345995	0.2862	0.5782
chr19	59128983	3547468	0.06	0.2598
chr20	63025520	11099088	0.1761	0.4599
chr21	48129895	9133944	0.1898	0.4882
chr22	51304566	2927370	0.0571	0.2553
chrMT	16571	1695	0.1023	0.3115
chrX	155270560	19722832	0.127	0.3709
chrY	59373566	2728267	0.046	0.23

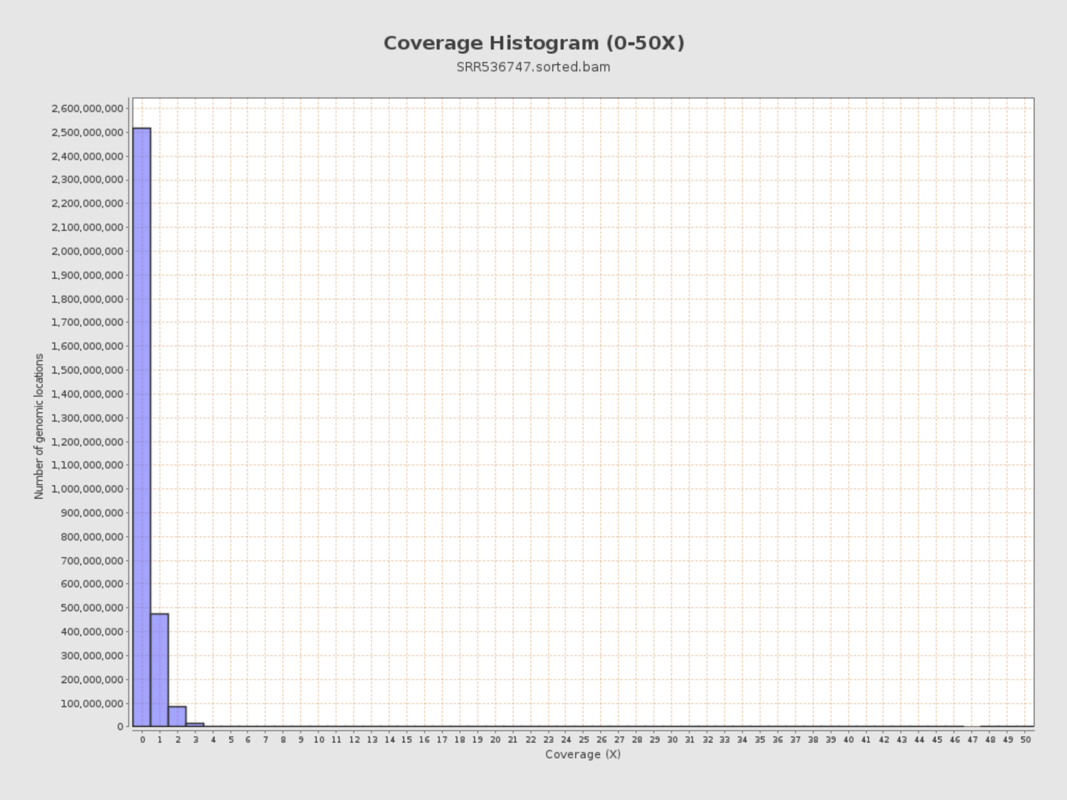
3. Results : Coverage across reference



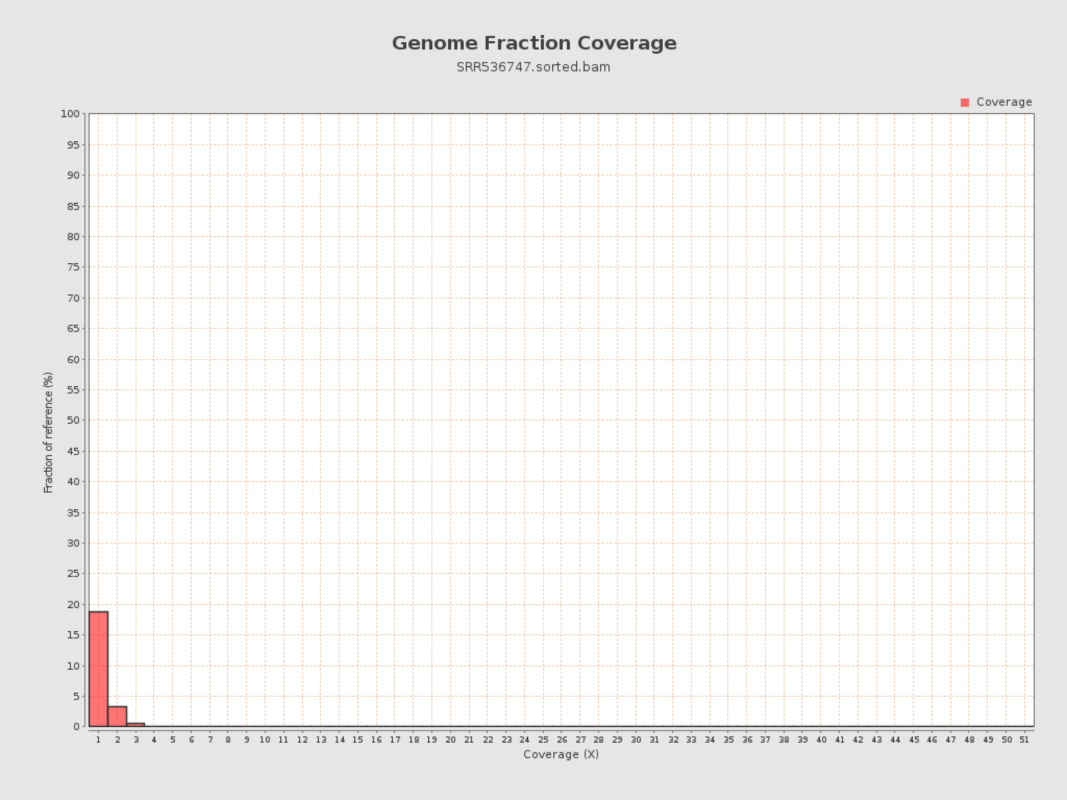
4. Results : Coverage Histogram



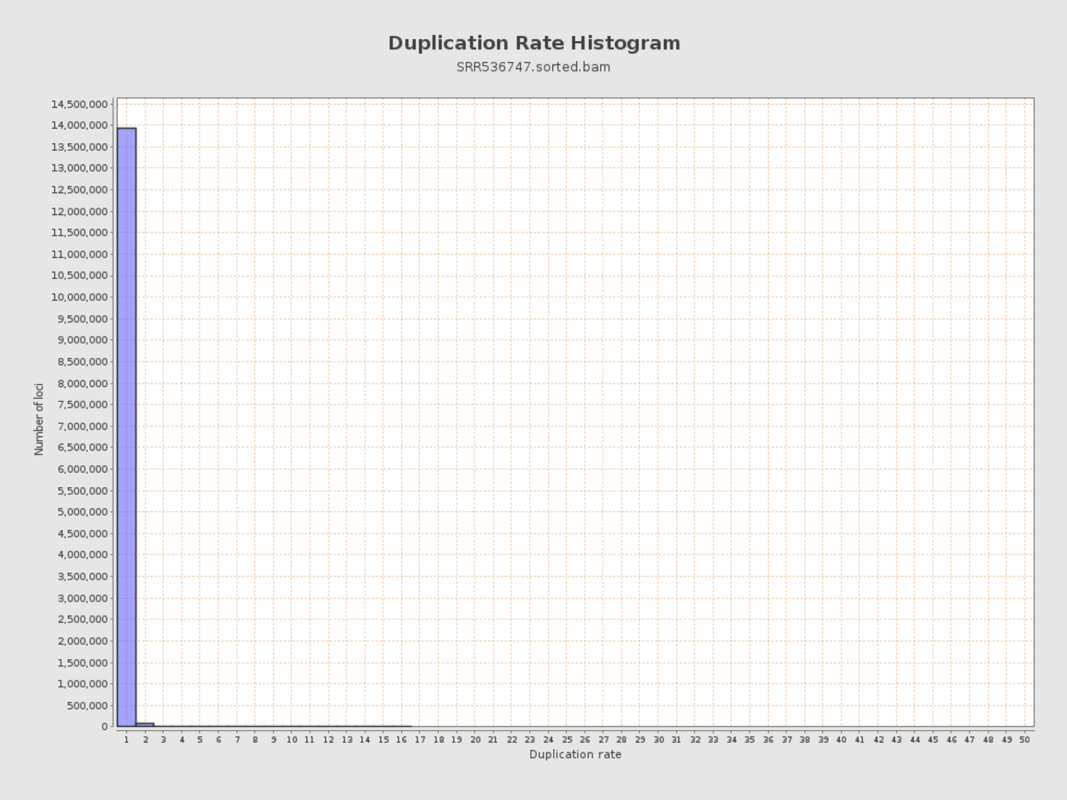
5. Results : Coverage Histogram (0-50X)



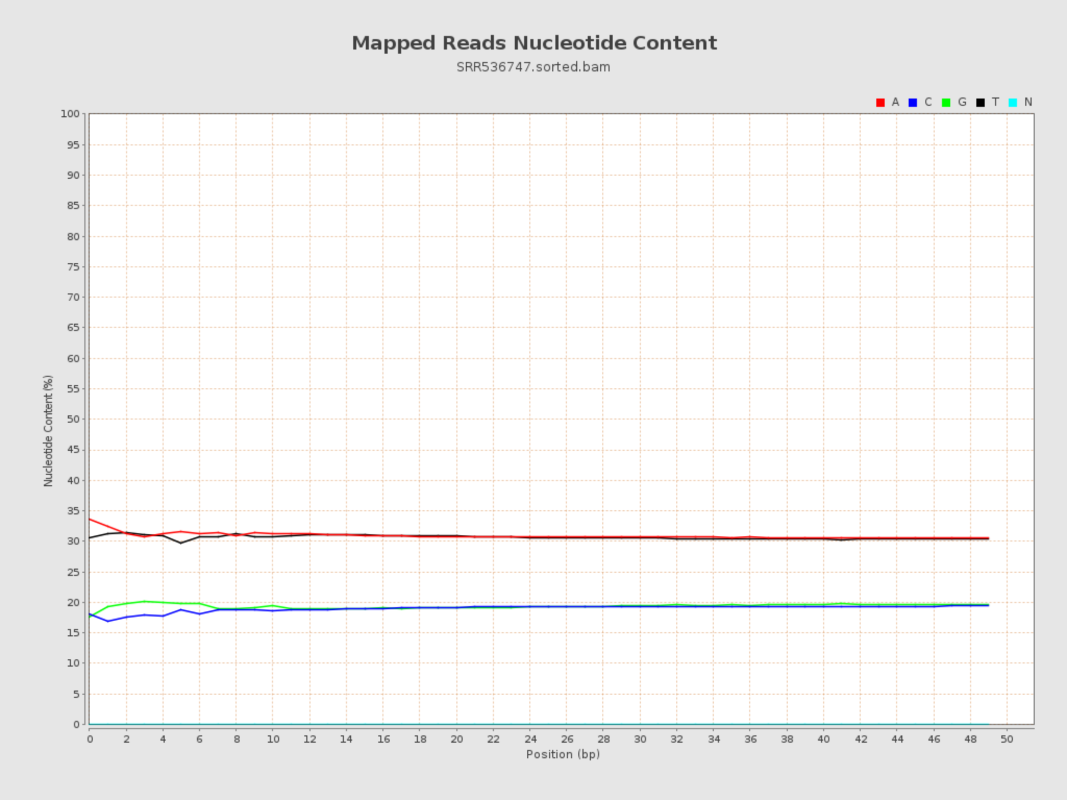
6. Results : Genome Fraction Coverage



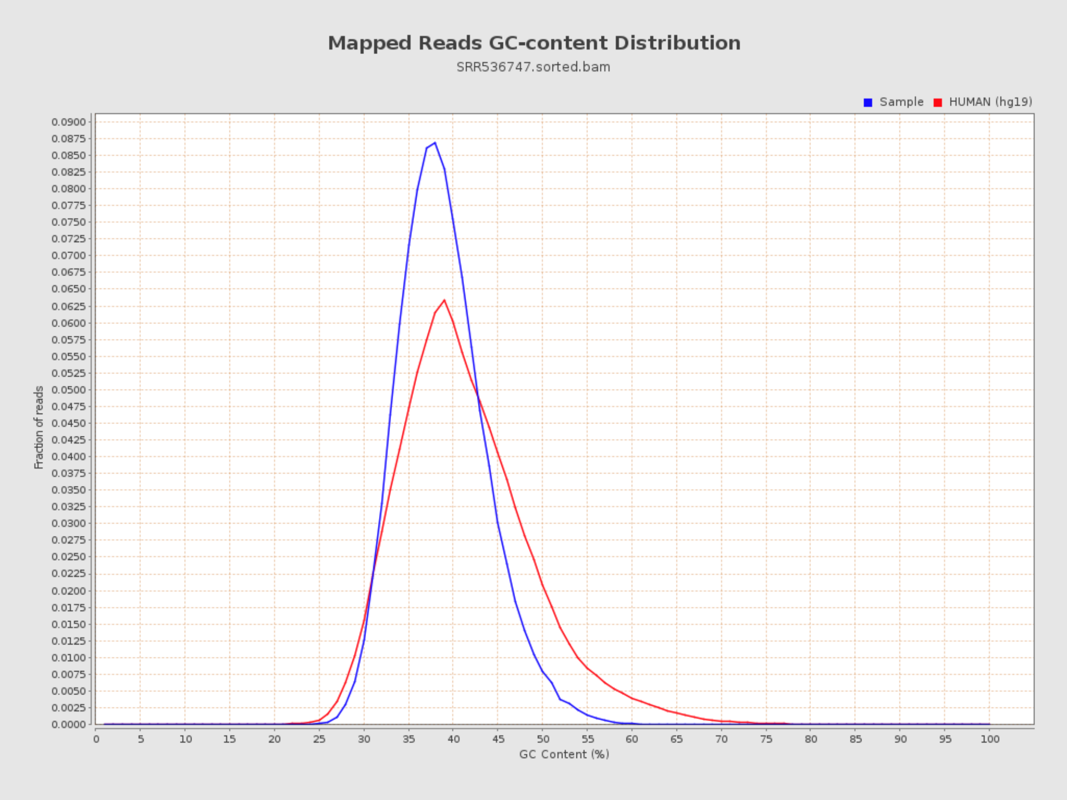
7. Results : Duplication Rate Histogram



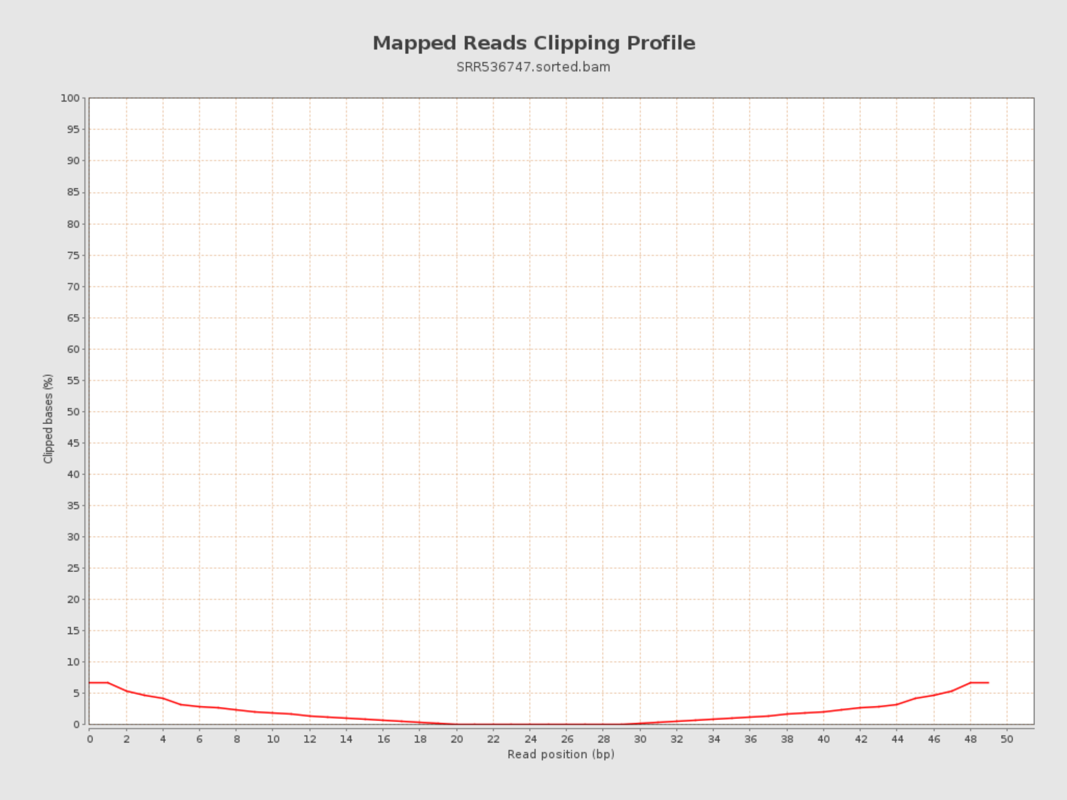
8. Results : Mapped Reads Nucleotide Content



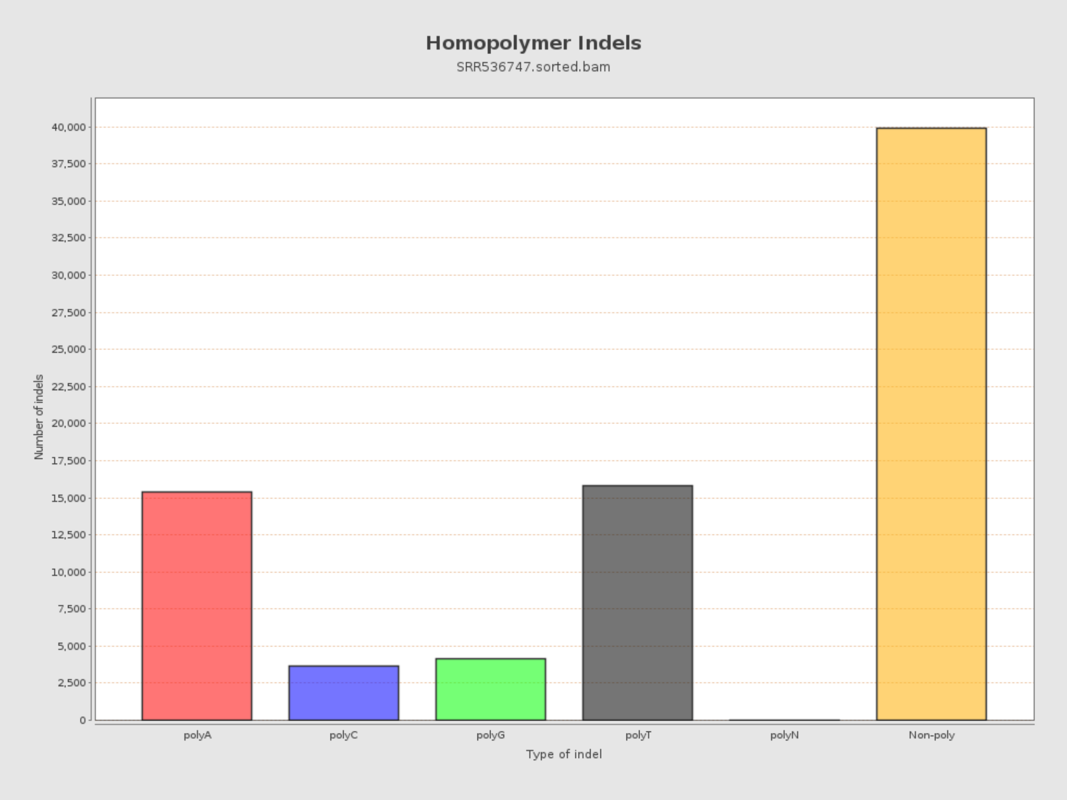
9. Results : Mapped Reads GC-content Distribution



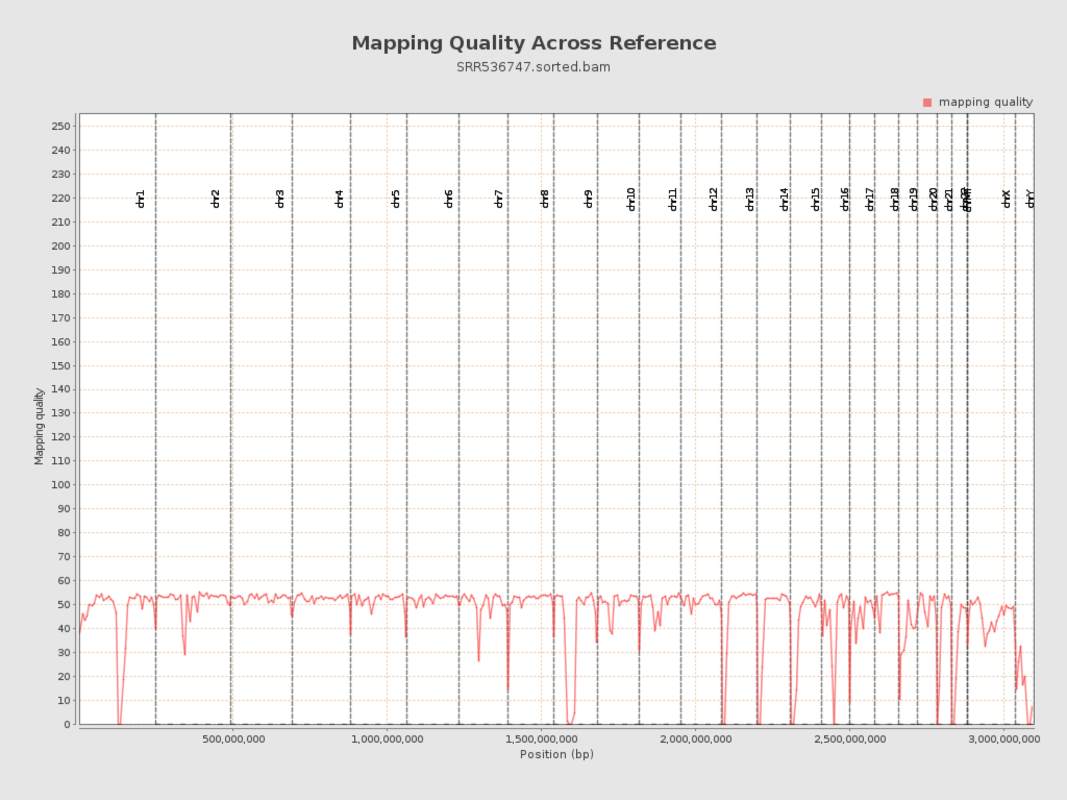
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram