

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2021/01/12 16:15:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam /opt/tsinghua/zhangwei/Pipeline_test/o_WGS-
PE/intermediate_result/step_05_bamsort/H1284-Pre_sorted.bam -nw 400 -
hm 3
```

1.2. Alignment

Command line:	"/home/zhangwei/software/miniconda3/envs/cfDNApipe/bin/bowtie2-align-s --wrapper basic-0 -x /home/zhangwei/Genome/hg19_bowtie2/hg19 -q -N 1 --time -p 60 --passthrough -1 /opt/tsinghua/zhangwei/Pipeline_test/o_WGS-PE/intermediate_result/step_03_adapterremoval/H1284-Pre.pair1.truncated.gz -2 /opt/tsinghua/zhangwei/Pipeline_test/o_WGS-PE/intermediate_result/step_03_adapterremoval/H1284-Pre.pair2.truncated.gz"
Draw chromosome limits:	no
Analyze overlapping paired-end reads:	no
Program:	bowtie2 (2.4.2)
Analysis date:	Tue Jan 12 16:15:29 CST 2021
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400

BAM file:

/opt/tsinghua/zhangwei/Pipeline_test/
o_WGS-
PE/intermediate_result/step_05_bam
sort/H1284-Pre_sorted.bam

2. Summary

2.1. Globals

Reference size	3,137,161,264
Number of reads	1,993,610
Mapped reads	1,872,193 / 93.91%
Unmapped reads	121,417 / 6.09%
Mapped paired reads	1,872,193 / 93.91%
Mapped reads, first in pair	940,704 / 47.19%
Mapped reads, second in pair	931,489 / 46.72%
Mapped reads, both in pair	1,854,122 / 93%
Mapped reads, singletons	18,071 / 0.91%
Secondary alignments	0
Read min/max/mean length	15 / 150 / 146.09
Duplicated reads (estimated)	196,089 / 9.84%
Duplication rate	11.03%
Clipped reads	0 / 0%

2.2. ACGT Content

Number/percentage of A's	79,162,934 / 28.97%
Number/percentage of C's	57,475,361 / 21.03%
Number/percentage of T's	79,239,719 / 29%
Number/percentage of G's	57,390,080 / 21%
Number/percentage of N's	6,786 / 0%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0871
Standard Deviation	0.6815

2.4. Mapping Quality

Mean Mapping Quality	32.17
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2.5. Insert size

Mean	10,053.98
Standard Deviation	987,275.68
P25/Median/P75	156 / 169 / 182

2.6. Mismatches and indels

General error rate	0.65%
Mismatches	1,656,650
Insertions	39,503
Mapped reads with at least one insertion	1.92%
Deletions	35,799
Mapped reads with at least one deletion	1.82%
Homopolymer indels	60.98%

2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

chr1	249250621	22473505	0.0902	1.2981
chr2	243199373	22779615	0.0937	0.4749
chr3	198022430	18039108	0.0911	0.4114
chr4	191154276	17233063	0.0902	0.422
chr5	180915260	16636566	0.092	0.4067
chr6	171115067	15490776	0.0905	0.5525
chr7	159138663	15168340	0.0953	0.8222
chr8	146364022	13602486	0.0929	0.436
chr9	141213431	11430401	0.0809	0.4044
chr10	135534747	14058934	0.1037	1.4378
chr11	135006516	12642494	0.0936	0.4529
chr12	133851895	12257726	0.0916	0.4048
chr13	115169878	8685791	0.0754	0.3686
chr14	107349540	8494347	0.0791	0.3778
chr15	102531392	8231225	0.0803	0.3817
chr16	90354753	8444263	0.0935	0.6345
chr17	81195210	7854195	0.0967	0.49
chr18	78077248	7184450	0.092	0.589
chr19	59128983	5819385	0.0984	1.1007
chr20	63025520	6006863	0.0953	0.4134
chr21	48129895	3552864	0.0738	0.4842
chr22	51304566	3599494	0.0702	0.3808
chrX	155270560	7415778	0.0478	0.3225
chrY	59373566	2348203	0.0395	0.649

chrM	16571	9618	0.5804	0.9926
chr1_gl00019 1_random	106433	5956	0.056	0.3081
chr1_gl00019 2_random	547496	49255	0.09	0.4044
chr4_ctg9_ha p1	590426	24023	0.0407	0.2717
chr4_gl00019 3_random	189789	48187	0.2539	0.8095
chr4_gl00019 4_random	191469	38784	0.2026	0.6229
chr6_apd_ha p1	4622290	29288	0.0063	0.104
chr6_cox_hap 2	4795371	76049	0.0159	0.1665
chr6_dbb_ha p3	4610396	63555	0.0138	0.1568
chr6_mann_h ap4	4683263	54967	0.0117	0.1435
chr6_mcf_ha p5	4833398	55733	0.0115	0.1458
chr6_qbl_hap 6	4611984	55614	0.0121	0.1478
chr6_ssto_ha p7	4928567	59596	0.0121	0.1461
chr7_gl00019 5_random	182896	65003	0.3554	0.8169
chr8_gl00019 6_random	38914	1803	0.0463	0.2862

chr8_gl00019 7_random	37175	1934	0.052	0.2946
chr9_gl00019 8_random	90085	27947	0.3102	0.8094
chr9_gl00019 9_random	169874	602145	3.5447	10.2227
chr9_gl00020 0_random	187035	5750	0.0307	0.24
chr9_gl00020 1_random	36148	2250	0.0622	0.3066
chr11_gl0002 02_random	40103	3076	0.0767	0.3635
chr17_ctg5_h ap1	1680828	37654	0.0224	0.1989
chr17_gl0002 03_random	37498	3304	0.0881	0.3864
chr17_gl0002 04_random	81310	5408	0.0665	0.3385
chr17_gl0002 05_random	174588	54555	0.3125	0.795
chr17_gl0002 06_random	41001	1200	0.0293	0.2195
chr18_gl0002 07_random	4262	450	0.1056	0.3073
chr19_gl0002 08_random	92689	45785	0.494	1.5943
chr19_gl0002 09_random	159169	7930	0.0498	0.2886
chr21_gl0002 10_random	27682	2246	0.0811	0.3666

chrUn_gl0002 11	166566	23454	0.1408	0.5318
chrUn_gl0002 12	186858	97901	0.5239	7.5005
chrUn_gl0002 13	164239	6166	0.0375	0.2617
chrUn_gl0002 14	137718	115814	0.841	3.5927
chrUn_gl0002 15	172545	6668	0.0386	0.2734
chrUn_gl0002 16	172294	86585	0.5025	1.7764
chrUn_gl0002 17	172149	24764	0.1439	0.5077
chrUn_gl0002 18	161147	31008	0.1924	0.6529
chrUn_gl0002 19	179198	69824	0.3896	0.9115
chrUn_gl0002 20	161802	883193	5.4585	8.3053
chrUn_gl0002 21	155397	34749	0.2236	0.6636
chrUn_gl0002 22	186861	21101	0.1129	0.5865
chrUn_gl0002 23	180455	8544	0.0473	0.2868
chrUn_gl0002 24	179693	173121	0.9634	2.4874
chrUn_gl0002 25	211173	283446	1.3422	2.8478

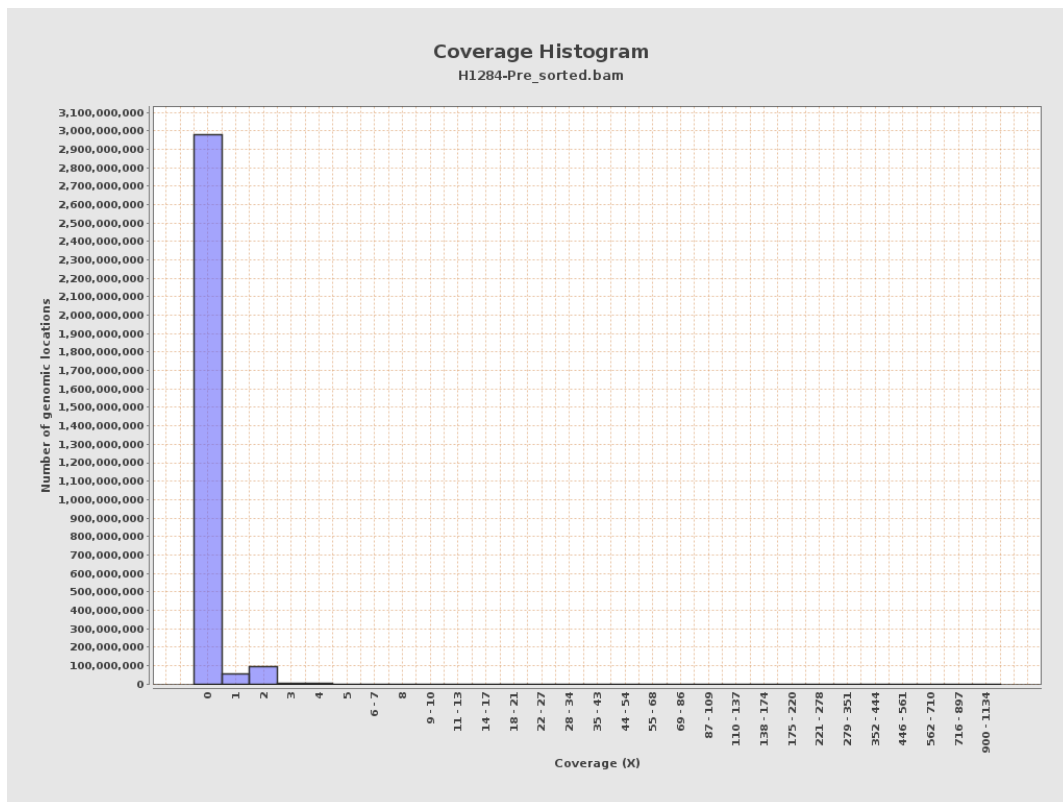
chrUn_gl0002 26	15008	390372	26.0109	21.3529
chrUn_gl0002 27	128374	8235	0.0641	0.3872
chrUn_gl0002 28	129120	47594	0.3686	2.5351
chrUn_gl0002 29	19913	6835	0.3432	0.8968
chrUn_gl0002 30	43691	3850	0.0881	0.3933
chrUn_gl0002 31	27386	6263	0.2287	0.6639
chrUn_gl0002 32	40652	18860	0.4639	0.9574
chrUn_gl0002 33	45941	5655	0.1231	0.5109
chrUn_gl0002 34	40531	20674	0.5101	0.9399
chrUn_gl0002 35	34474	10681	0.3098	1.0479
chrUn_gl0002 36	41934	3236	0.0772	0.3644
chrUn_gl0002 37	45867	12533	0.2732	0.7025
chrUn_gl0002 38	39939	3336	0.0835	0.4108
chrUn_gl0002 39	33824	8972	0.2653	0.7719
chrUn_gl0002 40	41933	5063	0.1207	0.4705

chrUn_gl0002 41	42152	15479	0.3672	0.8277
chrUn_gl0002 42	43523	1188	0.0273	0.2243
chrUn_gl0002 43	43341	11131	0.2568	0.7457
chrUn_gl0002 44	39929	3412	0.0855	0.3787
chrUn_gl0002 45	36651	9126	0.249	0.6425
chrUn_gl0002 46	38154	1200	0.0315	0.2351
chrUn_gl0002 47	36422	4981	0.1368	0.4813
chrUn_gl0002 48	39786	3126	0.0786	0.3716
chrUn_gl0002 49	38502	1382	0.0359	0.2576

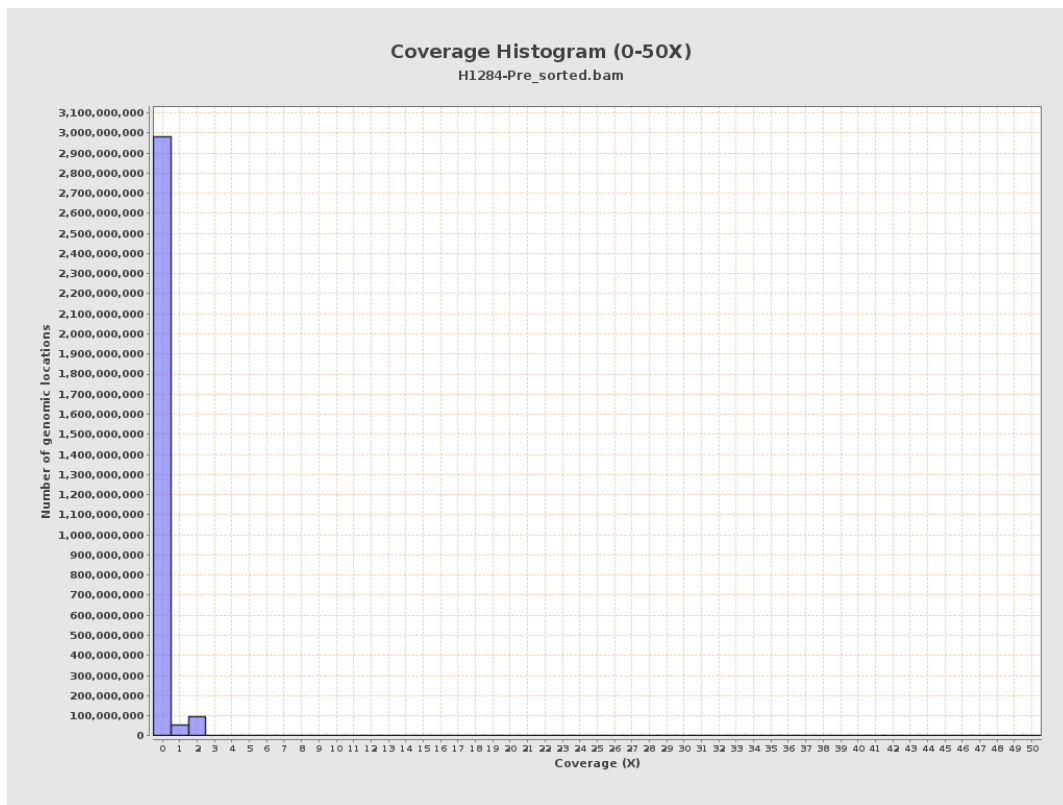
3. Results : Coverage across reference



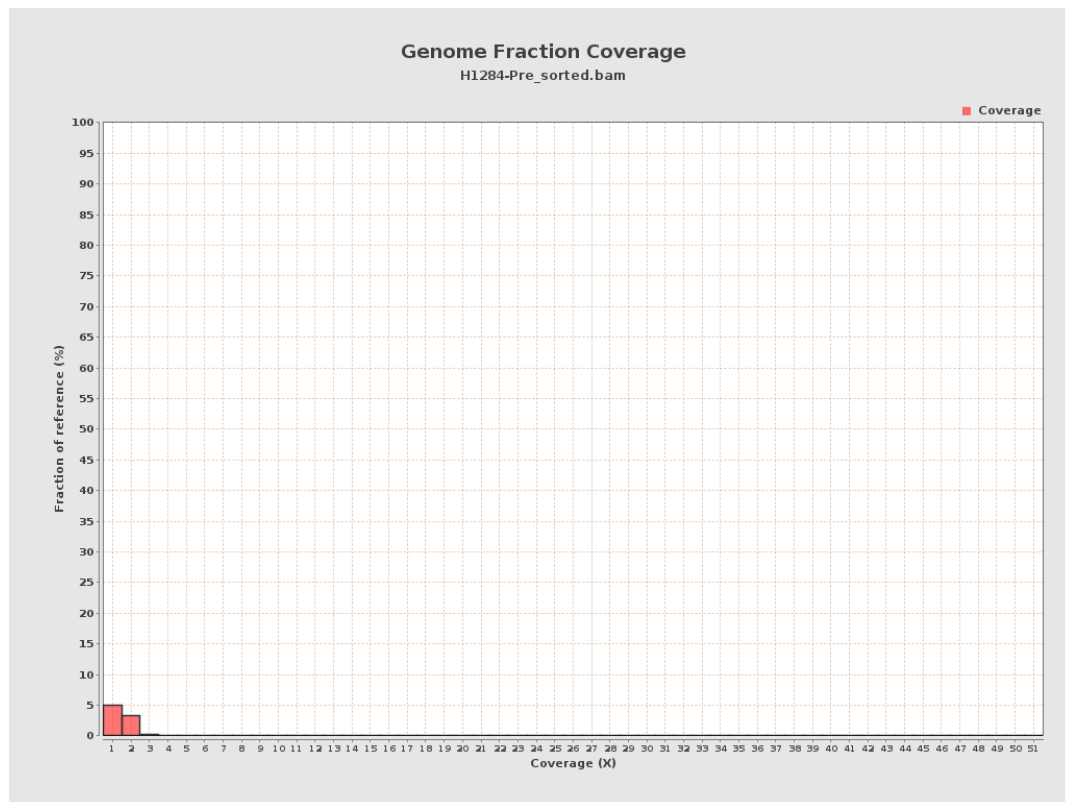
4. Results : Coverage Histogram



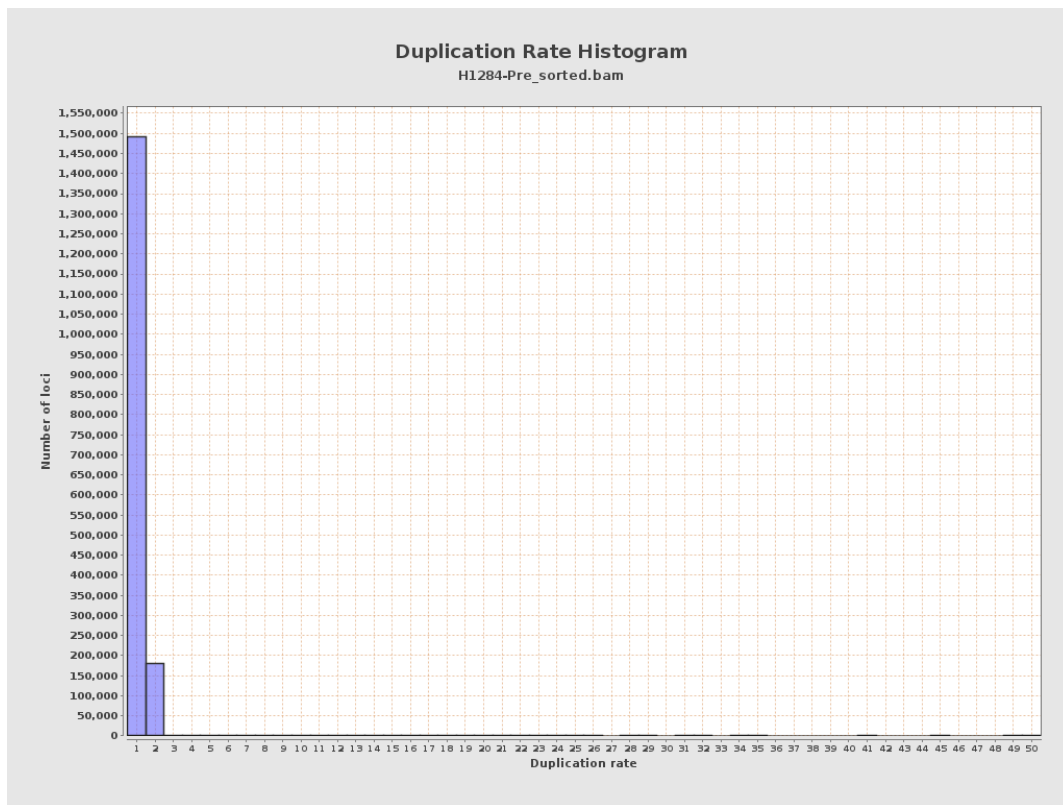
5. Results : Coverage Histogram (0-50X)



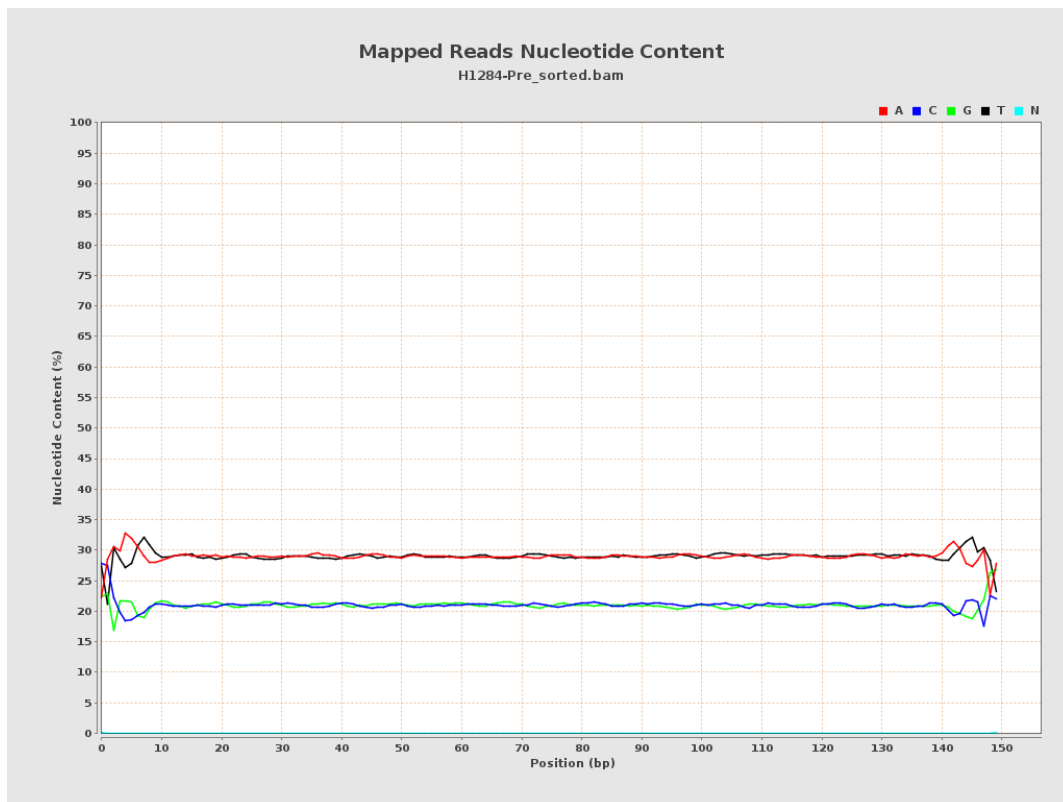
6. Results : Genome Fraction Coverage



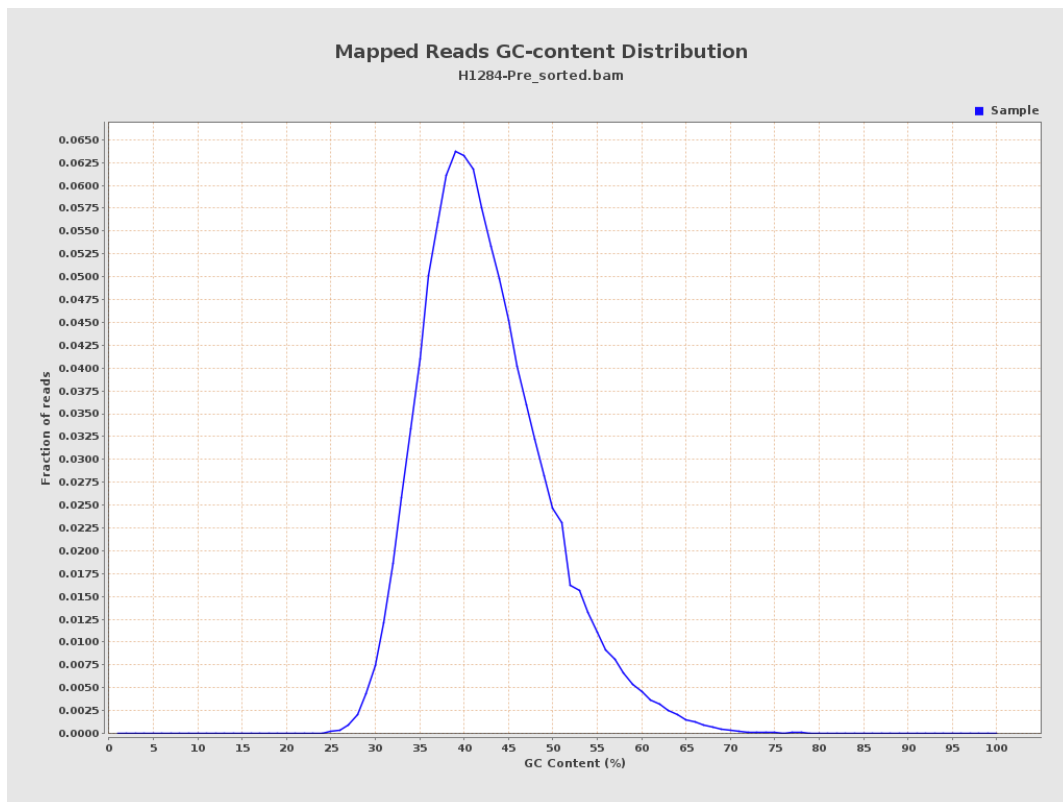
7. Results : Duplication Rate Histogram



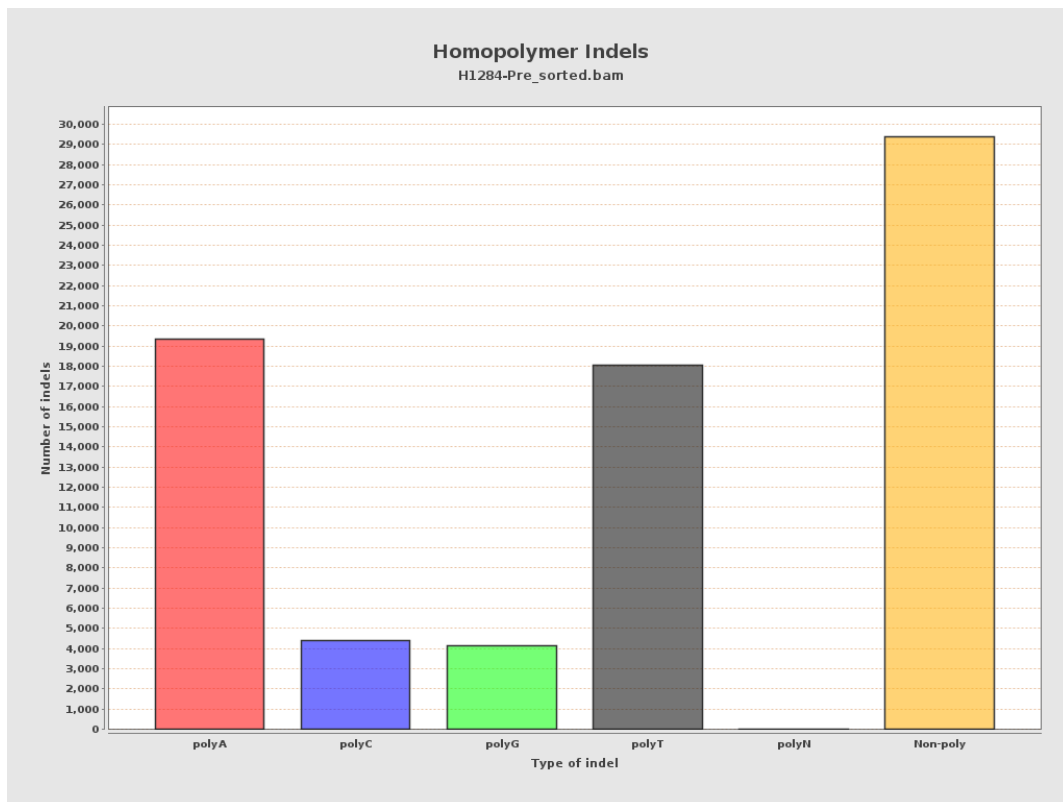
8. Results : Mapped Reads Nucleotide Content



9. Results : Mapped Reads GC-content Distribution



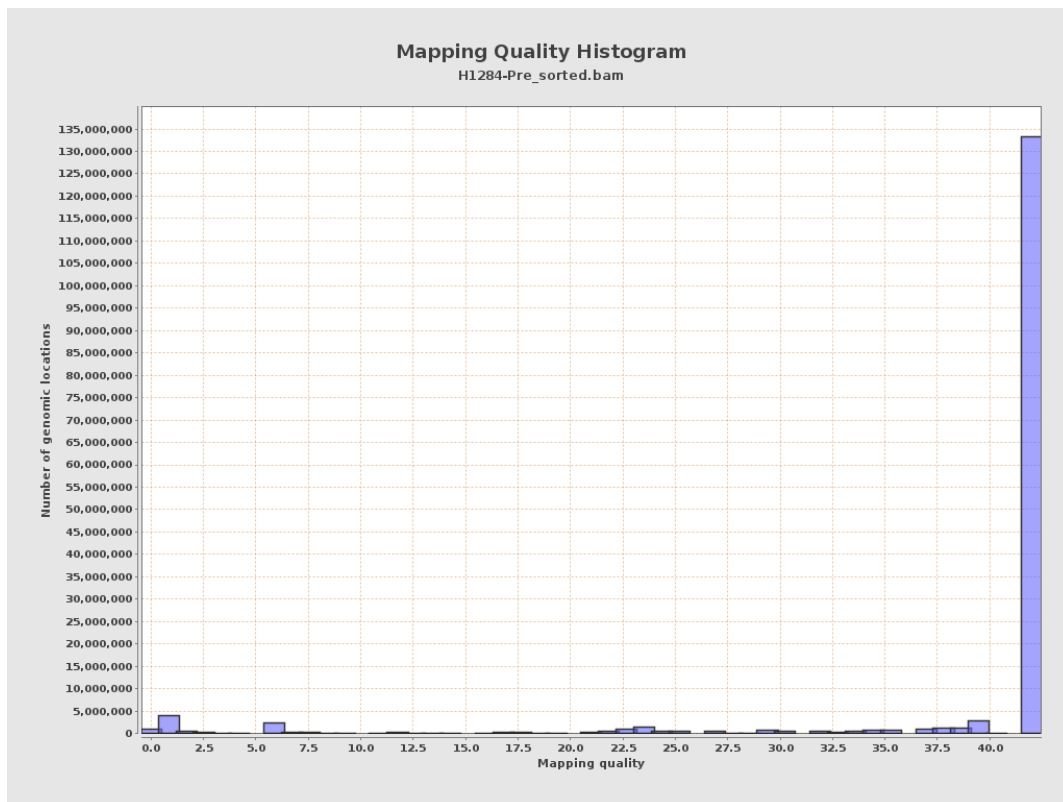
10. Results : Homopolymer Indels



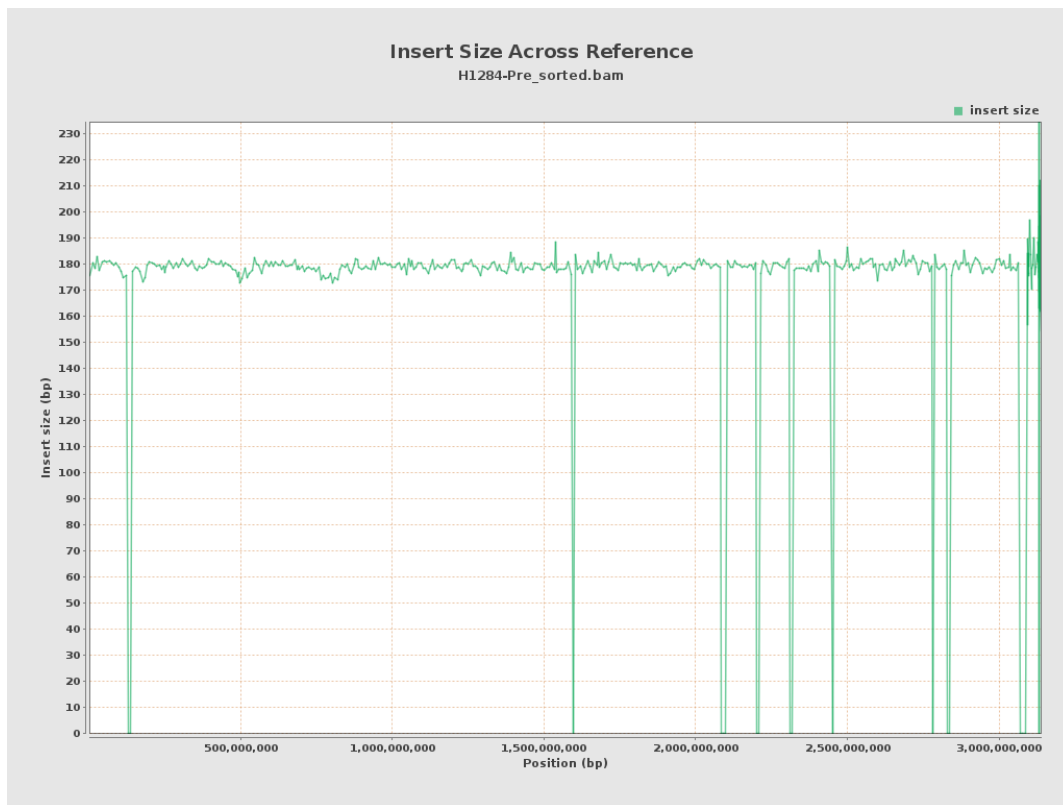
11. Results : Mapping Quality Across Reference



12. Results : Mapping Quality Histogram



13. Results : Insert Size Across Reference



14. Results : Insert Size Histogram

