Table S1. The QV value assessment by Merqury.

| Chr | length (bp) | K-mers in genome only | common K-mers in both | QV | error possiblity |
|---|---|---|---|---|---|
| Chr01 | 20702373 | 171 | 20702357 | 63.1347 | 4.86E-07 |
| Chr02 | 8410284 | 9 | 8410268 | 72.0102 | 6.29E-08 |
| Chr03 | 15280781 | 864 | 15280765 | 54.7807 | 3.33E-06 |
| Chr04 | 19018323 | 128 | 19018307 | 64.0241 | 3.96E-07 |
| Chr05 | 19017521 | 468 | 19017505 | 58.3935 | 1.45E-06 |
| Chr06 | 16775540 | 273 | 16775524 | 60.1896 | 9.57E-07 |
| Chr07 | 14042223 | 343 | 14042207 | 58.4259 | 1.44E-06 |
| Chr08 | 16314353 | 2 | 16314337 | 81.4199 | 7.21E-09 |
| Chr09 | 16821697 | 451 | 16821681 | 58.0214 | 1.58E-06 |
| Chr10 | 17761834 | 233 | 17761818 | 61.1258 | 7.72E-07 |
| Chr11 | 21704787 | 2725 | 21704787 | 51.3161 | 7.38E-06 |
| Chr12 | 17837365 | 84 | 17837349 | 65.575 | 2.77E-07 |
| Chr13 | 17878236 | 53 | 17878220 | 67.585 | 1.74E-07 |
| Chr14 | 13548894 | 9 | 13548878 | 74.0811 | 3.91E-08 |
| Chr15 | 18557905 | 6 | 18557889 | 77.2083 | 1.90E-08 |
| Chr16 | 14425536 | 8 | 14425520 | 74.8649 | 3.26E-08 |
| Chr17 | 16893552 | 122 | 16893536 | 63.7181 | 4.25E-07 |
| Chr18 | 15944915 | 60 | 15944899 | 66.5492 | 2.21E-07 |
| Chr19 | 15019242 | 2 | 15019226 | 81.0607 | 7.83E-09 |
| Chr20 | 12704505 | 400 | 12704489 | 57.3234 | 1.85E-06 |
| Chr21 | 15389305 | 21 | 15389289 | 70.9545 | 8.03E-08 |
| Chr22 | 18521747 | 46 | 18521731 | 68.3537 | 1.46E-07 |
| Chr23 | 21555315 | 29 | 21555299 | 71.016 | 7.91E-08 |
| Chr24 | 18056436 | 184 | 18056420 | 62.2226 | 5.99E-07 |
| Chr25 | 14611429 | 556 | 14611413 | 56.5006 | 2.24E-06 |
| Chr26 | 11594696 | 0 | 11594680 | inf | 0 |
| Chr27 | 10985051 | 640 | 10985035 | 54.6506 | 3.43E-06 |
| Chr28 | 10634025 | 28 | 10634009 | 68.0999 | 1.55E-07 |

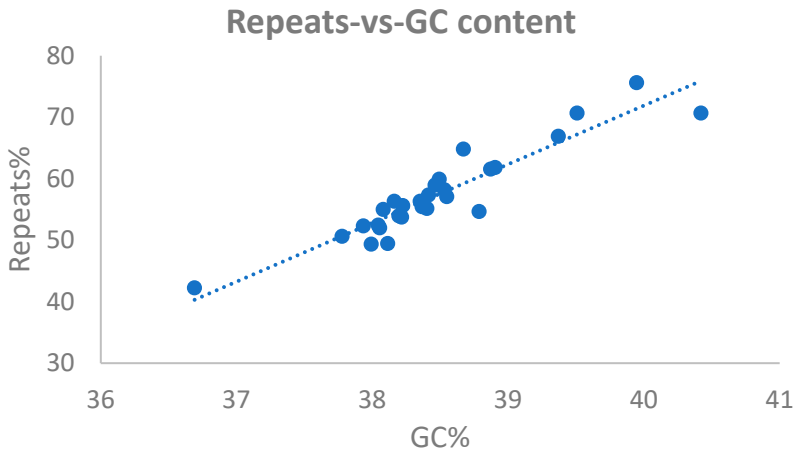



Figure S1 the content of repeats is positively correlated with GC content of each chromosome.