

Column Assignments for human LCT SNPs (rhesus reference)

This is a tab-separated file with the following columns:

1. cont - contig
2. cpos - contig position
3. A - reference allele
4. B - variant allele
5. Q - overall SNP quality
6. rchr - reference chromosome (rheMac2)
7. rpos - reference position
8. rnuc - reference nucleotide

For each of 12 individual humans there are four columns, giving count of the reference allele, count of the variant allele, count of ambiguous alleles, and quality of the called genotype. The values occupy columns 9-56.

- 9-12. individual 1: E1 European 1
- 13-16. individual 2: E2 European 2
- 17-20. individual 3: E3 European 3
- 21-24. individual 4: E4 European 4
- 25-28. individual 5: E5 European 5
- 29-32. individual 6: F1 African 1
- 33-36. individual 7: F2 African 2
- 37-40. individual 8: F3 African 3
- 41-44. individual 9: F4 African 4
- 45-48. individual 10: S1 Asian 1
- 49-53. individual 11: S2 Asian 2
- 53-56. individual 12: S3 Asian 3