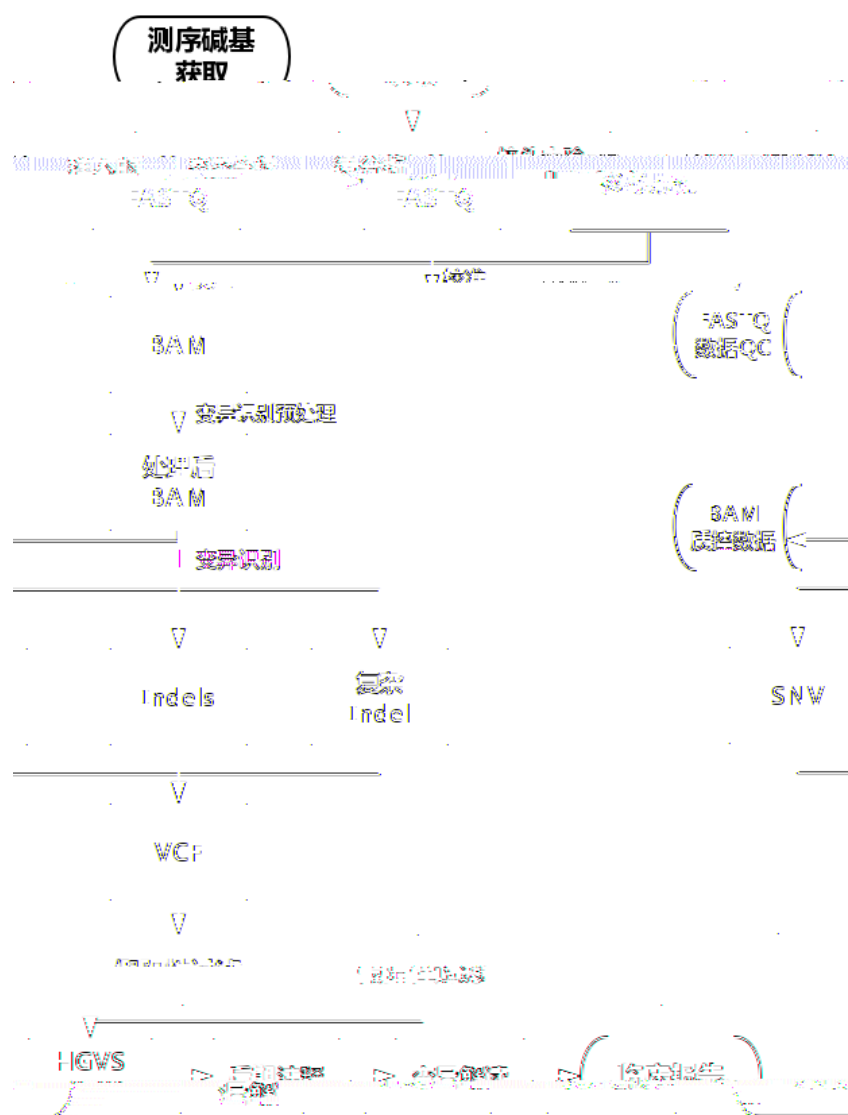
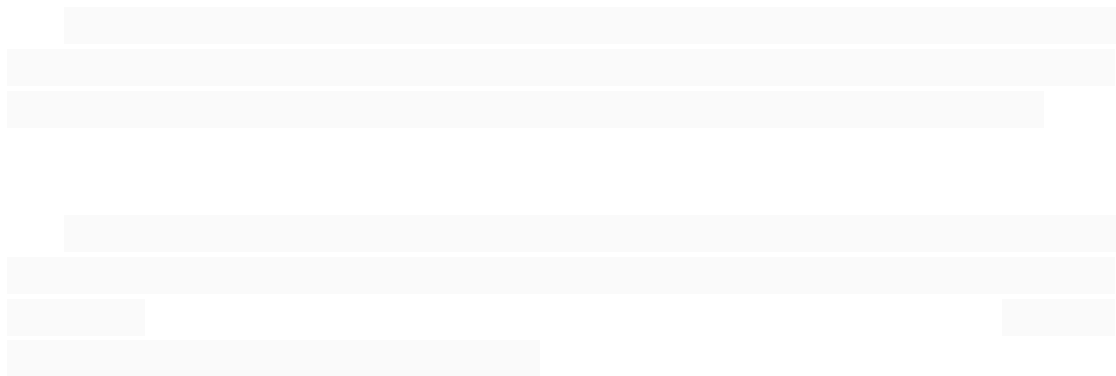


The Quality Standard of Using High-throughout Sequencing Data to Interpretate
Human Whole Genome Variation

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ABCDEF2<=&%G: : HI@K1; @ 31L41=|@29M=2?>K12<>@E41=€?OE?=9?@, 121€??2F€LK: P<; ?F@€?F: EK9?@
: 0€?=?9341KH@ + &@|=; @=; ?R@?=: 2SL?@1RFRM@ @-Tl@UVWtXB@TzBU[@
; : \BZMBZ-]^=Q2MT]-X@@

@
ATC@: 3=@_M@ R?1KS^B^ I@ : FF@JK1-23a1-2?^B^I@29M@ : 4L1K<=>@) 1K<1=2@ 1RR@ <R?F@: K@&?K0: K41=9?@
J?=?9341KH<=>@ 0@+?b25_?=?K12<: =@ ?OE?=?9<=>@) 1K<1=2@ 1RR<=>€<L?R<=?F@ @ =R<=?@' E>M@T@
TZBX@ : \@322L^^; bM; : <M: K>^BZMBBZB^ZT-dXUM@

@
A-C@1=@_E: @^IfI@ER=@/1-@I?29M@4LK: P?4?=?2F@|=; @4L192F@ 0@_ ' . 3-]@E41=€(??K?=?9?@ =€>3@
23K: E>3LE2€?OE?=?9<=>@ 121@|=1RSF-F@ BZg@TZBd[@]-WgZM@
; : \BZMBZBV^hMS>?=: MTZBdMzBMZZX@

@
AUC@) 1R?K<?@' M@ 93=?<; ?K^B^I@#<=1@_K1P??F57<=: F1SI?29M@*P1RE12<: =@ 0@_ ' . 3-]@|=; @ ?@=: P: @31LR: <; @
>?=: 4?@FF?4QR<?F@ ?4: =F2K12?F@3?@?=: EK<=>@E1R2S@ 0@3?€(??K?=?9?@FF?4QRSM@
M@ : <BZMBBZB^>KMTB-VBBMBBV@

@
AXC@ 21=: 1K; F@|=; @_E<; ?R<=?F@: K@) 1R<; 12<=>@+?b25_?=?K12<: =@ ?OE?=?9<=>@J< <=0: K412-9F€<L?R<=?F\@
" @: <=2@ ?9: 44?=: 12<: =@ 0@3?@' FF: 9<12<: =@: K@%: R?9ER1K&123: R: >S@|=; @ : RR?>?@ 0@' 4?K<91=@
&123: R: >F2FM@ @/(M@BZMBZBV^hM4: R; bMTZBdMzBMZZ-[@

@
AVC@61@ 1=>^B^I@%<=>S1: @<^I@|=; €\$1H: =€\$1H: =1KF: =^B^I@' ++ () "' \@E=92<: =1R@|==: 212<: =@ 0@
>?=?2-9@1K<1=2F@K: 4@>3523K: E>3LE2€?OE?=?9<=>@ 121 M@TZBZ@ ?L@-]YBV[\@
?BVUM&EQR-F3?; @ =R<=?@TZBZ@ER@-M@ : \BZMBZg-^=1K^>HOVZ-@

@