NextSeq−150PE (more miscalibration in base quality scores)
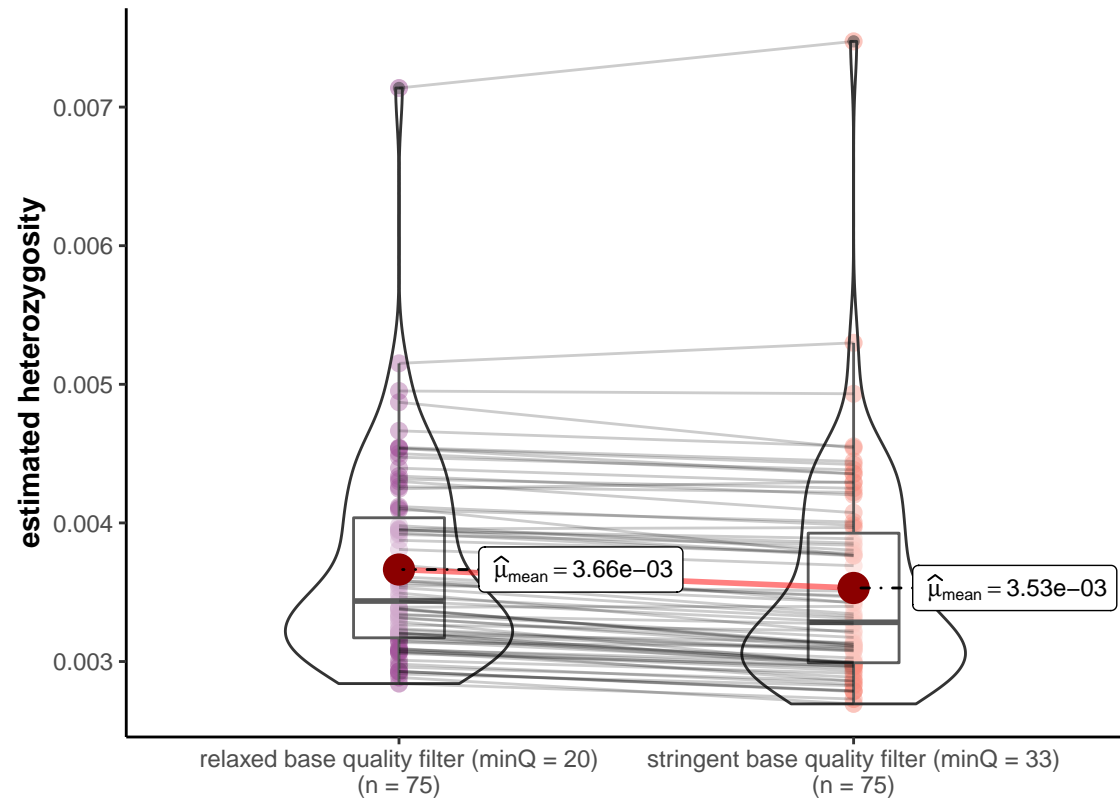
$t_{\text{Student}}(74) = 11.39$, $p = 6.16e{-}18$, $\widehat{g}_{\text{Hedges}} = 1.30$, $CI_{95\%}$ [1.00, 1.62], $n_{\text{pairs}} = 75$

estimated heterozygosity

$\widehat{\mu}_{\text{mean}} = 3.66e{-}03$

$\widehat{\mu}_{\text{mean}} = 3.53e{-}03$

relaxed base quality filter (minQ = 20)
(n = 75)

stringent base quality filter (minQ = 33)
(n = 75)

HiSeq−125SE (less miscalibration in base quality scores)

$t_{\text{Student}}(87) = -2.71$, $p = 0.008$, $\widehat{g}_{\text{Hedges}} = -0.29$, $CI_{95\%}$ [−0.50, −0.07], $n_{\text{pairs}} = 88$

estimated heterozygosity

$\widehat{\mu}_{\text{mean}} = 3.69e{-}03$

$\widehat{\mu}_{\text{mean}} = 3.70e{-}03$

relaxed base quality filter (minQ = 20)
(n = 88)

stringent base quality filter (minQ = 33)
(n = 88)