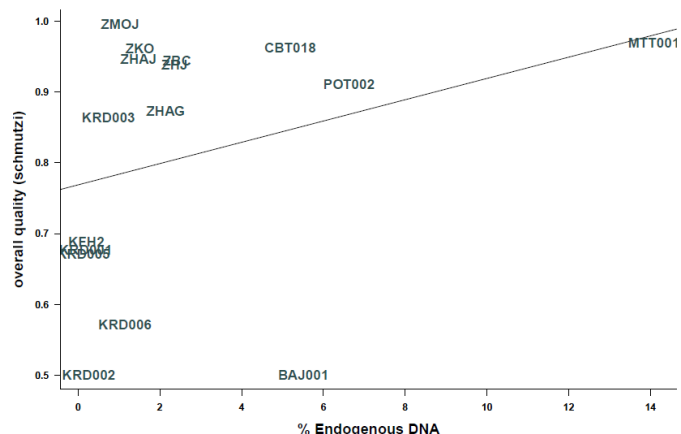
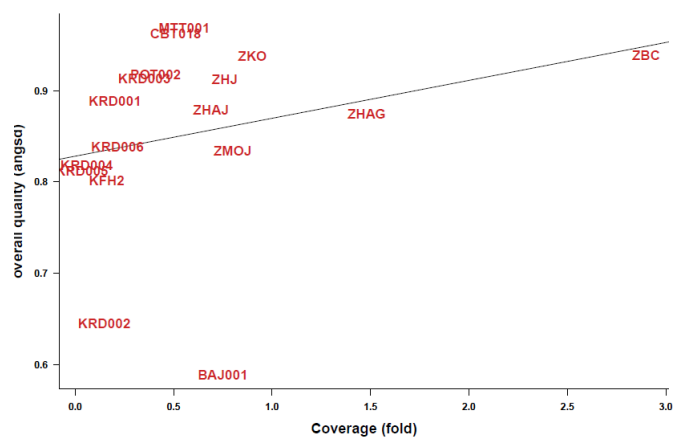


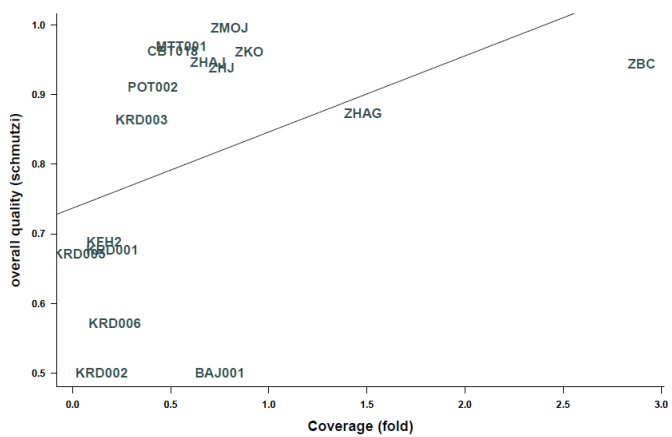
(a)



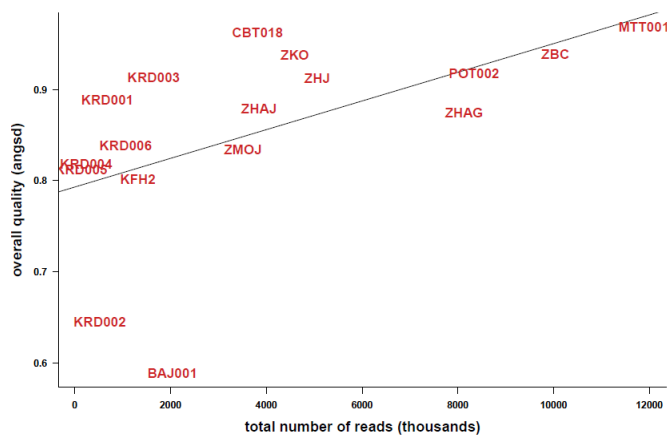
(b)



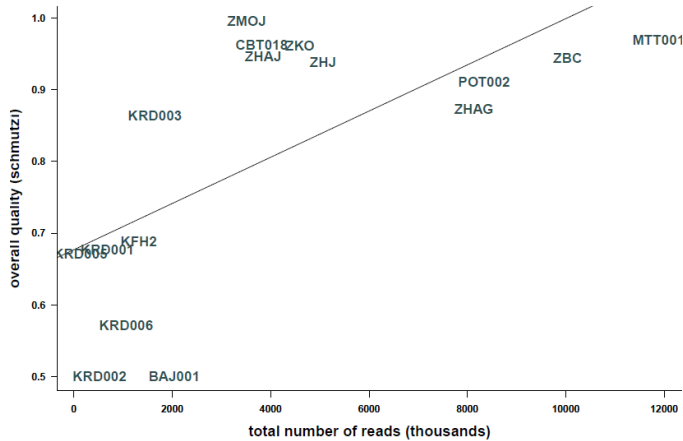
(c)



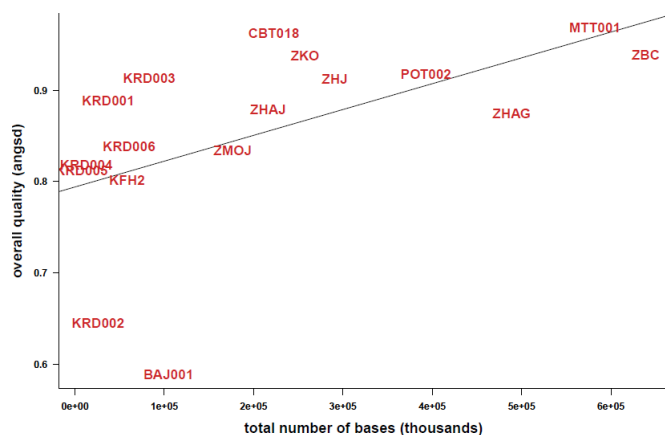
(d)



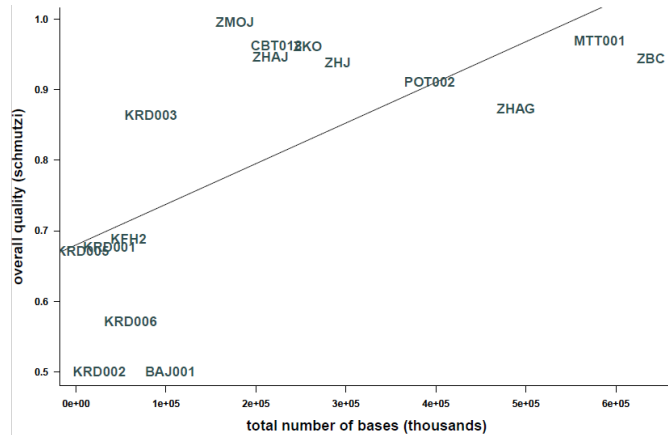
(e)



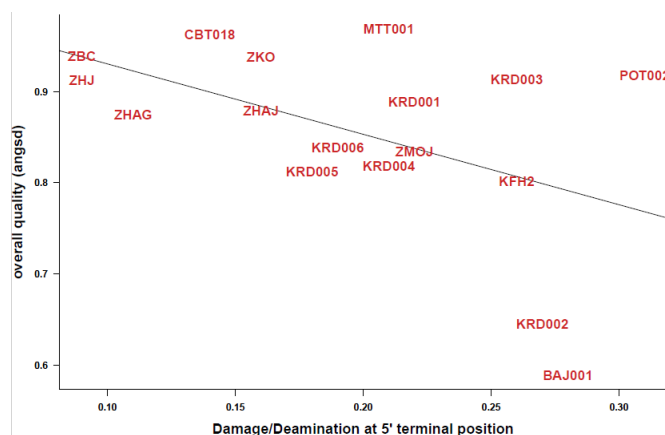
(f)



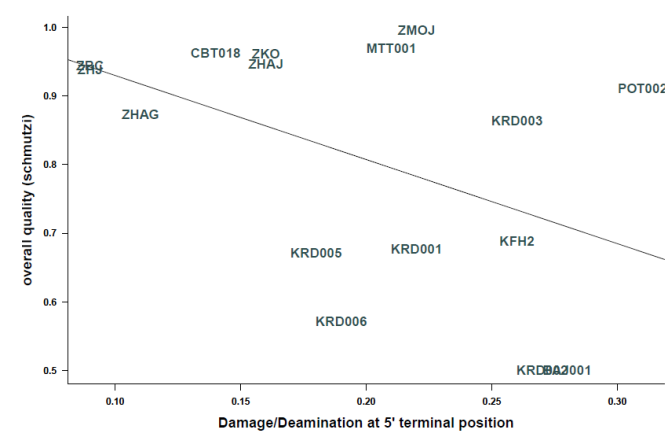
(g)



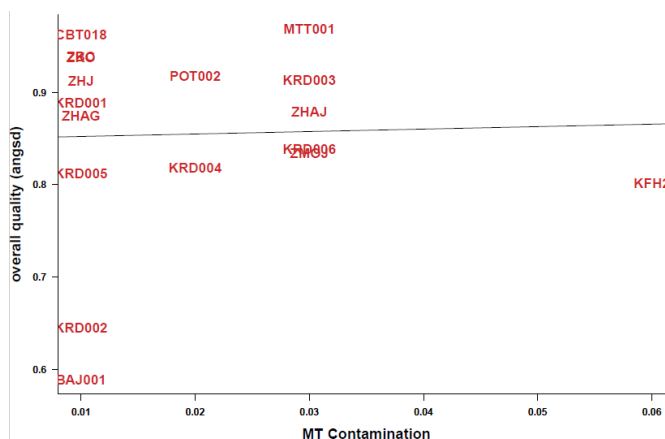
(h)



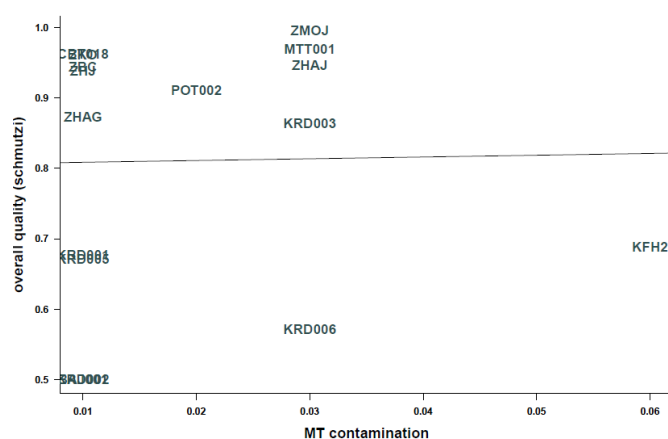
(i)



(j)



(k)



(l)

Figure S3. Association between different sample characteristics and derived sequence quality, by two alternative tools and pipelines (ANGSD *vs* schmutzi): (a) Proportional endogenous DNA *vs* overall ANGSD-derived sequence quality; (b) Proportional endogenous DNA *vs* overall schmutzi-derived sequence quality; (c) Coverage *vs* overall ANGSD-derived sequence quality; (d) Coverage *vs* overall schmutzi-derived sequence quality; (e) Total number of reads *vs* overall ANGSD-derived sequence quality; (f) Total number of reads *vs* overall schmutzi-derived sequence quality; (g) Total number of bases *vs* overall ANGSD-derived sequence quality; (h) Total number of bases *vs* overall schmutzi-derived sequence quality; (i) Damage at 5' position *vs* overall ANGSD-derived sequence quality; (j) Damage at 5' position *vs* overall schmutzi-derived sequence quality; (k) MT contamination *vs* overall ANGSD-derived sequence quality; (l) MT contamination *vs* overall schmutzi-derived sequence quality.