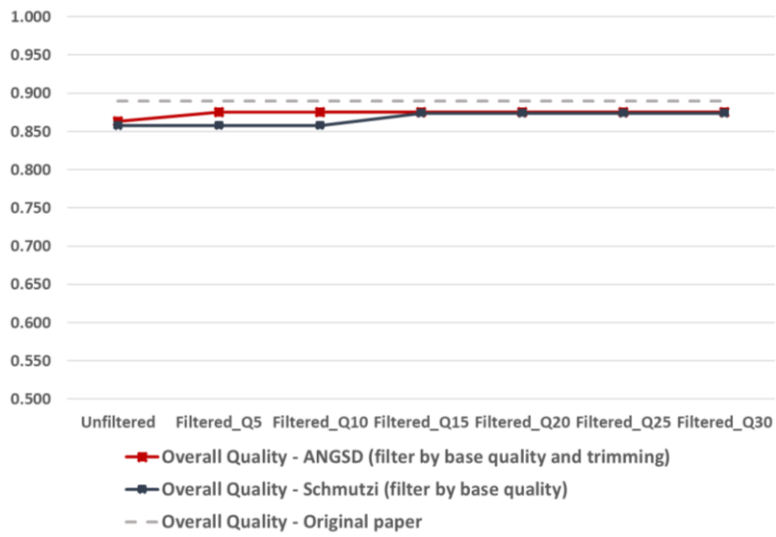


Overall Quality - ANGSD (filter by base quality and trimming)

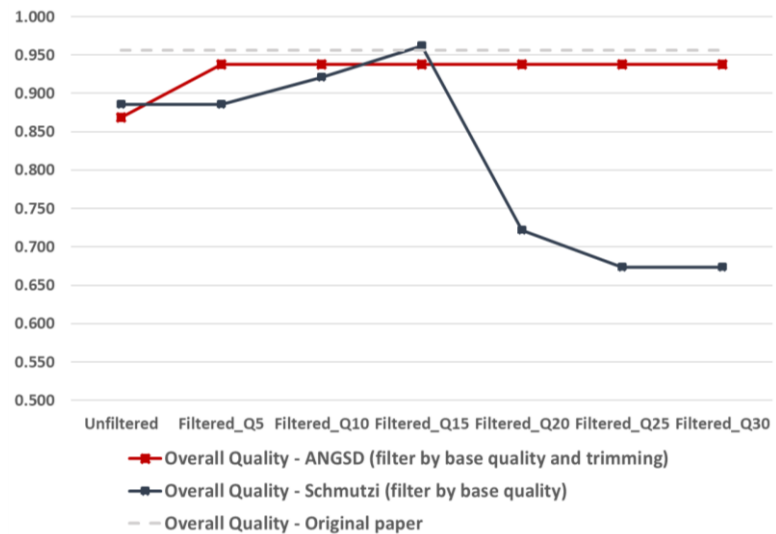
Overall Quality - Schmutzi (filter by base quality)

Overall Quality - Original paper

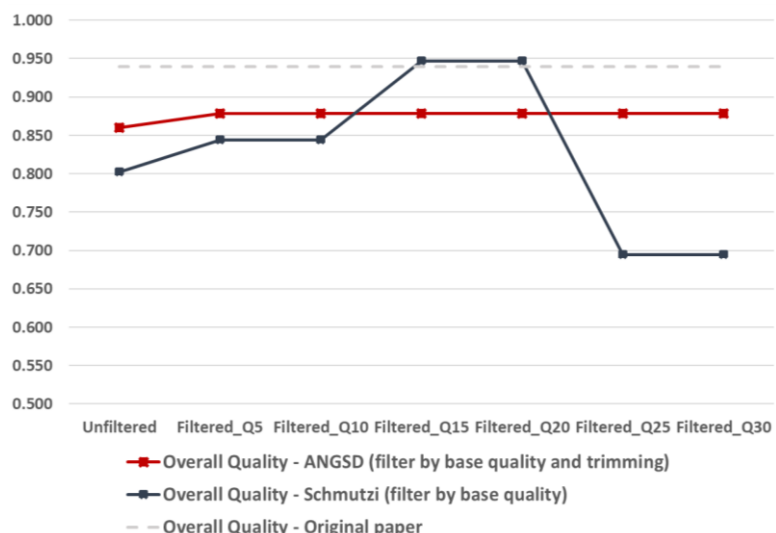
Filtering Step	ANGSD Overall Quality	Schmutzi Overall Quality	Original paper Overall Quality
Unfiltered	~0.935	~0.895	~0.960
Filtered_Q5	~0.940	~0.895	~0.960
Filtered_Q10	~0.925	~0.905	~0.960
Filtered_Q15	~0.925	~0.910	~0.960
Filtered_Q20	~0.940	~0.910	~0.960
Filtered_Q25	~0.940	~0.945	~0.960
Filtered_Q30	~0.940	~0.945	~0.960

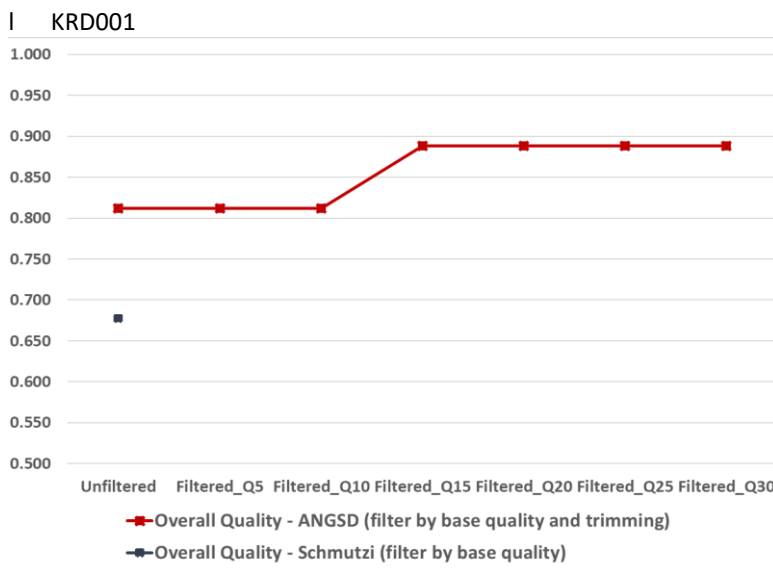
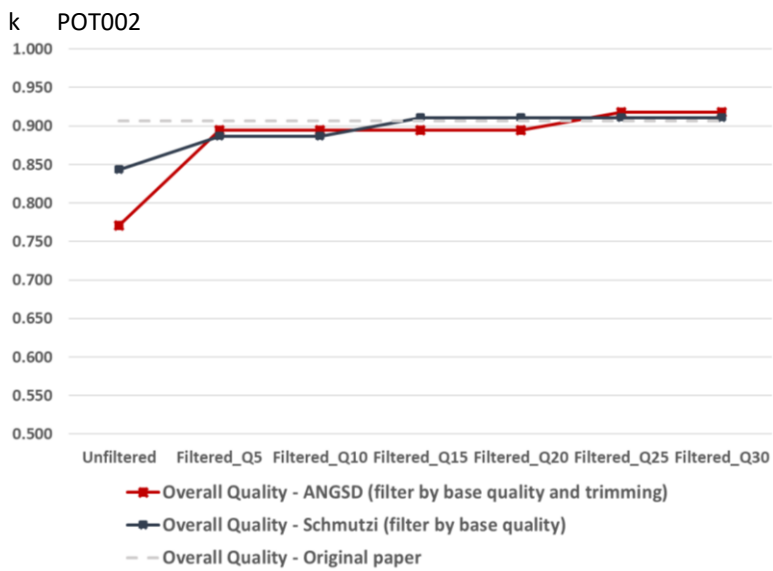
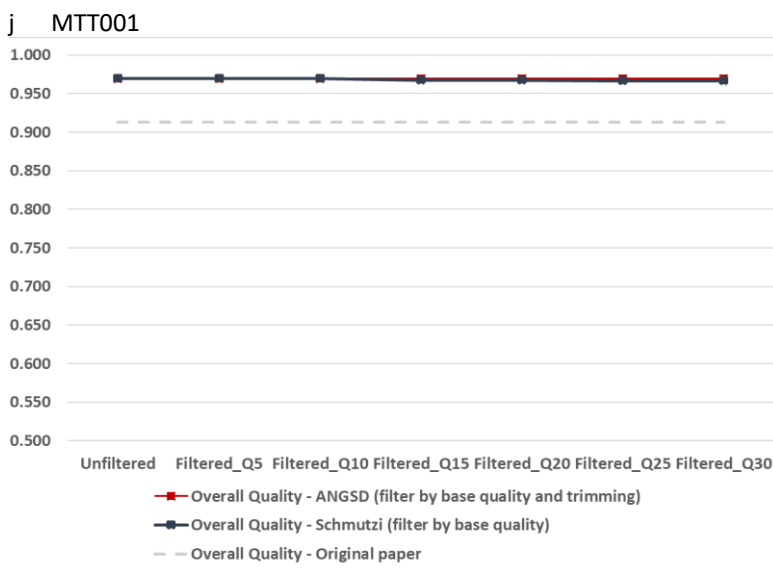
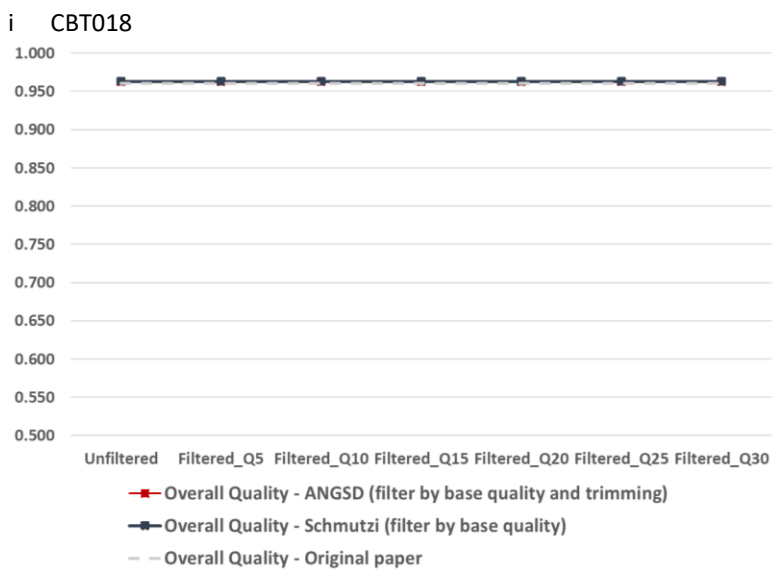
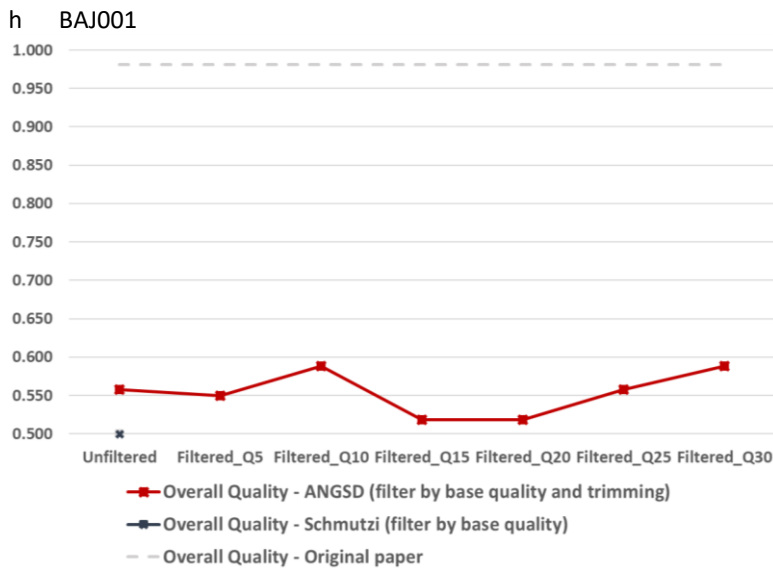
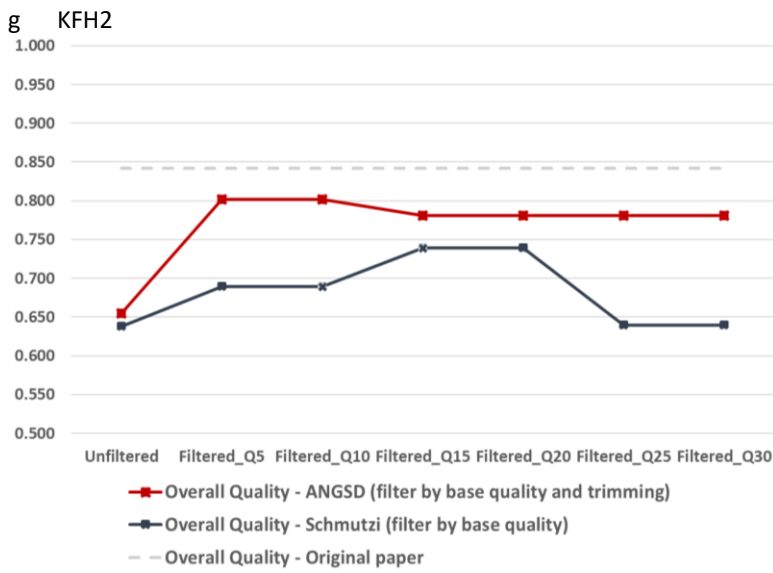


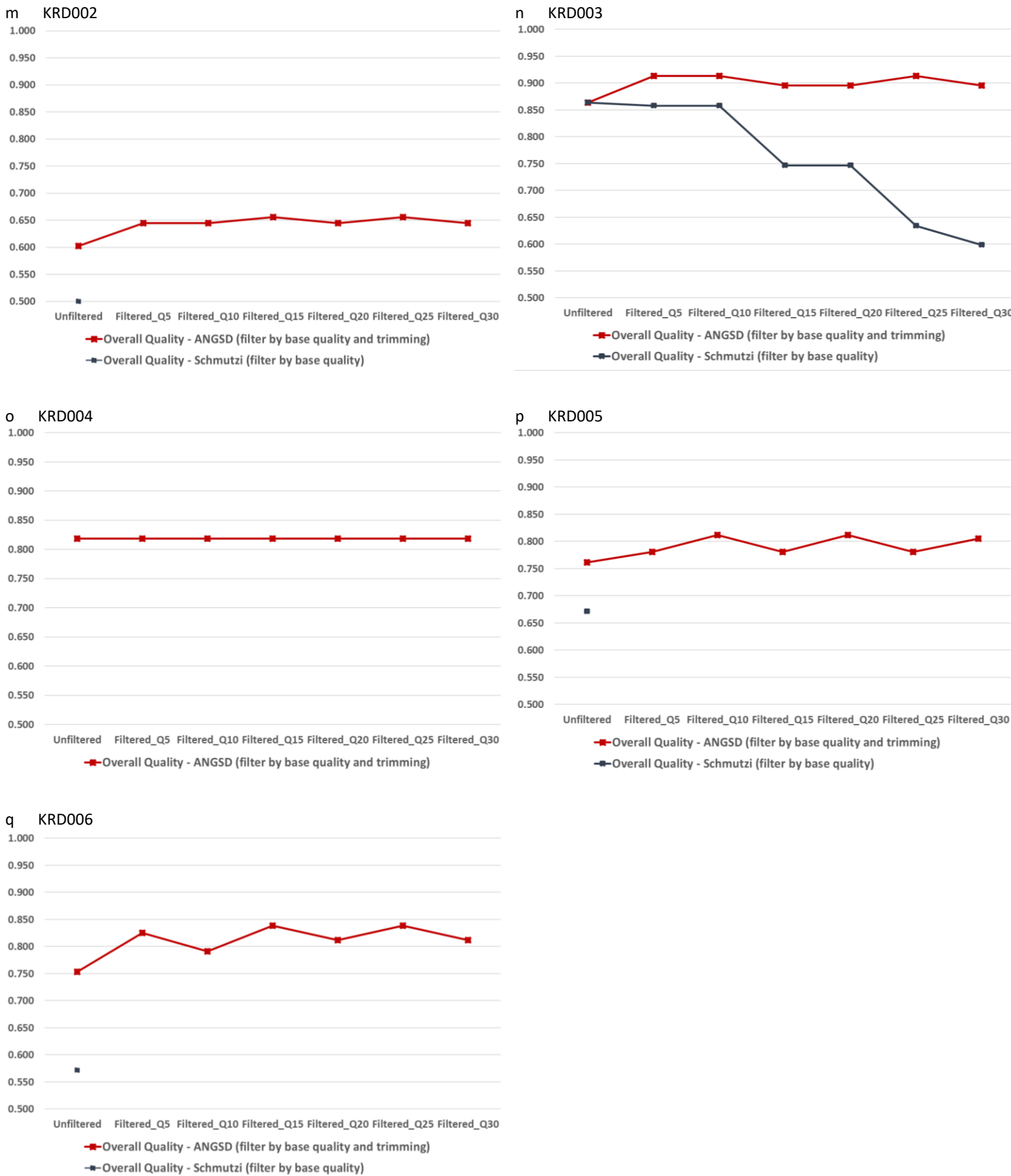
Filtering Threshold	Overall Quality - ANGSD (filter by base quality and trimming)	Overall Quality - Schmutzi (filter by base quality)	Overall Quality - Original paper
Unfiltered	0.785	0.910	0.615
Filtered_Q5	0.795	0.945	0.615
Filtered_Q10	0.795	1.000	0.615
Filtered_Q15	0.795	0.645	0.615
Filtered_Q20	0.820	0.645	0.615
Filtered_Q25	0.835	0.620	0.615
Filtered_Q30	0.795	0.615	0.615



Filtering Step	Overall Quality - ANGSD (filter by base quality and trimming)	Overall Quality - Schmutzi (filter by base quality)	Overall Quality - Original paper
Unfiltered	0.905	0.935	0.925
Filtered_Q5	0.905	0.935	0.925
Filtered_Q10	0.905	0.935	0.925
Filtered_Q15	0.905	0.935	0.925
Filtered_Q20	0.905	0.935	0.925
Filtered_Q25	0.905	0.935	0.925
Filtered_Q30	0.915	0.940	0.930







**Figure S1.** Haplogroup prediction accuracy for analyzed samples using mitogenome consensus sequence extracted from whole genome data, as derived by two alternative tools and pipelines (ANGSD *vs* schmutzi). Samples for which a quality curve is missing for one of the two tools, indicates that the approach did not result in a consensus mitogenome sequence, particularly after filtering: (a) sample ZBC; (b) sample ZHAG [29]; (c) sample ZMOJ [29]; (d) sample ZKO [29]; (e) sample ZHJ [29]; (f) sample ZHAJ [29]; (g) sample KFH2 [29]; (h) sample BAJ001 [29]; (i) sample CBT018 [30]; (j) sample MTT001 [30]; (k) sample POT002 [30]; (l) sample KRD001 [30]; (m) sample KRD002 [30]; (n) sample KRD003 [30]; (o) sample KRD004 [30]; (p) sample KRD005 [30]; (q) sample KRD006 [30].