Indicator	Threshold	Interpretation	Comments
Genetic diversity within populations ($\Delta H = H2 - H1$) H1: Heterozygosity at first point in time H2: Heterozygosity at second point in time	≤ 0.05% reduction per year*	Good	Focus on H_E but also considers H_O, A_R, N_A, P_L, as well as π, F_{ROH}, HP when available.
	0.06-0.3% reduction per year**	Warning	
	> 0.3% reduction per year***	Alarm	
Effective population size (N_e)	$N_e \geq 500$	Good	Applies to single isolated populations, metapopulations, or sub-areas of the total range. For metapopulations, subpopulation N_e is also considered.
	$50 < N_e < 500$	Warning	
	$N_e \leq 50$	Alarm	
Genetic diversity between populations ($\Delta F_{ST} = F_{ST}2 - F_{ST}1$) $F_{ST}1$: Genetic differences between two or more subpopulations at first point in time $F_{ST}2$: Genetic differences between two or more subpopulations at second point in time	ΔF_{ST} no/minor change	Good	Change of the number of genetically distinct populations is also considered in this indicator.
	ΔF_{ST} reflects c. 25% reduction of genetic exchange between subpopulations, or c. 50% increase of genetic exchange among subpopulations	Warning	
	ΔF_{ST} reflects >50% reduction of genetic exchange among subpopulations, or >100% increase of genetic exchange among subpopulations	Alarm	

*≥95% retention of H over 100 years; **75-94% retention of H over 100 years; ***<75% retention of H over 100 years