APPENDIX 1

Summary of the type and format of genetic data relevant for each of the MSP goals addressed in this report and the suggestions made by the Focus Group regarding how the genetic data could be reformatted for use in an MSP tool.

MSP Goal		Data type	Genetic data format	Suggested MSP format	Relevance for MSP
Defining Units	Individuals & kin-relationships	• Microsatellites	• Probability of identity • Probability of parentage/kinship • Pedigrees • Relatedness measures • Relatedness networks	• Individual kernel distributions • Relatedness/kinship measures (continuous metric)	• Estimates of levels of in/outbreeding • Vulnerability assessment of family groups (i.e., leading to the disproportionate loss of biodiversity) • Assessment of population sub-structure to inform management unit definitions • Habitat use and preferences • Estimates of connectivity
	Demographic populations	• Microsatellites • SNPs • Mitochondrial sequences	• Genetic differentiation indices (e.g., F_{ST}, ϕ_{ST}) • Clustering algorithms • Assignment probabilities • PCA-based analyses	• Kernel distribution of genetic differences • Haplotype distributions • Heat map of population specific F_{ST} • Sliding window analysis • Principle component	• Protection of different population units ensures long-term species persistence • Population units need to be defined to quantify a number of measures

				analysis • Isolation by distance • Ecological analysis (e.g., isolation by environmental distance) • Clustering analysis	management such as population size, genetic diversity, vulnerability, connectivity, etc. • Once identified, population unit boundaries can be used to define MSP zoning boundaries
	Species	• Nuclear gene sequences • Nuclear introns • Mitochondrial sequences • Genome	• Phylogenetic trees	• Species identification • Levels of species diversity within a defined area • Diversity hot-spots or cold-spots	• Identification of cryptic management priority species • Quantification of levels of biodiversity to inform management prioritization
	Community/ Ecosystems	• Nuclear gene sequences • Nuclear introns • Mitochondrial sequences • Genome • Environmental DNA	• Phylogenetic trees • Clustering algorithms • Species and community diversity/ richness/ evenness indices	• Similarity/ differentiation indices between pre-defined areas (continuous metric) • Spatial interpolation of clustering of units sampled in different areas	• Management prioritization of areas with high levels of diversity • Quantification of levels of biodiversity to inform management prioritization
Assessing connectivity	Historic connectivity	• Microsatellites • Mitochondrial control region sequences	• Network • Connectivity matrix	• Network Connectivity matrix	• May not occur on a timescale relevant for marine spatial planning
	Demographic	• Microsatellites	• Network	• Network	• Understanding the

	connectivity		• Connectivity matrix	• Connectivity matrix	spatial dynamics of metapopulations (i.e., source/sink dynamics, isolation, etc.) and therefore proposing effective management plans
	Individual movements	• Microsatellites	• Genotypic matches	• Straight lines connecting two sampling locations • Individual range maps, kernel distributions or densities • Polygons proportional to the number of recaptures in a single location across time.	• Quantification real-time movements indicate levels of contemporary connectivity and inform assessments of population structure • Habitat preferences and use, including estimates of putative migration routes • Ecological processes underlying genetic structure (e.g., seascape genetics)
Measuring status & trends	Population reduction & bottlenecks	• Microsatellites • DNA sequences	• Allele frequency distribution • Time since bottleneck • Change in population size over time	• Color-coding to indicate expansion, stability, or decline • Supplementary charts that document change in population size across time	• Assessments of population decline/recovery (informing management measures and prioritization)
	Effective population	• Microsatellites	• Ne (continuous metric)	Most measures of genetic diversity and Ne can be	• Assessments of

	size (Ne)	• DNA sequences		described by a simple summary statistic. For example: • Diversity indices (color-coded) • Standardized variables (color coded) • Composite variable of multiple diversity indices	population size (and vulnerability) • Assessments of genetic diversity of different populations to inform management prioritization measures • Assessments of the biodiversity value of a defined area to inform management prioritization measures
	Population diversity	• Microsatellites • SNPs • Mitochondrial sequences	• Diversity indices (continuous metric)		
	Species diversity	• Nuclear gene sequences • Nuclear introns • Mitochondrial sequences • Genome • Environmental DNA	• Phylogenetic trees • Clustering algorithms • Species and community diversity indices		