**Supplemental C. Genetic Methods**

Samples within each collection event (i.e., for each site in every collection round) were reviewed by WGI by randomly assigning each sample a number, excluding samples that did not appear to be bear hair. In the first tier of sample selection, samples with more than one guard hair and 20 or more underfur hairs (considered high quality samples) were randomly selected for analysis. If we lacked high-quality samples in the first tier of sub-selection, samples with one guard hair and five to 19 underfur hairs (otherwise considered marginal samples) were selected. Samples with less hair than this were treated as inadequate and not selected for analysis. However, we had to make exceptions to this rule with 36 collection events in which all available samples were classified as inadequate. As such, the best available hair samples as determined by the lab were analyzed from this collection (Table 1).

Table 1**.** Genetic sub-sampling rules for a given collection event in which multiple hair samples were collected at a single hair snag site, during the BMA 1 Grizzly Bear Program.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Number of Available Samples from single collection event | **1-4** | **5-6** | **7-9** | **10-12** | **13-16** | **16+** |
| Number of Samples Genetically analyzed | All | 4 | 5 | 6 | 7 | 8 |