Elfström *et al*.

**Appendix A**

**Diet composition analysis**

We extracted, cleaned and purified total DNA from about 10 mg of sample using the DNeasy Blood and Tissue Kits (QIAGEN GmbH), according to the DNeasy Blood and Tissue Handbook, 7/2006, QIAGEN. Mock extractions were systematically performed to monitor for possible contaminations. The first multiplex PCR contained the primer sets g/h (amplifying the P6 loop of the chloroplast trnL (UAA) intron in angiosperms and gymnosperms ([Taberlet et al. 2007](#_ENREF_21); [Valentini et al. 2009](#_ENREF_22))), 12SV5F/12SV5R (amplifying the V5 loop of the mitochondrial 12S gene in vertebrates ([Riaz et al. 2011](#_ENREF_19))), and MAVF/MAVR (targeting a short portion of the mitochondrial 16S gene of mollusks, annelids, and vertebrates; unpublished) with the *Ursus* V5 blocking primer, mammalian MAVB1 blocking primer, and *Homo* blocking primer to prevent amplification of bear and human DNA in the vertebrate samples, and mammalian DNA in the invertebrate samples. The second multiplex PCR contained the primer sets ITS1-F/ITS1Poa-R (Poaceae ITS1 ([Baamrane et al. 2012](#_ENREF_1))), ITS1-F/ITS1Ast-R (Asteraceae ITS1 ([Baamrane et al. 2012](#_ENREF_1))), ITS1-F/ITS1Cyp-R (Cyperaceae ITS1(P. Taberlet unpublished)) targeting a short fragment of the internal transcribed spacer region 1 (ITSI) of nuclear ribosomal DNA of the Asteraceae, Cyperaceae, and Poaceae, and ITSRosF/ITSRosR (Rosaceae ITS2 ([De Barba et al. 2014](#_ENREF_4)) amplifying a short fragment of the internal transcribed spacer region 2 (ITS2) of nuclear ribosomal DNA of the Rosaceae. We conducted four replicate PCRs per multiplex PCR for each fecal sample, and conditions for both reactions were as described in De Barba ([2014](#_ENREF_4)). We uniquely tagged universal primers (each tag was composed by CC or GG followed by eight variable nucleotides and was added on the 5’ end of the primers) to allow for individual sample recognition in downstream bioinformatic analyses after pooling of PCR products for sequencing ([Coissac et al. 2012](#_ENREF_2)). PCR products of multiplex 1 and multiplex 2 were purified, mixed together in equimolar concentration ([De Barba et al. 2014](#_ENREF_4)) and sequenced on one region of the Illumina HiSeq 2000 (Illumina Inc.), following the manufacturer’s instructions. We sequenced a total of 100 nucleotides on each extremity of the DNA fragments.

The direct and reverse reads corresponding to single molecules were aligned and a consensus sequence and quality score were generated using the *solexaPairEnd* script. We identified primers and tags using *ngsfilter,* and excluded those sequences with errors in the tags and a maximum of two errors in the primers from further analysis*.* The amplified regions, excluding primers and tags, were kept for further analysis. For each marker dataset, identical sequences were clustered using *obiuniq*, while still keeping the information about their distribution among samples. We excluded sequences shorter than 10 bp (gh, mav, cyp, ros markers) or 30 bp (v5, ast, poa markers), or with occurrence <1000 from the dataset using the *obigrep* script. The *obiclean* script was implemented to detect PCR and sequencing errors: each unique sequence within a PCR product was given the status “head” (most common sequence among all those sequences that can be linked by a single indel or substitution), “singleton” (no other variant with a single difference in the relevant PCR product), or “internal” (all other sequences not being “head” or “singleton”, i.e. corresponding to amplification/sequencing errors). We excluded all sequences designated more often as “internal” than “head” or “singleton” from further analysis.

We gave each unique sequence a taxonomic assignment using the *ecoTag* script for all amplified regions. The *ecoTag* script identifies the taxon corresponding to the last common ancestor node of the NCBI (National Center for Biotechnology Information) taxonomic tree of all the taxids annotating those sequences matching the query in a marker-specific reference database generated by extracting the relevant part of the EMBL (European Molecular Biology Laboratory) nucleotide database using the *ecoPCR* script ([Ficetola et al. 2010](#_ENREF_6)). We then conducted a final filtering of the dataset. We removed unique sequence groups from the dataset that 1) occurred in <3 of the four PCR replicates, 2) had a best identity match <0.95, 3) accounted for <1% of the total sequences generated for that marker across all samples (presumably items of little dietary significance), or 4) were identified as human or bear. Those unique sequence groups within the chloroplast trnL marker dataset that were identified as belonging to the Asteraceae, Cyperaceae, Poaceae, or Rosaceae were excluded to avoid overlap in detection with the family-specific ITS marker datasets. Finally, we collapsed unique sequence groups with identical taxonomic assignments at the species level into a single representative grouping. We then created a concatenated fecal sample versus dietary item matrix from all the samples from which all seven markers were successfully amplified and sequenced. The matrix was then rarified to an even sequencing depth of 75,000 reads per sample, and converted to presence-absence data, as differences in primer efficiencies and PCR bias render abundances noncomparable among the different markers.

**Appendix B**

**Diet quality analysis**

Commonly used indices for dietary quality include the fecal constituents of nitrogen, crude fiber, acid detergent lignin (ADL), neutral detergent fiber (NDF), and dry matter (DM) ([Pritchard and Robbins 1990](#_ENREF_17); [Dixon and Coates 2009](#_ENREF_5)). Unknown sample concentrations can be predicted with NIRS, by linking spectral signatures with that from a calibration set ([Næs et al. 2001](#_ENREF_13)). NIRS analyses and preprocessing optimization functions were performed using the Opus 6.5 SP2 software from Bruker Optics (Bruker Optik GmbH), and followed the descriptions in Steyaert et al. ([2012](#_ENREF_20)). We used standard lab procedures (Kjeldahl, Weender and detergent fiber analysis) to obtain measures of fecal nutritive content from each of 174 reference samples ([Nehring 1960](#_ENREF_15); [Naumann and Bassler 1976](#_ENREF_14); [van Soest et al. 1991](#_ENREF_23)). We analyzed five fecal constituents for our reference set: crude fat (CFA), crude protein (CP), ADL, and NDF, measured relative to the fecal DM content (% of DM). The spectroscopy was performed with a MPA Multi Purpose FT – NIR spectrometer (Bruker Optik GmbH). We used partial least square regression (PLSR) for multivariate calibration on the 3600-12,500 cm-1 spectral range ([Conzen 2006](#_ENREF_3)), and created calibration methods for each of the components analyzed with wet-chemistry. We used the cross validation with one leave-out sample to examine the R² and the Root Mean Square Error of Cross Validation (RMSECV) to assess the quality of the calibration methods.

**Appendix C**

**Diet composition and quality combined; model selection and validation**

Global Nonmetric Multidimensional Scaling (GNMDS) ([Kruskal 1964a](#_ENREF_9), [b](#_ENREF_10); [Minchin 1987](#_ENREF_12)) and Detrended Correspondence Analysis (DCA) ([Hill 1979](#_ENREF_7); [Hill and Gauch Jr 1980](#_ENREF_8)) ordinations were conducted in parallel on a presence-absence matrix of fecal samples versus diet items using the *vegan* package implemented in R ([Oksanen et al. 2011](#_ENREF_16); [R Development Core Team 2011](#_ENREF_18)). GNMDS was run with the following options [following recommendations by T. Økland ([1996](#_ENREF_26)) and Liu et al. ([2008](#_ENREF_11))]: distance measure = Bray-Curtis distance, dimensions = 2 or 3, initial configurations = 100, maximum iterations = 200, convergence ratio for stress = 0.9999999. We used the default options in DCA analyses. We inspected both ordinations for outliers and known artefacts, like the arch effect (in GNMDS) and the tongue effect (in DCA) ([Økland 1990](#_ENREF_24); [Økland and Eilertsen 1993](#_ENREF_25)). The nonparametric Kendall’s rank correlation coefficient τ was used to calculate correlations between DCA and GNMDS axes.

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| **Table A.1**. Kendall’s Tau correlation tests of Scandinavian brown bears’ diet between detrended correspondence analysis (DCA) and global nonmetric multidimensional scaling (GNMDS) axes for GNMDS ordinations run in two dimensions. Significant correlation between axes (*P*<0.05) is indicated by bold font. |
|  | **GMDS 1** | **GNMDS 2** |
|  | **Kendall’s tau** | ***P*τ (>τ)** | **Kendall’s tau** | ***P* τ (>τ)** |
| **DCA1** | 0.309 | **<0**.**001** | -0.401 | **<0**.**001** |
| **DCA2** | 0.565 | **<0**.**001** | 0.343 | **<0**.**001** |

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| **Table A.2**. Frequency and identity of 228 diet items recovered from analysis based on DNA metabarcoding of 106 fecal remains of brown bears in south-central Sweden 2010. Plant species are indicated on light-gray, insects on dark-gray, and vertebrates on white background. |
| **OTU Name**¶ | **Kingdom/Phylum** | **Species** | **Frequency** | **Reads** | **Best identity** |
| gh\_00001 | Plantae | *Vaccinium vitis-idaea* | 91 | 4034929 | 1.00 |
| mav\_00001 | Arthropoda | *Formica* sp. | 87 | 2572392 | 1.00 |
| ast\_00001 | Plantae | *Tussilago farfara* | 86 | 1067530 | 1.00 |
| ast\_00003 | Plantae | *Taraxacum* | 84 | 533355 | 1.00 |
| v05\_00002 | Chordata | *Alces alces* | 83 | 241930 | 1.00 |
| ast\_00002 | Plantae | *Cirsium palustre* | 79 | 927587 | 1.00 |
| poa\_00003 | Plantae | *Avenella flexuosa* | 68 | 310499 | 1.00 |
| ros\_00001 | Plantae | *Rubus idaeus* | 66 | 282754 | 1.00 |
| poa\_00004 | Plantae | *Deschampsia* sp*.* | 59 | 209737 | 1.00 |
| summed6 | Plantae | *Cicerbita alpina* | 59 | 345647 | 1.00 |
| gh\_00003 | Plantae | *Vaccinium myrtillus* | 54 | 1429792 | 0.98 |
| mav\_00002 | Arthropoda | *Oliarces clara* | 53 | 1767672 | 0.97 |
| v05\_00010 | Chordata | *Bos* sp*.* | 53 | 30189 | 1.00 |
| ast\_00012 | Plantae | *Hieracium* sp*.* | 52 | 83706 | 1.00 |
| poa\_00001 | Plantae | *Avena* sp*.* | 51 | 404048 | 1.00 |
| v05\_00003 | Chordata | *Sus scrofa* | 50 | 78161 | 1.00 |
| poa\_00002 | Plantae | Poeae | 43 | 355698 | 1.00 |
| cyp\_00002 | Plantae | *Carex* sp. 1 | 42 | 51055 | 1.00 |
| poa\_00008 | Plantae | Poeae | 41 | 81144 | 1.00 |
| summed7 | Plantae | *Crepis paludosa* | 40 | 235110 | 0.97 |
| mav\_00004 | Arthropoda | *Camponotus herculeanus* | 39 | 1453732 | 1.00 |
| ast\_00010 | Plantae | *Cirsium* sp*.* | 37 | 91064 | 1.00 |
| gh\_00002 | Plantae | Asterales | 37 | 1540008 | 0.98 |
| gh\_00007 | Plantae | Poeae | 33 | 540600 | 0.98 |
| gh\_00005 | Plantae | *Empetrum* sp*.* | 26 | 1166872 | 0.94 |
| gh\_00016 | Plantae | *Asterales* sp. | 23 | 279616 | 0.98 |
| mav\_00007 | Arthropoda | *Lasius* sp*.* | 23 | 337584 | 1.00 |
| gh\_00036 | Plantae | *Pinus resinosa* | 21 | 64671 | 0.98 |
| poa\_00010 | Plantae | *Triticum aestivum* | 21 | 43586 | 1.00 |
| summed11 | Plantae | *Phleum pratense* | 21 | 27849 | 1.00 |
| cyp\_00004 | Plantae | *Carex* sp. 2 | 20 | 32019 | 1.00 |
| mav\_00005 | Arthropoda | *Provespa barthelemyi* | 20 | 1198307 | 0.97 |
| poa\_00031 | Plantae | Loliinae | 20 | 10376 | 1.00 |
| summed14 | Plantae | *Alnus* sp*.* | 20 | 54561 | 1.00 |
| v05\_00007 | Chordata | *Tetrao urogallus* | 20 | 46519 | 1.00 |
| ros\_00011 | Plantae | *Potentilla anglica* | 19 | 11185 | 1.00 |
| poa\_00005 | Plantae | Agrostidinae | 18 | 105960 | 1.00 |
| ast\_00019 | Plantae | *Hieracium* sp*.* | 17 | 19194 | 1.00 |
| cyp\_00025 | Plantae | *Carex* sp. 3 | 17 | 5385 | 1.00 |
| cyp\_00003 | Plantae | *Carex* sp. 4 | 16 | 44303 | 1.00 |
| gh\_00008 | Plantae | Salicaceae | 16 | 400681 | 0.98 |
| gh\_00017 | Plantae | *Musineon vaginatum* | 16 | 247771 | 0.98 |
| poa\_00023 | Plantae | Triticeae | 15 | 15192 | 1.00 |
| v05\_00004 | Chordata | *Oryctolagus cuniculus* | 15 | 76285 | 1.00 |
| v05\_00009 | Chordata | Anatidae | 15 | 33497 | 1.00 |
| v05\_00035 | Chordata | *Gallus* sp*.* | 15 | 4165 | 1.00 |
| summed2 | Plantae | *Ambrosia artemisiifolia* | 14 | 9198 | 0.99 |
| mav\_00009 | Arthropoda | Vespoidea | 13 | 158702 | 0.97 |
| summed5 | Plantae | *Chamerion angustifolium* | 13 | 192289 | 1.00 |
| v05\_00016 | Chordata | *Ovis* sp*.* | 13 | 14080 | 1.00 |
| gh\_00038 | Plantae | *Picea breweriana* | 12 | 57292 | 0.98 |
| poa\_00019 | Plantae | Poeae | 12 | 19278 | 1.00 |
| poa\_00024 | Plantae | Triticeae | 12 | 12742 | 1.00 |
| ros\_00005 | Plantae | *Rubus arcticus* | 12 | 26093 | 1.00 |
| summed1 | Plantae | *Carex vaginata* | 12 | 6712 | 0.99 |
| summed13 | Plantae | *Poa trivialis* | 12 | 4581 | 1.00 |
| ast\_00032 | Plantae | Asteracea | 11 | 8739 | 1.00 |
| ros\_00003 | Plantae | *Potentilla* sp. | 11 | 67184 | 1.00 |
| v05\_00011 | Chordata | *Tetrao* sp*.* | 11 | 25117 | 1.00 |
| v05\_00405 | Chordata | *Cervus elaphus* | 11 | 149 | 1.00 |
| ast\_00022 | Plantae | *Hieracium* sp. | 10 | 6736 | 0.99 |
| ast\_00030 | Plantae | *Cirsium* sp. | 10 | 10712 | 0.99 |
| gh\_00032 | Plantae | *Rumex hastatulus* | 9 | 79844 | 0.97 |
| gh\_00039 | Plantae | *Calluna vulgaris* | 9 | 44191 | 1.00 |
| mav\_00057 | Arthropoda | *Eriesthis* cf.*'rhodesiana'* | 9 | 13059 | 1.00 |
| poa\_00057 | Plantae | *Hordeum vulgare* | 9 | 3805 | 1.00 |
| ros\_00032 | Plantae | *Alchemilla* sp. | 9 | 1359 | 1.00 |
| gh\_00042 | Plantae | *Lathyrus pratensis* | 8 | 42330 | 1.00 |
| gh\_00046 | Plantae | *Vaccinium uliginosum* | 8 | 29965 | 1.00 |
| mav\_00033 | Arthropoda | Protostomia | 8 | 27815 | 0.97 |
| poa\_00007 | Plantae | *Agrostidinae* | 8 | 59721 | 1.00 |
| ros\_00193 | Plantae | *Sorbus* sp. | 8 | 375 | 1.00 |
| summed15 | Plantae | *Vaccinium microcarpum* | 8 | 63599 | 0.98 |
| ast\_00017 | Plantae | *Tussilagininae* | 7 | 14876 | 0.99 |
| mav\_00013 | Arthropoda | *Bombus* sp. | 7 | 93199 | 1.00 |
| poa\_00012 | Plantae | *Triticum* sp. | 7 | 9840 | 1.00 |
| summed9 | Plantae | *Malus* sp. | 7 | 70 | 1.00 |
| v05\_00059 | Chordata | *Sylvia crassirostris* | 7 | 3796 | 1.00 |
| v05\_00693 | Chordata | *Erinaceus concolor* | 7 | 111 | 1.00 |
| ast\_00356 | Plantae | *Tragopogon* sp. | 6 | 927 | 1.00 |
| cyp\_00007 | Plantae | *Carex* sp. 5 | 6 | 22570 | 0.99 |
| mav\_00027 | Arthropoda | Mycetophilidae | 6 | 33444 | 1.00 |
| ros\_00014 | Plantae | *Comarum palustre* | 6 | 6775 | 1.00 |
| v05\_00558 | Chordata | *Felis catus* | 6 | 131 | 1.00 |
| ast\_00027 | Plantae | Gnaphalieae | 5 | 12468 | 0.95 |
| ast\_00498 | Plantae | Cichorieae | 5 | 656 | 1.00 |
| cyp\_00045 | Plantae | *Carex* sp. 6 | 5 | 3378 | 0.97 |
| mav\_00014 | Arthropoda | Protostomia | 5 | 92869 | 0.97 |
| mav\_00028 | Arthropoda | *Pyrobombus* sp. | 5 | 33332 | 1.00 |
| mav\_00046 | Arthropoda | *Argulus americanus* | 5 | 17976 | 0.97 |
| ros\_00600 | Plantae | *Prunus* sp. | 5 | 61 | 1.00 |
| v05\_00037 | Chordata | *Lepus* sp. | 5 | 5018 | 1.00 |
| ast\_00011 | Plantae | *Lactuca* sp. | 4 | 82117 | 1.00 |
| mav\_00032 | Arthropoda | *Sylvicola fenestralis* | 4 | 29681 | 1.00 |
| poa\_00048 | Plantae | Loliinae | 4 | 5730 | 1.00 |
| poa\_00081 | Plantae | Poeae | 4 | 2248 | 0.97 |
| ros\_00052 | Plantae | *Prunus* sp. | 4 | 1463 | 1.00 |
| v05\_00113 | Chordata | *Actitis hypoleucos* | 4 | 2174 | 1.00 |
| ast\_00047 | Plantae | Cichorieae | 3 | 3108 | 0.99 |
| ast\_01398 | Plantae | *Prenanthes purpurea* | 3 | 86 | 1.00 |
| cyp\_00052 | Plantae | *Carex* sp. 7 | 3 | 2363 | 1.00 |
| gh\_00056 | Plantae | *Luzula pilosa* | 3 | 18877 | 1.00 |
| gh\_00095 | Plantae | *Melampyrum sylvaticum* | 3 | 5178 | 1.00 |
| mav\_00044 | Arthropoda | *Symydobius kabae* | 3 | 17348 | 1.00 |
| mav\_00064 | Arthropoda | Pancrustacea | 3 | 10493 | 0.97 |
| mav\_00065 | Arthropoda | Ditrysia | 3 | 10021 | 0.97 |
| poa\_00054 | Plantae | *Milium effusum subsp. effusum* | 3 | 3783 | 1.00 |
| poa\_00077 | Plantae | Poeae | 3 | 2792 | 1.00 |
| ros\_00042 | Plantae | *Alchemilla* sp. | 3 | 2714 | 1.00 |
| ros\_00377 | Plantae | *Rubus* sp. | 3 | 11 | 1.00 |
| v05\_00066 | Chordata | *Sylvaemus* sp*.* | 3 | 3605 | 1.00 |
| v05\_00577 | Chordata | *Canis* sp. | 3 | 62 | 1.00 |
| cyp\_00010 | Plantae | *Carex* sp. 8 | 2 | 32 | 1.00 |
| cyp\_00170 | Plantae | *Carex* sp. 9 | 2 | 493 | 1.00 |
| gh\_00018 | Plantae | *Cannabis sativa* | 2 | 241885 | 1.00 |
| gh\_00047 | Plantae | *Areca triandra* | 2 | 27985 | 0.98 |
| gh\_00052 | Plantae | Brassicaceae | 2 | 15432 | 0.97 |
| gh\_00065 | Plantae | *Melampyrum pratense* | 2 | 11255 | 1.00 |
| gh\_00115 | Plantae | *Lotus japonicus* | 2 | 5716 | 0.98 |
| gh\_00117 | Plantae | *Polygonum cognatum* | 2 | 6509 | 0.96 |
| gh\_00125 | Plantae | Hypnales | 2 | 4842 | 0.96 |
| gh\_00137 | Plantae | *Geranium* sp. | 2 | 4885 | 0.96 |
| gh\_00174 | Plantae | *Viola bulbosa subsp. tuberifera* | 2 | 1055 | 0.98 |
| gh\_00259 | Plantae | *Sphagnum* sp. | 2 | 2697 | 0.96 |
| mav\_00019 | Arthropoda | *Bombus sporadicus* | 2 | 55845 | 1.00 |
| mav\_00036 | Arthropoda | *Cosmophasis micarioides* | 2 | 25046 | 0.97 |
| mav\_00048 | Arthropoda | *Bombus* sp. | 2 | 17569 | 0.97 |
| mav\_00126 | Arthropoda | Athetini | 2 | 4427 | 1.00 |
| mav\_00143 | Arthropoda | Caeciliusidae | 2 | 3838 | 1.00 |
| mav\_00164 | Arthropoda | Pancrustacea | 2 | 3286 | 0.97 |
| mav\_00177 | Arthropoda | *Stemonyphantes* sp. | 2 | 2635 | 1.00 |
| mav\_00193 | Arthropoda | *Bombus* sp. | 2 | 3015 | 1.00 |
| mav\_00228 | Arthropoda | *Evarcha* sp. | 2 | 1946 | 1.00 |
| mav\_00270 | Arthropoda | Pancrustacea | 2 | 2001 | 0.97 |
| poa\_00039 | Plantae | *Alopecurus japonicus* | 2 | 7616 | 1.00 |
| poa\_00055 | Plantae | Pooideae | 2 | 758 | 0.99 |
| poa\_00060 | Plantae | *Oryza* sp. | 2 | 4304 | 1.00 |
| poa\_00072 | Plantae | *Vahlodea atropurpurea* | 2 | 1599 | 0.99 |
| poa\_00086 | Plantae | Poeae | 2 | 2134 | 0.97 |
| poa\_00140 | Plantae | *Dactylis glomerata* | 2 | 1047 | 1.00 |
| poa\_00152 | Plantae | *Holcus lanatus* | 2 | 855 | 1.00 |
| ros\_00077 | Plantae | *Rubus* sp. | 2 | 729 | 1.00 |
| summed10 | Plantae | *Molinia caerulea* | 2 | 8994 | 0.99 |
| ast\_00075 | Plantae | *Cirsium* sp. | 1 | 2528 | 0.99 |
| ast\_00078 | Plantae | Cichorieae | 1 | 2417 | 0.99 |
| ast\_00125 | Plantae | *Cirsium arvense* | 1 | 2065 | 1.00 |
| ast\_01047 | Plantae | *Cirsium* sp. | 1 | 20 | 0.99 |
| ast\_01267 | Plantae | *Leontodon hispidus* | 1 | 133 | 1.00 |
| ast\_01693 | Plantae | Tussilagininae | 1 | 19 | 0.98 |
| cyp\_00099 | Plantae | *Carex* sp. 10 | 1 | 917 | 1.00 |
| cyp\_00112 | Plantae | *Carex* sp. 11 | 1 | 205 | 1.00 |
| cyp\_00173 | Plantae | *Carex* sp. 12 | 1 | 533 | 0.96 |
| cyp\_00223 | Plantae | *Carex* sp. 13 | 1 | 361 | 1.00 |
| cyp\_00254 | Plantae | *Carex* sp. 14 | 1 | 344 | 1.00 |
| cyp\_00469 | Plantae | *Carex* sp. 15 | 1 | 142 | 1.00 |
| cyp\_00634 | Plantae | *Carex* sp. 16 | 1 | 58 | 1.00 |
| gh\_00006 | Plantae | *Vaccinium ovalifolium* | 1 | 2028 | 1.00 |
| gh\_00105 | Plantae | *Teucrium* sp. | 1 | 4779 | 0.98 |
| gh\_00106 | Plantae | *Morella diversifolia* | 1 | 7598 | 0.96 |
| gh\_00138 | Plantae | *Trifolium gymnocarpon* | 1 | 5259 | 0.98 |
| gh\_00157 | Plantae | *Musa rosea* | 1 | 1705 | 0.98 |
| gh\_00160 | Plantae | *Trifolium* sp. | 1 | 4100 | 0.98 |
| gh\_00179 | Plantae | *Ptilium crista-castrensis* | 1 | 3667 | 1.00 |
| gh\_00198 | Plantae | *Trientalis europaea* | 1 | 1941 | 1.00 |
| gh\_00261 | Plantae | *Leucothoe* sp. | 1 | 2532 | 0.98 |
| gh\_00340 | Plantae | *Allium* sp. | 1 | 1140 | 0.98 |
| gh\_00366 | Plantae | *Vicia cracca* | 1 | 1798 | 1.00 |
| gh\_00484 | Plantae | Arecaceae | 1 | 1192 | 0.96 |
| gh\_01045 | Plantae | *Tumamoca macdougalii* | 1 | 354 | 0.96 |
| gh\_01574 | Plantae | *Juncus balticus* | 1 | 241 | 0.98 |
| gh\_02455 | Plantae | *Asparagus* sp. | 1 | 148 | 0.98 |
| mav\_00018 | Arthropoda | *Bombus campestris* | 1 | 66625 | 1.00 |
| mav\_00026 | Arthropoda | Aphidomorpha | 1 | 34608 | 0.97 |
| mav\_00061 | Arthropoda | Pancrustacea | 1 | 11508 | 0.97 |
| mav\_00078 | Arthropoda | *Prosarthria teretrirostris* | 1 | 8368 | 0.97 |
| mav\_00083 | Arthropoda | Pancrustacea | 1 | 7388 | 0.97 |
| mav\_00159 | Arthropoda | Schizophora | 1 | 3398 | 0.97 |
| mav\_00230 | Arthropoda | Pancrustacea | 1 | 2538 | 0.97 |
| mav\_00239 | Arthropoda | Scarabaeidae | 1 | 1405 | 1.00 |
| mav\_00240 | Arthropoda | Obtectomera | 1 | 1928 | 0.97 |
| mav\_00243 | Arthropoda | Pancrustacea | 1 | 1818 | 0.97 |
| mav\_00276 | Arthropoda | *Metoecus* sp. | 1 | 1855 | 1.00 |
| mav\_00283 | Arthropoda | Mandibulata | 1 | 1776 | 0.97 |
| mav\_00290 | Arthropoda | Cicadellidae | 1 | 1436 | 0.97 |
| mav\_00293 | Arthropoda | *Deroceras reticulatum* | 1 | 1873 | 1.00 |
| mav\_00299 | Arthropoda | *Macrosteles fascifrons* | 1 | 1787 | 1.00 |
| mav\_00300 | Arthropoda | Lycosidae | 1 | 1807 | 0.97 |
| mav\_00360 | Arthropoda | Pancrustacea | 1 | 1197 | 0.97 |
| mav\_00371 | Arthropoda | Polyphaga | 1 | 1322 | 0.97 |
| mav\_00377 | Arthropoda | Nicrophorinae | 1 | 1306 | 0.97 |
| mav\_00387 | Arthropoda | Protostomia | 1 | 1282 | 0.97 |
| mav\_00411 | Arthropoda | Aleocharinae | 1 | 587 | 1.00 |
| mav\_00437 | Arthropoda | Miridae | 1 | 1054 | 1.00 |
| mav\_00458 | Arthropoda | *Evarcha* sp. | 1 | 348 | 0.97 |
| mav\_00472 | Arthropoda | *Pardosa* sp. | 1 | 650 | 1.00 |
| mav\_00480 | Arthropoda | *Thrips flavidulus* | 1 | 678 | 0.97 |
| mav\_00492 | Arthropoda | *Syneta adamsi* | 1 | 886 | 1.00 |
| mav\_00530 | Arthropoda | *Bolitochara pulchra* | 1 | 778 | 1.00 |
| mav\_00587 | Arthropoda | *Isotoma viridis* | 1 | 541 | 0.97 |
| mav\_00722 | Arthropoda | Polyphaga | 1 | 433 | 0.97 |
| mav\_00754 | Arthropoda | *Paralamyctes* sp. | 1 | 382 | 1.00 |
| mav\_01252 | Arthropoda | Endopterygota | 1 | 146 | 0.97 |
| mav\_01374 | Arthropoda | Mandibulata | 1 | 165 | 0.97 |
| mav\_01381 | Arthropoda | *Ampedus* sp. | 1 | 156 | 1.00 |
| poa\_00062 | Plantae | Agrostidinae | 1 | 444 | 0.99 |
| poa\_00074 | Plantae | *Poa* sp. | 1 | 158 | 1.00 |
| poa\_00098 | Plantae | Triticeae | 1 | 285 | 1.00 |
| poa\_00132 | Plantae | Poeae | 1 | 807 | 0.99 |
| poa\_00182 | Plantae | Poeae | 1 | 808 | 0.96 |
| poa\_00197 | Plantae | Loliinae | 1 | 872 | 0.99 |
| poa\_00298 | Plantae | Poeae | 1 | 388 | 0.99 |
| poa\_00385 | Plantae | *Melica picta* | 1 | 295 | 1.00 |
| poa\_00530 | Plantae | Poeae | 1 | 113 | 0.97 |
| poa\_00689 | Plantae | Poeae | 1 | 239 | 0.97 |
| ros\_00053 | Plantae | *Potentilla reptans* | 1 | 57 | 1.00 |
| ros\_00073 | Plantae | *Fragaria* sp. | 1 | 21 | 1.00 |
| ros\_00468 | Plantae | *Rosa* sp. | 1 | 52 | 1.00 |
| summed3 | Arthropoda | *Apis mellifera* | 1 | 201 | 1.00 |
| summed4 | Arthropoda | *Bradysia amoena* | 1 | 557 | 0.97 |
| v05\_00114 | Chordata | *Meleagris gallopavo* | 1 | 163 | 1.00 |
| v05\_00130 | Chordata | *Dama dama* | 1 | 1516 | 1.00 |
| v05\_00184 | Chordata | *Tetrastes bonasia* | 1 | 108 | 1.00 |
| v05\_00192 | Chordata | *Sorex araneus* | 1 | 731 | 1.00 |
| v05\_00216 | Chordata | *Anas* sp. | 1 | 647 | 1.00 |
| v05\_00269 | Chordata | *Turdus philomelos* | 1 | 74 | 1.00 |
| v05\_00356 | Chordata | *Rana temporaria* | 1 | 195 | 1.00 |
| v05\_00516 | Chordata | *Lutra lutra* | 1 | 201 | 1.00 |
| v05\_00821 | Chordata | *Canis lupus familiaris* | 1 | 38 | 1.00 |
| ¶ OTU-Operational taxonomic unit |

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| **Table A.3**. Model selection based on AICc values (w*i*= AICc weights) finding the most parsimonious linear mixed-effect model when fitting 120 samples of fecal crude protein (CP) of brown bears in relation to sex, age and reproductive categories and areas (prior to visit to settlements, settlements, and remote areas), and bear duration at settlements, in south-central Sweden between May and September 2010. BC=bear category, Fe=field exposure, d=Julian date, Sd=settlement duration, SR= prior to visit to a settlement, settlement, and remote areas |
| **Candidate models** | **K** | **AICc** | **ΔAICc** | ***wi*** | ***wi* cum.** |
| BC + d | 8 | 681.77 | 0.00 | 0.98 | 0.98 |
| SR + d | 6 | 690.07 | 8.30 | 0.02 | 1.00 |
| Fe + d  | 5 | 707.49 | 25.71 | 0.00 | 1.00 |
| Intercept only  | 3 | 708.12 | 26.35 | 0.00 | 1.00 |
| BC + Fe + Sd + d | 10 | 710.79 | 29.01 | 0.00 | 1.00 |
| BC + SR + Fe + Sd + d | 12 | 711.72 | 29.95 | 0.00 | 1.00 |
| Fe + Sd + d  | 6 | 718.91 | 37.13 | 0.00 | 1.00 |
| SR + Fe + Sd + d | 8 | 719.76 | 37.99 | 0.00 | 1.00 |

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| **Table A.4**. Fecal crude protein (CP) among categories of brown bears during May – September 2010, based on the most parsimonious linear mixed-effect model with bear identity as random effect (Table S3). Markov Chain Monte Carlo (MCMC)-simulated *β* and its 95% highest posterior density interval (HPD) and P-values are given with *β* and standard errors (SE) based on a *t*-distribution. Variances of random effects are 11.06 for bear identity and 12.04 for residuals for highest ranked model. Adult males are reference level within the bear category factor. |
| **ΔAICc = 0.00, *w* = 0.98** | ***β*** | **SE** | ***β*MCMC** | **HPD 95% lower** | **HPD 95% upper** | ***P*MCMC** |
| (Intercept) | 30.77 | 3.01 | 29.54 | 24.15 | 35.11 | 0.001 |
| Females w cubs of the year | -1.57 | 2.38 | -1.93 | -5.71 | 2.00 | 0.294 |
| Females with yearlings | -5.05 | 2.89 | -4.56 | -9.01 | -0.18 | 0.024 |
| Lone adult females | -0.29 | 1.99 | -0.24 | -3.46 | 2.61 | 0.904 |
| Subadult females and males | -0.06 | 1.99 | -0.06 | -2.98 | 2.98 | 0.972 |
| Julian date | -0.08 | 0.01 | -0.07 | -0.10 | -0.05 | 0.001 |

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| **Table A.5**. Model selection based on AICc values (w*i*= AICc weights) finding the most parsimonious linear mixed-effect model when fitting 120 samples of fecal crude fat (CFA) of brown bears in relation to sex, age and reproductive categories and areas (prior to visit to settlements, settlements, and remote areas), and bear duration at settlements, in south-central Sweden between May and September 2010. BC=bear category, Fe=field exposure, d=Julian date, Sd=settlement duration, SR= prior to visit to a settlement, settlement, and remote areas |
| **Candidate models** | **K** | **AICc** | **ΔAICc** | ***wi*** | ***wi* cum.** |
| Intercept only  | 3 | 488.59 | 0.00 | 0.92 | 0.92 |
| BC + d | 8 | 493.75 | 5.15 | 0.07 | 0.99 |
| SR + d  | 6 | 498.15 | 9.55 | 0.01 | 1.00 |
| Fe + d | 5 | 518.16 | 29.57 | 0.00 | 1.00 |
| BC + SR + Fe + Sd + d  | 12 | 526.60 | 38.01 | 0.00 | 1.00 |
| BC + Fe + Sd + d | 10 | 527.42 | 38.83 | 0.00 | 1.00 |
| SR + Fe + Sd + d  | 8 | 531.25 | 42.66 | 0.00 | 1.00 |
| Fe + Sd + d | 6 | 531.70 | 43.11 | 0.00 | 1.00 |

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| **Table A.6**. Model selection based on AICc values (w*i*= AICc weights) finding the most parsimonious linear mixed-effect model when fitting 120 samples of fecal crude acid detergent lignin/neutral detergent fiber (ADL/NDF) of brown bears in relation to sex, age and reproductive categories and areas (prior to visit to settlements, settlements, and remote areas), and bear duration at settlements, in south-central Sweden between May and September 2010. BC=bear category, Fe=field exposure, d=Julian date, Sd=settlement duration, SR= prior to visit to a settlement, settlement, and remote areas |
| **Candidate models** | **K** | **AICc** | **ΔAICc** | ***wi*** | ***wi* cum.** |
| Intercept only  | 3 | 36.91 | 0.00 | 1.00 | 1.00 |
| SR + d | 6 | 58.57 | 21.66 | 0.00 | 1.00 |
| BC + d | 8 | 64.65 | 27.74 | 0.00 | 1.00 |
| Fe + d | 5 | 70.54 | 33.63 | 0.00 | 1.00 |
| Fe + Sd + d  | 6 | 86.55 | 49.64 | 0.00 | 1.00 |
| SR + Fe + Sd + d | 8 | 96.53 | 59.63 | 0.00 | 1.00 |
| BC + Fe + Sd + d | 10 | 102.97 | 66.06 | 0.00 | 1.00 |
| BC + SR + Fe + Sd + d | 12 | 112.68 | 75.78 | 0.00 | 1.00 |

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| **Table A.7**. Correlation and significance of factors and vectors fitted to the detrended correspondence analysis (DCA) ordination for dietary composition of brown bears in south-central Sweden. Significant factors and vectors are indicated in bold. *P*-values are based on 999 random permutations. |
| **Factor** | **r2** | ***P* r(>r)** |
| Settlement visit | 0.75 | **0**.**001** |
| Area | 0.02 | 0.349 |
| Bear identity | 0.52 | **0**.**001** |
| Sex, age, repr. category | 0.09 | **0**.**021** |
| Date | 0.54 | **0**.**001** |
| Fat (% feces) | 0.08 | **0**.**014** |
| ADL/NDF (% feces) | 0.01 | 0.856 |
| Protein (% feces) | 0.34 | **0**.**001** |
| Visit duration | 0.03 | 0.283 |
| Field exposure | 0.08 | 0.140 |
| r**2** – the maximized correlation vector.  |
| ADL/NDF – acid detergent lignin/neutral detergent fiber |