**Supplementary File 2**

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| **VCF** | **Description** | **Use** | **Filter Parameters** | **Availability** | **Software used** |
| soft-filtered | Unfiltered variant set with soft-filters appended at variant and sample level | initial variant calling | Depth (DP) > 10; Mapping Quality (MQ) > 40; Variant quality (QUAL) > 10; ((AD) / (DP)) ratio > 0.5; high\_heterozygosity: >10% het calls ; high\_missing > 90% sites missing | **CeNDR**https://storage.googleapis.com/elegansvariation.org/releases/20180527/variation/WI.20180527.soft-filter.vcf.gz | BCFtools - variant calling and variant level filters; vcf-kit - append sample-level filters |
| hard-filtered | Any variant site flagged by the soft filters is removed, Any sample genotype with a soft-filter flag are set to missing | processed variant set | Same as soft-filter | **CeNDR**https://storage.googleapis.com/elegansvariation.org/releases/20180527/variation/WI.20180527.hard-filter.vcf.gz | BCFtools - remove soft-filter sites |
| PopGen  | Processed variant set for population genomics analyses | pi;tajima's D; Fst; phylogeny; neighbor-net;admixture; treemix; haplotype | No missing genotypes sites | **Supplementary Data 3** https://github.com/AndersenLab/HawaiiMS/raw/master/data/elife\_files/Supplemental\_Data\_3.vcf.gz | BCFtools - remove sites with missing genotypes |