Biocultural vulnerability of traditional crops in the Indian Trans Himalaya

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Abstract

Traditional agricultural landscapes are vital reservoirs of biocultural heritage and agro-biodiversity, yet traditional farming systems and their unique crop landraces face increasing marginalization and genetic erosion. Using northwest Himalaya as a case study, we examine the ecological resilience and genetic diversity of an understudied traditional crop, black pea (scientific name unclear), alongside barley (*Hordeum vulgare*), and compare them to the introduced cash crop, green pea (*Pisum sativum L.*). Participatory field experiments with local farmers revealed that traditional crops outperform introduced varieties in survival and reproduction traits across sites. We generate the first whole-genome sequencing data for black peas. Clustering and nutritional analyses highlight black pea's genetic richness and dietary potential. Our findings underscore the importance of integrating Traditional Ecological

Knowledge with ecological science to sustain agrobiodiversity, enhance climate resilience, and promote sustainable food systems. We provide insights for global agri-food innovations and socio-ecological stability in fragile mountain ecosystems.

Teaser

Traditional understudied black pea and barley in Indian Trans Himalaya offer unique ecological, genetic, and nutritional potential.

1 Introduction

Traditional farming landscapes and mountain communities are important reservoirs for conservation of biodiversity, biocultural diversity and agro-ecological resources [1, 2, 3, 4, 5]. Traditional farming knowledge (in the form of, e.g., local crop landraces and seedbanks) results from complex cultural and environmental selection [6] and supports diverse ecosystem services [7, 8]. However, traditional practices have often been overlooked in conservation and modern agronomic research [9] even as researchers have noted declines in the diversity of landraces and crop genetic erosion [10]. This is concerning because traditonal production systems (*e.g* locally adapted crop varieties) may inform nutritional, cultural and ecological stability, especially in adverse climates [11, 12]. Therefore, research on local production systems is important for supporting regional livelihoods, sustaining socio-ecological stability and preserving cultural knowledge [13, 9].

The stability and productivity of food systems is increasingly vulnerable to increased variation in weather patterns, and in the frequency of extreme events (such as episodes of drought) often due to climate change [14, 15]. The high-altitude Trans-Himalayan landscape presents excellent case studies to examine traditional food systems and the impacts of climate change on agricultural production in mountainous communities. In that region, and more broadly over Asian montane rangelands, climate is changing even faster than the global average [16, 17], threatening both the agroecological landscape and local economy. These rangelands provide exceptional biodiversity and cultural richness [18, 19], and are also known as the Third Pole, because they hold the next largest reserves of freshwater and glacial ice after the polar regions. The human communities in these cold desert ecosystems share habitat with diverse wildlife, including the iconic but vulnerable snow leopard *Panthera uncia*, and depend closely on ecosystem services [20].

Our research examines traditional agricultural systems and their vulnerability in the fragile ecosystems of northwest Himalaya, in the state of Himachal Pradesh, India in the Spiti district (Fig. 1). Agricultural production in Spiti was traditionally subsistence-based [21]. The main crops grown were barley *Horedum vulgare* (*neh* or *jau* in Tibetan), and a local variety of pea called black pea (*sanmoh nako* or *dhoopchum* in Tibetan). The scientific name for black pea remains unclear (as we later explain) and until recently [22, 23] there were no scientific research articles on black peas. In 1983, an agro-economic revolution in Spiti was spearheaded by a family that experimentally planted green pea or garden peas *Pisum sativum L.* [21]. In the subsequent two decades, the predominantly subsistence-based production of the village communities has been increasingly replaced by the market-oriented production of cash crops (mainly green peas, apples), destabilizing the sustainability of the cropping system [24, 25, 26].

During our socio-cultural work, we learnt that black pea and barley (Fig. **??**) are an integral part of ethnodietary recipes and of a climate-resilient farming system, but their cultivation has drastically declined due to market forces and lack of information [26]. The practice of polyvarietal cultivation of barley (*kneu, soha, nenak, and eumo*) is nearly extinct [21]. *kneu* is the only variety grown currently with small quantities of *soha* for religious ceremonies. Without adequate research, the understudied black peas are close to facing cultural extinction. Grown for around 3000 years in the Tibetan-Qinghai plateau [27, 28, 29, 30, 31], barley and black peas are likely well adapted to the region's geo-climatic conditions and irrigation regimes.

In this research, we use a multipronged approach to provide an ecological, genetic and nutritional characterization of black pea, which to our knowledge has not been done before. Using Indian Trans-Himalaya as a case study, we compared several traits (such as germination, flowering) for traditional crops (we include black peas and barley) and cash crops of green peas. The key research questions are as follows: firstly, we examined whether traditional crops are better adapted to changing climatic conditions in terms of their survival and reproductive traits (such as stem height, number of pods, among others). Secondly, we examined whether black pea differs in genetic diversity from other peas in the *Pisus* genus. We expected genetic differences between black peas and green peas, but did not have a prior on the magnitude and nature of those differences. Thirdly, we examined the nutritional profile of back pea to address the lack of existing data on this crop.

We performed field experiments (March-September 2023) to compare the three different crops (black pea, barley, and green pea) for reproductive and photosynthetic traits under variable water treatments across three elevation gradients (see Materials and Methods). We co-designed the

experiments with local farmers who advised on sowing density, soil depth, and bed preparation to ensure optimal growth conditions. To examine the second research question, we generated the first whole-genome sequencing (shotgun sequencing using the Illumina platform) for black pea using leaf sample (see Materials and Methods). We then performed a chromosome-wide clustering analysis and Principal Component Analysis (PCA) to compare our black pea sample with pea accessions published in [32]. For the third question, we collaborated with the Central Food Technological Research Institute (CFTRI) in India to provide a standardized nutritional profile for black peas.

Our study establishes ecological, genetic and nutritional baseline data for black peas, addressing the existing knowledge gap on this crop. Previous studies [33, 25, 22] have noted trends in cropping patterns, but there has not been a comprehensive assessment of traditional food systems in the region, especially black peas, with respect to its ecology and genetic diversity, as well as their impacts on local communities that depend on them. In the next sections, we describe the study system, research methods, results and recommendations. We close with a discussion on integrating local knowledge and modern science to examine lesser-known and underutilized crops to foster food systems that are environmentally sustainable and adaptable to changing climatic conditions.

2 Results: Traditional production systems

2.1 Survival and reproductive traits from field experiments

We focused on three key aspects: ecology, genetics, and nutrition for traditional crops and cash crops. We hypothesized that traditional crops are more resilient than cash crops as measured by traits such as stem height, number of pods, among others. We expected genetic differences between black peas and green peas, but did not have a prior on the magnitude and nature of those differences. Nutritionally, we expected that black peas have a distinct and high nutritional profile compared to green peas because cash crops are consistently selected for particular nutritional values and sold in markets for this trait [34, 35].

We first want to note that the results are averaged across water treatments because of high rainfall in the summer of 2023. The drought treatments received rainfall and we therefore treated different treatments as replicates. Our first result from the field experiment shows both black peas and

barley have higher survival probability (or establishment rate since few seeds are eaten by birds, livestock and ungulates) in comparison with green peas across all sites. The results are consistent across three different ecological settings as shown in Fig. 2 A. The site Kiamo (at 4000m) has highest average establishment rate for black peas with 0.51 overall. The high establishment rates for black peas (evidenced by the higher mean value) underscore a possible genetic or phenotypic advantage over green peas. These findings suggest that black peas may possess attributes that confer greater survival advantages under the diverse conditions represented by the study sites.

Except one site (Tashigang) at 4500m elevation, barley establishment rates are lower than green peas across all sites. Please note there are no error bars for barley because some of our barley plots were destroyed and we were only able to preserve one plot per site. We also added another experimental site Thinam at 4600m without replicates to note seed survival in high elevation. Farmers noted they had been experimenting growing crops at even higher elevation (4600m) due to better availability of snow melt and access to water. We find low success at this elevation across all crops at Thinam as shown in last panel of Fig. 2 A.

Next, we evaluate non-reproductive traits such as average stem height and average number of leaves (correspond to higher photosynthetic activity). As shown in the Supplement fig. (S1:S3), black peas outperform green peas consistently across all sites. The average stem height for black peas is 38.12cm, 24.3cm, 25cm compared to 18.2cm, 12.48cm, 10.7cm, across Kiamo, Kibber, and Tashigang, respectively. We do not consider barley in these plots because barley is a grass species from *Poaceae* family.

Important covariates for farmers include the reproductive traits such as proportion of flowering plants and pea pods. Fig. 3 A describes the distribution of survival-weighted proportion of flowering plants. Through the cropping season, we noted the proportion of flowering plants and weighted it by survival. We find black peas have higher proportion of flowering plants for black peas on average (0.62) than green peas (0.27) at Kiamo site (4000m) during peak flowering time. Black peas (0.5) have higher flowering proportion than green peas (0.31) at Kibber site (4200m). However, at the highest elevation Tashigang (4500m), green peas (0.3) outperform black peas (0.2) though both perform worse than at the two other sites. Similarly, the average number of pods per individual plant are also higher for black peas than green peas as shown in Fig. 3 B.

Finally, we evaluate the growth rate for all crops by taking stem height as a predictor in an ordinary least squares (OLS) regression and find black peas, barley and green peas have growth rates 0.83, 0.6, and 0.38 as shown in Fig. 2 (B). OLS ignores site variance, assuming a single growth rate across all sites. Therefore, we also performed a linear mixed model with site as a ran-

dom effect, allowing for variation in baseline growth across different sites (fig. S3). For black pea, the growth rate was 0.8951 (SE = 0.0687, p-value < 0.01) in LMM, compared to 0.8266 (SE = 0.0703, pvalue < 0.01) in OLS. For green pea, the estimated growth rate using the LMM was 0.428 (SE = 0.038), whereas the OLS regression estimated a slightly lower growth rate of 0.383 (SE = 0.039), indicating that accounting for site-level variation in LMM resulted in a slightly higher estimate. For barley, the growth rate estimated by LMM was 0.604 (SE = 0.040), while OLS produced a similar estimate of 0.600 (SE = 0.041), suggesting that site-specific effects had minimal impact on growth rate estimation for this crop. The table and figure are presented in the Supplement (table S1 and fig. S3). Our results are consistent, though the site variation is notably high for black peas. We want to note that our dataset consists of observations from a single year (2023-2024 with a pilot in 2022). Therefore, we used simple statistical regression in the absence of repeated measurements across multiple years. Future studies over multiple years will provide a better estimate of growth rates and effects of site variation.

2.2 Genetic diversity of black peas

Pea belongs to the most ancient set of cultivated plants and is known to be domesticated about 10,000 years ago in the Middle East and Mediterranean region (also known as Fertile Crescent) [36, 37]. Although the taxonomy of *Pisum* genus is complex and still under debate [32, 38], there is consensus that the genus consists of two species- wild *P. fulvum* and *P. sativum* [39]. *P. sativum* includes wild (subsp. *elatius*) and domesticated taxa (subsp. *sativum*).

We generated the first whole genome sequencing data for the black pea and have mapped it to the P. sativum reference genome. The average depth of coverage of our black pea data was 15X with a breadth of coverage across the reference genome of 86.6% . We combined this data with data for pea accessions in [32], and performed a chromosome wide-PCA analysis to infer the structure of Pisum collection. Since we were interested in our black pea subpopulation, we used samples from *P. sativum* and admixed accessions. In addition, we included *Pisum sativum var. arvense* (Accession SRR19543725) and performed a PCA for each chromosome to compare the samples.

Our PCA results reveal the three principal components (PCs) explain approximately 50% of the observed genetic variation in the collection. We find pea accessions were separated based on the *P. sativum* subspecies consistent with previous studies [40, 32]. As shown in Fig. 4 (A and B), for chromosome NC_066584 and NC_066585 our sample clusters neither with domesticated varieties nor the wild germplasms. In addition, the black pea sample (Kibber) clustered distinctly

away from *P. sativum subsp. sativum var. arvense* sample. Although morphological study of black pea supports two recent studies [23, 22] from Himalayan region that identify the local black pea to be *Pisum sativum var. arvense* or field pea, a winter legume belonging to the Fabaceae (Leguminosae) family, our genetic results question the claim.

Next, to validate the robustness of observed genetic variation from the PCA results we performed clustering analysis on the covariance data. First, we implemented hierarchical clustering analysis of 18 different accessions for all chromosomes. Fig. 5 illustrates the results for two chromosomes NC_066581 and NC_066583. PC1 and PC2 accounted for about 25% and 16% of the observed genetic variance for each chromosome. Across both chromosomes, five genetically distinct clusters are consistently observed. The black pea sample formed a closely related subcluster with a traditional Indian landrace, *Pisum sativum asiaticum* (PSII30), while maintaining phylogenetic separation from other accessions. The results suggest that the black pea shares a genetic affinity with Indian landraces while exhibiting divergence, potentially underscoring localized evolutionary or selective pressures. Consistent with [32], *P. fulvum*, *P. abyssinicum* and cultivated *P. sativum* of Pisum formed separate single clusters as before. The results are also consistent for all chromosomes as shown in Fig. 6. We present the results in two separate plots because, for chromosomes NC_066581 and NC_066583, the black pea sample (Kibber) clustered into a group of two, whereas for the remaining five chromosomes (NC_066580, NC_066579, NC_066584, NC_066585, and NC_066582), black pea grouped into a cluster of four, indicating possible chromosome-specific genetic structuring. We present the plots for optimal clustering in the Supplement (fig. S4:S10).

We further implemented spectral clustering and k-means algorithms, which verified clustering patterns across all methods, reinforcing the reliability of observed population structure (as shown in Supplement fig. S11:S17. Overall, by generating the first whole-genome sequencing data for black peas from the Trans-Himalayan region, we discovered substantial genetic diversity and demonstrated that black peas form a distinct genetic clusters, suggesting their importance as a genetic resource for future breeding programs. Our research emphasizes that high-altitude Himalayan mountains are a relevant secondary center of pea diversity, rich in primitive cultivated forms of field peas [40].

2.3 Nutritional composition of black peas

Anecdotally, black peas are known for their diverse nutritional profile but the nutrient content for black peas from the Trans-Himalayas has been unclear. We collaborated with CFTRI based in Mysuru, Karnataka, India to create a nutritional profile for black peas. We find these legumes are rich in a variety of essential nutrients and offer a diverse combination of protein, fiber, vitamins, and minerals, making them not only culturally and ecologically important but also a valuable addition to a balanced diet. Table 1 provides a measure of nutrients and daily recommendation averages taken from NIH for a adult of body weight 70kg. Firstly, black peas are notably high in protein, with approximately 21.20% protein content per 100 grams. This makes them an excellent plant-based protein source, especially beneficial for individuals following vegetarian or vegan diets. Furthermore, black peas are a good source of dietary fiber (15.9% per 100 grams) in addition to crude fiber at 6.23% per 100 grams. Black peas also provide a range of essential vitamins such as Vitamin C (13.1 mg/100g), Vitamin B1 (0.61 mg/100g), Vitamin B3 (1.62 mg/100g). They are a good source of minerals such as iron (9.11 mg/100g), zinc (2.48 mg/100g), calcium (108.09 mg/100g), and magnesium (109.28 mg/100g).

3 Discussion

Our multi-pronged approach provides a comprehensive baseline for traditional crops in high-altitude Trans-Himalaya as these food systems are crucial to the stability of humans and their ecosystems [41, 42, 43]. The results of our ecological study find potential for lesser-known, understudied and underutilized traditional crops (black peas and barley) in terms of their survival and reproductive traits. We find black peas outperform green peas (cash crop) in terms of their establishment rates, survival-weighted proportion of flowering plants, and average stem height (Fig. 2 (A), 4 (A), S2). The findings align with our socio-cultural research during which local farmers underscored black peas are better adapted and more resilient (in terms of ease of growing, and drought resistance) than green peas [26]. We note that although we did not have sufficient replicates for barley, we included the crop in our study because barley holds profound cultural and religious importance in the Himalayan and Tibetan-Qinghai communities, and is the primary crop for traditional farming. Ethnobotanical work has repeatedly underlined how the crop performs the function of a 'cultural keystone species' [44].

We generated the first whole genome sequencing data for black peas from the Trans-Himalayan region to assess how genetically similar they are to other pea species. By generating first whole-genome sequencing data for black peas, we uncovered substantial genetic diversity and demonstrated that black peas form a distinct genetic clusters using three clustering algorithms along with principal component analysis. Our research suggests their importance as a genetic resource for future breeding programs. We expected genetic differences between black peas and green peas, but did not have a priori knowledge on the magnitude and nature of those differences. Although earlier studies [22, 23] identify black pea to be *P. sativum subsp. sativum var. arvense*, our findings show black peas to be distinct from *arvense*. Our research aligns with previous research [40] that emphasizes the high-altitude Himalayan mountains to be a relevant secondary centre of pea diversity, rich in primitive cultivated forms of field peas [40]. As a future direction, LD-based SNP pruning would be necessary for studies such as GWAS to identify trait-associated loci, selection scans to detect regions under adaptive evolution, or demographic history inference using coalescent-based methods [45, 46]. We also find black peas have high nutritional profile, offering high percentage of protein, dietary fiber, zinc, magnesium, among others. This makes them an excellent plant-based protein source, especially beneficial for individuals following vegetarian/vegan diets [26].

Many studies [47, 48] have noted wild pea diversity in peripheral regions is not adequately rep-

resented in the existing germplasm collections. [47] found two small populations of the wild pea *Pisum sativum subsp. elatius* in the Zagros Mts, Iran. They note wild pea populations are rare, small in size and suffer from climatic change and land exploitation c[47]. Another example is *Pisum sativum subsp. abyssinicum*, locally known as Dekoko peas, a unique subspecies endemic to Amhara and highland areas of Tigray, Ethiopia and to South Yemen [49, 48]. Dekoko peas are an important crop, widely mixed with the main cereal crops such as, sorghum, barley and teff. The crop qualifies for species status on the basis of its phenotype (early flowering and strongly serrate leaflets) and biological isolation [50]. Although cultivation of Dekoko peas had drastically declined due to drought and political disruption, in the past 10 years, there has been a considerable renewal of interest, resulting in Dekoko germplasm collections, characterization studies aimed at crop improvement and extending the areas of cultivation [51].

Looking beyond the *Pisum* genus, studies note that *Coffea stenophylla* can tolerate higher temperatures than the commercial species *Coffea arabica*, under threat from climate warming. Communities in Sierra Leone helped researchers at the Royal Botanic Gardens (Kew) to find coffee berries from *Coffea stenophylla* in the wild [52]. In southwestern Ethiopia, the banana-like Enset (*Ensete ventricosum*)has starch-filled stems that are a main source of calories and nutrients, while the leaves are used for basket making, to feed cattle, and to provide shade and build roofs. Additionally, this species is remarkably tolerant of drought and short-term temperature variations [9]. And as a final example, we note that the UN recognized 2023 as the International Year of Millets [53], calling attention to their many nutritional and health benefits, their suitability for cultivation under adverse and changing climatic conditions, and their potential to contribute to the UN 2030 Agenda for Sustainable Development. Our research emphasizes greater recognition of and research on lesser-known traditional crops in collaboration with communities who have long been using them, and who can be the main beneficiaries.

Our findings have important policy implications. Given the genetic variation revealed in black peas, we see great potential for modern analytical approaches and crop wild relatives (CWRs) to harness this diversity for crop improvement [54, 55]. Approaches such as genomic prediction, machine learning, and multi-trait gene editing offer innovative pathways to accelerate breeding efforts, enhancing the adaptability, yield, and nutritional quality of crops to meet future global food demands amidst increasing heat and drought stress [56]. Recently, [57] emphasized utilization of CWRs to enhance resilience in the Indian mustard *Brassica juncea (L.) Czern. and Coss.* cultigen pool. We recommend research using introgression techniques to improve adaptive traits for green peas via hybridization with black peas. These approaches may also improve the ability

to expand the cultivation of cash crops such as green peas, into adverse environments of drought conditions and extreme environments [58].

GIAHS, Globally Important Agricultural Heritage Systems (identified by the Food and Agriculture Organization, United Nations) recognize and designate bioculturally important sites to safeguard agrobiodiversity, protect agricultural heritage and recognize the knowledge and practices of local communities [59, 60, 42]. These declarations have triggered the development of different tourism activities related to biocultural inheritance. There are several successful examples: the Indigenous 'Bari System of Farming' practiced by the native people of North Eastern India (Assam) is recognized from the perspective of consumption, conservation, and biodiversity management [61]. Another example is the campesino cooperatives in Mapuche-Pewenche territory (southern Andes) who practice community-based tourism incorporating Mapuche rural culture and agricultural practices that support local food systems/economy with a strong identity component [62].

Based on our results, we recommend the Trans-Himalayan agricultural systems for recognition within the GIAHS framework due to their exceptional biocultural importance, ecological fragility, and potential to serve as models of sustainable agri-food systems [26]. The region's traditional farming practices have evolved over centuries in response to unique environmental pressures, resulting in agroecosystems that sustain both biodiversity and cultural heritage. Inclusion within the GIAHS framework could offer multiple benefits [27, 44]. First, it would safeguard local farming practices and associated traditional knowledge systems that are at risk of being lost due to the growing shift toward high-yield cash crops, thereby ensuring the continued cultivation of regionally meaningful landraces. Second, this could stimulate the creation of local and regional markets for traditional crops, such as black peas, which have demonstrated high nutritional value and resilience. Third, the GIAHS designation could promote sustainable tourism by drawing attention to the region's cultural and ecological uniqueness (such as snow leopards), creating considerable economic opportunities. Finally, the recognition would facilitate greater statewide, national and international collaboration, drawing resources for research, conservation, and sustainable development agro-initiatives. As the impacts of climate change intensify, safeguarding these bioculturally rich and ecologically sensitive systems becomes critical not only for local food security but also for global agrobiodiversity conservation efforts [9]. Overall, environmental and conservation outcomes could improve by recognizing and honoring the relationships between people and their landscapes, and proposing actions based on local priorities [63, 64].

Future research should address the limitations of our study, particularly the single-year dataset,

by conducting long-term studies to assess demographic vulnerabilities under varying climatic conditions. Such long-term data is needed to not only identify effects of climate change on the agro-ecosystem but also genetic variation in traditional crops. The long-term datasets may also shed light on other demographic patterns- which stage in life-cycle of crop is most vulnerable to water stress and plant pathogens? What makes traditional crops more resilient? A quantitative understanding of demographic tradeoffs as well as effects of stochasticity on dispersal patterns will yield important insights for farmers and management interventions [65, 66]. Further research is needed to identify the level of genetic variation and what genes and loci may be associated with adaptive traits [54]. This includes identification of desirable genes and traits from unadapted materials, such as CWRs, and the transformation of these traits so they can be used for creating resilient cultivars [31].

4 Materials and Methods

4.1 Study site

In the state of Himachal Pradesh (HP), about 26,000 km^2 area is potential snow leopard habitat [18]. Within this habitat, we focused on Lahaul-Spiti district (Fig. 1). The area lies in the rain-shadow of the main Greater Himalayan range, within the Trans-Himalaya region, bordering Tibetan plateau in the east. The landscape is typically above the treeline, between 3000-6000 m elevation range. Temperatures range from -30°C in peak winter to 30°C in peak summer. The landscape is mountainous cold desert and rocky, with steep slopes largely dominated by grasses and shrubs. Precipitation is received primarily in the form of snow in between November and March, and starts to melt by April.

The major river system is the Spiti river that originates from Kunzum range and travels 150 km in Kinnaur district before its confluence at Khap with Satluj river (from Tibet). Spiti river flows in deep chasms and gorges for most of its length with a catchments area is about $\sim$ 12000km^2 [67], most part being barren rocky land covered with thick moraines. The heavy snowfall in the winter months contributes to the Satluj's flow in spring. The Pin is the largest tributary of the Spiti River and Lingti, Parechu are other important tributaries. The townships and settlements are clustered close to the river systems or near a glacier from which they harvest water.

Spiti valley has a low human population density (c. 1 person/km^2). Agriculture is the backbone

of the economy, in addition to animal husbandry and tourism and 80% of the population in Spiti and Kinnaur are predominantly agro-pastoralists [68]. According to the 2011 census, the per capita annual income of the district is 2,289.57 USD (1,92,292 INR).

Ecologically, there is a robust community of small and large carnivores [19], including the vulnerable snow leopard (*Panthera uncia*). The two main prey species of the snow leopard – blue sheep *Pseudois nayaur* and ibex *Capra sibirica* – mostly occur in high altitude pastures and in relatively rugged terrain [69]. The livestock reared are sheep *Ovis aries*, goat *Capra hircus*, donkey *Equus asinus*, yak *Bos grunniens*, cattle *Bos indicus*, dzomo (a yak-cattle hybrid), and horses *Equus caballus*. The community has access to grazing pastures near the village over an area of approximately 70–100 km^2 with traditional grazing and collection rights in the pastures, where cultivation is not permitted. Relatively smaller-bodied livestock such as goats, sheep, donkeys, cows and dzomo are taken grazing every day during the summer months while larger bodied livestock such as yak and horses are left to free-graze over most of the year except for a few weeks during extreme winter [70]. All livestock are stall fed during the winter months. Fodder is collected from the pastures and crop fields and stored as winter forage.

We used a multidisciplinary approach to study traditional production systems in the Indian-Trans Himalaya. We first used an ecological lens to perform field experiments comparing green pea, black pea, and barley on their growth performance. We then examined the genetic and nutritional diversity for black pea to assess how well these results align with farmers perceptions.

4.2 Field experiment for survival and reproductive traits

The field study was conducted in March-September 2023 to evaluate the growth performance of three crop species: green peas, black peas, and barley under variable water treatments across altitudinal gradients. The experiment was carried at three sites characterized: low (4000m), mid (4200m), and high (4500m) elevations. The experiment was laid out in a randomized block design with a factorial arrangement, incorporating three factors: crop species, water treatments, and elevation levels. Each treatment combination was replicated three times, and thus a total of 81 plots were monitored. The seeds were sown uniformly across all plots and spacing was determined by interacting with farmers. The sowing density for green pea was lower than black pea seeds since black pea seeds are relatively smaller. The farmers also advised on sowing depth and bed preparation to ensure optimal growth conditions. The IRB eprotocol number is 71749.

We set up plots for green, black pea, and barley (1.5 by 1 meter) along a climate gradient in three

villages (at elevations 4000m, 4200m, 4500m) with three water treatments. The water treatments represented varying levels of water availability: low, medium, and regular. The low water treatment simulated drought conditions, medium represented the less than standard recommended irrigation practice for the region, and regular simulated conditions of water used by farmers. The adjustment was made by altering the number of irrigation times rather than the quantity of water.

Throughout the cropping season, we monitored the plants for photosynthetic, non-reproductive and reproductive traits such as, germination rate, flowering time, height at maturity, leaf coloration (disease infestation), and flower/pod production. Data on growth parameters (plant height, leaf area, and biomass) were collected at regular intervals (every 7-10 days). Yield components were assessed at the time of harvest. Our dataset consists of observations from a single year (2023-2024 with a pilot in 2022), and so we used ordinary least squares (OLS) regression to estimates growth rates with stem height as predictor variable for the crops. OLS ignores site variance, assuming a single growth rate across all sites. Therefore, we also performed a linear mixed model with site as a random effect, allowing for variation in baseline growth across different sites. To compare site-level crop means we analyzed the traits using ANOVA to determine the effects of the crop type, water treatment, elevation, and their interactions. All statistical analyzes were performed using the R software.

4.3 Genetic diversity

For the genetic analysis, we first sampled fresh leaves and performed DNA extraction using DNeasy Plant Pro kit (Cat #69204). Illumina libraries were constructed using KAPA HyperPrep Kit and whole genome sequencing was performed at Medgenome labs (based out of Delhi, India) on an Illumina NovaSeq platform using a paired 150bp configuration. Illumina reads were mapped to the *P. sativum* reference genome (accession GCF_024323335.1) using BWA-MEM and depth and breadth were calculated using SAMtools [71]. We want to note that the whole genome sequencing data generated for the black pea as part of this study has been deposited on NCBI - BioSample accession SAMN44380099.

We downloaded additional whole genome sequencing data from the recent paper [32] for P. sativum II, P. sativum III, P. sativum IV, and Pisum sativum var. arvense and also mapped these data to the reference genome using BWA-MEM. We list the whole genome sequencing data for the PCA analyses in the Supplement (table S2). The resultant alignment files (.bam files) were then run through ANSGD with the following flags "-uniqueOnly 1 -remove_bads 1 -only_proper_pairs 1

-trim 0 -C 50 -baq 1 -minMapQ 20 -minQ 20 -doCounts 1 -GL 1 -doMajorMinor 1 -doMaf 1 -skipTriallelic 1 -SNP_pval 1e-3 -doGeno 32 -doPost 1" to generate posterior probability of genotypes. We then used the ngsCover function from NGStools [72] to generate a covariance matrix for each of the 7 chromosomes (2n=14) and visualized the population structure using Principal Component Analysis.

Next, we employed three clustering algorithms: hierarchical, spectral and k-means clustering to delineate population structure among different *Pisum sativum* accessions. Hierarchical clustering builds a tree-like structure (dendrogram), allowing us to infer nested genetic relationships without a priori assumptions about cluster numbers [73]. For k-means and spectral clustering, which require a predefined number of clusters, we determined the optimal clusters (k) using two methods: first we implemented the elbow method which minimizes within-cluster sum of squares and then we implemented silhouette analysis which maximizes intra-cluster cohesion and inter-cluster separation. These validation metrics were calculated across a range of k values (2–10) to avoid subjective bias. We performed spectral clustering because it uses graph-based similarity matrices and is better at capturing non-linear, non-convex genetic patterns that distance-based methods such as, k-means might overlook [73]. These methods were applied to principal components derived from covariance matrices. Our multi-method approach strengthened confidence in the inferred genetic subdivisions among accessions.

We note that our analysis does not rely on SNP array design or GWAS methodologies and does not require LD-based SNP pruning. The approach allows us to retain a representation of genomic variation without concerns of pseudo-replication from LD-linked SNPs, as covariance matrices inherently capture genome-wide patterns of variation rather than treating each SNP independently.

4.4 Nutritional composition of black peas

The nutritional analysis for the black pea samples was done in collaboration with CSIR- Central Food Technological Research Institute (CFTRI) based out of Mysuru, India. The aim was to create a nutritional profile for black peas that includes the percentage per 100g of protein, carbohydrates, energy (kCal), and micronutrients such as zinc, magnesium, and iron.

References

[1] Joern Fischer, Tibor Hartel, and Tobias Kuemmerle. “Conservation policy in traditional farming landscapes”. *Conservation letters* 5.3 (2012), pp. 167–175.

[2] Fausto O Sarmiento, J Tomás Ibarra, Antonia Barreau, J Cristóbal Pizarro, Ricardo Rozzi, Juan A González, and Larry M Frolich. “Applied montology using critical biogeography in the Andes”. *Mountains: Physical, Human-Environmental, and Sociocultural Dynamics*. Routledge, 2018, pp. 179–191.

[3] Michael-Shawn Fletcher, Rebecca Hamilton, Wolfram Dressler, and Lisa Palmer. “Indigenous knowledge and the shackles of wilderness”. *Proceedings of the National Academy of Sciences* 118.40 (2021), e2022218118.

[4] Victoria Reyes-García, Rodrigo Cámara-Leret, Benjamin S Halpern, Casey O’Hara, Delphine Renard, Noelia Zafra-Calvo, and Sandra Díaz. “Biocultural vulnerability exposes threats of culturally important species”. *Proceedings of the National Academy of Sciences* 120.2 (2023), e2217303120.

[5] José Tomás Ibarra, Julián Caviedes, Carla Marchant, Sarah-Lan Mathez-Stiefel, Silvia Navarro-Manquilef, and Fausto O Sarmiento. “Mountain social-ecological resilience requires transdisciplinarity with Indigenous and local worldviews”. *Trends in ecology & evolution* (2023).

[6] Eduardo Aguilera, Cipriano Díaz-Gaona, Raquel García-Laureano, Carolina Reyes-Palomo, Gloria I Guzmán, Livia Ortolani, Manuel Sánchez-Rodríguez, and Vicente Rodríguez-Estévez. “Agroecology for adaptation to climate change and resource depletion in the Mediterranean region. A review”. *Agricultural Systems* 181 (2020), p. 102809.

[7] Devra I Jarvis, Toby Hodgkin, Bhuwon R Sthapit, Carlo Fadda, and Isabel Lopez-Noriega. “An heuristic framework for identifying multiple ways of supporting the conservation and use of traditional crop varieties within the agricultural production system”. *Critical Reviews in Plant Sciences* 30.1-2 (2011), pp. 125–176.

[8] Eduardo S Brondízio, Yildiz Aumeeruddy-Thomas, Peter Bates, Joji Carino, Álvaro Fernández-Llamazares, Maurizio Farhan Ferrari, Kathleen Galvin, Victoria Reyes-García, Pamela McElwee, Zsolt Molnár, Aibek Samakov, and Uttam B Shrestha. “Locally based, regionally manifested, and globally relevant: Indigenous and local knowledge, values, and practices for nature”. *Annual Review of Environment and Resources* 46.1 (2021), pp. 481–509.

[9] Alexandre Antonelli. “Indigenous knowledge is key to sustainable food systems”. *Nature* 613.7943 (2023), pp. 239–242.

[10] Colin K Khoury, Stephen Brush, Denise E Costich, Helen Anne Curry, Stef De Haan, Johannes MM Engels, Luigi Guarino, Sean Hoban, Kristin L Mercer, Allison J Miller, Gary P. Nabhan, Hugo R. Perales, Chris Richards, Chance Riggins, and Imke Thormann. “Crop genetic erosion: understanding and responding to loss of crop diversity”. *New Phytologist* 233.1 (2022), pp. 84–118.

[11] RP Singh. “Integration and commercialization of local varieties under sub-optimal environments for food security, promoting sustainable agriculture and agro-biodiversity conservation”. *MOJ Eco Environ Sci* 3.2 (2018), pp. 65–67.

[12] Teresa Borelli, Danny Hunter, Stefano Padulosi, Nadezda Amaya, Gennifer Meldrum, Daniela Moura de Oliveira Beltrame, Gamini Samarasinghe, Victor W Wasike, Birgül Güner, Ayfer Tan, Gaia Dembélé Yara Koreissi amd Lochetti, Amadou Sidibé, and Florence Tartanac. “Local solutions for sustainable food systems: The contribution of orphan crops and wild edible species”. *Agronomy* 10.2 (2020), p. 231.

[13] Alexander Wezel, Barbara Gemmill Herren, Rachel Bezner Kerr, Edmundo Barrios, Andre Luiz Rodrigues Goncalves, and Fergus Sinclair. “Agroecological principles and elements and their implications for transitioning to sustainable food systems. A review”. *Agronomy for Sustainable Development* 40 (2020), pp. 1–13.

[14] Martin Beniston. “Climatic change in mountain regions: a review of possible impacts”. *Climatic change* 59.1 (2003), pp. 5–31.

[15] Josh M Maurer, JM Schaefer, S Rupper, and AJSA Corley. “Acceleration of ice loss across the Himalayas over the past 40 years”. *Science advances* 5.6 (2019), eaav7266.

[16] Pashupati Chaudhary and Kamaljit S Bawa. “Local perceptions of climate change validated by scientific evidence in the Himalayas”. *Biology Letters* 7.5 (2011), pp. 767–770.

[17] Mayank Kohli, Tserennadmid Nadia Mijiddorj, Kulbhushansingh Ramesh Suryawanshi, Charudutt Mishra, Bazartseren Boldgiv, and Mahesh Sankaran. “Grazing and climate change have site-dependent interactive effects on vegetation in Asian montane rangelands”. *Journal of Applied Ecology* 58.3 (2021), pp. 539–549.

[18] Kulbhushansingh Suryawanshi, Abinand Reddy, Manvi Sharma, Munib Khanyari, Ajay Bijoor, Devika Rathore, Harman Jaggi, Abhirup Khara, Aditya Malgaonkar, Abhishek Ghoshal, Jenis Patel, and Charudutt Mishra. "Estimating snow leopard and prey populations at large spatial scales". *Ecological Solutions and Evidence* 2.4 (2021), e12115.

[19] J Patel, M Sharma, M Khanyari, A Bijoor, C Mishra, A Harihar, and K Suryawanshi. "Influence of predator suppression and prey availability on carnivore occurrence in western Himalaya". *Journal of Zoology* 322.1 (2024), pp. 3–11.

[20] Ranjini Murali, Purevjav Ikhagvajav, Venera Amankul, Kubanych Jumabay, Koustubh Sharma, Yash Veer Bhatnagar, Kulbushansingh Suryawanshi, and Charudutt Mishra. "Ecosystem service dependence in livestock and crop-based production systems in Asia's high mountains". *Journal of Arid Environments* 180 (2020), p. 104204.

[21] Charudutt Mishra, Herbert HT Prins, and Sipke E Van Wieren. "Diversity, risk mediation, and change in a Trans-Himalayan agropastoral system". *Human Ecology* 31.4 (2003), pp. 595–609.

[22] Astha Sharma and Mahesh Gupta. "Characterization of physicochemical, functional and antioxidant properties of western Himalayan black pea". *Journal of Agriculture and Food Research* 13 (2023), p. 100607.

[23] Shriya Bhatt, Rashim Kumari, and Mahesh Gupta. "Development of soluble dietary fiber incorporated black pea protein slice: Physicochemical, textural, and rheological properties". *Measurement: Food* 12 (2023), p. 100112.

[24] Aghaghia Rahimzadeh. "Socio-economic and environmental implications of the decline of chilgoza pine nuts of Kinnaur, Western Himalaya". *Conservation and Society* 18.4 (2020), pp. 315–326.

[25] Sumit Mukherjee. "Changing Economy and Culture of Food in Spiti". *Food and Power: Expressions of Food-Politics in South Asia* (2020), p. 1.

[26] Harman P. K. Jaggi. "Dynamics at Multiple Scales : Sites, Individuals, and Populations". English. Copyright - Database copyright ProQuest LLC; ProQuest does not claim copyright in the individual underlying works; Last updated - 2025-01-27. PhD thesis. 2024, p. 220. ISBN: 9798342113458.

[27] Alexandra Witze. "Barley fueled farmers' spread onto Tibetan Plateau". *Nature News* (2014).

[28] Jade d'Alpoim Guedes, Hongliang Lu, Yongxian Li, Robert N Spengler, Xiaohong Wu, and Mark S Aldenderfer. "Moving agriculture onto the Tibetan plateau: the archaeobotanical evidence". *Archaeological and Anthropological Sciences* 6 (2014), pp. 255–269.

[29] Fahu H Chen, Guanghui H Dong, Dongju J Zhang, Xinyi Y Liu, Xin Jia, Cheng-Bang An, Minmin M Ma, Yaowen W Xie, Loukas Barton, XY Ren, Z. J. Zhao, X. H. Wu, and M. K. Jones. "Agriculture facilitated permanent human occupation of the Tibetan Plateau after 3600 BP". *science* 347.6219 (2015), pp. 248–250.

[30] Li Tang, Hongliang Lu, Jixiang Song, Shargan Wangdue, Xinzhou Chen, Zhengwei Zhang, Xinyi Liu, Nicole Boivin, and Robert N Spengler III. "The transition to a barley-dominant cultivation system in Tibet: First millennium BC archaeobotanical evidence from Bangga". *Journal of Anthropological Archaeology* 61 (2021), p. 101242.

[31] Katarina Perić, Tihomir Čupić, Goran Krizmanić, Branimir Tokić, Luka Andrić, Marija Ravlić, Vladimir Meglič, and Marijana Tucak. "The Role of Crop Wild Relatives and Landraces of Forage Legumes in Pre-Breeding as a Response to Climate Change". *Agronomy* 14.7 (2024), p. 1385.

[32] Tao Yang, Rong Liu, Yingfeng Luo, Songnian Hu, Dong Wang, Chenyu Wang, Manish K Pandey, Song Ge, Quanle Xu, Nana Li, Guan Li, Yuning Huang, Rachit K. Saxena, Yishan Ji, Mengwei Li, Xin Yan, Yuhua He, Yujiao Liu, Xuejun Wang, Chao Xiang, Rajeev K. Varshney, Hanfeng Ding, Shenghan Gao, and Xuxiao Zong. "Improved pea reference genome and pan-genome highlight genomic features and evolutionary characteristics". *Nature genetics* 54.10 (2022), pp. 1553–1563.

[33] N. Kumar, Singh G., and Kumar D. "Kala Matar: An Indigenous Legume Crop of Spiti Valley in the Trans-Himalayan Cold Desert of India Facing Threat of Extinction". *International Journal of Current Research in Life Sciences* (2015), pp. 346–348.

[34] Rakesh K Maikhuri, Kottapalli S Rao, and KG Saxena. "Traditional crop diversity for sustainable development of Central Himalayan agroecosystems". *The International Journal of Sustainable Development & World Ecology* 3.3 (1996), pp. 8–31.

[35] M Santalla, Juana Marina Amurrio, and AM De Ron. "Food and feed potential breeding value of green, dry and vegetable pea germplasm". *Canadian Journal of plant science* 81.4 (2001), pp. 601–610.

[36] Shahal Abbo, Simcha Lev-Yadun, and Avi Gopher. "Agricultural origins: centers and non-centers; a Near Eastern reappraisal". *Critical Reviews in Plant Science* 29.5 (2010), pp. 317–328.

[37] Petr Smỳkal, Clarice J Coyne, Mike J Ambrose, Nigel Maxted, Hanno Schaefer, Matthew W Blair, Jens Berger, Stephanie L Greene, Matthew N Nelson, Naghmeh Besharat, Tomás Vymyslický, Cengiz Toker, Rachit K. Saxena, Manish Roorkiwal, Manish K. Pandey, Jinguo Hu, Ying H. Li, Li X. Wang, Yong Guo, Li J. Qiu, Robert J. Redden, and Rajeev K. Varshney. "Legume crops phylogeny and genetic diversity for science and breeding". *Critical Reviews in Plant Sciences* 34.1-3 (2015), pp. 43–104.

[38] Nicolas Rispail, Osman Zakaria Wohor, Salvador Osuna-Caballero, Eleonora Barilli, and Diego Rubiales. "Genetic diversity and population structure of a wide Pisum spp. core collection". *International Journal of Molecular Sciences* 24.3 (2023), p. 2470.

[39] Erez Naim-Feil, Maya Toren, Gregoire Aubert, Mor Rubinstein, Ada Rosen, Ravit Eshed, Amir Sherman, Ron Ophir, Yehoshua Saranga, and Shahal Abbo. "Drought response and genetic diversity in Pisum fulvum, a wild relative of domesticated pea". *Crop Science* 57.3 (2017), pp. 1145–1159.

[40] Runchun Jing, Alexander Vershinin, Jacek Grzebyta, Paul Shaw, Petr Smỳkal, David Marshall, Michael J Ambrose, TH Noel Ellis, and Andrew J Flavell. "The genetic diversity and evolution of field pea (Pisum) studied by high throughput retrotransposon based insertion polymorphism (RBIP) marker analysis". *BMC Evolutionary Biology* 10 (2010), pp. 1–20.

[41] Fabrice AJ DeClerck, Sarah Kate Jones, Simon Attwood, Deborah Bossio, Evan Girvetz, B Chaplin-Kramer, E Enfors, Alexander K Fremier, LJ Gordon, Fred Kizito, I Lopez Noriega, N Matthews, M McCartney, M Meacham, Noble, M Quintero, Roseline Remans, Richard Soppe, L Willemen, SLR Wood, and W Zhang. "Agricultural ecosystems and their services: the vanguard of sustainability?" *Current opinion in environmental sustainability* 23 (2016), pp. 92–99.

[42] FAO. "Indigenous Peoples' food systems: Insights on sustainability and resilience from the front line of climate change". *Rome: Alliance of Biodiversity International, International Centre for Tropical Agriculture (CIAT)* (2021).

[43] Ivette Perfecto and John Vandermeer. "Reflections on research agendas in agroecology: In search of a practical guide". *Journal of Agriculture, Food Systems, and Community Development* 13.3 (2024), pp. 1–7.

[44] Yannick Laurent. "The Tibetans in the making—Barley cultivation and cultural representations". *Revue d'Etudes Tibétaines* 33 (2015), pp. 78–108.

[45] Christopher S Carlson, Michael A Eberle, Mark J Rieder, Qian Yi, Leonid Kruglyak, and Deborah A Nickerson. “Selecting a maximally informative set of single-nucleotide polymorphisms for association analyses using linkage disequilibrium”. *The American Journal of Human Genetics* 74.1 (2004), pp. 106–120.

[46] Jon Slate, Jake Gratten, Dario Beraldi, Jessica Stapley, Matt Hale, and Josephine M Pemberton. “Gene mapping in the wild with SNPs: guidelines and future directions”. *Genetica* 136 (2009), pp. 97–107.

[47] OE Kosterin, VS Bogdanova, and AV Mglinets. “Wild pea (Pisum sativum L. subsp. elatius (Bieb.) Aschers. et Graebn. sl) at the periphery of its range: Zagros Mountains”. *Vavilov Journal of Genetics and Breeding* 24.1 (2020), p. 60.

[48] Yirga Gufi, Alemtsehay Tsegay, Morgan L Ruelle, Kassa Teka, Sarah Tewolde-Berhan, and Alison G Power. “Field pea diversity and its contribution to farmers’ livelihoods in northern Ethiopia”. *Legume Science* 4.4 (2022), e141.

[49] Berhane Gebreslassie and Berhanu Abraha. “Distribution and productivity of Dekoko (Pisum sativum var. abyssinicum A. Braun) in Ethiopia”. *Glob J Sci Front Res Biol Sci* 16 (2016), pp. 45–57.

[50] Gemechu Keneni, Fassil Assefa, M Imtiaz, and Endashaw Bekele. “Genetic diversity for attributes of biological nitrogen fixation in Abyssinian field pea (Pisum sativum var. Abyssinicum) germplasm accessions”. *Ethiopian Journal of Applied Science and Technology* 4.2 (2013), pp. 1–20.

[51] Berhanu Abraha Tsegay and Berhane G Gebreegziabher. “Effects of terrains’ soil and altitude on performance of Abyssinian pea (Pisum sativum var. abyssinicum A. Braun) landraces of Ethiopia”. *Biodiversitas Journal of Biological Diversity* 20.12 (2019).

[52] Aaron P Davis, Roberta Gargiulo, Michael F Fay, Daniel Sarmu, and Jeremy Haggar. “Lost and found: Coffea stenophylla and C. affinis, the forgotten coffee crop species of West Africa”. *Frontiers in Plant Science* 11 (2020), p. 521618.

[53] Rahul Verma. “The revival of ancient grains: Millets”. *International Journal of Political Science and Governance* (2023).

[54] Rae Page, Shuyi Huang, Moshe Ronen, Hanan Sela, Amir Sharon, Sandesh Shrestha, Jesse Poland, and Brian J Steffenson. “Genome-wide association mapping of rust resistance in Aegilops longissima”. *Frontiers in Plant Science* 14 (2023), p. 1196486.

[55] Rodomiro Ortiz, Filippo M Bassi, Mahesh Rao, and Diego Rubiales. “Trends and perspectives for the use of crop wild relatives in crop breeding”. *Frontiers in Plant Science* 15 (2024), p. 1424160.

[56] Andrés J Cortés and Felipe López-Hernández. “Harnessing crop wild diversity for climate change adaptation”. *Genes* 12.5 (2021), p. 783.

[57] Swati Verma, Namo Dubey, KH Singh, Nehanjali Parmar, Lal Singh, Dipika Sharma, Dipika Rana, Kalpana Thakur, Devina Vaidya, and Ajay Kumar Thakur. “Utilization of crop wild relatives for biotic and abiotic stress management in Indian mustard [Brassica juncea (L.) Czern. & Coss.]” *Frontiers in Plant Science* 14 (2023), p. 1277922.

[58] Emily Warschefsky, R Varma Penmetsa, Douglas R Cook, and Eric JB Von Wettberg. “Back to the wilds: tapping evolutionary adaptations for resilient crops through systematic hybridization with crop wild relatives”. *American journal of botany* 101.10 (2014), pp. 1791–1800.

[59] Parviz Koohafkan and Miguel A Altieri. *Globally important agricultural heritage systems: a legacy for the future*. Food and Agriculture Organization of the United Nations Rome, 2011.

[60] Antonio Santoro, Martina Venturi, Remo Bertani, and Mauro Agnoletti. “A review of the role of forests and agroforestry systems in the FAO Globally Important Agricultural Heritage Systems (GIAHS) programme”. *Forests* 11.8 (2020), p. 860.

[61] Anwesha Borthakur and Pardeep Singh. “Indigenous knowledge systems in sustainable water conservation and management”. *Water conservation and wastewater treatment in BRICS Nations*. Elsevier, 2020, pp. 321–328.

[62] Santiago Kaulen-Luks, Carla Marchant, Fernanda Olivares, and José Tomás Ibarra. “Biocultural heritage construction and community-based tourism in an important indigenous agricultural heritage system of the southern Andes”. *International Journal of Heritage Studies* 28.10 (2022), pp. 1075–1090.

[63] Roy C Dudgeon and Fikret Berkes. “Local understandings of the land: Traditional ecological knowledge and indigenous knowledge”. *Nature across cultures: Views of nature and the environment in non-Western cultures*. Springer, 2003, pp. 75–96.

[64] Patricia Kefilwe Mogomotsi, Goemeone EJ Mogomotsi, Keaoleboga Dipogiso, Nametso D Phonchi-Tshekiso, Lesego S Stone, and Dandy Badimo. “An analysis of communities’ attitudes toward wildlife and implications for wildlife sustainability”. *Tropical Conservation Science* 13 (2020), p. 1940082920915603.

[65] Harman Jaggi, David Steinsaltz, and Shripad Tuljapurkar. “Temporal variability can promote migration between habitats”. *Theoretical Population Biology* 158 (2024), pp. 195–205.

[66] Harman Jaggi, Wenyun Zuo, Rosemarie Kentie, Jean-Michel Gaillard, Tim Coulson, and Shripad Tuljapurkar. “Density dependence shapes life-history trade-offs in a food-limited population”. *Ecology Letters* 27.11 (2024), e14551.

[67] Pradeep Srivastava, Yogesh Ray, Binita Phartiyal, and Anupam Sharma. “Late Pleistocene-Holocene morphosedimentary architecture, Spiti River, arid higher Himalaya”. *International Journal of Earth Sciences* 102 (2013), pp. 1967–1984.

[68] Ranjini Murali, Stephen Redpath, and Charudutt Mishra. “The value of ecosystem services in the high altitude Spiti Valley, Indian Trans-Himalaya”. *Ecosystem Services* 28 (2017), pp. 115–123.

[69] Sumanta Bagchi and Charudutt Mishra. “Living with large carnivores: predation on livestock by the snow leopard (Uncia uncia)”. *Journal of zoology* 268.3 (2006), pp. 217–224.

[70] Ranjini Murali, Ajay Bijoor, Tanzin Thinley, Kalzang Gurmet, Kesang Chunit, Rinchen Tobge, Tanzin Thuktan, Kulbhushansingh Suryawanshi, Harini Nagendra, and Charudutt Mishra. “Indigenous governance structures for maintaining an ecosystem service in an agro-pastoral community in the Indian Trans Himalaya”. *Ecosystems and People* 18.1 (2022), pp. 303–314.

[71] Heng Li, Bob Handsaker, Alec Wysoker, Tim Fennell, Jue Ruan, Nils Homer, Gabor Marth, Goncalo Abecasis, Richard Durbin, and 1000 Genome Project Data Processing Subgroup. “The sequence alignment/map format and SAMtools”. *bioinformatics* 25.16 (2009), pp. 2078–2079.

[72] Matteo Fumagalli, Filipe G Vieira, Tyler Linderoth, and Rasmus Nielsen. “ngsTools: methods for population genetics analyses from next-generation sequencing data”. *Bioinformatics* 30.10 (2014), pp. 1486–1487.

[73] Trevor Hastie. *The elements of statistical learning: data mining, inference, and prediction*. 2009.

Positionality statement

We are 8 scientists and practitioners who deeply value agro-cultural and ecological diversity. Together we represent many places including India, United States, and Colombia. Two of us are native to the Trans-Himalayan region, and have been farming in this landscape for over two decades. Six of us have post-graduate and above academic backgrounds spanning interdisciplinary conservation science, population ecology, ethnobiology, and demography. We recognize that our current team composition may not fully encompass the breadth of interdisciplinary perspectives, particularly in Social sciences, agro-economics, and political ecology. However, our team includes both local perspective and researchers with expertise in conservation science, environmental policy and community engagement. We write this piece from our position of privilege when it comes to our educational backgrounds.

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Author Contributions

Conceptualization: H.J., A.A, A.E, K.Suryawanshi, and S.T. Data Curation: H.J., A.A., R.T., and T.T. Methodology: H.J., K.Solari, A.A, A.E, K.Suryawanshi, R.T. and S.T. Formal analysis: H.J., K.Solari., A.A, and S.T. Investigation: H.J., A.A., A.E., K.Suryawanshi, S.T., R.T., and T.T. Visualization: H.J., A.A., K.Solari, and A.E. Project administration: H.J., A.A., K.Suryawanshi, S.T., R.T., and T.T. Original draft: H.J., A.E., and S.T. Writing- review & editing: H.J., A.A, A.E., K.Suryanwanshi, and S.T. Funding acquisition: H.J., A.E., K.Suryawanshi, and S.T. Software: H.J. Supervision: H.J., A.E., K.Suryawanshi, and S.T. Validation: H.J., K.Suryawanshi, S.T. Resources: H.J., K. Suryawanshi, S.T.

All authors declare that they have no competing interests.

5 Figures

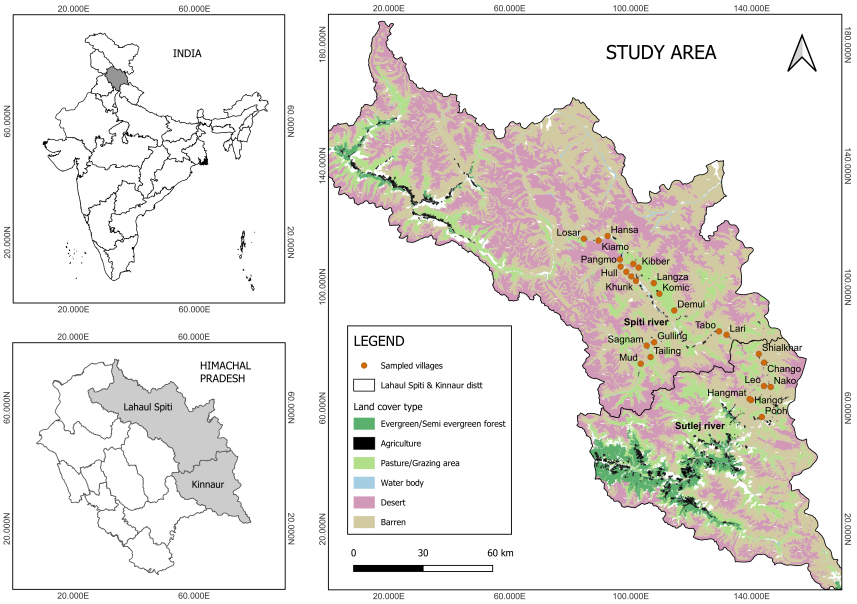

Figure 1: **Study site**. Study sites within Spiti Valley and Kinnaur district where we interviewed local community members across 26 villages and helped co-design experimental plots at the three sites discussed in the Methods section. Different colors correspond to land use characterizations such as agriculture, grazing pastures, and barren among others. The orange circles correspond to the villages sampled. The bottom-left panel shows the extent of Spiti and Kinnaur district within the state of Himachal Pradesh, India.

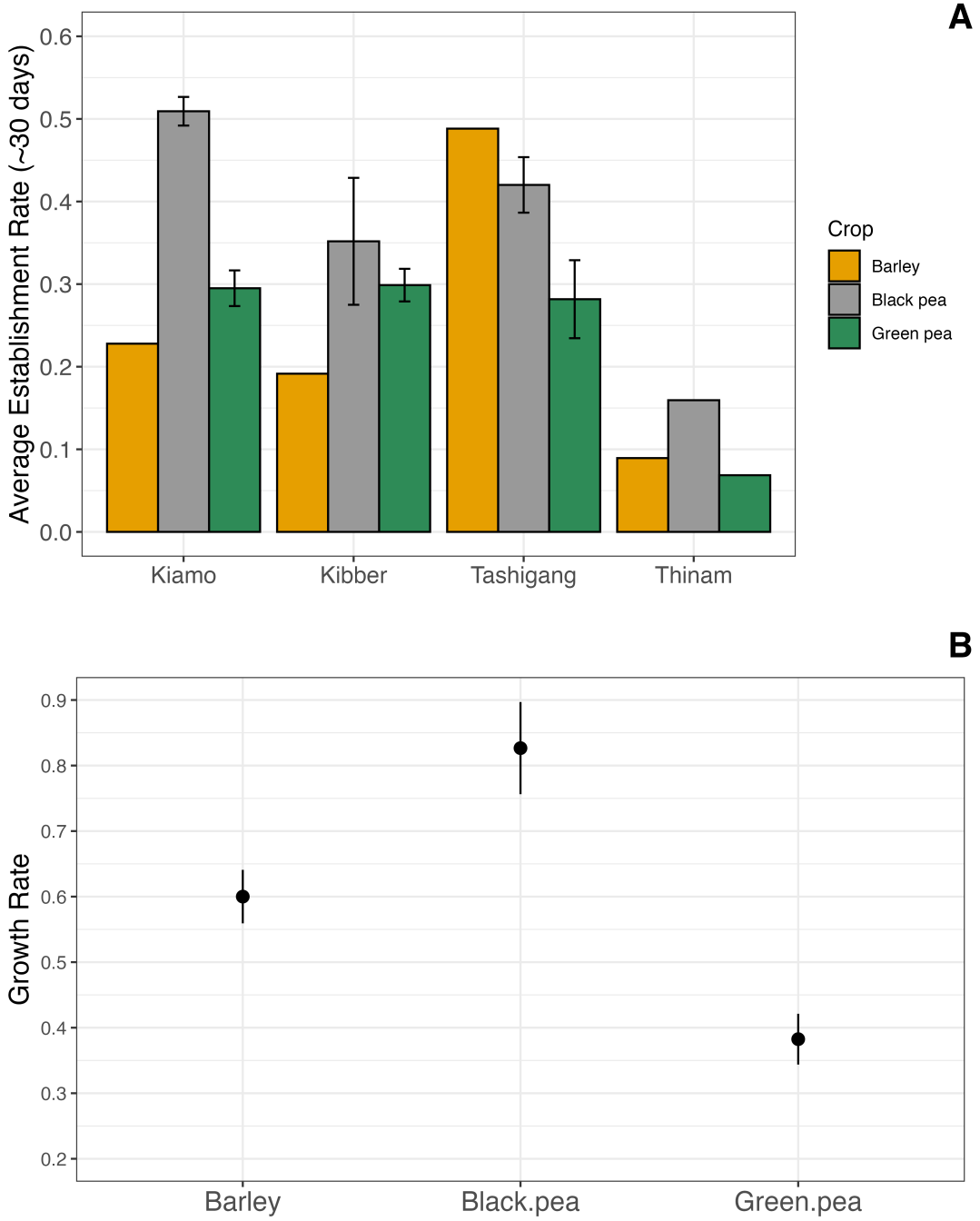

Figure 2: **Establishment and growth rate of black peas, green peas, and barley**. **(A)** The x-axis corresponds to four sites at different elevations: Kiamo (4000m), Kibber (4200m), Tashigang (4500m), and Thinam (4600m). The y-axis corresponds to average establishment rates for the crops. Each color corresponds to different crops: barley, black pea and green pea. The lack of error bars indicates that there was one replicate. **(B)** The y-axis corresponds to the log growth rates from the regression analysis and x-axis corresponds to crops- barley, black pea and green pea. The values are averaged over all sites and replicates.

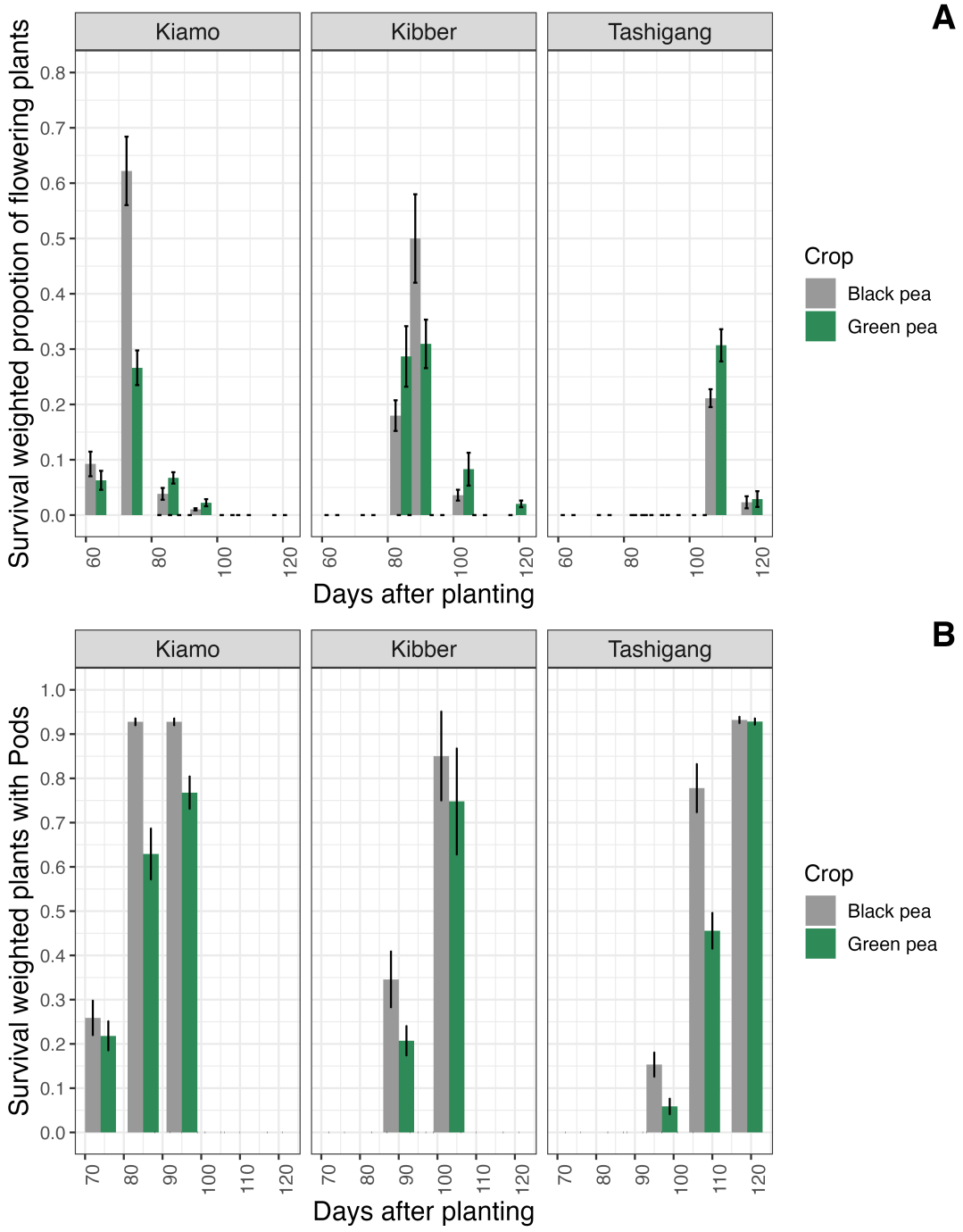

Figure 3: **Flowering and number of pods for green and black peas.** (**A** and **B**) Each panel corresponds to three sites at different elevations: Kiamo (4000m), Kibber (4200m), Tashigang (4500m). The x-axis corresponds to days after planting the seeds. The color corresponds to black peas and green peas. **(A)** The y-axis corresponds to survival-weighted proportion of flowering plants. **(B)** The y-axis corresponds to the survival weighted proportion of pods per plant.

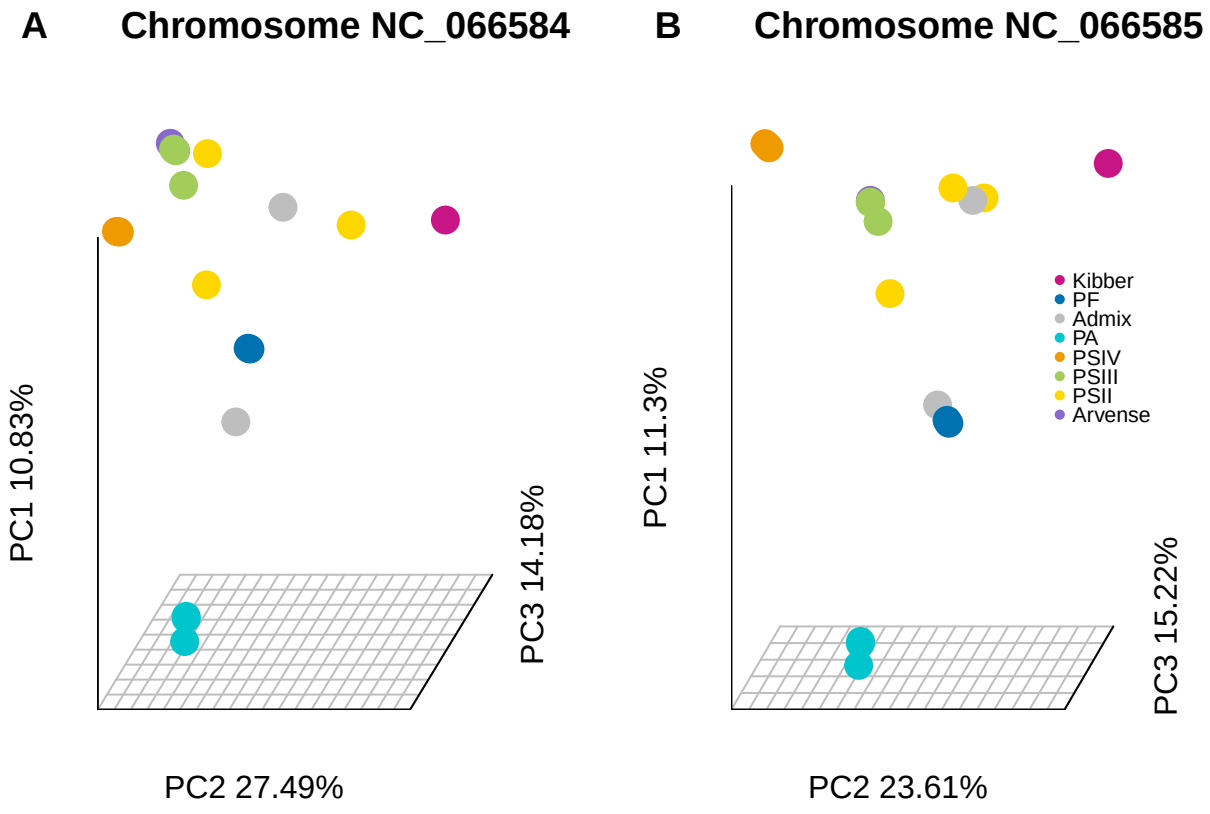

Figure 4: **Principal component analysis for chromosomes**. **(A)** Results for chromosome NC_066584 and **(B)** results for chromosome NC_066585. The black pea sample (Kibber) is in pink color and is distinct from *arvense* (in purple color) and other domesticated samples such as Pisum II and Pisum III (in green and yellow). PF and PA stand for *Pisum fulvum* and *Pisum sativum var. absynicum*, respectively.

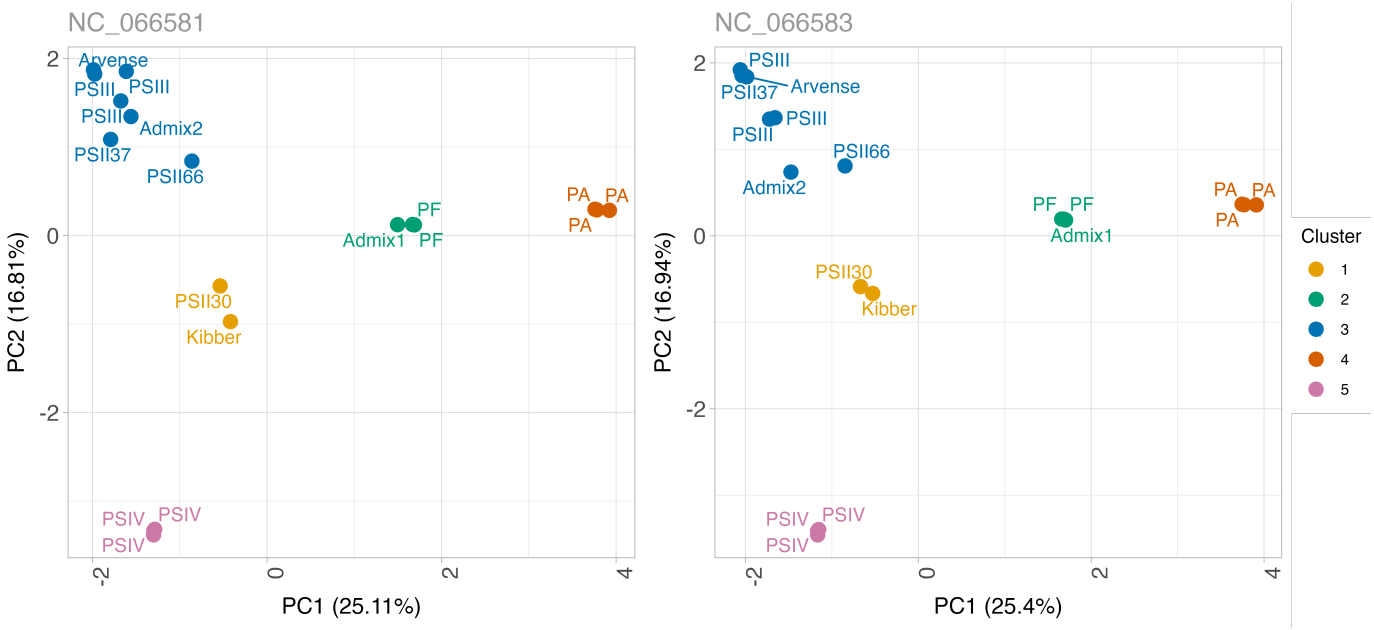

Figure 5: **Hierarchical clustering results for two chromosomes** Results for chromosom NC_066581 (left panel) and NC_066583 (right panel). Each color corresponds to a cluster. The black pea sample (Kibber) clusters with *Pisum sativum asiaticum* (PSII30) which is a traditional Indian landrace for all chromosomes. PF and PA stand for *Pisum fulvum* and *Pisum sativum var. absynicum*, respectively.

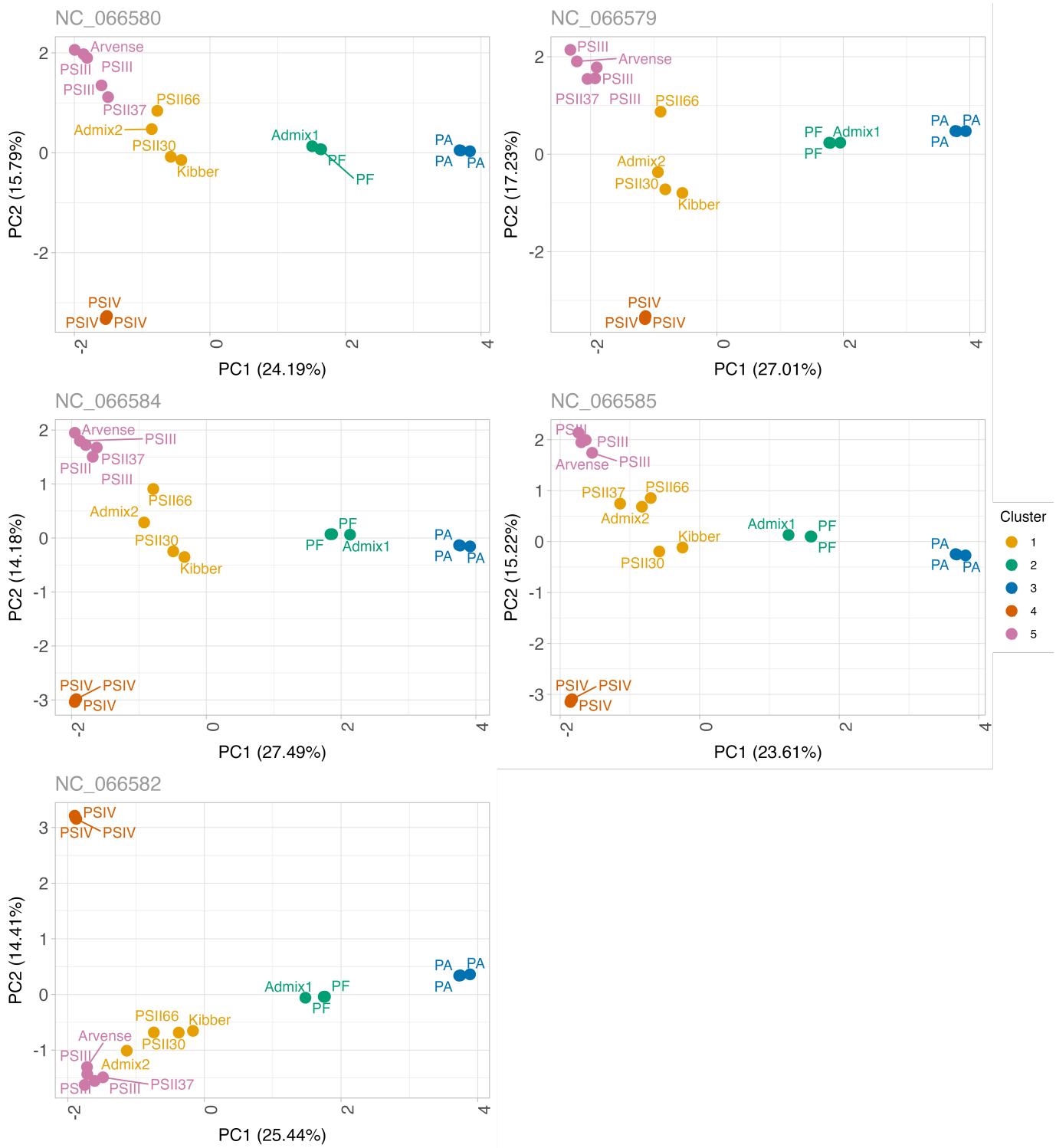

Figure 6: **Hierarchical clustering results for chromosomes** Results for chromosome NC_066580, NC_066579 (top panels); NC_066584, NC_066585 (middle panels); and NC_066582 (last panel) based on hierarchical clustering algorithm.Each color corresponds to a cluster. The black pea sample (Kibber) clusters with *Pisum sativum asiaticum* (PSII30) which is a traditional Indian landrace for all chromosomes. PF and PA stand for *Pisum fulvum* and *Pisum sativum var. absynicum*, respectively.

main text table

Table 1

Nutrient	Value per 100g	RDI (Unit per 100g)
Vitamin A	109 µg	900 µg
Vitamin E	2.74 mg	15 mg
Calcium	108.09 mg	1000 mg
Iron	9.11 mg	8 mg
Magnesium	109.28 mg	400 mg
Zinc	2.48 mg	11 mg
Fat	1.03%	-
Dietary Fiber	15.9%	25-35
Crude Fiber	6.23%	-
Protein	21.20%	10-36%
Vitamin C	13.1 mg	75.6-100mg
Vitamin B1	0.61 mg	-
Vitamin B2	0.09 mg	-
Vitamin B3	1.62 mg	-

table captions

Table 1: Nutritional Profile for black peas and Recommended Daily Intake (RDI) taken from National Institutes for Science (NIH) for an average adult of body weight 70 kg. The tests were performed at Central Food and Technological Research Institute, Mysuru, India. The % by wt corresponds to percentage of nutrient per 100 g.

Supplement: Biocultural vulnerability of traditional crops in the Indian Trans Himalaya

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Statistical analysis for crop growth rates

Data on growth parameters (plant height, leaf area, and biomass) were collected at regular intervals (every 7-10 days). Yield components were assessed at the time of harvest. Our dataset consists of observations from a single year (2023-2024 with a pilot in 2022), and so used ordinary least squares regression (OLS) to estimates growth rates with stem height as predictor variable for the crops. OLS ignores site variance, assuming a single growth rate across all sites. Therefore, we also performed a linear mixed model (LMM) with site as a random effect, allowing for variation in baseline growth across different sites. We show the results comparing OLS and LMM in fig. S3. All statistical analyzes were performed using the R software.

We compared LMM, which accounts for site-level variation, and OLS regression to estimate growth rates for different crops. The LMM estimates were consistently higher than OLS, suggesting that site variability influences growth rates. Growth rate estimates were statistically significant ($p < 0.001$) across all models. For black pea, the growth rate was 0.8951 (SE = 0.0687, p-value < 0.01) in LMM, compared to 0.8266 (SE = 0.0703, pvalue < 0.01) in OLS. LMM accounts for site-specific variation by introducing random intercepts, allowing growth rates to vary between locations.

We present the growth rates for all crops using OLS and LMM results.

Crop	**Model**	**Slope**	**SE**	**P-value**
Green pea	LMM	0.4278	0.0378	***
Green pea	OLS	0.3825	0.0387	***
Black pea	LMM	0.8951	0.0684	***
Black pea	OLS	0.8266	0.0703	***
Barley	LMM	0.6044	0.0403	***
Barley	OLS	0.6000	0.0408	***

Table S1: **Comparison of growth rate estimates**. We compare the growth rate (Slope) and standard errors (SE) between Linear Mixed Model (LMM) and Ordinary Least Squares (OLS) regression for different crops. Significance is denoted by *** ($p < 0.001$).

Optimal number of clusters for spectral and k-means analysis

K-means and spectral clustering are widely used clustering algorithms that identify patterns and structures in high-dimensional data [1]. K-means is an iterative algorithm that partitions data into k clusters by minimizing the sum of squared distances between points and their assigned cluster

centroids. Spectral clustering uses graph-based approach, and is particularly useful when clusters have non-convex shapes or complex structures. Spectral clustering constructs a similarity graph from the data, where each node represents a point and edges encode similarity. It then uses eigenvectors of a transformed matrix (Laplacian) and applies k-means to cluster them. Spectral clustering often outperforms k-means in complex data distributions, as it effectively captures global data structure.

Before performing PCA and clustering, we examine the optimal number of clusters (k). Figures S4:S10 illustrate the results using two methods: elbow and silhouette method for determining k. The elbow method plots within-cluster sum of squares (WCSS) versus k. The “elbow point" is where WCSS reduction slows down. The silhouette method computes how well points fit within their clusters using silhouette width and optimal k maximizes average silhouette score. For our analysis, the optimal clusters for most chromosomes is 5. However, for some chromosomes the optimal number of clusters was 4 or 7. To keep comparison consistent across chromosomes, we choose the optimal number of clusters to be 5 for our analysis. The analysis is performed in RStudio using “fviz_nbclust" function. Next, Figures S11:S17 illustrate the clustering results using three different methods (hierarchical, spectral, and k-means) for all chromosomes.

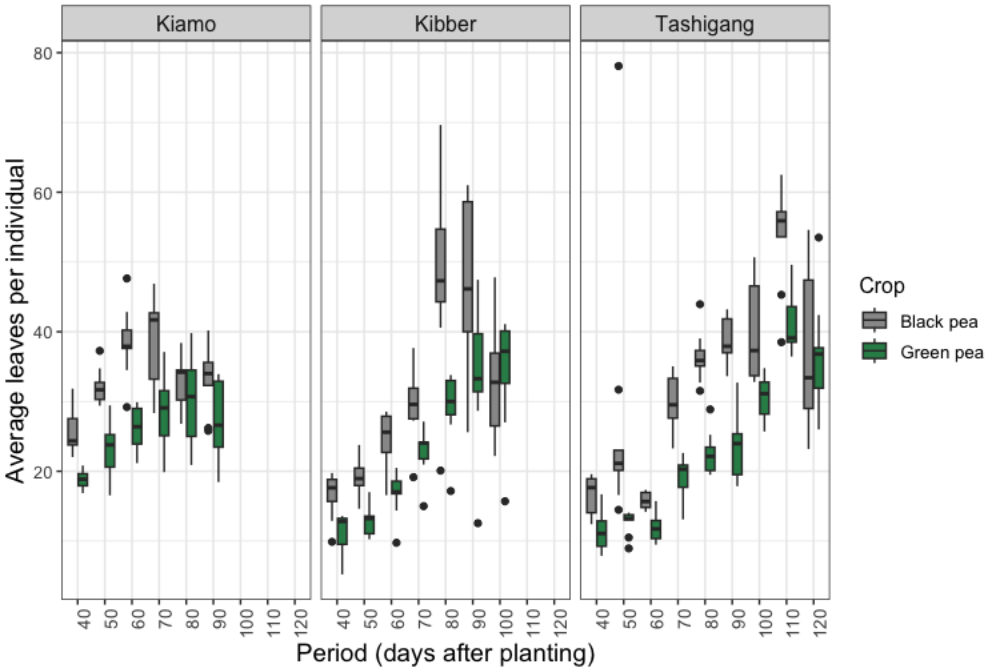

Figure S1: **Average number of leaves per individual**. The results are averaged across treatments and replicates for black peas, green peas, and barley across the three sites Kiamo (4000m), Kibber (4200m) and Tashigang (4500m).

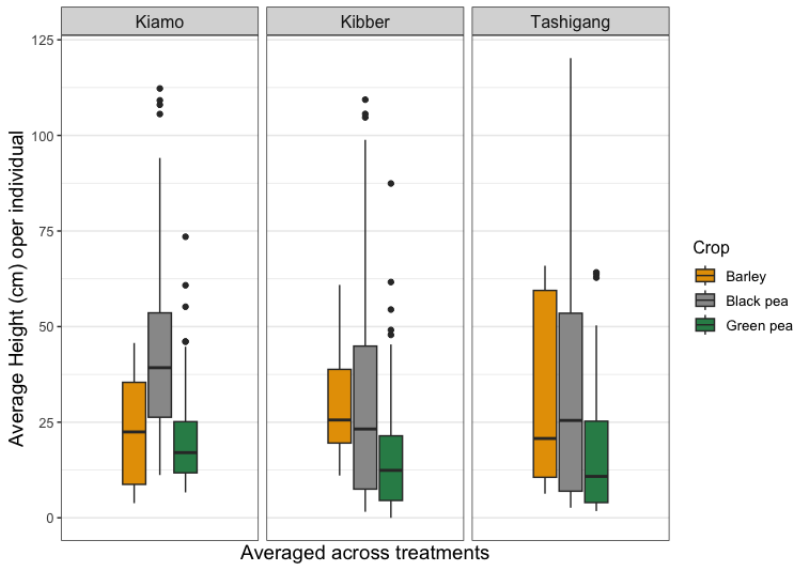

Figure S2: **Average stem height per individual**. The results are averaged across treatments and replicates for black peas, green peas, and barley across the three sites Kiamo (4000m), Kibber (4200m) and Tashigang (4500m).

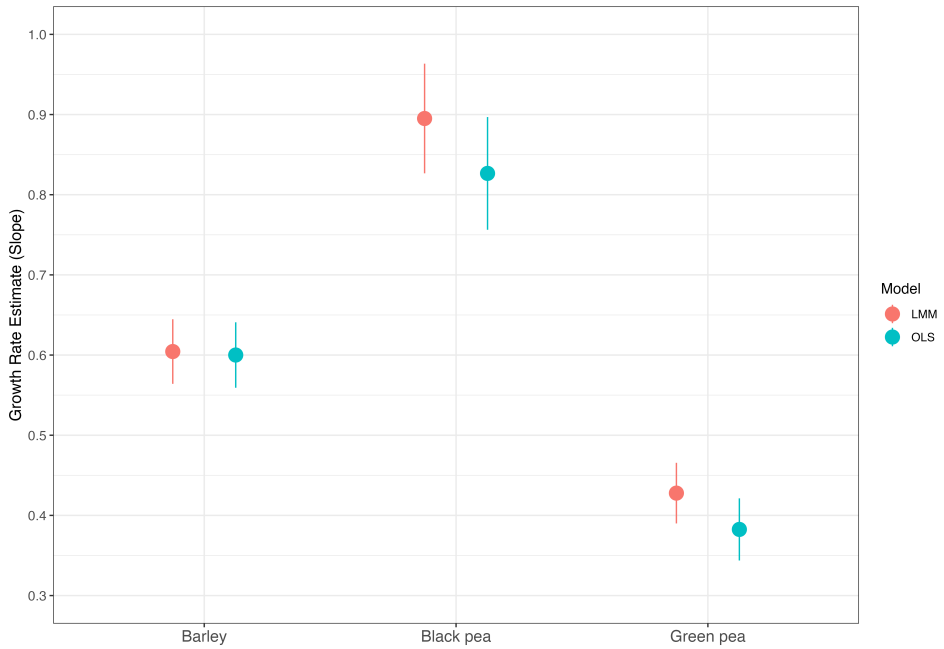

Figure S3: **Average growth rates using OLS and LMM**. The results are averaged across treatments and replicates for black peas, green peas, and barley across the three sites Kiamo (4000m), Kibber (4200m) and Tashigang (4500m).

Table S2: Whole genome sequencing data for PCA analyses

Run No.	Accension No.	Original taxa	Country	Type	Genetic groups SNPs at K=5	Genetic groups SVs at k=5
SRR19543730	PI 164779	P. sativum	India	Traditional Cultivar/Landrace	PSII	PSII
SRR19666966	AGG4020	P. sativum asiaticum	Afghanistan	Traditional Cultivar/Landrace	PSII	PSII
SRR19543737	G917	P. sativum	China, Tibet	Traditional Cultivar/Landrace	PSII	PSII
SRR3138890	PI180693	P. sativum sativum	GERMANY	Cultivar/Landrace	PSIII	PSIII
SRR19543723	AGG4064	P. sativum asiaticum	Algeria	Traditional Cultivar/Landrace	PSIII	PSIII
SRR19543716	AGG2380	P. sativum subsp. transcaucasicum	Former Soviet Union	Wild/Landrace	PSIV	PSIV
SRR19543715	AGG2384	P. sativum subsp. transcaucasicum	Sweden	Wild/Landrace	PSIV	PSIV
SRR3138882	JI281	P. sativum sativum	ETHIOPIA	Landrace	Admixture	Admixture
SRR19543696	AGG4107-1	P. sativum asiaticum	Tajikistan	Traditional Cultivar/Landrace	Admixture	PSII
SRR19543725	AGG190	P. sativum arvense	Finland	Traditional Cultivar/Landrace	PSIII	PSIII
SRR6702454	CGN3277	P. sativum sativum	HINDU KUSH	Landrace	PSII	PSII
SRR19543742	G626	P. sativum	China, Qinghai	Traditional Cultivar/Landrace	PSII	PSII
SRR6702455	JI103	P. sativum sativum	AFGHANISTAN	Landrace	Admixture	Admixture
ERR10478763	BACCARA	P. sativum		Uncertain	PSIII	PSIII
ERR10478950	DARK SKIN PERFECTION	P. sativum sativum		Cultivar	PSIII	PSIII
SRR19543723	AGG4064	P. sativum asiaticum	Algeria	Traditional Cultivar/Landrace	PSIII	PSIII
ERR10478829	DP	P. sativum sativum		Landrace	PSIII	PSIII
SRR19543719	ZW6	P. sativum		Breeding	PSIII	PSIII
SRR6702458	ATC6937	P. sativum sativum	MONGOLIA	Landrace	PSII	PSII
SRR14698499	G2686	P. sativum	China, Inner Mongolia	Traditional Cultivar/Landrace	PSII	PSII
SRR19543732	PI 116944	P. sativum	Afghanistan	Traditional Cultivar/Landrace	PSII	PSII
SRR19543731	PI 143485	P. sativum	Iran	Traditional Cultivar/Landrace	PSII	PSII

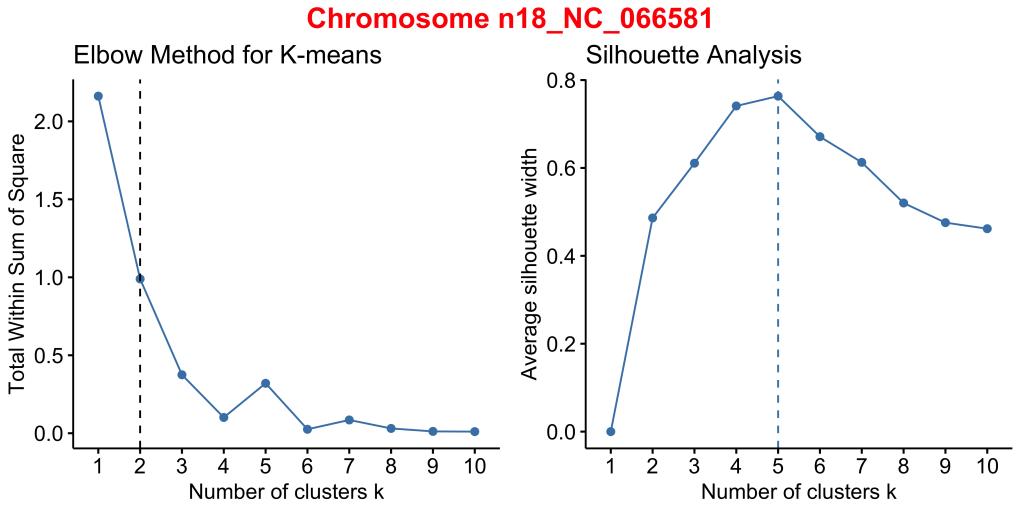

Figure S4: **Plot for optimal number of clusters for NC_066581**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

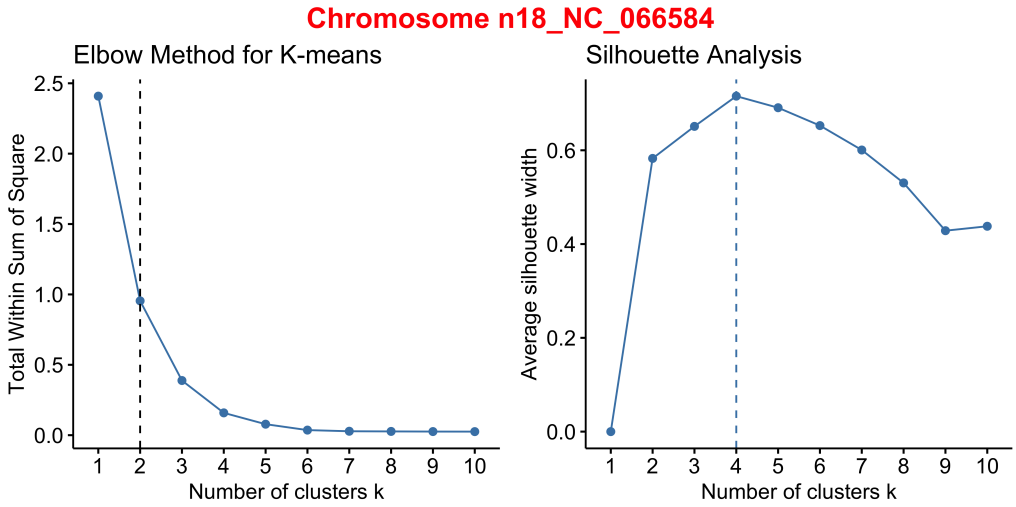

Figure S5: **Plot for optimal number of clusters for NC_066584**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

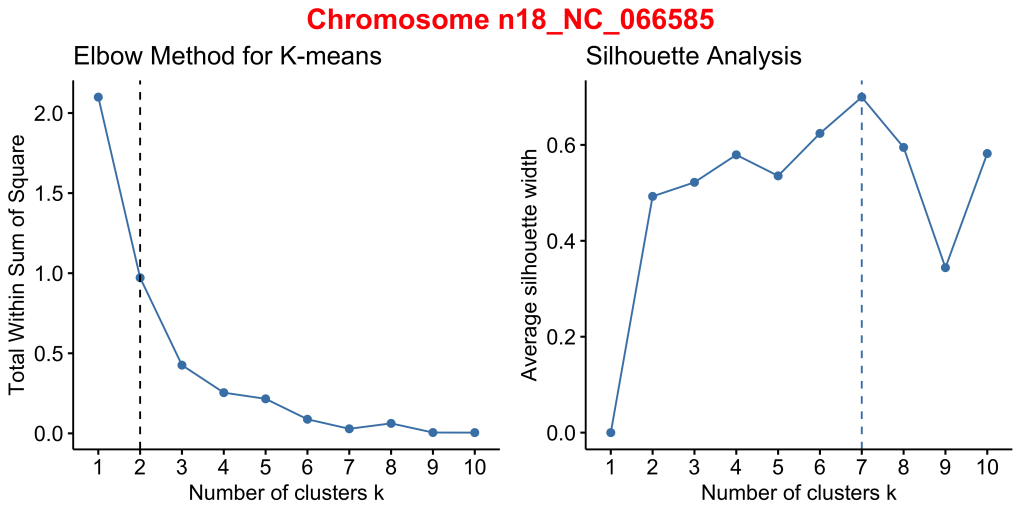

Figure S6: **Plot for optimal number of clusters for NC_066585**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

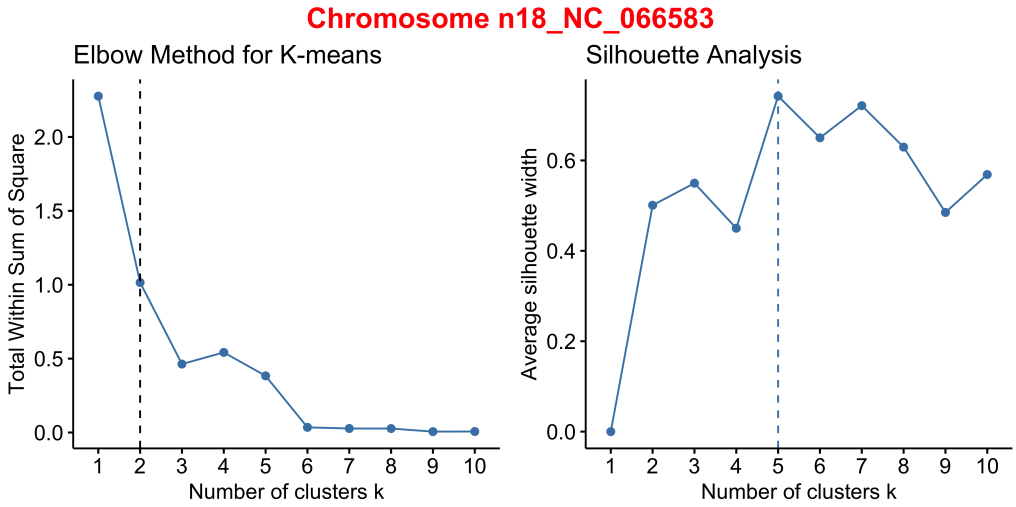

Figure S7: **Plot for optimal number of clusters for NC_066583**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

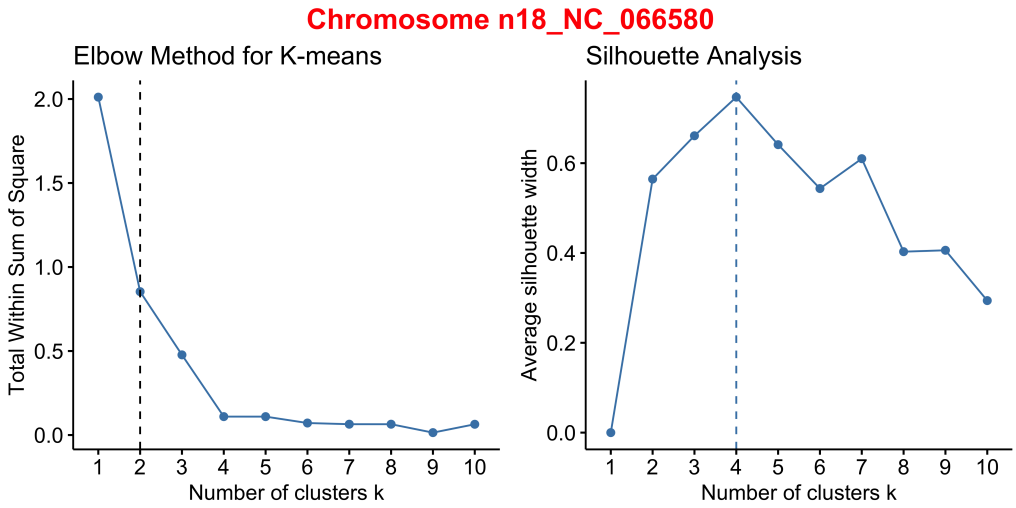

Figure S8: **Plot for optimal number of clusters for NC_066580**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

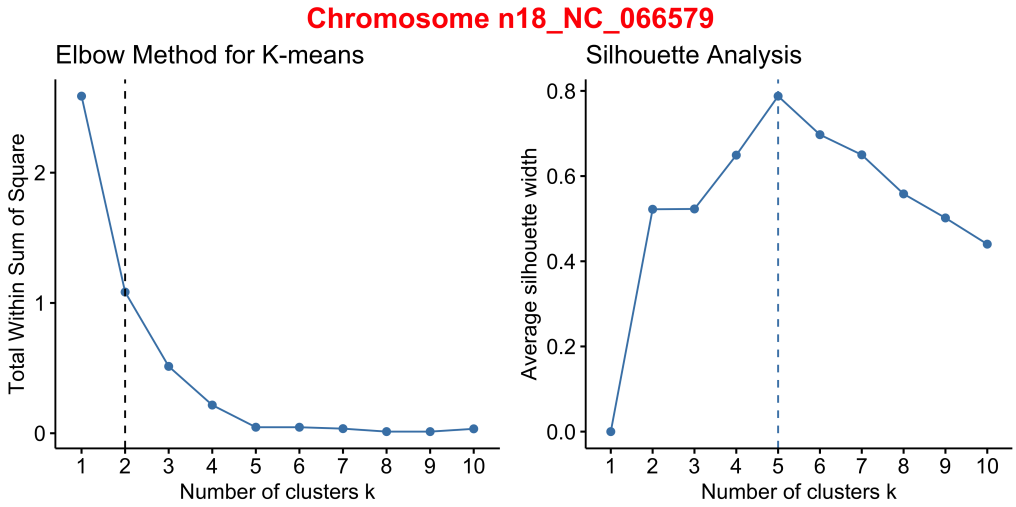

Figure S9: **Plot for optimal number of clusters for NC_066579**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

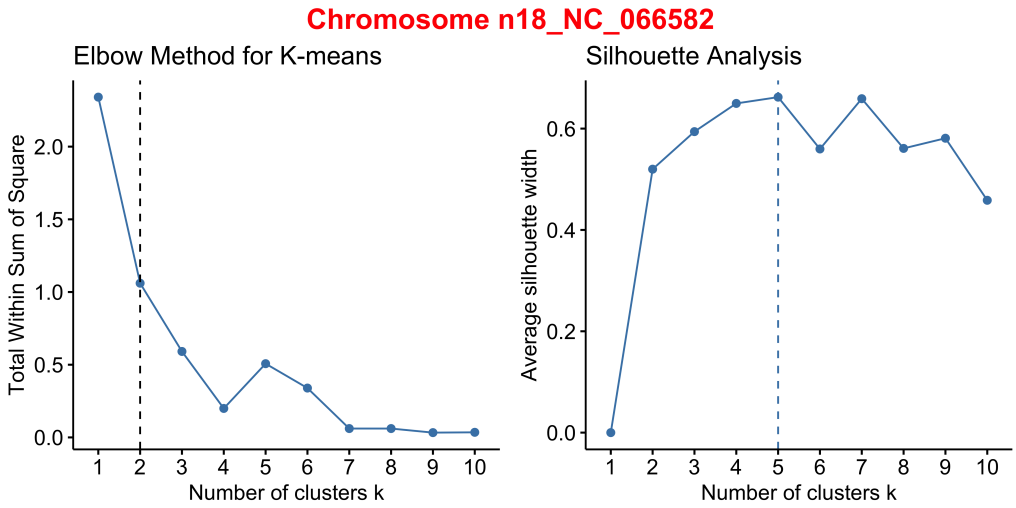

Figure S10: **Plot for optimal number of clusters for NC_066582**. The optimal number of clusters are used for the spectral and k-means clustering. The left panel corresponds to elbow method and the right hand panel corresponds to silhoutte method.

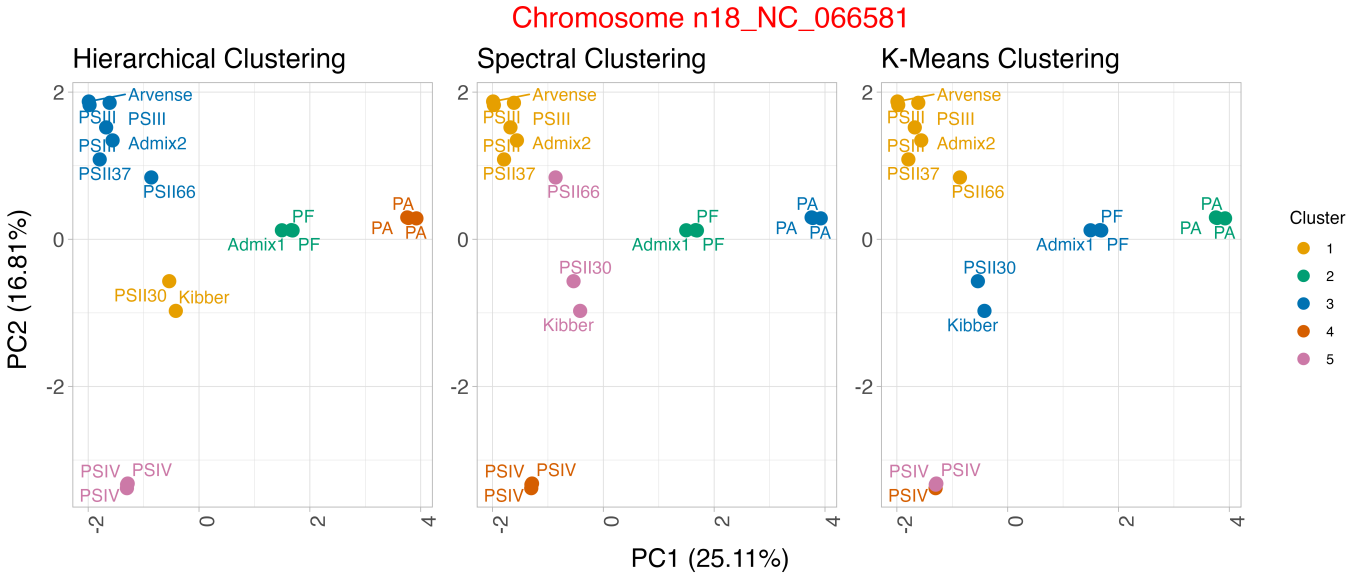

Figure S11: **Plot for results of different clustering algorithms for chromosome NC_066581**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.

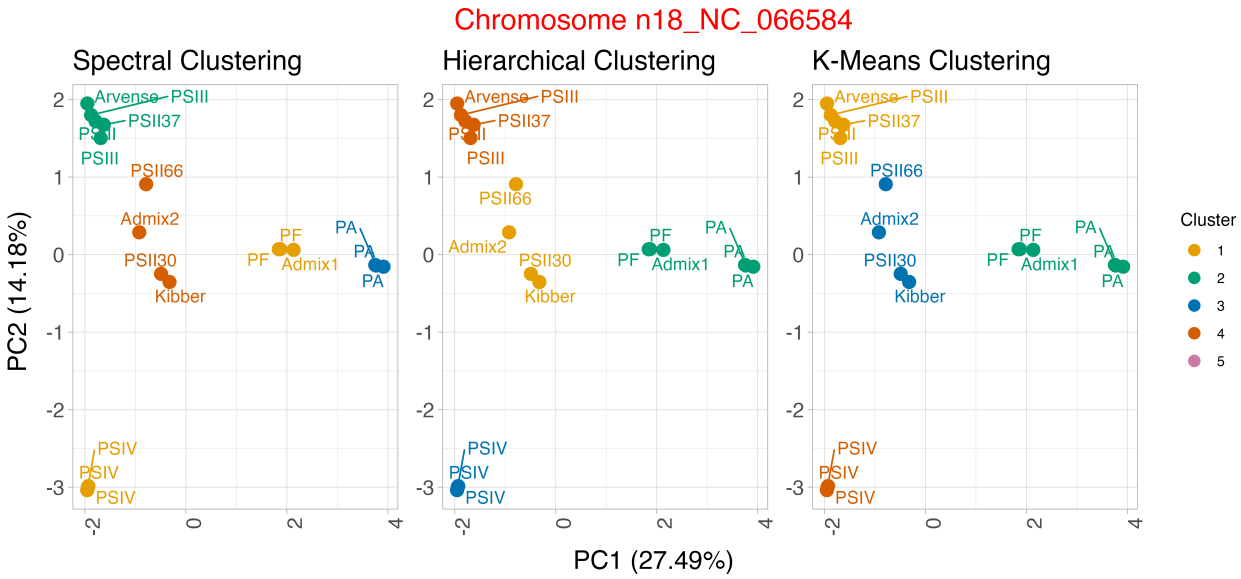

Figure S12: **Plot for results of different clustering algorithms for chromosome NC_066584**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.

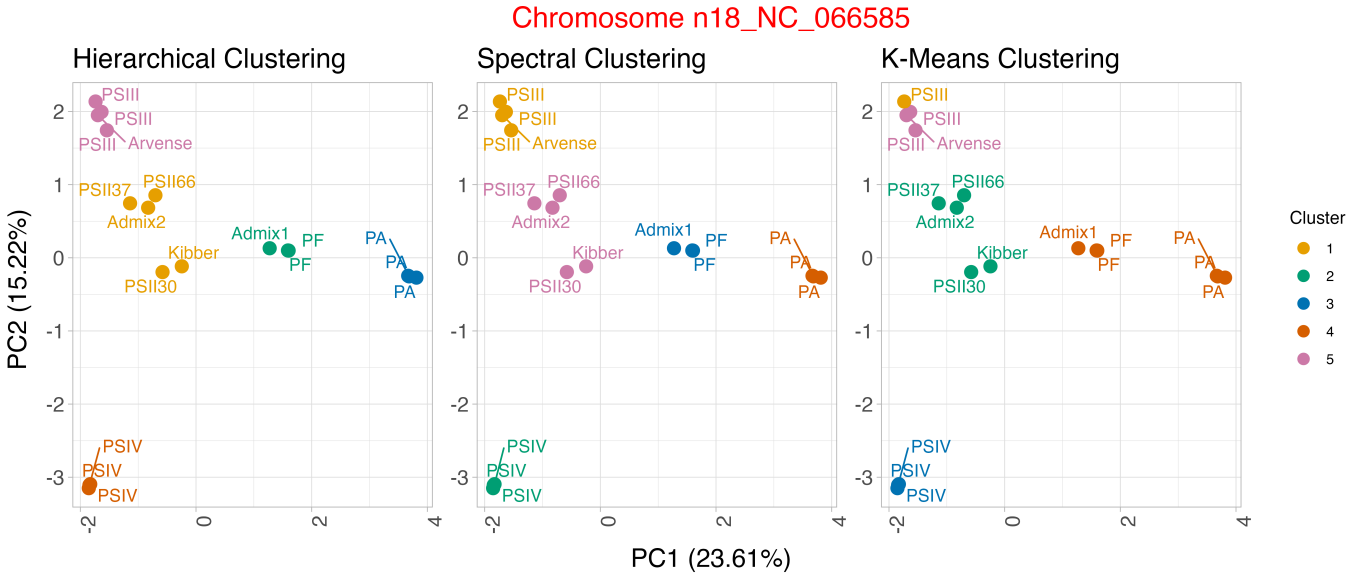

Figure S13: **Plot for results of different clustering algorithms for chromosome NC_066585**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.

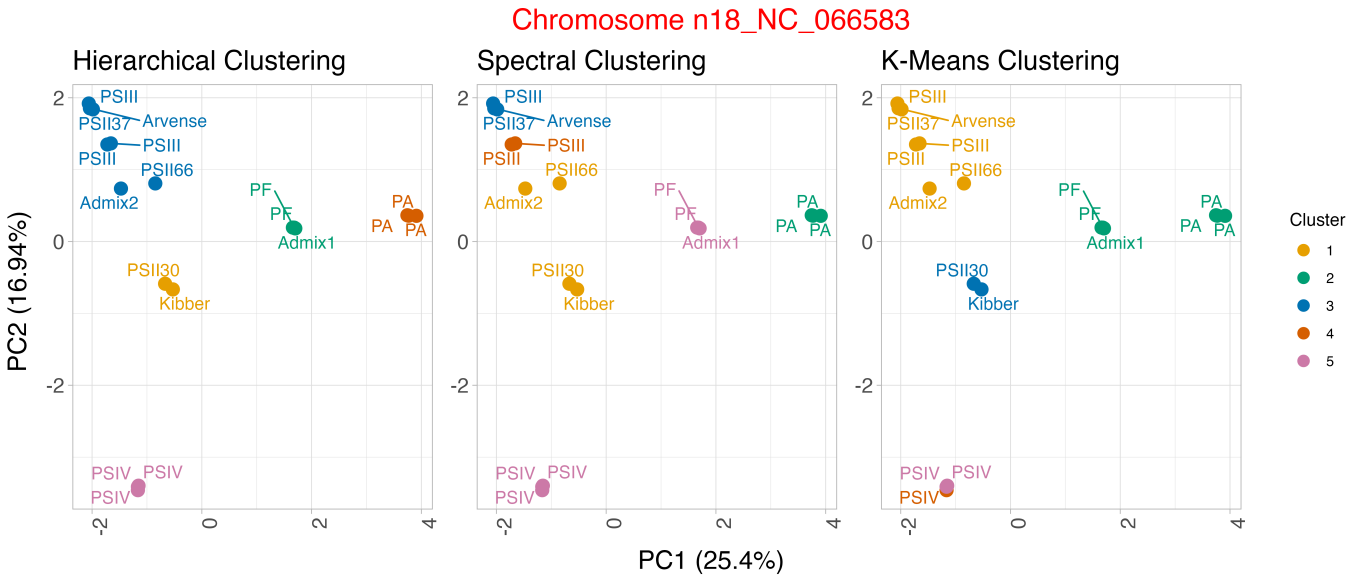

Figure S14: **Plot for results of different clustering algorithms for chromosome NC_066583**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.

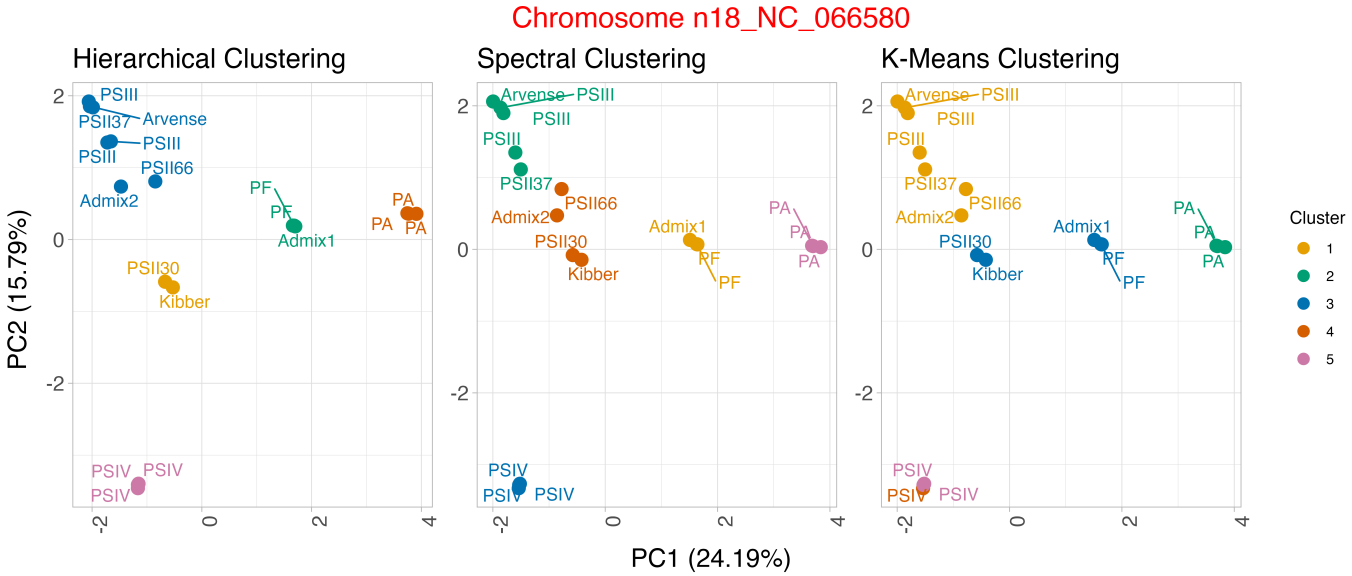

Figure S15: **Plot for results of different clustering algorithms for chromosome NC_066580**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.

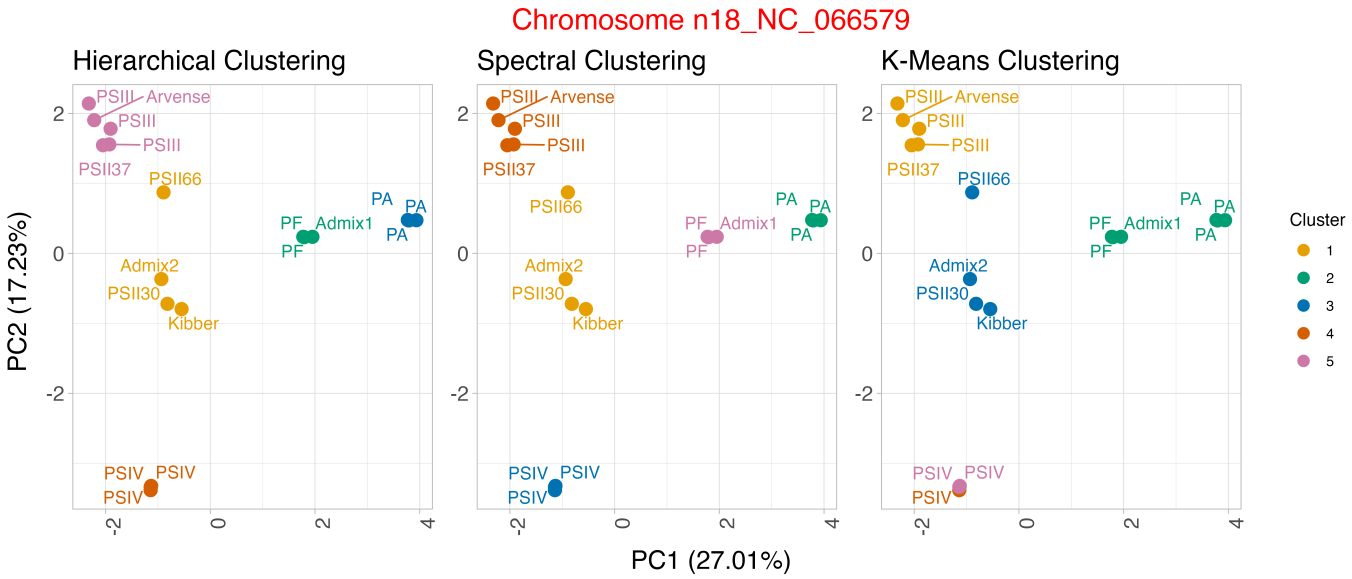

Figure S16: **Plot for results of different clustering algorithms for chromosome NC_066579**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.

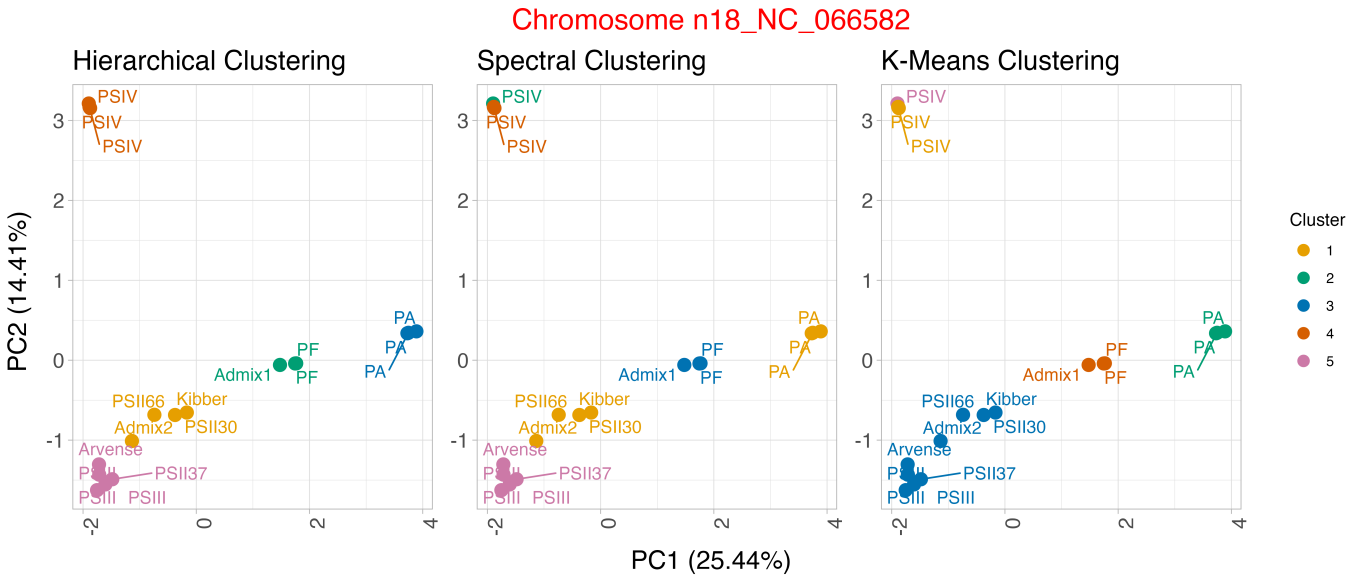

Figure S17: **Plot for results of different clustering algorithms for chromosome NC_066582**. The panel (left to right) illustrates results from hierarchical, spectral, and k-means clustering.