

1 Genomic and Chemical Diversity in *Cannabis*

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25 **Abstract**

26 Plants of the *Cannabis* genus are the only producers of phytocannabinoids, terpenoid compounds
27 that strongly interact with evolutionarily ancient endocannabinoid receptors shared by most
28 bilaterian taxa. For millennia, the plant has been cultivated for these compounds, but also for
29 food, rope, paper, and clothing. Today, specialized varieties yielding high-quality textile fibers,
30 nutritional seed oil or high cannabinoid content are cultivated across the globe. However, the
31 genetic identities and histories of these diverse populations remain largely obscured. We
32 analyzed the nuclear genomic diversity among 340 *Cannabis* varieties, including fiber and seed
33 oil hemp, high cannabinoid drug-types and feral populations. These analyses demonstrate the
34 existence of at least three major groups of diversity, with European hemp varieties more closely
35 related to narrow leaflet drug-types (NLDT) than to broad leaflet drug-types (BLDT). The BLDT
36 group appears to encompass less diversity than the NLDT, which reflects the larger geographic
37 range of NLDTs, and suggests a more recent origin of domestication of the BLDTs. As well as
38 being genetically distinct, hemp, NLDT and BLDT genetic groups each produce unique
39 cannabinoid and terpenoid content profiles. This combined analysis of population genomic and
40 trait variation informs our understanding of the potential uses of different genetic variants for
41 medicine and agriculture, providing valuable insights and tools for a rapidly emerging, valuable
42 legal industry.

43

44 **Significance Statement**

45 Despite millennia of cultivation and current widespread use across the globe, *Cannabis* is the
46 only multi-billion dollar crop for which the genetic identities and origins of most varieties are
47 unknown. As legalized cultivation of hemp and high-cannabinoid types continues to grow

48 rapidly in the US and other countries, the need for a better understanding of the diversity and
49 evolution of the species has increased. Through analyzing the genomes of 340 hemp, drug and
50 feral *Cannabis* individuals, we found significant evidence for at least three major genetic groups.
51 Importantly, each group produces distinct phytochemical profiles. Our results improve the
52 understanding of genetically and chemically diverse *Cannabis* strains currently cultivated, and
53 provide a roadmap for developing improved varieties.

54

55 **Introduction**

56 Plants of the genus *Cannabis* (Cannabaceae; hemp, drug-type) have been used for thousands of
57 years for fiber, nutritional seed oil and medicinal or psychoactive effects. Archaeological evidence
58 for hemp fiber textile production in China dates to at least as early as 6,000 years ago (1), but
59 possibly as early as 12,000 years ago (2), suggesting *Cannabis* was one of the first domesticated
60 fiber plants. Archeological evidence for medicinal or shamanistic use of *Cannabis* has been found
61 at Indian, central-Asian and middle-eastern sites (3), further illustrating the widespread extent of
62 *Cannabis* utilization throughout human history. A central Asian site of domestication is often cited
63 (4), although genetic analyses suggest two independent domestication events may have occurred
64 separately (5).

65 *Cannabis* plants are usually annual wind-pollinated dioecious herbs, though individuals
66 may live more than a year in subtropical climates (6) and monoecious populations exist (7). The
67 taxonomic composition of the genus remains unresolved, with two species (*C. indica* and *C. sativa*)
68 commonly cited (8), although *C. ruderalis* is sometimes proposed as a third species that contains
69 northern short-day or auto-flowering plants (9). Monospecific treatment of the genus as *Cannabis*
70 *sativa* L. is also common (10) and various alternative nomenclature schemes (e.g. *Cannabis sativa*

71 subsp. *indica* var. *kafiristanica*) are sometimes referenced (4). Even though an extensive
72 monograph on the genus has recently been published (11), limited genetic and experimental data
73 leaves the questions of taxonomy unresolved (12, 13).

74 The geographical and ecological range of *Cannabis* is unusually broad, with cultivated
75 populations growing outdoors on every continent except Antarctica in a wide range of
76 environments from sub-arctic to temperate to tropical, and from sea level to over 3,000 meters
77 elevation (14, 15). Feral or wild populations are also found as far north as the edge of the Arctic
78 Circle in Eurasia, but are most common in well drained soils of temperate continental ecosystems
79 in Eurasia and North America, while tropical populations are absent or rare (14). Perhaps
80 unsurprising, given this diversity of habitats, the species contains extensive phytochemical
81 diversity, particularly in cannabinoid and terpenoid profiles (5, 16), and also shows extensive
82 diversity of morphological and life-history characteristics, further fueling debate regarding the
83 taxonomic status and origins of *Cannabis* domestication.

84 One distinctive feature of the *Cannabis* genus is the production of a tremendous diversity
85 of compounds called *cannabinoids*, so named because they are not produced at high levels in any
86 other plant species (17). Cannabinoids are a group of at least 74 known C₂₁ terpenophenolic
87 compounds (18, 19) responsible for many reported medicinal and psychoactive effects of *Cannabis*
88 consumption (20). Some estimates for the total number of phytocannabinoids range to well over a
89 hundred (21), though this number includes breakdown products as well as compounds found at
90 extremely low levels. The plants produce a non-psychoactive carboxylic acid form of these
91 compounds, with heating required to convert cannabinoids into the psychoactive decarboxylated
92 forms. Interestingly, these compounds have pronounced neurological effects on a wide range of
93 vertebrate and invertebrate taxa, suggesting an ancient origin of the endocannabinoid receptors,

94 perhaps as old as the last common ancestor of all extant bilaterians, over 500 MYA (22). The plant
95 compounds thus produced have the potential to affect a broad range of metazoans, though their
96 ecological functions in nature are not well understood. Indeed, suggested roles for these
97 compounds include many biotic and abiotic defenses, such as suppression of pathogens and
98 herbivores, protection from UV radiation damage, and attraction of seed dispersers. These
99 hypotheses about the selective benefits of cannabinoid production remain speculative, as none
100 have been conclusively verified to date. We do know more, however, about the more recent
101 evolution of the plants under human cultivation.

102 High delta-9-tetrahydrocannabinolic acid (THCA) (23) content has been selected for in
103 many strains due to its potential to be converted to delta-9-tetrahydrocannabinol (THC), which has
104 potent psychoactive (24), appetite-stimulating (25), analgesic (26) and antiemetic (27) effects.
105 These effects are mediated through interactions with human endocannabinoid CB1 receptors found
106 in the brain (28), and CB2 receptors, which are concentrated in peripheral tissues (29). Other THC
107 receptor binding locations are hypothesized as well (30). After several decades of accelerated
108 clandestine cultivation technique and breeding improvements, some modern strains can now yield
109 dried un-pollenated pistillate inflorescence material that contains over 30% THCA by dry-weight
110 (31). However, other cannabinoids may also be present in high concentrations. In particular, high
111 cannabidiolic acid (CBDA) plants were historically used in some hashish preparations(32) and are
112 presently in high demand as an anti-seizure therapy (33). In contrast with THC, which acts as a
113 partial agonist of the CB1 and CB2 receptors, CBD does not have as strong psychoactive
114 properties, and instead has antagonist activity on agonists of the CB1- and CB2-receptors (34).
115 Thus, the two most abundant cannabinoids produced in *Cannabis* have, to some degree, opposing
116 neurological effects.

117 THCA and CBDA are alternative products of a shared precursor, CBGA (35). A single
118 locus with co-dominant alleles was proposed to explain patterns of inheritance for THCA to CBDA
119 ratios (7, 36). However more recent quantitative trait loci (QTL) mapping experiments (37),
120 expression studies (38) and genomic analyses (10) paint a more complex scenario with several
121 linked paralogs responsible for the various THCA and CBDA phenotypes. Other cannabinoids
122 such as cannabigerol (CBG) (39), cannabichromene (CBC) (40) and delta-9-
123 tetrahydrocannabivarin (THCV) (41) demonstrate pharmacological promise, and can also be
124 produced at high levels by the plant (42–44). Additionally, *Cannabis* secondary metabolites such
125 as terpenoids and flavonoids likely contribute to therapeutic or psychoactive effects (2), such as β -
126 myrcene, humulene and linalool proposed to produce sedative effects associated with specific
127 strains (45).

128 In this study, plants that produce low levels of total cannabinoids are herein referred to as
129 hemp, while high cannabinoid producing varieties are described as drug-type strains. Legal
130 definitions often use a maximum THCA threshold to delineate hemp from drug-types, thus some
131 high CBDA producing strains are categorized as hemp. However this definition ignores the
132 broader traditional usage of hemp for fibers or seed oils and historical presence of CBDA-
133 producing alleles in some drug-type populations (32). Additionally, hemp strains have a distinct
134 set of growth characteristics (46), with fiber varieties reaching up to 6 meters in height during a
135 growing season, exhibiting reduced flower set, increased internodal spacing and lower total
136 cannabinoid concentration per unit mass compared to drug-type relative. Despite the widespread
137 prohibition of drug-type *Cannabis* cultivation from the 1930s to present (47), hemp cultivation
138 and breeding continued in parts of Europe and China through this period, and experienced a brief
139 comeback during World War II in the USA through the Hemp for Victory campaign. Studies to

140 date have found hemp varieties are genetically distinct from drug-type strains (10), though
141 interestingly Hillig (5) found broad leaflet southeastern Asian hemp landraces to be more closely
142 related to Asian drug-type strains than to European hemp strains.

143 *Cannabis* has a diploid genome ($2n = 20$), and an XY/XX chromosomal sex-determining
144 system(48). The genome size is estimated to be 818 Mb for female plants and 843 Mb for male
145 plants (49). Currently, a draft genome consisting of 60,029 scaffolds is available for the Purple
146 Kush (PK) drug-type strain from the National Center for Biotechnology Information. Additional
147 whole genome data is available from NCBI for the Finola and USO31 hemp strains. Various
148 reduced representation genome, gene and RNA sequence data are also available from NCBI.
149 Presently *Cannabis* is the only multi-billion dollar legal crop without a sequence-based genetic
150 linkage or physical genome map. Indeed, the first genetic map for the species, using AFLP and
151 microsatellite markers, was only recently published, providing for the first time, quantitative trait
152 mapping of cannabinoid content and other traits (37).

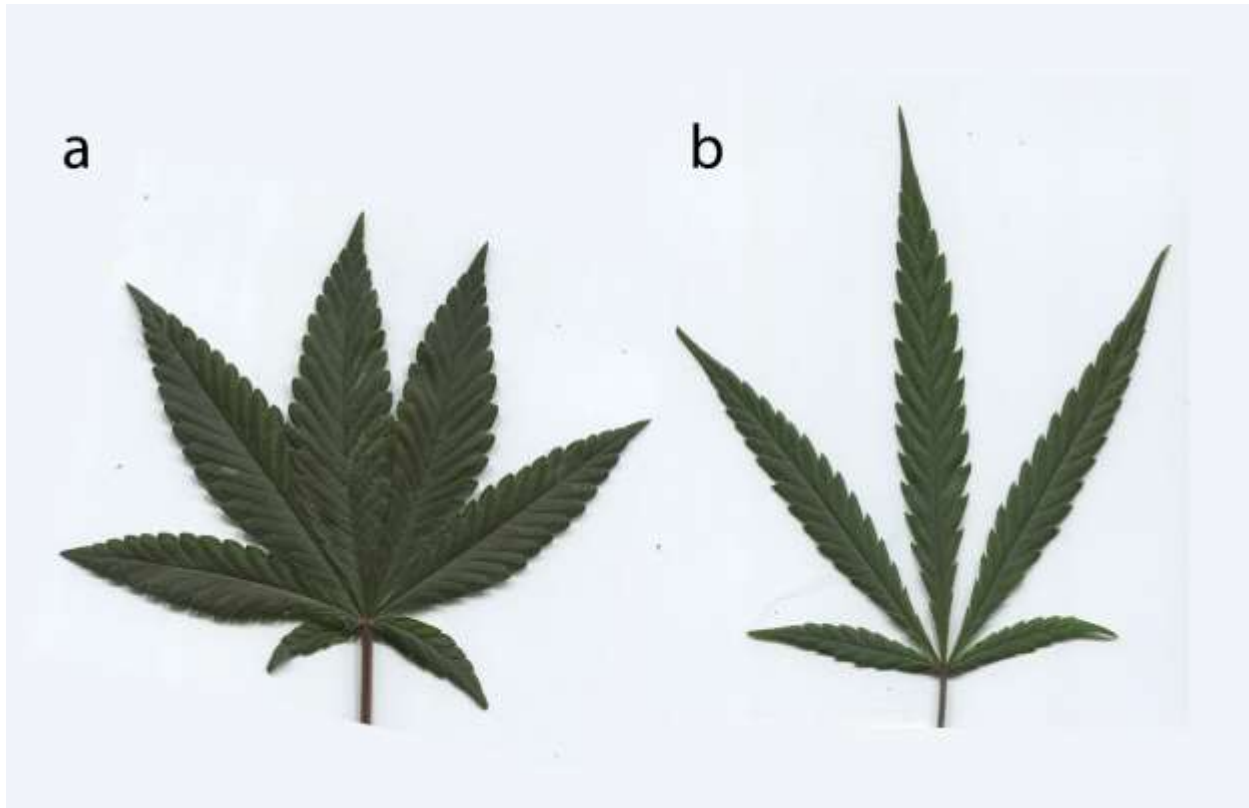
153 Initial studies of *Cannabis* genetic diversity examined either many samples with few
154 molecular markers (5) or whole genome wide data for relatively few samples types (10). Sawler
155 et al. (50) recently published a survey of *Cannabis* genomic diversity, using a reduced genomic
156 representation strategy to evaluate 81 marijuana (drug-type) and 43 hemp strains. The aim of this
157 present study is to assess the genomic diversity and phylogenetic relationships among 340 total
158 *Cannabis* plants that have distinct phenotypes, and that were described *a priori* by plant breeders
159 as various landraces, *indica*, *sativa*, hemp and drug-types, as well as commercially available
160 hemp and drug-types with unclear pedigrees. We have combined data from existing sources and
161 generated new data to create the largest sample set of *Cannabis* genomic sequence data
162 published to date. These data and analyses will continue to facilitate the development of

163 modernized breeding and quality assurance tools, which are lacking in the nascent legal
164 *Cannabis* industry.

165

166 **Results and Discussion**

167 **Sequencing and SNPs.** Summary information and raw sequencing libraries are publically
168 available from the NCBI short read archive (accessions pending). Detailed information about all
169 samples can be found in Dataset S1 and examples of wide and narrow leaflet forms are shown in
170 Figure 1. Of the 466,427,059 non-ambiguous base pairs in the PK reference, 77,810,563 bps
171 were removed due to excess self-similarity (≥ 97 % identity and ≥ 500 bps length, Figure S1).
172 After this filter, the total single copy portion the PK reference within the combined coverage
173 levels for all 67 WGS samples of 326x – 401x, a 95% Poisson confidence interval around a 362x
174 mean, was 71,236,365 bps (Figure S1). After quality (Q), genotype quality (GQ), allele
175 frequency (AF), missing data, biallelic and ambiguous base filters, the following SNP counts
176 remained: 491,341 WGS, 2,894 GBS (this study), SNPs 4,105 GBS Sawler (50). Forty-five
177 SNPs overlapped both GBS datasets, and the WGS samples.



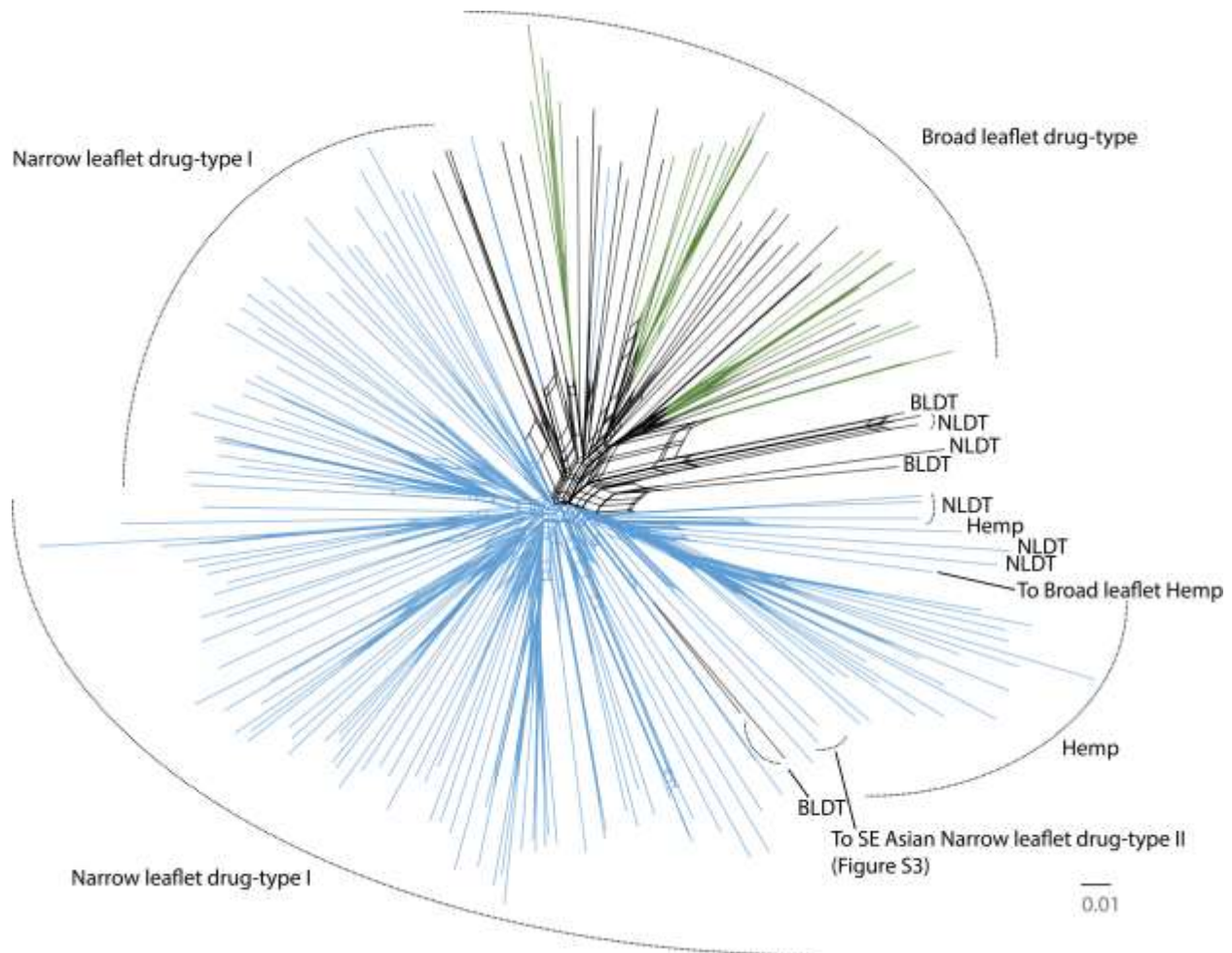
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179 Figure 1. Example of broad leaflet type (a, R4) and narrow leaflet type (b, Super Lemon Haze)
180 strains. Photograph credits: D. Vergara.

181

182 **Phylogenetic Relationships.** Bifurcating trees are commonly used to model mutation driven
183 divergence and speciation events. Whole genome wide sequence datasets include information
184 about recombination, hybridization, and gene loss or genesis events, some of which may be
185 incongruent with one and other (51). Phylogenetic networks can represent incompatible
186 phylogenetic signals across large character matrices in a visually informative manner. Figure 2
187 contains 195 *Cannabis* samples including WGS and GBS data, and shows that all European
188 hemp strains form a distinct clade, separated from drug-type strains by a consistent band of
189 parallel branches. Broad leaflet drug-type strains clustered with purported Afghan Kush landrace
190 samples (Dataset S1 and Figure S3), while narrow leaflet drug-type strains appear to contain

191 several groups with only faint visible distinctions between them, perhaps influenced by the
192 inclusion of hybrid strains in the analysis.



194 Figure 2. Phylogenetic neighbor network of a 2,894 SNP alignment from the single-copy portion
195 of the *Cannabis* genome. Clade names on the periphery were inferred via FLOCK (where $K \geq 3$
196 was most likely). Colored branches indicate fastStructure population membership of $\geq 70\%$
197 assignment (where $K=2$ was most likely). NLDT = Narrow Leaflet Drug-Type and BLDT =
198 Broad Leaflet Drug-Type. To SE Asian NLDT II points to Dr. Grinspoon and Somali Taxi Cab
199 samples. To Broad Leaflet Hemp points to a Chinese hemp sample. A high-resolution version of
200 this figure that includes each sample name is available from:
201 https://figshare.com/articles/Cannabis_Tree/1585470/4

202

203 We found significantly more heterozygosity in drug-type strains than in hemp varieties
204 (31 % v 22 %, $p < 0.001$, two-tailed Mann-Whitney U-test, Table 1). This likely reflects the

205 widespread hybridization of strains in North America during the transition to indoor cultivation
206 of drug-types starting in the 1970s (52), as well as the extensive reliance on clonal propagation
207 for indoor commercial cultivation, which does not require trait stable seed stock. Conversely,
208 fiber and seed oil hemp are grown on multi-acre scales that have necessitated the stabilization of
209 agronomically important traits in seed stocks, likely leading to reduced heterozygosity at some
210 loci.

211 Group Genetic Information

	Mean Within Distances	Heterozygosity %
Hemp	0.195	0.22*
All Drug-types	0.244	0.31*
NLDT	0.237	0.32
BLDT	0.221	0.30
	Mean Between Distances	F _{ST}
Hemp v. All Drug-types	0.273	0.098530
Hemp v. NLDT	0.269	0.091679
Hemp v. BLDT	0.281	0.10131
NLDT v. BLDT	0.258	0.036156

212

213 Table 1. Summary of genetic distance, heterozygosity and F_{st} information for major *Cannabis*
214 groups. * = significantly different (p < 0.001, two-tailed Mann-Whitney U-test).

215

216 **Population Structure.** To determine the statistical likelihood of various population scenarios
217 represented in our samples, we first applied the FLOCK model to our data set of 195 GBS and
218 WGS *Cannabis* samples, which is an iterative reallocation clustering algorithm that does not
219 require non-admixed individuals to make population assignments (53). Using the K-partitioning
220 method suggested by the authors (53), we determined that $K \geq 3$, after testing K values of one to
221 eight (Table 2 and peripheral population names in Figure 2). FLOCK was able to assign all
222 samples to one of the three populations, although it does not calculate admixture proportions.
223 Sample population assignments were largely consistent with the known history of these samples,

224 and appear visually consistent with MDS analysis (Figure S2). For example all fiber and seed oil
 225 hems were assigned to an exclusive population, with the exception of sample AC/DC, a high
 226 CBDA producing variety, with likely hybrid hemp origins (Figure 2, Table 2).

227 Sample Names

A-train	Original_Sour_Diesel	C36	H11	Schemp
Afghan_Kush	Phantom_Cookies	C37	H5	Skunk_#1
Afghan_Kush	Platinum_OG	Canna_Tsu	Harlequin	Somali_Taxi_Cab
Afghan_Kush	Purple_Kryptonite	Cannatonic	Hash_Plant	Spectrum-11
Afghan_Kush	Purple_Kush	CBD_Diesel	Hawaiian	Spectrum-14
Afghan_Kush	Purple_Urkle	CBD_Shark_F-6	Holy_Grail	Super_Lemon_Haze
Boss_Hogg	R4	CBD-0	Holy_Grail_Kush	Sweet_Afghani_Delicious
Bubba_Kush	San_Fran_Valley_OG_Kush	CBD18	Jack_47	Sweet_Skunk
Char_Tango	Screaming_Haze	Charlottes_Web	Jack_Flash	Tangerine_Haze
Chem_91'	SFV	Cheese_Quake	Jack_Herer	Train_Wreck
Chem91	Skywalker_OG	Cherry	Jack_Herrer	Trainwreck
Chemdawg	Snowcap	Cherry_Afghan	Jack_Herrer	Violator_Kush
Chocolate_Kush	Snowcap	Chocolope	Jack_Skellington	White_Cookies
Crippd_Out_Cookies	Sour_Diesel	Chocolope	Juicy_Fruit	White_Widdow
Cript_out_Cookies	Sour_Patch_Kush	Colombia_Rio_Negro	Lebanese	White_Widow
Dead_Head_OG	Sour_Willie	Critical_Kush	Lemon_Skunk	Wonder_Woman
Dog_Walker	Sshrek	Critical_Kush	Liberty_Haze	XJ_13
Flo	The_Sauce	Critical_Mass	Lions_Tabernacle	AC/DC
Girl_Scout_Cookie_#6	The_Sauce	Dr_Grinspoon	Low_Ryder	AZ_Star_#1
Girl_Scout_Cookies	Tora_Bora	Durban_Poison	LSD	Carmagnola
Girl_Scout_Cookies	WAF_B	Durban_Poison	Mad_Cow	Carmagnola
Goast_Train_Haze	4-Jack	Easy_Sativa	Mango_Stomper	Carmagnola
Grapefruit	Afghan_Mango	Exodus_Cheese	Maui_Waui	Carmagnola
Guido_OG	Afghan_Mango	G13	Mazar	Carmagnola
Headband	Afghan_Mango	G13_Haze-31	Medical_Mass	Carmagnola
Hindu_Kush	Alaskan_Thunderfuck	Gin	Melon_Gum	Chinese_hemp
Kandy_Kush	Appalachian_Mad_Sun	Girl_Scout_Cookies	Mexican_E	Dagestani_hemp
King_Chem	Auto_AK47	Glass_Slipper	MO	EuroOil_2
King_Louie_Cookies	B-5	Golden_Goat	Nuclear_Fruit	Feral_Kansas
Kool_Aid_Kush	BC_HQ	Grand_Daddy_Purps	Otto	Feral_Nebraska
Kosher_Kush	Black_Cherry	Grape_AK-47	Peaches_and_Cream	Feral_Nebraska
Kosher_Kush	Black_Jack	Grape_Ape	Pineapple	Finola
Kosher_Kush_#1	Blue_Cheese	Grape_Ape	Pineapple_Express	J7
Kunduz	Blue_Dream	Grape_Kush	Pink_Lady	J20
Larry_OG	Blue_Dream	Grape_Kush	Pre-98_Bubba_Kush	J28
Medibud	Blue_OG	Green_Crack	Purps	Kompolti_1
OG_18	Blueberry_DJ	Green_Crack	R4	Kompolti_2
OG_Kush_1	Bubble_Gum	Green_Mandarine	Red_Purps	Sievers_Infinity
Old_Skool_OG	Bubble_Gum_XL	Green_Poison	Rocky_Mountain_Blueberry	US031

228

229 Table 2. Sample names and FLOCK assignment to three groups, represented with different cell
230 colors. Green are BLDT, blue are NLDT and yellow are hemp.

231

232 Additionally we applied the admixture model based Bayesian clustering method of
233 fastStructure to the same 195 samples (54). The most likely population structure analysis of $K=2$
234 (Figure 2, Dataset S1), shows consistent separation between BLDT and NLDT and hemp strains.
235 Some hemp and NLDT strains were each assigned with near 100% population membership to the
236 same population (Figure 2, light blue samples, Dataset S1), despite the clear separation
237 visualized in the tree and statistically significant mean between-group genetic distance measured
238 (Table 1). The separation of BLDT and NLDT strains into fastStructure populations was stable
239 when hemp samples were excluded from the analysis (Dataset S1). Sawler et al. (50) used
240 fastStructure to delineate hemp from drug-types as the major division of *Cannabis* diversity, and
241 found two drug-type sub-groups within their samples when hemp types were excluded from the
242 analysis. Likewise using a smaller dataset, Lynch (55) found support for $K=3$, consisting of two
243 separate drug-type populations and hemp types, using the original Structure implementation (56)
244 and the Evanno method to select the best value of K (57). However, we caution that despite
245 many claims for the availability of “landrace genetics” (strains) from *Cannabis* producers,
246 breeders and seed sellers, these may or may not represent non-admixed individuals (52)—a
247 situation that can be problematic for the Structure and fastStructure approaches (56).

248 The GBS samples from Sawler et al. (50) appear to contain an additional divergent
249 NLDT clade, with likely SE Asian origins (Supplementary Figures 3 and 4), that did not emerge
250 from our main analyses. Due to very limited overlap between sequence fragments from the two
251 GBS datasets, which results from using different restriction enzymes, we were required to re-
252 analyze the Sawler data in combination with only our 67 WGS samples. A connection was made

253 across the two GBS analyses to this SE Asian NLDT group through two WGS samples (Dr.
254 Grinspoon and Somali Taxi Cab, Figure 2, Supplementary Figures 3) that were included in both
255 sets of GBS analyses. Although only 45 SNPs overlapped between both types of GBS data and
256 the WGS data, a phylogeny of this limited alignment also supports the existence of an additional
257 distinct SE Asian NLDT clade (Figure S4). Collectively these analyses lend support to a total
258 lower bound of four *Cannabis* populations, although clearly more extensive sampling with
259 consistent sequencing is required to fully access standing biogeographic diversity.

260

261 **Tests of Tree Models.** To test hypotheses of tree-like evolution for the three genetic groups, we
262 first applied the three-population test for admixture (58), and found no evidence for admixture in
263 any of the pairwise comparisons (positive f statistic values). Next we constructed maximum
264 likelihood trees based on the aggregate SNP frequencies for the three genetic groups and
265 simulated a variety of ‘migration’ events (0-10), but no simulation produced non-zero migration
266 graph edges (Figure 3). F_{ST} analysis shows little divergence among lineages for most loci, but a
267 substantial number of highly-divergent regions are unique to each clade (Figure 4). This
268 reinforces the importance of using many, high-quality, single-copy regions of the genome, rather
269 than smaller numbers of loci that could lead to less resolution or even misleading results.

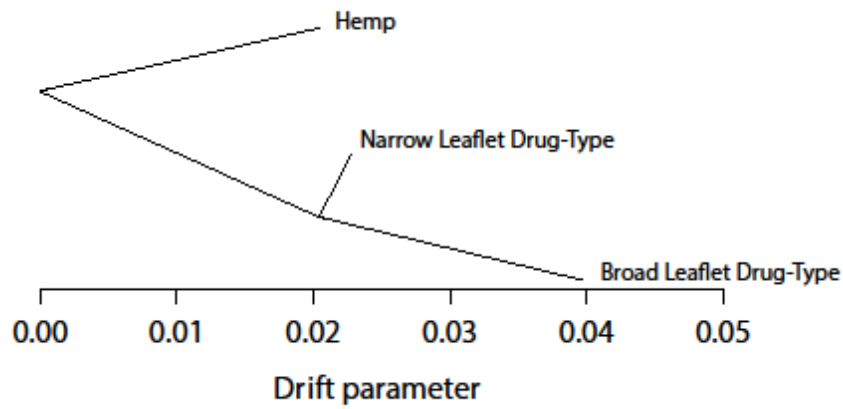
270 Although lore (52), Figure 2 and Figure S2 strongly suggest at least some individuals have
271 hybrid origins, these tree models for the overall SNP frequencies of the population groups
272 inferred by FLOCK (Table 2) imply each group contains strong genetic signals from ancestral
273 biogeographic gene pools.

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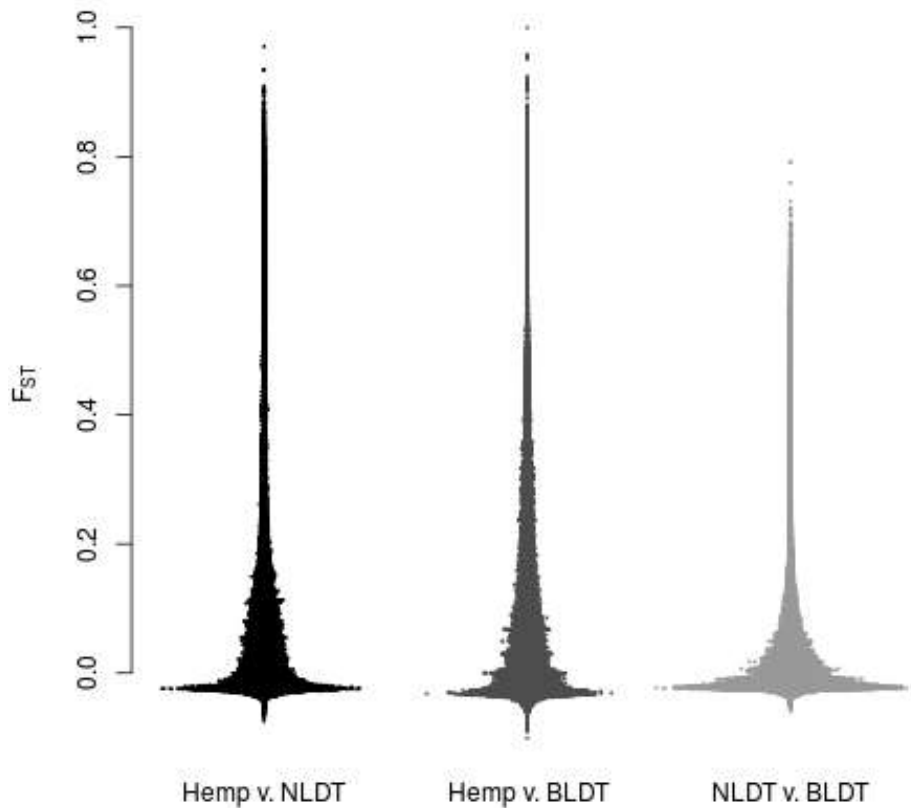
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278

279 Figure 3. Maximum likelihood tree of three *Cannabis* populations. We found no evidence for
280 extensive admixture or deviations from this tree model.

281



282

283 Figure 4. Distribution of Weir-Cockerham F_{ST} estimates for each population comparison. Each
284 population pair has some portion of segregated sites.

285

286 Additional *Cannabis* diversity likely remains to be sampled. Notably absent from all
287 genome sequence datasets published to date are putative *C. ruderalis* (59) samples. These are
288 short weedy plants, with free shattering inflorescences found widely from northern Siberia,
289 through central Asia and into Eastern Europe (60). Whether these populations represent
290 ancestral, pre-domesticated wild *Cannabis*, more recent feral escapes or some combination of
291 both remains unclear. Even though we were not able to sample putative *C. ruderalis* populations,
292 Finola is an early maturing seed hemp strain from Finland with purported northern Russian
293 landrace ancestry (52), and Low Ryder and Auto AK-47 are auto-flowering drug-type strains

294 with possible *C. ruderalis* heritage included in our samples (Table 2). Our analyses found Finola
295 fits within the hemp group while Low Ryder and Auto AK-47 are close relatives of each other
296 within the NLDT group (Figure S3). Further genomic analyses are required to determine the
297 extent to which *C. ruderalis* populations are genetically distinct from hemp and drug-type
298 groups, and whether they may in fact harbor an ancestral wild-type gene pool from which
299 European hemp varieties were domesticated (5, 16).

300 Broad leaflet Asian hemp is also underrepresented, although we included one putative
301 Chinese hemp sample that occupies an area between the core hemp and BLDT populations
302 (Table 2, Figure 2 and Figure S2). Hillig's (5) analysis of alloenzymes concluded that Asian
303 hemp strains were more similar to Asian drug-type strains than they were to narrow leaflet
304 European hemp. Likewise, Gao et al. (61) found genetic dissimilarity between European hemp
305 and Chinese hemp, using microsatellites, and showed at least several distinct groups of hemp
306 occur across the vast geography of Asia. Overall, Asian and European hemp strains appear
307 dissimilar genetically, possibly reflecting independent domestication events (60).

308 One major complication obscuring the understanding of *Cannabis* diversity and history is
309 the lack of information about the native range or ranges of *Cannabis*. In addition to divergent
310 breeding efforts and human-vectored transport of seeds, the tendency of *Cannabis* is to escape
311 into feral populations wherever human cultivation occurs in temperate climates (62). This,
312 coupled with wind pollination biology and no known reproductive barriers, makes the existence
313 of pure wild native *Cannabis* populations unlikely. The weedy tendencies of *Cannabis* are
314 exemplified by the mid-western USA populations of feral hemp that flourish despite the
315 eradication efforts by the Drug Enforcement Agency, which have for decades totaled millions of
316 plants removed per year. A comprehensive evaluation of *Cannabis* diversity, which includes

317 feral and wild Eurasian populations, is required to ascertain if the levels of divergence and gene
318 flow are consistent with one or more origins of domestication (5). Even if these extant
319 populations are highly admixed with modern varieties, their study promises to offer insight into
320 *Cannabis* ecology and evolution, given how different the selective regime of the feral setting is
321 compared to that of agricultural fields. Considering the similar debates regarding the timing and
322 origins of *Oryza* domestication that remain as of yet unresolved (63), *Cannabis* requires
323 substantially more work to unravel its complicated relationship with humans.

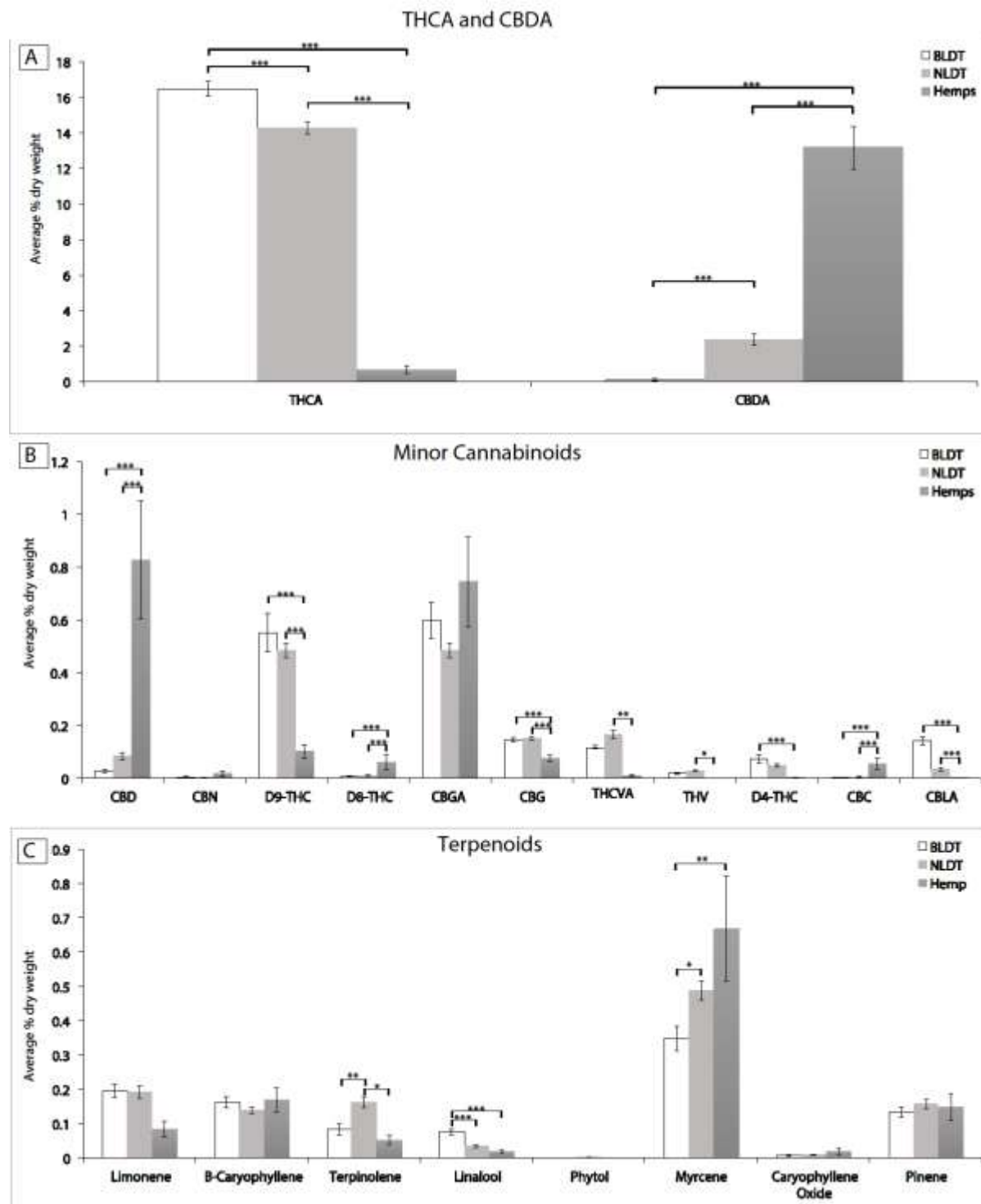
324 'Indica' and 'sativa' are commonly used terms ascribed to plants that have certain
325 characteristics, often related to leaflet morphology and the perceived effects of consuming the
326 plant (8). However these names are rooted in taxonomic traditions dating to Linnaeus who first
327 classified the genus as monotypic (*Cannabis sativa*) based on hemp specimens from Virginia and
328 Europe (64). Lamarck subsequently designated *Cannabis indica* to accommodate the shorter
329 stature potent narrow leaflet drug-type plants from the Indian subcontinent (65). Although
330 currently the term 'indica' is typically used to refer to BLDTs, this biotype from the Hindu-Kush
331 mountains (14) was not clearly documented until a 1929 survey of Afghani agriculture by
332 Vavilov (66). This absence of historical documentation until the 20th century, a very narrow
333 geographic range, and some evidence for a broader NLDT gene pool (Table 1, Supplementary
334 Figures 3 and 4), suggest a separate and more recent origin of the BLDT clade. This origin could
335 represent a domestication event of a wild or feral BLDT population, or perhaps hybridization
336 events between NLDT and BLDT populations. Final resolution of *Cannabis* taxonomy will
337 require complete assessment of standing global genetic diversity and experimental evaluation of
338 reproductive compatibility across all major genetic groups (67), in conjunction with
339 morphological circumscriptions. Given the current absence of evidence for reproductive barriers,

340 and overall limited genetic distances between hemp and drug-type strains analyzed in this study
341 we suggest continued monotypic treatment of plants in this genus as *Cannabis sativa* L. is
342 warranted.

343 **Cannabinoid and Terpenoid Diversity.** THCA and CBDA are the most abundant cannabinoids
344 produced by the majority of strains on the North American market today (Figure 5a), and both
345 compounds show an impressive range of medicinal potential (33, 68), although
346 endocannabinoid-based therapy trials have a history of significant rates of study withdraws and
347 adverse effects (69). Historical breeding efforts have resulted in mostly high THCA plants that
348 produce strong intoxicating effects when consumed, and that synthesize only very low levels of
349 alternative cannabinoids (Figure 5b). High CBDA plants have only recently become more
350 available in North America over the last several years in response to demand. Interestingly, these
351 high CBDA-producing plants form several clusters within the both the NLDT and BLDT groups,
352 as well as within the hemp group (Dataset S1), but rarely reach equivalent quantities total
353 cannabinoid production as those found in high THCA plants (Figure 4a). The minor
354 cannabinoids that are commonly assayed, CBGA, CBCA, THCVA and CBDVA are also of
355 interest, despite strains producing high levels of these compounds being largely unavailable for
356 research currently (70). With at least 74 cannabinoids identified in *Cannabis*, modernized
357 genetic and breeding techniques are required to diversify and optimize *Cannabis* varieties.
358 Efforts should also be made to document and preserve feral, wild and heirloom populations that
359 can serve as reservoirs of cultural and genetic diversity.

360 Aromatic terpenoids impart many of the characteristic fragrances to *Cannabis*, and
361 possibly contribute to the effects of consumption (2). Terpenoids are synthesized in many plant
362 species, and play a role in relieving various abiotic and biotic stresses through direct and indirect

363 mechanisms (71). Our analysis of strains sharing common genetic groups shows that each group
364 has a distinct terpenoid profile (Figure 5c and Figure S5). We found NLDTs to contain
365 significantly more β -myrcene and α -terpinolene than BLDTs, although interestingly the two
366 hemp strains for which we analyzed chemical data for had significantly more β -myrcene than
367 either drug-type group (Figure 5c). Similarly Hillig (72) found NLDTs to yield significantly
368 more β -myrcene than Afghani BLDTs, yet European hemp and un-cultivated accessions labeled
369 as *C. ruderalis* contained the highest levels. Hillig also reported that Afghani BLDTs contained
370 the highest levels of guaiol and eudesmol isomers, which we did not measure, although we found
371 BLDTs contained more linalool than NLDTs or hemp. Understanding the ecological functions
372 and evolutionary origins of terpenoids and cannabinoids in *Cannabis* could improve therapeutic
373 potential, and possibly reduce the need for pesticide application during cultivation.



374

375

376 Figure 5. Average percentage of mass for dried and un-pollinated female flowers of *Cannabis*
 377 genetic groups. (a) THCA and CBDA cannabinoids (b) Minor cannabinoids (c) Terpenoids.

378 THCA = delta-9-tetrahydrocannabinolic acid. CBDA = cannabidiolic acid. CBD = cannabidiol.

379 CBN = cannabinol. D9-THC = delta-9-tetrahydrocannabinol. D8-THC = delta-8-
380 tetrahydrocannabinol. CBGA = cannabigerolic acid. CBG = cannabigerol. THCVA =
381 Tetrahydrocannabivarin carboxylic acid. THCV = Tetrahydrocannabivarin. D4-THC = delta-4-
382 tetrahydrocannabinol. CBC = cannabichromene. CBLA = cannabicyclolic acid.

383

384 **Conclusions.** *Cannabis* genomics offers a window into the past, but also a road forward.

385 Although historical and clandestine breeding efforts have been clearly successful in many
386 regards (21, 31), *Cannabis* lags decades behind other major crop species in many other respects.
387 Developing stable *Cannabis* lines capable of producing the full range of potentially therapeutic
388 cannabinoids is important for the research and medical communities, which currently lack access
389 to diverse high-quality material in the USA (73).

390 In this paper we extended the initial *Cannabis* genome study (10), by re-mapping WGS
391 and GBS sequence reads to the existing PK draft scaffolds, to understand diversity and
392 evolutionary relationships among the major lineages. Although hybridization of cultivated
393 varieties (52) and human transport of seeds across the globe was hypothesized to have obscured
394 much of the ancestral genetic signal (13), we found significant evidence for apparent ancestral
395 signals in genomic data derived largely from modern cultivated varieties (Table 2, Figures 2 and
396 3). Re-analysis of previously published GBS data (50) provides additional limited evidence for a
397 fourth group (Supplementary Figures 4 and 5). Interestingly, unique cannabinoid and terpenoid
398 profiles were associated with three of the genetic groups, lending support to their validity,
399 despite the limitations of our sampling scheme. Overall, we hope the publicly available data and
400 analyses from this study will facilitate the continued research on the history of this controversial
401 plant and the development of the agricultural and therapeutic potential of *Cannabis*.

402

403

404 **Materials and Methods**

405 **Sample collection.** DNA was obtained from numerous sources, including a variety of breeding
406 and production facilities. The strain names, descriptions and putative origins used in this paper
407 were recorded from the providers of the DNA and sequence data (Dataset S1). For data not
408 previously published, DNA extractions were performed using the Qiagen DNeasy Plant Mini Kit
409 (Valencia, CA) according to the manufacturer's protocol.

410

411 **Whole genome shotgun (WGS) sequencing.** 60 samples were sequenced using standard
412 Illumina multiplexed library preparation protocols for two 2 x 125 HiSeq 2500 lanes and one 2 x
413 150 NextSeq 500 run. Sequencing efforts were targeted for approximately 4-6x coverage of the
414 *Cannabis* genome per sample.

415

416 **Genotype-by-Sequencing (GBS).** 182 samples were sequenced on two 1 x 100 HiSeq 2500
417 lanes, following a multiplexed library preparation protocol described previously (74).

418

419 **Publicly available data.** We obtained three WGS datasets available from NCBI (10) and
420 received seven additional WGS datasets from Medicinal Genomics Corporation
421 (www.medicinalgenomics.com). GBS data for 143 samples from Sawler et al. (50) were also
422 included in this study.

423

424 **Sequence Processing, Alignment and SNP calling.** Trimmomatic (75) was used to trim any
425 remaining adaptor sequence from raw fastq reads and remove sequences with low quality regions
426 or ambiguous base calls using the following settings:

427 ILLUMINACLIP:IlluminaAdapters:2:20:10 LEADING:20 TRAILING:20
428 SLIDINGWINDOW:5:15 MINLEN:100. Trimmed raw reads from the 67 total WGS samples
429 were then aligned to the only publicly available draft genome of PK (JH226140-JH286168)
430 using the Burrows-Wheeler Alignment tool (BWA mem) (76). Chloroplast and mitochondrial
431 regions were excluded. We collated the individual alignments to produce a single variant call
432 format table (.vcf) for all samples using samtools mpileup -uf | bcftools view -bvcg (77). We
433 filtered the vcf table to include only high quality informative SNP sites using vcftools (78), bash
434 and awk with the following vcf parameters: Q (>200), GQ (>10), AF1 (.1 - .9), biallelic sites
435 only and no ambiguous bases. Next, data filters were applied through plink (79) to require that
436 individuals have a minimum 50% informative sites and that sites each have data for minimum
437 20% of samples. Finally we used an estimate of expected coverage for the single copy portion of
438 the genome based on the estimated genome size and number of reads being aligned. This was
439 adjusted empirically based on total coverage level (across all WGS samples) per SNP site
440 (Figure S1) and bounded by a 95% Poisson confidence interval (mean 362x coverage). Further
441 removal of repetitive content was achieved by aligning the PK reference to itself with BLASTN
442 and removing all sites that were within regions of $\geq 97\%$ identity for at ≥ 500 bp alignments.
443 These aforementioned processing, alignment and SNP calling procedures were then performed
444 separately on the 182 GBS samples generated for this study and the 143 GBS samples previously
445 published (50), resulting in three vcf tables and filtered SNP sets. GBS SNPs were additionally
446 required to have a minimum of 5x coverage per sample. Due to limited overlap between the SNP
447 sites produced by the two GBS libraries, most downstream analyses were performed separately
448 for each GBS library along with its corresponding set of WGS SNPs. Code used for these
449 analyses is available at <https://github.com/KaneLab>.

450

451 **SNP Analyses.** To visualize genetic relationships, divergence, and ancestral hybridization
452 among lineages, a phylogenetic neighbor network was inferred using simple p-distance
453 calculations (51). Heterozygosity counts and Multidimensional Scaling (MDS) analyses were
454 calculated with Plink (79). Average within and between group genetic distances, and a 45 SNP
455 alignment neighbor joining tree based on p-distances, were calculated with MEGA6 (80).
456 Population structure inferences were made through FastStructure (54) and FLOCK (53). Tests
457 for reticulation within the trees and admixture between populations were performed in TreeMix
458 (81) F_{ST} estimates were calculated with vcftools (78).

459

460 **Chemical Analyses of Genetic Groups.** The cannabinoid and terpenoid information
461 (chemotype) for a portion of the strains in the genome analysis were generated by Steep Hill
462 Labs (<http://steephill.com/>). Only strains with matching data in the genomic analysis were
463 analyzed, for a total of 112 individuals from 17 strains from the BLDT group, 278 individuals
464 from 35 unique strains from the NLDT group, and 33 individuals from two strains of hemp, for a
465 total of 423 individuals in this analysis (Dataset S1). This chemotype analysis was performed
466 using high performance liquid chromatography (HPLC) with Agilent (1260 Infinity, Santa Clara,
467 CA) and Shimadzu (Prominence HPLC, Columbia, MD) equipment. Between 400 and 600
468 milligrams of each sample was extracted into methanol, diluted and analyzed by HPLC. A
469 mobile phase consisting of 0.1% formic acid in water and 0.1% formic acid in methanol was
470 used with a gradient starting at 72% methanol and ending at 99% methanol. Terpenoid standards
471 were purchased from Sigma-Aldrich (St. Louis, MO). Cannabinoid standards were purchased
472 from Cerilliant (Round Rock, TX), RESTEK (Bellefonte, PA) and Lipomed (Cambridge, MA).

473 A C18 column from RESTEK (Raptor ARC-18, Bellefonte, PA) or Phenomenex (Kinetex C18,
474 Torrance, CA) was used. Concentrations of cannabinoids without commercially available
475 standards were estimated using published absorptivities (82). The chemotype data analyzed for
476 this research includes 13 cannabinoids and eight terpenoids. Each compound was quantified
477 using a linear calibration curve. Analytes were measured as percent mass in sample and not
478 corrected for moisture content.

479 We performed a one-way ANOVA for each cannabinoid and terpenoid separately, with
480 the group (NLDT, BLDT, and hemp) as the predictor variable. We used Bonferroni corrections
481 for multiple comparisons. We also implemented a Principal Component Analysis (PCA) with
482 `prcomp` function in base R, and `car` was used to visualize 95% confidence ellipses for each group
483 (www.R-project.org). Individuals with missing data values for any cannabinoid or terpenoid
484 were removed. After removing the individuals with missing values, we had a total of 351
485 individuals: 94 BLDT, 229 NLDT, and 28 hemp.

486

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497 bioinformatics analyses. KdC, DPL and TCR generated chemical data. DV and SBT performed
498 chemical data analyses. RCL, DV and NCK wrote the paper.

499

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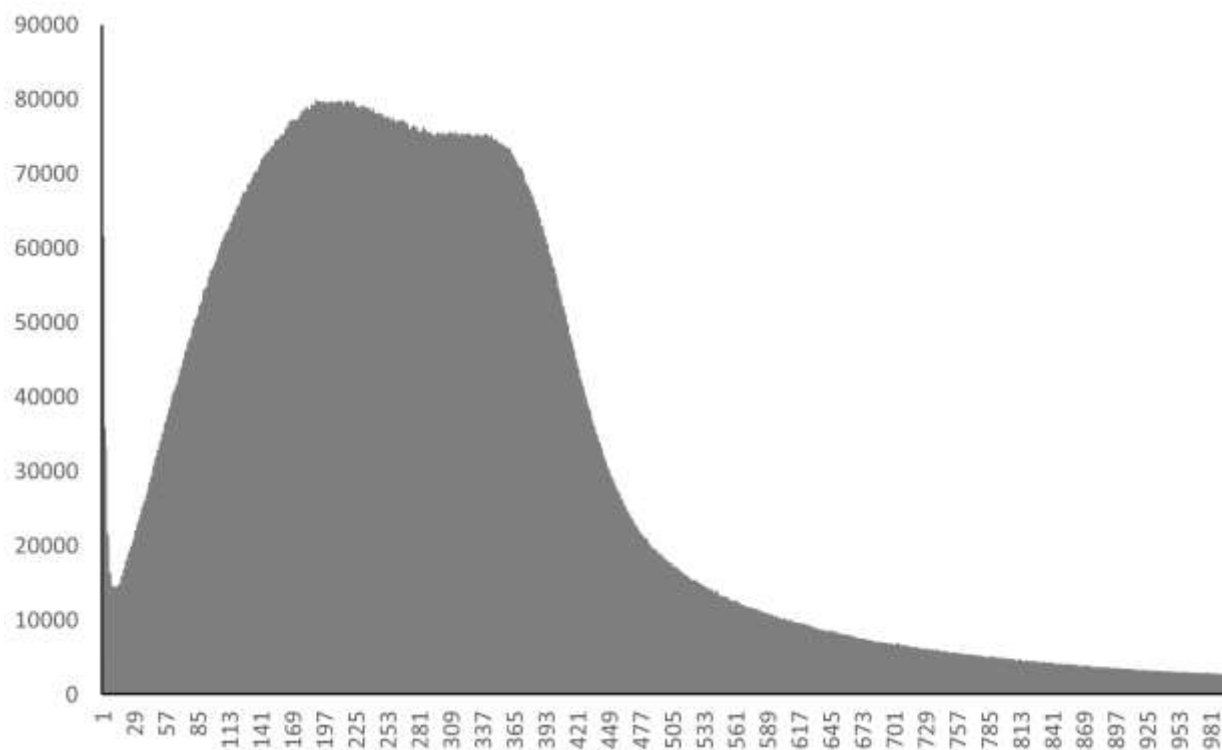
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679 **Supplementary Information**

680 a)



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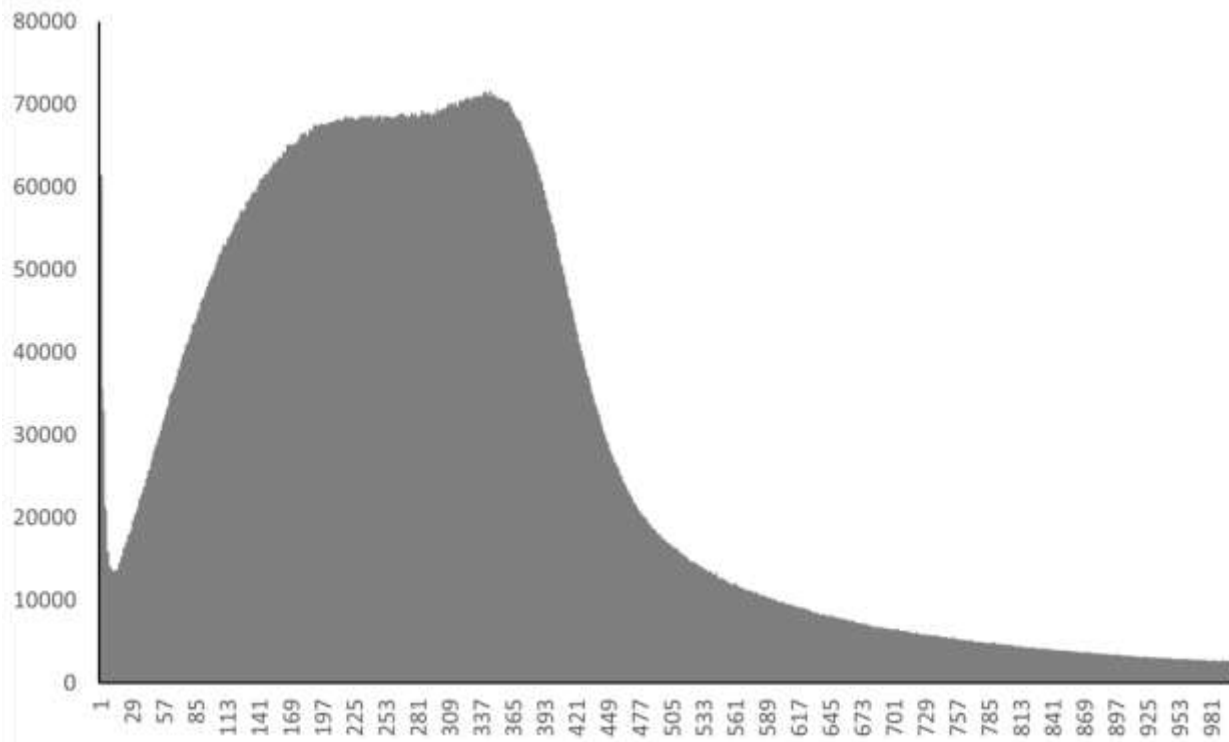
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695 b)



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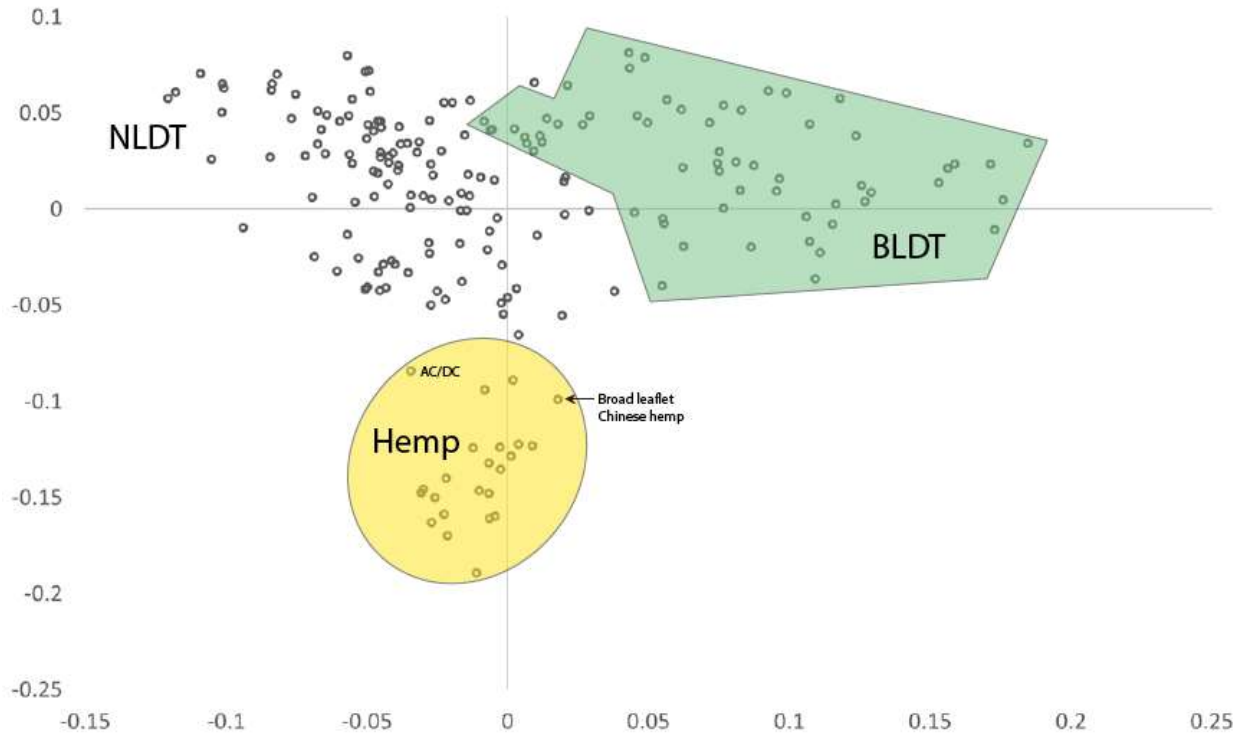
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699 Figure S1. Histograms of WGS read depths at variant loci. a) before PK reference self-
700 similarity filter. b) after self-similarity filter.

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707 Figure S2. Multidimensional Scaling plot of GBS and WGS SNPs. Hemp, NLDT and BLDT
708 group assignments were made by FLOCK.

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712 Figure S3. Phylogenetic neighbor network of WGS samples combined with Sawler GBS SNPs
713 (4,105) in separate high resolution pdf.

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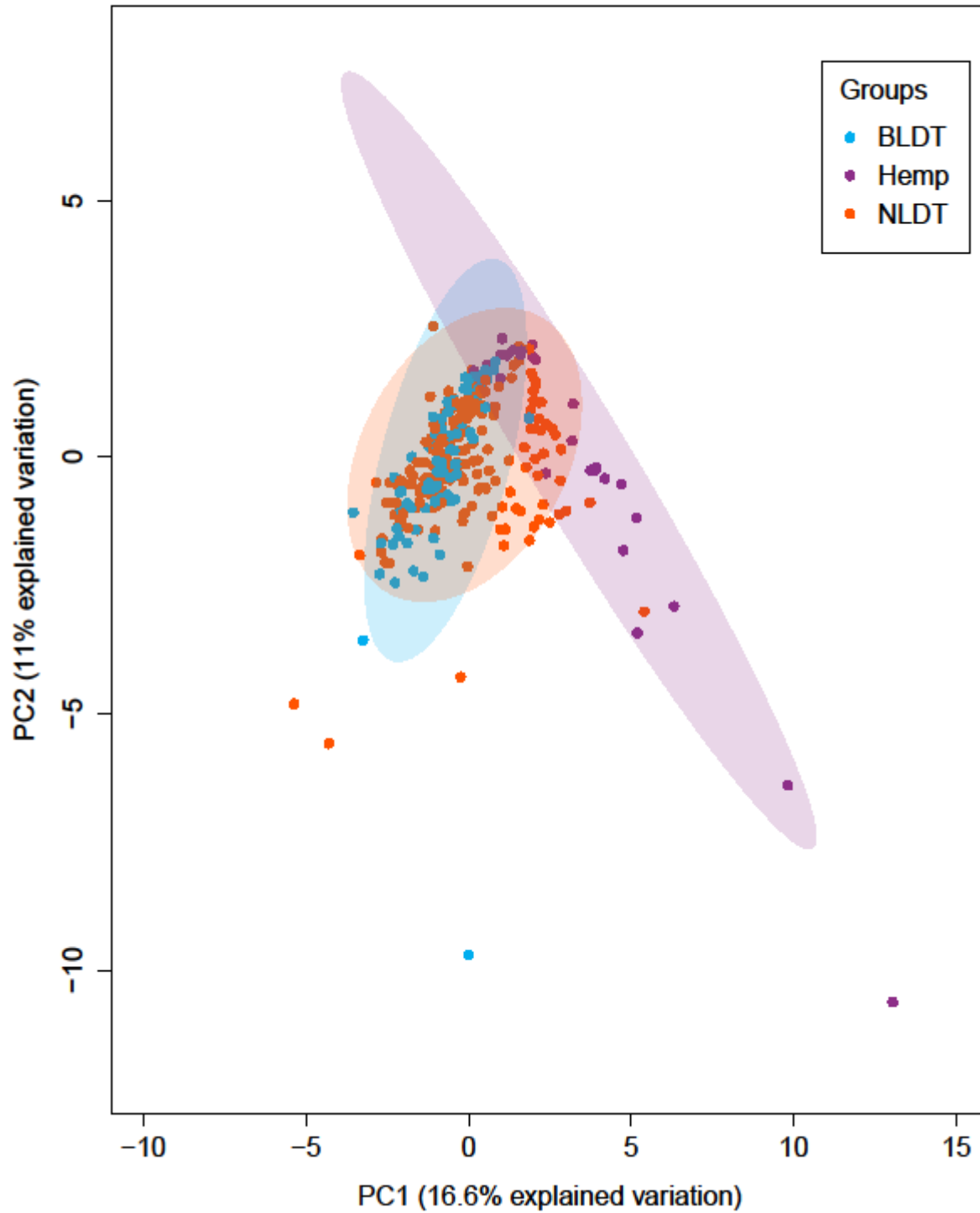
717 Figure S4. Neighbor joining tree from 45 SNP alignment of 289 GBS and WGS samples in
718 separate high resolution pdf.

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724 Figure S5. Principal Components Analysis of cannabinoid and terpene profiles colored by

725 FLOCK derived genetic groups.