

# Kannapedia

Library of Cannabis Genetics

## Wild Thailand

SRR 14708216 · Grower: [Lanzhou University, Guangpeng Ren](#)

### General Information

**Sample Name**

THD

**Accession Date**

May 31, 2021

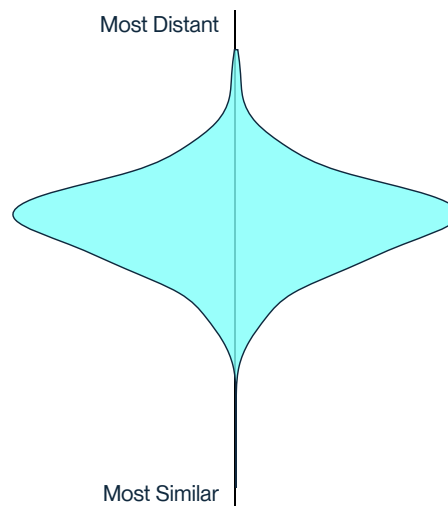
**Reported Plant Sex**

[not reported](#)

**Report Type**

[Whole-Genome Sequencing](#)

Rarity: **Rare**



## Chemical Information

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*Cannabinoid and terpenoid information provided by the grower.*

### **CANNABINOIDS**

*No information provided.*

### **TERPENOIDS**

*No information provided.*

# Genetic Information

## Plant Type

Type I

## FILE DOWNLOADS

VCF ([https://mgcdata.s3.amazonaws.com/SS2/vcf\\_JL/SRR14708216\\_blockchain.vcf.gz](https://mgcdata.s3.amazonaws.com/SS2/vcf_JL/SRR14708216_blockchain.vcf.gz))

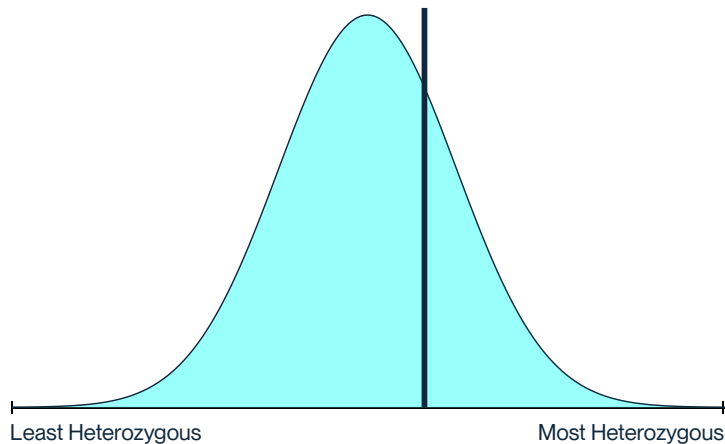
Annotated VCF (<https://mgcdata.s3.amazonaws.com/SS2/vcf-snpEff-variants/SRR14708216.vcf.gz>)

Annotated VCF Index (<https://mgcdata.s3.amazonaws.com/SS2/vcf-snpEff-variants/SRR14708216.vcf.gz.tbi>)

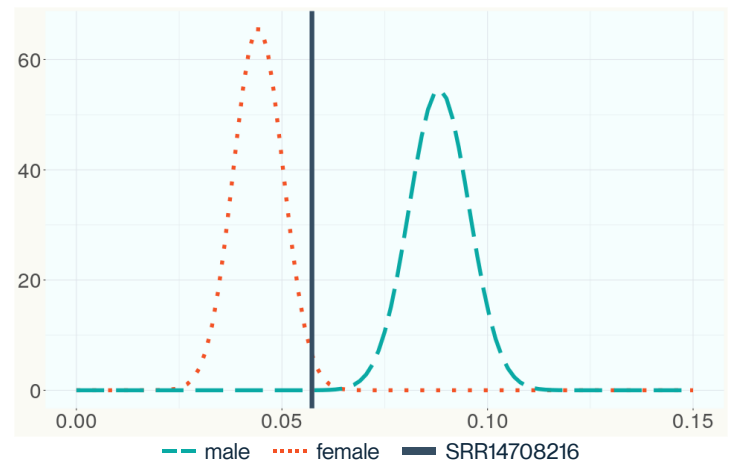
BAM (<https://mgcdata.s3.amazonaws.com/SS2/bams/public/SRR14708216.bam>)

BAM Index (<https://mgcdata.s3.amazonaws.com/SS2/bams/public/SRR14708216.bam.bai>)

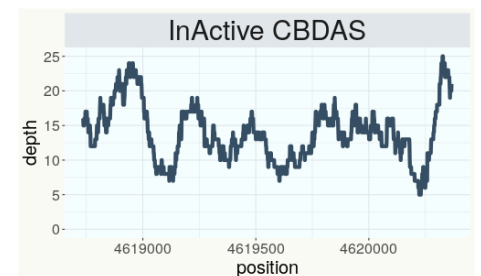
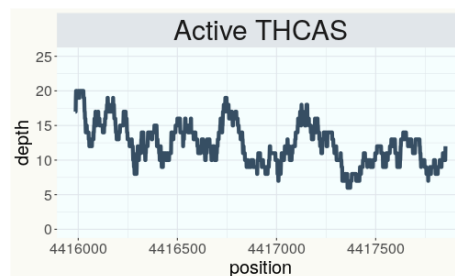
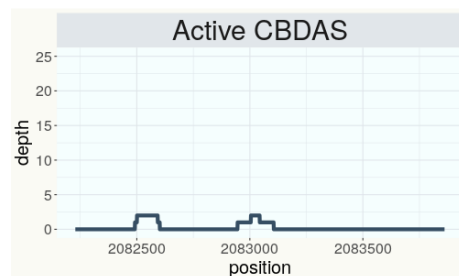
Heterozygosity: **1.34%**



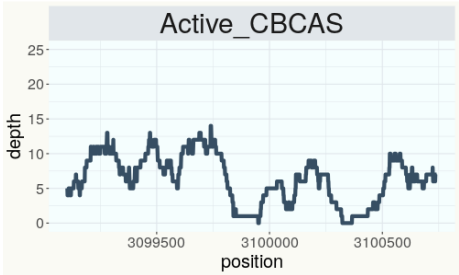
Y-Ratio Distribution: **0.0573**



## Bt/Bd Allele Coverage



CBCAS Coverage



**Variants (THCAS, CBDAS, and CBCAS)**

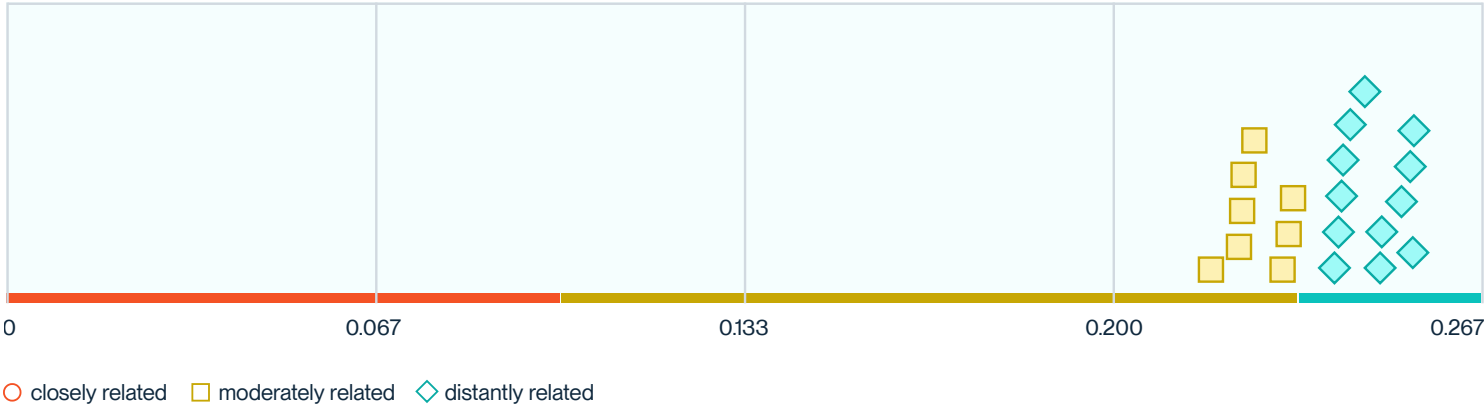
GENE	HGVS.C	HGVS.P	ANNOTATION	ANNOTATION IMPACT	CONTIG	CONTIG POS	REF/ALT	VAR FREQ
THCAS	c.1229G>A	p.Gly410Glu	missense variant	moderate	contig741	4416599	C/T	NGS: 0.039 C90: 0.000
THCAS	c.749C>A	p.Ala250Asp	missense variant	moderate	contig741	4417079	G/T	NGS: 0.127 C90: 0.632

Variants (Select Genes of Interest)

GENE	HGVS.C	HGVS.P	ANNOTATION	ANNOTATION IMPACT	CONTIG	CONTIG POS	REF/ALT	VAR FREQ
PHL-2	c.455A>C	p.Asp152Ala	missense variant	moderate	contig2621	339191	A/C	NGS: 0.018 C90: 0.507
PHL-2	c.977A>C	p.His326Pro	missense variant	moderate	contig2621	340255	A/C	NGS: 0.007 C90: 0.000
PHL-2	c.1057A>G	p.Arg353Gly	missense variant	moderate	contig2621	340335	A/G	NGS: 0.096 C90: 0.555
PHL-2	c.1540A>G	p.Thr514Ala	missense variant	moderate	contig2621	340818	A/G	NGS: 0.042 C90: 0.282
PHL-2	c.3467A>G	p.Gln1156Arg	missense variant	moderate	contig2621	343510	A/G	NGS: 0.064 C90: 0.713
OAC-2	c.22G>A	p.Val8Ile	missense variant	moderate	contig931	110317	C/T	NGS: 0.018 C90: 0.000
ELF3	c.358G>A	p.Gly120Arg	missense variant	moderate	contig97	242064	G/A	NGS: 0.099 C90: 0.493
ELF3	c.772A>G	p.Ser258Gly	missense variant	moderate	contig97	242478	A/G	NGS: 0.112 C90: 0.000
ELF3	c.1230-2_1230-1delAG		splice acceptor variant & intron variant	high	contig97	243676	TAG/T	NGS: 0.088 C90: 0.450
ELF3	c.1630A>G	p.Thr544Ala	missense variant	moderate	contig97	244461	A/G	NGS: 0.103 C90: 0.545
ELF3	c.1966C>G	p.Pro656Ala	missense variant	moderate	contig97	244797	C/G	NGS: 0.123 C90: 0.632
ELF3	c.2141C>G	p.Pro714Arg	missense variant	moderate	contig97	244972	C/G	NGS: 0.088 C90: 0.335
ELF3	c.2198G>T	p.Arg733Leu	missense variant	moderate	contig97	245029	G/T	NGS: 0.125 C90: 0.531
ELF5	c.853C>T	p.Pro285Ser	missense variant	moderate	contig382	880715	C/T	NGS: 0.007 C90: 0.153
aPT1	c.406A>G	p.Ile136Val	missense variant	moderate	contig121	2839605	A/G	NGS: 0.579 C90: 0.761
aPT1	c.629C>T	p.Thr210Ile	missense variant	moderate	contig121	2840237	C/T	NGS: 0.561 C90: 0.598
aPT1	c.864C>G	p.Asn288Lys	missense variant	moderate	contig121	2842407	C/G	NGS: 0.075 C90: 0.062
AAE1-2	c.688G>A	p.Asp230Asn	missense variant	moderate	contig81	209650	G/A	NGS: 0.018 C90: 0.000
AAE1-2	c.1415G>A	p.Ser472Asn	missense variant	moderate	contig81	210377	G/A	NGS: 0.070 C90: 0.000
AAE1-2	c.1434G>T	p.Glu478Asp	missense variant	moderate	contig81	210396	G/T	NGS: 0.075 C90: 0.000
PKSG-2b	c.948T>G	p.Asp316Glu	missense variant	moderate	contig700	1950690	A/C	NGS: 0.456 C90: 0.000
PKSG-2b	c.945T>G	p.Ser315Arg	missense variant	moderate	contig700	1950693	A/C	NGS: 0.454 C90: 0.000
PKSG-2b	c.944G>A	p.Ser315Asn	missense variant	moderate	contig700	1950694	C/T	NGS: 0.445 C90: 0.000
PKSG-2b	c.934C>G	p.His312Asp	missense variant	moderate	contig700	1950704	G/C	NGS: 0.410 C90: 0.000
PKSG-2b	c.31A>T	p.Thr11Ser	missense variant	moderate	contig700	1951851	T/A	NGS: 0.844 C90: 0.880
TFL1	c.302-1G>A		splice acceptor variant & intron variant	high	contig1636	520616	C/T	NGS: 0.103 C90: 0.794

HDS-1	c.1618A>G	p.Ile540Val	missense variant	moderate	contig1891	885936	T/C	NGS: 0.099 C90: 0.861
HDS-1	c.136G>A	p.Val46Ile	missense variant	moderate	contig1891	889256	C/T	NGS: 0.088 C90: 0.593
HDS-1	c.56C>G	p.Ala19Gly	missense variant	moderate	contig1891	889336	G/C	NGS: 0.125 C90: 0.943
HDS-1	c.35G>A	p.Cys12Tyr	missense variant	moderate	contig1891	889357	C/T	NGS: 0.094 C90: 0.646
PIE1-2	c.710C>T	p.Pro237Leu	missense variant	moderate	contig1460	1193804	G/A	NGS: 0.072 C90: 0.866
PIE1-2	c.706T>C	p.Tyr236His	missense variant	moderate	contig1460	1193808	A/G	NGS: 0.059 C90: 0.737
EMF2	c.1772A>G	p.Gln591Arg	missense variant	moderate	contig954	3059929	A/G	NGS: 0.092 C90: 0.876
aPT4	c.97T>C	p.Tyr33His	missense variant	moderate	contig121	2828753	T/C	NGS: 0.439 C90: 0.000
aPT4	c.153A>C	p.Lys51Asn	missense variant	moderate	contig121	2828809	A/C	NGS: 0.375 C90: 0.000
aPT4	c.235_237delGTA	p.Val79del	conservative inframe deletion	moderate	contig121	2829031	TGTA/T	NGS: 0.002 C90: 0.000
FLD	c.2686G>A	p.Ala896Thr	missense variant	moderate	contig1450	2044848	C/T	NGS: 0.035 C90: 0.225
FLD	c.2681T>C	p.Ile894Thr	missense variant	moderate	contig1450	2044853	A/G	NGS: 0.020 C90: 0.144
AAE1-3	c.722G>A	p.Arg241Lys	missense variant	moderate	contig976	1083132	C/T	NGS: 0.070 C90: 0.000
AAE1-3	c.382T>C	p.Tyr128His	missense variant	moderate	contig976	1083643	A/G	NGS: 0.072 C90: 0.000
AAE1-3	c.293A>G	p.Asp98Gly	missense variant	moderate	contig976	1083732	T/C	NGS: 0.068 C90: 0.000
AAE1-3	c.125A>G	p.Glu42Gly	missense variant	moderate	contig976	1083950	T/C	NGS: 0.064 C90: 0.000
AAE1-3	c.104T>C	p.Leu35Pro	missense variant	moderate	contig976	1083971	A/G	NGS: 0.009 C90: 0.000
GGR	c.362A>T	p.Tyr121Phe	missense variant	moderate	contig2282	549354	A/T	NGS: 0.029 C90: 0.000
GGR	c.704A>T	p.His235Leu	missense variant	moderate	contig2282	549696	A/T	NGS: 0.121 C90: 0.000

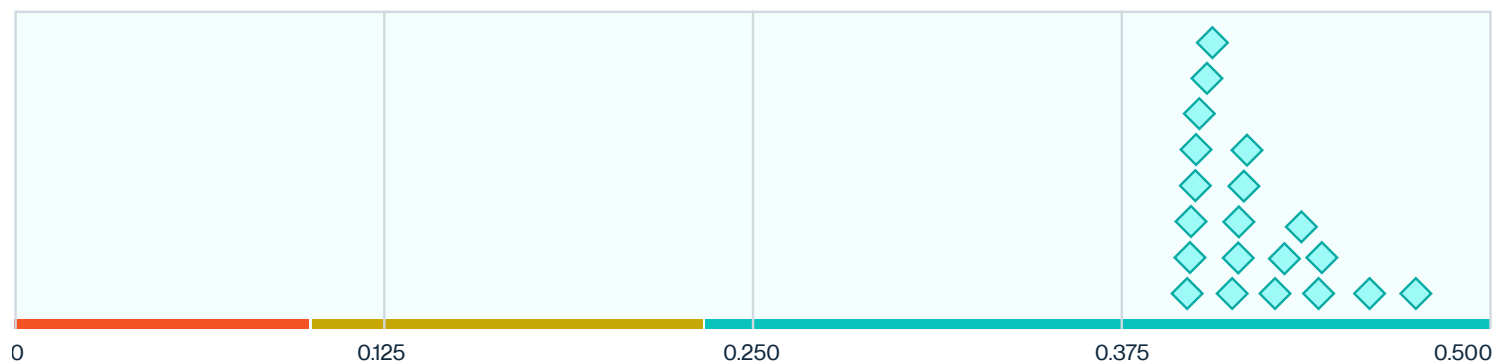
NEAREST GENETIC RELATIVES (ALL SAMPLES)



0.218 Durban Poison #1 (RSP11013) (<https://kannapedia.net/strains/rsp11013>)

- 0.223 Serious Happiness (RSP10763) (<https://kannapedia.net/strains/rsp10763>)
- 0.223 RKM-2018-025 (RSP1117) (<https://kannapedia.net/strains/rsp1117>)
- 0.224 Black Jack (RSP10603) (<https://kannapedia.net/strains/rsp10603>)
- 0.226 RKM-2018-016 (RSP11108) (<https://kannapedia.net/strains/rsp11108>)
- 0.231 BLACK JACK (RSP11346) (<https://kannapedia.net/strains/rsp11346>)
- 0.232 Lift (RSP11378) (<https://kannapedia.net/strains/rsp11378>)
- 0.233 Durban Poison #1 (RSP10996) (<https://kannapedia.net/strains/rsp10996>)
- ◇ 0.240 Durban Poison (RSP11014) (<https://kannapedia.net/strains/rsp11014>)
- ◇ 0.241 Strawberry Cough (RSP11356) (<https://kannapedia.net/strains/rsp11356>)
- ◇ 0.241 Doug s Varin (RSP11243) (<https://kannapedia.net/strains/rsp11243>)
- ◇ 0.242 Electra (RSP11366) (<https://kannapedia.net/strains/rsp11366>)
- ◇ 0.243 Durban Poison (RSP10998) (<https://kannapedia.net/strains/rsp10998>)
- ◇ 0.246 Miss X (RSP10999) (<https://kannapedia.net/strains/rsp10999>)
- ◇ 0.248 Saint Jack (RSP11179) (<https://kannapedia.net/strains/rsp11179>)
- ◇ 0.249 Liberty Haze (RSP11000) (<https://kannapedia.net/strains/rsp11000>)
- ◇ 0.252 UP Sunrise (RSP10989) (<https://kannapedia.net/strains/rsp10989>)
- ◇ 0.254 Blue Dream (RSP11007) (<https://kannapedia.net/strains/rsp11007>)
- ◇ 0.254 Domnesia (RSP11184) (<https://kannapedia.net/strains/rsp11184>)
- ◇ 0.254 RKM-2018-027 (RSP11119) (<https://kannapedia.net/strains/rsp11119>)

### MOST GENETICALLY DISTANT STRAINS (ALL SAMPLES)



○ closely related    □ moderately related    ◇ distantly related

- ◇ 0.475 Cherry Blossom (RSP11323) (<https://kannapedia.net/strains/rsp11323>)
- ◇ 0.459 Cherry Blossom (RSP11318) (<https://kannapedia.net/strains/rsp11318>)
- ◇ 0.443 Cherry Blossom (RSP11301) (<https://kannapedia.net/strains/rsp11301>)
- ◇ 0.442 Chematonic -Cannatonic x Chemdawg- (RSP11394) (<https://kannapedia.net/strains/rsp11394>)
- ◇ 0.436 Cherry Blossom (RSP11328) (<https://kannapedia.net/strains/rsp11328>)
- ◇ 0.431 Cherry Blossom (RSP11306) (<https://kannapedia.net/strains/rsp11306>)
- ◇ 0.427 Unknown--Cherry Wine---001- (RSP11268) (<https://kannapedia.net/strains/rsp11268>)
- ◇ 0.418 Cherry Blossom (RSP11325) (<https://kannapedia.net/strains/rsp11325>)



- ◇ 0.417 Tanao Sri -46- (RSP11486) (<https://kannapedia.net/strains/rsp11486>)
- ◇ 0.415 Cherry Blossom (RSP11274) (<https://kannapedia.net/strains/rsp11274>)
- ◇ 0.415 JL yellow (RSP11075) (<https://kannapedia.net/strains/rsp11075>)
- ◇ 0.413 Cherry Blossom (RSP11322) (<https://kannapedia.net/strains/rsp11322>)
- ◇ 0.406 JL 3rd Gen Mother (RSP11214) (<https://kannapedia.net/strains/rsp11214>)
- ◇ 0.404 Cherry Blossom (RSP11300) (<https://kannapedia.net/strains/rsp11300>)
- ◇ 0.402 Cherry Blossom (RSP11309) (<https://kannapedia.net/strains/rsp11309>)
- ◇ 0.401 JL Cross 1 (RSP11502) (<https://kannapedia.net/strains/rsp11502>)
- ◇ 0.400 YMCM (RSP11416) (<https://kannapedia.net/strains/rsp11416>)
- ◇ 0.399 Danny Noonan (RSP11070) (<https://kannapedia.net/strains/rsp11070>)
- ◇ 0.399 Avidelk 05MAY2017 (RSP10938) (<https://kannapedia.net/strains/rsp10938>)
- ◇ 0.398 Cherry Blossom (RSP11312) (<https://kannapedia.net/strains/rsp11312>)

#### NEAREST GENETIC RELATIVE IN PHYLOS DATASET

Phylos Strain SRR8346980  
(<https://www.ncbi.nlm.nih.gov/sra/SRR8346980>)

Overlapping SNPs: **17**

Concordance: **14**

#### NEAREST GENETIC RELATIVE IN LYNCH DATASET

Lynch Strain SRR3495200  
(<https://www.ncbi.nlm.nih.gov/sra/SRR3495200>)

Overlapping SNPs: **4**

Concordance: **4**

