

Kannapedia

Library of Cannabis Genetics

Haze

SRR 14708264 · Grower: [Lanzhou University, Guangpeng Ren](#)

General Information

Sample Name

HAE

Accession Date

May 31, 2021

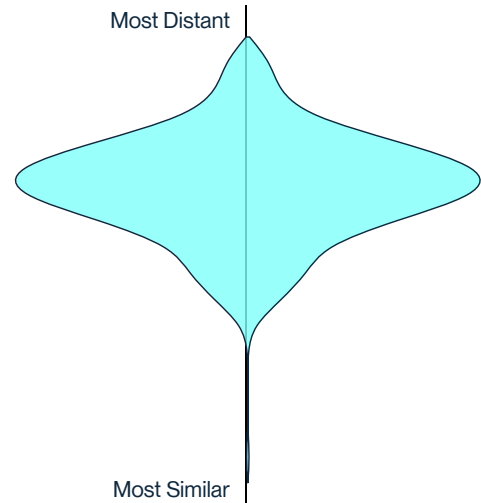
Reported Plant Sex

[not reported](#)

Report Type

[Whole-Genome Sequencing](#)

Rarity: **Rare**



Chemical Information

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/SRR14708264_blockchain.vcf.gz)

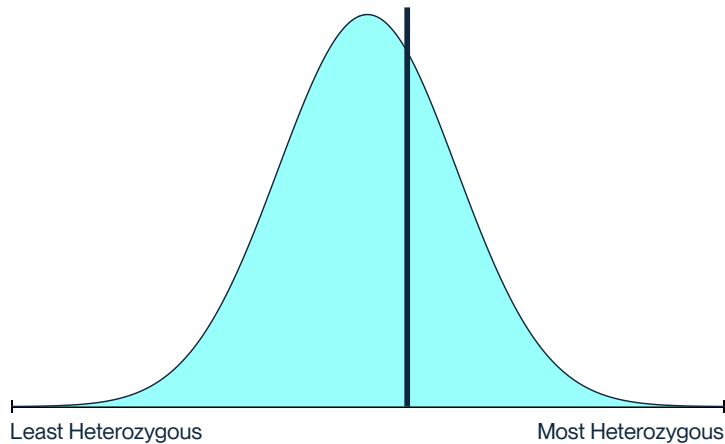
Annotated VCF (<https://mgcdata.s3.amazonaws.com/SS2/vcf-snpEff-variants/SRR14708264.vcf.gz>)

Annotated VCF Index (<https://mgcdata.s3.amazonaws.com/SS2/vcf-snpEff-variants/SRR14708264.vcf.gz.tbi>)

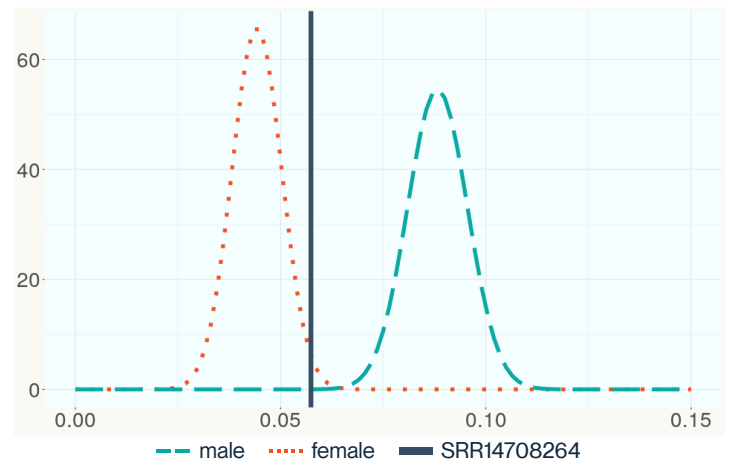
BAM (<https://mgcdata.s3.amazonaws.com/SS2/bams/public/SRR14708264.bam>)

BAM Index (<https://mgcdata.s3.amazonaws.com/SS2/bams/public/SRR14708264.bam.bai>)

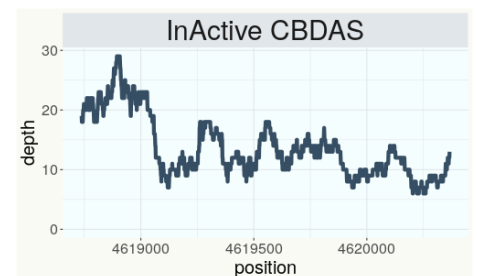
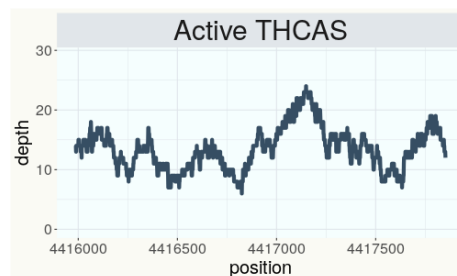
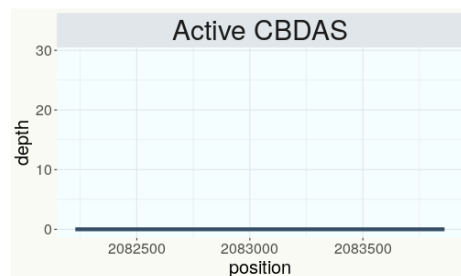
Heterozygosity: **1.27%**



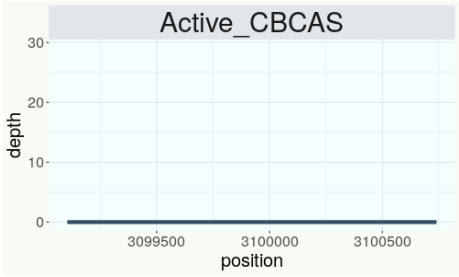
Y-Ratio Distribution: **0.0574**



Bt/Bd Allele Coverage



CBCAS Coverage



Variants (THCAS, CBDAS, and CBCAS)

No variants to report

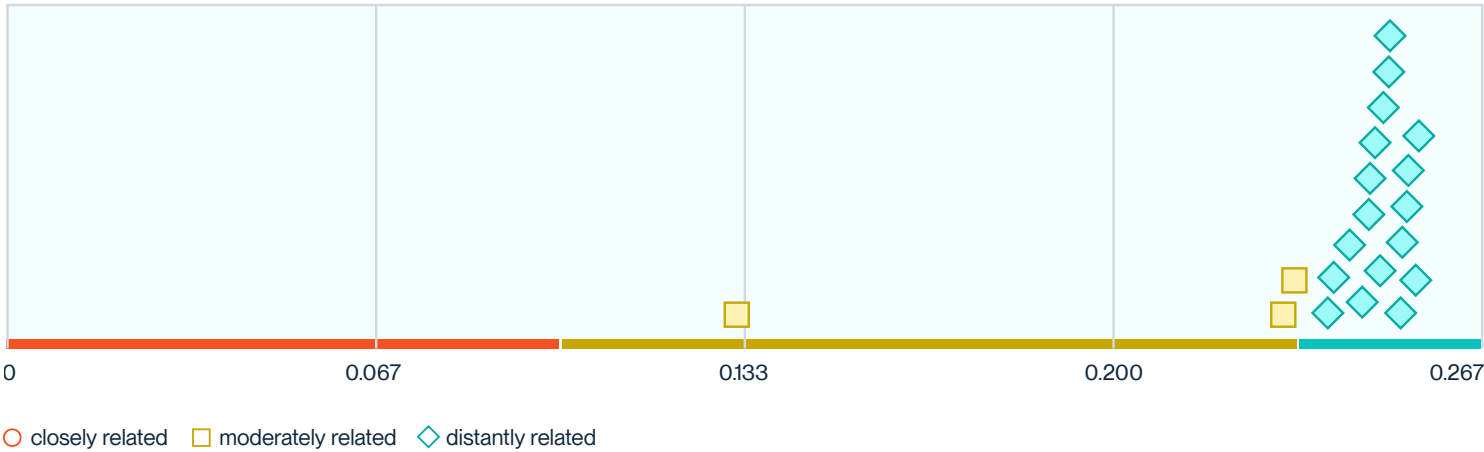
Variants (Select Genes of Interest)

GENE	HGVS.C	HGVS.P	ANNOTATION	ANNOTATION IMPACT	CONTIG	CONTIG POS	REF/ALT	VAR FREQ
GPPs1	c.845_848delAAAG	p.Glu282fs	frameshift variant	high	contig676	169629	TGAAA/T	NGS : 0.118 C90 : 0.000
PHL-2	c.44G>A	p.Arg15Lys	missense variant	moderate	contig2621	337613	G/A	NGS : 0.015 C90 : 0.167
PHL-2	c.932T>C	p.Leu311Pro	missense variant	moderate	contig2621	340210	T/C	NGS : 0.039 C90 : 0.268
PHL-2	c.1057A>G	p.Arg353Gly	missense variant	moderate	contig2621	340335	A/G	NGS : 0.096 C90 : 0.555
PHL-2	c.2564T>A	p.Phe855Tyr	missense variant	moderate	contig2621	342607	T/A	NGS : 0.064 C90 : 0.732
PHL-2	c.2578T>A	p.Leu860Ile	missense variant	moderate	contig2621	342621	T/A	NGS : 0.068 C90 : 0.746
PHL-2	c.2582C>G	p.Pro861Arg	missense variant	moderate	contig2621	342625	C/G	NGS : 0.002 C90 : 0.000
PHL-2	c.2624C>T	p.Ser875Phe	missense variant	moderate	contig2621	342667	C/T	NGS : 0.042 C90 : 0.268
PHL-2	c.2783G>A	p.Ser928Asn	missense variant	moderate	contig2621	342826	G/A	NGS : 0.107 C90 : 0.890
PHL-2	c.2830A>C	p.Asn944His	missense variant	moderate	contig2621	342873	A/C	NGS : 0.044 C90 : 0.000
PHL-2	c.2834A>G	p.Asn945Ser	missense variant	moderate	contig2621	342877	A/G	NGS : 0.004 C90 : 0.000
PHL-2	c.3020T>A	p.Ile1007Asn	missense variant	moderate	contig2621	343063	T/A	NGS : 0.000 C90 : 0.000
PHL-2	c.3209A>G	p.Gln1070Arg	missense variant	moderate	contig2621	343252	A/G	NGS : 0.103 C90 : 0.885
PKSG-4b	c.496A>G	p.Lys166Glu	missense variant	moderate	contig700	2721177	T/C	NGS : 0.651 C90 : 0.684
PKSG-4b	c.489delT	p.Phe163fs	frameshift variant	high	contig700	2721183	CA/C	NGS : 0.792 C90 : 0.761
PKSG-4b	c.485A>G	p.Lys162Arg	missense variant	moderate	contig700	2721188	T/C	NGS : 0.643 C90 : 0.301
PKSG-4b	c.316+2T>A		splice donor variant & intron variant	high	contig700	2723818	A/T	NGS : 0.070 C90 : 0.689
PKSG-4b	c.229G>A	p.Gly77Ser	missense variant	moderate	contig700	2724206	C/T	NGS : 0.042 C90 : 0.000
PKSG-4b	c.216G>C	p.Leu72Phe	missense variant	moderate	contig700	2724219	C/G	NGS : 0.044 C90 : 0.000
PKSG-4b	c.206T>C	p.Leu69Ser	missense variant	moderate	contig700	2724229	A/G	NGS : 0.044 C90 : 0.000
DXR-2	c.1319T>C	p.Ile440Thr	missense variant	moderate	contig380	285250	A/G	NGS : 0.480 C90 : 0.000
FAD2-2	c.58C>T	p.His20Tyr	missense variant	moderate	contig83	1803311	G/A	NGS : 0.013 C90 : 0.000
ELF3	c.1466G>A	p.Ser489Asn	missense variant	moderate	contig97	244297	G/A	NGS : 0.123 C90 : 0.000
ELF3	c.2198G>T	p.Arg733Leu	missense variant	moderate	contig97	245029	G/T	NGS : 0.125 C90 : 0.531
ELF3	c.2216A>G	p.His739Arg	missense variant	moderate	contig97	245047	A/G	NGS : 0.020 C90 : 0.182
aPT1	c.406A>G	p.Ile136Val	missense variant	moderate	contig121	2839605	A/G	NGS : 0.579 C90 : 0.761

AAE1-2	c.133T>A	p.Phe45Ile	missense variant	moderate	contig81	209095	T/A	NGS : 0.004 C90 : 0.000
AAE1-2	c.374A>G	p.His125Arg	missense variant	moderate	contig81	209336	A/G	NGS : 0.026 C90 : 0.000
AAE1-2	c.1006A>G	p.Lys336Glu	missense variant	moderate	contig81	209968	A/G	NGS : 0.116 C90 : 0.000
AAE1-2	c.1090A>G	p.Lys364Glu	missense variant	moderate	contig81	210052	A/G	NGS : 0.007 C90 : 0.000
PHL-1	c.2551A>G	p.Thr851Ala	missense variant	moderate	contig1439	1487246	T/C	NGS : 0.116 C90 : 0.890
Edestin	c.231G>T	p.Glu77Asp	missense variant	moderate	contig850	3065059	C/A	NGS : 0.002 C90 : 0.000
Edestin	c.130_131insATT	p.Gly43_Ser44insTyr	conservative inframe insertion	moderate	contig850	3065159	G/GAAT	NGS : 0.009 C90 : 0.000
PKSG-2b	c.1152T>A	p.Asn384Lys	missense variant	moderate	contig700	1950486	A/T	NGS : 0.715 C90 : 0.895
PKSG-2b	c.73A>T	p.Ile25Leu	missense variant	moderate	contig700	1951809	T/A	NGS : 0.011 C90 : 0.000
PKSG-2b	c.-2_1dupATA		start lost & conservative inframe insertion	high	contig700	1951880	A/ATAT	NGS : 0.410 C90 : 0.000
TFL1	c.302-1G>A		splice acceptor variant & intron variant	high	contig1636	520616	C/T	NGS : 0.103 C90 : 0.794
DXR-1	c.139A>G	p.Arg47Gly	missense variant	moderate	contig380	235296	T/C	NGS : 0.020 C90 : 0.000
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.35G>A	p.Cys12Tyr	missense variant	moderate	contig1891	889357	C/T	NGS : 0.094 C90 : 0.646
PIE1-2	c.5932A>G	p.Ile1978Val	missense variant	moderate	contig1460	1185552	T/C	NGS : 0.061 C90 : 0.268
PIE1-2	c.1872T>A	p.Asp624Glu	missense variant	moderate	contig1460	1190252	A/T	NGS : 0.086 C90 : 0.990
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.1415_1416insTT	p.His474fs	frameshift variant	high	contig954	3056602	A/ATT	NGS : 0.007 C90 : 0.000
EMF2	c.1418_1419insACA	p.Ser473_His474insGln	disruptive inframe insertion	moderate	contig954	3056605	C/CACA	NGS : 0.007 C90 : 0.029
EMF2	c.1419_1420insT	p.His474fs	frameshift variant	high	contig954	3056606	G/GT	NGS : 0.004 C90 : 0.000
FT	c.240C>G	p.Asn80Lys	missense variant	moderate	contig1561	3124664	C/G	NGS : 0.075 C90 : 0.000
aPT4	c.97T>C	p.Tyr33His	missense variant	moderate	contig121	2828753	T/C	NGS : 0.439 C90 : 0.000
aPT4	c.202T>A	p.Leu68Ile	missense variant	moderate	contig121	2828858	T/A	NGS : 0.068 C90 : 0.000
aPT4	c.235_236delGT	p.Val79fs	frameshift variant	high	contig121	2829030	ATG/A	NGS : 0.417 C90 : 0.000
aPT4	c.238delT	p.Ser80fs	frameshift variant	high	contig121	2829034	AT/A	NGS : 0.421 C90 : 0.000
FLD	c.2981T>C	p.Met994Thr	missense variant	moderate	contig1450	2044012	A/G	NGS : 0.064 C90 : 0.478
FLD	c.2962G>A	p.Asp988Asn	missense variant	moderate	contig1450	2044031	C/T	NGS : 0.009 C90 : 0.000

FLD	c.2585G>A	p.Arg862Gln	missense variant	moderate	contig1450	2045075	C/T	NGS : 0.007 C90 : 0.000
AAE1-3	c.634G>C	p.Gly212Arg	missense variant	moderate	contig976	1083220	C/G	NGS : 0.116 C90 : 0.000
AAE1-3	c.610delG	p.Glu204fs	frameshift variant	high	contig976	1083243	TC/T	NGS : 0.000 C90 : 0.000
AAE1-3	c.600_608del CAGTGGTGA	p.Ser201_Asp 203del	disruptive inframe deletion	moderate	contig976	1083245	ATCACCCTG/A	NGS : 0.000 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.284A>T	p.Glu95Val	missense variant	moderate	contig976	1083741	T/A	NGS : 0.053 C90 : 0.000
AAE1-3	c.260T>C	p.Val87Ala	missense variant	moderate	contig976	1083765	A/G	NGS : 0.000 C90 : 0.000
AAE1-3	c.233C>G	p.Ser78Cys	missense variant	moderate	contig976	1083842	G/C	NGS : 0.000 C90 : 0.000
AAE1-3	c.214G>T	p.Glu72*	stop gained	high	contig976	1083861	C/A	NGS : 0.009 C90 : 0.000
AAE1-3	c.212C>G	p.Thr71Arg	missense variant	moderate	contig976	1083863	G/C	NGS : 0.000 C90 : 0.000
AAE1-3	c.181G>A	p.Val61Ile	missense variant	moderate	contig976	1083894	C/T	NGS : 0.055 C90 : 0.000
AAE1-3	c.179C>T	p.Thr60Ile	missense variant	moderate	contig976	1083896	G/A	NGS : 0.009 C90 : 0.000
AAE1-3	c.167A>G	p.Glu56Gly	missense variant	moderate	contig976	1083908	T/C	NGS : 0.070 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
AAE1-3	c.79A>G	p.Thr27Ala	missense variant	moderate	contig976	1083996	T/C	NGS : 0.068 C90 : 0.000
AAE1-3	c.52G>A	p.Gly18Ser	missense variant	moderate	contig976	1084023	C/T	NGS : 0.064 C90 : 0.000
AAE1-3	c.8C>T	p.Ser3Leu	missense variant	moderate	contig976	1084067	G/A	NGS : 0.000 C90 : 0.000

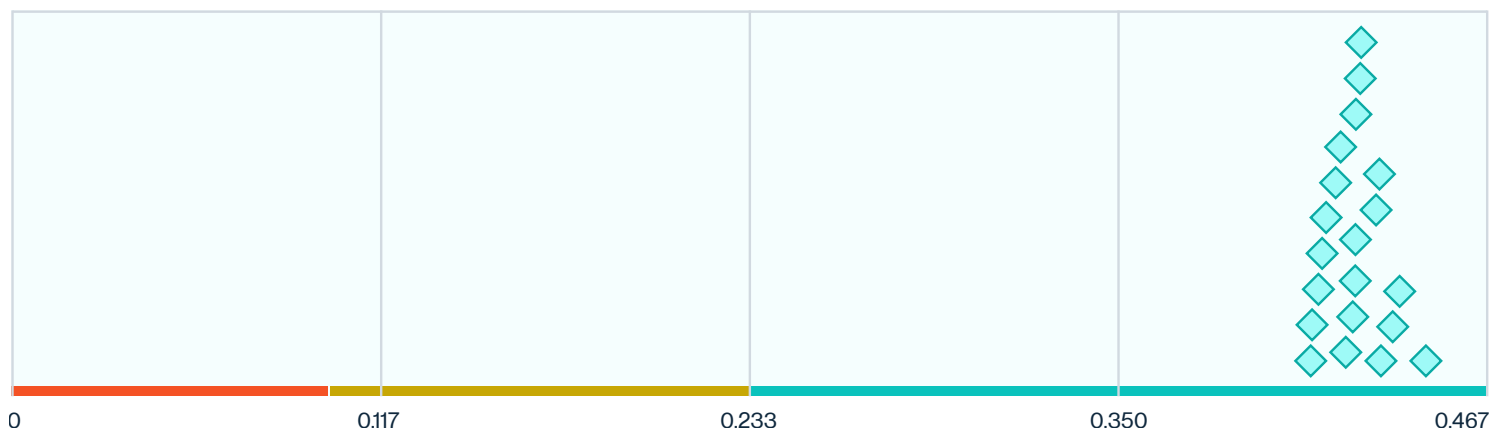
NEAREST GENETIC RELATIVES (ALL SAMPLES)



□ 0.132 Swaziland (SRR14708271) (<https://kannapedia.net/strains/srr14708271>)

- ◻ 0.231 RKM-2018-027 (RSP11119) (<https://kannapedia.net/strains/rsp11119>)
- ◻ 0.233 Blue Dream (RSP11017) (<https://kannapedia.net/strains/rsp11017>)
- ◇ 0.239 Black Jack (RSP10603) (<https://kannapedia.net/strains/rsp10603>)
- ◇ 0.240 Blue Dream (RSP11009) (<https://kannapedia.net/strains/rsp11009>)
- ◇ 0.243 Cheese (RSP10460) (<https://kannapedia.net/strains/rsp10460>)
- ◇ 0.245 Blue Dream (RSP11007) (<https://kannapedia.net/strains/rsp11007>)
- ◇ 0.246 Blue Dream (RSP11012) (<https://kannapedia.net/strains/rsp11012>)
- ◇ 0.247 RKM-2018-025 (RSP11117) (<https://kannapedia.net/strains/rsp11117>)
- ◇ 0.248 RKM-2018-016 (RSP11108) (<https://kannapedia.net/strains/rsp11108>)
- ◇ 0.248 Blue Dream (RSP11008) (<https://kannapedia.net/strains/rsp11008>)
- ◇ 0.249 Blue Dream (RSP11006) (<https://kannapedia.net/strains/rsp11006>)
- ◇ 0.250 Super Blue Dream (RSP11011) (<https://kannapedia.net/strains/rsp11011>)
- ◇ 0.250 Italian Kiss (RSP11034) (<https://kannapedia.net/strains/rsp11034>)
- ◇ 0.252 Domnesia (RSP11184) (<https://kannapedia.net/strains/rsp11184>)
- ◇ 0.252 Blue Dream (RSP11005) (<https://kannapedia.net/strains/rsp11005>)
- ◇ 0.253 Snoops Dream (RSP11003) (<https://kannapedia.net/strains/rsp11003>)
- ◇ 0.254 Snoops Dream (RSP11031) (<https://kannapedia.net/strains/rsp11031>)
- ◇ 0.255 BLACK JACK (RSP11346) (<https://kannapedia.net/strains/rsp11346>)
- ◇ 0.255 Italian Kiss (RSP10990) (<https://kannapedia.net/strains/rsp10990>)

MOST GENETICALLY DISTANT STRAINS (ALL SAMPLES)



◻ closely related ◻ moderately related ◇ distantly related

- ◇ 0.448 Cherry Blossom (RSP11318) (<https://kannapedia.net/strains/rsp11318>)
- ◇ 0.439 CHEM4 (RSP12090) (<https://kannapedia.net/strains/rsp12090>)
- ◇ 0.437 Cherry Blossom (RSP11334) (<https://kannapedia.net/strains/rsp11334>)
- ◇ 0.433 Cherry Blossom (RSP11323) (<https://kannapedia.net/strains/rsp11323>)
- ◇ 0.433 Unknown--Cherry Wine---001- (RSP11268) (<https://kannapedia.net/strains/rsp11268>)
- ◇ 0.432 Fatso (RSP11741) (<https://kannapedia.net/strains/rsp11741>)
- ◇ 0.427 Red Eye OG (RSP11190) (<https://kannapedia.net/strains/rsp11190>)
- ◇ 0.427 Cherry Blossom (RSP11308) (<https://kannapedia.net/strains/rsp11308>)

- ◇ 0.426 Cherry Blossom (RSP11311) (<https://kannapedia.net/strains/rsp11311>)
- ◇ 0.425 Cherry Blossom (RSP11335) (<https://kannapedia.net/strains/rsp11335>)
- ◇ 0.425 Right Mark (RSP11628) (<https://kannapedia.net/strains/rsp11628>)
- ◇ 0.425 RKM-2018-012 (RSP11103) (<https://kannapedia.net/strains/rsp11103>)
- ◇ 0.422 Black Triangle (RSP11638) (<https://kannapedia.net/strains/rsp11638>)
- ◇ 0.421 GMO x Garlic Breath (RSP12507) (<https://kannapedia.net/strains/rsp12507>)
- ◇ 0.419 JL Cross 6 (RSP11507) (<https://kannapedia.net/strains/rsp11507>)
- ◇ 0.416 Chem 91 (RSP11185) (<https://kannapedia.net/strains/rsp11185>)
- ◇ 0.415 Cherry Blossom (RSP11333) (<https://kannapedia.net/strains/rsp11333>)
- ◇ 0.414 GMO (RSP12091) (<https://kannapedia.net/strains/rsp12091>)
- ◇ 0.412 East side OG (RSP12089) (<https://kannapedia.net/strains/rsp12089>)
- ◇ 0.411 Cherry Blossom (RSP11328) (<https://kannapedia.net/strains/rsp11328>)

NEAREST GENETIC RELATIVE IN PHYLOS DATASET

Phylos Strain SRR4448825
(<https://www.ncbi.nlm.nih.gov/sra/SRR4448825>)

Overlapping SNPs: **12**

Concordance: **10**

NEAREST GENETIC RELATIVE IN LYNCH DATASET

Lynch Strain SRR3495276
(<https://www.ncbi.nlm.nih.gov/sra/SRR3495276>)

Overlapping SNPs: **5**

Concordance: **5**

