

## Lucky Charms

 Sample ID: BIA240912S0030  
 Strain: Lucky Charms

 Produced:  
 Collected:  
 Received: 09/13/2024  
 Completed: 09/19/2024  
 Batch#: HL4

 Client  
**PermaGanix**

 Matrix: Plant  
 Type: Flower - Cured  
 Sample Size: 6.75 g  
 Lot#:


### Summary

Test	Date Tested	Result
Sample		Complete
Cannabinoids	09/17/2024	Complete
Moisture	09/16/2024	9.60% - Complete
Water Activity	09/16/2024	0.467 aw - Complete
Terpenes	09/16/2024	Complete
Microbials	09/19/2024	Complete

### Cannabinoids

Completed

<b>13.61%</b> Total THC	<b>0.04%</b> Total CBD	<b>16.12%</b> Total Cannabinoids
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Analyte	LOQ	Results	Results	Mass
	mg/g	%	mg/g	mg/serving
CBDVa	0.0005	<LOQ	<LOQ	
CBDV	0.0012	<LOQ	<LOQ	
CBDa	0.0008	0.04	0.4	
CBGa	0.0008	0.54	5.4	
CBG	0.0019	0.07	0.7	
CBD	0.0019	<LOQ	<LOQ	
THCV	0.0021	0.05	0.5	
CBN	0.0013	<LOQ	<LOQ	
Δ9-THC	0.0020	0.75	7.5	
Δ8-THC	0.0019	<LOQ	<LOQ	
Δ10-THC	0.0002	<LOQ	<LOQ	
CBC	0.0024	<LOQ	<LOQ	
THCa	0.0034	14.67	146.7	
<b>Total THC</b>		<b>13.61</b>	<b>136.12</b>	
<b>Total CBD</b>		<b>0.04</b>	<b>0.36</b>	
<b>Total</b>		<b>16.12</b>	<b>161.15</b>	<b>0.00</b>

Analyst: 052

Cannabinoids Methodology: High Performance Liquid Chromatography (HPLC) using PerkinElmer FLEXAR™ with Photo Diode Array Detector (PDA)

Total CBD and total THC are calculated values, to account for assumed decarboxylation from the acid form (THCA or CBDA) to the neutral form, causing weight loss of the acid group. These values are calculated as follows:

$$\text{Total THC} = (\text{THCA} \times 0.877) + \Delta 9\text{-THC}$$

$$\text{Total CBD} = (\text{CBDA} \times 0.877) + \text{CBD Reagent}$$

Blanks: &lt; LOQs for all analytes

LOQ = The lowest quantity that this method can reliably detect. Any cannabinoid that was not detected is assumed to be less than the stated LOQ (&lt;LOQ).

All results reflect dry weight of material, based on % moisture of the sample.

Measurement of Uncertainty (MU): the parameter, associated with the result of a measurement, that characterizes the dispersion of the values that could reasonably be attributed to the particular quantity subject to measurement. Δ9-THC MU = ±0.005% Total THC MU = ±0.007%

All other cannabinoid MU values are available upon request.

All moisture analysis is determined by loss-on-drying measurement using OHAUS Model MB90 Moisture Content Readers.




 Luke Emerson-Mason  
 Laboratory Director  
 09/19/2024

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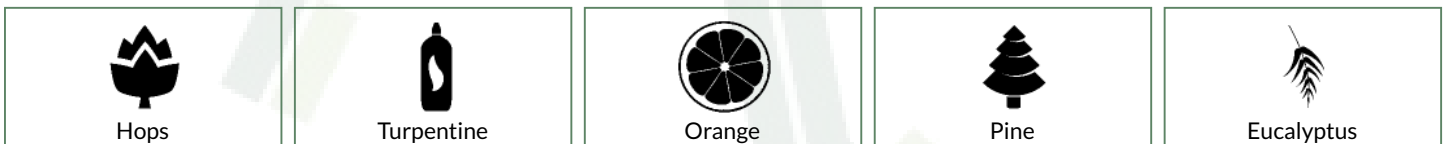
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## Terpenes

Completed

Analyte	LOQ	Results	Results
	mg/g	mg/g	%
β-Myrcene	0.010	11.732	1.173
Terpinolene	0.010	8.973	0.897
Limonene	0.010	3.727	0.373
β-Pinene	0.010	2.223	0.222
3-Carene	0.010	1.401	0.140
Ocimene	0.010	1.358	0.136
α-Pinene	0.010	1.347	0.135
β-Caryophyllene	0.010	1.318	0.132
α-Humulene	0.010	0.489	0.049
α-Terpinene	0.010	0.475	0.048
γ-Terpinene	0.010	0.405	0.041
Geraniol	0.010	0.391	0.039
α-Bisabolol	0.010	0.172	0.017
Guaiol	0.010	0.162	0.016
Eucalyptol	0.010	0.099	0.010
Linalool	0.010	0.072	0.007
Camphene	0.010	0.054	0.005
Caryophyllene Oxide	0.010	<LOQ	<LOQ
cis-Nerolidol	0.010	<LOQ	<LOQ
Isopulegol	0.010	<LOQ	<LOQ
p-Cymene	0.010	<LOQ	<LOQ
trans-Nerolidol	0.010	<LOQ	<LOQ
<b>Total</b>		<b>34.398</b>	<b>3.440</b>

## Primary Aromas



Analyst: 045

LOQ = The lowest quantity this method can reliably detect. Any terpene that was not detected is assumed to be less than the stated LOQ (&lt;LOQ).

Terpene Methodology: Headspace Sampler, Gas Chromatography-Mass Spectrometry (GC-MS), using Perkin Elmer Clarus® SQ8 GC MS

Reagent Blanks: &lt; LOQs for all analytes

All results reflect dry weight of material, based on % moisture of the sample.

All moisture analysis is determined by loss-on-drying measurement using OHAUS Model MB90 Moisture Content Readers.




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 Laboratory Director  
 09/19/2024

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## Pathogens

Completed

Pathogens	LOD	Results
	CFU/g	CFU/g
Aspergillus	5	Not Detected
Shiga Toxin E. Coli	5	Not Detected
Salmonella SPP	5	Not Detected

Analyst: 018

Test Methodology: Bio-Rad IQ-Check PCR Kits

cfu/g = colony forming units per gram

LOD = The lowest quantity that this method can reliably detect. Any microbial growth that was not detected is assumed to be less than the stated LOD (<LOD).

Reagent Blanks: <LOD for all analytes




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