

Supplementary Information

Untargeted metabolomics reveals molecular effects of ketogenic diet on healthy and tumor xenograft mouse models

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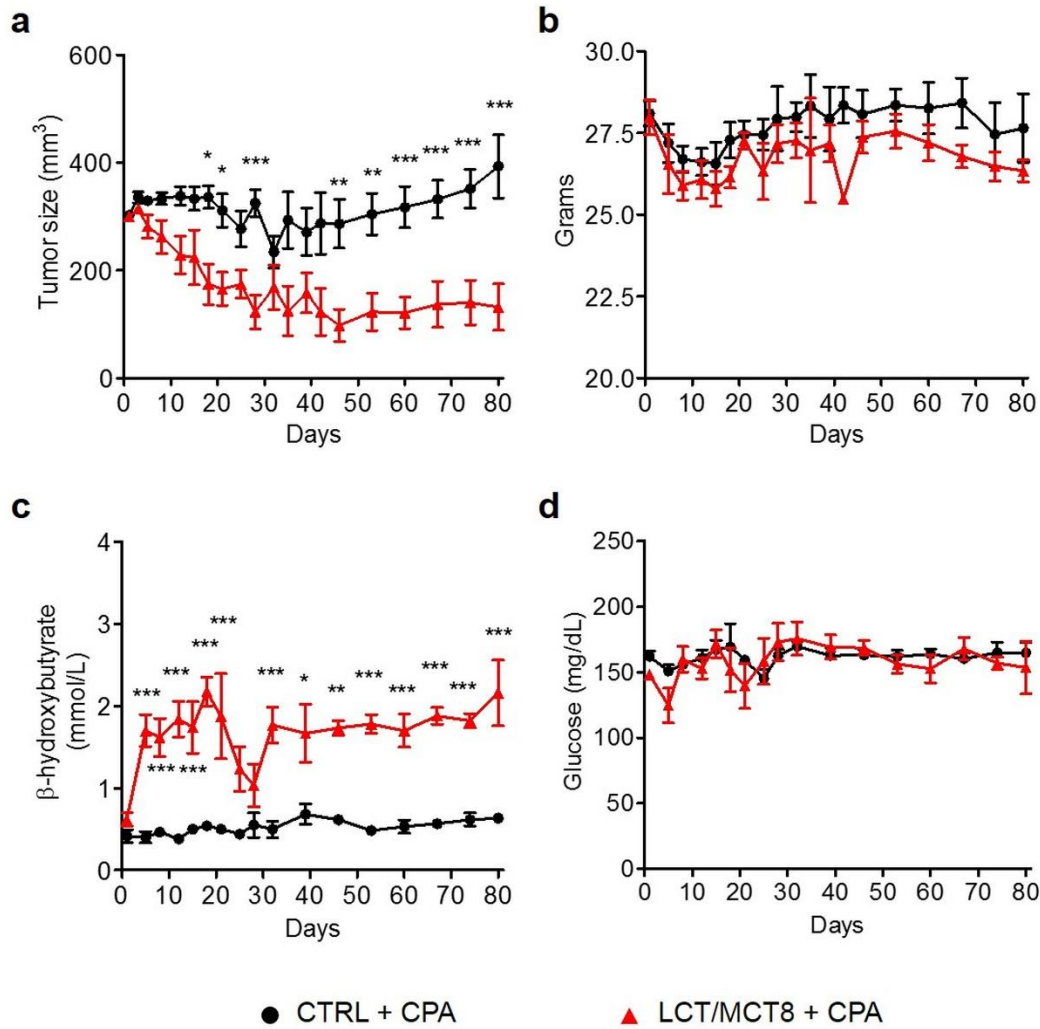
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Supplementary figure S1. Mean of the tumor size in MDA-MB-468 bearing mice under CTRL diet or LCT/MCT8 ketogenic diet (a). Average body weight variations in mice during dietary intervention (b). Average ketone bodies (mmol/L) (c) and blood glucose (mg/dL) levels (d) measured in blood of mice fed with the different diets.

Data are given as mean $\pm$ SEM. Statistical analysis was performed by using two-way ANOVA (Dunnett's multiple comparison test), * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$; $n = 5-6$ mice.

Supplementary table 1. Composition and energy supply of the different diets.

	CTRL	LCT/MCT8
Crude Protein %	16.1	8.1
LCT % ^a	7.1	49.6
MCT8 % ^b	0	25
MCT10 % ^b	0	0
Sugar %	6	1
Starch %	51.2	0
Crude fiber %	10	9.9
Crude ash %	4.5	4.4
Energy Kcal	3609	7098
	per Kg	per Kg
Vitamin A (IU/IE)	15	15
Vitamin D ₃ (IU/IE)	1.5	1.5
Vitamin E (mg)	150	150
Vitamin K ₃ (mg)	20	20
Vitamin C (mg)	30	30
Copper (mg)	11	11

CTRL, control; MCT8, 8-carbon medium-chain triglyceride;

^a LCT composition: butter fat 11.7% and pork lard 88.3%

^b MCT8 composition: pure oil

Supplementary table 2. Settings of PeakPickerHiRes

Parameter	Value
PeakPickerHiRes	
version	2.3.0
processOption	inmemory
debug	0
threads	1
no_progress	false
force	false
test	false
algorithm	
signal_to_noise	0.1
spacing_difference_gap	4.0
spacing_differnece	1.5
missing	1
ms_levels	1
report_FWHM	false
report_FWHM_unit	relative(ppm)
SignalToNoise	
max_intensity	-1
auto_max_stdev_factor	3.0
auto_max_percentile	95
auto_mode	0
win_len	200.0
bin_count	30
min_required_elements	10
noise_for_empty_window	1.0E20
write_log_messages	true

Supplementary table 3. Settings of FeatureFinderMetabo

Parameter	Value
FeatureFinderMetabo	
version	2.3.0
debug	0
threads	1
no_progress	false
force	false
test	false
common	
noise_threshold_int	3000.0
chrom_peak_snr	3.0
chorm_fwhm	5.0
mtd	
mass_error_ppm	5.0
reestimate_mt_sd	true
quant_method	area
trace_termination_criterion	outlier
trace_termination_outliers	5
min_sample_rate	0.5
min_trace_length	0.25
max_trace_length	-1.0
epd	
enabled	true
width_filtering	fixed
min_fwhm	0.25
max_fwhm	60.0
masstrace_snr_filtering	false
ffm	
local_ret_range	10.0
local_mz_range	6.5
charge_lower_bound	1
charge_upper_bound	3
report_summed_ints	false
enable_rt_filtering	true
isotope_filtering_model	metabolites (5% RMS)
mz_scoring_13c	false
use_smoothed_intensities	true
report_convex_hulls	true

Supplementary table 4. Settings of FeatureLinkerUnlabeled QT

Parameter	Value
FeatureLinkerUnlabeledQT	Value
version	2.3.0
keep_subelements	false
debug	0
threads	1
no_progress	true
force	false
test	false
algorithm	
use_identifications	false
nr_partitions	100
ignore_charge	false
distance_rt	
max_difference	10.0
exponent	1.0
weight	1.0
distance_mz	
max_difference	5.0
unit	ppm
exponent	2.0
weight	1.0
distance_intensity	
exponent	1.0
weight	0.0

Supplementary table 5. Settings of TextExporter

Parameter	Value
TextExporter	
version	2.1.0
replacement	–
quoting	None
no_ids	False
debug	0
threads	1
no_progress	false
force	false
test	false
feature	
minimal	false
add_metavalues	-1
id	
proteins_only	false
peptides_only	false
first_dim_rt	false
add_metavalues	-1
add_hit_metavalues	-1
consensus	
sorting_method	None
sort_by_maps	false
sort_by_size	false

Supplementary table 6. Settings of R Snippets in KNIME workflow

Parameter	Value
Blank Filter_1	
blankFilterPassed	14
ConsensusMapNormalization	
ignoreColsPattern	Blank
method	mean
outlier	0.68, 1/0.68
verbose	TRUE
Pool Filter/RSD Filter	
poolFilterCount	7
maxRSD	25
Biological Replicate Filter	
numInConditions	3
numInReplicates	4