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3 **Figure 3. Positive ion MALDI-IMS of DAG lipids in GSC xenografts.** (A) Relative
4 abundance of DAG (34:0), DAG (34:1), DAG (36:1), DAG (38:4), DAG (38:6), and DAG (40:6)
5 as determined by ESI-MS/MS. Values are mean \pm SEM (n = 9 for each phenotype) of the lipid
6 abundance as the ratio of lipid peak area to the peak area of an internal standard corrected for
7 protein concentration; * $p < 0.05$ and ** $p < 0.01$ (Student's *t*-test). (B) Positive ion image from
8 MALDI-IMS experiments of a representative attractor specimen, demonstrating the localization
9 and signal intensity of DAG (40:6) (m/z 707.1). Image color intensity corresponds to signal
10 strength. (C) H&E staining of corresponding tissue section analyzed by MALDI-IMS. The tumor
11 area is outlined in *blue*. (D) Positive ion image of DAG (40:6), m/z 707.1 from MALDI-IMS
12 experiments of a representative non-attractor specimen. (E) H&E staining of a corresponding
13 tissue section analyzed by MALDI-IMS. The tumor area is outlined in *blue*.
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32 **Figure 4. Tumor-specific localization of DHA.** (A and C) Negative ion images derived from
33 MALDI-IMS experiments showing the localization and signal intensity of DHA (22:6) m/z 327.0
34 in a representative non-attractor and attractor, respectively. (B and D) H&E stain of tissue
35 sections used in MALDI-IMS experiments in a non-attractor and attractor, respectively. The
36 tumor area is outlined in *blue*. (E) Relative abundance of DHA as determined by ESI-MS/MS (p
37 = 0.046). (F) Annotated negative ion MS/MS spectrum of m/z 327.0 with precursor ion (*inset*).
38 The most abundant peak, DHB [M-H]⁻, represents the matrix. MS/MS product ions are shown in
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48 **Table 1.**
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53 **Supplemental Figure S1.** Annotated MS/MS spectrum of DHA (22:6) standard for comparison
54 to tissue-acquired DHA in **Figure 4F**.
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8 **Supplemental Figure S2.** Annotated MS/MS spectrum of DAG (40:6) suggesting DHA-
9 containing DAG (22:6/18:0). Precursor ion of potassiated DAG (40:6) m/z 707.1 is shown
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12 (*inset*). Peak at m/z 191.9 is DHB matrix ion and the peak at 323.6 represents potassiated 18:0
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