

Supplemental Information

Supplemental Table S1 Demographic details from Dupuytren and Carpal

Tunnel cases.

Patient No.	Patient Group	Technique	Patient ID	Age	Gender	Ethnic Background	Anatomical Tissue Location
1	Cohort A	Metabolic Fingerprint Analysis with FT-IR Experiment 1	DD8	77	Male	White	Nodule, Cord, Fascia
2			DD9	58	Male	White	Nodule, Cord, Fascia, Fat, SON
3			DD10	76	Male	White	Nodule, Cord, Fascia
4			DD11	67	Male	White	Nodule, Cord, Fascia, Fat, SON
5			DD12	52	Male	White	Nodule, Cord, Fascia, Fat, SON
6			DD13	74	Female	White	Nodule, Cord, Fascia, Fat, SON
7	Cohort B		DD2	71	Male	White	Nodule, Cord, Fascia, Fat, SON
8			DD17	67	Male	White	Cord, Fascia
9			DD18	68	Male	White	Nodule, Cord
10			CT5	78	Male	White	Fascia
11			CT6	62	Female	White	Fascia
12			CT7	50	Female	White	Fascia
13	CT8		28	Male	White	Fascia	
14	Cohort C	Metabolic Identification with GC-MS Experiment 2	DD44	64	Male	White	Nodule, Cord, Fascia
15			DD60	67	Male	White	Nodule, Cord, Fascia
16			DD61	77	Male	White	Nodule, Cord, Fascia

Supplemental Table S2 List of categories and the sample set chosen for chemometric analyses of FT-IR and GC-MS data.

Experiment	Patient Cohort	Sample set
1.1 Metabolic Fingerprinting	A,B	DD N,C, F
1.2 Metabolic Fingerprinting	B	DD N,C, F & CT F*
1.3 Metabolic Fingerprinting	A,B	DD N,C, F ,T,S
1.4 Metabolic Fingerprinting	A,B	DD N,C, F ,T,S (Passage 0-6)
1.5 Metabolic Footprinting	A	DD N,C, F
2 Metabolic Profiling	C	DD N,C, F

*external control, N=Nodule, C=Cord, **F**=Fascia (internal control), T=Fat, S=Skin overlying nodule

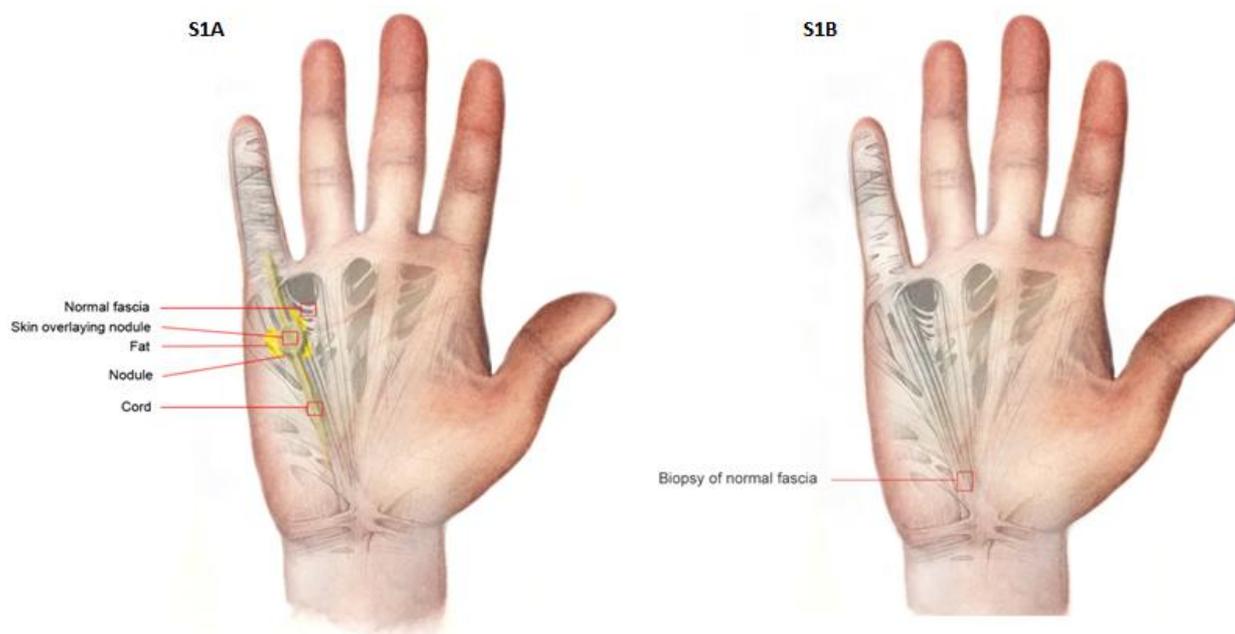
Supplemental Table S3

Table S3 List of 69 known detected metabolite features (peaks) and their involvement in corresponding pathways. 'Yes' to Definitive ID = the metabolite in the sample has matched (by retention index and mass spectrum) to an authentic chemical standard present in MMD's EI-MS mass spectral library. 'No' = the mass spectrum only matches to a metabolite in other mass spectral libraries (i.e. not the Manchester library). Definitive ID = Due to the nature of the analysis, not all metabolites detected can be accurately identified and some have similar chemical structure and were assigned by best possible match score.

Metabolite No	HMDB Accession ID	Metabolite Identification	Definitive	Pathway
1		trimethylamine-N-oxide	no	
2	HMDB00883	valine	yes	
3	HMDB00192	cystine	yes	
4	HMDB00929	tryptophan	yes	
5	HMDB00687	leucine	yes	
6	HMDB00050	adenosine	yes	
7	HMDB00172	isoleucine	yes	
8	HMDB00687	leucine	yes	
9	HMDB00172	isoleucine	yes	
10	HMDB00123	glycine	yes	
11	HMDB00162	proline	yes	
12	HMDB00187	serine	yes	
13	HMDB00161	alanine	yes	
14	HMDB00167	threonine	yes	
15	HMDB00191	aspartic acid	yes	
16	HMDB00191	aspartic acid	yes	
17	HMDB00574	cysteine	yes	Amino Acid Metabolism
18	HMDB00696	methionine	yes	
19	HMDB00574	cysteine	yes	
20	HMDB00696	methionine	yes	
21	HMDB00159	phenylalanine	yes	
22	HMDB00159	phenylalanine	yes	
23	HMDB00159	phenylalanine	yes	
24	HMDB00123	glycine	yes	
25	HMDB00182	lysine	yes	
26	HMDB00182	lysine	yes	
27	HMDB00182	lysine	yes	
28	HMDB11733	glycylglycine	no	
29	HMDB00158	tyrosine	yes	
30	HMDB00158	tyrosine	yes	
31	HMDB00883	valine	yes	
32	HMDB00167	threonine	yes	
33	HMDB00191	aspartic acid	yes	
34	HMDB00143	galactose	yes	
35		sugar	no	
36		inositol	no	
37		sugar	no	
38		sugar	no	
39		sugar	no	Carbohydrate Metabolism
40		sugar	no	
41		sugar	no	
42		sugar	no	
49		sugar	no	
43	HMDB00827	octadecanoic acid	yes	
44	HMDB10368	cholesterol	yes	Fatty Acid Metabolism
45	HMDB00482	octanoic acid	yes	
46	HMDB00220	hexadecanoic acid	yes	
47	HMDB00131	glycerol	yes	Glycerolipid Metabolism
48	HMDB00131	glycerol	yes	
50	HMDB00126	glycerol-3-phosphate	yes	Glycolysis pathway
51	HMDB01401	glucose-6-phosphate	yes	
52	HMDB01401	glucose-6-phosphate	yes	
53	HMDB02730	nicotinamide	yes	Metabolism of Cofactors and Vitamins
54	HMDB00210	Pantothenic acid	yes	
55		3-ureidopropionic acid and/or beta-alanine	no	
56	HMDB00641	glutamine	yes	Metabolism of Other Amino Acids
57	HMDB00641	glutamine	yes	
58	HMDB00641	glutamine	yes	
59	HMDB00300	uracil	yes	
60	HMDB00300	uracil	yes	
61		sucrose	no	Starch and sucrose metabolism
62		sucrose	no	
63	HMDB00254	succinic acid	yes	Tricarboxylic acid cycle
64	HMDB00094	citric acid	yes	
65	HMDB00243	pyruvic acid	yes	
66		thiourea	no	Urea cycle
67		thiourea	no	
68		thiourea	no	
69		à-D-Galactopyranosiduronic acid	no	Uronic acid pathway

Figure Legends

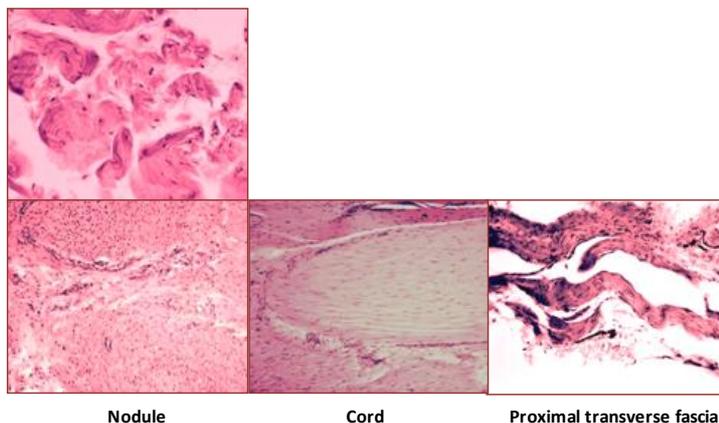
Supplemental Figure S1A The five sites from the diseased hand. The Dupuytren's disease-associated tissues that are subjected to analysis in this study. Five different Dupuytren's disease-associated tissues in each patient's hand are collected, the normal fascia (unaffected transverse fascia), palmar nodule and cord, skin overlying nodule, and fat. **Supplemental Figure S1B** The palm of an unaffected individual used as control. The palm of the hand of a control subject, where the overlying skin has been removed to demonstrate the position of the palmar fascia harvested. Skin, palmar fascia (transverse carpal ligament) and fat were obtained from control subjects, individuals undergoing carpal tunnel release.



Supplemental Figure S2 Hematoxylin and eosin slides displaying cross sections
from disease and control tissues.

S 2

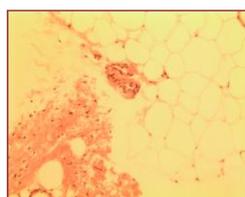
Carpel ligamentous fascia - Control



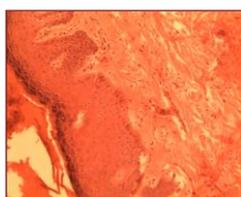
Nodule

Cord

Proximal transverse fascia

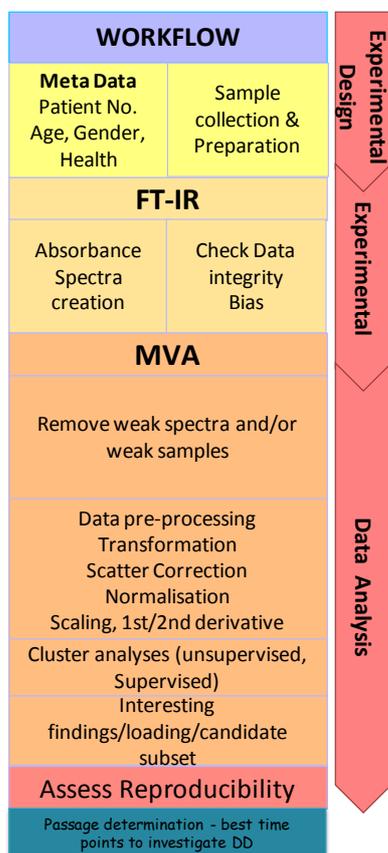


Fibroblasts in fat cushioning nodule

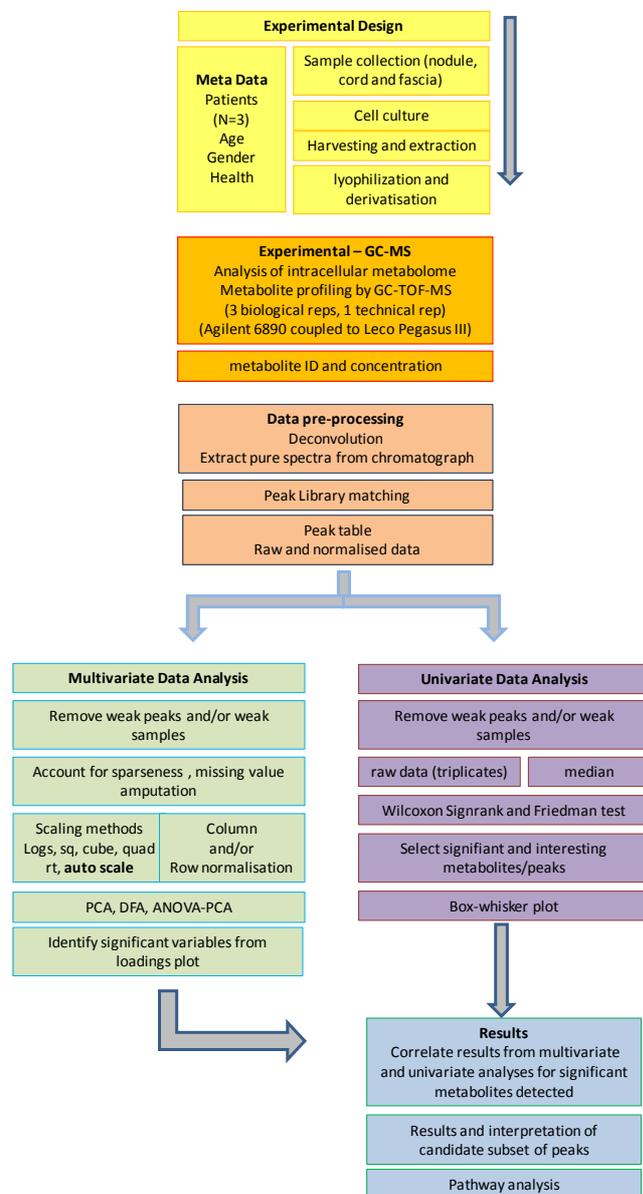


Fibroblasts in skin overlying the nodule

Supplemental Figure S3 A workflow representing the procedure implemented to analyse the samples from Dupuytren's disease and control fibroblast cell cultures.



Supplemental Figure S4 Flowchart of metabolomics experiment – from experimental design through to data analysis.



Supplemental Figure S5 Mass spectrometry spectra of metabolites features reported in Figures 8A-F.

8 a) L-Leucine MW 131.173

Reference Spectrum - Reference "Samrina May10", Analyte "Samrina May10 16"

