Supplemental Table 3: Summary of gene sets overrepresented in FL-PDLS compared to 2D cultures

UPREGULATED GENE SETS	Gene Sets	NES (Max)	FDR q-val (min)
Proliferation			
Cell cycle regulation	114	3,27	0
DNA replication	21	2,87	0
MYC regulated genes	1	1,72	0,001
Transcription factors	5	1,93	0
Cyclins	2	1,83	0,001
Immune modulation			
B cell receptor signaling	1	1,59	0,018
Survival pathways			
DNA repair	26	2,73	0
mTOR signaling	2	2,21	0
Cellular processes			
Regulation of cytoskeleton	17	2,61	0
Epigenetic regulation	7	2,33	0
Organelle organization	20	2,59	0
Metabolic pathways			
Oxidative phosphorylation (OXPHOS)	19	2,6	0
Nucleotide metabolism	25	2,09	0
Amino acid metabolism	12	1,72	0,003
Glucose metabolism	7	1,84	0,001
Others			
Ribosome structure	8	2,13	0
DNA structure	3	2,19	0
Metabolite transport	5	1,85	0,001
Catalytic activity	19	2,3	0

DOWNREGULATED GENE SETS	Gene Sets	NES (Min)	FDR q-val (min)
Proliferation			
MAPK signaling	5	-1,8	0,005
Immune modulation			
Chemokines	6	-1,8	0,009
Inflammation	2	-2,44	0
Allograft reaction	1	-1,63	0,012
T cell receptor signaling	2	-1,63	0,028
Cytokines	27	-1,96	0
Immune response	41	-2,03	0
Survival pathways			
NF-kappaB pathway	3	-1,9	0,003
Notch signaling	5	-1,83	0,002
TNF signaling	4	-3,14	0
TGF-beta signaling	4	-1,99	0
Toll-like receptor signaling	8	-2,05	0
KRAS pathway	2	-1,61	0,013
Wnt signaling	4	-1,65	0,021
Cellular processes			
Regulation of cell death	21	-1,95	0,002
Angiogenesis	4	-1,79	0,01
Cell migration	9	-1,78	0,01
Cell adhesion	11	-1,7	0,01
Response to stress	6	-1,93	0,003

GSEA was used to test for significant enrichment of defined gene signatures. NES indicates Normalized Enriched Score; FDR, False Discovery Rate. Threshold FDR<0.05 and NES>1.5. Custom genes set were experimentally derived and downloaded from http://lymphochip.nih.gov/signaturedb/index.html. C2CP, C5, C6 and H gene sets were obtained from the Molecular Signature Database (v2.5).