

## Molecular signatures reflecting microenvironmental metabolism and chemotherapy-induced immunogenic cell death in colorectal liver metastases

### SUPPLEMENTARY MATERIALS

**Supplementary Table 1: Primers used for RT-qPCR validation**

Gene symbol	ID (Pubmed)	Forward primer		Reverse primer	
<i>AXIN2</i>	6653583	2066	AGTCAGCAGAGGGACAGGAA	2182	GTGGACACCTGCCAGTTTCT
<i>APC2</i>	57242791	8769	ACCCCCAGTTAACTGCTG	8888	GGCACACCTCGGTGACTTAT
<i>DMBT1</i>	157423469	4259	ATCTCCAATCCTTGGGCTTT	4380	GCAGCCTGAGTAGGGAATTG
<i>PLA2G2A</i>	13543520	765	CCCTCCCTACCCTAACCAAG	882	GCTGGAAATCTGCTGGATGT
<i>TGFBR3</i>	223459585	1445	ACCCTGTCATTCCCAGCATA	1561	CAGCCACGATCATCTTCTCA
<i>HOXA7A</i>	84105267	1216	TATCCCAACTGGCAGACA	1339	GGCACTAGGTAGCAGGCAAG
<i>CECR1</i>	30704989	2572	TCCCATAGCTGGTGAAGGAC	2692	GATGAGGGATGCGTTCTGAT
<i>CSF1R</i>	28833090	966	CCAAAAAGTCCTGACCCTCA	1086	CTCTACCACCCGGAAGAACA
<i>FABP6</i>	894182	146	CGCAACTTCAAGATCGTCAC	264	ATGTTGCTTTCCTTGCCAAC
<i>TFF3</i>	17389673	349	CAGGCACTGTTTCATCTCAGC	455	GAGCATGGGACCTTTATTTCG
<i>TRIM7</i>	124376611	1937	AAGCCAGTCTGCTGTTCTC	2059	GAGGTCCCAACCTCTCAA
<i>PLA2G2F</i>	145553988	1234	GTGGCTACTTTGGGCTTGAA	1356	ACACTCAGCACTGCACATCC
<i>GAPDH</i>	53734501	1045	GGCCTCCAAGGAGTAAGACC	1166	AGGGGAGATTGAGTGTGGTG
<i>CHKA</i>	34192558	1187	GCCTGCATTCCAAAATGACT	1301	TCCCCAGAGGAAATGAGATG

**Supplementary Table 2: Somatic variants**

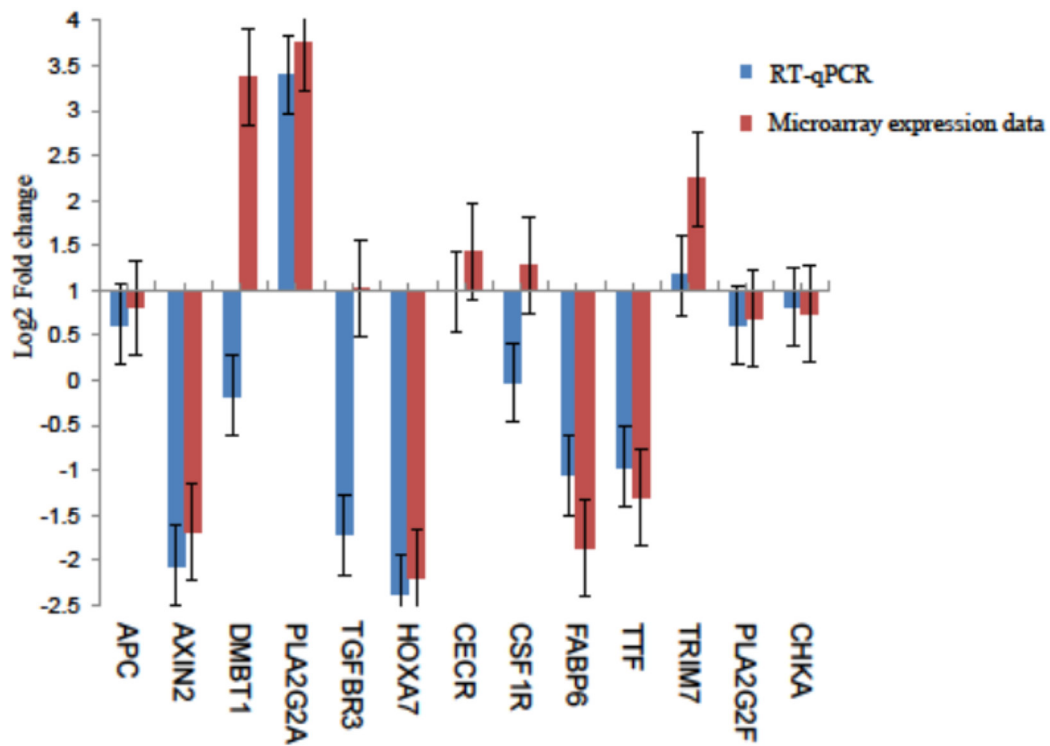
See Supplementary File 1

**Supplementary Table 3: Univariable Cox proportional hazard analysis of OS and DFS, including DEGs**

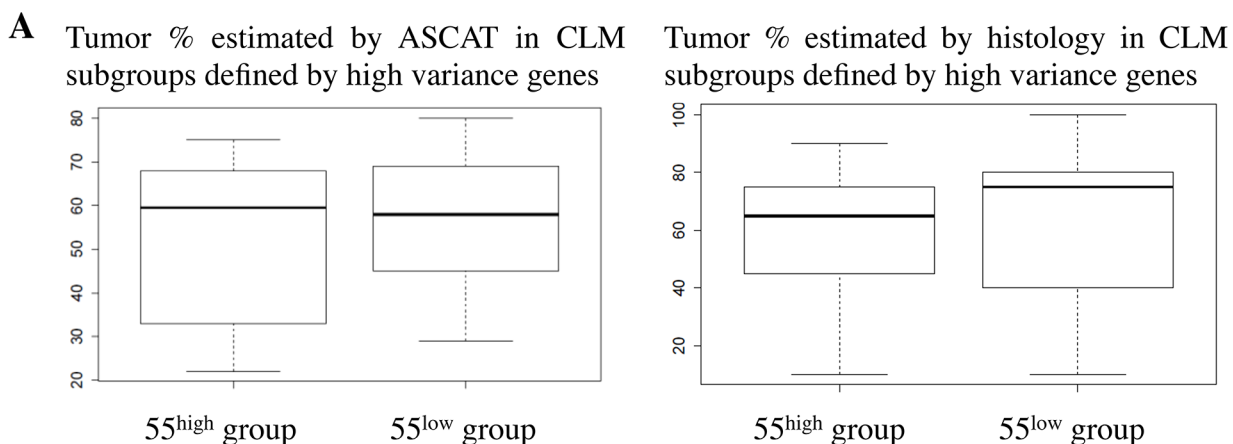
See Supplementary File 2

**Supplementary Data\_set1-12: Gene expression data**

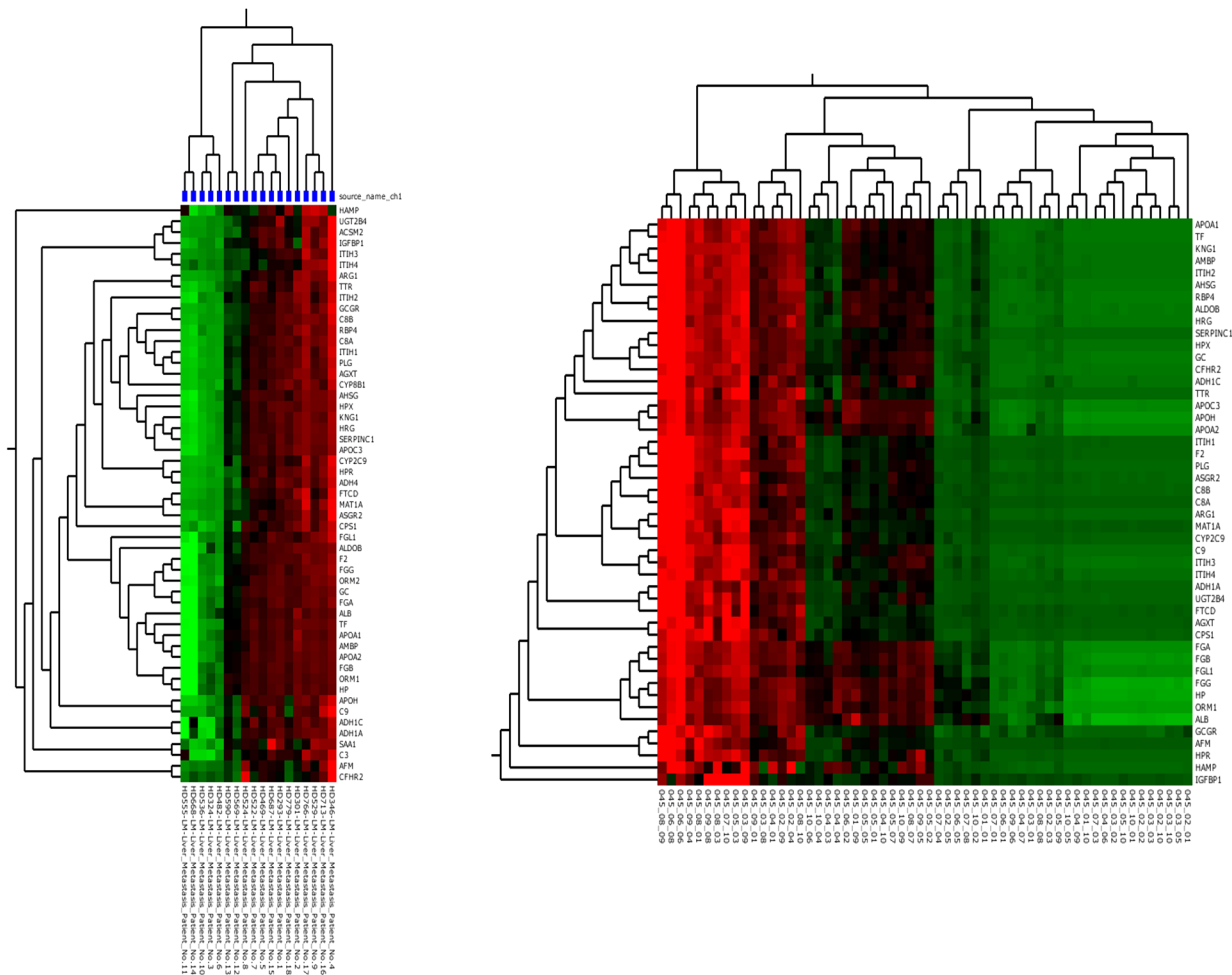
See Supplementary File 3



**Supplementary Figure 1: RT-qPCR Validation.** Validation of differentially expressed genes by RT-qPCR. Log<sub>2</sub> fold changes in microarray data (red bars) were validated by RT-qPCR (blue bars) using *GAPDH* as a reference gene.



**B**



**Supplementary Figure 2: Tumor percentage estimation.** (A) Estimation of tumor percentage in samples by ASCAT and histology in the two subgroups of metastases differing by high or low expression of 55 genes exhibiting high variance in the gene expression data set. Neither estimate showed significant differences in tumor content between the two groups. (B) Expression pattern of the 55 gene cluster in CLM in two publicly available cohorts (GSE14297 [15], GSE5851 [16]). The samples/genes were subjected to clustering analysis. Red-green scale: red represents high expression and green low expression. The expression of the 55 genes is commonly up- or down-regulated, forming two main subgroups and parallel to the CoMet gene expression pattern.