

Figure S1. Cnetplot analysis of commonly deregulated targeted genes and pathways in (A and B) newly diagnosed and (C and D) recurrent liver metastases. CTCs, circulating tumor cells.

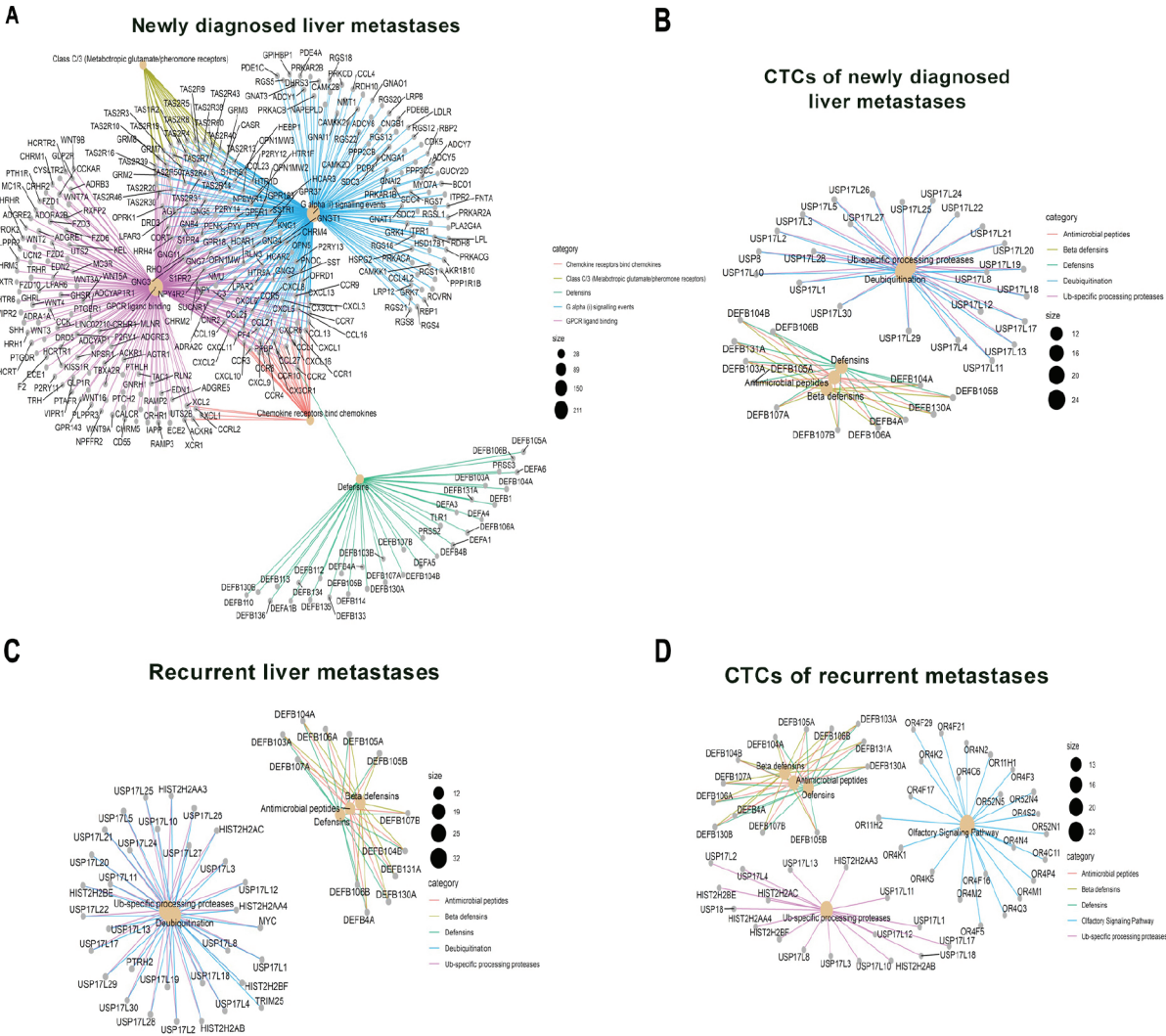


Table S1. CTC analysis data of clinical samples from breast cancer liver metastasis patients by three-color immunofluorescence.

Case ID ^a	CK8 ⁺ /Nucleus ⁺ /CD45 ⁻ (CTC)	CK8 ⁻ /Nucleus ⁺ /CD45 ⁺ (WBC)	CK8 ⁺ /Nucleus ⁺ /CD45 ⁻ (EPC)
BCLM01L	6	2	0
BCLM02H	151	43	21
BCLM03L	6	4	0
BCLM04L	9	2	2
BCLM05H	94	28	35
BCLM06H	17	10	2
BCLM07L	7	5	0
BCLM08L	11	2	1
BCLM09L	12	4	2
BCLM10H	91	12	27
BCLM11H	55	12	9
BCLM12H	49	29	4
BCLM13H	248	120	76
BCLM14L	14	3	0
BCLM15L	12	5	3
BCLM16H	215	31	34
BCLM17L	12	3	7
BCLM18L	9	0	0
BCLM19L	14	2	0
BCLM20L	6	6	0
BCLM21H	102	18	8
BCLM22L	7	7	0
BCLM23L	8	3	0
BCLM24H	87	59	13
BCLM25H	69	11	15
BCLM26H	48	9	33
Total	1,359	430	292

^aLow-CTCs are counted as ≤ 15 CTCs/7.5 ml and high-CTCs > 15 CTCs/7.5 ml. CTC-positive patients were considered if at least 5 CTCs/7.5 ml were present. BCLML, breast cancer liver metastasis that were categorized as low-CTCs; BCLMH, breast cancer liver metastasis patients that were categorized as high-CTCs; CTC, circulating tumor cell; WBC, white blood cell; EPC, epithelial cell; CK, cytokeratin.