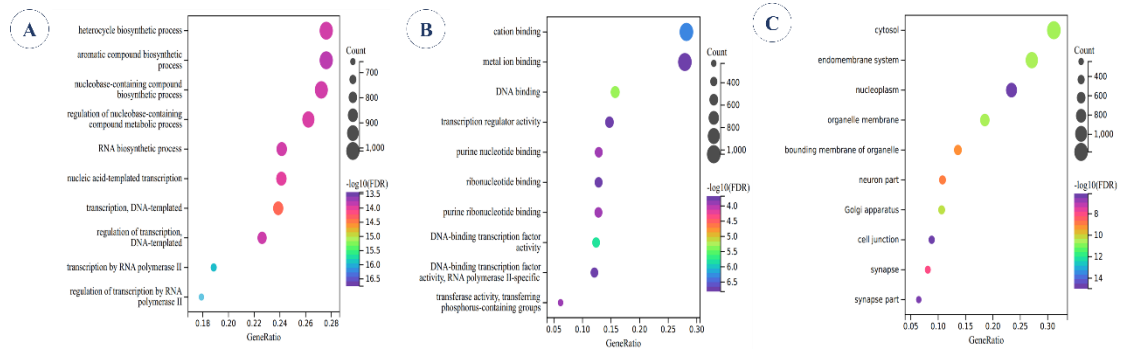
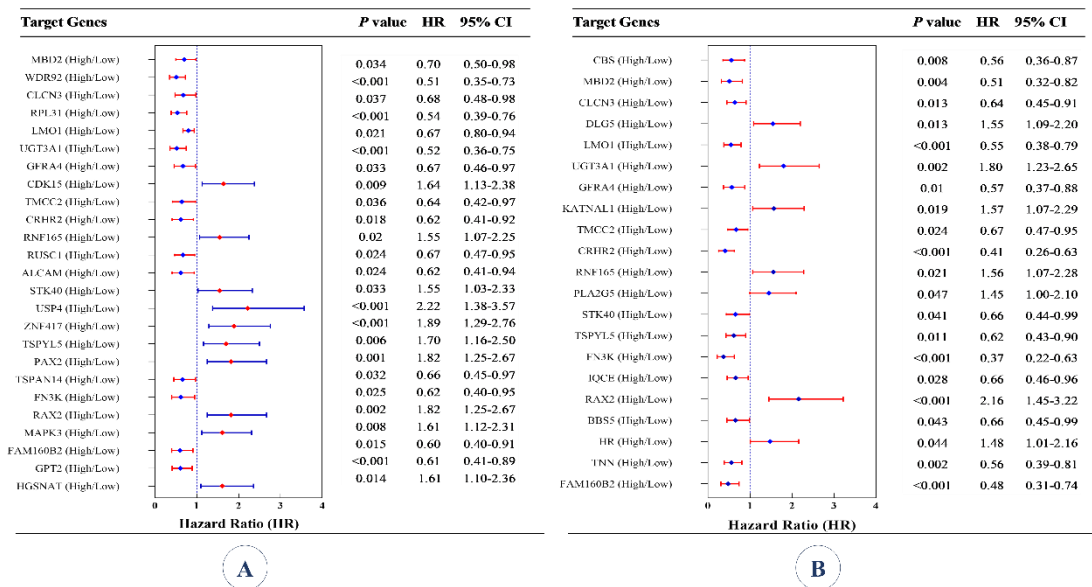


Supplementary Figure 1 The heatmap and volcano plots of exosome DEMiRNAs in the timepoints of pre-nCRT and post-nCRT, in poor-responders (A and B), and in well-responders (C and D).



Supplementary Figure 2 The bioinformatics GO analysis of target genes of exosome hsa-miR-483-5p, A, B, and C represent the GO items of “BP”, “MF”, and “CC”, respectively.



Supplementary Figure 3 The forest plots of survival analysis in the 46 common target genes of exosome hsa-miR-483-5p as identified in the TCGA database. The results identified that the low-expression of 22 target genes (9 genes positively, and 13 genes negatively) were correlated with RFS in CRC patients (A), and 21 target genes (7 genes positively, and 14 genes negatively) correlated with OS (B).

Supplementary Table 1 The differential expression levels of exosome plasma miRNAs pre- and post-nCRT

Poor-responders (G1 versus G3)				Well-responders (G2 versus G4)			
MiRNAs	Log2FC	P value	Regulation	MiRNAs	Log2FC	P value	Regulation
MiR-2116-3p	4.51	0.009	Up	MiR-122-3p	5.61	0.003	Up
MiR-514a0-3p	4.31	0.029	Up	MiR-516a-5p	4.65	0.025	Up
MiR-4503	4.14	0.047	Up	MiR-3202	4.21	0.048	Up
MiR-4504	3.90	0.027	Up	MiR-3913-5p	3.50	0.039	Up
MiR-935	2.19	0.038	Up	MiR-483-5p	1.20	0.001	Up
MiR-378g	-3.23	0.047	Down	MiR-337-5p	-4.58	0.032	Down
MiR-3913-5p	-3.09	0.032	Down	MiR-133a-3p	-4.42	0.025	Down
MiR-150-3p	-2.30	0.031	Down	MiR-330-3p	-3.80	0.049	Down
MiR-485-3p	-1.85	0.036	Down	MiR-1468-5p	-3.14	0.033	Down
MiR-548j-5p	-1.65	0.008	Down	MiR-493-5p	-3.05	0.037	Down