## Univariate Analysis Hazard Ratio Plot - OS

Factors	beta	HR (95% CI for HR)		P value	significance
Gender	-0.063	0.94 (0.68–1.3)	<b>→</b>	0.71	
Age	-0.0038	1 (0.98–1)	•	0.6	
CRC_location	0.12	1.1 (0.77–1.6)	<b>→</b>	0.54	
Tstage	-0.12	0.89 (0.53-1.5)	<b>├</b>	0.65	
Nstage	0.28	1.3 (0.95–1.8)	1	0.098	
RAS_mutation	0.077	1.1 (0.68–1.7)	<b>├</b>	0.75	
CEA	0.0015	1 (1–1)	•	0.0012	**
DFI	0.0093	1 (1–1)	•	0.076	
liver_M_distribution	0.35	1.4 (1–2)	<b>——</b>	0.038	*
liver_M_number	0.017	1 (0.99–1)	•	0.3	
liver_M_size	0.067	1.1 (0.99–1.1)	•	0.069	
RR	0.61	1.8 (1.3–2.7)	<b>—</b>	0.0012	**
radio_ablation	0.17	1.2 (0.79–1.8)	<b>—</b>	0.42	
CRS_score	0.29	1.3 (1.1–1.6)	<b>I</b> → <b></b>	0.0019	**
CRS_group	0.44	1.6 (1.1–2.1)	<b>├──</b>	0.0056	**
post_chemotherapy	-0.17	0.84 (0.59-1.2)	<b>—</b>	0.35	
STR_Proportion	-0.092	0.91 (0.78–1.1)	H+1	0.25	
Entropy	-0.079	0.92 (0.79-1.1)	1-0-1	0.32	
LYM_Proportion	-0.23	0.79 (0.68-0.93)	10-1	0.0051	**
STR_interaction	-0.062	0.94 (0.8-1.1)	1-0-1	0.43	
LYM_interaction	-0.15	0.86 (0.73-1)	<b>!→</b>	0.065	
Within_cluster_disp	0.099	1.1 (0.94–1.3)	1	0.22	
Between_cluster_disp	-0.058	0.94 (0.81-1.1)	1-0-1	0.47	
CH_score	0.15	1.2 (1–1.4)	<b>├</b>	0.051	
far_STR	-0.16	0.85 (0.72-1)	<b>I</b> →I	0.055	
around_STR	-0.17	0.85 (0.72-0.99)	I-0-I	0.037	*
inside_STR	-0.089	0.92 (0.78-1.1)	1-0-1	0.26	
far_LYM	-0.16	0.85 (0.73-0.99)	1-0-1	0.037	*
around_LYM	-0.2	0.82 (0.7-0.96)	10-1	0.013	*
inside_LYM	-0.12	0.89 (0.76-1)	<b>I-0-I</b>	0.13	
infiltrated_LYM	-0.17	0.84 (0.72-0.98)	10-1	0.028	*
infiltrated_STR	-0.16	0.85 (0.72-1)	H=H	0.052	
whole_slide_LYM	-0.24	0.79 (0.67-0.93)	10-1	0.004	**
whole_slide_STR	-0.16	0.85 (0.73-1)	I-0-I	0.053	