

	pvalue	Hazard ratio
Grade	<0.001	2.847(2.114–3.833)
IDH_mutation	0.332	1.182(0.844–1.655)
codeletion_1p19q	<0.001	3.075(2.105–4.492)
MGMTp_methylation	0.399	1.128(0.853–1.493)
metabolismcluster	0.003	1.625(1.180–2.237)

