

	pvalue	Hazard ratio
Grade	<0.001	2.866(2.221–3.697)
IDH_mutation	<0.001	2.272(1.765–2.924)
codeletion_1p19q	<0.001	3.630(2.637–4.996)
MGMTp_methylation	0.083	1.250(0.971–1.608)
metabolismcluster	<0.001	2.868(2.228–3.693)

