

SUPPLEMENTARY INFORMATION

Germline pathogenic variants in *HNRNPU* are associated with alterations in blood methylome

Short title: *HNRNPU* episinature

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[Supplementary Table 1] Number of sequencing coverage and mapped reads

Supplementary Table 1 Number of mapped reads

Sample	Total reads processed	Number of mapped reads (bismarkcov)
Patient 1	33,864,153	9,476,634
Patient 2	54,583,274	11,312,506
Patient 3	19,416,856	8,915,639
Patient 4	46,392,754	15,680,389
Patient 5	48,211,581	9,990,357
Patient 6	34,989,055	9,476,001
Patient 7	51,053,405	11,073,213