

**Supplementary Table 1: Summary of sequencing data**

<b>Patient</b>	<b>P4</b>	<b>P6</b>	<b>P10</b>	<b>P14</b>	<b>P15</b>
Total trimmed reads (no.)	462,212	7,083,940	1,207,286	540,480	386,112
Duplicates (%)	0.17	0.25	0.41	0.42	0.32
HCMV reads (no.)	365,711	261,202	1,141,561	460,559	287,305
HCMV reads (%)	79.12	3.69	94.56	85.21	74.41
Mean read length	284	196	289	288	283
Average coverage depth + std	453±128	224±73	1355±825	577±176	355±124