

Table S4. RNA-seq mapping statistics of PDX-Bone in the presence of five drug treatments

| Samples | Total Reads | Mapped Reads | Mapping Rate | has_mRNA_ mapped Reads (hg19) | mmu_mRNA_ mapped Reads (mm10) | lncRNA_ mapped Reads | Virus_ mapped Reads |
|-------------------------|--------------------|---------------------|---------------------|--|--|---------------------------------|--------------------------------|
| C. PDX-B Con | 58,401,590 | 46,254,346 | 79.20% | 42,263,187 | 2,903,561 | 1,048,497 | 39,101 |
| 1. PDX-B GEM | 49,892,923 | 40,809,157 | 81.79% | 36,141,204 | 3,880,058 | 747,034 | 40,861 |
| 2. PDX-B GSK | 52,431,848 | 41,927,970 | 79.97% | 38,660,867 | 2,285,473 | 938,664 | 42,966 |
| 3. PDX-B DEC | 43,372,857 | 35,266,107 | 81.31% | 31,677,112 | 2,860,299 | 696,647 | 32,049 |
| 4. PDX-B PAL | 28,730,565 | 23,583,377 | 82.08% | 20,456,801 | 2,659,627 | 429,511 | 37,438 |
| 5. PDX-B GEM+PAL | 32,784,657 | 27,282,576 | 83.22% | 23,489,568 | 3,196,872 | 540,098 | 56,038 |

The mapping rate of RNA-Seq of each sample was ~80%. EBV transcripts comprised 0.1–0.2% of the total mapped transcripts