Table S2

| | | | | **DRB (-)** | **DRB (+)** | **Mock** | |
|---|---|---|---|---|---|---|---|
| start | end | gene | strand | counts | Counts | counts | **DRB+/DRB-** (Normalized to reads mapping to reads mapping to HSV-1) |
| **46672** | **47802** | **UL23/b** | **-** | **7502** | **7670** | **0** | **1,685695147** |
| 47737 | 48546 | UL24/g1 | + | 1718 | 1719 | 1 | 1,649732193 |
| 113734 | 115272 | UL54/a | + | 5447 | 4902 | 5 | 1,483804432 |
| 26946 | 28502 | UL13/g | - | 873 | 753 | 1 | 1,422137095 |
| 28256 | 28915 | UL14/g2 | - | 411 | 346 | 1 | 1,388017716 |
| **25007** | **26887** | **UL12/b** | **-** | **5822** | **4765** | **2** | **1,349433341** |
| **18224** | **20476** | **UL8/b** | **-** | **2096** | **1665** | **2** | **1,30973578** |
| **107010** | **108125** | **UL50/b** | **+** | **3764** | **2946** | **2** | **1,290457958** |
| 127232 | 131128 | RS1/a | - | 745 | 583 | 2 | 1,290247464 |
| 2261 | 2317 | RL2/a | + | 54 | 42 | 0 | 1,282378602 |
| 134053 | 134928 | US2/g2 | - | 1367 | 1058 | 0 | 1,276079951 |
| 69633 | 70460 | UL34/g1 | + | 2509 | 1902 | 2 | 1,249886518 |
| **58463** | **62053** | **UL29/b** | **-** | **7961** | **6034** | **4** | **1,249678834** |
| 24801 | 25091 | UL11/g | - | 2552 | 1899 | 0 | 1,226888306 |
| 29020 | 30048 | UL15/g | + | 464 | 344 | 1 | 1,222365811 |
| 48813 | 50555 | UL25/g2 | + | 2477 | 1805 | 0 | 1,201467236 |
| 142744 | 143223 | US8A/ | + | 1318 | 957 | 1 | 1,197173954 |
| **89926** | **90948** | **UL40/b** | **+** | **9251** | **6632** | **9** | **1,18199753** |
| **86444** | **89857** | **UL39/b** | **+** | **9981** | **7142** | **7** | **1,179794922** |
| **20704** | **23259** | **UL9/b** | **-** | **4387** | **3122** | **8** | **1,173345728** |
| 69161 | 69553 | UL33/g2 | + | 359 | 253 | 0 | 1,1619483 |
| 147105 | 151001 | RS1_2/a | + | 822 | 578 | 1 | 1,159355838 |
| 55802 | 58159 | UL28/g | - | 2953 | 2072 | 0 | 1,156876599 |
| 141243 | 142895 | US8/g1 | + | 3859 | 2660 | 4 | 1,136495159 |
| 135222 | 136667 | US3/g1 | + | 2160 | 1487 | 0 | 1,135057727 |
| 124054 | 124110 | RL2_6/a | - | 77 | 53 | 0 | 1,134869375 |
| 67372 | 69162 | UL32/g2 | - | 1878 | 129 0 | 1 | 1,132543403 |
| **62807** | **66514** | **UL30/b** | **+** | **9663** | **6537** | **5** | **1,115391261** |
| 80713 | 84084 | UL37/g1 | - | 3897 | 2632 | 3 | 1,113566639 |
| 17135 | 18025 | UL7/g1 | + | 1813 | 1223 | 0 | 1,112216632 |
| 66459 | 67379 | UL31/g | - | 4293 | 2862 | 2 | 1,099181659 |
| 53080 | 55794 | UL27/g1 | - | 39282 | 25983 | 26 | 1,090577251 |
| 112179 | 113195 | UL53/g | + | 2217 | 1449 | 0 | 1,077614495 |
| **93113** | **94579** | **UL42/b** | **+** | **10668** | **6934** | **7** | **1,071671207** |
| 51727 | 52716 | UL26.5/g | + | 7453 | 4807 | 5 | 1,063417329 |
| 11823 | 12422 | UL4/a | - | 1240 | 799 | 0 | 1,062394531 |
| 50809 | 52716 | UL26/g | + | 9504 | 6114 | 5 | 1,060668666 |
| 31386 | 33497 | UL17/g | - | 1217 | 773 | 0 | 1,047248261 |
| **12483** | **15131** | **UL5/b** | **-** | **2948** | **1870** | **4** | **1,045863146** |
| 143313 | 143585 | US9/g | + | 3122 | 1976 | 1 | 1,043553632 |
| 115496 | 116056 | UL55/g2 | + | 1107 | 696 | 2 | 1,036626605 |
| 70566 | 70904 | UL35/g2 | + | 3483 | 2189 | 3 | 1,036222503 |
| 43866 | 46382 | UL22/g | - | 5785 | 3621 | 6 | 1,032014725 |
| 9884 | 10888 | UL2/b/g1 | + | 3277 | 2051 | 2 | 1,031929318 |
| 40820 | 41488 | UL20/g1 | - | 737 | 459 | 1 | 1,026847452 |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 137731 | 138009 | US5/g | + | 333 | 206 | 0 | 1,019961359 |
| 30174 | 31295 | UL16/g1 | - | 1771 | 1087 | 0 | 1,011979501 |
| 15130 | 17160 | UL6/g | + | 2155 | 1316 | 1 | 1,006860601 |
| 94748 | 96052 | UL43/g | + | 876 | 528 | 0 | 0,993780678 |
| 23204 | 24625 | UL10/g2 | + | 5311 | 3171 | 5 | 0,984420554 |
| 136744 | 137460 | US4/g1 | + | 5270 | 3146 | 0 | 0,984257732 |
| 36404 | 40528 | UL19/g | - | 12788 | 7622 | 13 | 0,982713787 |
| 84531 | 85928 | UL38/g2 | + | 2819 | 1635 | 1 | 0,956276346 |
| 132644 | 133906 | US1/a | + | 13921 | 8042 | 8 | 0,952476715 |
| 35095 | 36051 | UL18/g1 | - | 4373 | 2519 | 4 | 0,949750263 |
| 145311 | 145577 | US12/a | - | 4233 | 2436 | 2 | 0,948832928 |
| 116221 | 116925 | UL56/g2 | - | 1764 | 1008 | 2 | 0,942155708 |
| 33635 | 34813 | UL15_2/g | + | 1249 | 710 | 0 | 0,937252576 |
| 71049 | 80543 | UL36/g2 | - | 3148 | 1775 | 5 | 0,929660473 |
| 3083 | 3749 | RL2_2/a | + | 699 | 393 | 2 | 0,926992258 |
| 98796 | 100952 | UL46/g1 | - | 11267 | 6232 | 6 | 0,911968594 |
| 108277 | 109011 | UL51/g1 | - | 944 | 521 | 2 | 0,909968715 |
| **109048** | **112224** | **UL52/b** | **+** | **3662** | **2005** | **3** | **0,902727701** |
| 105486 | 106391 | UL49/g? | - | 10342 | 5535 | 5 | 0,882416914 |
| 9337 | 10011 | UL1/g1 | + | 2884 | 1500 | 2 | 0,857544637 |
| 139785 | 140957 | US7/g1 | + | 9935 | 5161 | 9 | 0,856498723 |
| 122622 | 123288 | RL2_5/a | - | 718 | 371 | 2 | 0,851942331 |
| 138419 | 139603 | US6/g | + | 9851 | 4977 | 7 | 0,833005855 |
| 98032 | 98550 | UL45/g2 | + | 4281 | 2117 | 1 | 0,815335519 |
| 42074 | 43681 | UL21/g | + | 2483 | 1219 | 0 | 0,809445696 |
| 103607 | 105079 | UL48/g | - | 14375 | 6975 | 9 | 0,800013086 |
| 10957 | 11664 | UL3/a | + | 1334 | 629 | 0 | 0,777419712 |
| 101035 | 103116 | UL47/g1 | - | 3444 | 1623 | 2 | 0,776991216 |
| 144761 | 145246 | US11/g2 | - | 18454 | 8494 | 4 | 0,758896365 |
| 106718 | 106993 | UL49A/ | - | 888 | 408 | 1 | 0,757544117 |
| 144157 | 145095 | US10/g1 | - | 35080 | 16080 | 16 | 0,755765725 |
| 120882 | 122485 | RL2_4/a | - | 1263 | 557 | 1 | 0,72713086 |
| 3886 | 5489 | RL2_3/a | + | 1223 | 539 | 1 | 0,726646256 |
| 91168 | 92637 | UL41/g1 | - | 3106 | 1361 | 3 | 0,722465988 |
| 96311 | 97846 | UL44/g2 | + | 13727 | 5318 | 17 | 0,638753704 |

Evaluation of RNA-Seq experiments performed in the presence or absence of 25 μM DRB. DRB was added at 6 h.p.i. and cells from the two experiments were harvested at 13 h.p.i.. The total number of reads obtained in the absence of DRB was 3 826 721 and 425 319 reads (11%) mapped to the HSV-1 genome. For the experiment performed in the presence of DRB 3 725 564 reads were obtained and 257 961 reads (6.9%) mapped to the HSV-1 genome. For the mock infection experiment 8 855 884 reads were obtained and 274 mapped to the HSV-1 genome. The early genes (b) are highlighted in bold print. Immediate early and late genes are designated as a, g1 and g2.