

**Suppl. Table S3.** Protein coding genes *H. lucertense* SVX82 with cTAG methylation within 20 bp upstream of the start codon

| Locus Tag  | $\Delta^*$ | Methylation <sup>†</sup> |    |     |    | RPKM <sup>‡</sup> |        |        |        | Gene annotation   |
|------------|------------|--------------------------|----|-----|----|-------------------|--------|--------|--------|---|
|            |            | I                        | II | III | IV | I                 | II     | III    | IV     |   |
| SIVHX_0538 | -3         | +                        | +  | +   | +  | 44                | 0      | 44     | 0      | HAD superfamily hydrolase   |
| SIVHX_2584 | -4         | +                        | +  | +   | +  | 82                | 47     | 0      | 62     | Sugar-specific transcriptional regulator TrmB                           |
| SIVHX_0106 | -5         | +                        | +  | +   | +  | 70                | 73     | 0      | 0      | Uncharacterized protein   |
| SIVHX_0772 | -5         | --                       | +  | +   | +  | 238               | 217.5  | 47     | 147    | CbpA; DnaJ-class molecular chaperone                                    |
| SIVHX_1729 | -5         | +                        | +  | +   | +  | 37.5              | 13.5   | 59     | 31     | Uncharacterized membrane protein, Yip1 family                           |
| SIVHX_1861 | -5         | +                        | +  | +   | +  | 813.5             | 585.5  | 121    | 541.5  | Ndk; Nucleoside diphosphate kinase                                      |
| SIVHX_2482 | -5         | --                       | +  | +   | +  | 21                | 19.5   | 25     | 0      | BglX; Beta-glucosidase, glycosyl hydrolase family 3                     |
| SIVHX_3282 | -5         | +                        | +  | +   | +  | 0                 | 23     | 0      | 0      | Uncharacterized protein   |
| SIVHX_0549 | -6         | +                        | -- | +   | +  | 1229.5            | 707.5  | 267.5  | 821.5  | Predicted redox protein, regulator of disulfide bond formation          |
| SIVHX_2487 | -6         | +                        | +  | +   | +  | 202.5             | 275.5  | 230    | 351.5  | SalX; ABC-type antimicrobial peptide transport system                   |
| SIVHX_3146 | -6         | +                        | +  | +   | +  | 95                | 151    | 96     | 100.5  | OmpR; REC domain  |
| SIVHX_5036 | -8         | +                        | +  | --  | +  | 183.5             | 285    | 0      | 187.5  | ArsR; Transcriptional regulator containing HTH domain, ArsR family      |
| SIVHX_0132 | -9         | +                        | +  | +   | +  | 135.5             | 149    | 32     | 42.5   | RIO1; Serine/threonine protein kinase involved in cell cycle control    |
| SIVHX_1326 | -9         | --                       | +  | +   | -- | 429.5             | 510.5  | 74     | 348.5  | Transcriptional regulator, contains HTH domain                          |
| SIVHX_2851 | -9         | +                        | -- | +   | +  | 259.5             | 289.5  | 586.5  | 254    | CopA; Copper-translocating P-type ATPase                                |
| SIVHX_0064 | -10        | --                       | +  | +   | +  | 817.5             | 540    | 346    | 598    | Rubredoxin family protein   |
| SIVHX_0624 | -10        | --                       | +  | +   | +  | 716               | 1950.5 | 38.5   | 2863.5 | THI4; Sulfide-dependent adenosine diphosphate thiazole synthase         |
| SIVHX_0972 | -11        | +                        | +  | +   | +  | 123               | 65.5   | 70.5   | 182.5  | Archaea-specific RecJ-like exonuclease                                  |
| SIVHX_1140 | -11        | +                        | +  | +   | -- | 1056              | 537.5  | 561.5  | 3172   | AldH; Aldehyde dehydrogenase (NAD+)                                     |
| SIVHX_2840 | -11        | +                        | +  | +   | +  | 311               | 179    | 285.5  | 229.5  | Fdx; DnaJ-like chaperone fused to ferredoxin                            |
| SIVHX_0241 | -12        | +                        | +  | +   | +  | 136.5             | 27     | 108.5  | 121    | ICC-like phosphoesterase  |
| SIVHX_0476 | -12        | --                       | +  | +   | +  | 25.5              | 32     | 0      | 36.5   | Uncharacterized protein   |
| SIVHX_0761 | -12        | +                        | +  | --  | +  | 72.5              | 50     | 330.5  | 197    | Membrane protein implicated in regulation of membrane protease activity |
| SIVHX_1096 | -12        | +                        | +  | +   | +  | 62                | 0      | 129.5  | 0      | Uncharacterized protein   |
| SIVHX_1193 | -12        | --                       | +  | +   | +  | 143.5             | 113    | 279    | 344.5  | Twin-arginine translocation signal domain-containing protein            |
| SIVHX_1769 | -12        | +                        | +  | +   | +  | 55.5              | 36.5   | 0      | 0      | Uncharacterized protein   |
| SIVHX_2246 | -12        | +                        | +  | --  | +  | 91                | 107.5  | 0      | 0      | Uncharacterized protein   |
| SIVHX_2274 | -12        | --                       | +  | --  | +  | 20                | 25     | 96.5   | 28     | AcrR; Transcriptional regulator, TetR/AcrR family                       |
| SIVHX_2438 | -12        | +                        | +  | +   | +  | 31.5              | 18.5   | 189.5  | 0      | Cytochrome cbb3 oxidase subunit I                                       |
| SIVHX_2809 | -12        | --                       | +  | +   | +  | 95                | 104    | 0      | 43.5   | Uncharacterized protein   |
| SIVHX_4082 | -12        | --                       | +  | +   | +  | 301.5             | 89.5   | 96     | 75     | NosL family protein   |
| SIVHX_0095 | -13        | +                        | +  | +   | +  | 104.5             | 131    | 56.5   | 0      | NMD3; NMD protein affecting ribosome stability and mRNA decay           |
| SIVHX_0302 | -13        | +                        | +  | +   | +  | 381.5             | 398    | 267    | 511.5  | eRF1; Peptide chain release factor eRF1                                 |
| SIVHX_0432 | -13        | +                        | +  | +   | +  | 205               | 300.5  | 1091.5 | 295    | Uncharacterized archaeal Zn-finger protein                              |
| SIVHX_0545 | -13        | +                        | +  | +   | +  | 51.5              | 8      | 0      | 142.5  | HisC; Histidinol-phosphate aminotransferase                             |
| SIVHX_1192 | -13        | --                       | +  | +   | +  | 524               | 501    | 232    | 433.5  | Sco1; Cytochrome oxidase Cu insertion factor, SCO1/SenC/PrrC family     |
| SIVHX_1297 | -13        | +                        | +  | +   | +  | 116.5             | 208    | 0      | 139.5  | ArsR; Transcriptional regulator containing HTH domain, ArsR family      |
| SIVHX_1533 | -13        | +                        | +  | +   | +  | 80.5              | 119    | 0      | 32     | ArgA; Acetyltransferase (GNAT) family                                   |
| SIVHX_1600 | -13        | +                        | +  | --  | +  | 40.5              | 87     | 280.5  | 246.5  | Zn finger protein, C2C2 type  |
| SIVHX_1767 | -13        | +                        | +  | +   | +  | 132.5             | 167.5  | 106    | 177    | AstE; Succinylglutamate desuccinylase                                   |
| SIVHX_2142 | -13        | +                        | +  | --  | +  | 90                | 142    | 125    | 374    | Uncharacterized protein, DUF2062 family                                 |
| SIVHX_2574 | -13        | --                       | +  | --  | +  | 6.5               | 0      | 0      | 0      | FepB; ABC-type Fe3+-hydroxamate transport system                        |
| SIVHX_2595 | -13        | +                        | +  | +   | +  | 67.5              | 13.5   | 0      | 72.5   | Uncharacterized protein   |
| SIVHX_4056 | -13        | +                        | +  | +   | +  | 0                 | 0      | 0      | 0      | FrdA; Fumarate reductase flavoprotein subunit                           |
| SIVHX_0267 | -14        | +                        | +  | +   | +  | 11.5              | 27     | 0      | 53.5   | CinA; Nucleotide-utilizing enzyme related to molybdopterin-biosynthesis |
| SIVHX_1073 | -14        | +                        | -- | --  | +  | 509.5             | 559.5  | 421.5  | 420.5  | PetE; Halocyanin  |
| SIVHX_1520 | -14        | --                       | +  | +   | -- | 146               | 175    | 321    | 536    | GyrB; DNA gyrase subunit B  |
| SIVHX_2227 | -14        | +                        | -- | +   | +  | 5                 | 6      | 0      | 0      | Uncharacterized surface protein, possible component of pili like system |
| SIVHX_1137 | -15        | +                        | +  | --  | +  | 1624              | 3529   | 1263   | 1974   | Uncharacterized protein   |
| SIVHX_2494 | -16        | +                        | +  | +   | +  | 41.5              | 112.5  | 17.5   | 51.5   | Uncharacterized protein with Ig-like domain                             |
| SIVHX_3150 | -16        | +                        | +  | +   | +  | 50.5              | 65.5   | 0      | 0      | hypothetical protein  |
| SIVHX_3282 | -16        | +                        | +  | +   | +  | 0                 | 23     | 0      | 0      | Uncharacterized protein   |
| SIVHX_4004 | -16        | +                        | +  | +   | +  | 1475              | 2009   | 145    | 7173.5 | Pilin/Flagellin, FlaG/FlaF family                                       |
| SIVHX_1072 | -17        | --                       | +  | +   | +  | 666.5             | 742    | 209    | 554.5  | Zn ribbon containing protein  |
| SIVHX_3327 | -17        | +                        | +  | +   | +  | 58                | 56.5   | 0      | 45     | SufS; Cysteine desulfurase/selenocysteine lyase                         |
| SIVHX_0202 | -18        | +                        | +  | --  | +  | 33.5              | 116.5  | 0      | 49     | Predicted transcriptional regulator, ArsR family                        |
| SIVHX_0279 | -18        | +                        | +  | +   | +  | 403               | 541.5  | 3387   | 540    | Predicted RNA-binding protein, contains TRAM domain                     |
| SIVHX_1893 | -18        | +                        | +  | +   | +  | 236               | 71.5   | 29     | 38.5   | IolE; Sugar phosphate isomerase/epimerase                               |
| SIVHX_3284 | -18        | +                        | +  | +   | +  | 36.5              | 91.5   | 0      | 0      | Transcriptional regulator, contains HTH domain                          |
| SIVHX_3288 | -18        | +                        | +  | +   | +  | 30                | 66.5   | 23     | 30.5   | Protein containing two CBS domains                                      |
| SIVHX_0562 | -19        | +                        | +  | +   | +  | 28                | 81     | 0      | 21     | Transposase   |
| SIVHX_2215 | -19        | +                        | +  | +   | +  | 4                 | 24.5   | 0      | 0      | Transposase   |
| SIVHX_3124 | -19        | --                       | +  | --  | +  | 7                 | 15.5   | 0      | 0      | Transposase   |
| SIVHX_5067 | -19        | +                        | +  | +   | +  | 163.5             | 246.5  | 251    | 0      | Transcriptional regulator, PadR family                                  |
| SIVHX_0522 | -20        | +                        | +  | +   | +  | 77                | 34     | 60     | 77     | Two-component system, OmpR family, sensor kinase                        |
| SIVHX_1115 | -20        | +                        | +  | --  | +  | 1454              | 2612.5 | 807    | 1201.5 | TatA; Sec-independent protein secretion pathway component               |
| SIVHX_3021 | -20        | +                        | +  | +   | +  | 7.5               | 24.5   | 0      | 0      | Transposase   |
| SIVHX_3300 | -20        | --                       | +  | +   | +  | 215               | 66     | 71.5   | 21     | Transposase   |

\*Distance from the methylated cytosine to the start codon;

†Methylation occurrence in four experiments I, II, III and IV.

‡RPKM (reads per kilo base per million mapped reads) values of gene expression in four experiments I, II, III and IV.