

**Table S1.** Sequencing and assembly metrics for tissue assemblies, based on two individuals per tissue for all samples except Corn snake skin (see methods). *Eco*, Painted saw-scaled viper (*Echis coloratus*); *Pgu*, Corn snake (*Pantherophis guttatus*); *Oae*, Rough green snake (*Opheodrys aestivus*); *Pre*, Royal python (*Python regius*); *Ema*, Leopard gecko (*Eublepharis macularius*). VG, venom gland (pooled 24 and 48 hours post-milking); SAL, salivary gland; SCG, scent gland; SK, skin.

| Species    | Tissue | Total number of reads | Total number of bases | Number of contigs | Number of contigs >300bp | Contig N50 (bp) | Max contig (bp) |
|------------|--------|-----------------------|-----------------------|-------------------|--------------------------|-----------------|-----------------|
| <i>Eco</i> | VG     | 4,478,521             | 78,297,821            | 84,846            | 56,805                   | 1,684           | 15,819          |
|            | SCG    | 4,615,745             | 159,597,029           | 138,852           | 87,389                   | 2,444           | 36,612          |
|            | SK     | 2,436,702             | 70,078,381            | 77,402            | 50,860                   | 1,725           | 30,610          |
| <i>Pgu</i> | SAL    | 3,911,929             | 64,843,188            | 64,595            | 43,565                   | 1,916           | 17,102          |
|            | SCG    | 4,325,490             | 121,928,061           | 110,016           | 70,265                   | 2,345           | 17,065          |
|            | SK     | 1,354,205             | 41,671,078            | 51,199            | 35,969                   | 1,329           | 19,348          |
| <i>Oae</i> | SAL    | 3,557,997             | 62,132,339            | 65,393            | 42,558                   | 1,780           | 17,524          |
|            | SCG    | 4,728,785             | 129,085,282           | 126,321           | 77,954                   | 2,064           | 17,135          |
|            | SK     | 2,807,701             | 90,620,560            | 92,597            | 57,242                   | 1,918           | 33,155          |
| <i>Pre</i> | SAL    | 4,094,700             | 79,553,343            | 73,492            | 48,727                   | 2,265           | 33,655          |
|            | SCG    | 4,128,123             | 216,585,760           | 163,065           | 104,329                  | 3,156           | 20,966          |
|            | SK     | 2,687,104             | 66,158,208            | 67,200            | 47,819                   | 1,864           | 25,879          |
| <i>Ema</i> | SAL    | 5,024,551             | 127,979,189           | 111,345           | 73,027                   | 2,439           | 24,285          |
|            | SCG    | 4,306,502             | 141,161,398           | 129,951           | 85,014                   | 2,330           | 29,392          |
|            | SK     | 2,531,638             | 91,521,947            | 92,506            | 61,456                   | 2,057           | 27,091          |

**Table S2.** Sequencing metrics for additional Painted saw-scaled viper (*Echis coloratus*) venom gland samples used for RSEM abundance estimation.

| Time post-milking | Total number of reads | Total number of bases |
|-------------------|-----------------------|-----------------------|
| 16 hours          | 44,678,609            | 4,512,539,509         |
| 24 hours          | 38,711,180            | 3,909,829,180         |

**Table S3.** Sequence and assembly metrics for King cobra (*Ophiophagus hannah*) venom gland, accessory gland and pooled tissue (heart, lung, spleen, brain, testes, gall bladder, pancreas, small intestine, kidney, liver, eye, tongue and stomach) data from Vonk et al. (2013).

| Tissue          | Total number of reads | Total number of bases | Number of contigs | Number of contigs >300bp | Contig N50 (bp) | Max contig (bp) |
|-----------------|-----------------------|-----------------------|-------------------|--------------------------|-----------------|-----------------|
| Venom gland     | 15,166,590            | 2,458,479             | 6123              | 2,925                    | 424             | 4,585           |
| Accessory gland | 11,209,677            | 3,381,052             | 9046              | 4,113                    | 377             | 3,740           |
| Pooled tissue   | 17,858,289            | 3,557,109             | 8877              | 4,135                    | 413             | 5,733           |

**Table S4.** Sequencing and assembly metrics for reference transcriptome assemblies used for transcript abundance estimation.

| Reference assembly  | Total number of bases | Number of contigs | Number of contigs >300bp | Contig N50 (bp) | Max contig (bp) |
|---------------------|-----------------------|-------------------|--------------------------|-----------------|-----------------|
| <i>EcoTissueRef</i> | 228,063,624           | 206,147           | 149,821                  | 2,445           | 38,875          |
| <i>PguTissueRef</i> | 166,312,211           | 152,359           | 112,327                  | 2,315           | 23,951          |
| <i>OaeTissueRef</i> | 210,451,256           | 204,942           | 147,597                  | 2,200           | 52,645          |
| <i>PreTissueRef</i> | 301,328,500           | 219,070           | 166,578                  | 3,407           | 34,165          |
| <i>EmaTissueRef</i> | 266,096,501           | 228,645           | 167,623                  | 2,746           | 33,255          |

**Table S5.** Transcript abundance estimation values given in FPKM for each Leopard gecko (*Eublepharis macularius*) tissue. See methods section in the main text for further explanation.

| Gene                       | Salivary gland |       |        | Scent gland |        |        | Skin   |        |        |
|----------------------------|----------------|-------|--------|-------------|--------|--------|--------|--------|--------|
|                            | 1              | 2     | Mean   | 1           | 2      | Mean   | 1      | 2      | Mean   |
| ache transcript 1          | 9.08           | 8.18  | 8.63   | 6.62        | 2.36   | 4.49   | 5.48   | 2.65   | 4.07   |
| complement c3              | 121.32         | 0.06  | 60.69  | 53.85       | 22.52  | 38.19  | 7.85   | 82.24  | 45.05  |
| cystatin-e/m               | 14.97          | 11.57 | 13.27  | 37.6        | 57.06  | 47.33  | 20.15  | 25.77  | 22.96  |
| cystatin-f                 | 1.21           | 1.79  | 1.50   | 0.36        | 1.1    | 0.73   | 0.66   | 4.26   | 2.46   |
| lao-a                      | 0              | 4.78  | 2.39   | 8.48        | 5.58   | 7.03   | 15.47  | 50.14  | 32.81  |
| lao-a                      | 109.19         | 16.39 | 62.79  | 259.98      | 3.31   | 131.65 | 1.71   | 0.26   | 0.99   |
| esp-e1                     | 47.71          | 45.91 | 46.81  | 26.36       | 50.32  | 38.34  | 35.12  | 38.27  | 36.70  |
| ficolin                    | 7.07           | 0.9   | 3.99   | 5.16        | 5.43   | 5.30   | 0.21   | 0.95   | 0.58   |
| kallikrein                 | 1.53           | 0.12  | 0.83   | 4.28        | 1.83   | 3.06   | -      | -      | -      |
| kunitz 1                   | 2.06           | 0.24  | 1.15   | 0           | 3.87   | 1.94   | 0      | 1.11   | 0.56   |
| kunitz 2                   | 103.1          | 102   | 102.55 | 140.59      | 192.61 | 166.6  | 111.37 | 111.52 | 111.45 |
| lipa-a                     | 5.69           | 6.31  | 6.00   | 6.57        | 8.84   | 7.71   | 14.05  | 25.33  | 19.69  |
| ngf                        | 2.67           | 2.16  | 2.42   | 1.34        | 2.08   | 1.71   | 1.87   | 3.06   | 2.47   |
| PLA <sub>2</sub> group IIE | 9.41           | 22.27 | 15.84  | -           | -      | -      | -      | -      | -      |
| plb                        | 4.68           | 6.25  | 5.47   | 44.19       | 53.66  | 48.93  | 72.02  | 91.27  | 81.65  |
| renin                      | -              | -     | -      | 1           | 7.01   | 4.01   | -      | -      | -      |
| vegf-a                     | 2.34           | 0.82  | 1.58   | 5.38        | 1.24   | 3.31   | 2.89   | 2.19   | 2.54   |
| vegf-b                     | 1.61           | 0.97  | 1.29   | 1.27        | 1.63   | 1.45   | 1.86   | 1.53   | 1.70   |
| vegf-c                     | 1.83           | 1.81  | 1.82   | 1.35        | 2.15   | 1.75   | 0.39   | 1.2    | 0.80   |
| vespryn                    | -              | -     | -      | 7.29        | 10.72  | 9.01   | 1.42   | 29.91  | 15.67  |
| waprin                     | 74.86          | 81.24 | 78.05  | 22.71       | 25.55  | 24.13  | 4.25   | 2.52   | 3.39   |

**Table S6.** Transcript abundance estimation values given in FPKM for each Royal python (*Python regius*) tissue. See methods section in the main text for further explanation.

| Gene                       | Salivary gland |        |        | Scent gland |          |          | Skin  |        |        |
|----------------------------|----------------|--------|--------|-------------|----------|----------|-------|--------|--------|
|                            | 1              | 2      | Mean   | 1           | 2        | Mean     | 1     | 2      | Mean   |
| 3ftx-a                     | 6.16           | 2.14   | 4.15   | -           | -        | -        | -     | -      | -      |
| ache transcript 1          | 0              | 1.47   | 0.74   | 0           | 0        | 0        | 2.74  | 1.25   | 2.00   |
| ache transcript 2          | -              | -      | -      | 0.82        | 1.12     | 0.97     | -     | -      | -      |
| complement c3              | 26.23          | 1.61   | 13.92  | 1.2         | 2.2      | 1.70     | -     | -      | -      |
| crisp-a                    | -              | -      | -      | 6.39        | 4.92     | 5.66     | -     | -      | -      |
| cystatin-e/m               | 270.35         | 135.03 | 202.69 | 861.58      | 681.05   | 771.32   | 35.3  | 49.76  | 42.53  |
| cystatin-f                 | 1.61           | 0.8    | 1.21   | 5.1         | 5.7      | 5.40     | 0.73  | 0.37   | 0.55   |
| dpp3                       | 6.84           | 5.16   | 6.00   | 28.07       | 28.3     | 28.19    | 25.51 | 25.75  | 25.63  |
| dpp4                       | 124.71         | 33.41  | 79.06  | 20.01       | 24.63    | 22.32    | 2.72  | 4.23   | 3.48   |
| esp-e1                     | 2.54           | 1.16   | 1.85   | 9.3         | 10.85    | 10.08    | 2.99  | 5.4    | 4.20   |
| ficolin                    | 3.76           | 0      | 1.88   | -           | -        | -        | -     | -      | -      |
| kallikrein                 | 0.34           | 0      | 0.17   | 1.35        | 2.08     | 1.72     | 0     | 16.9   | 8.45   |
| kunitz 1                   | 5.36           | 4.49   | 4.93   | 13.45       | 16.6     | 15.03    | 4.45  | 3      | 3.73   |
| kunitz 2                   | 35.72          | 17.57  | 26.65  | 50.1        | 53       | 51.55    | 44.08 | 60.63  | 52.36  |
| lao-b1                     | -              | -      | -      | 1,066.83    | 1,242.33 | 1,154.58 | -     | -      | -      |
| lipa-a                     | 0.95           | 0.92   | 0.94   | 3.49        | 2.41     | 2.95     | 32.37 | 41.21  | 36.79  |
| lipa-b                     | -              | -      | -      | 4.13        | 3.88     | 4.01     | -     | -      | -      |
| ngf                        | -              | -      | -      | -           | -        | -        | 5.03  | 2.15   | 3.59   |
| PLA <sub>2</sub> group IIE | 138.12         | 111.14 | 124.63 | -           | -        | -        | -     | -      | -      |
| plb                        | 0              | 2.56   | 1.28   | 16.8        | 12.24    | 14.52    | 16.33 | 34.61  | 25.47  |
| vegf-a                     | 0.82           | 0.09   | 0.46   | 2.98        | 2.5      | 2.74     | 0.36  | 0.15   | 0.26   |
| vegf-b                     | 3.93           | 3.97   | 3.95   | 1.95        | 0.85     | 1.40     | 0     | 0.86   | 0.43   |
| vegf-c                     | 0.94           | 0.58   | 0.76   | 17.38       | 10.43    | 13.91    | 0.46  | 0      | 0.23   |
| vespryn                    | -              | -      | -      | 15.3        | 4.24     | 9.77     | 99.86 | 141.84 | 120.85 |

**Table S7.** Transcript abundance estimation values given in FPKM for each Rough green snake (*Opheodrys aestivus*) tissue. See methods section in the main text for further explanation.

| Gene                       | Salivary gland |        |        | Scent gland |        |        | Skin  |       |       |
|----------------------------|----------------|--------|--------|-------------|--------|--------|-------|-------|-------|
|                            | 1              | 2      | Mean   | 1           | 2      | Mean   | 1     | 2     | Mean  |
| 3ftx-a                     | 120.53         | 0.36   | 60.45  | -           | -      | -      | 1.67  | 0     | 0.84  |
| 3ftx-b                     | -              | -      | -      | 0           | 10.59  | 5.30   | -     | -     | -     |
| ache transcript 1          | 2.43           | 0      | 1.22   | 8.48        | 9.7    | 9.09   | -     | -     | -     |
| ache transcript 2          | -              | -      | -      | 8.48        | 9.7    | 9.09   | -     | -     | -     |
| AVIT                       | -              | -      | -      | 0           | 0.91   | 0.46   | -     | -     | -     |
| complement c3              | 18.29          | 1.63   | 9.96   | 102.28      | 52.24  | 77.26  | 0.81  | 8.77  | 4.79  |
| crisp-a                    | -              | -      | -      | 0           | 5.3    | 2.65   | 0     | 0     | 0     |
| cystatin-e/m               | 168.58         | 213.23 | 190.91 | 25.12       | 18.03  | 21.58  | 23.94 | 12.78 | 18.36 |
| cystatin-f                 | 0.59           | 0      | 0.30   | 1.75        | 2.27   | 2.01   | 0.14  | 0.47  | 0.31  |
| dpp3                       | 0              | 6.34   | 3.17   | 0           | 3.37   | 1.69   | 0     | 6.43  | 3.22  |
| dpp4                       | 4.33           | 5.61   | 4.97   | 9.61        | 9.64   | 9.63   | 2.59  | 2.27  | 2.43  |
| esp-e1                     | 20.13          | 11.16  | 15.65  | 76.01       | 84.29  | 80.15  | 17.44 | 20.41 | 18.93 |
| ficolin                    | 17.32          | 1.93   | 9.63   | 269.16      | 1.6    | 135.38 | -     | -     | -     |
| kallikrein                 | -              | -      | -      | 1.34        | 8.11   | 4.73   | -     | -     | -     |
| kunitz 1                   | 17.35          | 26.32  | 21.84  | 22.93       | 60.7   | 41.82  | 2.26  | 2.91  | 2.59  |
| kunitz 2                   | 60.5           | 79.52  | 70.01  | 144.05      | 309.27 | 226.66 | 18.91 | 36.53 | 27.72 |
| lao-b1                     | -              | -      | -      | 2.44        | 0.44   | 1.44   | -     | -     | -     |
| lipa-a                     | 7.4            | 2.87   | 5.14   | 26.2        | 44.7   | 35.45  | 11.74 | 6.66  | 9.20  |
| ngf                        | -              | -      | -      | 2.8         | 0.74   | 1.77   | 1.15  | 1.11  | 1.13  |
| PLA <sub>2</sub> group IIE | 8.28           | 24.89  | 16.59  | -           | -      | -      | -     | -     | -     |
| plb                        | -              | -      | -      | 9.11        | 34.64  | 21.88  | 7.38  | 42.55 | 24.97 |
| vegf-a                     | 0.25           | 3.57   | 1.91   | 0.6         | 4.44   | 2.52   | 0.7   | 0.78  | 0.74  |
| vegf-b                     | 1.17           | 0.72   | 0.95   | 1.06        | 0.92   | 0.99   | 0.59  | 0     | 0.29  |
| vegf-c                     | 1.17           | 1.42   | 1.30   | 3.85        | 2.04   | 2.95   | 1.21  | 1.17  | 1.19  |
| vespryn                    | -              | -      | -      | 0.31        | 2      | 1.16   | 0     | 0.39  | 0.19  |
| waprin                     | 41.85          | 41.26  | 41.56  | 277.5       | 75.5   | 176.50 | 3.4   | 0.58  | 1.99  |

**Table S8.** Transcript abundance estimation values given in FPKM for each Corn snake (*Pantherophis guttatus*) tissue. See methods section in the main text for further explanation.

| Gene                       | Salivary gland |        |       | Scent gland |        |        | Skin  |
|----------------------------|----------------|--------|-------|-------------|--------|--------|-------|
|                            | 1              | 2      | Mean  | 1           | 2      | Mean   | 1     |
| 3ftx-a                     | 7.00           | 0.57   | 3.79  | 0           | 1.04   | 0.52   | 6.15  |
| ache transcript 1          | 3.31           | 2.97   | 3.14  | 1.07        | 1.92   | 1.50   | 1.12  |
| complement c3              | 41.33          | 76.08  | 58.71 | 2.12        | 3.27   | 2.70   | 0.49  |
| crisp-a                    | 0              | 4.48   | 2.24  | 3.11        | 7.95   | 5.53   | 37.27 |
| crisp-b                    | 0.11           | 13.15  | 6.63  | -           | -      | -      | -     |
| cystatin-e/m               | 0.85           | 61.01  | 30.93 | 204.32      | 657.41 | 430.87 | 90.14 |
| cystatin-f                 | 1.05           | 0.77   | 0.91  | 1.42        | 1.4    | 1.41   | 1.58  |
| dpp3                       | 2.43           | 12.31  | 7.37  | 9.58        | 0      | 4.79   | 2.49  |
| dpp4                       | 17.67          | 21.74  | 19.71 | 5.06        | 2.08   | 3.57   | 6.98  |
| esp-e1                     | 10.58          | 13.77  | 12.18 | 20.53       | 68.15  | 44.34  | 23.83 |
| ficolin                    | 8.67           | 39.06  | 23.87 | 6.75        | 13.22  | 9.99   | 2.98  |
| kallikrein                 | -              | -      | -     | 4.52        | 72.05  | 38.29  | -     |
| kunitz 1                   | 12.2           | 14.89  | 13.55 | 46.68       | 16.63  | 31.66  | 2.27  |
| kunitz 2                   | 50.24          | 112.88 | 81.56 | 121.72      | 79.8   | 100.76 | 65.64 |
| lao-b1                     | -              | -      | -     | 97.78       | 0.26   | 49.02  | -     |
| lipa-a                     | 1.04           | 0      | 0.52  | 19.19       | 0.1    | 9.65   | 6.96  |
| ngf                        | 0.9            | 0.5    | 0.70  | 2.09        | 0      | 1.05   | -     |
| PLA <sub>2</sub> group IIE | 49.24          | 53.99  | 51.62 | -           | -      | -      | -     |
| Pgu svmp-a                 | 0.42           | 4.13   | 2.28  | -           | -      | -      | -     |
| Pgu svmp-b                 | 0              | 7.05   | 3.53  | -           | -      | -      | -     |
| plb                        | 1.06           | 5.52   | 3.29  | 17.96       | 146.36 | 82.16  | 20.76 |
| vegf-a                     | 0.88           | 0.22   | 0.55  | 1.01        | 0.86   | 0.94   | -     |
| vegf-b                     | 2.37           | 4.97   | 3.67  | 3.84        | 0.22   | 2.03   | 1.88  |
| vegf-c                     | 1.27           | 1.13   | 1.20  | 6.44        | 0.63   | 3.54   | 1.93  |
| vespryn                    | 2.58           | 1.47   | 2.03  | 4.97        | 5.07   | 5.02   | -     |
| waprin                     | 72.16          | 34.98  | 53.57 | -           | -      | -      | -     |



**Table S9.** Transcript abundance estimation values given in FPKM for each Painted saw-scaled viper (*Echis coloratus*) tissue. See methods section in the main text for further explanation.

| Gene              | Venom gland |          |           |         |           | Scent gland |        |        | Skin  |        |        |
|-------------------|-------------|----------|-----------|---------|-----------|-------------|--------|--------|-------|--------|--------|
|                   | 1           | 2        | 3         | 4       | Mean      | 1           | 2      | Mean   | 1     | 2      | Mean   |
| 3ftx-a            | 6.04        | 199.4    | 18.33     | 1,234.1 | 364.47    | 28.68       | 368.33 | 198.51 | 3.61  | 11.84  | 7.73   |
| 3ftx-b            | 0.15        | 3.42     | 316.94    | 367.29  | 171.95    | 1,491.4     | 1.21   | 746.31 | -     | -      | -      |
| ache transcript 1 | 6.02        | 10.07    | 3.61      | 6.68    | 6.60      | 4.75        | 3.4    | 4.07   | -     | -      | -      |
| ache transcript 2 | -           | -        | -         | -       | -         | 0.52        | 0.33   | 0.43   | 1.16  | 0.38   | 0.77   |
| complement c3     | 1.24        | 22.41    | 29.94     | 180.95  | 58.64     | 6.9         | 495.67 | 251.29 | 0.99  | 0.88   | 0.94   |
| crisp-a           | 0.04        | 0        | 0.96      | 1.45    | 0.61      | 0.12        | 72.76  | 36.44  | 35.54 | 0      | 17.77  |
| crisb-b           | 7,791.91    | 1,422.35 | 4,851.14  | 14.88   | 3,520.07  | -           | -      | -      | -     | -      | -      |
| crotamine-like    | 0           | 29.66    | 0         | 14.15   | 10.95     | -           | -      | -      | -     | -      | -      |
| ctl-a             | 1.23        | 127.05   | 50.80     | 741.17  | 230.06    | 1.34        | 168.13 | 84.73  |       |        |        |
| ctl-b             | 25,656.2    | 555.52   | 70,262.94 | 14.97   | 24,122.41 | -           | -      | -      | -     | -      | -      |
| ctl-c             | 4,202.8     | 319.98   | 10,294.96 | 7.1     | 3,706.21  | -           | -      | -      | -     | -      | -      |
| ctl-d             | 8,795.51    | 310.09   | 19,238.23 | 177.65  | 7,130.37  | -           | -      | -      | -     | -      | -      |
| ctl-e             | 2,694.03    | 393.99   | 2,814.17  | 1.33    | 1,475.88  | -           | -      | -      | -     | -      | -      |
| ctl-f             | 11,158.35   | 428.25   | 15,385    | 147.73  | 6,779.83  | -           | -      | -      | -     | -      | -      |
| ctl-g             | 5,605.99    | 13.86    | 14,010.27 | 13.48   | 4,910.90  | -           | -      | -      | -     | -      | -      |
| ctl-h             | 1,203.55    | 139.1    | 144.89    | 1.58    | 372.28    | -           | -      | -      | -     | -      | -      |
| ctl-i             | 1.73        | 0        | 1.46      | 0       | 0.80      | -           | -      | -      | -     | -      | -      |
| ctl-j             | 21,250.16   | 725.85   | 40,076.36 | 88.99   | 15,535.34 | -           | -      | -      | -     | -      | -      |
| ctl-k             | 1.29        | 1.54     | 4.85      | 0       | 1.92      | -           | -      | -      | -     | -      | -      |
| cystatin-e/m      | 12.38       | 158.77   | 5.11      | 19.45   | 48.93     | 270.94      | 36.2   | 153.57 | 55.64 | 186.06 | 120.85 |
| cystatin-f        | 0.1         | 2.7      | 0.38      | 4.01    | 1.79      | 0.22        | 2.95   | 1.59   | -     | -      | -      |
| dpp3              | 15.47       | 2.06     | 5.81      | 0.98    | 6.08      | 4.88        | 3.32   | 4.10   | 5.75  | 1.22   | 3.49   |
| dpp4              | 6.74        | 1.74     | 3.2       | 0.1     | 2.95      | 8.58        | 1.53   | 5.06   | 1.46  | 2.46   | 1.96   |
| esp-e1            | 3.27        | 10.52    | 6.17      | 16.39   | 9.09      | 12.87       | 14.55  | 13.71  | 2.46  | 14.82  | 8.64   |
| ficolin           | 0.15        | 55.94    | 10.76     | 241.81  | 77.17     | 4.3         | 117.87 | 61.09  | 4.55  | 6.4    | 5.48   |
| kallikrein        | 0           | 0.27     | 0.05      | 4.32    | 1.16      | 23.08       | 5.6    | 14.34  | 79.86 | 0      | 39.93  |

|                            |           |          |           |        |           |        |        |        |       |       |       |
|----------------------------|-----------|----------|-----------|--------|-----------|--------|--------|--------|-------|-------|-------|
| kunitz 1                   | 3.87      | 1.64     | 4.28      | 3.71   | 3.38      | 1.83   | 8.4    | 5.12   | 1.26  | 2.09  | 1.68  |
| kunitz 2                   | 176.97    | 58.15    | 128.89    | 78.54  | 110.64    | 83.65  | 134.46 | 109.06 | 54.04 | 8.95  | 31.49 |
| laao-a                     | 2.57      | 3.24     | 2.97      | 4.58   | 3.34      | 5.22   | 6.01   | 5.62   | 3.16  | 2.62  | 2.89  |
| laao-b1                    | 107.96    | 22.6     | 85.47     | 0      | 54.01     | -      | -      | -      | -     | -     | -     |
| laao-b2                    | 776.96    | 20.01    | 1,710.19  | 8.18   | 628.84    | -      | -      | -      | -     | -     | -     |
| lipa-a                     | 5,080.21  | 942.08   | 7,259.94  | 67.08  | 3,337.33  | 940.15 | 28.83  | 484.49 | 21.9  | 23.67 | 22.79 |
| lipa-b                     | 0         | 0        | 10.01     | 1.83   | 2.96      | 6.02   | 4.55   | 5.29   | -     | -     | -     |
| ngf                        | 730.19    | 1.98     | 1,370.8   | 0.3    | 525.82    | 0.08   | 0.28   | 0.18   | 0.28  | 0.88  | 0.58  |
| PLA <sub>2</sub> IIA-a     | -         | -        | -         | -      | -         | 0.21   | 2.48   | 1.35   | -     | -     | -     |
| PLA <sub>2</sub> IIA-b     | -         | -        | -         | -      | -         | 0.21   | 2.48   | 1.35   | -     | -     | -     |
| PLA <sub>2</sub> IIA-c     | 35,965.07 | 1,285.85 | 52,775.79 | 54.91  | 22,520.41 | -      | -      | -      | -     | -     | -     |
| PLA <sub>2</sub> IIA-d     | 3,312.33  | 141.9    | 3,253.47  | 0.89   | 1,677.15  | -      | -      | -      | -     | -     | -     |
| PLA <sub>2</sub> IIA-e     | 914.26    | 36.52    | 787.89    | 0      | 434.67    | -      | -      | -      | -     | -     | -     |
| PLA <sub>2</sub> group IIE | 27.5      | 15.45    | 5.21      | 0.32   | 12.12     | -      | -      | -      | -     | -     | -     |
| plb                        | 196.04    | 32.79    | 191.94    | 37.14  | 114.48    | 30.18  | 11.51  | 20.85  | 99.02 | 8.01  | 53.52 |
| renin                      | 27.39     | 2.53     | 17.88     | 0.5    | 12.08     | 0      | 0      | 0      | 0     | -     | -     |
| sp-a                       | 3,726.15  | 8.9      | 17,693.55 | 0      | 5,357.15  | -      | -      | -      | -     | -     | -     |
| sp-b                       | 7,471.91  | 17.79    | 23,258.4  | 0      | 7,687.03  | -      | -      | -      | -     | -     | -     |
| sp-c                       | 2,525.53  | 131.58   | 9,646.92  | 0      | 3,076.01  | -      | -      | -      | -     | -     | -     |
| sp-d                       | 2,079.25  | 1,205.26 | 1,108.08  | 1.2    | 1,098.45  | -      | -      | -      | -     | -     | -     |
| sp-e                       | 2,742.78  | 1,131.13 | 16,149.18 | 0      | 5,005.77  | -      | -      | -      | -     | -     | -     |
| sp-f                       | 39.22     | 115.65   | 254.5     | 0      | 102.34    | -      | -      | -      | -     | -     | -     |
| svmp-a                     | 7,881.36  | 2.45     | 14,258.65 | 68.91  | 5,552.84  | -      | -      | -      | -     | -     | -     |
| svmp-b                     | 49,469.53 | 2,682.3  | 8,163.04  | 158.76 | 15,118.41 | -      | -      | -      | -     | -     | -     |
| svmp-c                     | 149.97    | 29.9     | 1.45      | 2.32   | 45.91     | -      | -      | -      | -     | -     | -     |
| svmp-d                     | 19,267.95 | 845.58   | 3,839.82  | 84.51  | 6,009.47  | -      | -      | -      | -     | -     | -     |
| svmp-e                     | 2,772.71  | 472.08   | 2,641.5   | 243.87 | 1,532.54  | -      | -      | -      | -     | -     | -     |
| svmp-f                     | 0.66      | 0        | 1.23      | 8.04   | 2.48      | -      | -      | -      | -     | -     | -     |
| svmp-g                     | 2,772.71  | 472.08   | 2,641.5   | 243.87 | 1,532.54  | -      | -      | -      | -     | -     | -     |
| svmp-h                     | -         | -        | -         | -      | -         | 0.98   | 0      | 0.49   | -     | -     | -     |
| svmp-i                     | 16,986.24 | 974.82   | 20,413.99 | 705.04 | 9,770.02  | -      | -      | -      | -     | -     | -     |

|        |           |          |          |        |          |      |      |      |      |      |      |
|--------|-----------|----------|----------|--------|----------|------|------|------|------|------|------|
| svmp-j | 2,772.71  | 472.08   | 2,641.5  | 243.87 | 1,532.54 | -    | -    | -    | -    | -    | -    |
| svmp-k | 2,772.71  | 472.08   | 2,641.5  | 243.87 | 1,532.54 | -    | -    | -    | -    | -    | -    |
| svmp-l | -         | -        | -        | -      | -        | -    | -    | -    | 5.54 | 0    | 2.77 |
| svmp-m | 251.21    | 0        | 294.07   | 0      | 136.32   | -    | -    | -    | -    | -    | -    |
| svmp-n | 2,772.71  | 472.08   | 2,641.5  | 243.87 | 1,532.54 | 0.06 | 0    | 0.03 | -    | -    | -    |
| svmp-o | -         | -        | -        | -      | -        | 0    | 10.7 | 5.35 | -    | -    | -    |
| svmp-p | 1,273.16  | 103.84   | 2,546.07 | 4.67   | 981.94   | -    | -    | -    | -    | -    | -    |
| svmp-q | 15,356.06 | 2,247.57 | 3,951.69 | 313.12 | 5,467.11 | -    | -    | -    | -    | -    | -    |
| svmp-r | -         | -        | -        | -      | -        | 0.06 | 0    | 0.03 | -    | -    | -    |
| svmp-s | -         | -        | -        | -      | -        | 0.06 | 0    | 0.03 | -    | -    | -    |
| svmp-t | 4.4       | 0.68     | 25.3     | 1.56   | 7.99     | -    | -    | -    | -    | -    | -    |
| svmp-u | -         | -        | -        | -      | -        | 0    | 0.26 | 0.13 | -    | -    | -    |
| vegf-a | 7.64      | 0.27     | 4.1      | 0.96   | 3.24     | 2.62 | 0    | 1.31 | 0.57 | 1.18 | 0.88 |
| vegf-b | 1.05      | 1.36     | 0.57     | 2.12   | 1.28     | 4.92 | 5.83 | 5.38 | 0.47 | 3.21 | 1.84 |
| vegf-c | 1.47      | 1.74     | 1.02     | 1.92   | 1.54     | 2.37 | 2.06 | 2.22 | 0.57 | 1.81 | 1.19 |
| vegf-f | 294.23    | 362.01   | 90.07    | 0.62   | 186.73   | -    | -    | -    | -    | -    | -    |
| waprin | 0.35      | 19.91    | 9.82     | 73.58  | 25.92    | -    | -    | -    | 1.59 | 2.04 | 1.82 |