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| **Table S2 Genes responding to SM1 in R. chinensis** |
|  | Isoform\_id | RC1\_expression | RC2\_expression | RC3\_expression | SM\_RC1\_expression | SM\_RC2\_expression | SM\_RC3\_expression | logFC | Pvalue | FDR | NR\_Subject\_id | NR\_Subject\_description | KO\_ID|KO\_name|Hyperlink | BLAST results in NCBI | Abbreviation |
| Metabolism | RC\_transcript\_10586 | 5.55 | 0 | 0 | 0 | 0 | 0 | -22.63474454 | 6.95617E-09 | 2.55471E-06 | XP\_023706492.1 | UTP--glucose-1-phosphate uridylyltransferase isoform X1 [Cryptotermes secundus] | K00963|UGP2, galU, galF|http://www.genome.jp/dbget-bin/www\_bget?ko:K00963 |  | UGP |
| RC\_transcript\_15564 | 0 | 0 | 2.99 | 0 | 0 | 0 | -21.40951211 | 4.35025E-08 | 9.45558E-06 | XP\_023710871.1 | beta-glucuronidase-like isoform X1 [Cryptotermes secundus] | K01195|uidA, GUSB|http://www.genome.jp/dbget-bin/www\_bget?ko:K01195 |  | GUSB |
| RC\_transcript\_19718 | 0 | 0 | 20.54 | 0 | 0 | 0 | -23.5505613 | 1.66807E-09 | 8.88286E-07 | XP\_021934970.1 | 2-oxoglutarate dehydrogenase, mitochondrial isoform X1 [Zootermopsis nevadensis] | K00164|OGDH, sucA|http://www.genome.jp/dbget-bin/www\_bget?ko:K00164 |  | OGDH |
| RC\_transcript\_23551 | 0 | 0 | 24.51 | 0 | 0 | 0 | -23.09704182 | 3.40473E-09 | 1.45048E-06 | XP\_023710798.1 | phosphoglycerate mutase 2 [Cryptotermes secundus] | K01834|PGAM, gpmA|http://www.genome.jp/dbget-bin/www\_bget?ko:K01834 |  | PGAM |
| RC\_transcript\_18688 | 0 | 0 | 20.88 | 0 | 0 | 0 | -23.71014928 | 1.29379E-09 | 8.10561E-07 | XP\_023719217.1 | pyruvate kinase-like isoform X4 [Cryptotermes secundus] | K00873|PK, pyk|http://www.genome.jp/dbget-bin/www\_bget?ko:K00873 |  | PK |
| RC\_transcript\_13401 | 0 | 0 | 5.24 | 0 | 0 | 0 | -22.37119117 | 1.03943E-08 | 3.30461E-06 | XP\_021922242.1 | inositol-3-phosphate synthase isoform X1 [Zootermopsis nevadensis] | K01858|INO1, ISYNA1|http://www.genome.jp/dbget-bin/www\_bget?ko:K01858 |  | ISYNA |
| RC\_transcript\_15246 | 3.88 | 0 | 0 | 0 | 0 | 0 | -21.74839235 | 2.64252E-08 | 6.701E-06 | XP\_021939065.1 | V-type proton ATPase subunit B [Zootermopsis nevadensis] | K02147|ATPeV1B, ATP6B|http://www.genome.jp/dbget-bin/www\_bget?ko:K02147 |  | ATPeV1B |
| RC\_transcript\_19129 | 0 | 0 | 25 | 0 | 0 | 0 | -23.85916152 | 1.0191E-09 | 6.62748E-07 | AAV84268.1 | vacuolar atpase 16kDa subunit [Culicoides sonorensis] | K02155|ATPeV0C, ATP6L|http://www.genome.jp/dbget-bin/www\_bget?ko:K02155 | Vtype proton ATPase 16 kDa proteolipid subunit | ATPeV0C |
| RC\_transcript\_24835 | 0 | 0 | 11.11 | 0 | 0 | 0 | -21.58918056 | 3.34257E-08 | 7.73915E-06 | PNF36160.1 | hypothetical protein B7P43\_G10666 [Cryptotermes secundus] | K03964|NDUFB8|http://www.genome.jp/dbget-bin/www\_bget?ko:K03964 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8 | NDUFB8 |
| RC\_transcript\_5851 | 0 | 0 | 1.86 | 0 | 0 | 0 | -21.64695227 | 3.06979E-08 | 7.34714E-06 | XP\_023710822.1 | lissencephaly-1 homolog [Cryptotermes secundus] | K16794|PAFAH1B1, LIS1|http://www.genome.jp/dbget-bin/www\_bget?ko:K16794 |  | LIS |
| RC\_transcript\_16451 | 0 | 0 | 3.13 | 0 | 0 | 0 | -21.39278301 | 4.45797E-08 | 9.59183E-06 | XP\_023720103.1 | guanine deaminase-like isoform X1 [Cryptotermes secundus] | K01487|E3.5.4.3, guaD|http://www.genome.jp/dbget-bin/www\_bget?ko:K01487 |  | GDA |
| RC\_transcript\_4156 | 0 | 4 | 0 | 0 | 0 | 0 | -22.70680922 | 6.22827E-09 | 2.36908E-06 | PNF40356.1 | cAMP-specific 3',5'-cyclic phosphodiesterase, isoform F [Cryptotermes secundus] | K13293|PDE4|http://www.genome.jp/dbget-bin/www\_bget?ko:K13293 |  | PDE |
| RC\_transcript\_11673 | 0 | 3.31 | 0.01 | 0 | 0 | 0 | -21.73567936 | 2.69257E-08 | 6.74758E-06 | KDR20892.1 | hypothetical protein L798\_04756, partial [Zootermopsis nevadensis] | K00933|E2.7.3.2|http://www.genome.jp/dbget-bin/www\_bget?ko:K00933 | arginine kinase | AK |
| RC\_transcript\_5141 | 4.97 | 4.02 | 1.61 | 1.13 | 1.15 | 1.12 | -1.617478766 | 0.000753731 | 0.049947504 | XP\_023712909.1 | ornithine decarboxylase-like [Cryptotermes secundus] | K01581|E4.1.1.17, ODC1, speC, speF|http://www.genome.jp/dbget-bin/www\_bget?ko:K01581 |  | ODC |
| RC\_transcript\_20745 | 7.14 | 0 | 0 | 0 | 0 | 0 | -21.90776284 | 2.08566E-08 | 5.7697E-06 | XP\_021936872.1 | juvenile hormone epoxide hydrolase 1-like [Zootermopsis nevadensis] | K10719|JHEH|http://www.genome.jp/dbget-bin/www\_bget?ko:K10719 |  | JHEH |
| RC\_transcript\_16113 | 4.39 | 0 | 0 | 0 | 0 | 0 | -21.80028038 | 2.44695E-08 | 6.33442E-06 | XP\_023724120.1 | dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit [Cryptotermes secundus] | K12670|WBP1|http://www.genome.jp/dbget-bin/www\_bget?ko:K12670 |  | DDOST |
| Immune | RC\_transcript\_20068 | 10.85 | 24.25 | 11.2 | 4.33 | 5.91 | 5.55 | -1.508192026 | 0.000240331 | 0.021509586 | XP\_023724387.1 | hemolymph lipopolysaccharide-binding protein-like isoform X4 [Cryptotermes secundus] | \* |  | LBP |
| RC\_transcript\_20278 | 16.33 | 15.58 | 12.17 | 8.18 | 6.04 | 6.36 | -1.080068061 | 1.56257E-06 | 0.000237745 | XP\_023727848.1 | galectin-3-like [Cryptotermes secundus] | \* |  | Gal-3 |
| RC\_transcript\_26038 | 0 | 0 | 44.97 | 0 | 0 | 0 | -22.90846682 | 4.56381E-09 | 1.83422E-06 | AFZ78835.1 | apolipophorin-III isoform 2 [Coptotermes formosanus] | \* |  | apoLp-Ⅲ |
| RC\_transcript\_26574 | 240.82 | 288.6 | 295.39 | 144.65 | 40.31 | 85.8 | -1.613866259 | 0.000276444 | 0.024014781 | XP\_013420610.2 | uncharacterized protein LOC106180967 [Lingula anatina] | K07937|ARF1|http://www.genome.jp/dbget-bin/www\_bget?ko:K07937 | ADP-ribosylation factor | ARF |
| RC\_transcript\_1885 | 0.21 | 0.14 | 0.2 | 0 | 0 | 0 | -6.160321473 | 0.000229923 | 0.020752464 | XP\_023713191.1 | cation-independent mannose-6-phosphate receptor isoform X1 [Cryptotermes secundus] | K06564|IGF2R|http://www.genome.jp/dbget-bin/www\_bget?ko:K06564 |  | IGF2R |
| RC\_transcript\_15246 | 3.88 | 0 | 0 | 0 | 0 | 0 | -21.74839235 | 2.64252E-08 | 6.701E-06 | XP\_021939065.1 | V-type proton ATPase subunit B [Zootermopsis nevadensis] | K02147|ATPeV1B, ATP6B|http://www.genome.jp/dbget-bin/www\_bget?ko:K02147 |  | ATPeV1B |
| RC\_transcript\_19129 | 0 | 0 | 25 | 0 | 0 | 0 | -23.85916152 | 1.0191E-09 | 6.62748E-07 | AAV84268.1 | vacuolar atpase 16kDa subunit [Culicoides sonorensis] | K02155|ATPeV0C, ATP6L|http://www.genome.jp/dbget-bin/www\_bget?ko:K02155 | Vtype proton ATPase 16 kDa proteolipid subunit | ATPeV0C |
| RC\_transcript\_5926 | 3.46 | 1.76 | 0 | 0 | 0 | 0 | -8.926800112 | 0.000625762 | 0.043555686 | XP\_021933582.1 | lysosomal-associated transmembrane protein 4A [Zootermopsis nevadensis] | K12387|LAPTM|http://www.genome.jp/dbget-bin/www\_bget?ko:K12387 |  | LAPTM |
| RC\_transcript\_15564 | 0 | 0 | 2.99 | 0 | 0 | 0 | -21.40951211 | 4.35025E-08 | 9.45558E-06 | XP\_023710871.1 | beta-glucuronidase-like isoform X1 [Cryptotermes secundus] | K01195|uidA, GUSB|http://www.genome.jp/dbget-bin/www\_bget?ko:K01195 |  | GUSB |
| RC\_transcript\_6887 | 4.28 | 2.81 | 5.41 | 1.25 | 1.86 | 1.58 | -1.413469572 | 0.000566723 | 0.040995231 | PNF32288.1 | hypothetical protein B7P43\_G16846, partial [Cryptotermes secundus] | K01373|CTSF|http://www.genome.jp/dbget-bin/www\_bget?ko:K01373 | cathepsin F | CTSF |
| RC\_transcript\_20097 | 0 | 0 | 15.41 | 0 | 0 | 0 | -23.05469776 | 3.63691E-09 | 1.48981E-06 | BAG48838.1 | hexamerin 1 [Reticulitermes speratus] | \* |  | Hex-1 |
| RC\_transcript\_23309 | 73.96 | 281.02 | 498.68 | 69.41 | 33.49 | 6.91 | -2.96710802 | 0.000687253 | 0.046621565 | AAU20852.2 | hexamerin II [Reticulitermes flavipes] | \* |  | Hex-2 |
| RC\_transcript\_12775 | 0.83 | 0.97 | 0.33 | 0 | 0 | 0 | -6.972929615 | 1.43362E-05 | 0.001862043 | AAN03488.1 | transferrin [Mastotermes darwiniensis] | \* |  | Tf1 |
| RC\_transcript\_4124 | 49.64 | 40.74 | 56.43 | 28.59 | 14.42 | 24.49 | -1.124164609 | 0.000206938 | 0.018999938 | AAN03488.1 | transferrin [Mastotermes darwiniensis] | \* |  | Tf2 |
| Signal transduction | RC\_transcript\_24406 | 0 | 0 | 206.71 | 0 | 0 | 0 | -25.75081785 | 4.36468E-11 | 6.15902E-08 | XP\_023727041.1 | ADP,ATP carrier protein [Cryptotermes secundus] | K05863|SLC25A4S, ANT|http://www.genome.jp/dbget-bin/www\_bget?ko:K05863 |  | ANT |
| RC\_transcript\_1461 | 1.25 | 0 | 0 | 0 | 0 | 0 | -21.61440872 | 3.22061E-08 | 7.62248E-06 | XP\_023711709.1 | sodium/potassium-transporting ATPase subunit alpha isoform X5 [Cryptotermes secundus] | K01539|ATP1A|http://www.genome.jp/dbget-bin/www\_bget?ko:K01539 |  | ATP1A |
| RC\_transcript\_4156 | 0 | 4 | 0 | 0 | 0 | 0 | -22.70680922 | 6.22827E-09 | 2.36908E-06 | PNF40356.1 | cAMP-specific 3',5'-cyclic phosphodiesterase, isoform F [Cryptotermes secundus] | K13293|PDE4|http://www.genome.jp/dbget-bin/www\_bget?ko:K13293 |  | PDE |
| RC\_transcript\_13791 | 0 | 0 | 11.84 | 0 | 0 | 0 | -22.34035275 | 1.08151E-08 | 3.33872E-06 | PNF42561.1 | hypothetical protein B7P43\_G05427 [Cryptotermes secundus] | K04437|FLNA|http://www.genome.jp/dbget-bin/www\_bget?ko:K04437 | filamin-A | FLNA |
| RC\_transcript\_26574 | 240.82 | 288.6 | 295.39 | 144.65 | 40.31 | 85.8 | -1.613866259 | 0.000276444 | 0.024014781 | XP\_013420610.2 | uncharacterized protein LOC106180967 [Lingula anatina] | K07937|ARF1|http://www.genome.jp/dbget-bin/www\_bget?ko:K07937 | ADP-ribosylation factor | ARF |
| RC\_transcript\_15246 | 3.88 | 0 | 0 | 0 | 0 | 0 | -21.74839235 | 2.64252E-08 | 6.701E-06 | XP\_021939065.1 | V-type proton ATPase subunit B [Zootermopsis nevadensis] | K02147|ATPeV1B, ATP6B|http://www.genome.jp/dbget-bin/www\_bget?ko:K02147 |  | ATPeV1B |
| Genetic information | RC\_transcript\_2742 | 0 | 0 | 1.44 | 0 | 0 | 0 | -21.64695227 | 3.06979E-08 | 7.34714E-06 | XP\_021920764.1 | 5'-3' exoribonuclease 1 isoform X1 [Zootermopsis nevadensis] | K12618|XRN1, SEP1, KEM1|http://www.genome.jp/dbget-bin/www\_bget?ko:K12618 |  | XRN1 |
| RC\_transcript\_22572 | 0 | 0 | 13.27 | 0 | 0 | 0 | -22.4805111 | 8.80385E-09 | 2.97668E-06 | AGM32529.1 | BTG1-like protein [Coptotermes formosanus] | K14443|TOB|http://www.genome.jp/dbget-bin/www\_bget?ko:K14443 |  | TOB |
| RC\_transcript\_12901 | 0 | 0 | 6.52 | 0 | 0 | 0 | -22.72021169 | 6.10156E-09 | 2.36308E-06 | PNF15393.1 | Eukaryotic translation initiation factor 3 subunit F-1 [Cryptotermes secundus] | K03249|EIF3F|http://www.genome.jp/dbget-bin/www\_bget?ko:K03249 |  | EIF3F |
| RC\_transcript\_16113 | 4.39 | 0 | 0 | 0 | 0 | 0 | -21.80028038 | 2.44695E-08 | 6.33442E-06 | XP\_023724120.1 | dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit [Cryptotermes secundus] | K12670|WBP1|http://www.genome.jp/dbget-bin/www\_bget?ko:K12670 |  | DDOST |
| RC\_transcript\_13048 | 0 | 0 | 3.22 | 0 | 0 | 0 | -21.34538124 | 4.74775E-08 | 1.00131E-05 | XP\_023708319.1 | transcription initiation factor TFIID subunit 12 isoform X2 [Cryptotermes secundus] | K03126|TAF12|http://www.genome.jp/dbget-bin/www\_bget?ko:K03126 |  | TAF12 |
| RC\_transcript\_27362 | 33.68 | 46.78 | 41.93 | 17.77 | 7.77 | 15.16 | -1.57981947 | 0.000551187 | 0.040346529 | XP\_023055329.1 | 60S ribosomal protein L31-like [Piliocolobus tephrosceles] | K02910|RP-L31e, RPL31|http://www.genome.jp/dbget-bin/www\_bget?ko:K02910 |  | RPL31 |