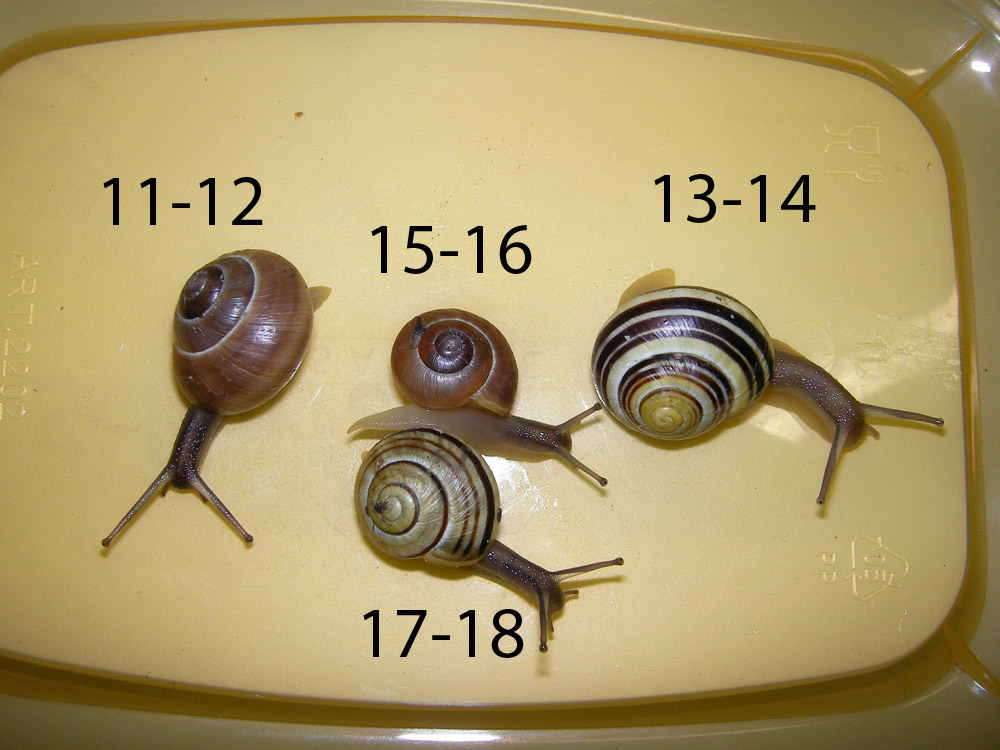
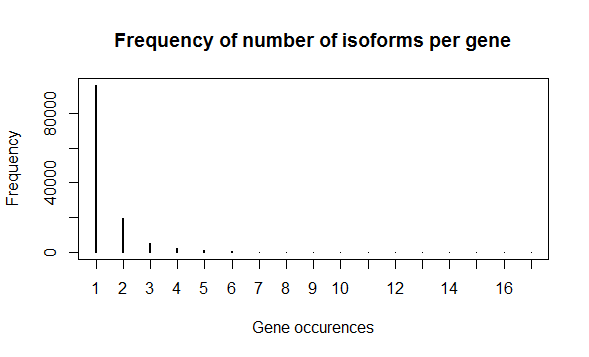
Supplementary material to:

**Candidate genes for shell colour polymorphism in *Cepaea nemoralis***

Jesse Kerkvliet, Tjalf de Boer, Menno Schilthuizen, Ken Kraaijeveld



**Figure S1** Snails used in this study.



**Figure S2** Frequency distribution of the number of isoforms per gene.

**Table S1** Overview of the alignment statistics for each sample.

|  |  |  |
| --- | --- | --- |
| Sample | Reads aligned at least once | Properly paired reads |
| 11 | 38,337,898 (53.6%) | 33,244,620 (46.4%) |
| 12 | 52,000,948 (72.6%) | 45,560,146 (63.6%) |
| 13 | 50,780,782 (65.9%) | 44,080,380 (57.2%) |
| 14 | 47,651,676 (71,4%) | 41,350,714 (62.0%) |
| 15 | 47,852,396 (74.9%) | 42,796,990 (67.0%) |
| 16 | 54,298,143 (78.1%) | 49,089,688 (70.6%) |
| 17 | 91,448,178 (75.1%) | 82,673,624 (67.9%) |
| 18 | 106,823,206 (76.6%) | 96,221,182 (69.0%) |

**Table S2** Number of SNPS after filtering on sequence depth (>10) for each sample.

|  |  |
| --- | --- |
| Sample | SNPs |
| 11 | 81,233 |
| 12 | 132,825 |
| 13 | 135,232 |
| 14 | 117,458 |
| 15 | 155,511 |
| 16 | 98,933 |
| 17 | 200,068 |
| 18 | 155,360 |
| Total | 1,076619 |
| Total (unique) | 461,799 |

**Table S3** Annotations and predicted SNP effects. For each transcript, we report only the best hit based on e-value.

|  |  |  |
| --- | --- | --- |
| **Contig name** | **Functional annotationKolom2** | **SNPEff effect** |
| c264073\_g1\_i1 | Camelus bactrianus mucin-2-like | frameshift\_variant&stop\_gained |
| inframe\_insertion |
| c280576\_g1\_i1 | Biomphalaria glabrata glycine and methionine-rich –like | synonymous\_variant |
| c280925\_g1\_i2 | Parasteatoda tepidariorum keratin-associated 6-2-like | synonymous\_variant |
| c321814\_g1\_i1 | Euhadra herklotsi mRNA for Dermatopontin1 | intergenic\_region |
| c323639\_g1\_i1 | Aplysia californica multiple coagulation factor deficiency | synonymous\_variant |
| 5\_prime\_UTR\_variant |
| c344946\_g1\_i1 | Physa acuta G-type lysozyme mRNA, complete cds | missense\_variant |
| c348138\_g1\_i1 | Biomphalaria glabrata annexin A7-like | chromosome\_number\_variation |
| c350256\_g1\_i1 | Anas platyrhynchos BPI fold-containing family B member 3 | synonymous\_variant |
| c354311\_g1\_i1 | Biomphalaria glabrata sorting nexin-5-like | 5\_prime\_UTR\_variant |
| c355427\_g1\_i1 | Euhadra herklotsi mRNA for Dermatopontin1 | stop\_gained |
| missense\_variant |
| c356371\_g1\_i1 | Aplysia californica tyramine beta-hydroxylase-like | missense\_variant |
| c357948\_g1\_i2 | Aplysia californica nucleoside-diphosphatase | missense\_variant |
| c358175\_g7\_i1 | AF109924Helix pomatia sulfatase 1 precursor | intergenic\_region |
| c358705\_g4\_i1 | Aplysia californica carbonic anhydrase 1-like | stop\_gained |
| missense\_variant |
| c358903\_g6\_i2 | Aplysia californica toll-like receptor 3 | 5\_prime\_UTR\_variant |
| c360655\_g1\_i2 | AF109924Helix pomatia sulfatase 1 precursor | disruptive\_inframe\_insertion |
| missense\_variant |
| synonymous\_variant |
| 5\_prime\_UTR\_premature\_start\_codon\_gain\_variant |
| c360728\_g7\_i2 | Aplysia californica UPF0462 C4orf33 homolog | missense\_variant |
| c361453\_g1\_i1 | Biomphalaria glabrata peroxidasin-like | 3\_prime\_UTR\_variant |
| missense\_variant |
| c361590\_g1\_i1 | Aplysia californica aquaporin-4-like | missense\_variant |
| synonymous\_variant |
| c362006\_g8\_i2 | Helix pomatia Cd-specific metallothionein gene | intergenic\_region |
| c362358\_g3\_i1 | AF109924Helix pomatia sulfatase 1 precursor | intergenic\_region |
| c362887\_g2\_i1 | AF109924Helix pomatia sulfatase 1 precursor | 3\_prime\_UTR\_variant |
| c363384\_g6\_i1 | Helix pomatia Cd-specific metallothionein gene | intergenic\_region |
| c363875\_g1\_i3 | Lepisosteus oculatus ficolin-2-like | missense\_variant |
| c365069\_g1\_i1 | Biomphalaria glabrata tyrosinase | 5\_prime\_UTR\_variant |
| c365850\_g1\_i1 | Biomphalaria glabrata formin BNR1-like | missense\_variant |
| synonymous\_variant |
| c366293\_g1\_i1 | Biomphalaria glabrata mucin-2-like | missense\_variant |
| c367319\_g1\_i1 | Aplysia californica sodium-coupled monocarboxylate transporter | 5\_prime\_UTR\_variant |
| c368154\_g1\_i1 | Lethenteron camtschaticum clone BAC 238J5 homeobox Hox-delta3 (Hox-delta3) and homeobox Hox-delta2 (Hox-delta2) genes | missense\_variant |
| 3\_prime\_UTR\_variant |
| c368572\_g1\_i1 | Aplysia californica epithelial splicing regulatory 1-like | synonymous\_variant |
| c368766\_g1\_i1 | Aplysia californica mesenchyme-specific cell surface glyco -like | missense\_variant |
| c369092\_g1\_i1 | Biomphalaria glabrata perivitellin-2 67 kDa subunit-like | synonymous\_variant |
| missense\_variant |
| c369237\_g1\_i2 | Biomphalaria glabrata amine oxidase | synonymous\_variant |
| c369245\_g1\_i1 | Helix pomatia Cd-specific metallothionein gene | 3\_prime\_UTR\_variant |
| synonymous\_variant |
| missense\_variant |
| c369506\_g2\_i1 | Aplysia californica solute carrier family 2, facilitated glucose transporter member | 5\_prime\_UTR\_premature\_start\_codon\_gain\_variant |
| 5\_prime\_UTR\_variant |
| c369765\_g4\_i2 | Biomphalaria glabrata ferric-chelate reductase 1-like | synonymous\_variant |
| c369942\_g2\_i3 | Aplysia californica ATP-binding cassette sub-family G member 2-like | missense\_variant |
| c371799\_g2\_i1 | Biomphalaria glabrata sushi, von Willebrand factor type A, EGF and pentraxin domain-containing 1-like | synonymous\_variant |

**Table S4** Transcripts with hits on the four RAD tags near the supergene.

|  |  |  |
| --- | --- | --- |
| RAD tag ID | Contig | Blastn annotation |
| Cne\_RAD02 | c364559\_g2\_i4 | None |
| Cne\_RAD02 | c366252\_g1\_i1 | None |
| Cne\_RAD02 | c366252\_g1\_i2 | None |
| Cne\_RAD02 | c366252\_g1\_i3 | None |
| Cne\_RAD02 | c366252\_g1\_i6 | None |
| Cne\_RAD08 | c365766\_g3\_i1 | *Helix pomatia* methallothionein |
| Cne\_RAD08 | c363423\_g3\_i3 | *Helix pomatia* methallothionein |
| Cne\_RAD08 | c337572\_g1\_i1 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c360230\_g9\_i1 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c360230\_g8\_i1 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c367196\_g3\_i3 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c367196\_g3\_i2 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c367196\_g3\_i1 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c325228\_g1\_i2 | *Helix pomatia* methallothionein |
| Cne\_RAD10 | c325228\_g1\_i1 | *Helix pomatia* methallothionein |