Supplemental Table 1. Primers used in qPCR studies.

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| **Gene Name**  **(*Gene symbol*)**  **1(Gene ID)** | **2DE groups** | **3Nucleotide sequence (5’-3’)** | **4Efficiency**  **(%)** | **Amplicon**  **size (bp)** |
| activating transcription factor 3 (*atf3*) (CN\_DN168212\_c0\_g1\_i7) | HPE vs HPC A2 | F: CACCAAATGCAGGAACAAGA | 97.9 | 102 |
| R: CGCTGAATTTCCGTCTTGAG |
| AF-10 protein (*af10*) (HL\_DN75831\_c2\_g2\_i5) | HCE vs HCC A1 | F: CACACGTGGTTTGTGCTCTT | 100.3 | 149 |
| R: GACTGCTCTGCTCTCCTTGC |
| argonaute 2 (*ago2*) (CN\_DN165091\_c1\_g2\_i1) | HPE vs HPC A2 | F: AAGGCACCACAAGGTTATGC | 104.2 | 149 |
| R: TCCTCGGGCAATCTTACAAC |
| ATP-dependent RNA helicase DDX31 (*ddx31*) (CN\_DN179580\_c1\_g1\_i1) | HPE vs HPC A2 | F: AGAGCCTTCAAGAGCAGCAG | 86.0 | 103 |
| R: AGACTCATGCCTGCCAGTTT |
| ATP-dependent RNA helicase DDX46 (*ddx46*) (CN\_DN185084\_c5\_g3\_i4) | HPC vs HCC | F: TGCTGAAGTTTTCCGAGCTT | 101.1 | 105 |
| R: TTCTTGCCTTCTCCTTCCAA |
| ATP synthase F1 subunit beta (*atp5f1b*) (HP\_DN123930\_c2\_g1\_i1) | HPE vs HPC A1 | F: TCCTAGTGACGGGGATCAAG | 104.4 | 102 |
| R: TCAGAACAGTCTTGCCAACG |
| broad complex protein (*brc*) (HP\_DN112978\_c0\_g1\_i3) | HPE vs HPC A1 | F: GTGCCAAGAGCTTTCAGTCC | 103.1 | 147 |
| R: CCTTGCCATGGACTGTGATA |
| C-type lectin (*clec*) (CN\_DN173887\_c0\_g3\_i7) | HCE vs HCC A2 | F: CCCTGGTAGTGCTGCTTCTC | 93.4 | 123 |
| R: AGGAGTCCGCCAGAATACAA |
| C-type lectin (*clec*) (CN\_DN185002\_c3\_g4\_i3) | HCE vs HCC A2 | F: AAGTAGGCACCATGGCAGAG | 96.3 | 135 |
| R: TCACCTGTGTGGGGTTGTTA |
| cathepsin A (*ctsa*) (CN\_DN169514\_c8\_g1\_i1) | HPE vs HPC A2 | F: CTATGCAACGACGAGGTGAA | 94.1 | 100 |
| R: TGTAGATGAGTCCCCGAACC |
| cathepsin D (*ctsd*) (CN\_DN168300\_c3\_g5\_i1) | HCE vs HCC A2 | F: CAGCTCCACAATCGCTATGA | 98.6 | 117 |
| R: CACGTGGTCACTTGAGAGGA |
| cathepsin L (*ctsl*) (CN\_DN185508\_c3\_g3\_i3) | HCE vs HCC A2 | F: AGGAACTGCCCACCACTATG | 91.3 | 142 |
| R: ACTAGCTTTCCGGTGCTGAA |
| cationic amino acid transporter (*cat*) (HP\_DN125120\_c1\_g1\_i8) | HPE vs HPC A1 | F: GCCTGCTGTGACCTCTTCTC | 92.8 | 108 |
| R: TACACCTGTCCCGAACACTG |
| chitinase 2 (*chi2*) (CN\_DN181507\_c2\_g1\_i1) | HCE vs HCC A2 | F: GGTGGACCGTAGTGAACGA | 94.1 | 114 |
| R: ACTCAGCCTTGGTCTTGACG |
| chitinase 3 (*chi3*) (CN\_DN179961\_c3\_g3\_i1) | HCE vs HCC A2 | F: GGCGTGGTGATGTGCTACTA | 97.4 | 103 |
| R: AGACGTAGTGCGTGCAGAGA |
| chromodomain-helicase-DNA-binding protein 1 (*chd1*) (HP\_DN116676\_c1\_g1\_i16) | HPE vs HPC A1 | F: GCAGTGCCCAGCTCTTAAAC | 104.1 | 122 |
| R: GCCAATTAACCCCTTCCATT |
| clotting factor B (*cfb*) (CN\_DN182827\_c0\_g1\_i18) | HPC vs HCC | F: CTCCATTGCTTCCTCTTTCG | 99.2 | 150 |
| R: AATGTCGTGGTAGGCCTGAG |
| cuticle protein CBM (*cbm*) (HP\_DN85003\_c0\_g1\_i1) | HPE vs HPC A1 | F: AATGCGGTCAATGTCAAGTG | 100.8 | 97 |
| R: TACAGGCGCAGTACATGGAG |
| cytochrome P450 CYP330A1 (*cyp330a1*) (CN\_DN185431\_c1\_g1\_i13) | HPC vs HCC | F: GAAGCGTGACTCCATCATCA | 101.8 | 106 |
| R: CAGTGTGCGCAGGGTAAAC |
| DNA-directed RNA polymerase I subunit RPA12 (*rpa12*) (HP\_DN111005\_c0\_g2\_i2) | HPE vs HPC A1 | F: GGATCCCCATCGAGAGTGTA | 98.5 | 90 |
| R: ATGGTCTGTCCCTCATCTGC |

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| dnaJ homolog subfamily C member 5 (*dnajc5*) (CN\_DN173656\_c0\_g1\_i13) | HPE vs HPC A2 | F: AGAAGACCTACCGCAAGCTG | 95.4 | 150 |
| R: GGGAGCCGTAGTTGTCGTAA |
| dual oxidase maturation factor 1 (*duoxa1*) (HL\_DN99704\_c4\_g3\_i1) | HCE vs HCC A1 | F: TCCAAAGGGCCTTCAGACAC | 100.3 | 133 |
| R: TGAGCGTACCACCCAGAGTA |
| E3 ubiquitin-protein ligase TRIM38 (*trim38*) (CN\_DN182146\_c3\_g2\_i1) | HPC vs HCC | F: AACCAATTTGAGTGCGAAAA | 94.0 | 105 |
| R: ATGGCCAGAGTAGAGGCAGA |
| gamma-interferon induced thiol reductase GILT1 (*gilt1*) (CN\_DN183562\_c3\_g1\_i1) | HPC vs HCC | F: TGAATTGCCTTCTCTCAGCA | 97.0 | 114 |
| R: TTTGACCCTCCAAAGAGCTG |
| gamma-interferon induced thiol reductase GILT3 (*gilt3*) (CN\_DN171981\_c0\_g1\_i3) | HPC vs HCC | F: TGGATTACGTGCCATGGATA | 102.2 | 108 |
| R: TATCCCCCTTGTACGTCTCG |
| glutathione peroxidase 3 (*gpx3*) (CN\_DN157621\_c0\_g1\_i3) | HCE vs HCC A2 | F: CGGCCAACGAACTTATGAAT | 95.4 | 115 |
| R: AAGATTGGGTCCTCGTCCTT |
| hemocyanin subunit 6 (*hcy6*)  (CN\_DN180669\_c4\_g1\_i1) | HCE vs HCC A2 | F: ATGAACATCCACCACGTCAC | 92.9 | 106 |
| R: GGACCCAGAAGAAGCTCTCA |
| hemocyanin C chain (*hcyc*)  (CN\_ DN173241\_c0\_g2\_i1) | HCE vs HCC A2 | F: GCTGCACGAAAACACTTCCT | 99.5 | 108 |
| R: ATACGGTCATCGTCAACACG |
| histone-lysine N-methyltransferase 2D (*kmt2d*) (HL\_DN95434\_c3\_g1\_i18) | HCE vs HCC A1 | F: ACGCAACCCATTATTTGAGC | 106.1 | 102 |
| R: CGTATGCCGTGGTACCTCTT |
| integral membrane protein DGCR2/IDD (*dgcr2, idd*) (HP\_DN109964\_c9\_g1\_i4) | HPE vs HPC A1 | F: TTTGCCTGGACGACATGTTA | 94.9 | 132 |
| R: GCCTGTGAATGAGGAAGAGC |
| integrin, subunit beta (*itgb*) (HL\_DN74060\_c3\_g6\_i1) | HCE vs HCC A1 | F: CCAGGAACCTGACTGGAGAG | 93.7 | 110 |
| R: CTCATGGACATCGCTTTCAC |
| interferon regulatory factor (*irf*)  (CN\_DN180562\_c0\_g1\_i7) | HCE vs HCC A2 | F: GAGCTGAAGCAGAGCCTGAG | 100.3 | 106 |
| R: TGCTCTCACCTGTGAACCTG |
| interferon regulatory factor 2-binding protein (*irf2bp*) (CN\_DN179152\_c4\_g1\_i10) | HPC vs HCC | F: ACACCCACTTCGTCCAGTG | 88.3 | 111 |
| R: CGCTCGGACAGTACACCTC |
| interleukin 16 (*il16*) (CN\_DN175539\_c3\_g1\_i10) | HPC vs HCC | F: CCATTTCTCCTCCCAGTTCA | 101.6 | 141 |
| R: TGTCACTGTCTTCGGCTCTG |
| leucine-rich repeat-containing protein 24 (*lrrc24*) (CN\_DN174586\_c3\_g1\_i1) | HPC vs HCC | F: CGCAAAGGAGTTCTCTACGG | 95.9 | 146 |
| R: TGTCGTGCAGGTACAGCTTC |
| macrophage mannose receptor 1 (*mrc1*) (CN\_DN185070\_c2\_g1\_i1) | HPC vs HCC | F: ATGTATTTGCCTGGGCTGAC | 90.7 | 130 |
| R: TTCCACCGGAAGTCTTTGAC |
| myoferlin (*myof*) (CN\_DN187140\_c4\_g1\_i13) | HPE vs HPC A2 | F: GGAGAACCGCTACCTTACCC | 98.8 | 149 |
| R: ACAGAGGTCCCTCCAGGTTT |
| period circadian regulator isoform 1 (*per1*) (CN\_DN187046\_c1\_g1\_i11) | HCE vs HCC A2 | F: ACATTGGCATCTTCCTGGAC | 93.4 | 139 |
| R: TTACTGGGGTCCTTGTACGC |
| programmed cell death 6-interacting protein (*pdcd6ip*) (CN\_DN173756\_c3\_g1\_i1) | HPE vs HPC A2 | F: GCTGGAGGAGTGTGATAGGC | 93.3 | 138 |
| R: CTGTATTTCTGGGCGTTGGT |
| pyruvate dehydrogenase (acetyl-transferring) kinase, mitochondrial (*pdk2*) (HL\_DN86705\_c3\_g1\_i13) | HCE vs HCC A1 | F: AGTTCAACCCTTCGCCTCTT | 100.9 | 102 |
| R: GCACAGGCAGTTCCTTCTTC |
| radical S-adenosyl methionine domain-containing protein 1, mitochondrial (*rsad1*) (CN\_DN181710\_c2\_g2\_i2) | HPC vs HCC | F: TGTCCATTGGCATACAGAGC | 92.7 | 123 |
| R: TGGAGACTCTGTTGGGGAAG |
| regulator of G-protein signaling 2 (*rgs2*) (HL\_DN74312\_c5\_g2\_i2) | HCE vs HCC A1 | F: AATACGGACAGGCGTTGTTC | 102.4 | 104 |
| R: AGTAACGCGGGTCTTCTTGA |
| retinol dehydrogenase 13 (*rdh13*) (HL\_DN83898\_c3\_g2\_i9) | HCE vs HCC A1 | F: GATGGCCATGGTTATGCTTC | 90.4 | 119 |
| R: ATTTCCCAGACACCCCTTCT |
| rho GTPase-activating protein 45 (*arhgap45*) (CN\_DN183466\_c0\_g2\_i13) | HPC vs HCC | F: TCTACCGGGTGTCTGGAGTC | 94.9 | 138 |
| R: GTAGTTGGCGGAGGTACAGC |
| sacsin (*sacs*) (CN\_DN143706\_c0\_g1\_i1) | HPC vs HCC | F: TGAGCAGACATTCGATGAGC | 98.4 | 122 |
| R: AGGCTTCGGAGAGGAATGTT |
| sacsin (*sacs*)  (CN\_DN144441\_c0\_g1\_i1) | HPC vs HCC | F: ACATTGTGTGTGCCGAGAAG | 92.9 | 108 |
| R: GCTGGGTGGGTATGCAAG |
| sacsin (*sacs*) (CN\_DN162290\_c0\_g1\_i1) | HPC vs HCC | F: CGGCAGTCTGCGTCTAGGATAT | 97.5 | 87 |
| R: ACTGGCCTCCACTTTGAATG |
| sacsin (*sacs*) (CN\_DN186766\_c3\_g1\_i13) | HPC vs HCC | F: AGACACTGCCTTGACCTGCT | 94.9 | 152 |
| R: GTTTACTGCTCTCCTGTCCACC |
| sacsin (*sacs*) (CN\_DN186766\_c3\_g1\_i2) | HPC vs HCC | F: TCACACCATGCGTATCACCA | 88.1 | 117 |
| R: TAGGAGCAGGTGAGGGCAGT |
| sel-1 1 protein (*sel1l*) (HP\_DN115550\_c6\_g2\_i4) | HPE vs HPC A1 | F: TTGTATGAGGCAGCCATGAG | 94.4 | 94 |
| R: GATGACCAAGTTCAGCAGCA |
| selenium-dependent glutathione peroxidase (*gpx5*) (CN\_DN169580\_c4\_g1\_i5) | HCE vs HCC A2 | F: ACTTGGAGATCCTCGGGTTT | 95.7 | 136 |
| R: TTGGTGAACATGGTGAAGGA |
| signal transducer and activator of transcription (*stat*) (CN\_DN187176\_c0\_g1\_i7) | HPC vs HCC | F: AGTTGCTGACATGCTCGATG | 95.5 | 107 |
| R: GACTCCTGTCCAGCCTGAAG |
| spectrin alpha chain-like protein (*sptan1*)  (HL\_DN101947\_c2\_g2\_i1) | HCE vs HCC A1 | F: CATGTCAAGGCCGAGGAGTT | 106.0 | 114 |
| R: GTTGTGGATCCCCTCGTGTT |
| sphingomyelin phosphodiesterase (*smpd*) (HP\_DN122162\_c4\_g1\_i11) | HPE vs HPC A1 | F: GTGGCTGGATGTTTGGTCTT | 97.6 | 111 |
| R: GGGTAGGTTGTTGGGGTTCT |
| sulfotransferase 1C4 (*sult1c4*) (HP\_DN110901\_c3\_g3\_i1) | HPE vs HPC A1 | F: CTTCTGGTGCCGAGATTTGT | 94.4 | 91 |
| R: GAAAAGAACGTTGCGGTGAT |
| tetraspanin-like protein CD9 (*cd9*) (CN\_DN168186\_c8\_g1\_i2) | HCE vs HCC A2 | F: CATCCAGGAACAGATGCGTA | 93.8 | 147 |
| R: TTGGGTATGGGCAGGTGTAT |
| toll-interacting protein (*tollip*) (CN\_DN184135\_c6\_g1\_i2) | HPC vs HCC | F: TGAGGGTCGGTCACTACGTT | 101.5 | 105 |
| R: TGACACCCTTAGGGAACTGG |
| toll-like receptor (*tlr*) (CN\_DN172344\_c2\_g2\_i8) | HPC vs HCC | F: ATTGACCAGAGCATCGAGGA | 103.5 | 107 |
| R: GCTTTACAGTGGGCAGTTTTG |
| toll-like receptor (*tlr*) (CN\_DN183609\_c2\_g1\_i12) | HPC vs HCC | F: CCGGGTGAGTACATCCAGAA | 99.3 | 96 |
| R: CCACACACTCTCCAGGAAGC |
| vacuolar protein sorting-associated protein 26 (*vps26*) (HL\_DN75510\_c4\_g2\_i8) | HCE vs HCC A1 | F: GCGGGACATCAACAAAAAGT | 103.8 | 106 |
| R: GCGCCATAATGTGATTTCCT |

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| vitelline membrane outer layer 1 (*vmo1*) (HP\_DN126169\_c3\_g1\_i9) | HPE vs HPC A1 | F: ACCATCGACAACGGACTGA | 98.8 | 148 |
| R: TCTCGCAGTACAGCCTGATG |
| 5elongation factor 1-alpha (*ef1a*) | N/A | F: AGATCCAGGCTGGCTACTCC | 95.8 | 132 |
| R: ACTTGATCTGCTTGGGGTTG |
| 5ribosomal protein 49 (alias 60S ribosomal protein L32) *(rp49/rpl32*) | N/A | F: GAAGCCCAAGGGTATTGACA | 96.4 | 104 |
| R: GCAGCATGTGCTTGGTTCT |

1Gene identifier (ID) from RNA-seq studies. For the individual cell/tissue type assemblies (i.e. RNA-seq analysis method 1), the ID includes a cell/tissue type-specific prefix [HL: hemolymph (hemocytes); HP: hepatopancreas]. For the hemocytes-hepatopancreas co-assembly (i.e. RNA-seq analysis method 2), the gene ID includes a generic prefix (CN: crab noise). See methods for details.

2Two group comparison in which the transcript was identified as being differentially expressed (DE) in RNA-seq studies. HCC: hemocytes control; HCE: hemocytes exposed to chronic noise; HPC: hepatopancreas control; HPE: hepatopancreas exposed to chronic noise; A1: RNA-seq analysis method 1; A2: RNA-seq analysis method 2. See Supplemental File 3 for complete DET lists and additional information [e.g. log2 fold change values, transcripts per million (tpm) counts, BLAST results, functional annotations and nucleotide sequences]. See Supplemental File 1 for a summary of the BLASTx, RNA-seq and qPCR results for these 61 transcripts.

3Primers were designed with a melting temperature (Tm) of 60°C. See methods for details.

4Primers were quality tested on cDNA pools representing the two groups in which the transcript of interest (TOI) had been identified as differentially expressed in RNA-seq studies. The exceptions were all TOIs identified in the HCE vs HCC analysis 2 (expect for *per1*) which were quality tested in HPC and HPE cDNA pools due to low/no expression levels in hemocytes. Amplification efficiencies were calculated for each of the two groups using a 5-point 1:3 dilution series starting with cDNA representing 10 ng of input total RNA; the reported values are an average of the two values; the exceptions were *cyp330a1*, *gilt1*, *gilt3*, *lrrc24, myof*, *per1* (HPC only); *mrc1*, *cfb* (HCC only) due to low/no expression levels in the other group. See methods for details.

5Normalizers (Hall et al., 2021)