| Case | Sex | NEU(*10^9/L) | HGB(g/L) | PLT(*10^9/L) | RET(*10^9/L) |
|------|-----|--------------|-----------|--------------|--------------|
| 1    | Male | 0.35         | 68        | 27           | 5            |
| 2    | Male | 0.13         | 73        | 28           | 4.8          |
| 3    | Female | 0.02       | 83        | 1            | 10.3         |
| 4    | Female | 0.19       | 84        | 12           | 19.9         |
| 5    | Female | 0.47       | 85        | 24           | 15.3         |
| 6    | Male | 0.45         | 53        | 15           | 4.7          |
| 7    | Female | 0.22       | 68        | 17           | 3.1          |
| 8    | Male | 0.37         | 61        | 15           | 3.6          |
| 9    | Female | 0.3        | 51        | 43           | 2.6          |
| 10   | Female | 0.61       | 88        | 9            | 19.2         |
| 11   | Male | 0.39         | 90        | 39           | 5.7          |
| 12   | Female | 0.04       | 96        | 25           | 10.6         |
| 13   | Female | 0.37       | 54        | 16           | 9.5          |
| 14   | Female | 0.79       | 37        | 4            | 4.9          |
| 15   | Female | 0.24       | 56        | 11           | 5.5          |

**Supplemental Table 1. Clinical characteristics of all AA patients.**
| gene    | Forward (5’-3’)                  | Reverse (5’-3’)                  |
|---------|----------------------------------|----------------------------------|
| PRSS1   | CCCAGACGAGCTGCAGTG               | GGGCCACCAGAATCACCCCT             |
| KCNJ18  | TGCATGAAATTGACGAGGCCAG           | CTCATTGGCCAGGTAGGAGC             |
| DGKK    | TGTTGGAATGCATTGTTGTAATCCAG       | TTGCTCTCAAGCACAATCTGTGAG         |
| PRSS2   | TGAACAGTTCTCATCAATGCAGC          | CTTGATCAGCAGGATGTCATTT           |
| β-actin | CATGTACGTGGCTATCCAGGC            | CTCCTTAATGTACACGACGAT            |

Supplemental Table 2. The sequences of primer used for RT-PCR.
| GO          | Category                | Description                                | Count | %    | Log10(P) |
|------------|-------------------------|--------------------------------------------|-------|------|----------|
| GO:0008527 | Molecular Functions     | taste receptor activity                   | 5     | 5.56 | -7.32    |
| GO:0050907 | Biological Processes    | detection of chemical stimulus involved in sensory perception | 11    | 12.22| -6.42    |
| GO:0032963 | Biological Processes    | collagen metabolic process                 | 4     | 4.44 | -3.38    |
| GO:0035591 | Molecular Functions     | signaling adaptor activity                 | 3     | 3.33 | -2.83    |
| GO:0007599 | Biological Processes    | hemostasis                                 | 5     | 5.56 | -2.29    |
| GO:0046165 | Biological Processes    | alcohol biosynthetic process               | 3     | 3.33 | -1.86    |
| GO:0022613 | Biological Processes    | ribonucleoprotein complex biogenesis       | 5     | 5.56 | -1.75    |
| GO:0140013 | Biological Processes    | meiotic nuclear division                   | 3     | 3.33 | -1.74    |
| GO:0097529 | Biological Processes    | myeloid leukocyte migration                | 3     | 3.33 | -1.47    |
| GO:0045089 | Biological Processes    | positive regulation of innate immune response | 3    | 3.33 | -1.46    |
| GO:0072594 | Biological Processes    | establishment of protein localization to organelle | 5    | 5.56 | -1.42    |
| GO:0048568 | Biological Processes    | embryonic organ development                | 4     | 4.44 | -1.36    |
| GO:0000228 | Cellular Components     | nuclear chromosome                         | 3     | 3.33 | -1.33    |

**Supplemental Table 3. GO Pathway and Process Enrichment Analysis.** Top 13 clusters with their representative enriched terms (one per cluster). "Count" is the number of genes in the user-provided lists with membership in the given ontology term. "%" is the percentage of all of the user-provided genes that are found in the given ontology term (only input genes with at least one ontology term annotation are included in the calculation). "Log10(P)" is the p-value in log base 10.
| GO    | Category        | Description                                      | Count | %   | Log10(P) |
|-------|-----------------|--------------------------------------------------|-------|-----|----------|
| hsa04742 | KEGG Pathway   | Taste transduction                               | 5     | 5.56| -5.15    |
| hsa04740 | KEGG Pathway   | Olfactory transduction                           | 6     | 6.67| -2.64    |
| hsa04974 | KEGG Pathway   | Protein digestion and absorption                 | 3     | 3.33| -2.46    |

**Supplemental Table 4. KEGG Pathway Enrichment Analysis.** Top 3 clusters with their representative enriched terms (one per cluster). "Count" is the number of genes in the user-provided lists with membership in the given ontology term. "%" is the percentage of all of the user-provided genes that are found in the given ontology term (only input genes with at least one ontology term annotation are included in the calculation). "Log10(P)" is the p-value in log base 10.
| KEGG pathway                                      | Genes                  |
|--------------------------------------------------|------------------------|
| Hsa04022 cGMP-PKG signaling pathway              | PDE5A                  |
| Hsa04923 Regulation of lipolysis in adipocytes   | AQP7                   |
| Hsa04072 Phospholipase D signaling pathway       | DGKK                   |
| Hsa04921 Oxytocin signaling pathway              | AQP7                   |
| Hsa04144 Endocytosis                             | IQSEC1                 |
| Hsa04080 Neuroactive ligand-receptor interaction | PRSS1 PRSS2 AVPR2     |
| Hsa05224 Breast cancer                          | FZD8                   |
| Hsa04014 Ras signaling pathway                   | KSR2                   |

Supplemental Table 5. The ten candidate genes in the KEGG enrichment pathway of the differently expressed genes.