

## 🌟 Thyroid stimulating hormone levels (Zhou, 2020)

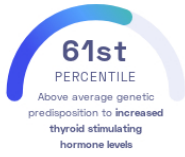
Wei Zhou, et al.  
Nature Communications

Cancer Metabolism

### STUDY SUMMARY

Identification of 28 novel regions associated with thyroid stimulating *hormone* levels.

#### YOUR RESULT



#### STUDY DESCRIPTION

The thyroid is a butterfly-shaped gland located at the front of the neck. It plays a critical role in controlling the body's metabolism by regulating how fast we burn calories and many other things. The thyroid itself is controlled by the pituitary gland, which is located in the brain, and releases thyroid stimulating *hormone* (TSH) that spurs the thyroid into action. TSH levels are commonly used to diagnose a variety of thyroid disorders, including hypothyroidism, hyperthyroidism, and thyroid cancer. This genome-wide association study examined nearly 120,000 individuals of European ancestry to better understand how genetics may influence TSH levels. The study identified 74 regions in the genome that appear to associate with TSH levels, 28 of which are newly discovered. One of the regions harbors the TSHR gene, which acts as a receptor for the thyroid stimulating *hormone*. The study also found that genetic predisposition to higher TSH levels is associated with a reduced risk of thyroid cancer.































#### DID YOU KNOW?

Women are between 5-8x more likely to develop disorders of the thyroid than men. On average, 1 in 8 women will be afflicted with a thyroid disorder during their lifetime.

#### YOUR DETAILED RESULTS

To calculate your genetic predisposition to increased thyroid stimulating hormone levels we summed up the effects of genetic variants that were linked to increased thyroid stimulating hormone levels in the study that this report is based on. These variants can be found in the table below. The variants highlighted in green have **positive effect sizes** and increase your genetic predisposition to increased thyroid stimulating hormone levels. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to increased thyroid stimulating hormone levels. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to increased thyroid stimulating hormone levels. By adding up the effect sizes of the highlighted variants we calculated your **polygenic score for increased thyroid stimulating hormone levels to be 0.14**. To determine whether your score is high or low, we compared it to the scores of 5,000 other Nebula Genomics users. We found that your polygenic score for increased thyroid stimulating hormone levels is in the **61st percentile**. This means that it is higher than the polygenic scores 61% of people. We consider this to be an **above average genetic predisposition to increased thyroid stimulating hormone levels**. However, please note that genetic predispositions do not account for important non-genetic factors like lifestyle. Furthermore, the genetics of most traits has not been fully understood yet and many associations between traits and genetic variants remain unknown. For additional explanations, click on the column titles in the table below and visit our [Nebula Library tutorial](#).

| VARIANT <sup>Ⓞ</sup> | YOUR GENOTYPE <sup>Ⓞ</sup> | EFFECT SIZE <sup>Ⓞ</sup> | VARIANT FREQUENCY <sup>Ⓞ</sup> | SIGNIFICANCE <sup>Ⓞ</sup> |
|----------------------|----------------------------|--------------------------|--------------------------------|---------------------------|
| rs1479567_A          | G / G                      | 0.16 (-)                 | 39%                            | 1.44 x 10 <sup>-269</sup> |
| rs2983511_C          | C / C                      | -0.12 (↓)                | 31%                            | 1.39 x 10 <sup>-120</sup> |
| rs11732089_C         | C / C                      | -0.12 (↓)                | 20%                            | 6.77 x 10 <sup>-83</sup>  |
| rs1317983_C          | T / C                      | 0.10 (↑)                 | 69%                            | 2.37 x 10 <sup>-86</sup>  |
| rs2928167_G          | A / A                      | -0.14 (-)                | 13%                            | 1.86 x 10 <sup>-86</sup>  |
| rs13020935_A         | A / A                      | 0.10 (↑)                 | 72%                            | 2.97 x 10 <sup>-78</sup>  |
| rs58722186_T         | C / C                      | -0.09 (-)                | 33%                            | 4.21 x 10 <sup>-78</sup>  |
| rs12138950_C         | A / A                      | -0.12 (-)                | 15%                            | 1.83 x 10 <sup>-72</sup>  |
| rs9381266_C          | T / T                      | -0.08 (-)                | 24%                            | 5.11 x 10 <sup>-62</sup>  |
| rs334726_A           | A / A                      | 0.16 (↑)                 | 95%                            | 2.94 x 10 <sup>-50</sup>  |
| rs17477923_C         | T / T                      | -0.07 (-)                | 25%                            | 8.30 x 10 <sup>-44</sup>  |
| rs17020122_T         | C / C                      | 0.11 (-)                 | 9%                             | 1.96 x 10 <sup>-43</sup>  |
| rs6675306_G          | A / A                      | 0.08 (-)                 | 20%                            | 2.21 x 10 <sup>-42</sup>  |
| rs12284404_A         | G / G                      | -0.07 (-)                | 30%                            | 2.72 x 10 <sup>-41</sup>  |
| rs139352934_A        | NA                         | 1.10 (-)                 | < 1%                           | 4.16 x 10 <sup>-40</sup>  |
| rs12027702_T         | G / G                      | 0.07 (-)                 | 33%                            | 3.95 x 10 <sup>-39</sup>  |
| rs10748781_A         | C / A                      | -0.06 (↓)                | 58%                            | 6.20 x 10 <sup>-35</sup>  |
| rs73234178_A         | G / G                      | -0.06 (-)                | 25%                            | 1.55 x 10 <sup>-34</sup>  |
| rs925488_A           | A / A                      | 0.06 (↑)                 | 66%                            | 4.95 x 10 <sup>-34</sup>  |
| rs4804416_G          | T / T                      | 0.06 (-)                 | 44%                            | 1.78 x 10 <sup>-32</sup>  |
| rs1348005_G          | A / G                      | -0.06 (↓)                | 33%                            | 1.09 x 10 <sup>-31</sup>  |
| rs121908872_A        | NA                         | 1.63 (-)                 | < 1%                           | 2.35 x 10 <sup>-31</sup>  |
| rs116909374_T        | NA                         | -0.17 (-)                | 4%                             | 7.94 x 10 <sup>-30</sup>  |
| rs10814915_C         | T / C                      | -0.05 (↓)                | 55%                            | 1.33 x 10 <sup>-29</sup>  |
| rs61938844_A         | NA                         | 0.19 (-)                 | 3%                             | 6.14 x 10 <sup>-29</sup>  |
| rs1203949_C          | C / C                      | 0.06 (↑)                 | 77%                            | 2.88 x 10 <sup>-28</sup>  |
| rs8020969_T          | C / T                      | -0.06 (↓)                | 23%                            | 2.36 x 10 <sup>-27</sup>  |
| rs118039499_C        | NA                         | -0.18 (-)                | 2%                             | 6.30 x 10 <sup>-27</sup>  |
| rs1042678_A          | G / A                      | 0.05 (↑)                 | 45%                            | 1.99 x 10 <sup>-26</sup>  |
| rs59381142_A         | G / G                      | -0.06 (-)                | 24%                            | 8.83 x 10 <sup>-26</sup>  |
| rs310755_A           | A / A                      | -0.06 (↓)                | 75%                            | 1.31 x 10 <sup>-26</sup>  |
| rs13100823_T         | C / C                      | -0.05 (-)                | 30%                            | 8.45 x 10 <sup>-23</sup>  |
| rs7873463_C          | A / C                      | -0.05 (↓)                | 73%                            | 1.14 x 10 <sup>-22</sup>  |
| rs59148743_C         | T / T                      | -0.05 (-)                | 30%                            | 6.49 x 10 <sup>-22</sup>  |
| rs12893151_A         | C / C                      | -0.06 (-)                | 21%                            | 6.70 x 10 <sup>-22</sup>  |
| rs117764941_A        | NA                         | -0.26 (-)                | 2%                             | 7.76 x 10 <sup>-22</sup>  |
| rs56009477_G         | A / A                      | -0.06 (-)                | 15%                            | 1.40 x 10 <sup>-21</sup>  |
| rs11156905_A         | G / A                      | -0.04 (↓)                | 62%                            | 3.98 x 10 <sup>-21</sup>  |

|   |       |           |      |                          |
|---|-------|-----------|------|--------------------------|
| rs12942923_A  | G / A | -0.04 (↓) | 53%  | 5.89 × 10 <sup>-21</sup> |
| rs6724073_C   | T / C | -0.05 (↓) | 26%  | 2.48 × 10 <sup>-20</sup> |
| rs544873_A  | A / A | 0.04 (↑)  | 37%  | 2.04 × 10 <sup>-18</sup> |
| rs10186921_T     | T / T | 0.04 (↑)  | 54%  | 3.13 × 10 <sup>-18</sup> |
| rs9497965_T   | C / T | 0.04 (↑)  | 39%  | 9.73 × 10 <sup>-18</sup> |
| rs2242602_T   | A / A | 0.04 (-)  | 29%  | 1.58 × 10 <sup>-17</sup> |
| rs179256_G  | G / G | -0.07 (↓) | 91%  | 2.82 × 10 <sup>-17</sup> |
| rs4445669_C   | T / T | 0.04 (-)  | 54%  | 4.69 × 10 <sup>-17</sup> |
| rs7318607_A   | A / A | 0.04 (↑)  | 64%  | 8.09 × 10 <sup>-17</sup> |
| rs141751376_C   | NA    | 1.37 (-)  | < 1% | 8.68 × 10 <sup>-17</sup> |
| rs12590163_C  | T / C | -0.04 (↓) | 44%  | 1.53 × 10 <sup>-16</sup> |
| rs1265091_T   | C / C | 0.06 (-)  | 19%  | 4.97 × 10 <sup>-16</sup> |
| rs28133_C   | T / C | -0.07 (↓) | 91%  | 1.25 × 10 <sup>-14</sup> |
| rs34046483_A  | G / A | 0.08 (↑)  | 7%   | 5.74 × 10 <sup>-14</sup> |
| rs7966590_A      | G / A | 0.04 (↑)  | 55%  | 5.93 × 10 <sup>-14</sup> |
| rs9678281_G   | C / G | 0.04 (↑)  | 38%  | 1.02 × 10 <sup>-13</sup> |
| rs4933466_G   | A / G | -0.04 (↓) | 40%  | 1.37 × 10 <sup>-13</sup> |
| rs11926459_C  | T / T | -0.03 (-) | 43%  | 1.47 × 10 <sup>-13</sup> |
| rs1157994_G   | G / G | 0.10 (↑)  | 96%  | 1.58 × 10 <sup>-13</sup> |
| rs10415188_G  | A / G | -0.04 (↓) | 71%  | 2.21 × 10 <sup>-13</sup> |
| rs11592436_G  | C / C | 0.04 (-)  | 17%  | 7.43 × 10 <sup>-13</sup> |
| rs700750_A       | C / A | 0.03 (↑)  | 64%  | 7.90 × 10 <sup>-13</sup> |
| rs191633940_A   | NA    | -0.79 (-) | < 1% | 1.28 × 10 <sup>-12</sup> |
| rs116956554_A   | A / A | 0.05 (↑)  | 18%  | 3.49 × 10 <sup>-12</sup> |
| rs2993047_A      | G / A | -0.03 (↓) | 59%  | 3.71 × 10 <sup>-12</sup> |
| rs115683886_A    | G / G | -0.04 (-) | 31%  | 3.83 × 10 <sup>-12</sup> |
| rs1045774_G      | A / A | 0.03 (-)  | 38%  | 3.87 × 10 <sup>-12</sup> |
| rs1045476_G   | G / G | -0.04 (↓) | 83%  | 4.39 × 10 <sup>-12</sup> |
| rs6721104_C    | NA    | 0.09 (-)  | 4%   | 4.45 × 10 <sup>-12</sup> |
| rs35587648_A   | G / G | 0.03 (-)  | 38%  | 4.53 × 10 <sup>-12</sup> |
| rs3104389_A   | C / C | 0.06 (-)  | 42%  | 5.84 × 10 <sup>-12</sup> |
| rs751171_C     | T / T | 0.03 (-)  | 34%  | 1.04 × 10 <sup>-11</sup> |
| rs6717283_G    | A / G | 0.05 (↑)  | 14%  | 1.04 × 10 <sup>-11</sup> |
| rs10735341_G  | G / G | 0.05 (↑)  | 88%  | 1.76 × 10 <sup>-11</sup> |
| rs145153320_T  | NA    | 0.49 (-)  | < 1% | 2.04 × 10 <sup>-11</sup> |
| rs62174422_G   | NA    | -0.08 (-) | 4%   | 2.09 × 10 <sup>-11</sup> |
| rs1801690_G    | C / C | -0.07 (-) | 6%   | 2.76 × 10 <sup>-11</sup> |
| rs2979181_T    | T / T | -0.04 (↓) | 50%  | 3.82 × 10 <sup>-11</sup> |
| rs9298749_C   | A / A | 0.03 (-)  | 39%  | 5.79 × 10 <sup>-11</sup> |
| rs3184504_C    | T / C | -0.03 (↓) | 52%  | 7.37 × 10 <sup>-11</sup> |
| rs72978712_C   | T / T | 0.04 (-)  | 20%  | 9.42 × 10 <sup>-11</sup> |
| rs12743883_G   | A / G | 0.03 (↑)  | 59%  | 1.00 × 10 <sup>-10</sup> |
| rs7083359_T   | C / T | -0.03 (↓) | 30%  | 1.42 × 10 <sup>-10</sup> |
| rs12029562_A   | A / A | -0.03 (↓) | 53%  | 1.66 × 10 <sup>-10</sup> |
| rs546738875_G  | NA    | 0.39 (-)  | < 1% | 1.95 × 10 <sup>-10</sup> |
| rs6989821_C   | T / C | 0.03 (↑)  | 29%  | 6.92 × 10 <sup>-10</sup> |
| rs6085658_T    | C / C | -0.03 (-) | 40%  | 1.32 × 10 <sup>-9</sup>  |
| rs77994712_G   | C / G | -0.07 (↓) | 5%   | 1.44 × 10 <sup>-9</sup>  |
| rs4571283_A    | A / A | 0.04 (↑)  | 88%  | 2.72 × 10 <sup>-9</sup>  |
| rs1373851_T   | T / T | -0.06 (↓) | 94%  | 6.09 × 10 <sup>-9</sup>  |
| rs3731890_T   | T / T | 0.03 (↑)  | 63%  | 7.02 × 10 <sup>-9</sup>  |
| rs4719486_A    | G / G | -0.03 (-) | 42%  | 8.44 × 10 <sup>-9</sup>  |
| rs4393429_C    | T / C | -0.03 (↓) | 26%  | 8.75 × 10 <sup>-9</sup>  |
| rs10421676_G   | A / G | 0.03 (↑)  | 60%  | 1.05 × 10 <sup>-8</sup>  |
| rs10878986_C   | T / T | -0.03 (-) | 39%  | 2.40 × 10 <sup>-8</sup>  |
| rs74888443_T   | C / C | 0.06 (-)  | 5%   | 2.70 × 10 <sup>-8</sup>  |
| rs30233_A   | G / A | -0.03 (↓) | 56%  | 3.29 × 10 <sup>-8</sup>  |
| rs9865818_G    | A / A | -0.03 (-) | 43%  | 3.42 × 10 <sup>-8</sup>  |
| rs72682433_C   | T / T | 0.04 (-)  | 10%  | 4.22 × 10 <sup>-8</sup>  |
| rs5997969_C    | T / C | -0.03 (↓) | 67%  | 4.37 × 10 <sup>-8</sup>  |

N/A indicates variants that could not be imputed using the 1000 genomes project datasets and variants that have a frequency of < 5%. Your genome was sequenced at 30x/100x coverage and is not imputed. However, to calculate percentiles, we need to compare your data with other users imputed data. To make the data comparable, we need to exclude some of the variants from your data.