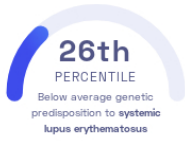


## STUDY SUMMARY

Identification of 132 regions of the genome associated with systemic lupus erythematosus.

## YOUR RESULT



## STUDY DESCRIPTION




Systemic lupus erythematosus (SLE) is an autoimmune disorder. This means that it is caused by the body's immune system mistakenly attacking organs and tissues. Individuals with SLE may experience joint pain, fatigue, fever, and numerous other symptoms. Genetic factors play a key role in the disease, with estimates of its heritability ranging from 43% to 66%. This genome-wide association study of over 35,000 individuals of East Asian and European ancestry identified 132 genomic regions associated with SLE risk, 38 of which were newly-discovered in this study. Many of the genes that were linked to SLE are important for the functioning of the immune system. For instance, TRAF3 plays a critical role in activating an immune response, while CTLA4 is important for turning down the activity of the immune system.

































## DID YOU KNOW?


Systemic lupus erythematosus affects nearly 10 times as many women as men.

## YOUR DETAILED RESULTS

To calculate your genetic predisposition to systemic lupus erythematosus we summed up the effects of genetic variants that were linked to systemic lupus erythematosus 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 systemic lupus erythematosus. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to systemic lupus erythematosus. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to systemic lupus erythematosus. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for systemic lupus erythematosus to be -2.05**. 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 systemic lupus erythematosus is in the **26th percentile**. This means that it is higher than the polygenic scores 26% of people. We consider this to be a **below average genetic predisposition to systemic lupus erythematosus**. 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>
rs1143679_A	G / G	0.59 (-)	15%	1.49 x 10 <sup>-60</sup>
rs11889341_T	C / C	0.46 (-)	22%	5.89 x 10 <sup>-137</sup>
rs4728142_A	G / A	0.37 (†)	50%	4.64 x 10 <sup>-71</sup>
rs9270984_G	G / G	-0.46 (↓)	90%	6.51 x 10 <sup>-68</sup>
rs2230926_G	NA	0.63 (-)	5%	7.34 x 10 <sup>-69</sup>
rs2205960_T	G / G	0.31 (-)	19%	2.52 x 10 <sup>-57</sup>
rs2736340_T	C / T	0.31 (†)	26%	2.01 x 10 <sup>-60</sup>
rs1128334_T	C / C	0.30 (-)	8%	6.41 x 10 <sup>-49</sup>
rs17849501_T	C / C	0.79 (-)	7%	1.50 x 10 <sup>-46</sup>
rs729302_C	A / A	-0.26 (-)	30%	2.80 x 10 <sup>-41</sup>
rs12531711_G	A / A	0.54 (-)	11%	7.38 x 10 <sup>-41</sup>
rs10036748_T	C / C	0.25 (-)	26%	5.65 x 10 <sup>-33</sup>
rs7097397_A	G / A	-0.22 (↓)	46%	1.82 x 10 <sup>-32</sup>
rs4917014_G	T / T	-0.23 (-)	37%	2.17 x 10 <sup>-31</sup>
rs2431697_C	T / C	-0.24 (↓)	44%	5.98 x 10 <sup>-29</sup>
rs548234_T	T / T	-0.21 (↓)	70%	2.39 x 10 <sup>-28</sup>
rs1385374_T	C / C	0.25 (-)	9%	2.62 x 10 <sup>-27</sup>
rs117026326_T	C / C	1.10 (-)	8%	7.35 x 10 <sup>-27</sup>
rs3734266_C	T / T	0.25 (-)	17%	9.40 x 10 <sup>-24</sup>
rs13385731_C	NA	-0.30 (-)	5%	5.09 x 10 <sup>-23</sup>
rs1418190_T	C / T	0.20 (†)	60%	2.14 x 10 <sup>-22</sup>
rs12599402_C	T / T	-0.17 (-)	47%	2.74 x 10 <sup>-22</sup>
rs7444_C	T / C	0.20 (†)	20%	8.99 x 10 <sup>-22</sup>
rs2280381_T	T / T	0.21 (†)	65%	3.94 x 10 <sup>-19</sup>
rs10028805_A	G / G	-0.16 (-)	37%	2.67 x 10 <sup>-17</sup>
rs11644034_A	G / A	-0.25 (↓)	16%	5.30 x 10 <sup>-17</sup>
rs2732552_C	T / C	0.16 (†)	55%	1.13 x 10 <sup>-16</sup>
rs7726414_T	C / C	0.28 (-)	9%	3.17 x 10 <sup>-16</sup>
rs1131265_C	G / G	-0.17 (-)	17%	8.35 x 10 <sup>-16</sup>
rs7579944_C	T / T	0.14 (-)	65%	1.17 x 10 <sup>-16</sup>
rs1801274_G	A / G	0.15 (†)	50%	5.05 x 10 <sup>-16</sup>
rs223881_C	C / C	-0.15 (↓)	77%	5.86 x 10 <sup>-16</sup>
rs463426_C	T / C	-0.14 (↓)	72%	6.57 x 10 <sup>-16</sup>
rs2476601_G	G / G	-0.34 (↓)	91%	3.04 x 10 <sup>-14</sup>
rs9630991_A 	A / A	-0.16 (↓)	50%	1.08 x 10 <sup>-13</sup>
rs1885889_G 	G / G	-0.14 (↓)	83%	2.05 x 10 <sup>-13</sup>
rs2297550_G	C / C	0.17 (-)	14%	6.22 x 10 <sup>-13</sup>
rs11264750_G 	NA	-0.28 (-)	1%	8.70 x 10 <sup>-13</sup>
rs763361_C	T / C	-0.12 (↓)	58%	3.03 x 10 <sup>-12</sup>

rs2009465_T	T / T	-0.12 (↓)	63%	4.22 x 10 <sup>-12</sup>
rs10774625_G	A / G	-0.19 (↓)	55%	7.28 x 10 <sup>-12</sup>
rs73135369_C	NA	0.30 (-)	2%	2.46 x 10 <sup>-11</sup>
rs2934498_G	A / G	0.14 (↑)	30%	2.56 x 10 <sup>-11</sup>
rs564799_T	T / T	-0.15 (↓)	35%	3.19 x 10 <sup>-11</sup>
rs7726169_A	C / A	0.13 (↑)	39%	6.04 x 10 <sup>-11</sup>
rs4948496_C	T / C	0.13 (↑)	50%	1.29 x 10 <sup>-10</sup>
rs13344313_A 	G / G	-0.16 (-)	29%	1.34 x 10 <sup>-10</sup>
rs28411034_A 	G / A	-0.15 (↓)	27%	1.50 x 10 <sup>-10</sup>
rs10936599_T	C / C	-0.12 (-)	22%	2.31 x 10 <sup>-10</sup>
rs8035957_C	T / T	0.12 (-)	25%	3.23 x 10 <sup>-10</sup>
rs6927090_T 	G / G	0.21 (-)	23%	3.48 x 10 <sup>-10</sup>
rs1061502_C	T / T	-0.18 (-)	28%	1.11 x 10 <sup>-9</sup>
rs1308020_A	G / A	-0.13 (↓)	37%	1.28 x 10 <sup>-9</sup>
rs12802200_A	C / C	-0.20 (-)	20%	1.59 x 10 <sup>-9</sup>
rs2381401_T 	C / C	0.14 (-)	22%	1.73 x 10 <sup>-9</sup>
rs7815944_G 	NA	-0.14 (-)	3%	2.21 x 10 <sup>-9</sup>
rs3760667_T 	C / T	-0.14 (↓)	22%	2.31 x 10 <sup>-9</sup>
rs405858_T 	C / T	-0.11 (↓)	69%	2.38 x 10 <sup>-9</sup>
rs12093154_A 	G / G	-0.18 (-)	6%	2.51 x 10 <sup>-9</sup>
rs6702599_C 	C / C	-0.18 (↓)	83%	3.18 x 10 <sup>-9</sup>
rs6705628_T	NA	-0.17 (-)	2%	4.61 x 10 <sup>-9</sup>
rs2841280_C	G / C	0.12 (↑)	44%	5.56 x 10 <sup>-9</sup>
rs7941765_C	T / C	0.13 (↑)	44%	6.37 x 10 <sup>-9</sup>
rs494003_A	G / G	0.16 (-)	23%	8.02 x 10 <sup>-9</sup>
rs1016140_T 	G / G	-0.11 (-)	9%	1.26 x 10 <sup>-8</sup>
rs438613_C 	T / C	0.10 (↑)	47%	1.32 x 10 <sup>-8</sup>
rs869310_G 	G / G	-0.13 (↓)	34%	1.90 x 10 <sup>-8</sup>
rs10845606_A	C / C	-0.13 (-)	23%	1.90 x 10 <sup>-8</sup>
rs8079075_G	NA	0.40 (-)	4%	2.15 x 10 <sup>-8</sup>
rs3087243_A 	G / A	-0.11 (↓)	52%	2.29 x 10 <sup>-8</sup>
rs1405209_C 	T / T	0.11 (-)	37%	2.42 x 10 <sup>-8</sup>
rs12148050_G 	G / G	-0.10 (↓)	67%	2.57 x 10 <sup>-8</sup>
rs7975703_T 	C / C	-0.12 (-)	20%	2.99 x 10 <sup>-8</sup>
rs6074813_T 	G / G	0.11 (-)	32%	3.23 x 10 <sup>-8</sup>
rs3795310_T 	C / C	-0.13 (-)	58%	3.36 x 10 <sup>-8</sup>
rs12680762_T	C / T	0.20 (↑)	24%	3.50 x 10 <sup>-8</sup>
rs76725306_A 	NA	0.15 (-)	3%	3.60 x 10 <sup>-8</sup>
rs10419308_A 	G / A	-0.17 (↓)	21%	3.60 x 10 <sup>-8</sup>
rs4745876_A 	G / G	-0.13 (-)	11%	3.66 x 10 <sup>-8</sup>
rs6871748_C 	T / C	-0.12 (↓)	24%	3.96 x 10 <sup>-8</sup>
rs549669428_G 	T / G	-0.18 (↓)	28%	4.53 x 10 <sup>-8</sup>
rs1099979_A 	NA	0.15 (-)	1%	4.65 x 10 <sup>-8</sup>
rs2384991_C 	A / A	0.10 (-)	19%	4.95 x 10 <sup>-8</sup>
rs4690055_A 	G / G	-0.10 (-)	46%	5.68 x 10 <sup>-8</sup>
rs4978037_C 	C / C	0.11 (↑)	81%	5.68 x 10 <sup>-8</sup>
rs11679484_A 	C / C	0.11 (-)	40%	6.26 x 10 <sup>-8</sup>
rs4697651_T 	C / C	-0.13 (-)	31%	6.36 x 10 <sup>-8</sup>
rs13260060_A 	G / G	-0.10 (-)	11%	7.94 x 10 <sup>-8</sup>
rs3768792_A	A / A	-0.14 (↓)	88%	8.36 x 10 <sup>-8</sup>
rs4639966_C	T / C	0.10 (↑)	26%	1.20 x 10 <sup>-7</sup>
rs7329174_G	NA	0.17 (-)	1%	1.40 x 10 <sup>-7</sup>
rs34889541_A	G / G	-0.18 (-)	7%	1.59 x 10 <sup>-7</sup>
rs1990760_T	C / T	0.10 (↑)	60%	1.82 x 10 <sup>-7</sup>
rs1547624_T 	T / T	0.12 (↑)	82%	1.95 x 10 <sup>-7</sup>
rs2445610_G 	A / G	-0.09 (↓)	31%	2.60 x 10 <sup>-7</sup>
rs61616683_T	T / T	0.11 (↑)	22%	3.46 x 10 <sup>-7</sup>
rs11603023_C	T / C	-0.09 (↓)	58%	4.28 x 10 <sup>-7</sup>
rs2305772_A	G / A	-0.09 (↓)	62%	4.50 x 10 <sup>-7</sup>
rs6740462_A	A / A	0.11 (↑)	71%	4.81 x 10 <sup>-7</sup>

rs35426045_A	A / A	0.20 (↑)	82%	$5.21 \times 10^{-7}$
rs2731783_G	G / G	-0.12 (↓)	82%	$6.68 \times 10^{-7}$
rs2327832_G	A / G	0.16 (↑)	21%	$1.14 \times 10^{-6}$
rs11235604_T	C / C	-0.25 (-)	10%	$1.26 \times 10^{-6}$
rs11773745_G	G / G	0.11 (↑)	24%	$1.41 \times 10^{-6}$
rs34562254_A	G / G	0.12 (-)	11%	$1.63 \times 10^{-6}$
rs2289583_A	C / C	0.11 (-)	30%	$2.36 \times 10^{-6}$
rs4690229_T	T / T	0.10 (↑)	47%	$2.45 \times 10^{-6}$
rs597325_G	G / G	0.08 (↑)	67%	$3.26 \times 10^{-6}$
rs9782955_C	C / C	0.12 (↑)	79%	$3.71 \times 10^{-6}$
rs9387400_A 	C / A	-0.11 (↓)	39%	$5.89 \times 10^{-6}$
rs2322659_C	C / C	0.10 (↑)	49%	$7.38 \times 10^{-6}$
rs1170426_T	C / T	-0.11 (↓)	75%	$8.30 \times 10^{-6}$
rs6445975_T	G / T	-0.09 (↓)	78%	$9.31 \times 10^{-6}$
rs930297_T	T / T	0.14 (↑)	84%	$1.60 \times 10^{-5}$
rs12874404_G	A / A	0.26 (-)	7%	$2.24 \times 10^{-5}$
rs6762714_T	C / T	0.10 (↑)	39%	$3.43 \times 10^{-5}$
rs3024505_A	G / G	0.13 (-)	12%	$5.26 \times 10^{-5}$
rs2366293_C	C / C	-0.14 (↓)	80%	$5.45 \times 10^{-5}$
rs2304256_A	C / C	-0.07 (-)	26%	$8.17 \times 10^{-5}$

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.