

# LDL cholesterol level (Richardson, 2020)

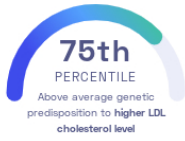
Tom Richardson, et al.  
PLoS Medicine

Heart Blood

## STUDY SUMMARY

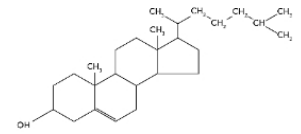
Identification of 220 genetic variants associated with the LDL *cholesterol* level in blood and analysis of its contribution to the risk of coronary heart disease.

### YOUR RESULT



### STUDY DESCRIPTION

Coronary heart disease (CHD) is a condition that develops when the heart's arteries cannot supply enough oxygen to the heart muscle. Coronary heart disease is the leading cause of death in the United States. It occurs when *plaque* builds up in the heart's arteries and blocks the blood flow to the heart. Arterial *plaque* consists of multiple substances that circulate in the blood. One of the substances that the study examined is LDL (low-density lipoprotein) *cholesterol*, also known as the "bad" *cholesterol*. To this end, this study analyzed genetic data of over 440,000 individuals of European descent to identify genomic regions associated with LDL *cholesterol* levels in the blood. The researchers identified 220 genetic variants, including 123 novel variants, associated with LDL *cholesterol* levels. The analysis showed that a high LDL *cholesterol* level is associated with an increased risk of coronary heart disease. However, this association weakened when the researchers considered all fats and proteins in the study. However, the results still suggest that LDL *cholesterol* plays an important role as a risk factor for heart disease.



The chemical structure of cholesterol resembles steroid hormones, bile acid and vitamin D because it is used for their biosynthesis.

























### DID YOU KNOW?

Coronary heart disease develops over many decades. A healthy lifestyle can significantly decrease the risk of developing coronary heart disease.

### YOUR DETAILED RESULTS

To calculate your genetic predisposition to higher LDL cholesterol level we summed up the effects of genetic variants that were linked to higher LDL cholesterol level 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 higher LDL cholesterol level. The variants highlighted in blue have **negative effect sizes** and decrease your genetic predisposition to higher LDL cholesterol level. Variants that are not highlighted are not found in your genome and do not affect your genetic predisposition to higher LDL cholesterol level. By adding up the effect sizes of the highlighted variants **we calculated your polygenic score for higher LDL cholesterol level to be 1.13**. 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 higher LDL cholesterol level is in the **75th percentile**. This means that it is higher than the polygenic scores 75% of people. We consider this to be an **above average genetic predisposition to higher LDL cholesterol level**. 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	YOUR GENOTYPE	EFFECT SIZE	VARIANT FREQUENCY	SIGNIFICANCE
rs6857_C	C / C	-0.16 (↓)	83%	$1.30 \times 10^{-71}$
rs143020224_C	C / C	0.17 (↑)	88%	$8.90 \times 10^{-605}$
rs1551891_G	G / G	0.17 (↑)	91%	$3.70 \times 10^{-490}$
rs11591147_G	G / G	0.35 (↑)	98%	$2.20 \times 10^{-421}$
rs4452060_C	C / C	-0.08 (↓)	58%	$6.90 \times 10^{-343}$
rs4970834_C	C / C	0.11 (↑)	81%	$2.00 \times 10^{-336}$
rs934197_G	G / G	-0.08 (↓)	66%	$9.40 \times 10^{-312}$
rs12916_T	C / C	-0.06 (-)	60%	$2.20 \times 10^{-187}$
rs28601761_C	C / C	0.06 (↑)	58%	$1.20 \times 10^{-184}$
rs8107974_A	A / A	0.11 (↑)	92%	$1.80 \times 10^{-158}$
rs4299376_G	T / T	0.05 (-)	32%	$3.50 \times 10^{-131}$
rs430096_A	A / A	0.05 (↑)	78%	$2.30 \times 10^{-103}$
rs118039278_G	G / G	-0.08 (↓)	92%	$2.20 \times 10^{-102}$
rs115478735_A	A / T	-0.06 (↓)	82%	$9.00 \times 10^{-96}$
rs2738447_A	A / C	-0.04 (↓)	41%	$3.50 \times 10^{-89}$
rs472495_G	T / T	-0.04 (-)	35%	$5.50 \times 10^{-85}$
rs964184_G	C / C	0.06 (-)	13%	$1.60 \times 10^{-78}$
rs77542162_A	A / A	-0.13 (↓)	98%	$5.50 \times 10^{-74}$
rs34042070_C	C / C	-0.05 (↓)	81%	$2.20 \times 10^{-73}$
rs1168127_C	A / A	-0.04 (-)	35%	$1.90 \times 10^{-70}$
rs556107_C	C / T	-0.04 (↓)	48%	$8.00 \times 10^{-64}$
rs1883711_G	G / G	-0.10 (↓)	97%	$1.40 \times 10^{-63}$
rs1260326_T	T / C	0.03 (↑)	40%	$5.60 \times 10^{-60}$
rs6874202_T	T / T	-0.03 (↓)	37%	$1.20 \times 10^{-50}$
rs3764261_C	C / A	0.03 (↑)	68%	$1.00 \times 10^{-49}$
rs79220007_T	T / C	0.06 (↑)	92%	$1.50 \times 10^{-48}$
rs174564_A	A / A	0.03 (↑)	65%	$3.10 \times 10^{-48}$
rs516316_G	C / C	-0.03 (-)	49%	$9.50 \times 10^{-47}$
rs4738684_A	A / G	0.03 (↑)	34%	$3.30 \times 10^{-46}$
rs34392107_G	G / A	-0.05 (↓)	88%	$5.80 \times 10^{-45}$
rs12208357_C	C / C	-0.06 (↓)	93%	$3.40 \times 10^{-44}$
rs59379014_C	C / C	-0.06 (↓)	93%	$3.30 \times 10^{-43}$
rs2073547_A	A / A	-0.04 (↓)	82%	$2.40 \times 10^{-40}$
rs6693893_T	T / T	0.07 (↑)	96%	$3.10 \times 10^{-40}$
rs6709904_A	A / G	0.04 (↑)	89%	$8.70 \times 10^{-40}$
rs56130071_G	G / G	-0.03 (↓)	78%	$4.70 \times 10^{-39}$
rs597808_A	A / G	-0.03 (↓)	48%	$2.00 \times 10^{-38}$
rs188247550_C	C / C	0.12 (↑)	99%	$9.20 \times 10^{-37}$

rs36043200_G	G / A	0.03 (↑)	48%	1.20 × 10 <sup>-36</sup>
rs9987289_A	A / G	-0.06 (↓)	9%	4.80 × 10 <sup>-36</sup>
rs61775180_C	C / T	0.03 (↑)	58%	1.70 × 10 <sup>-35</sup>
rs62116889_T	T / T	0.06 (↑)	93%	2.40 × 10 <sup>-33</sup>
rs11206517_T	T / T	-0.07 (↓)	97%	5.90 × 10 <sup>-32</sup>
rs150262789_C	C / C	0.10 (↑)	98%	2.00 × 10 <sup>-31</sup>
rs26185666_G	G / T	0.02 (↑)	34%	1.20 × 10 <sup>-29</sup>
rs2642438_A	A / G	-0.03 (↓)	30%	7.60 × 10 <sup>-29</sup>
rs35081008_C 	C / T	0.03 (↑)	85%	1.10 × 10 <sup>-27</sup>
rs1169294_G	G / A	-0.02 (↓)	69%	2.00 × 10 <sup>-27</sup>
rs117733303_A	A / A	-0.08 (↓)	98%	2.50 × 10 <sup>-27</sup>
rs2740488_A	A / C	0.03 (↑)	73%	7.80 × 10 <sup>-27</sup>
rs7746081_G	G / G	0.02 (↑)	70%	4.60 × 10 <sup>-26</sup>
rs7202323_T	T / G	0.03 (↑)	77%	7.50 × 10 <sup>-26</sup>
rs1801689_A	A / A	-0.06 (↓)	97%	1.60 × 10 <sup>-24</sup>
rs9884390_T 	T / T	-0.03 (↓)	77%	7.20 × 10 <sup>-24</sup>
rs150474434_G	G / G	0.03 (↑)	90%	1.40 × 10 <sup>-23</sup>
rs2287622_A 	G / G	0.02 (-)	40%	3.20 × 10 <sup>-23</sup>
rs65714927_C	C / C	0.03 (↑)	81%	3.70 × 10 <sup>-23</sup>
rs1800961_C	C / C	0.06 (↑)	97%	4.00 × 10 <sup>-23</sup>
rs6475606_C 	C / C	0.02 (↑)	52%	2.00 × 10 <sup>-22</sup>
rs17050272_G	G / A	0.02 (↑)	59%	3.10 × 10 <sup>-22</sup>
rs6602912_T 	T / T	-0.02 (↓)	72%	5.50 × 10 <sup>-22</sup>
rs6093446_G	G / A	-0.02 (↓)	71%	7.40 × 10 <sup>-22</sup>
rs76079263_G 	G / G	0.03 (↑)	91%	3.90 × 10 <sup>-21</sup>
rs72631343_C	C / C	0.03 (↑)	87%	4.90 × 10 <sup>-21</sup>
rs2068888_G 	G / A	0.02 (↑)	55%	5.30 × 10 <sup>-20</sup>
rs11621792_C	C / T	-0.02 (↓)	55%	1.30 × 10 <sup>-19</sup>
rs9391803_T 	T / T	-0.03 (↓)	85%	1.60 × 10 <sup>-19</sup>
rs3179865_G 	G / G	-0.02 (↓)	60%	1.90 × 10 <sup>-19</sup>
rs7562734_G	G / C	0.02 (↑)	68%	2.20 × 10 <sup>-19</sup>
rs116734477_C 	C / C	0.05 (↑)	96%	2.80 × 10 <sup>-19</sup>
rs7734476_G	A / A	-0.02 (-)	45%	3.90 × 10 <sup>-19</sup>
rs9834932_A	A / A	0.03 (↑)	91%	1.10 × 10 <sup>-18</sup>
rs113177823_G	G / G	0.04 (↑)	95%	1.20 × 10 <sup>-18</sup>
rs2737265_A	A / A	0.02 (↑)	72%	1.90 × 10 <sup>-18</sup>
rs233721_T 	T / A	-0.02 (↓)	36%	2.30 × 10 <sup>-18</sup>
rs13076933_T	T / T	0.02 (↑)	74%	3.00 × 10 <sup>-18</sup>
rs12948394_C 	T / T	0.02 (-)	52%	5.10 × 10 <sup>-18</sup>
rs261334_G 	G / C	0.02 (↑)	21%	8.70 × 10 <sup>-18</sup>
rs7569317_T 	T / T	-0.02 (↓)	47%	8.70 × 10 <sup>-18</sup>
rs4722551_T	T / C	-0.02 (↓)	84%	1.30 × 10 <sup>-17</sup>
rs76967117_G 	G / G	0.03 (↑)	89%	2.10 × 10 <sup>-17</sup>
rs3822855_G	G / T	-0.02 (↓)	60%	3.50 × 10 <sup>-17</sup>
rs907866_G	G / G	0.02 (↑)	55%	3.70 × 10 <sup>-17</sup>
rs2160994_T 	T / T	-0.02 (↓)	35%	4.10 × 10 <sup>-17</sup>
rs62118464_G	G / G	-0.03 (↓)	88%	4.90 × 10 <sup>-17</sup>
rs1229984_T 	NA	-0.05 (-)	3%	7.40 × 10 <sup>-17</sup>
rs13108218_A	A / G	0.02 (↑)	39%	2.10 × 10 <sup>-16</sup>
rs224424_A 	G / A	0.02 (↑)	79%	2.60 × 10 <sup>-16</sup>
rs8101801_C	C / C	0.05 (↑)	96%	6.20 × 10 <sup>-16</sup>
rs1458038_C 	T / T	0.02 (-)	71%	6.90 × 10 <sup>-16</sup>
rs114165349_G	G / G	-0.06 (↓)	98%	8.00 × 10 <sup>-16</sup>
rs1532085_A 	G / G	0.02 (-)	39%	8.90 × 10 <sup>-16</sup>
rs11601507_C 	C / C	-0.03 (↓)	93%	1.70 × 10 <sup>-16</sup>
rs2238162_C	C / C	0.02 (↑)	48%	3.50 × 10 <sup>-16</sup>
rs2250802_G	G / A	0.02 (↑)	28%	6.00 × 10 <sup>-16</sup>
rs4782568_C 	C / G	0.02 (↑)	55%	6.00 × 10 <sup>-16</sup>
rs77960347_A 	A / A	-0.07 (↓)	99%	7.50 × 10 <sup>-16</sup>
rs9929977_T 	T / A	-0.02 (↓)	63%	1.00 × 10 <sup>-14</sup>

rs12603885_G	A / A	-0.02 (↓)	30%	1.40 × 10 <sup>-14</sup>
rs1566662_G	G / T	-0.02 (↓)	21%	2.00 × 10 <sup>-14</sup>
rs71311871_A	A / A	0.03 (↑)	92%	6.60 × 10 <sup>-14</sup>
rs12246352_A	A / A	-0.03 (↓)	90%	6.80 × 10 <sup>-14</sup>
rs146534110_G	G / G	-0.07 (↓)	99%	8.70 × 10 <sup>-14</sup>
rs2925677_C	C / C	0.02 (↑)	79%	1.10 × 10 <sup>-13</sup>
rs11789603_C	C / T	-0.02 (↓)	89%	1.20 × 10 <sup>-13</sup>
rs9298506_A	A / A	-0.02 (↓)	79%	2.50 × 10 <sup>-13</sup>
rs10231941_T	T / T	-0.02 (↓)	82%	3.00 × 10 <sup>-13</sup>
rs10832963_T	T / G	-0.02 (↓)	26%	4.10 × 10 <sup>-13</sup>
rs9496567_G	G / G	0.02 (↑)	76%	5.90 × 10 <sup>-13</sup>
rs11786083_G	G / G	-0.02 (↓)	63%	7.10 × 10 <sup>-13</sup>
rs117139027_G	G / G	0.06 (↑)	98%	7.20 × 10 <sup>-13</sup>
rs704_G	A / A	-0.01 (-)	62%	8.60 × 10 <sup>-13</sup>
rs12990177_A	* / T	-0.02 (-)	48%	1.10 × 10 <sup>-12</sup>
rs13283282_C	C / C	0.02 (↑)	85%	2.60 × 10 <sup>-12</sup>
rs74869459_T	T / T	0.02 (↑)	76%	3.00 × 10 <sup>-12</sup>
rs3110609_T	C / C	0.02 (-)	66%	3.10 × 10 <sup>-12</sup>
rs145730801_T	T / T	-0.04 (↓)	96%	3.60 × 10 <sup>-12</sup>
rs1495741_G	G / A	0.02 (↑)	22%	4.60 × 10 <sup>-12</sup>
rs3732359_G	A / A	0.02 (-)	22%	4.70 × 10 <sup>-12</sup>
rs62120394_G	G / G	-0.02 (↓)	71%	5.50 × 10 <sup>-12</sup>
rs72823020_T	T / T	0.02 (↑)	87%	5.60 × 10 <sup>-12</sup>
rs4954192_C	C / C	-0.01 (↓)	63%	5.70 × 10 <sup>-12</sup>
rs880315_T	T / T	0.02 (↑)	66%	6.80 × 10 <sup>-12</sup>
rs7776054_A	A / A	0.02 (↑)	74%	7.00 × 10 <sup>-12</sup>
rs112987086_G	T / T	-0.02 (-)	28%	1.20 × 10 <sup>-11</sup>
rs62033400_A	A / G	0.01 (↑)	61%	1.20 × 10 <sup>-11</sup>
rs10448340_T	T / T	0.02 (↑)	68%	1.40 × 10 <sup>-11</sup>
rs2066714_T	T / T	-0.02 (↓)	87%	1.60 × 10 <sup>-11</sup>
rs9491699_C	C / T	-0.01 (↓)	62%	1.90 × 10 <sup>-11</sup>
rs9832727_C	C / G	0.01 (↑)	66%	2.10 × 10 <sup>-11</sup>
rs67050321_T	T / T	-0.02 (↓)	70%	2.20 × 10 <sup>-11</sup>
rs6073958_T	T / T	-0.02 (↓)	80%	2.60 × 10 <sup>-11</sup>
rs3780181_A	A / A	0.03 (↑)	93%	2.90 × 10 <sup>-11</sup>
rs6090101_G	G / G	-0.02 (↓)	80%	3.10 × 10 <sup>-11</sup>
rs1016988_T	T / C	0.02 (↑)	81%	5.20 × 10 <sup>-11</sup>
rs115458560_T	T / T	0.05 (↑)	98%	6.60 × 10 <sup>-11</sup>
rs6667939_C	T / T	-0.02 (-)	28%	7.10 × 10 <sup>-11</sup>
rs4818025_A	A / A	-0.01 (↓)	43%	8.70 × 10 <sup>-11</sup>
rs17476364_T	T / T	0.02 (↑)	89%	9.10 × 10 <sup>-11</sup>
rs9841897_T	T / T	-0.02 (↓)	84%	1.30 × 10 <sup>-10</sup>
rs1350559_C	C / G	-0.01 (↓)	60%	1.50 × 10 <sup>-10</sup>
rs549956721_A	A / A	0.04 (↑)	97%	1.80 × 10 <sup>-10</sup>
rs56113850_T	C / C	-0.01 (-)	42%	1.80 × 10 <sup>-10</sup>
rs11206788_G	G / C	-0.01 (↓)	41%	2.00 × 10 <sup>-10</sup>
rs28631087_T	T / T	0.02 (↑)	79%	2.20 × 10 <sup>-10</sup>
rs2718717_A	A / A	-0.02 (↓)	86%	2.60 × 10 <sup>-10</sup>
rs6573971_G	A / A	0.01 (-)	44%	3.40 × 10 <sup>-10</sup>
rs55921103_G	T / T	-0.01 (-)	35%	5.10 × 10 <sup>-10</sup>
rs140584594_A	A / A	0.01 (↑)	27%	5.80 × 10 <sup>-10</sup>
rs3932048_C	C / G	-0.01 (↓)	68%	5.80 × 10 <sup>-10</sup>
rs13107326_C	C / C	0.02 (↑)	93%	6.00 × 10 <sup>-10</sup>
rs34568880_C	C / C	-0.06 (↓)	99%	6.10 × 10 <sup>-10</sup>
rs541155877_C	C / C	0.07 (↑)	99%	6.30 × 10 <sup>-10</sup>
rs6589939_A	A / G	-0.01 (↓)	62%	7.00 × 10 <sup>-10</sup>
rs1731243_C	C / T	-0.01 (↓)	39%	7.10 × 10 <sup>-10</sup>
rs11568318_C	C / C	-0.03 (↓)	93%	7.40 × 10 <sup>-10</sup>
rs4808360_T	T / A	-0.01 (↓)	49%	8.10 × 10 <sup>-10</sup>
rs2021092_T	T / T	0.02 (↑)	81%	8.70 × 10 <sup>-10</sup>

rs59328596_G	G / G	0.02 (↑)	85%	$8.90 \times 10^{-10}$
rs73025516_A	A / A	0.03 (↑)	96%	$9.20 \times 10^{-10}$
rs12078100_C	G / G	-0.01 (-)	38%	$9.30 \times 10^{-10}$
rs191064667_C	C / C	0.04 (↑)	96%	$9.30 \times 10^{-10}$
rs12197047_G	G / A	-0.01 (↓)	33%	$1.10 \times 10^{-9}$
rs9471975_T	C / C	0.01 (-)	42%	$1.10 \times 10^{-9}$
rs960596_C	C / T	-0.01 (↓)	66%	$1.30 \times 10^{-9}$
rs115739682_T	T / T	0.02 (↑)	81%	$1.40 \times 10^{-9}$
rs551473284_T	T / T	-0.01 (↓)	37%	$1.40 \times 10^{-9}$
rs9894946_A	A / G	0.02 (↑)	16%	$1.50 \times 10^{-9}$
rs112758337_G	G / G	0.02 (↑)	81%	$1.60 \times 10^{-9}$
rs56212732_C	C / C	0.02 (↑)	92%	$1.80 \times 10^{-9}$
rs6050463_G	G / A	-0.01 (↓)	51%	$1.80 \times 10^{-9}$
rs61988556_T	T / T	0.02 (↑)	91%	$2.10 \times 10^{-9}$
rs72733928_A	A / A	-0.03 (↓)	94%	$2.30 \times 10^{-9}$
rs61778883_T	T / T	-0.02 (↓)	13%	$2.40 \times 10^{-9}$
rs12471768_T	C / C	-0.01 (-)	30%	$2.50 \times 10^{-9}$
rs576573069_T	T / T	-0.01 (↓)	33%	$2.90 \times 10^{-9}$
rs11014204_C	C / C	-0.01 (↓)	72%	$3.30 \times 10^{-9}$
rs438568_A	G / G	-0.01 (-)	39%	$4.00 \times 10^{-9}$
rs10910476_C	C / T	-0.01 (↓)	44%	$4.30 \times 10^{-9}$
rs12162782_T	T / G	-0.01 (↓)	66%	$4.40 \times 10^{-9}$
rs111338114_A	A / A	0.03 (↑)	94%	$4.70 \times 10^{-9}$
rs35882350_A	A / A	-0.01 (↓)	74%	$5.00 \times 10^{-9}$
rs11227247_A	A / A	-0.02 (↓)	87%	$5.70 \times 10^{-9}$
rs10851478_T	T / C	0.01 (↑)	58%	$6.00 \times 10^{-9}$
rs4148826_T	T / T	0.02 (↑)	82%	$6.50 \times 10^{-9}$
rs2256814_G	G / G	-0.02 (↓)	80%	$6.70 \times 10^{-9}$
rs1250258_C	T / T	-0.01 (-)	26%	$6.80 \times 10^{-9}$
rs56236159_T	T / T	-0.02 (↓)	87%	$7.00 \times 10^{-9}$
rs12445804_G	G / G	-0.02 (↓)	93%	$8.00 \times 10^{-9}$
rs6560499_G	A / A	0.01 (-)	42%	$8.10 \times 10^{-9}$
rs204469_A	NA	-0.03 (-)	4%	$8.60 \times 10^{-9}$
rs913499_A	A / G	0.01 (↑)	49%	$9.80 \times 10^{-9}$
rs9686661_C	C / C	-0.01 (↓)	80%	$1.10 \times 10^{-8}$
rs112403212_C	C / C	-0.02 (↓)	86%	$1.20 \times 10^{-8}$
rs61754230_C	C / C	-0.04 (↓)	98%	$1.20 \times 10^{-8}$
rs7241918_G	G / T	-0.02 (↓)	18%	$1.20 \times 10^{-8}$
rs869412_T	T / T	0.01 (↑)	77%	$1.20 \times 10^{-8}$
rs1007938_A	A / G	-0.01 (↓)	59%	$1.30 \times 10^{-8}$
rs28768427_G	G / A	-0.01 (↓)	48%	$1.30 \times 10^{-8}$
rs72638977_A	A / A	0.03 (↑)	97%	$1.30 \times 10^{-8}$
rs62011285_T	C / C	-0.01 (-)	66%	$1.60 \times 10^{-8}$
rs7090758_T	T / C	0.01 (↑)	53%	$1.60 \times 10^{-8}$
rs73075609_C	C / C	-0.04 (↓)	97%	$1.60 \times 10^{-8}$
rs77013160_G	G / G	-0.04 (↓)	98%	$1.70 \times 10^{-8}$
rs28406917_C	T / T	-0.01 (-)	57%	$1.80 \times 10^{-8}$
rs7108486_T	T / T	0.04 (↑)	98%	$1.80 \times 10^{-8}$
rs990619_C	C / G	0.01 (↑)	48%	$1.90 \times 10^{-8}$
rs12936113_T	T / C	-0.01 (↓)	24%	$2.30 \times 10^{-8}$
rs56208742_T	T / T	0.03 (↑)	97%	$2.30 \times 10^{-8}$
rs79828839_C	C / T	-0.01 (↓)	80%	$2.40 \times 10^{-8}$
rs61433703_G	G / G	-0.02 (↓)	84%	$2.70 \times 10^{-8}$
rs6714750_A	A / A	-0.01 (↓)	80%	$2.70 \times 10^{-8}$
rs144984216_C	C / C	0.04 (↑)	98%	$2.80 \times 10^{-8}$
rs8008068_A	A / G	-0.02 (↓)	84%	$3.70 \times 10^{-8}$
rs77257036_C	* / T	0.01 (-)	65%	$3.80 \times 10^{-8}$
rs72774870_C	C / T	0.02 (↑)	93%	$3.90 \times 10^{-8}$
rs146433259_C	C / C	0.06 (↑)	99%	$4.60 \times 10^{-8}$

rs4620259\_A 

A / A

-0.01 (↓)

81%

$4.60 \times 10^{-8}$

rs836550\_A 

A / G

-0.01 (↓)

59%

$4.60 \times 10^{-8}$

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.