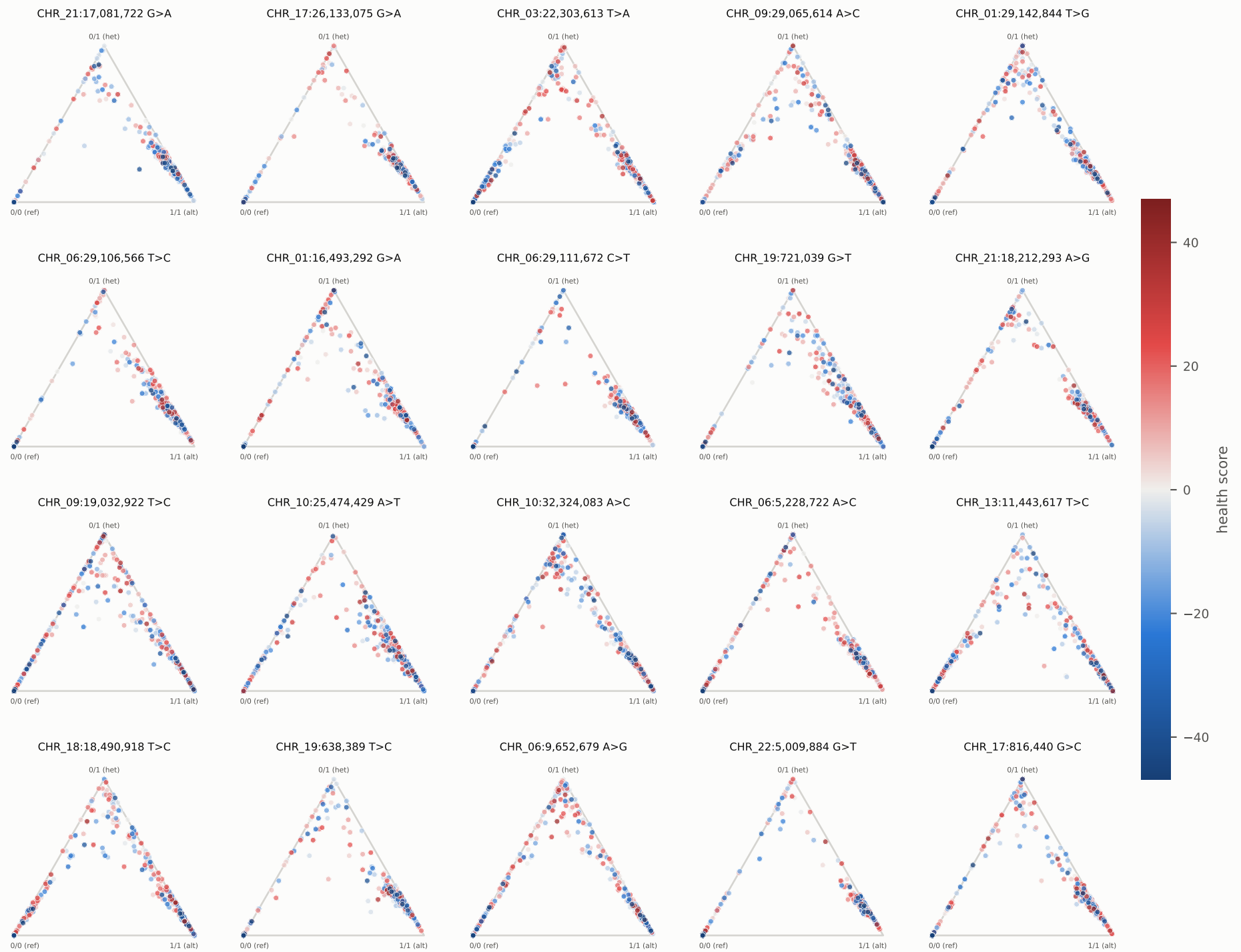
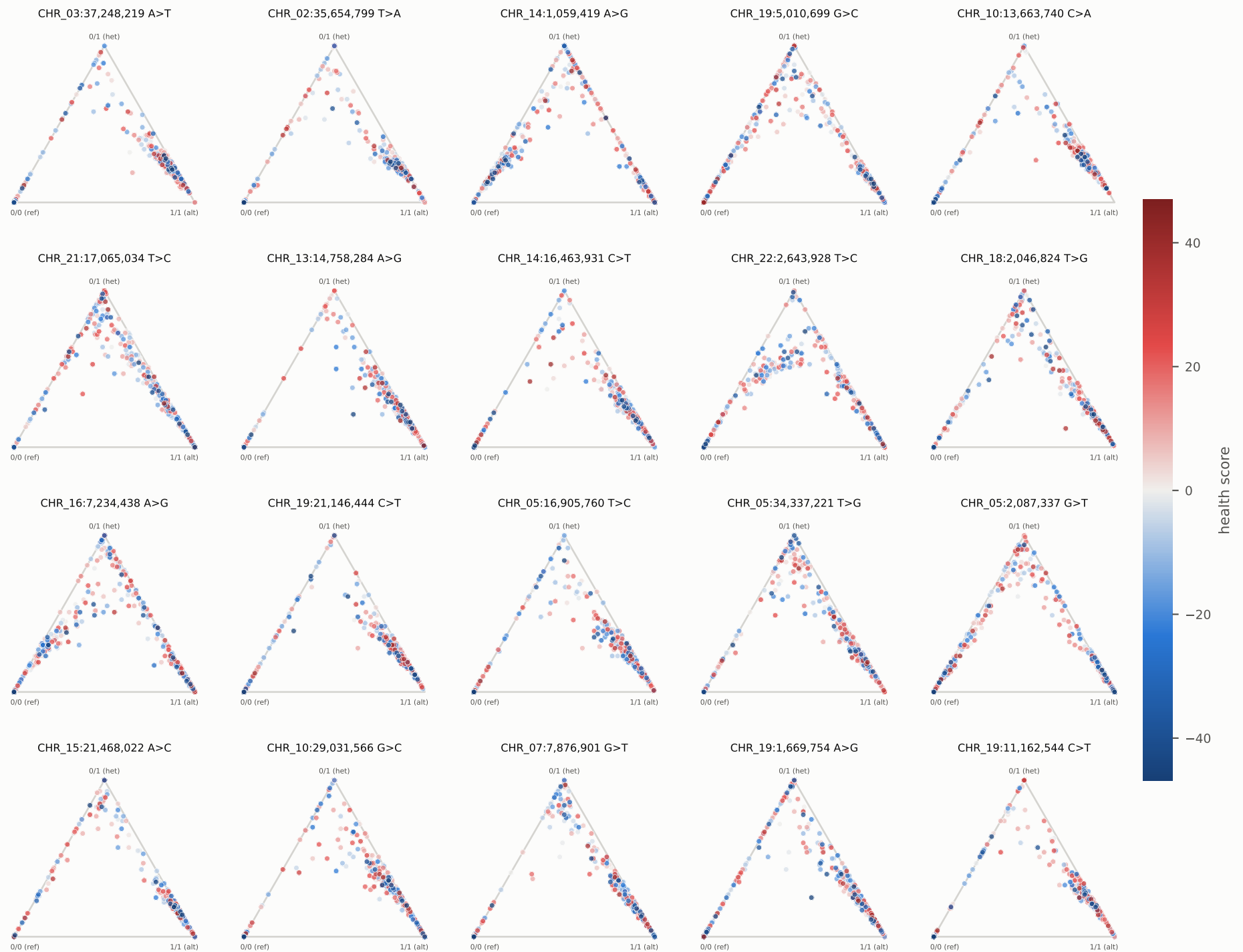


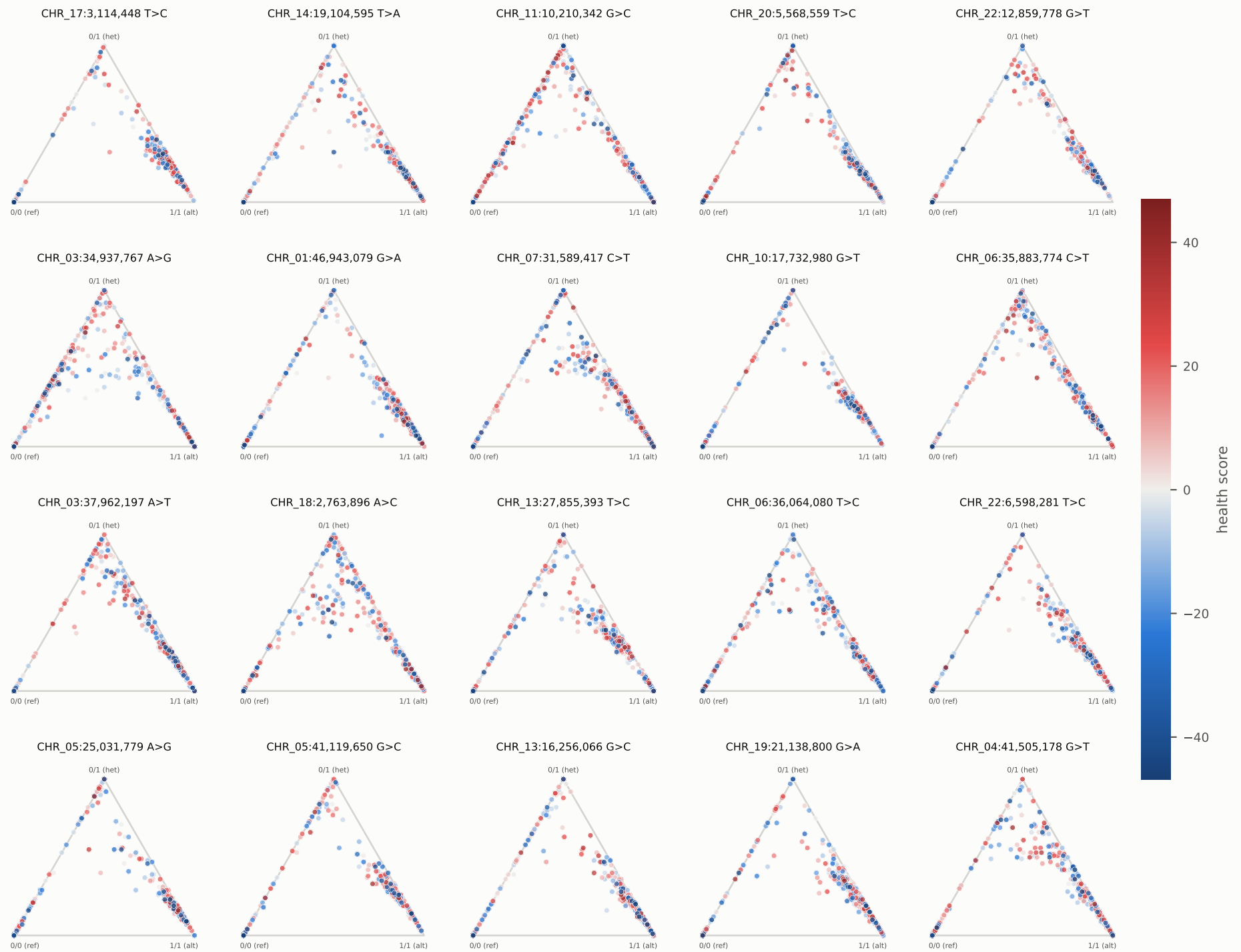
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 1/10



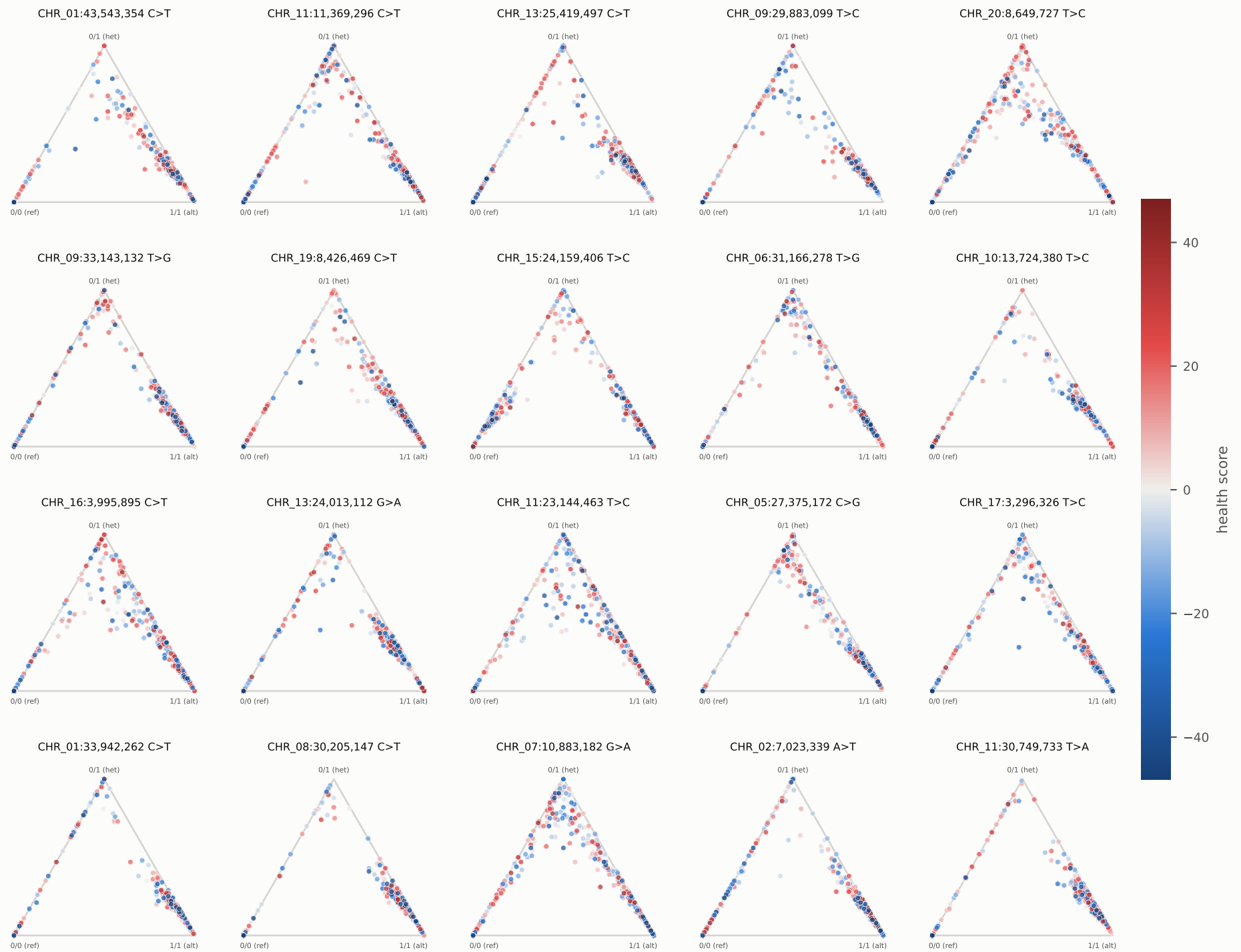
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 2/10



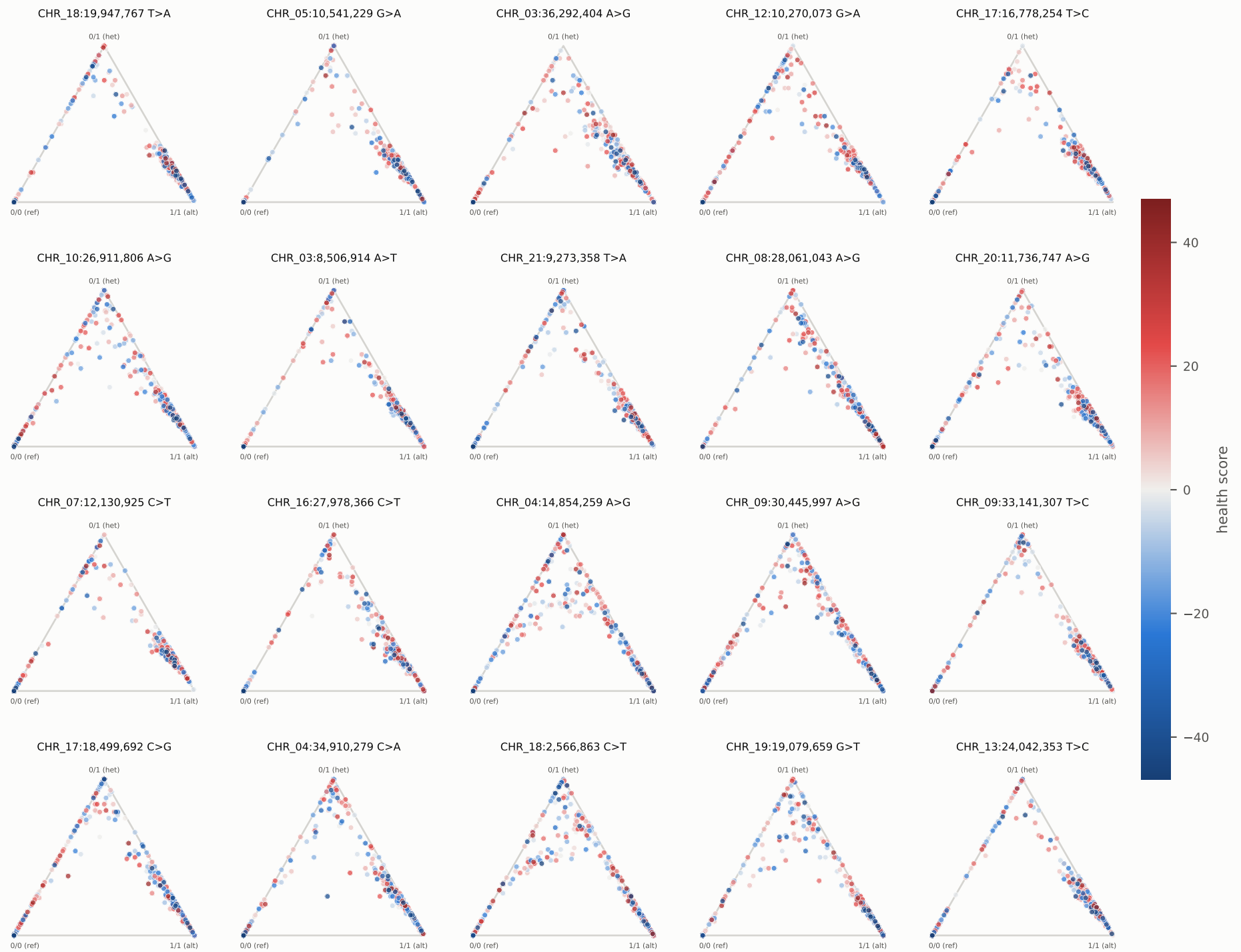
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 3/10



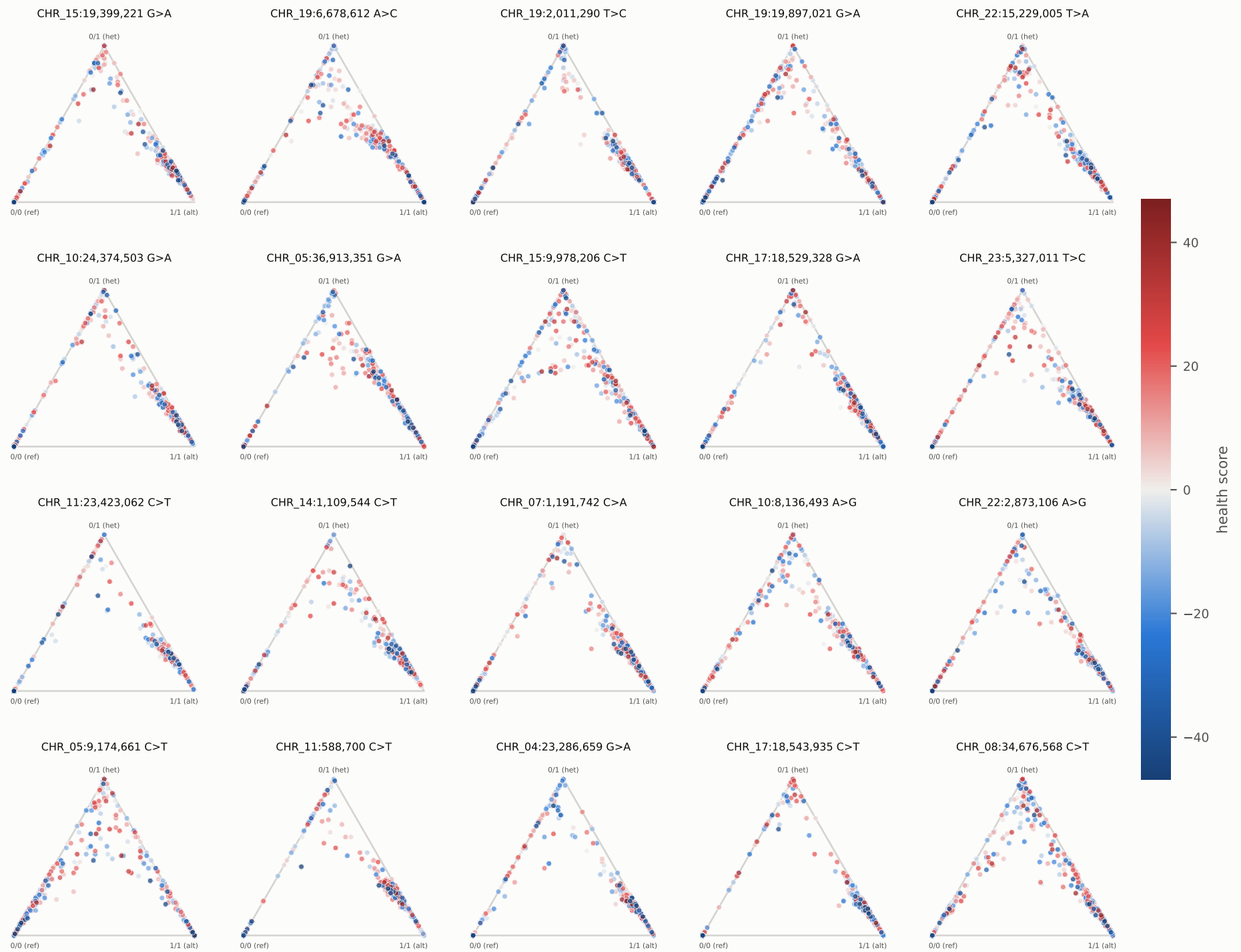
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 4/10



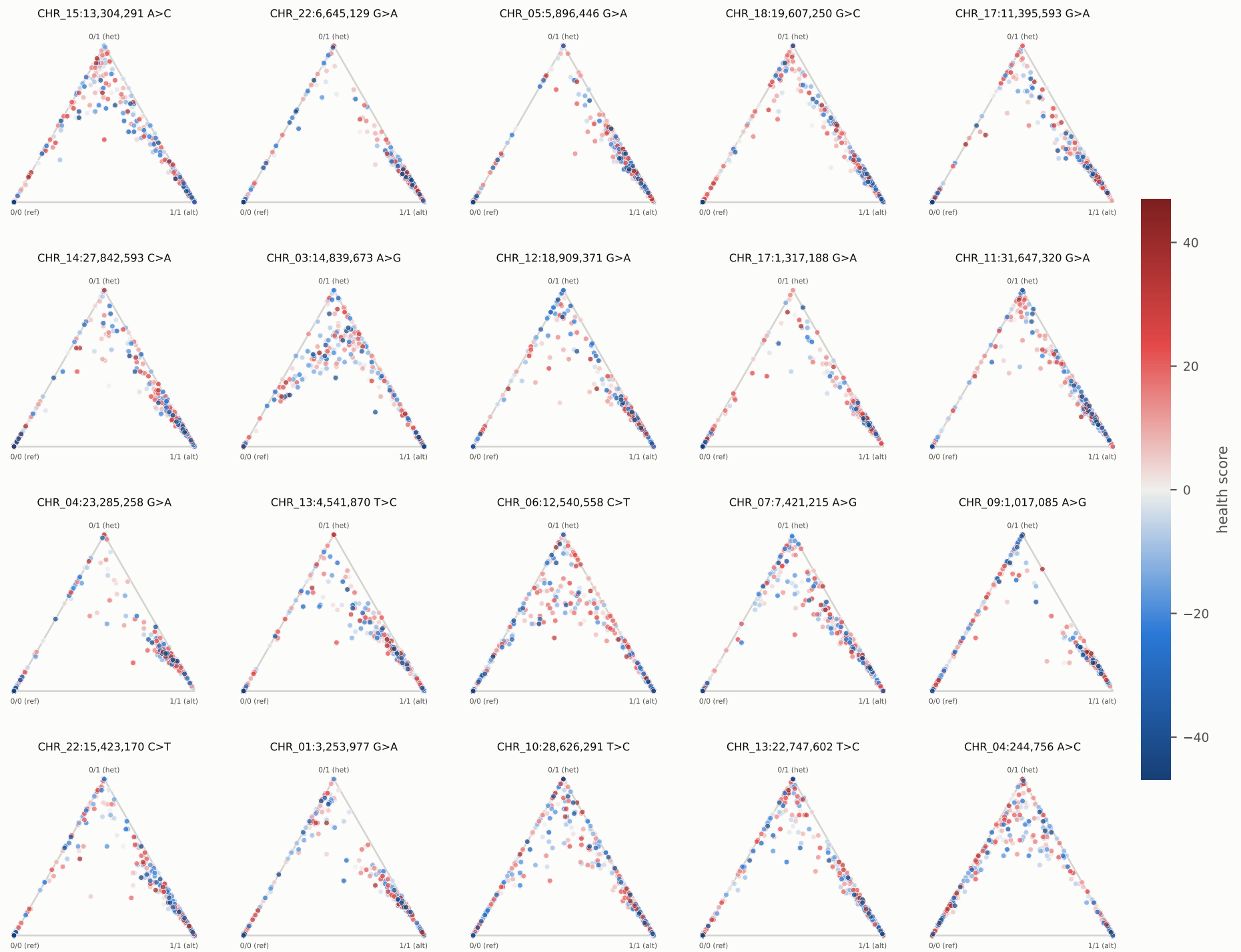
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 5/10



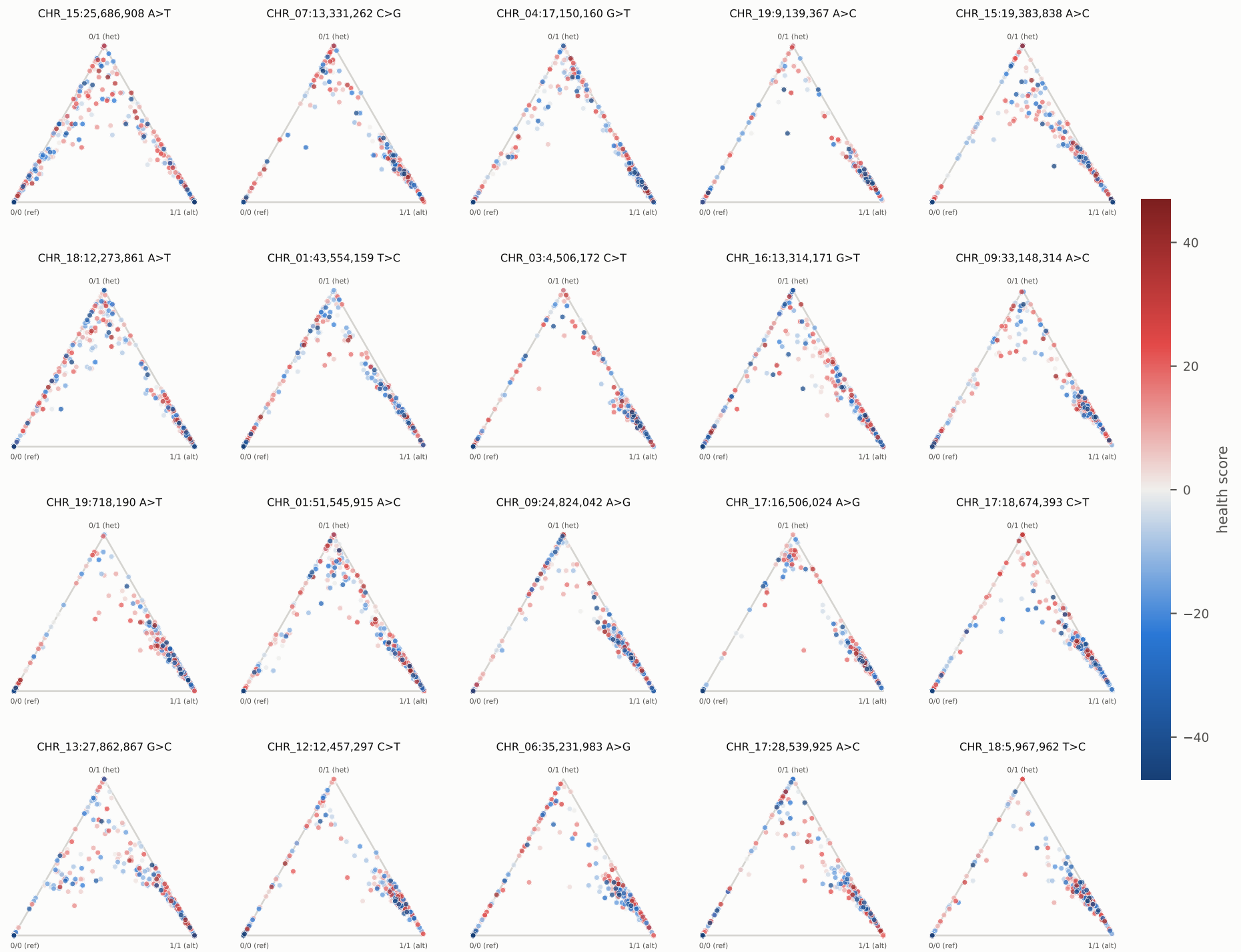
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 6/10

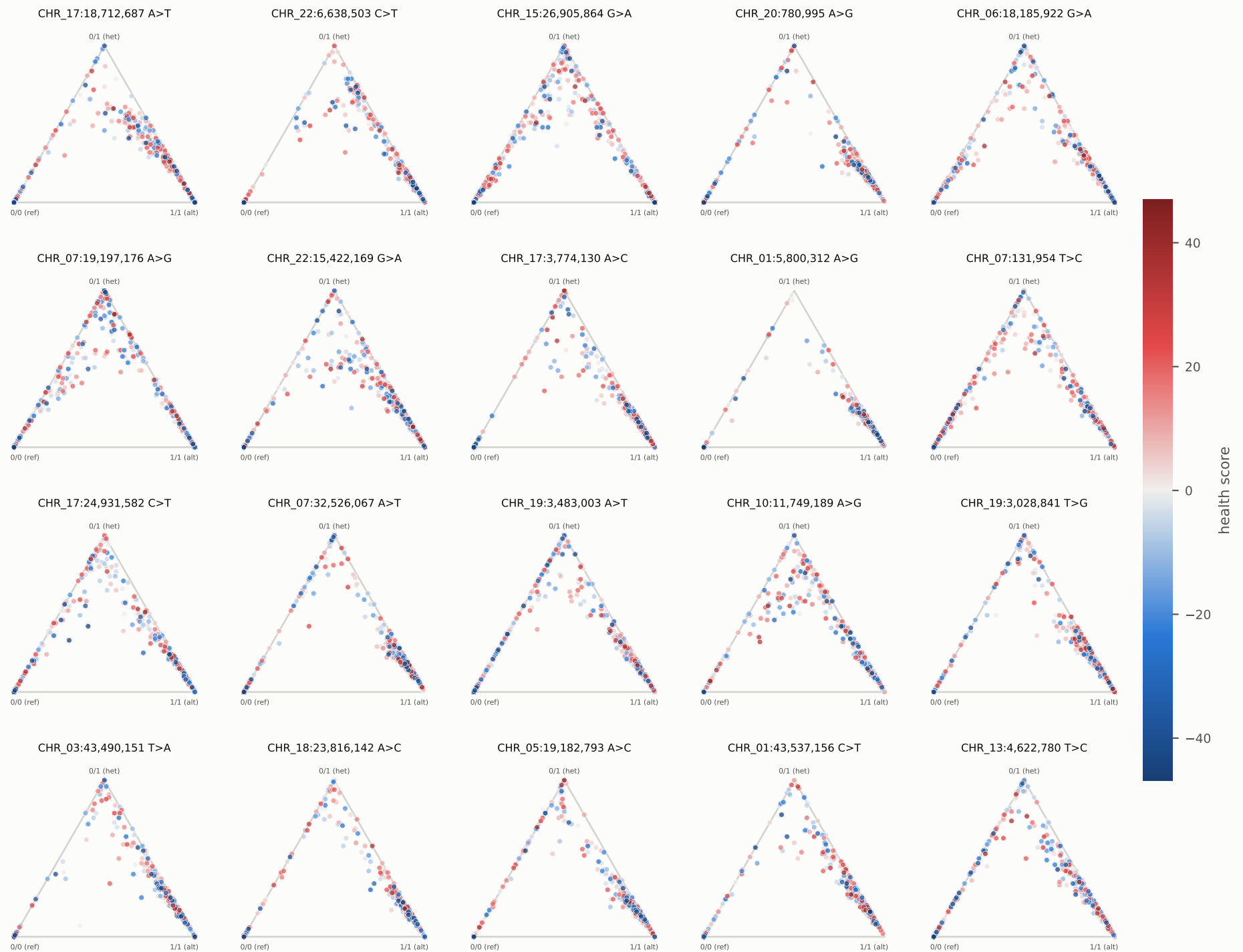


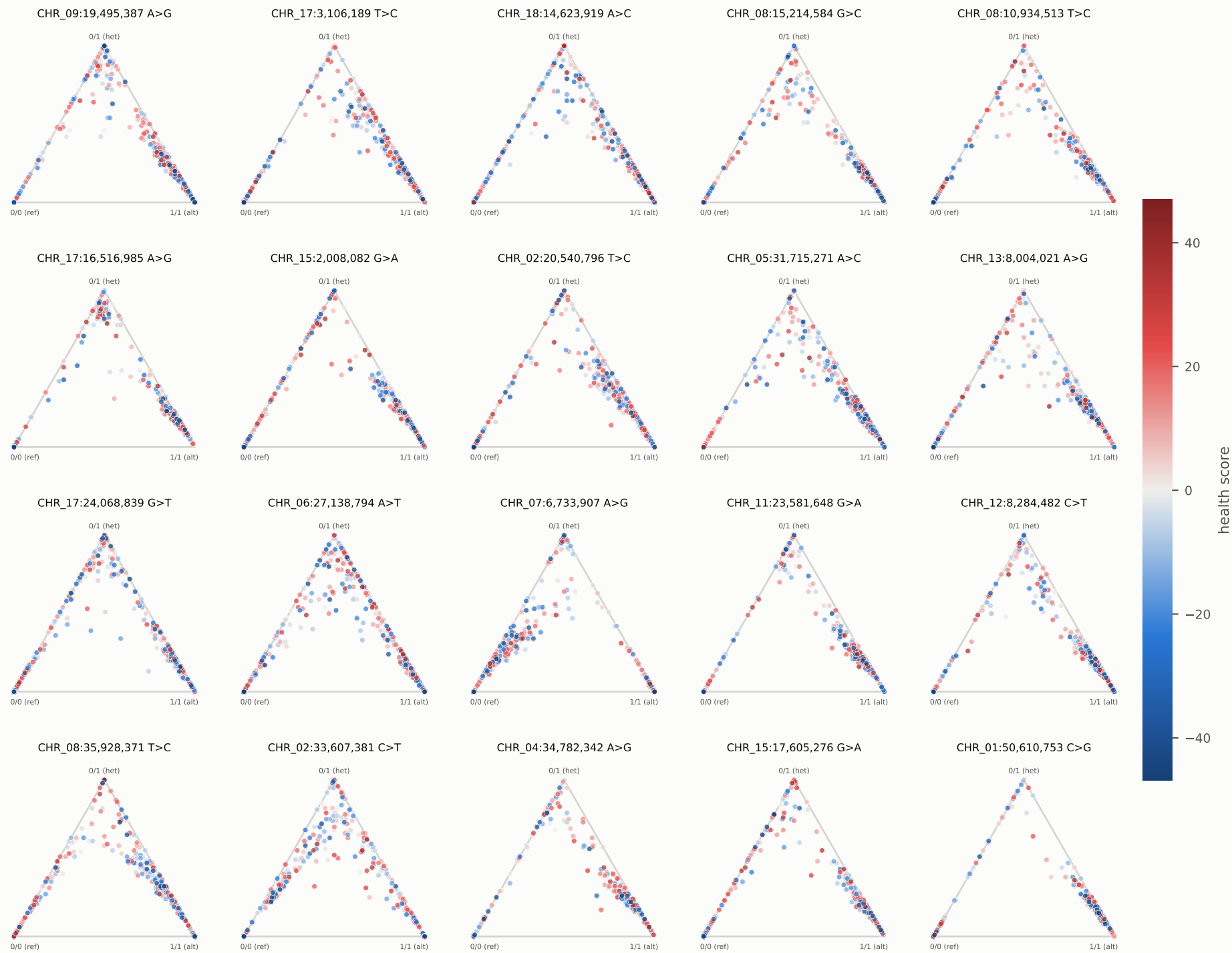
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 7/10



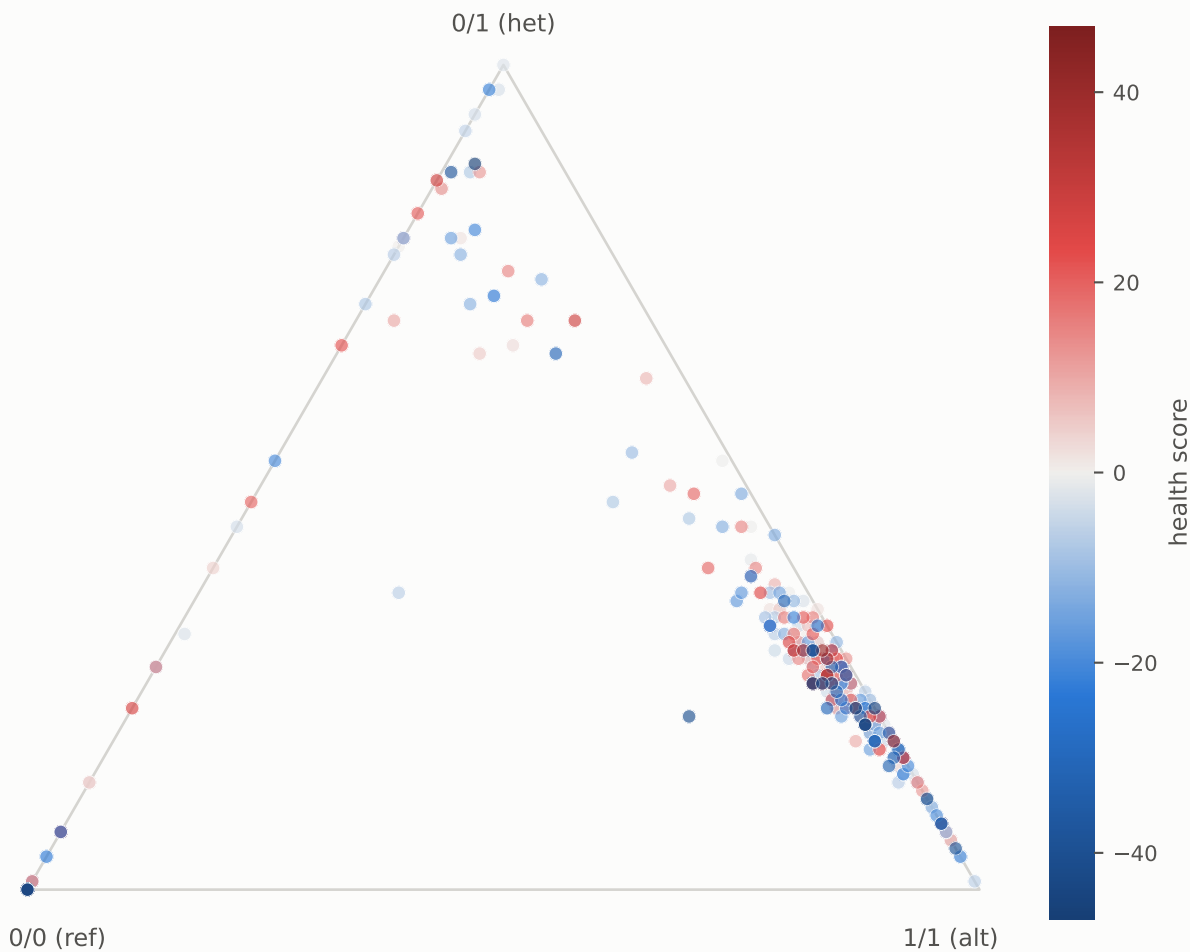
pruned — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 8/10



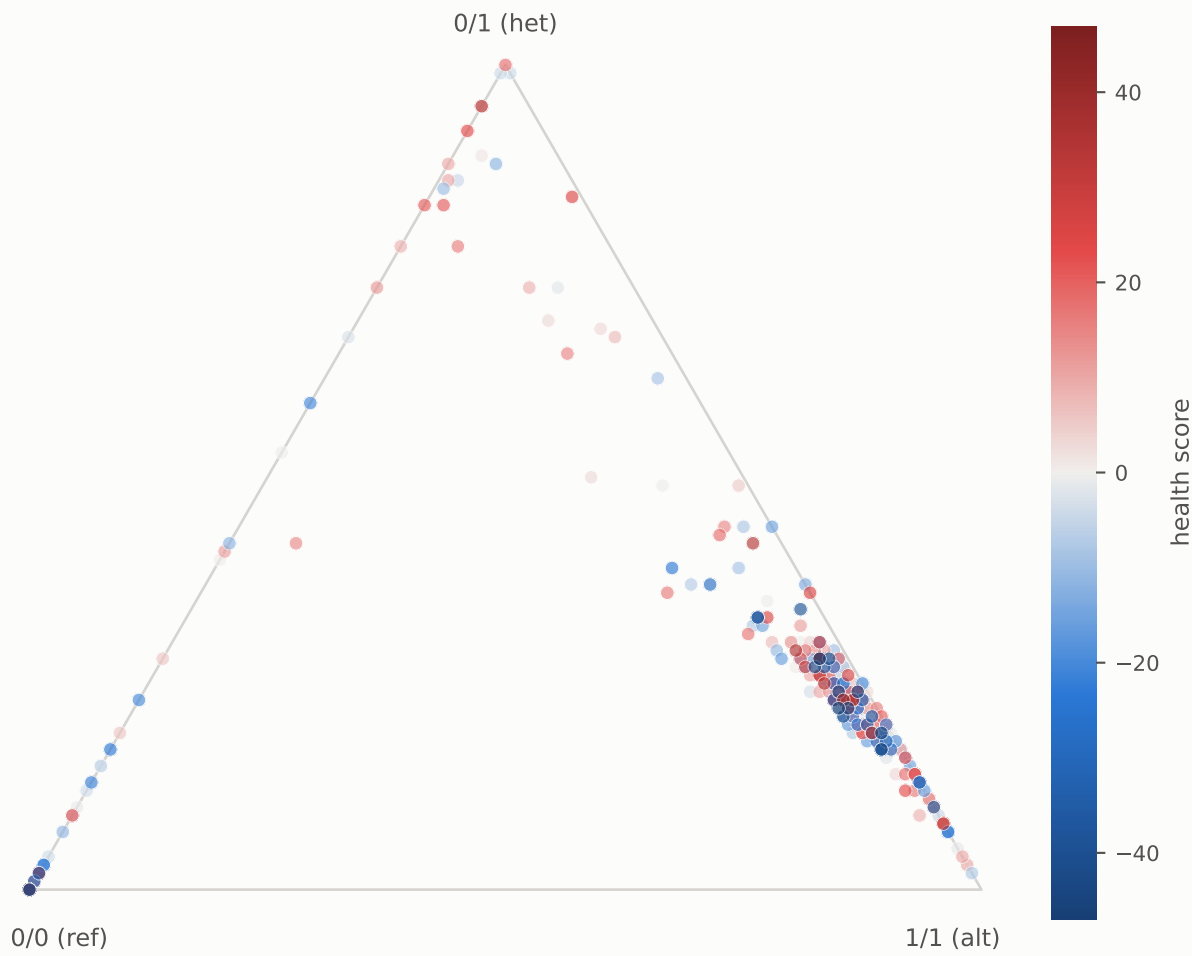




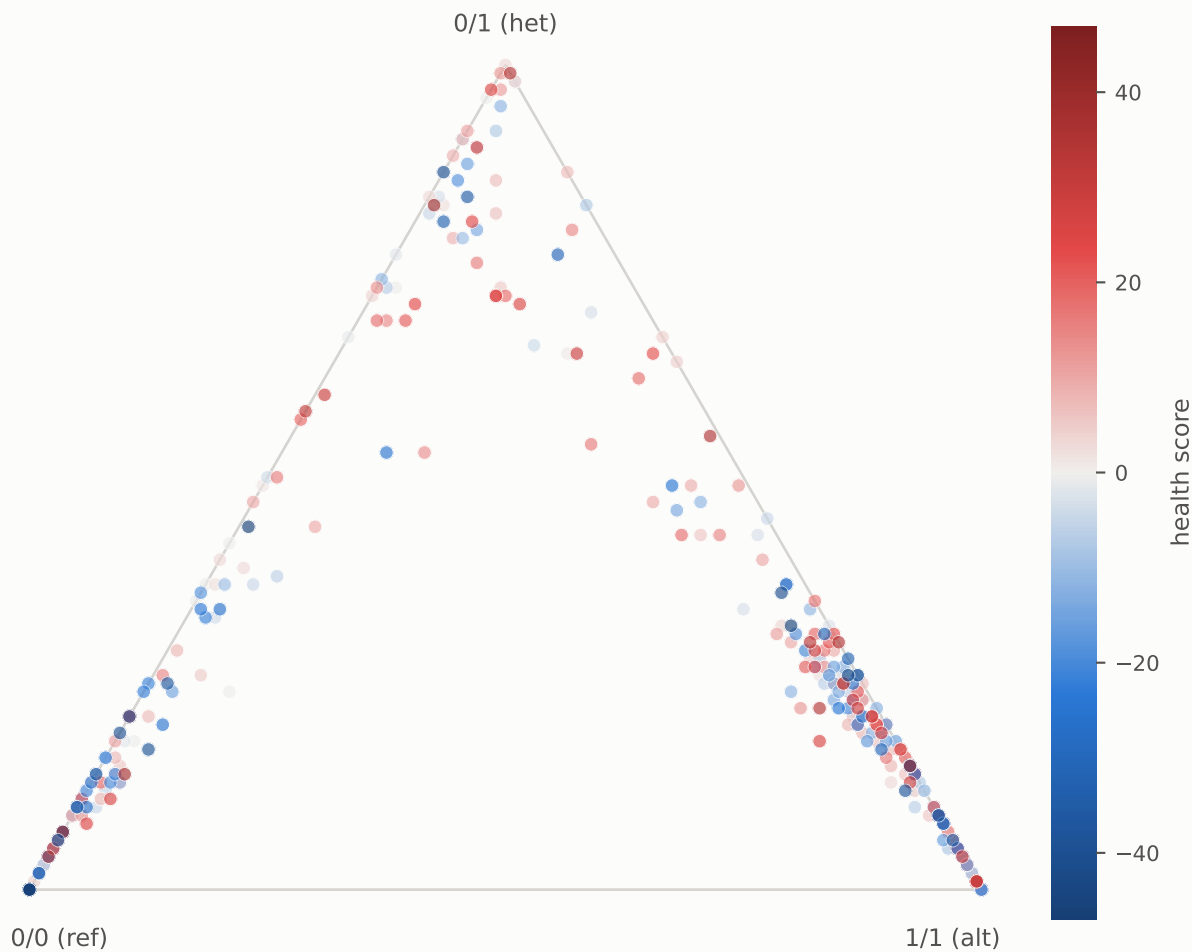
#1 by genotype uncertainty CHR_21:17,081,722 G>A
AF=0.49 DR2=0.81 r=-0.156 H=0.425 F=5.7



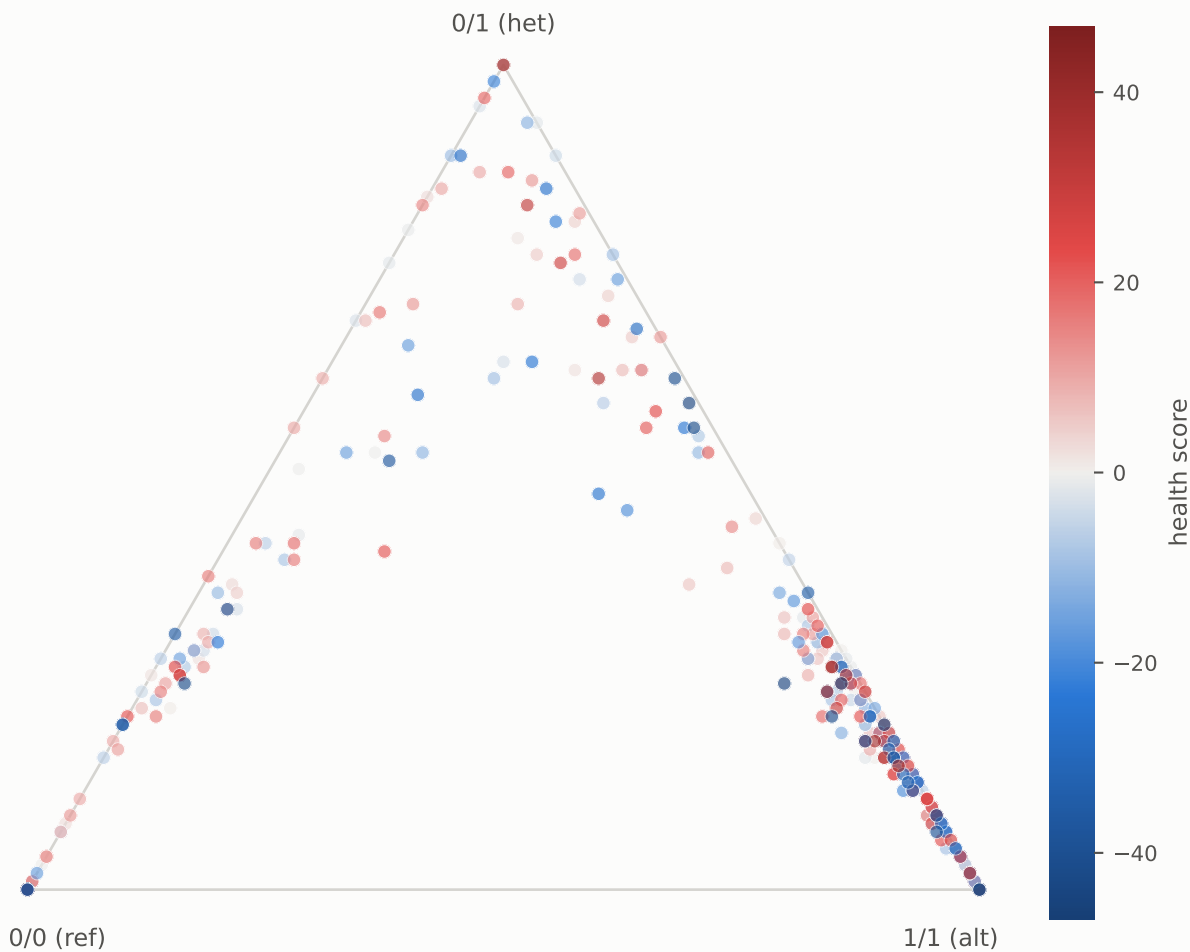
#2 by genotype uncertainty CHR_17:26,133,075 G>A
AF=0.52 DR2=0.81 r=+0.020 H=0.414 F=2.0



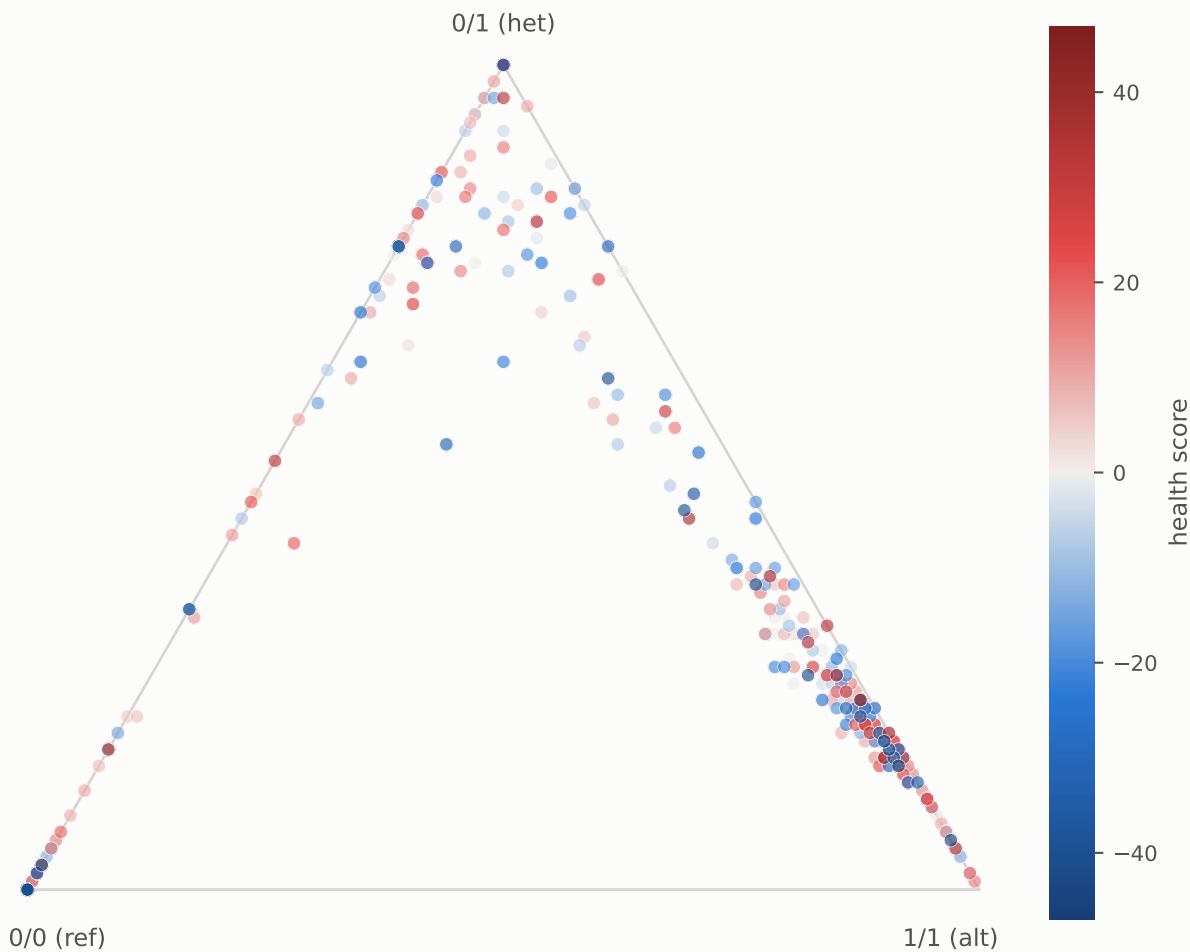
#3 by genotype uncertainty CHR_03:22,303,613 T>A
AF=0.48 DR2=0.81 r=+0.076 H=0.414 F=5.7



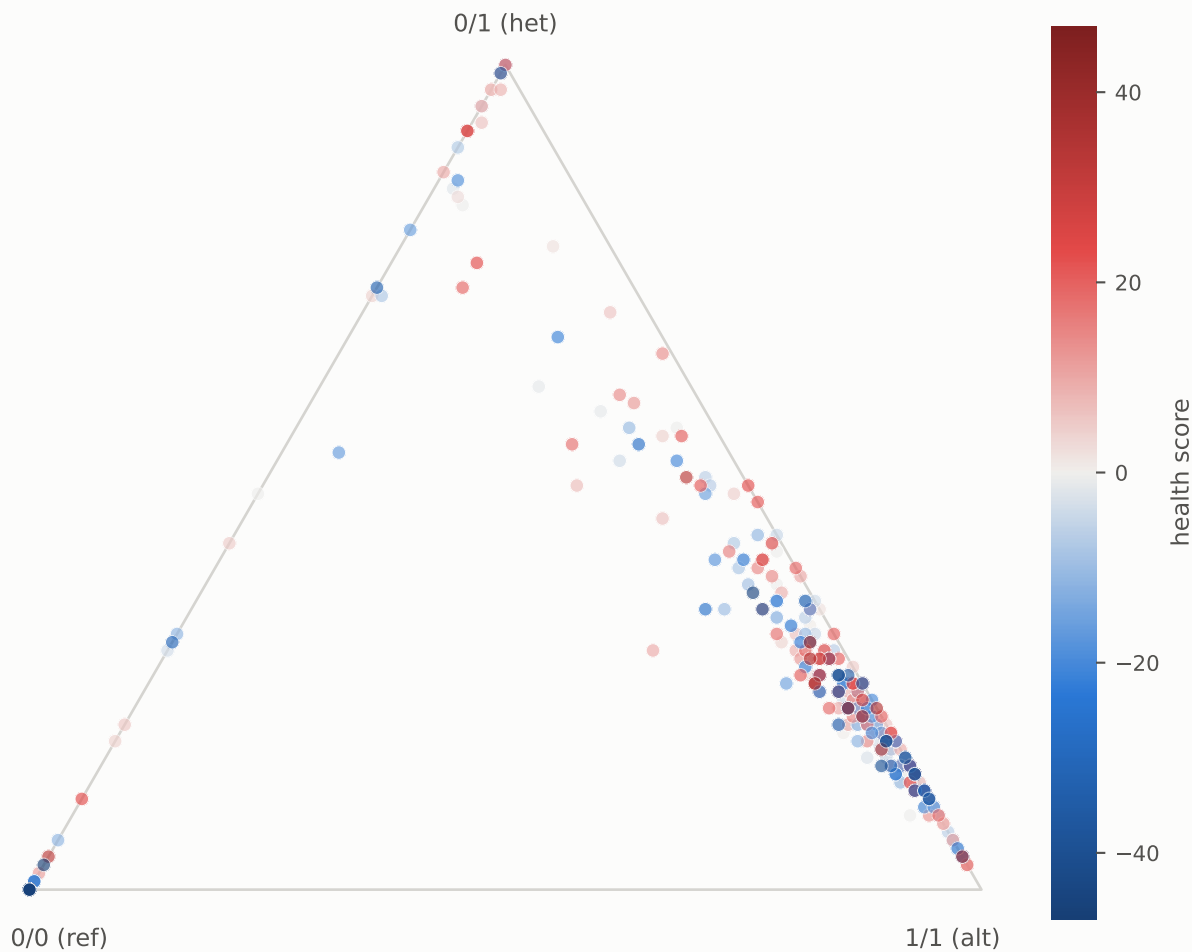
#4 by genotype uncertainty CHR_09:29,065,614 A>C
AF=0.54 DR2=0.81 $r=-0.015$ H=0.413 F=0.1



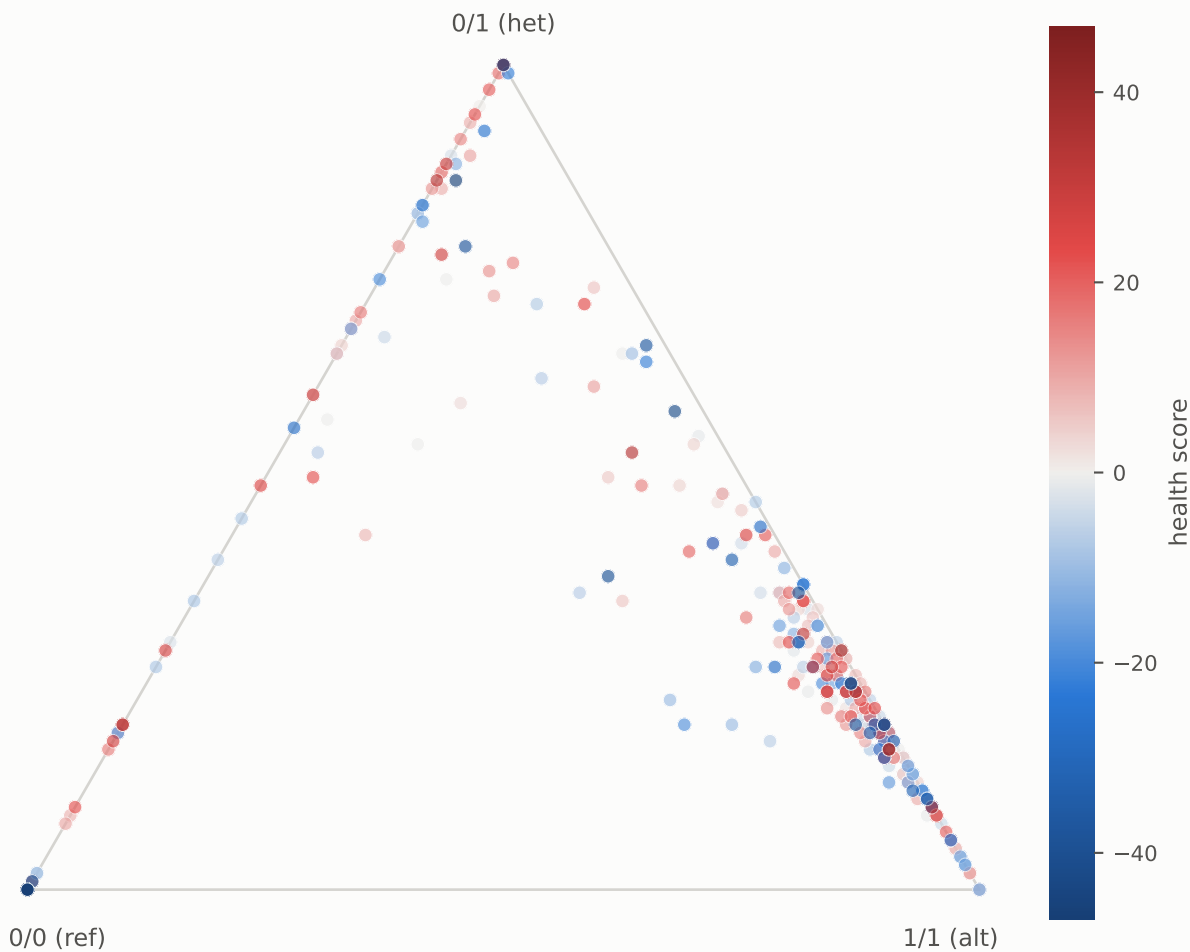
#5 by genotype uncertainty CHR_01:29,142,844 T>G
AF=0.47 DR2=0.81 r=-0.014 H=0.411 F=1.1



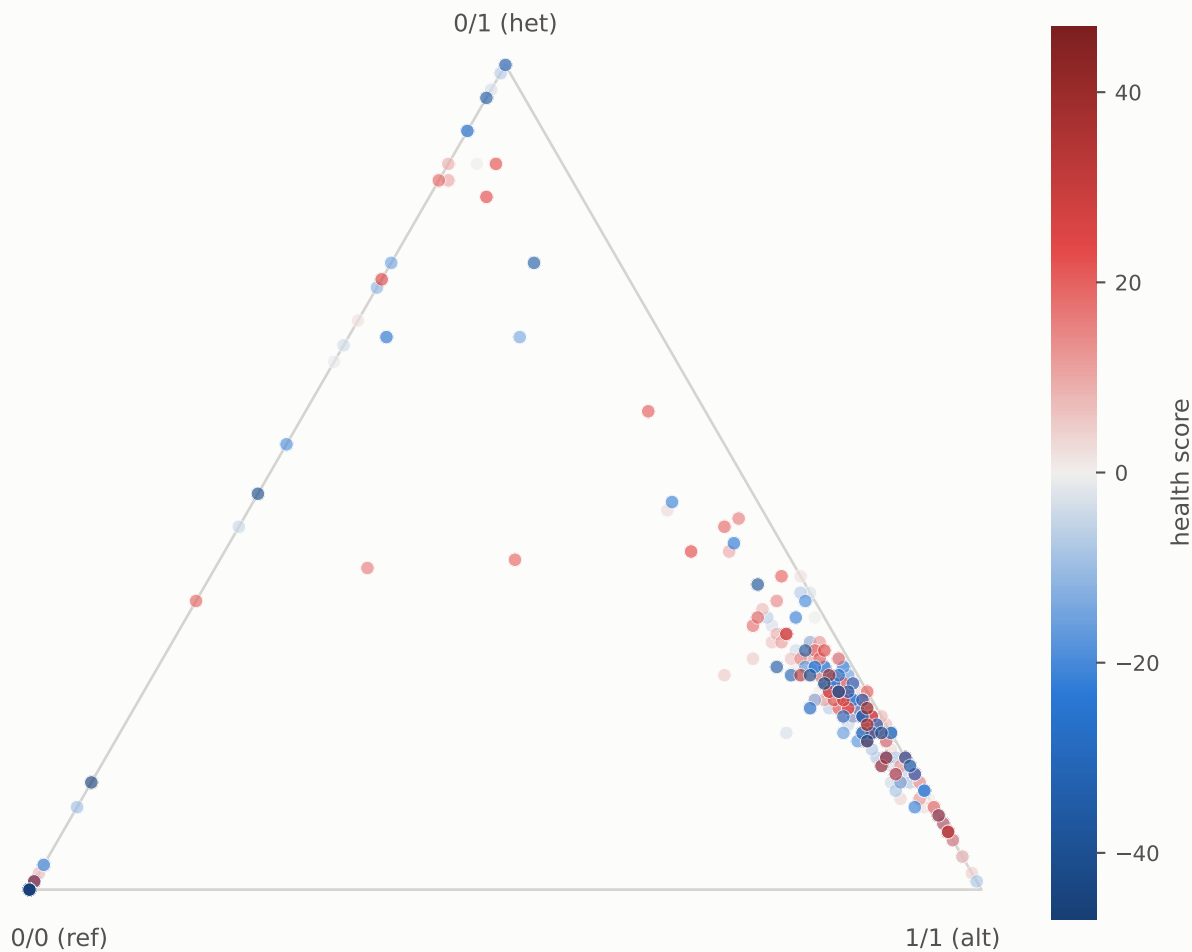
#6 by genotype uncertainty CHR_06:29,106,566 T>C
AF=0.54 DR2=0.81 r=-0.013 H=0.408 F=0.2



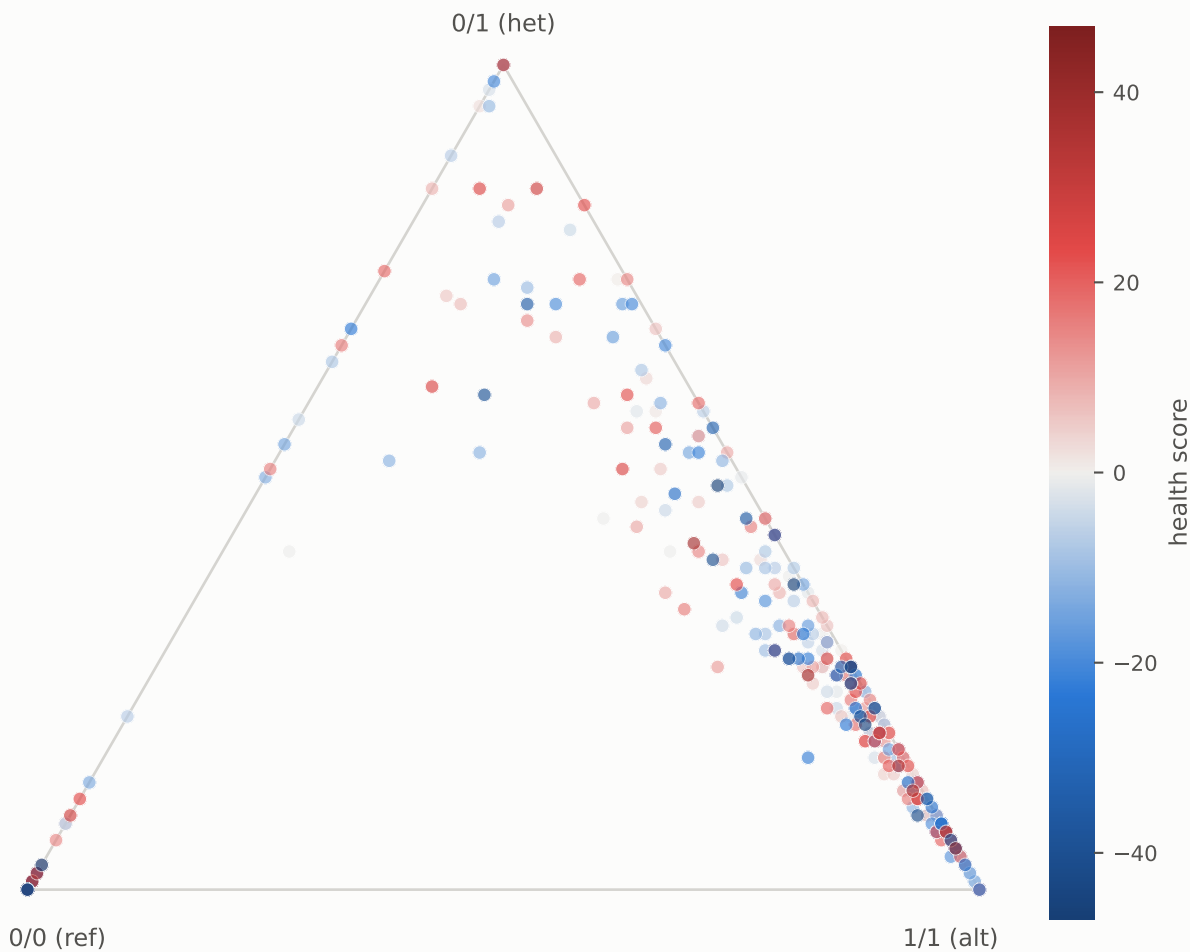
#7 by genotype uncertainty CHR_01:16,493,292 G>A
AF=0.5 DR2=0.81 r=+0.065 H=0.408 F=1.0



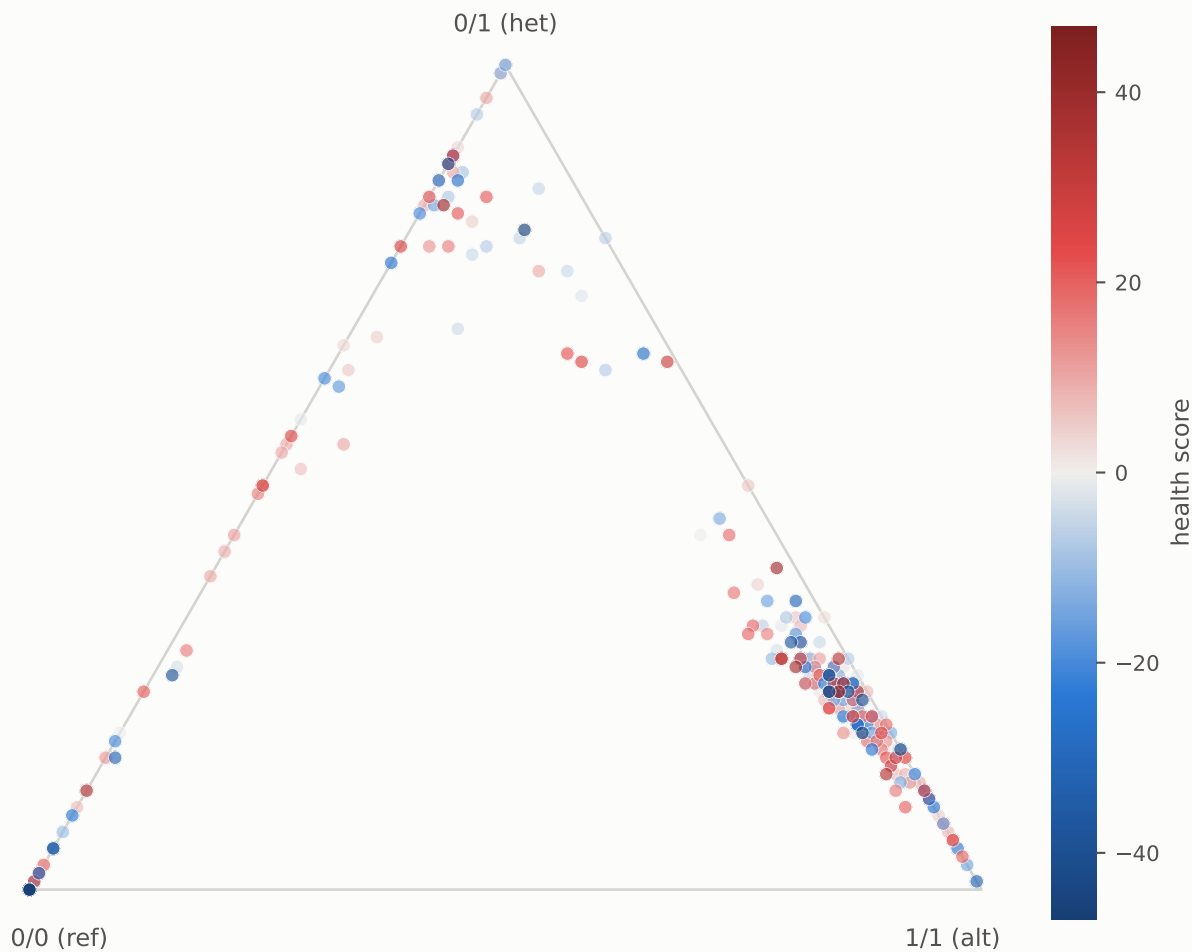
#8 by genotype uncertainty CHR_06:29,111,672 C>T
AF=0.54 DR2=0.81 $r=+0.006$ H=0.408 F=0.5



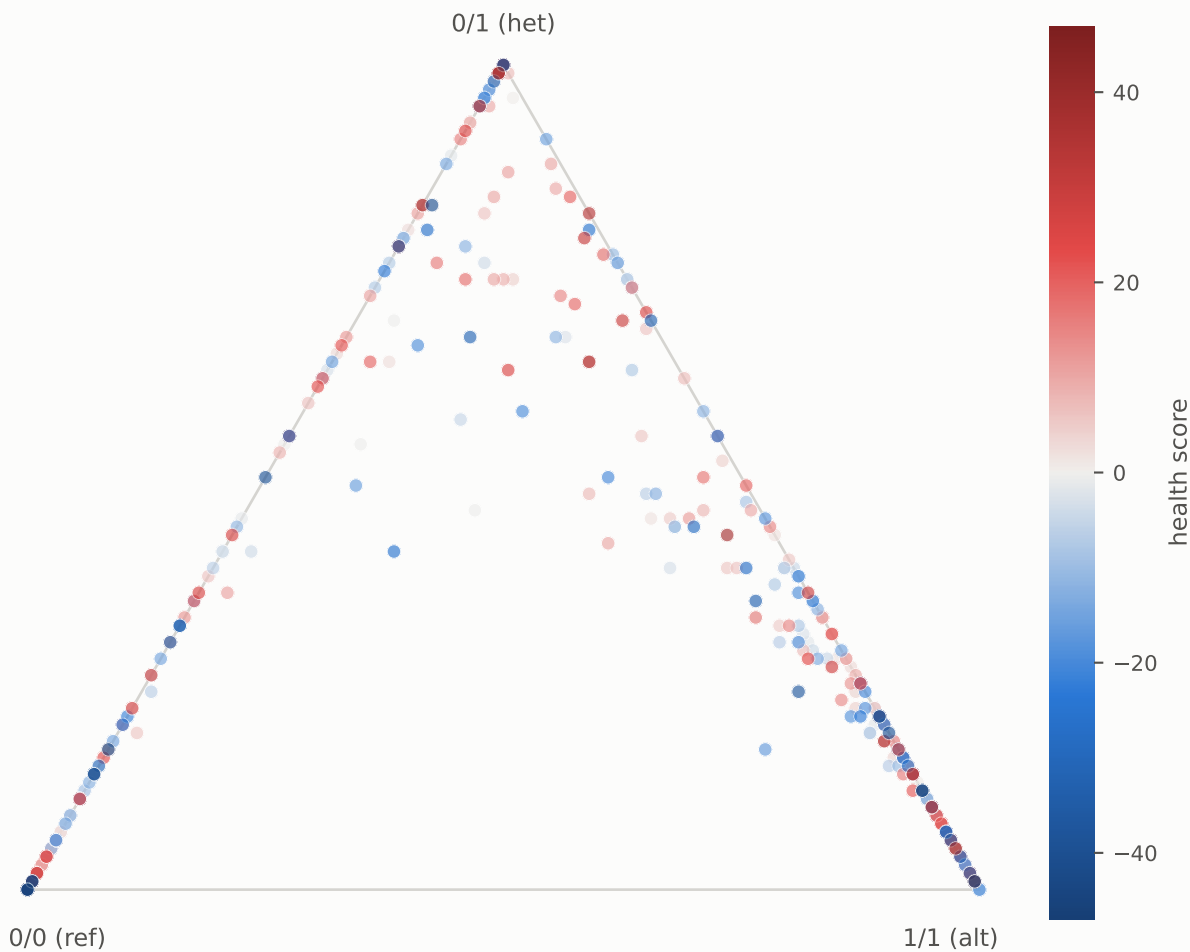
#9 by genotype uncertainty CHR_19:721,039 G>T
AF=0.53 DR2=0.81 $r=-0.065$ $\bar{H}=0.405$ $F=1.0$



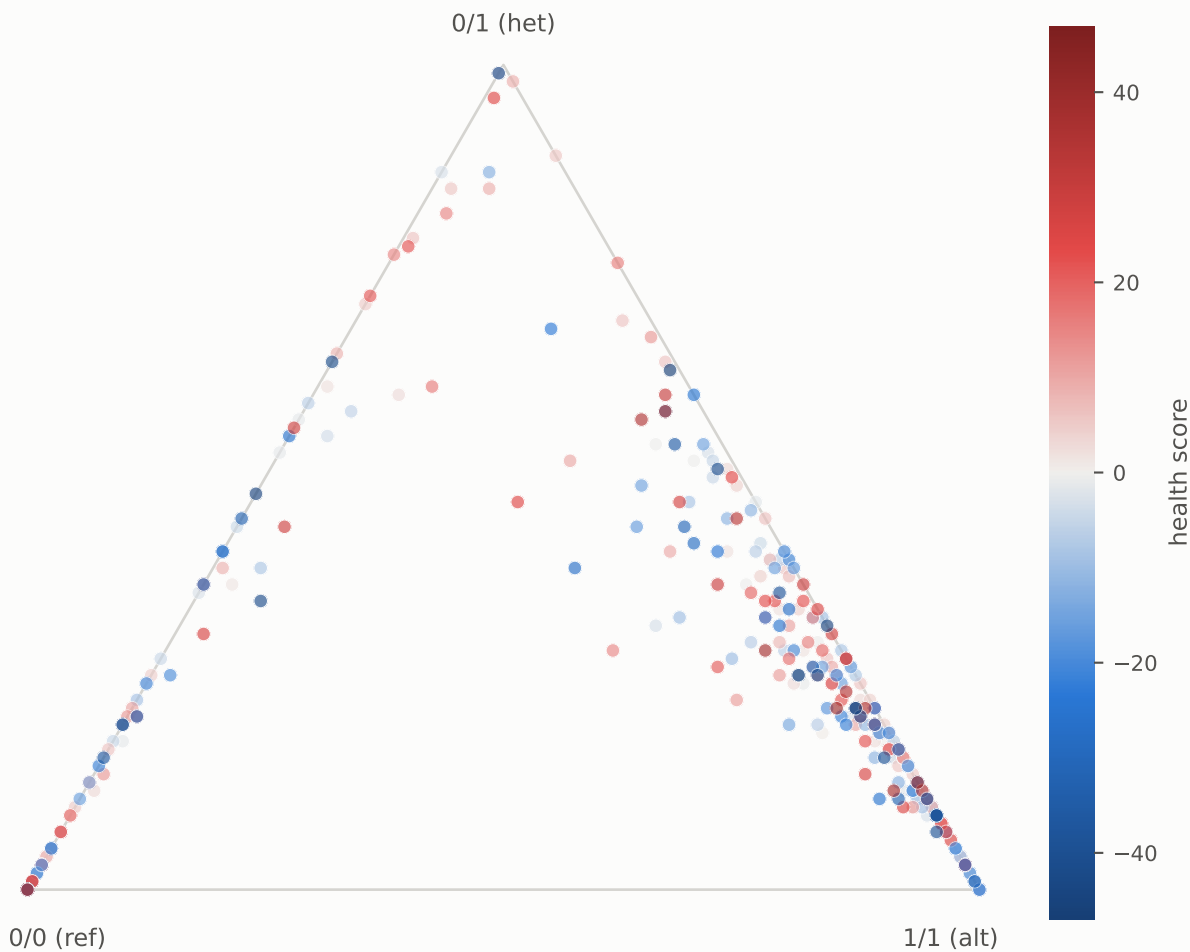
#10 by genotype uncertainty CHR_21:18,212,293 A>G
AF=0.46 DR2=0.82 $r=+0.016$ H=0.405 F=0.1



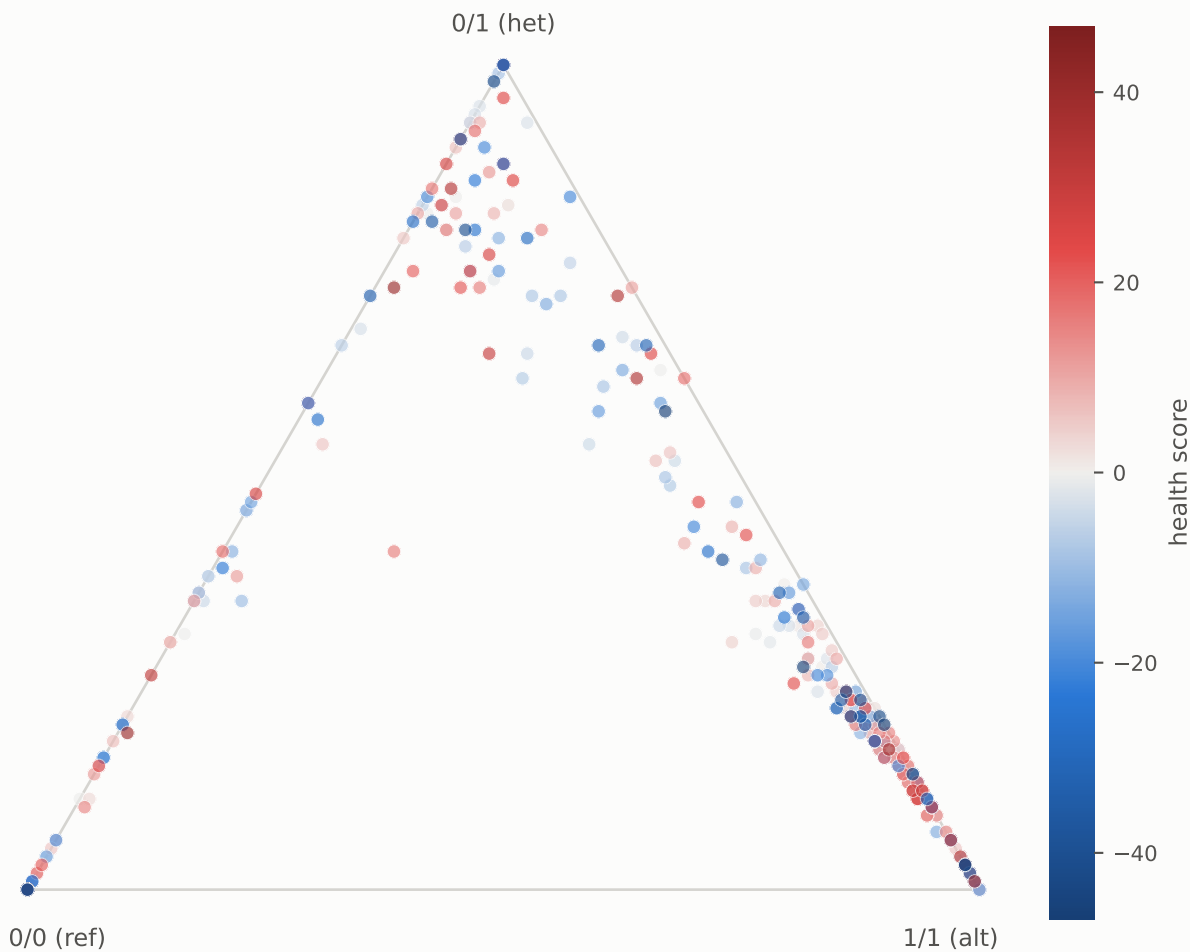
#11 by genotype uncertainty CHR_09:19,032,922 T>C
AF=0.48 DR2=0.81 r=+0.001 H=0.404 F=1.2



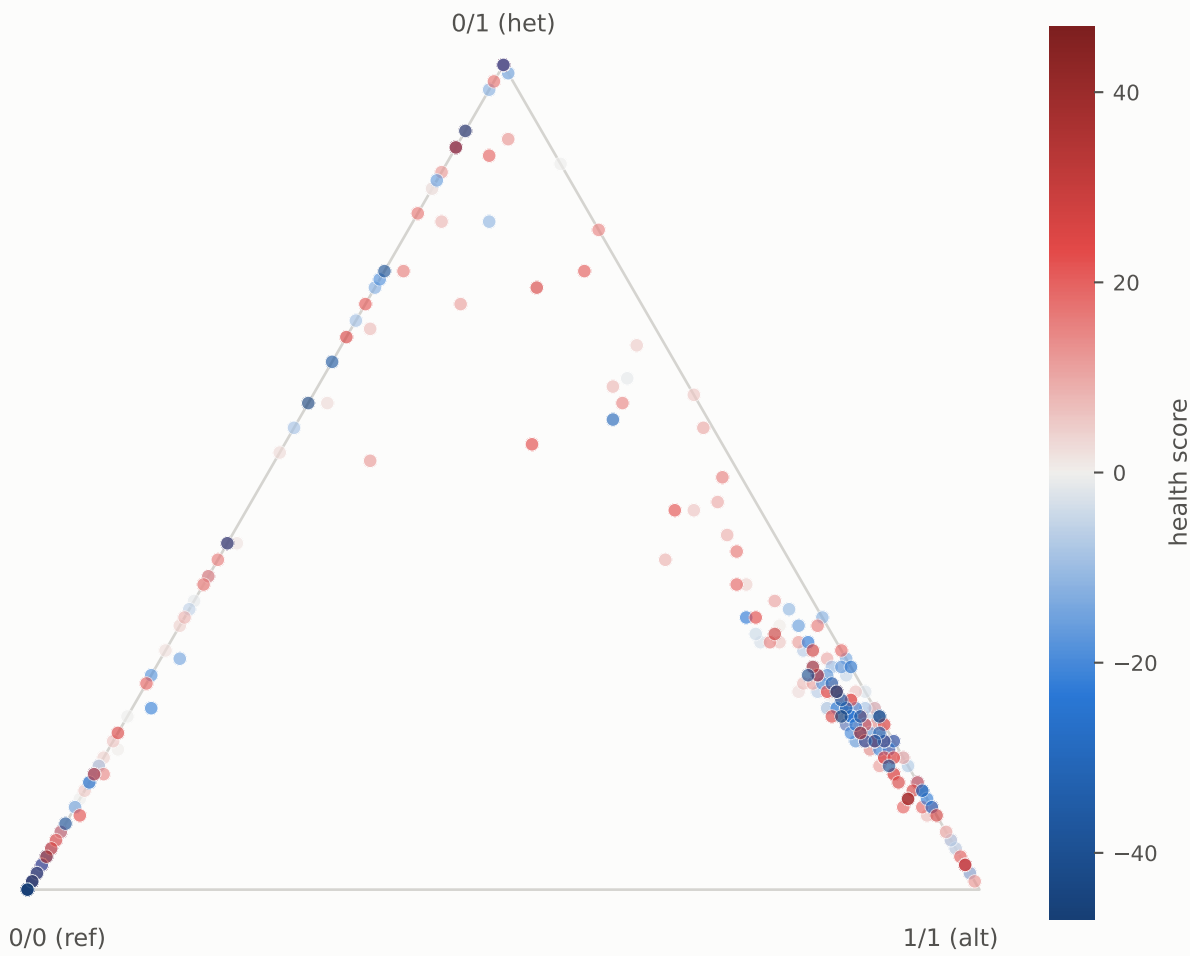
#12 by genotype uncertainty CHR_10:25,474,429 A>T
AF=0.48 DR2=0.81 $r=-0.101$ $\bar{H}=0.404$ F=1.4



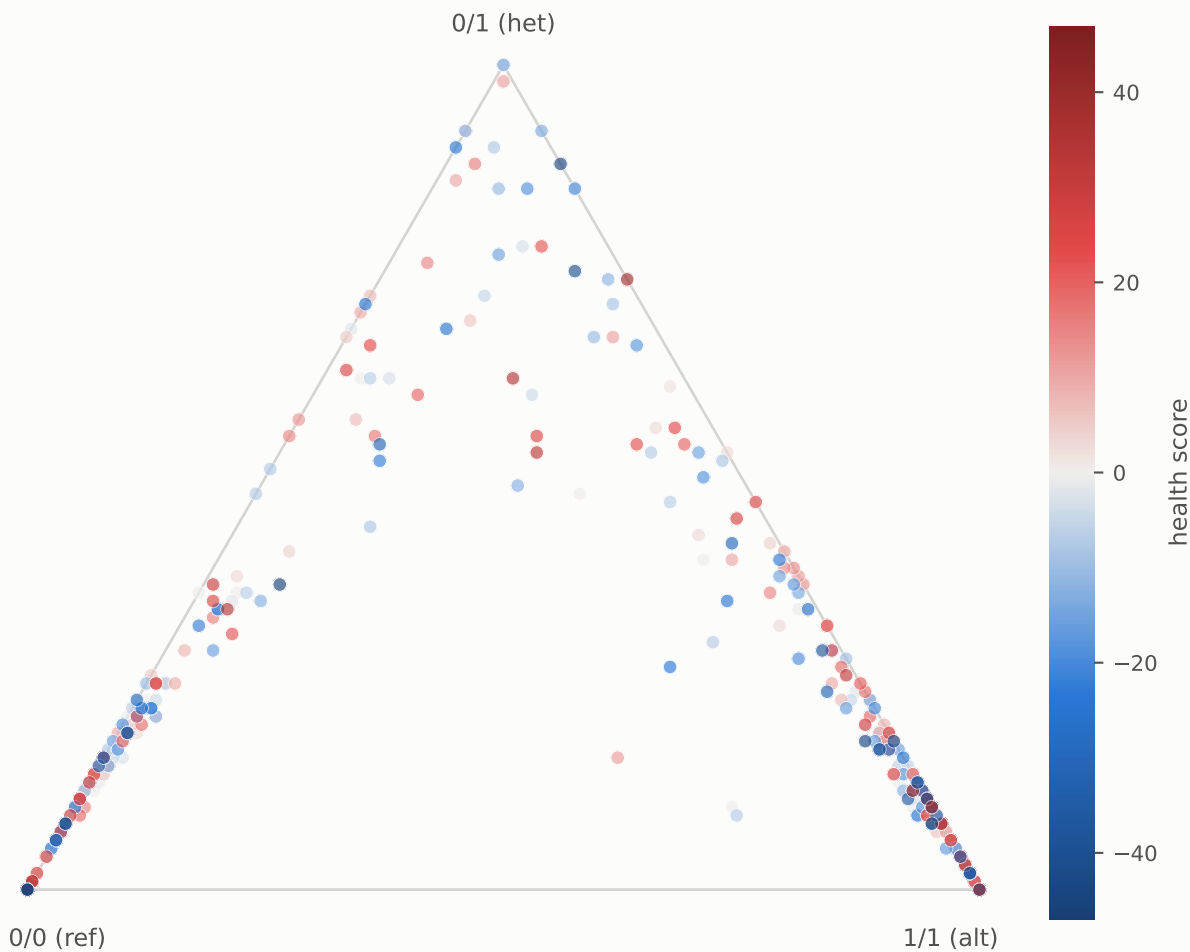
#13 by genotype uncertainty CHR_10:32,324,083 A>C
AF=0.47 DR2=0.81 $r=-0.049$ $\bar{H}=0.403$ F=0.8



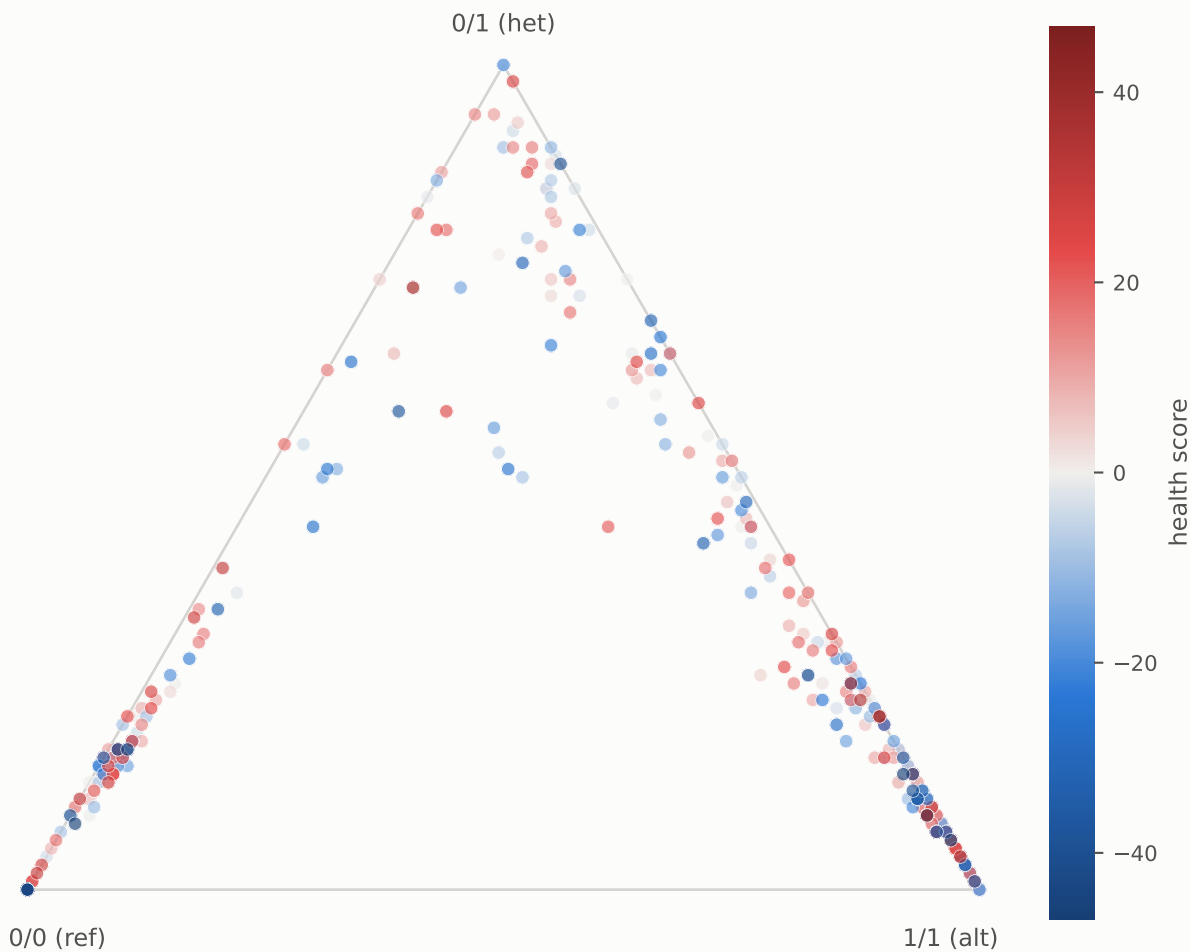
#14 by genotype uncertainty CHR_06:5,228,722 A>C
AF=0.5 DR2=0.81 $r=+0.022$ $\bar{H}=0.403$ F=0.9



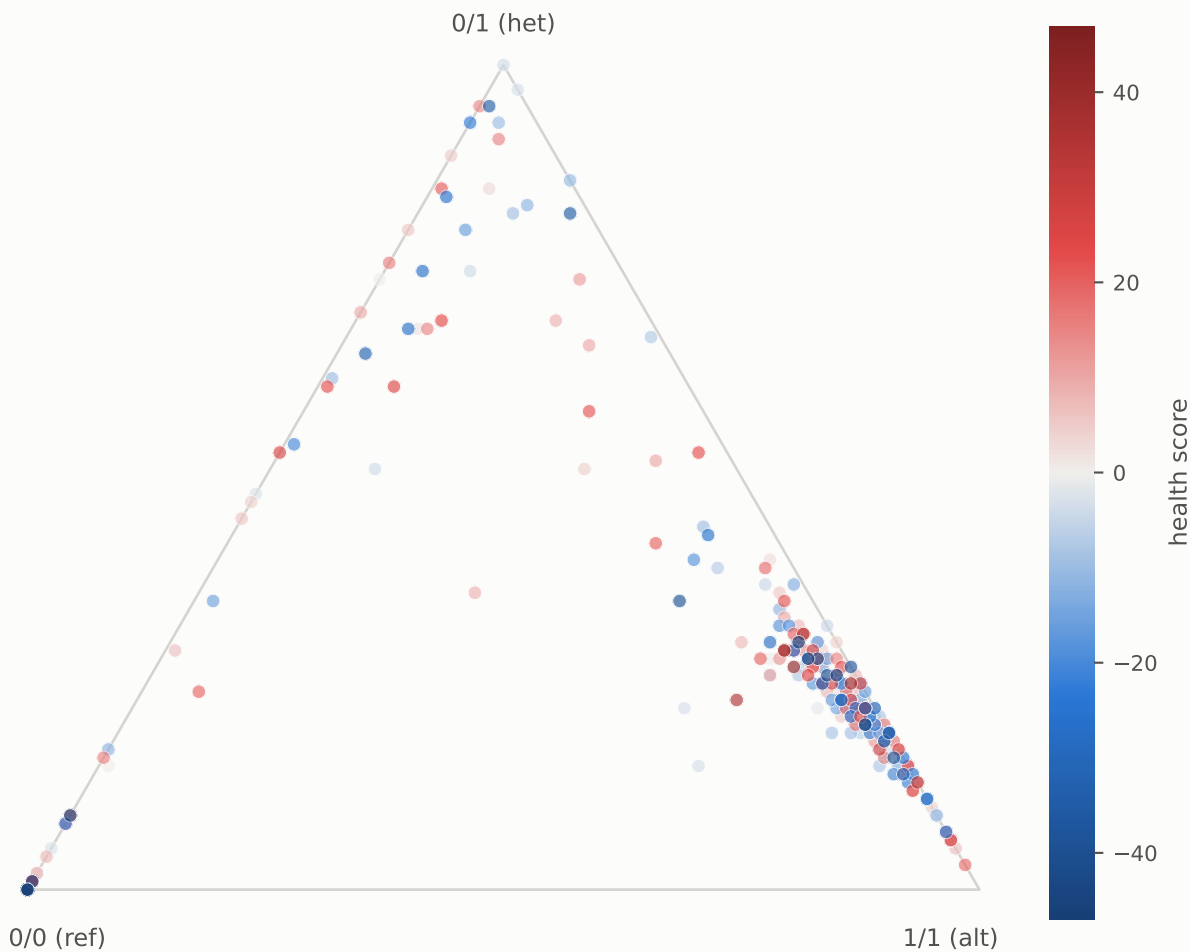
#15 by genotype uncertainty CHR_13:11,443,617 T>C
AF=0.5 DR2=0.81 $r=+0.005$ $\bar{H}=0.403$ F=0.1



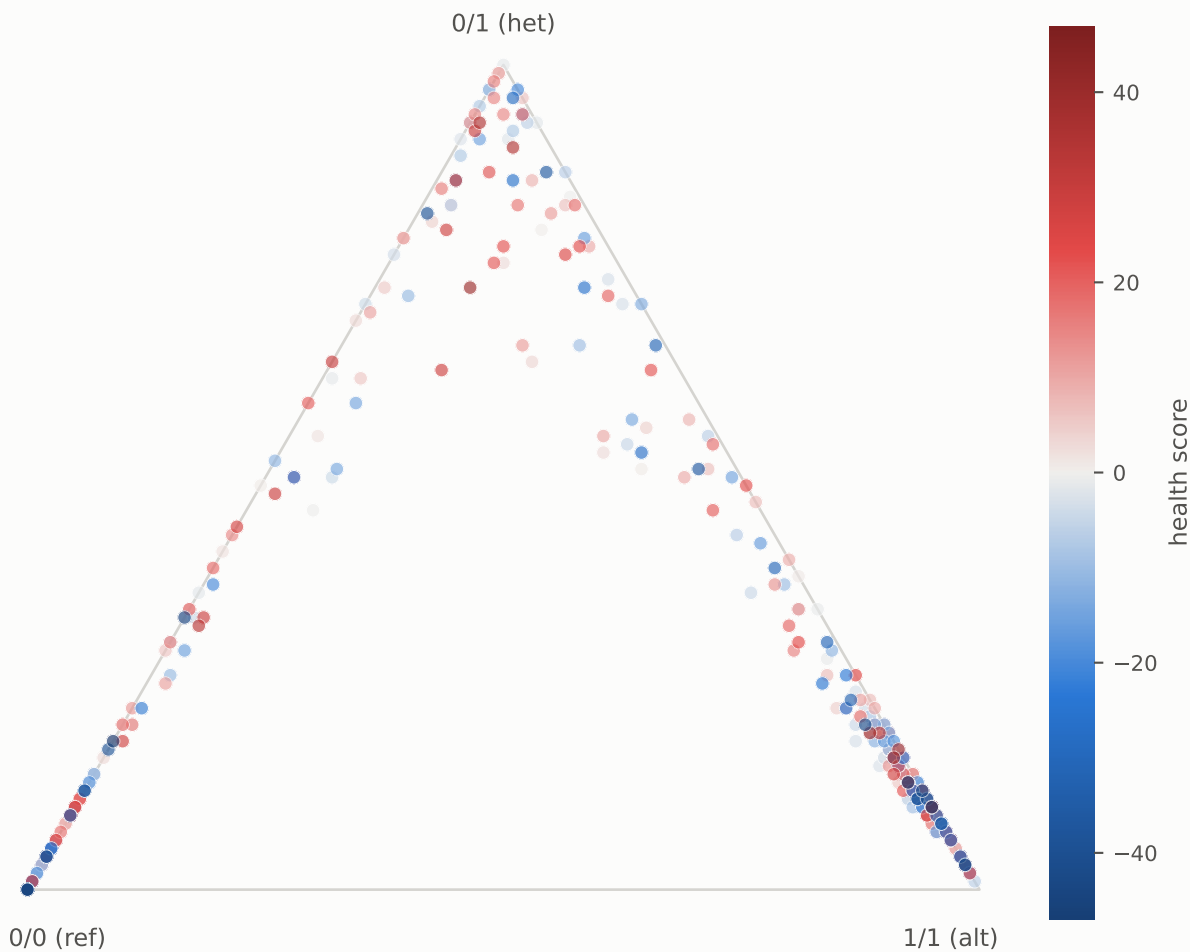
#16 by genotype uncertainty CHR_18:18,490,918 T>C
AF=0.52 DR2=0.81 $r=-0.006$ $\bar{H}=0.403$ $F=0.0$



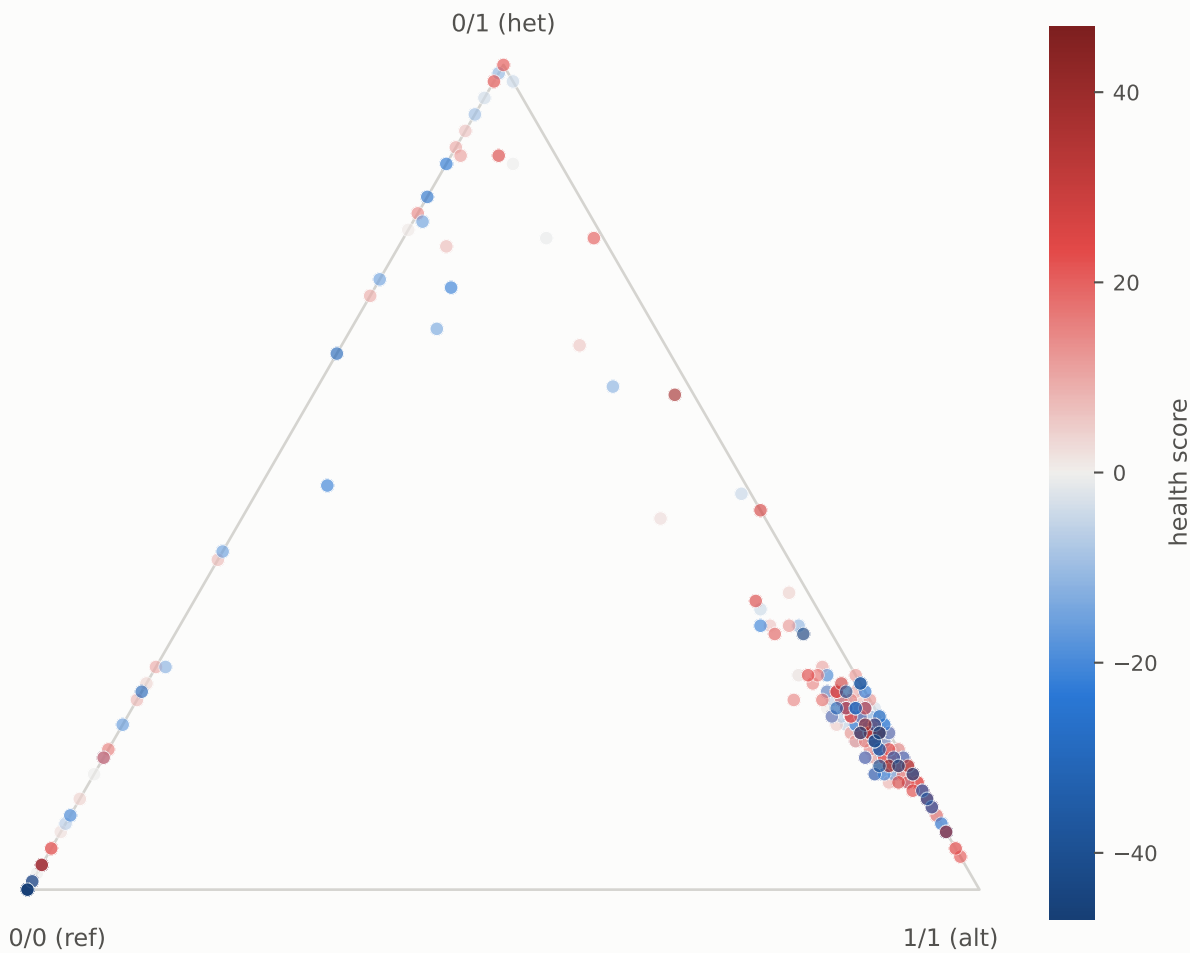
#17 by genotype uncertainty CHR_19:638,389 T>C
AF=0.45 DR2=0.81 $r=-0.057$ $H=0.402$ $F=0.8$



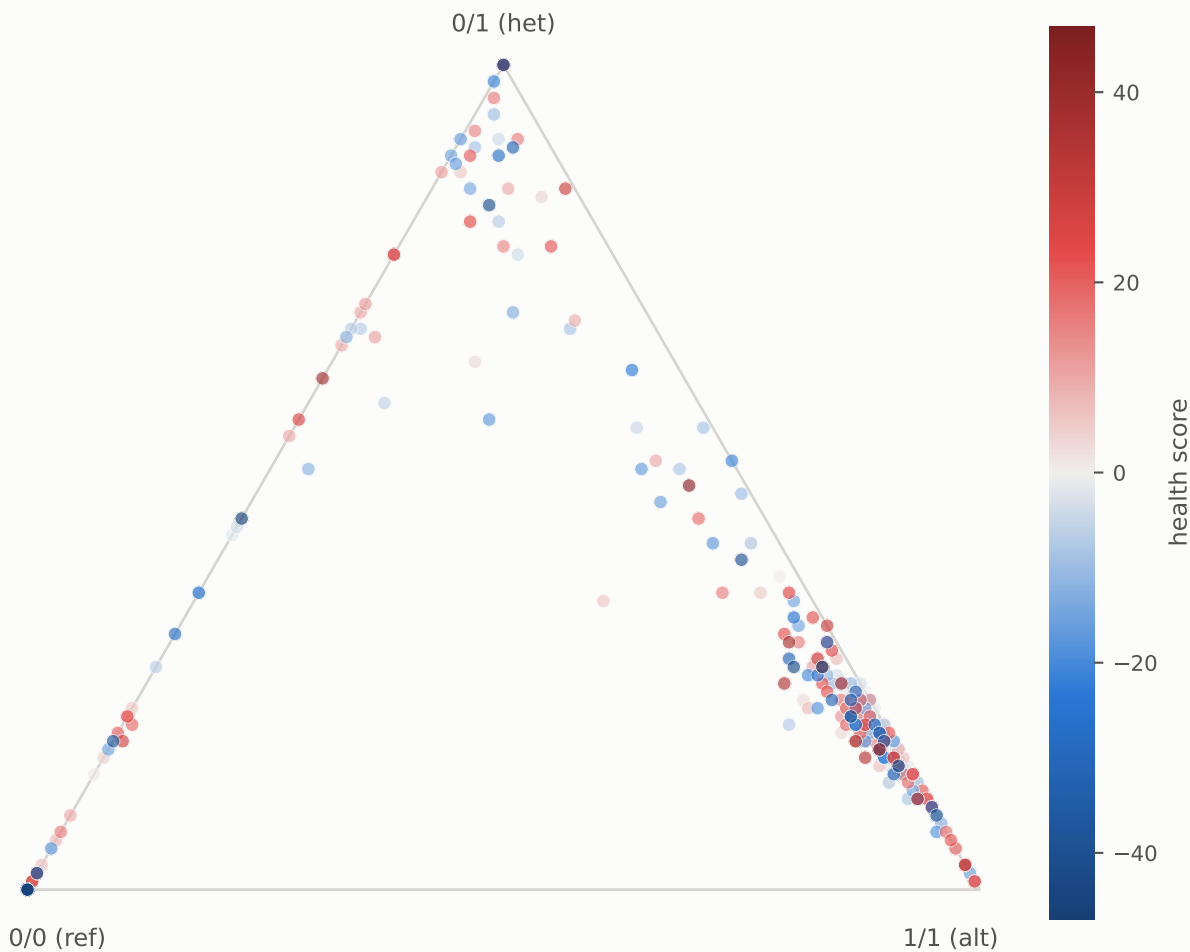
#18 by genotype uncertainty CHR_06:9,652,679 A>G
AF=0.55 DR2=0.81 $r=-0.014$ $\bar{H}=0.401$ F=1.2



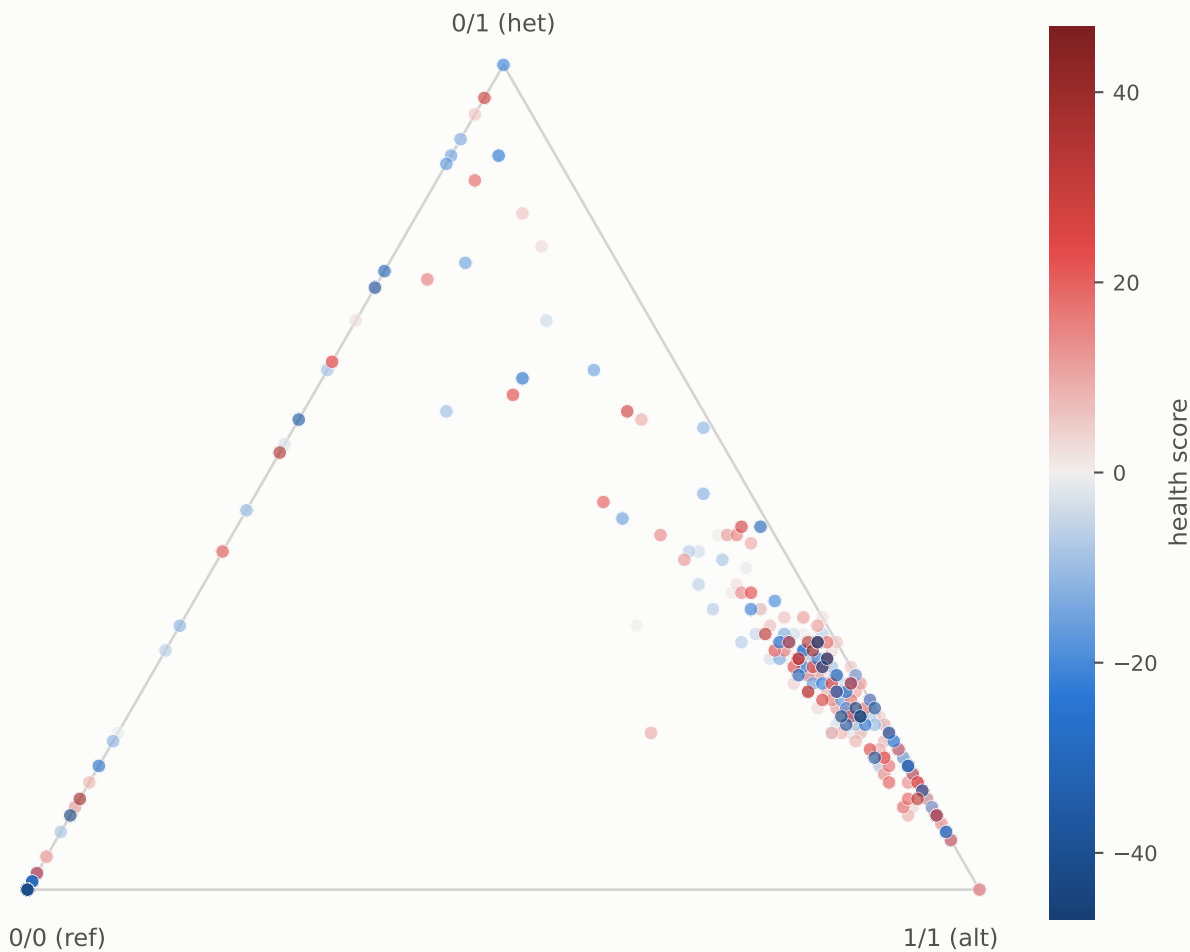
#19 by genotype uncertainty CHR_22:5,009,884 G>T
AF=0.58 DR2=0.81 $r=+0.066$ $\bar{H}=0.401$ F=0.8



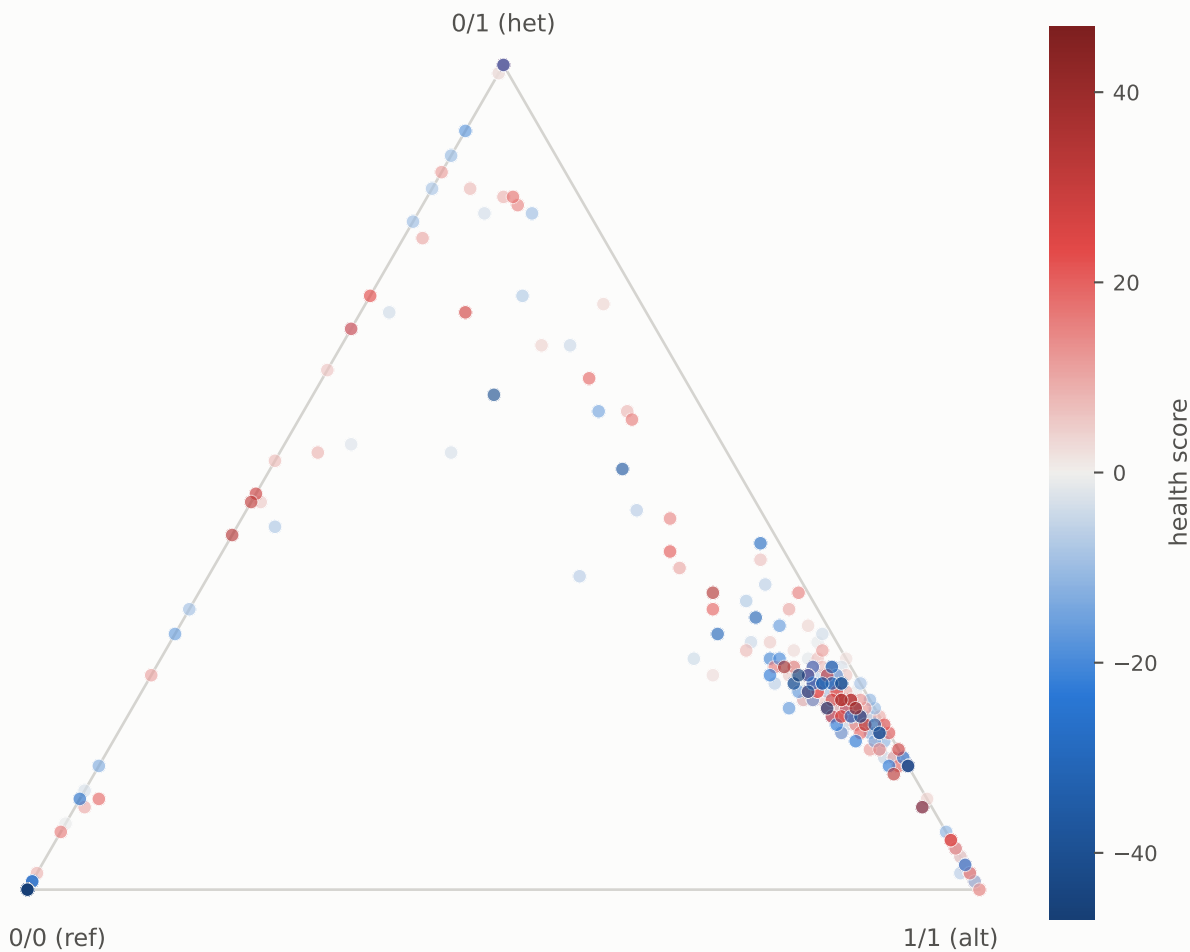
#20 by genotype uncertainty CHR_17:816,440 G>C
AF=0.53 DR2=0.81 $r=+0.041$ $\bar{H}=0.399$ $F=0.6$



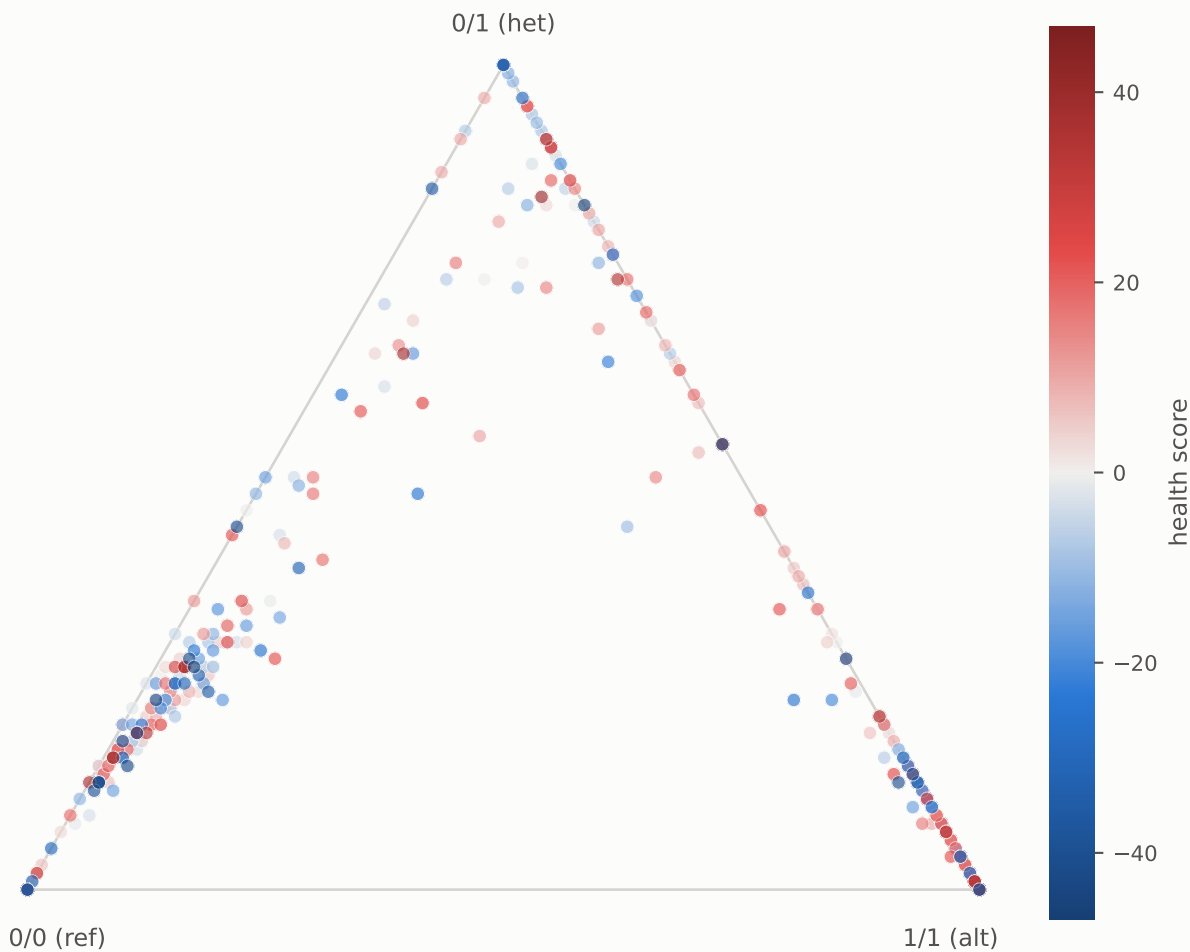
#21 by genotype uncertainty CHR_03:37,248,219 A>T
AF=0.46 DR2=0.81 $r=+0.019$ $\bar{H}=0.398$ F=0.4



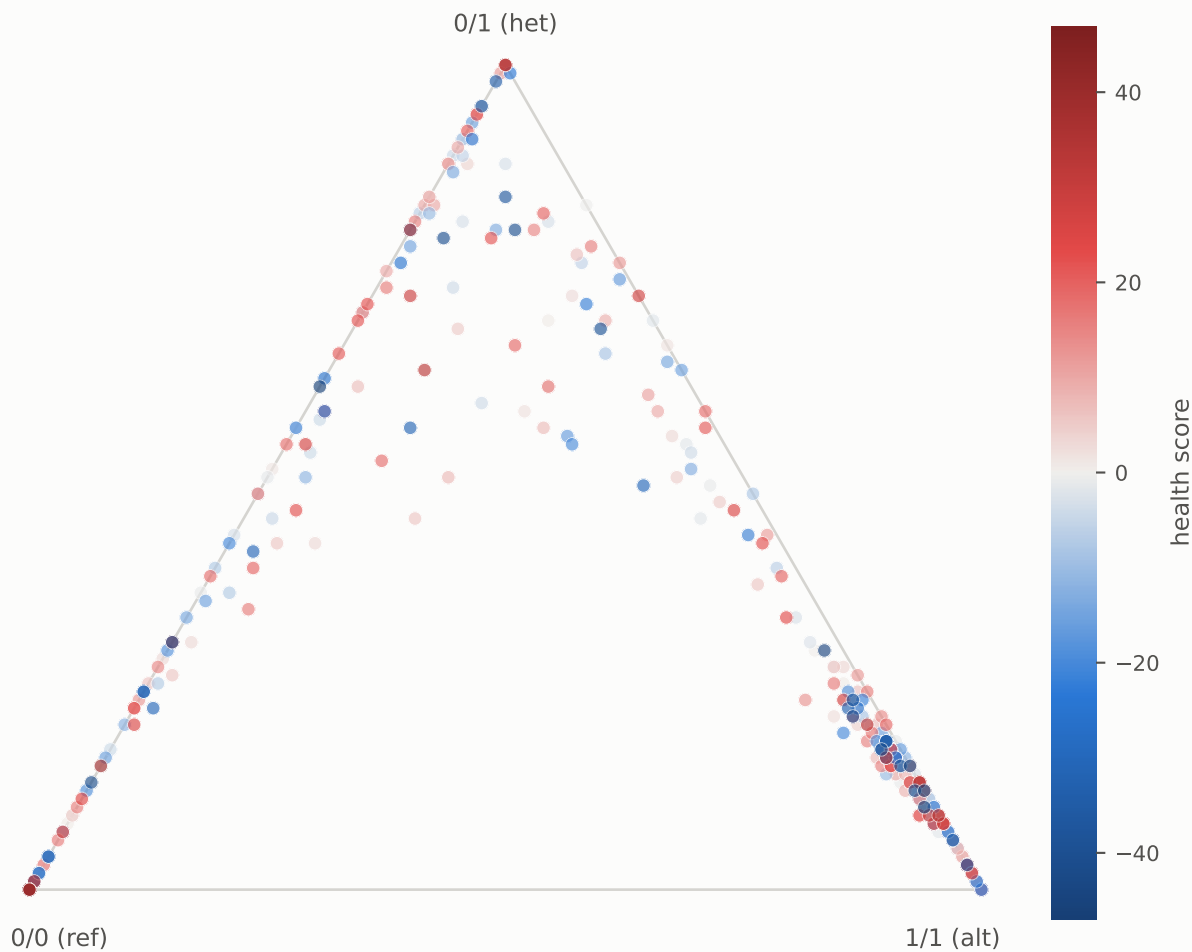
#22 by genotype uncertainty CHR_02:35,654,799 T>A
AF=0.48 DR2=0.81 $r=-0.001$ $\bar{H}=0.398$ F=0.2



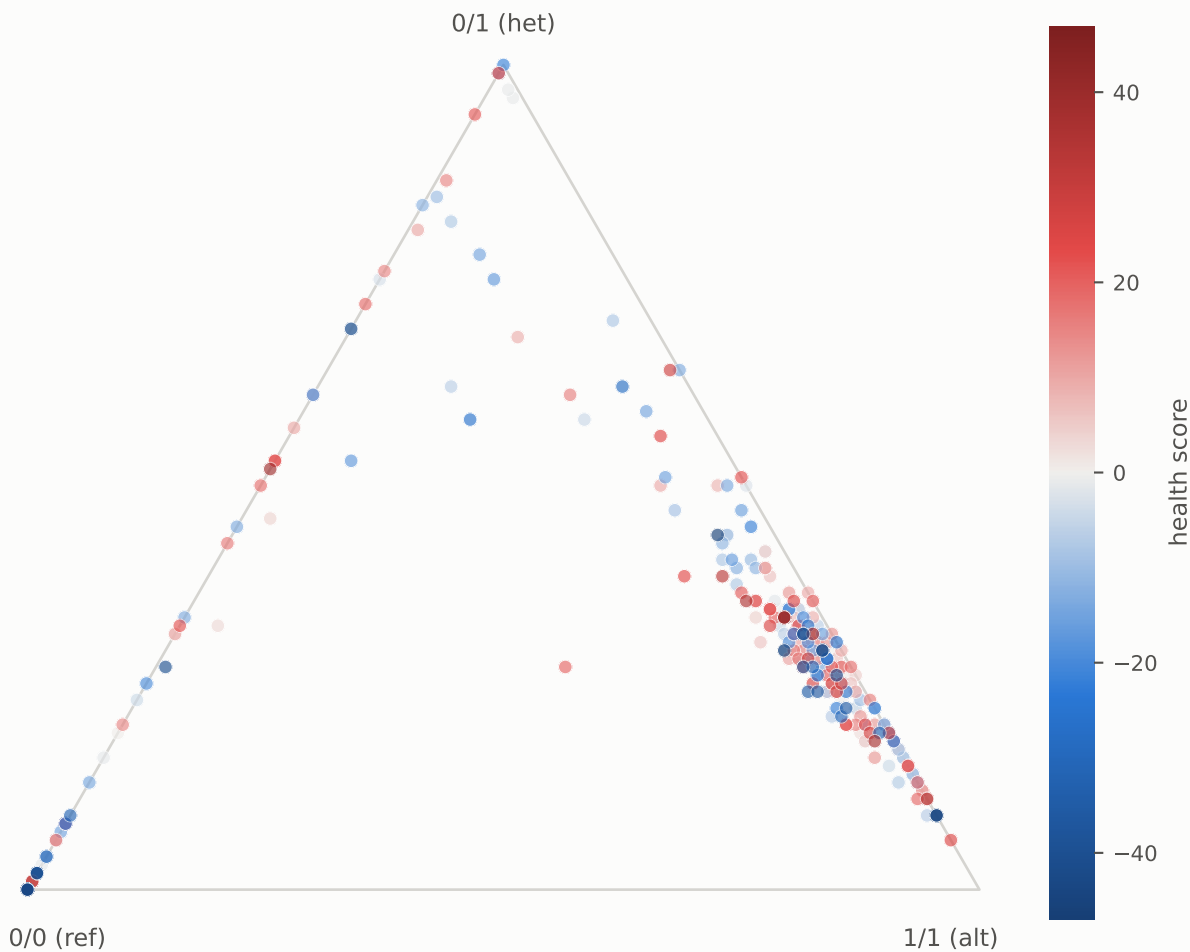
#23 by genotype uncertainty CHR_14:1,059,419 A>G
AF=0.53 DR2=0.81 $r=+0.053$ $\bar{H}=0.397$ F=1.1



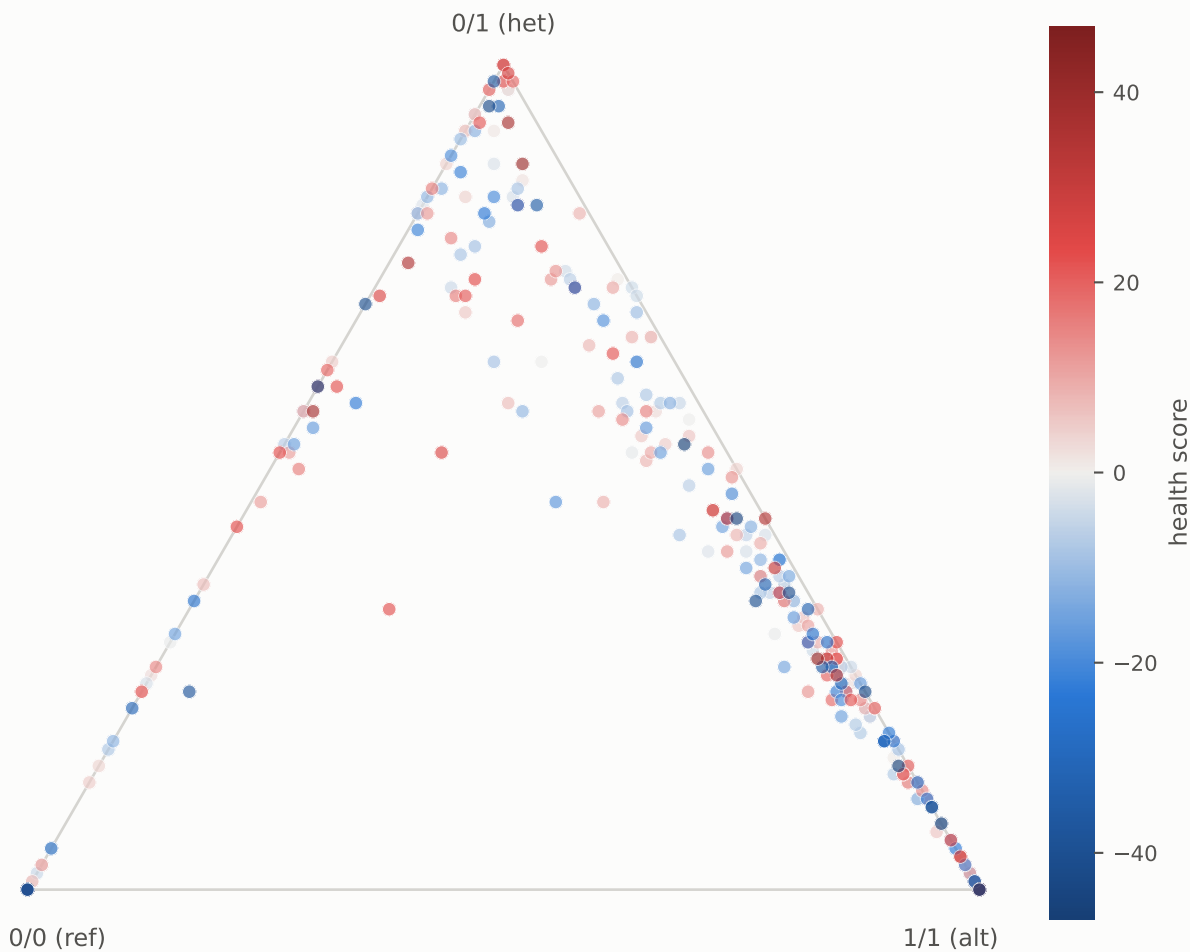
#24 by genotype uncertainty CHR_19:5,010,699 G>C
AF=0.49 DR2=0.81 $r=-0.041$ $\bar{H}=0.397$ F=0.3



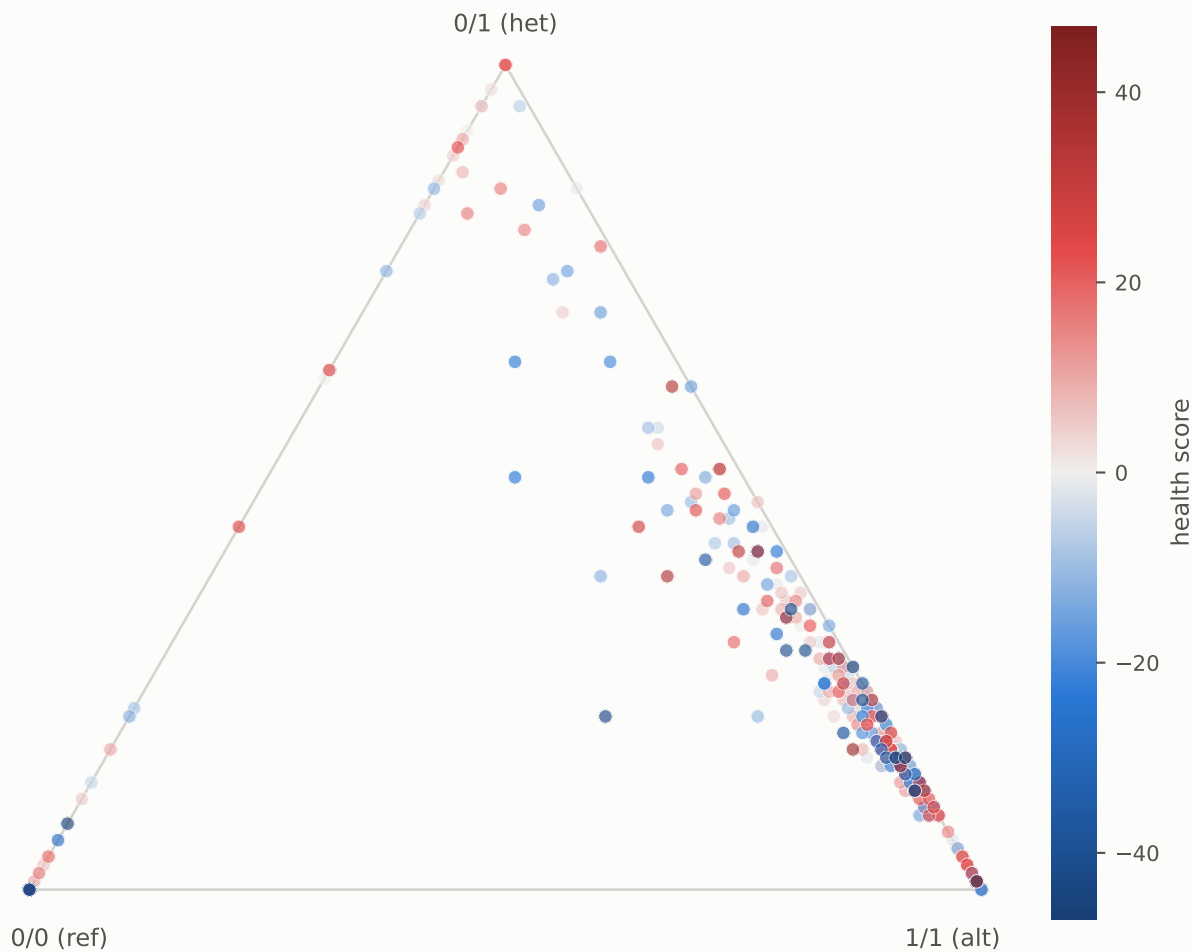
#25 by genotype uncertainty CHR_10:13,663,740 C>A
AF=0.43 DR2=0.81 r=+0.040 H=0.396 F=0.5



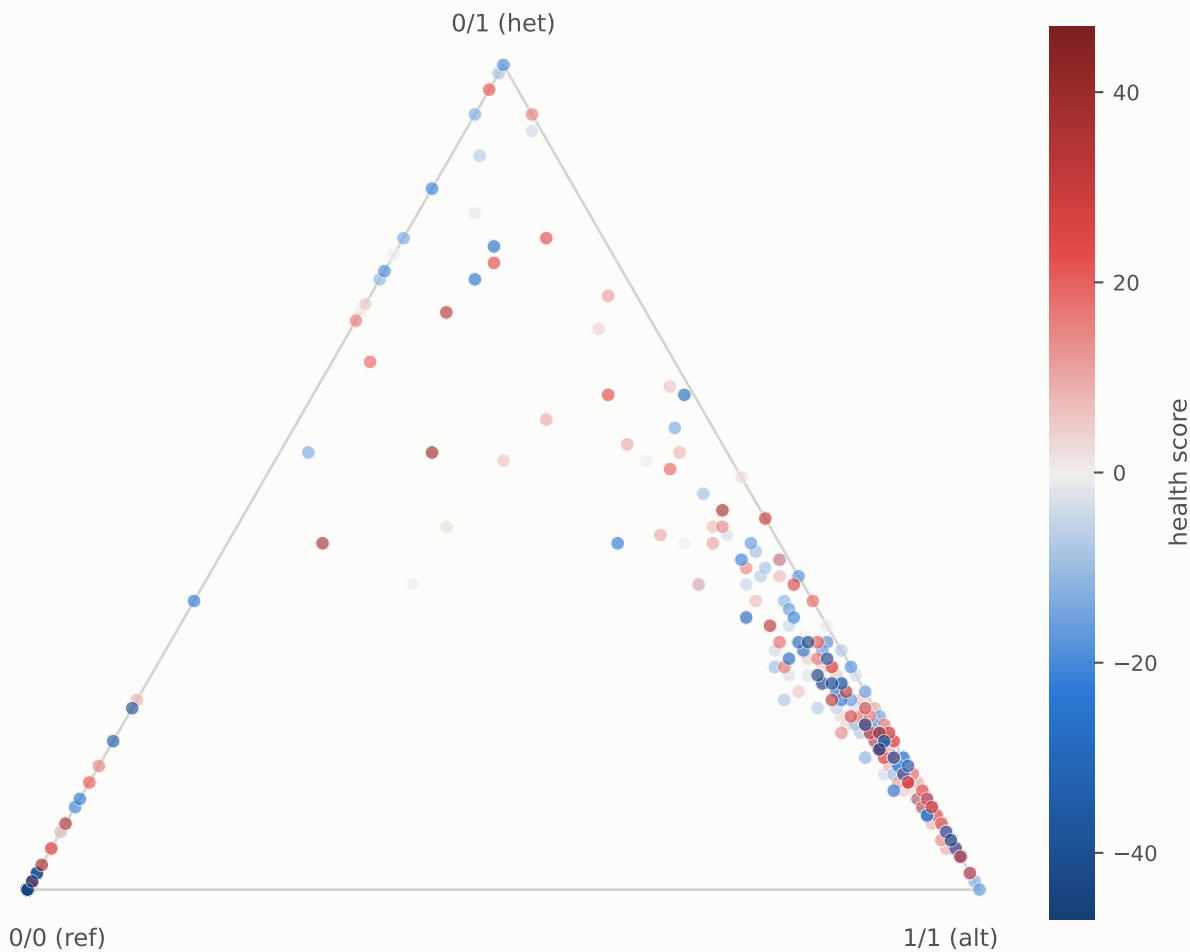
#26 by genotype uncertainty CHR_21:17,065,034 T>C
AF=0.5 DR2=0.81 r=-0.086 $\bar{H}$ =0.396 F=1.9



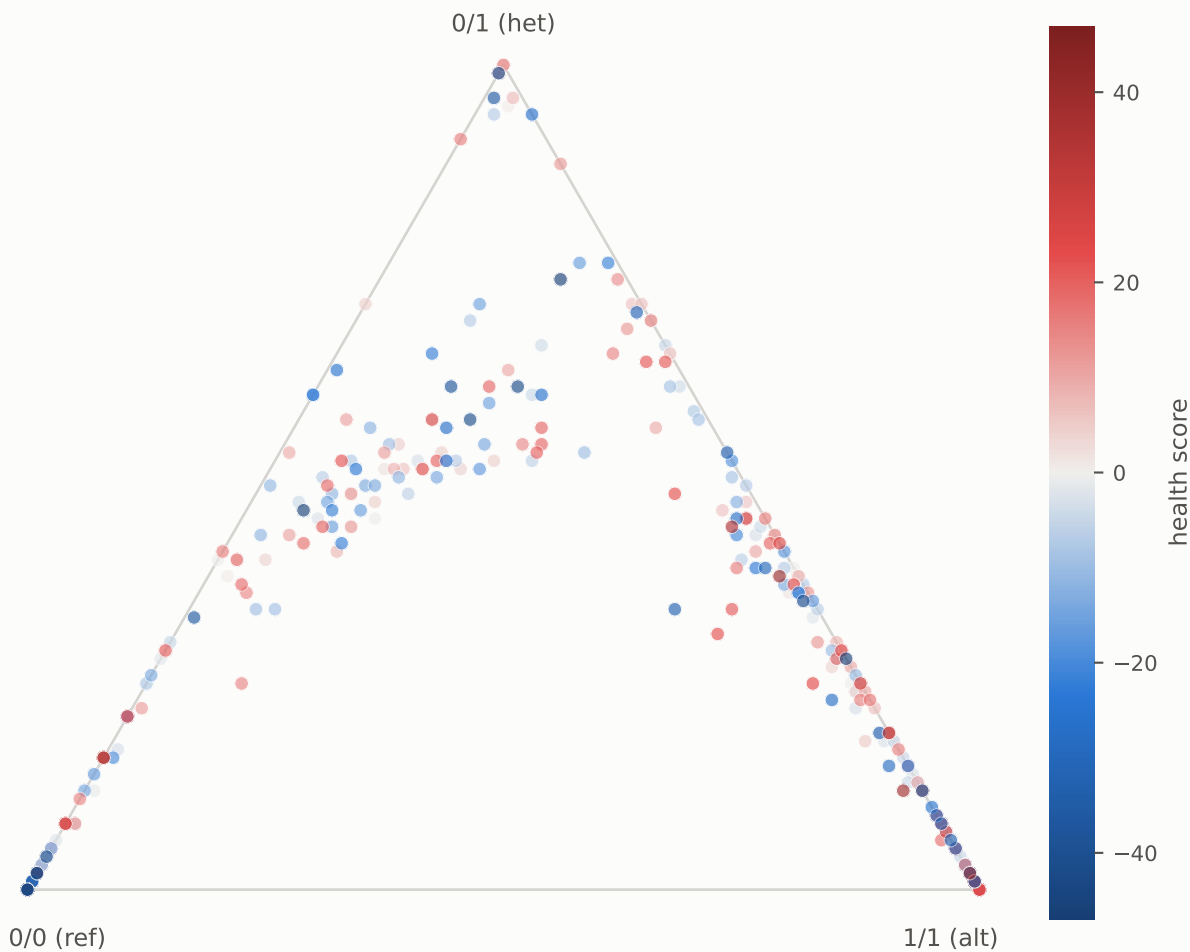
#27 by genotype uncertainty CHR_13:14,758,284 A>G
AF=0.58 DR2=0.81 $r=+0.008$ H=0.396 F=0.3



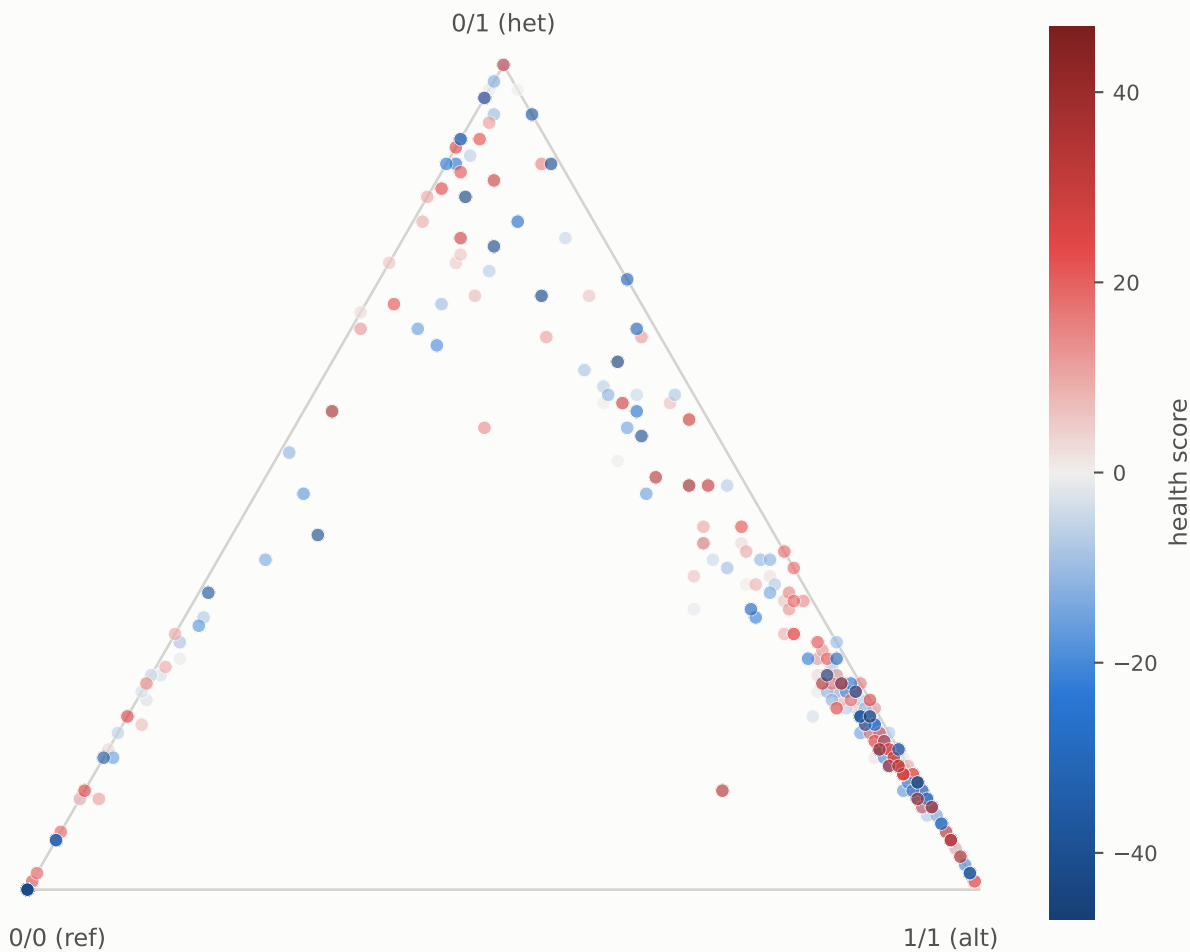
#28 by genotype uncertainty CHR_14:16,463,931 C>T
AF=0.58 DR2=0.81 $r=+0.038$ $\bar{H}=0.396$ $F=0.3$



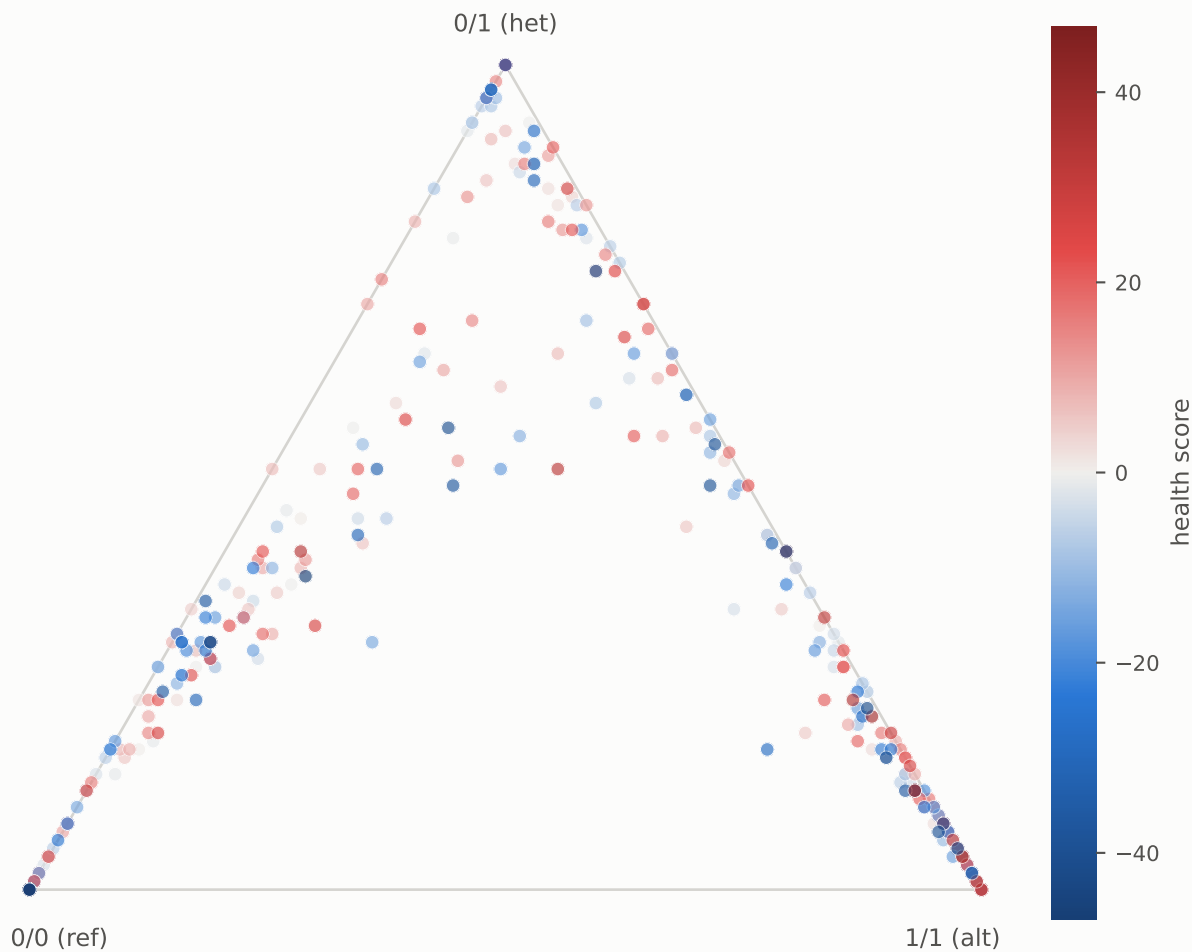
#29 by genotype uncertainty CHR_22:2,643,928 T>C
AF=0.46 DR2=0.81 r=+0.008 $\bar{H}$ =0.395 F=2.3



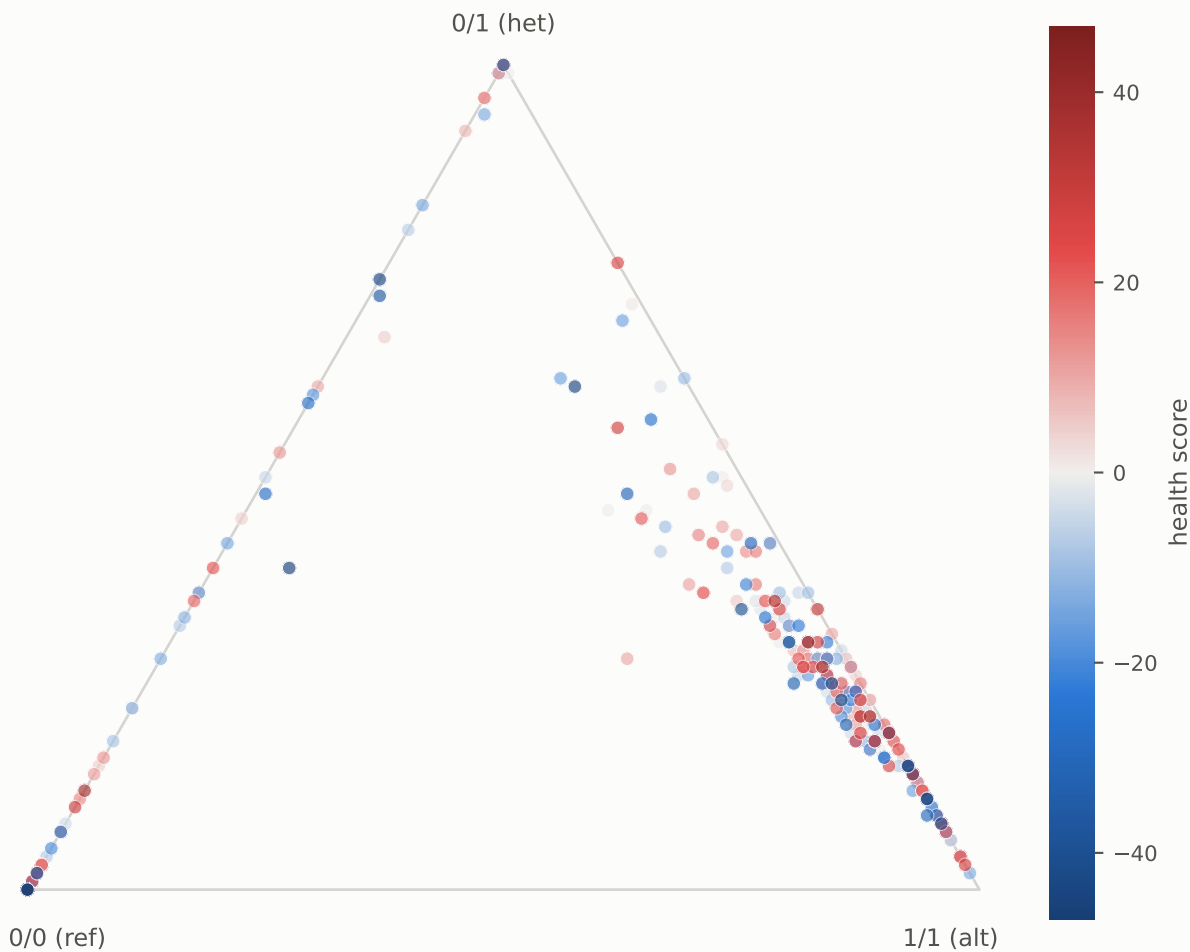
#30 by genotype uncertainty CHR_18:2,046,824 T>G
AF=0.51 DR2=0.81 $r=+0.007$ $\bar{H}=0.395$ F=1.0



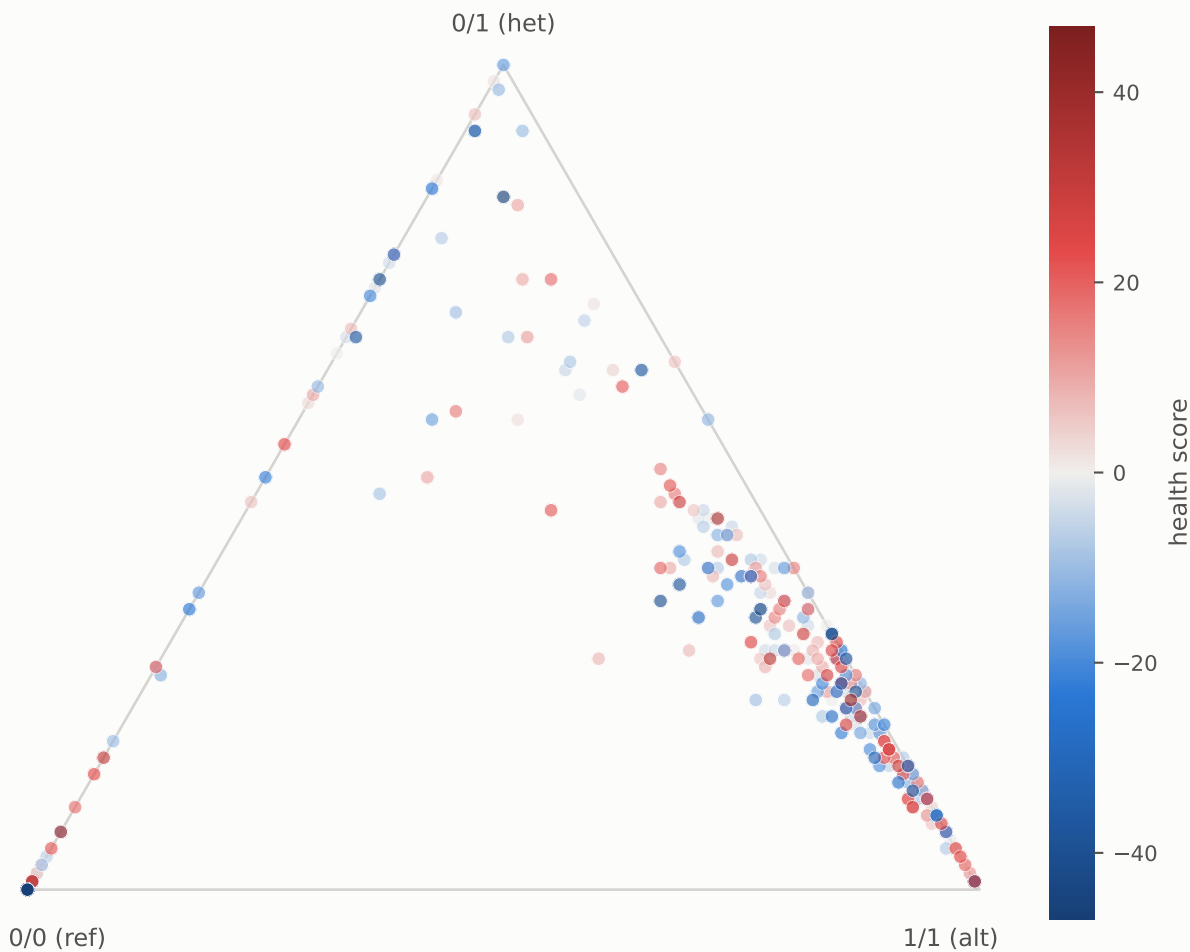
#31 by genotype uncertainty CHR_16:7,234,438 A>G
AF=0.44 DR2=0.81 $r=-0.031$ $\bar{H}=0.395$ F=0.1



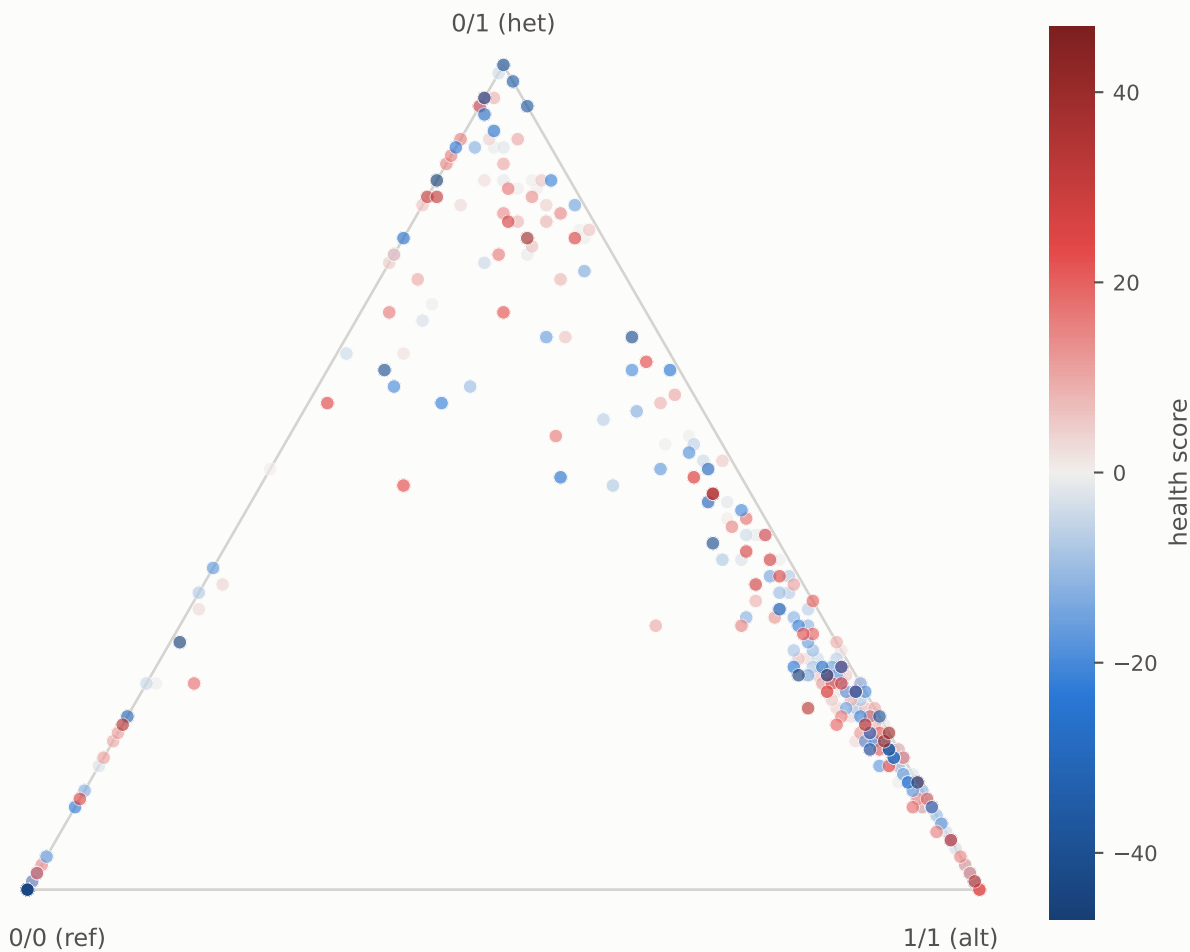
#32 by genotype uncertainty CHR_19:21,146,444 C>T
AF=0.49 DR2=0.81 $r=+0.045$ $\bar{H}=0.395$ F=1.6



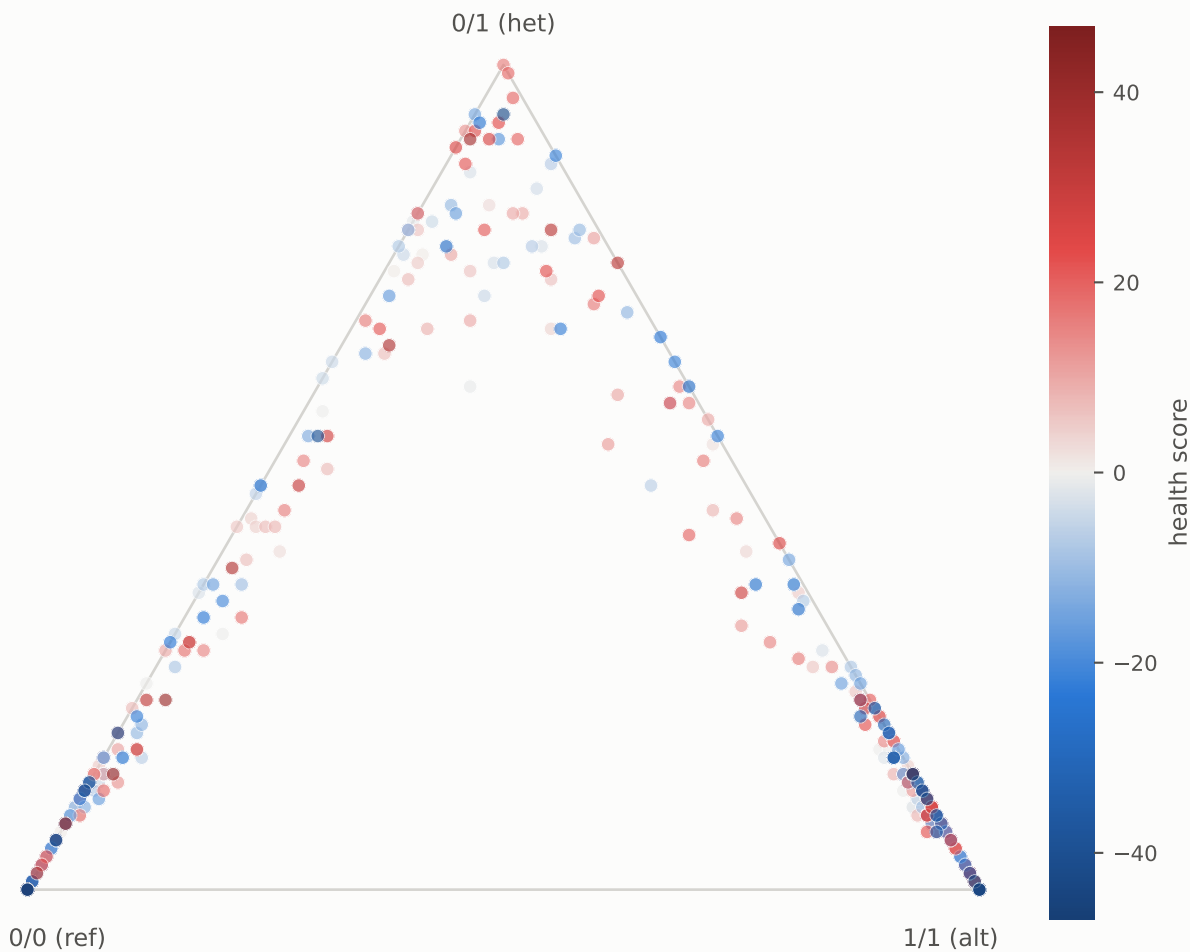
#33 by genotype uncertainty CHR_05:16,905,760 T>C
AF=0.46 DR2=0.81 $r=+0.007$ $\bar{H}=0.395$ $F=0.4$



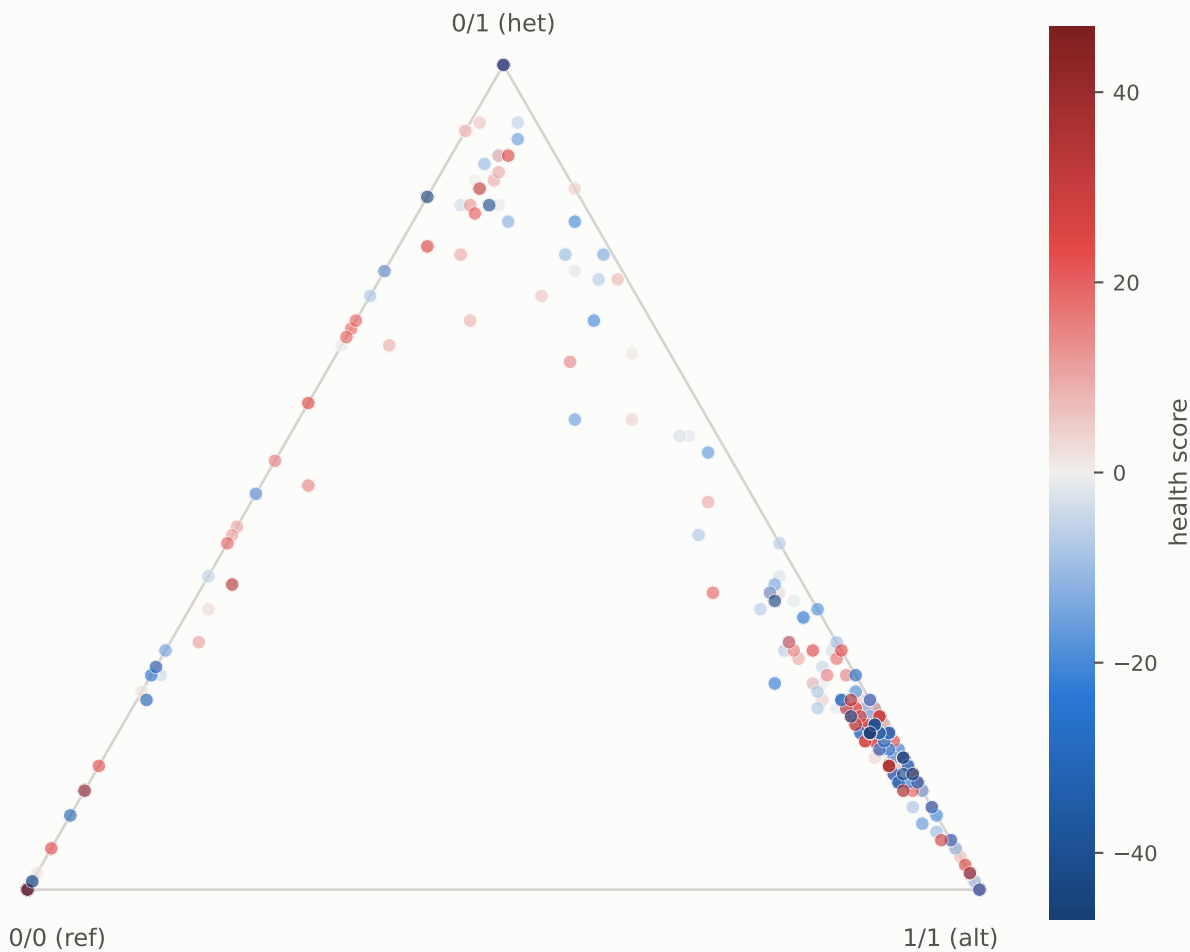
#34 by genotype uncertainty CHR_05:34,337,221 T>G
AF=0.5 DR2=0.81 r=+0.001 $\bar{H}$ =0.394 F=0.0



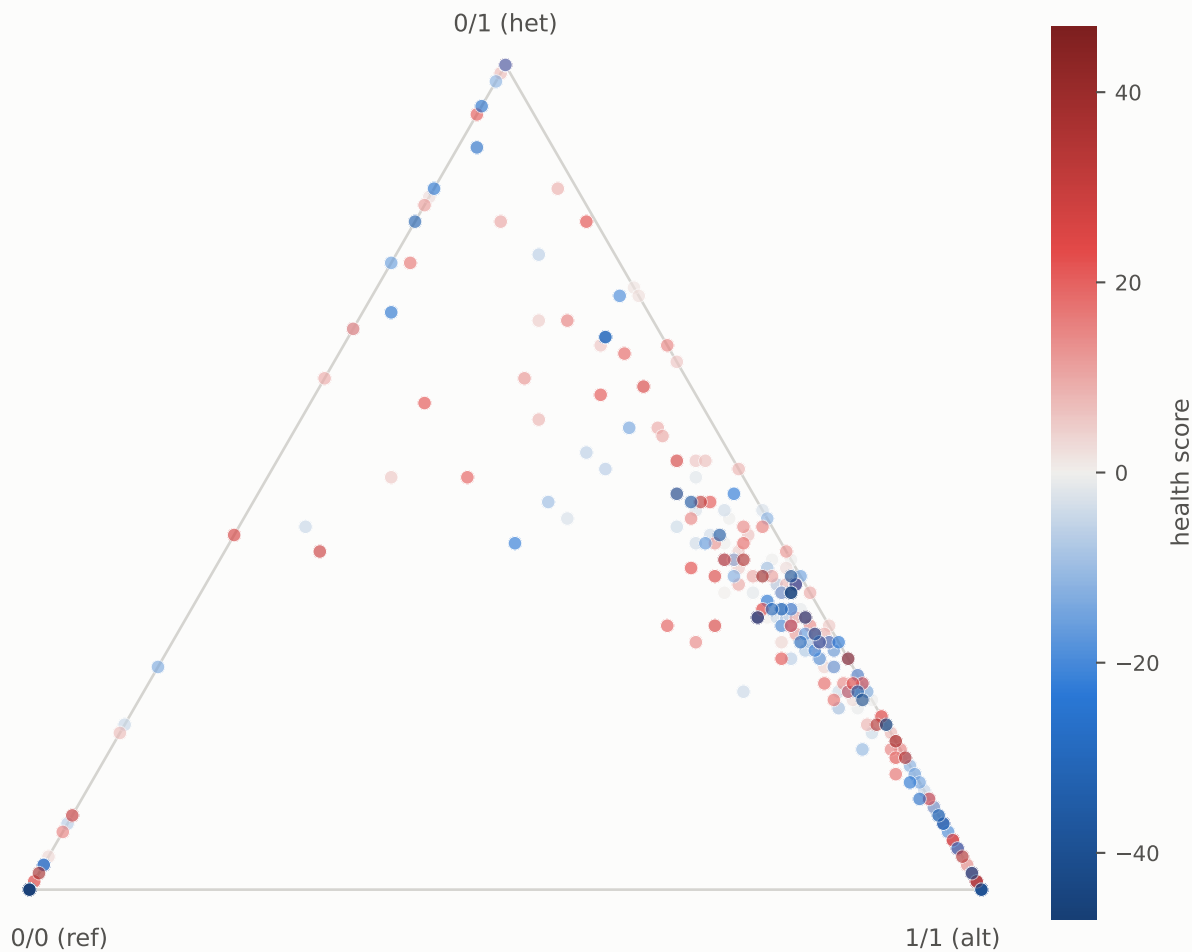
#35 by genotype uncertainty CHR_05:2,087,337 G>T
AF=0.56 DR2=0.82 $r=-0.004$ $\bar{H}=0.394$ F=1.8



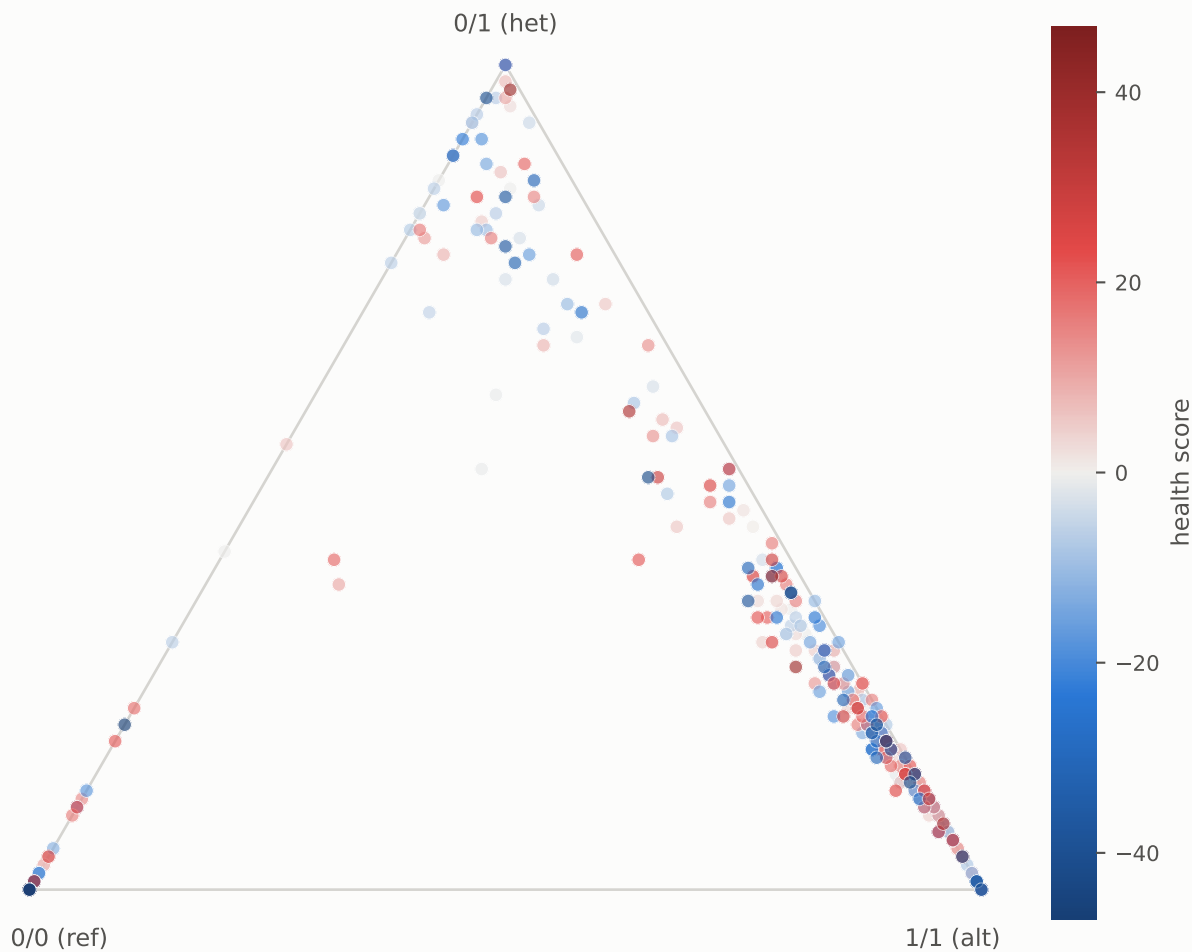
#36 by genotype uncertainty CHR_15:21,468,022 A>C
AF=0.6 DR2=0.81 r=+0.037 $\bar{H}$ =0.394 F=0.6



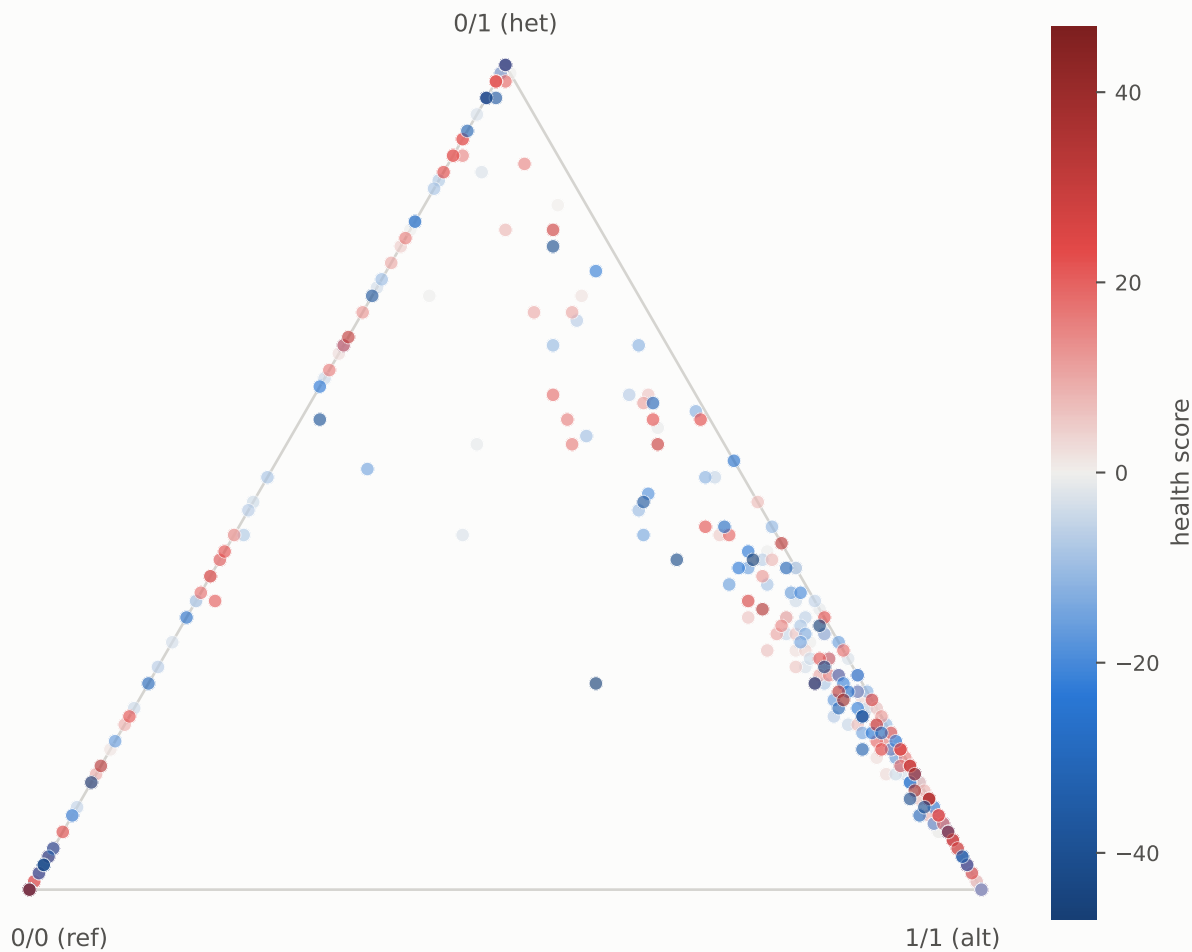
#37 by genotype uncertainty CHR_10:29,031,566 G>C
AF=0.52 DR2=0.81 $r=-0.034$ $\bar{H}=0.393$ F=0.5



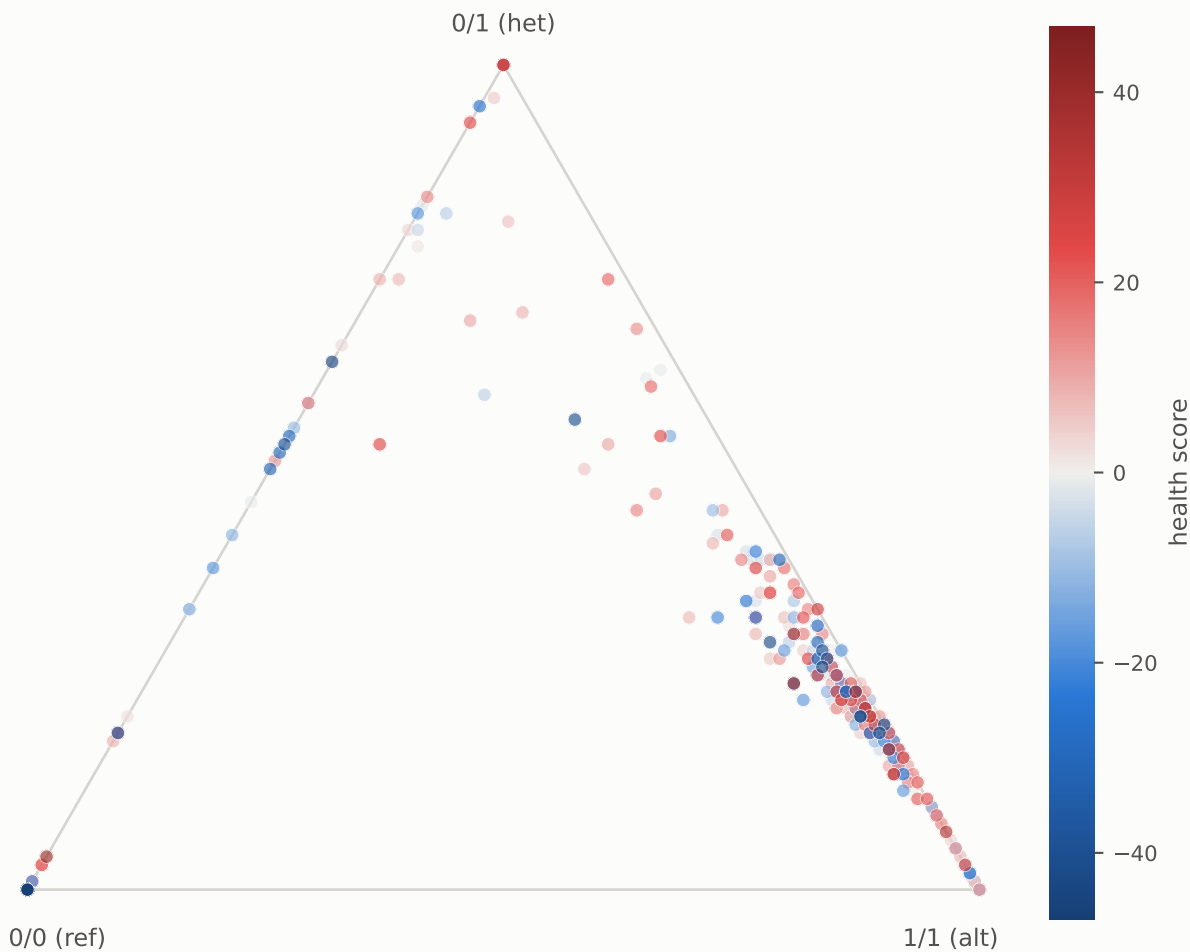
#38 by genotype uncertainty CHR_07:7,876,901 G>T
AF=0.56 DR2=0.81 $r=-0.031$ $\bar{H}=0.393$ F=1.0



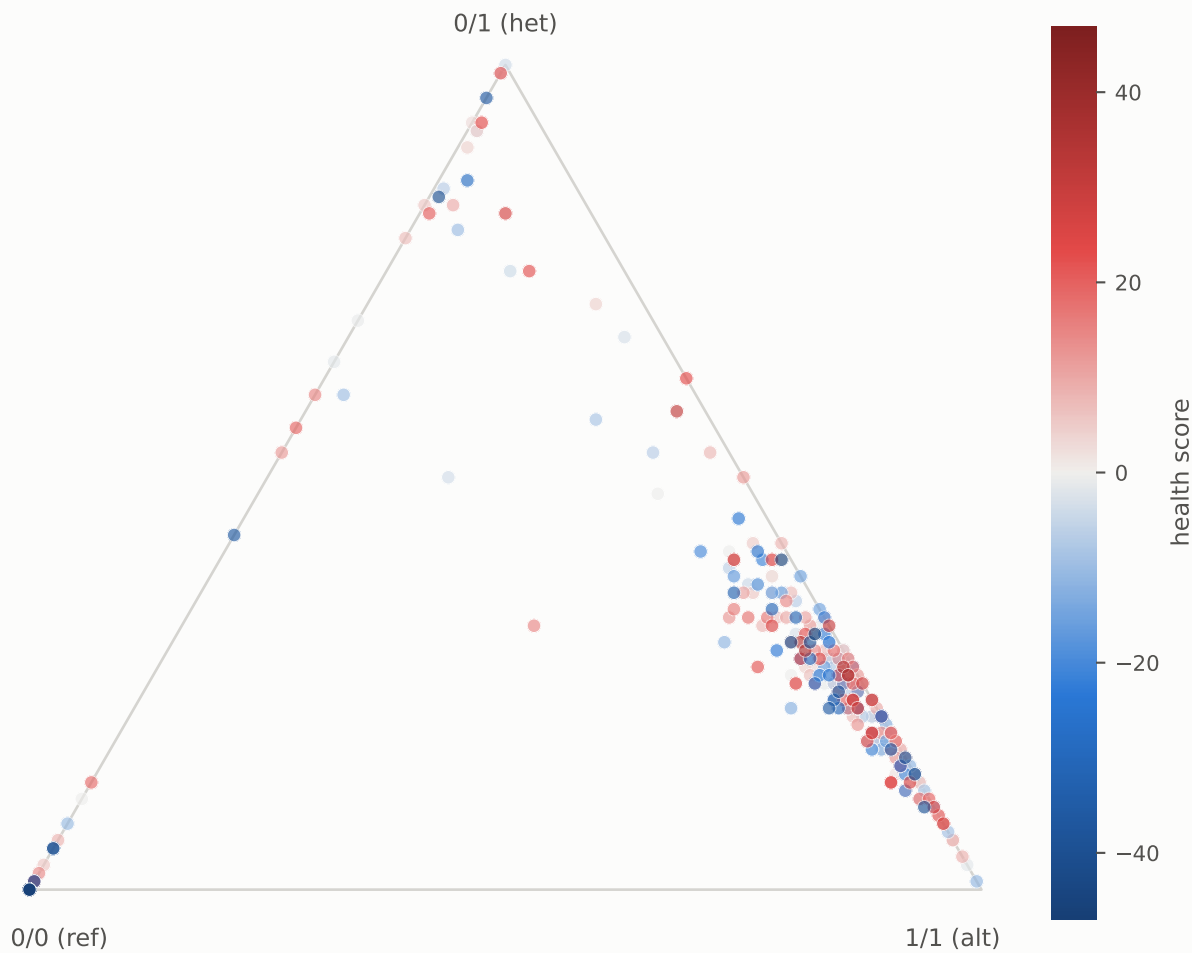
#39 by genotype uncertainty CHR_19:1,669,754 A>G
AF=0.51 DR2=0.81 $r=-0.005$ $\bar{H}=0.393$ F=0.4



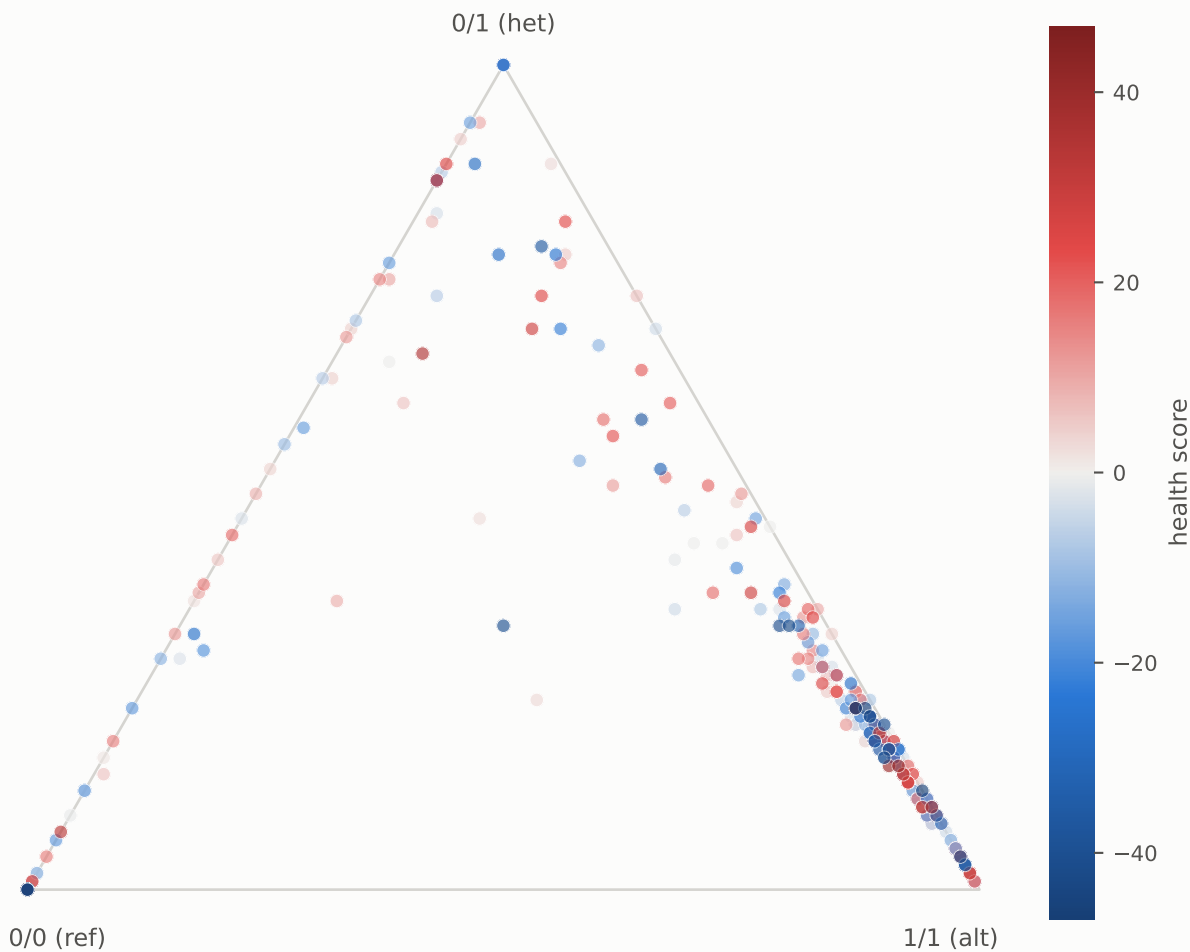
#40 by genotype uncertainty CHR_19:11,162,544 C>T
AF=0.54 DR2=0.81 $r=+0.091$ $\bar{H}=0.393$ $F=1.4$



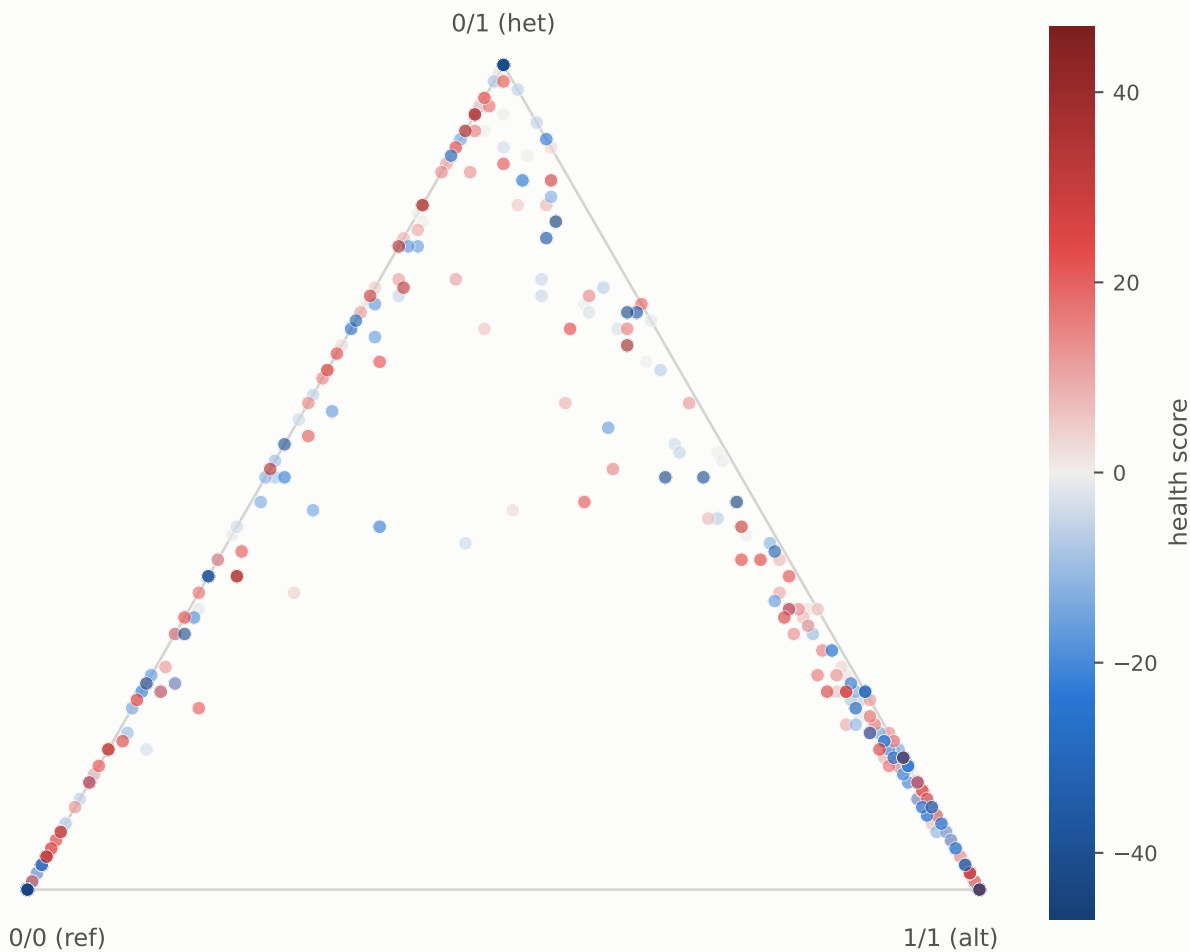
#41 by genotype uncertainty CHR_17:3,114,448 T>C
AF=0.51 DR2=0.81 $r=+0.059$ $\bar{H}=0.393$ F=1.3



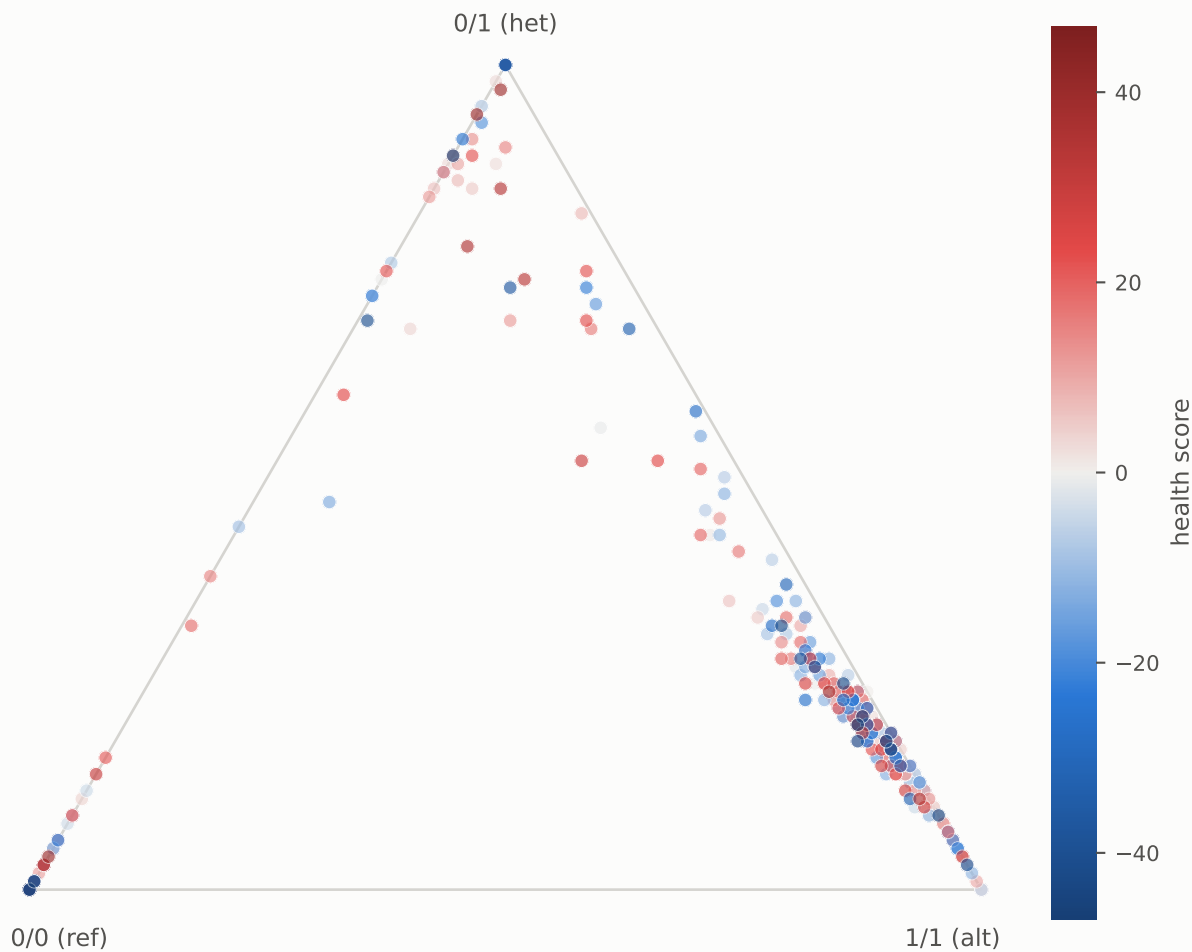
#42 by genotype uncertainty CHR_14:19,104,595 T>A
AF=0.57 DR2=0.81 $r=-0.044$ $\bar{H}=0.393$ F=0.6



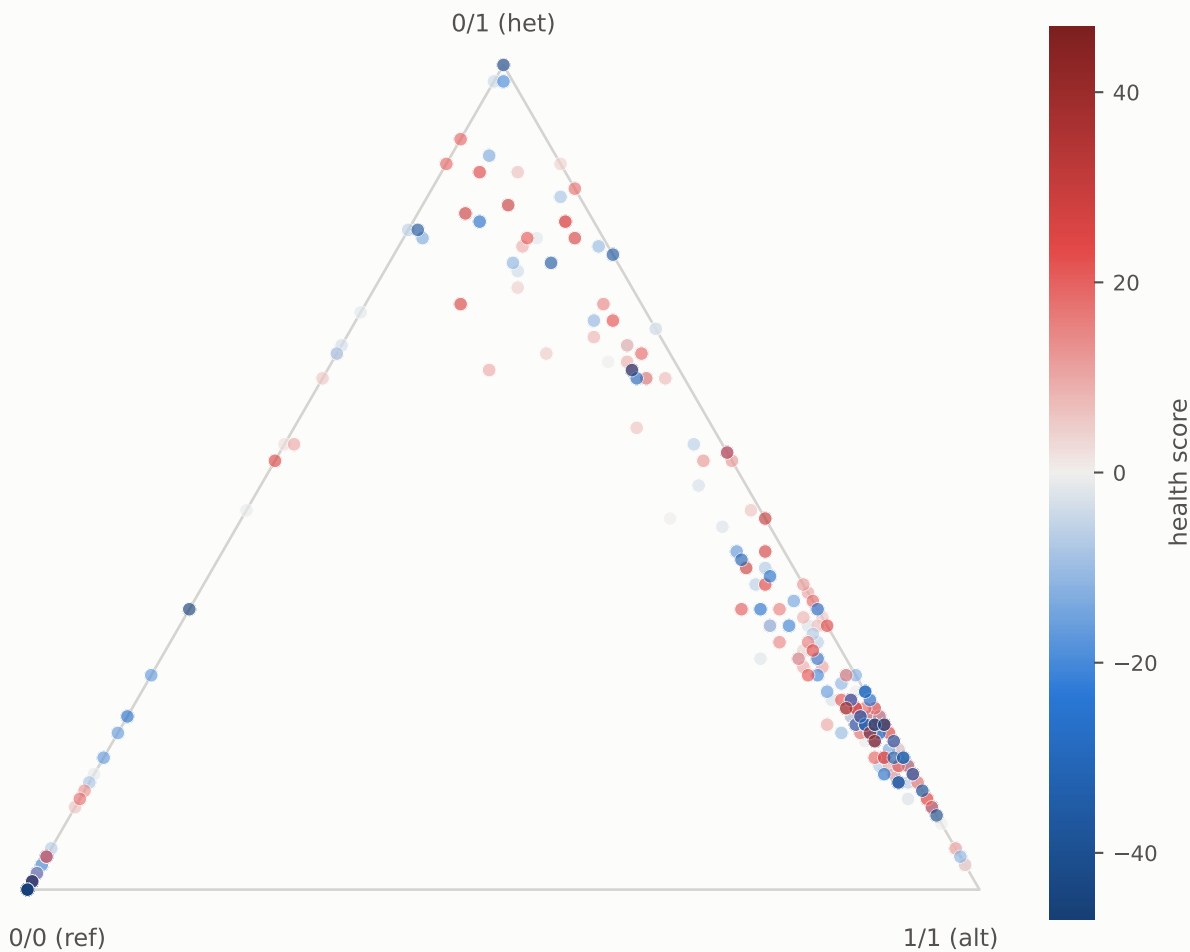
#43 by genotype uncertainty CHR_11:10,210,342 G>C
AF=0.48 DR2=0.81 $r=+0.005$ H=0.393 F=0.2



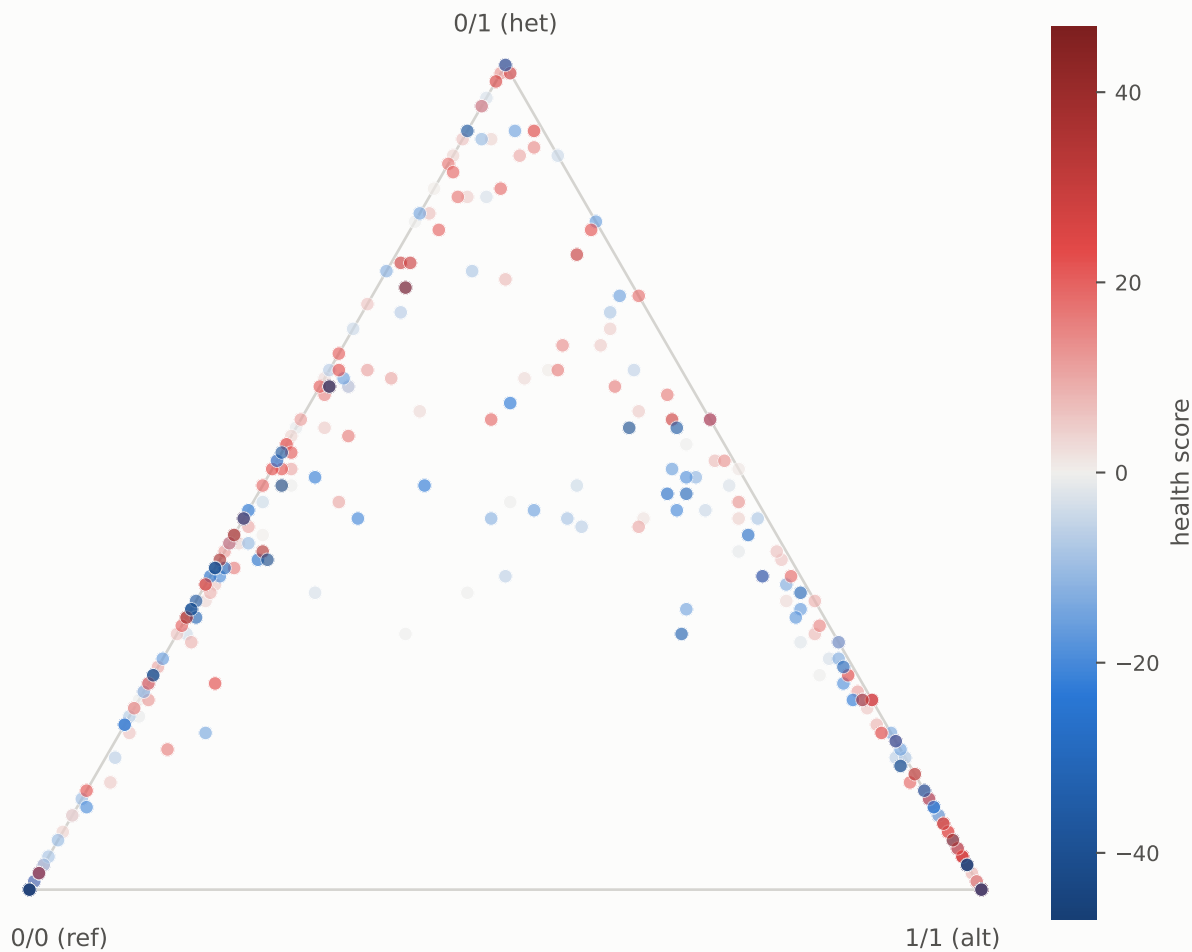
#44 by genotype uncertainty CHR_20:5,568,559 T>C
AF=0.55 DR2=0.81 $r=-0.057$ $\bar{H}=0.392$ F=1.1



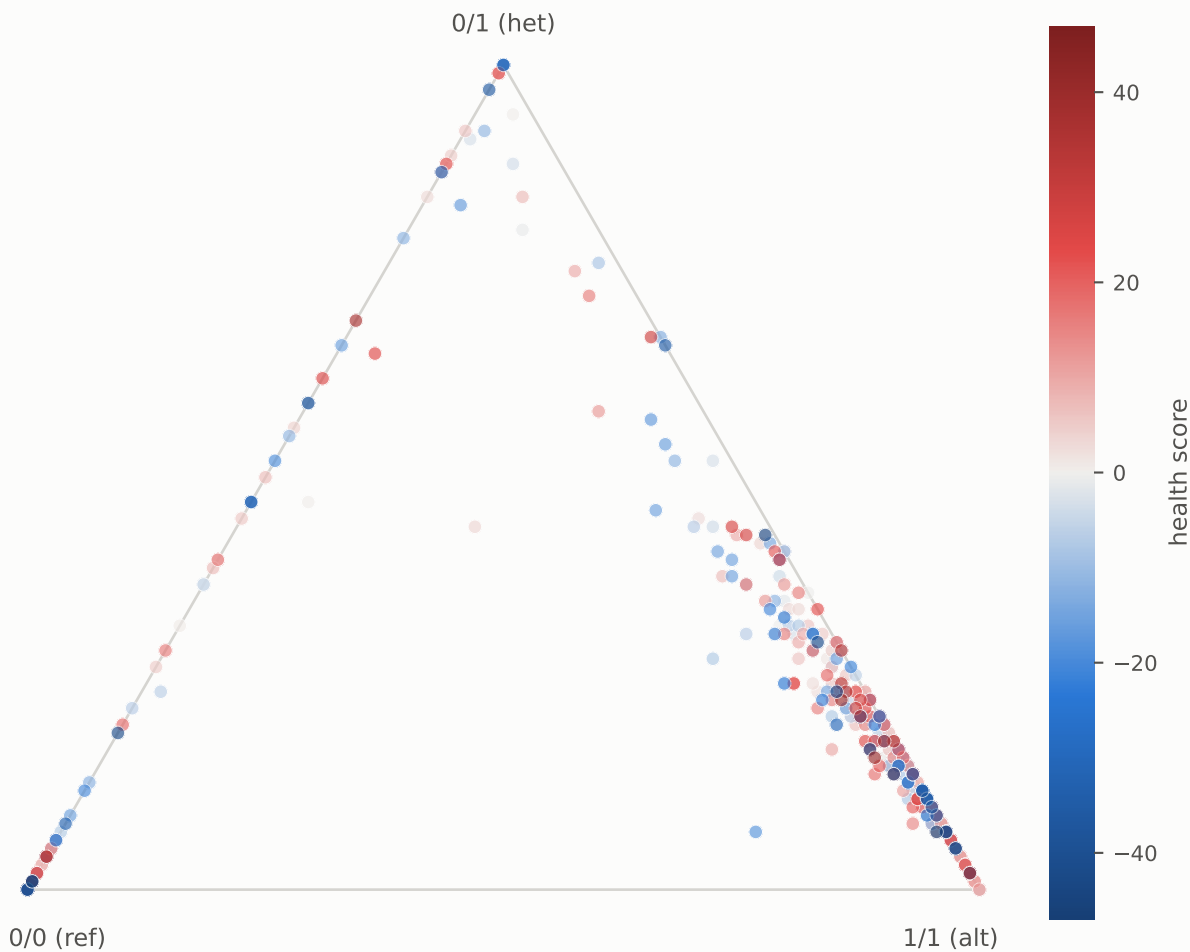
#45 by genotype uncertainty CHR_22:12,859,778 G>T
AF=0.54 DR2=0.81 $r=+0.014$ $H=0.392$ $F=0.5$



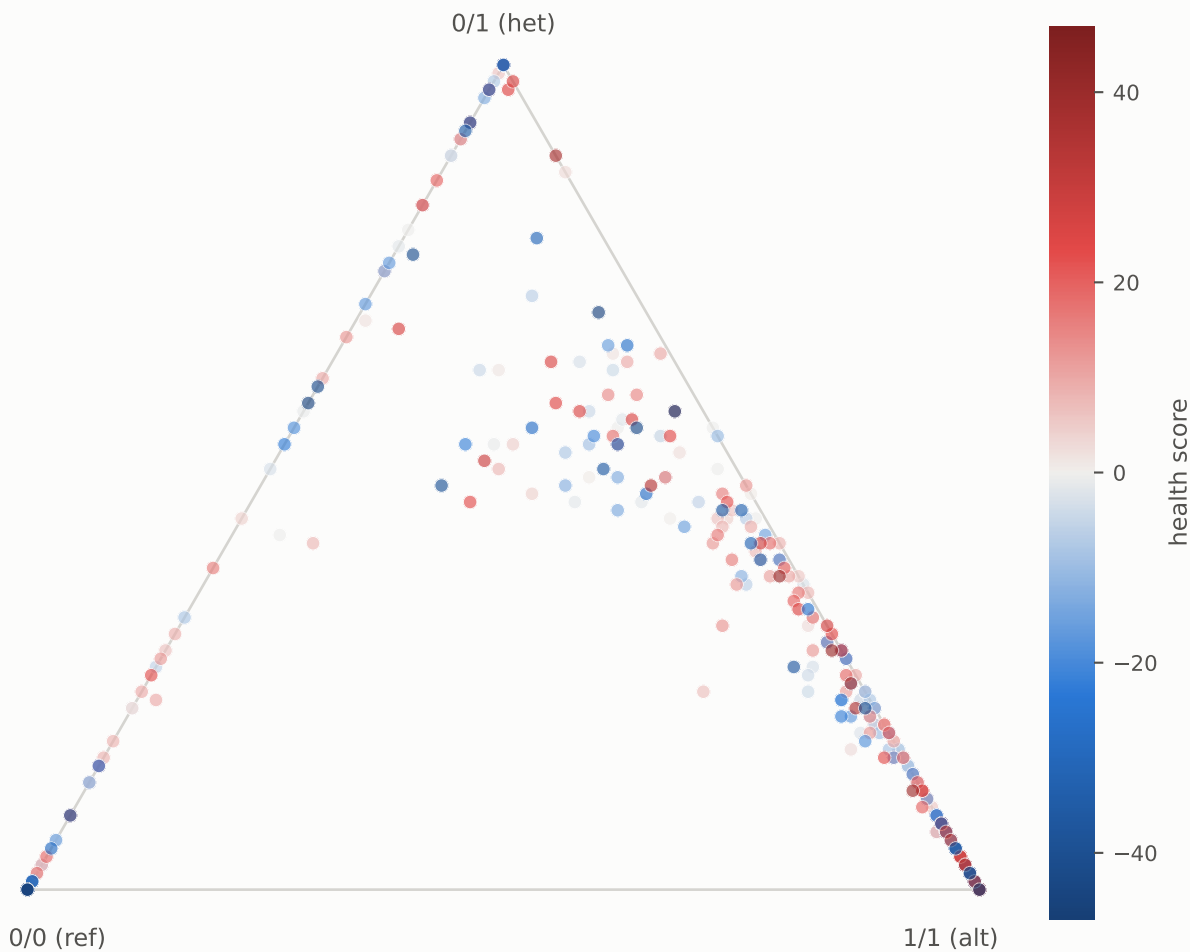
#46 by genotype uncertainty CHR_03:34,937,767 A>G
AF=0.46 DR2=0.81 $r=+0.027$ H=0.392 F=1.3



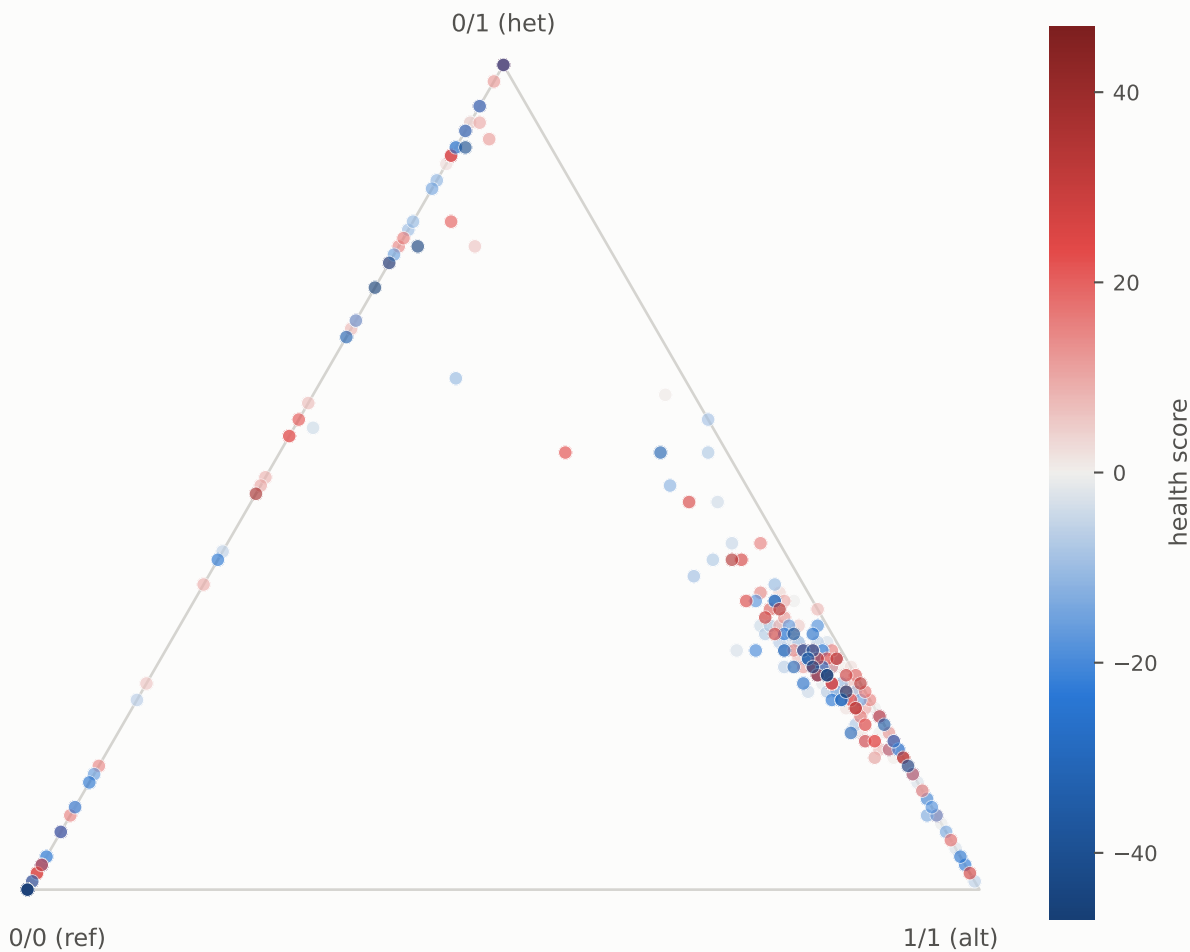
#47 by genotype uncertainty CHR_01:46,943,079 G>A
AF=0.59 DR2=0.81 $r=+0.013$ $H=0.392$ $F=0.8$



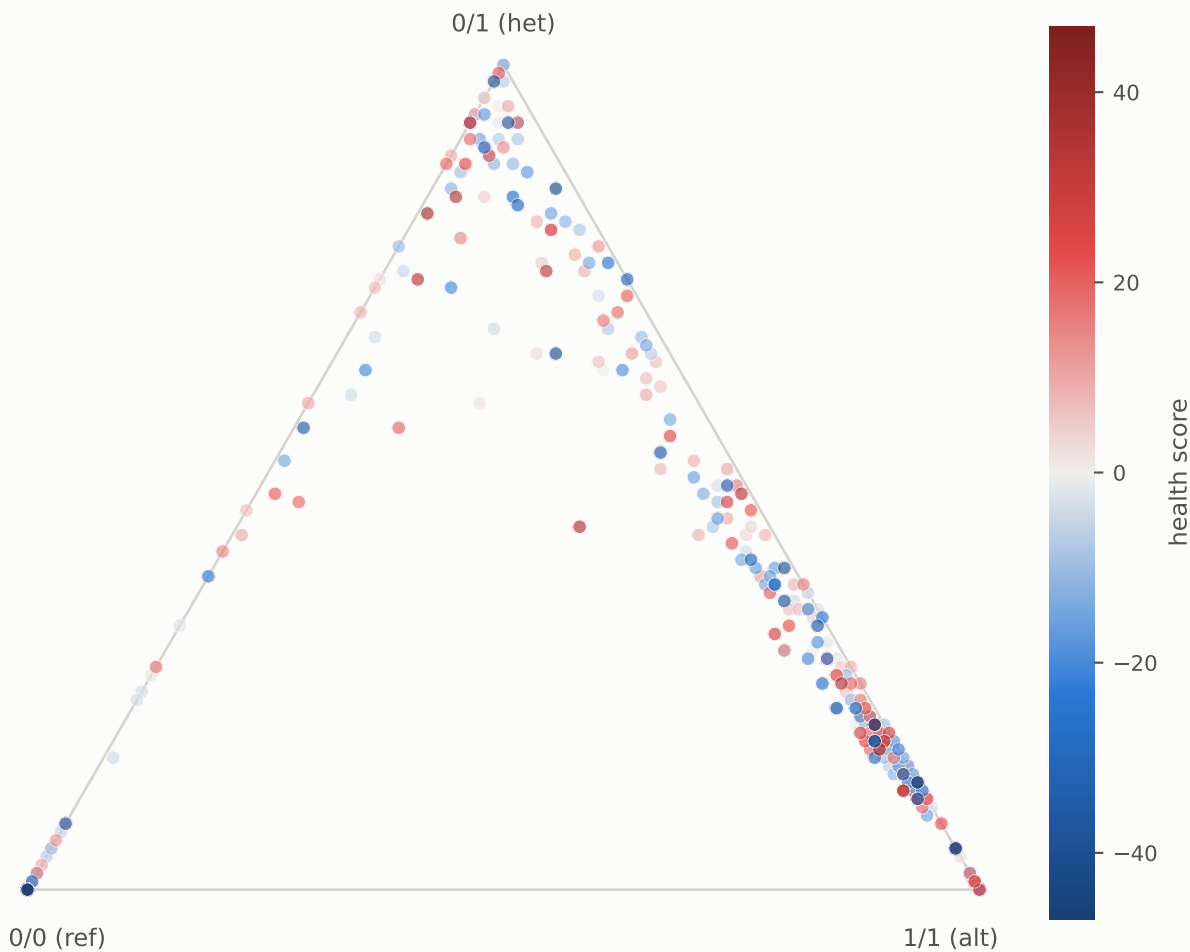
#48 by genotype uncertainty CHR_07:31,589,417 C>T
AF=0.61 DR2=0.81 $r=+0.088$ $H=0.392$ $F=2.6$



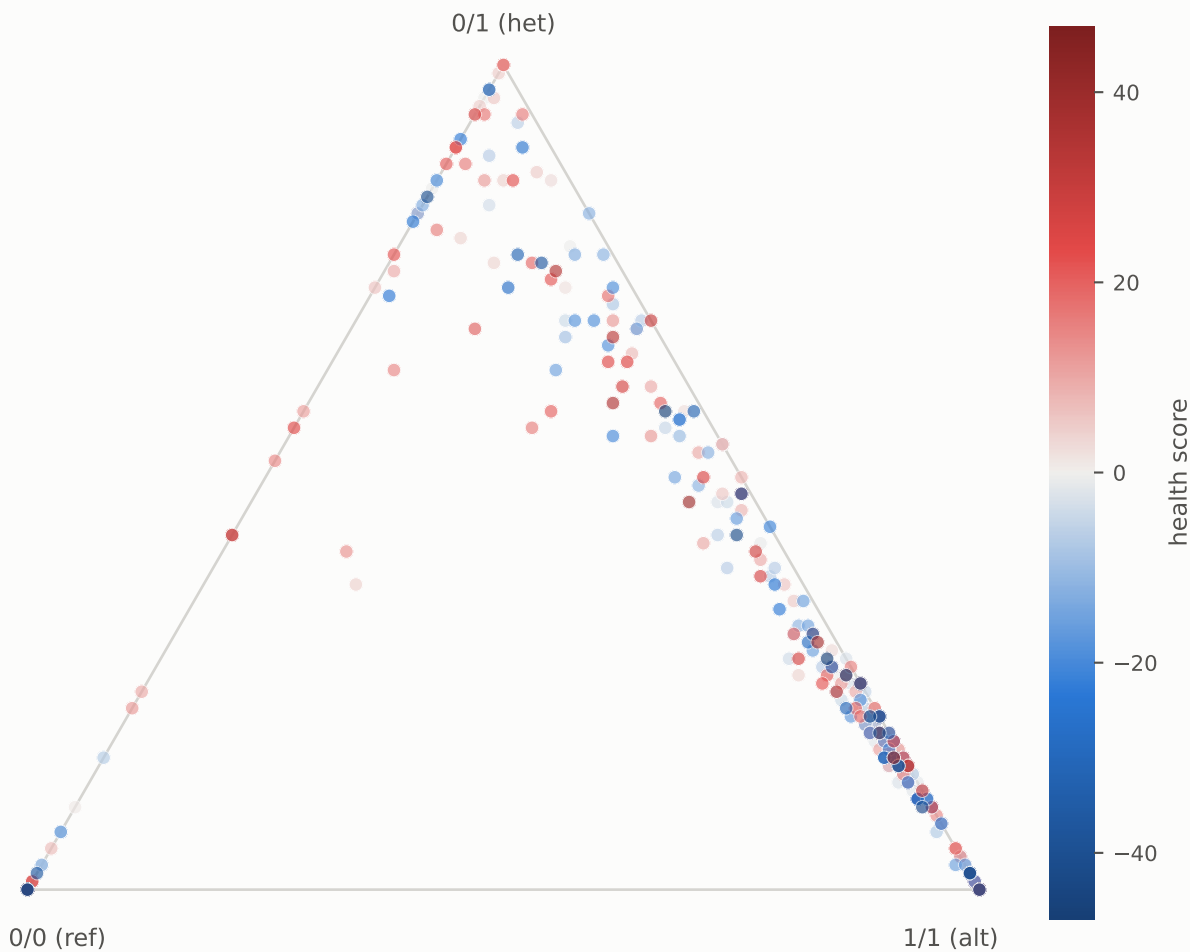
#49 by genotype uncertainty CHR_10:17,732,980 G>T
AF=0.44 DR2=0.82 $r=-0.045$ $\bar{H}=0.392$ F=1.0



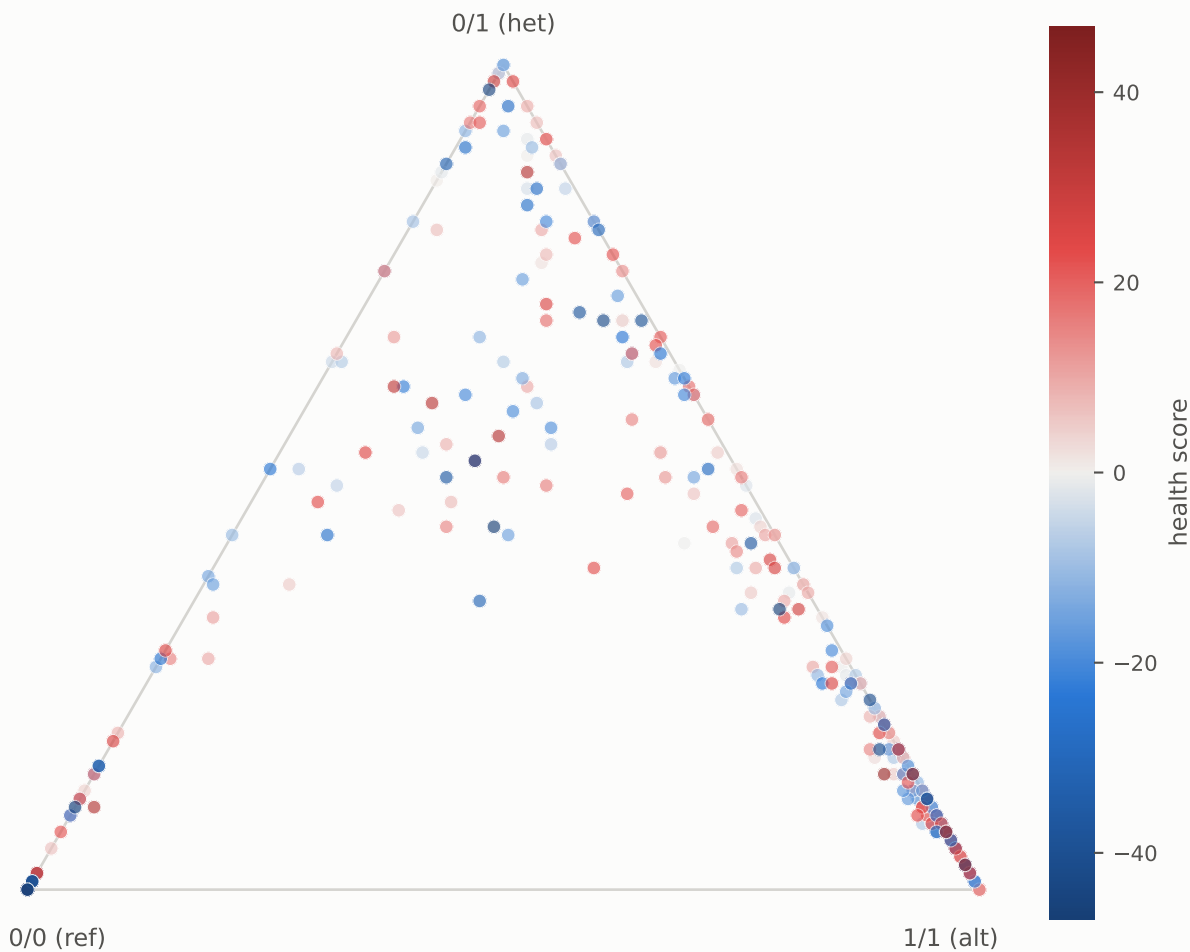
#50 by genotype uncertainty CHR_06:35,883,774 C>T
AF=0.51 DR2=0.81 $r=+0.004$ $\bar{H}=0.392$ $F=0.1$



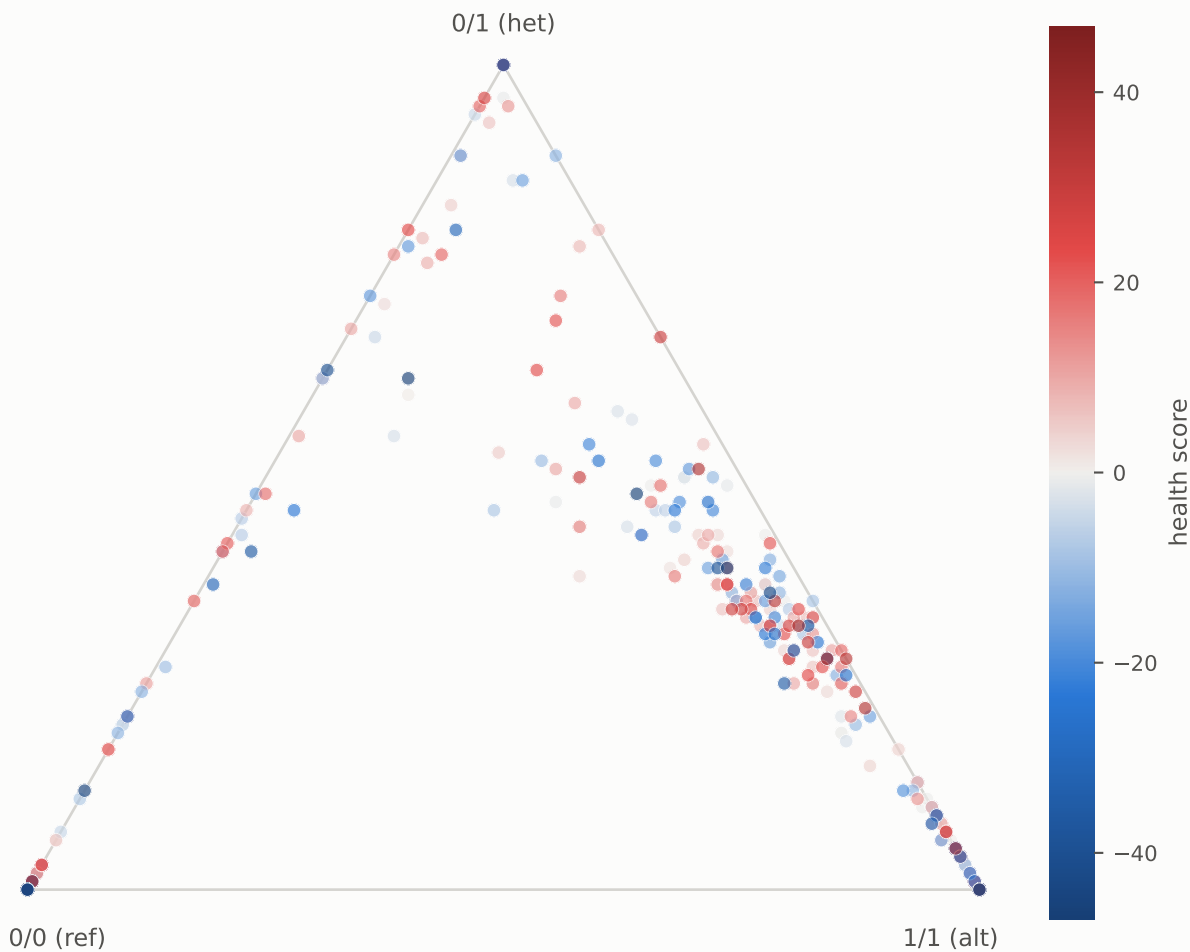
#51 by genotype uncertainty CHR_03:37,962,197 A>T
AF=0.54 DR2=0.81 $r=-0.121$ $\bar{H}=0.391$ F=4.1



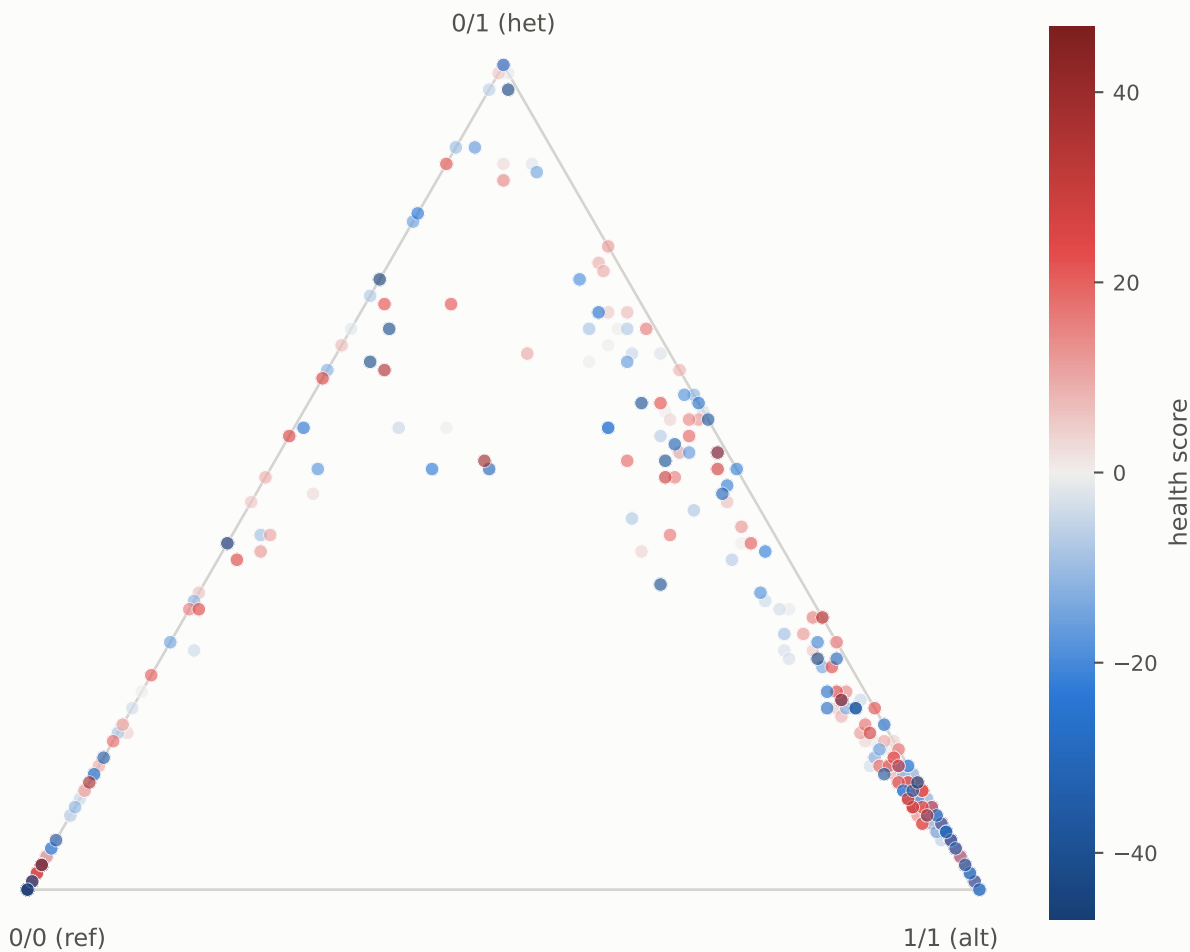
#52 by genotype uncertainty CHR_18:2,763,896 A>C
AF=0.58 DR2=0.81 $r=+0.024$ $\bar{H}=0.391$ F=0.6



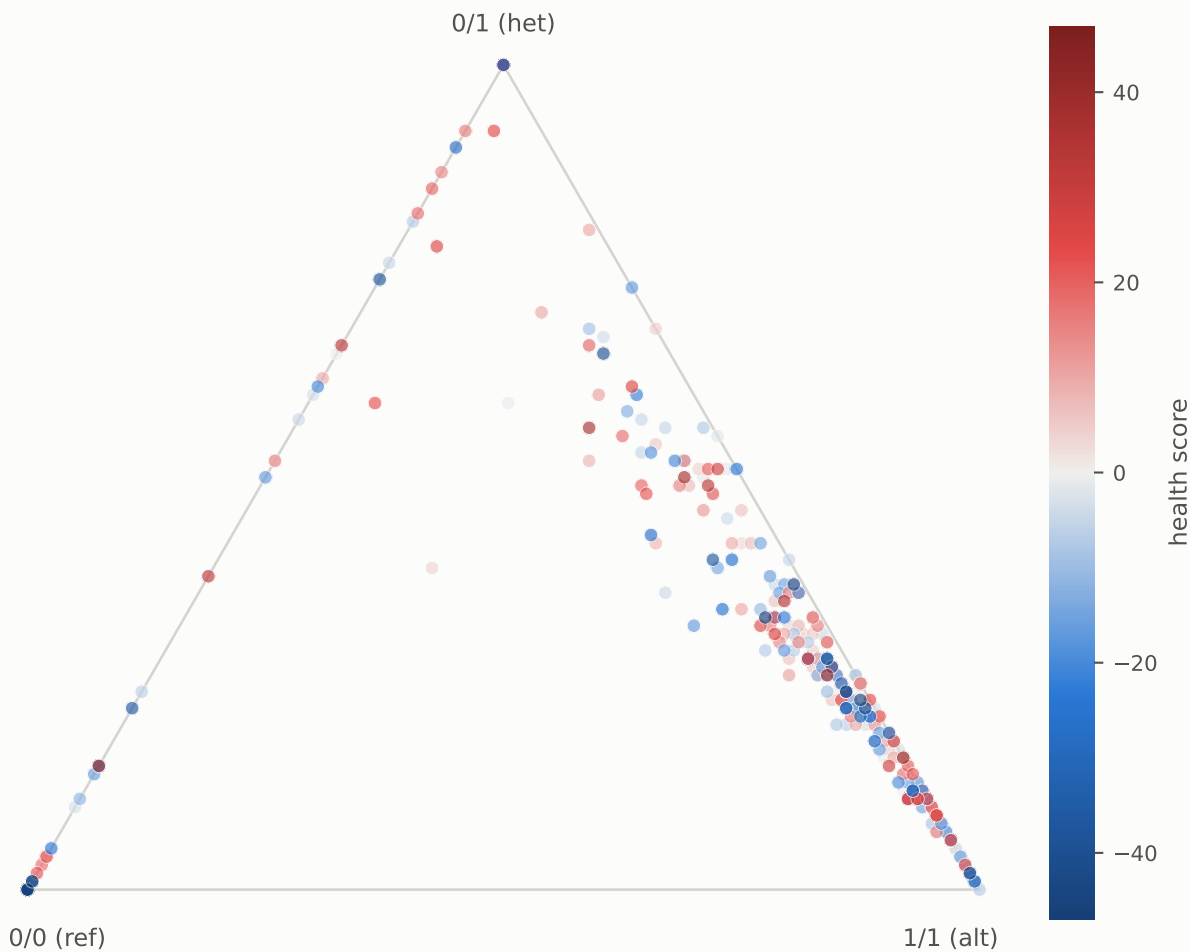
#53 by genotype uncertainty CHR_13:27,855,393 T>C
AF=0.46 DR2=0.81 r=-0.040 H=0.391 F=0.4



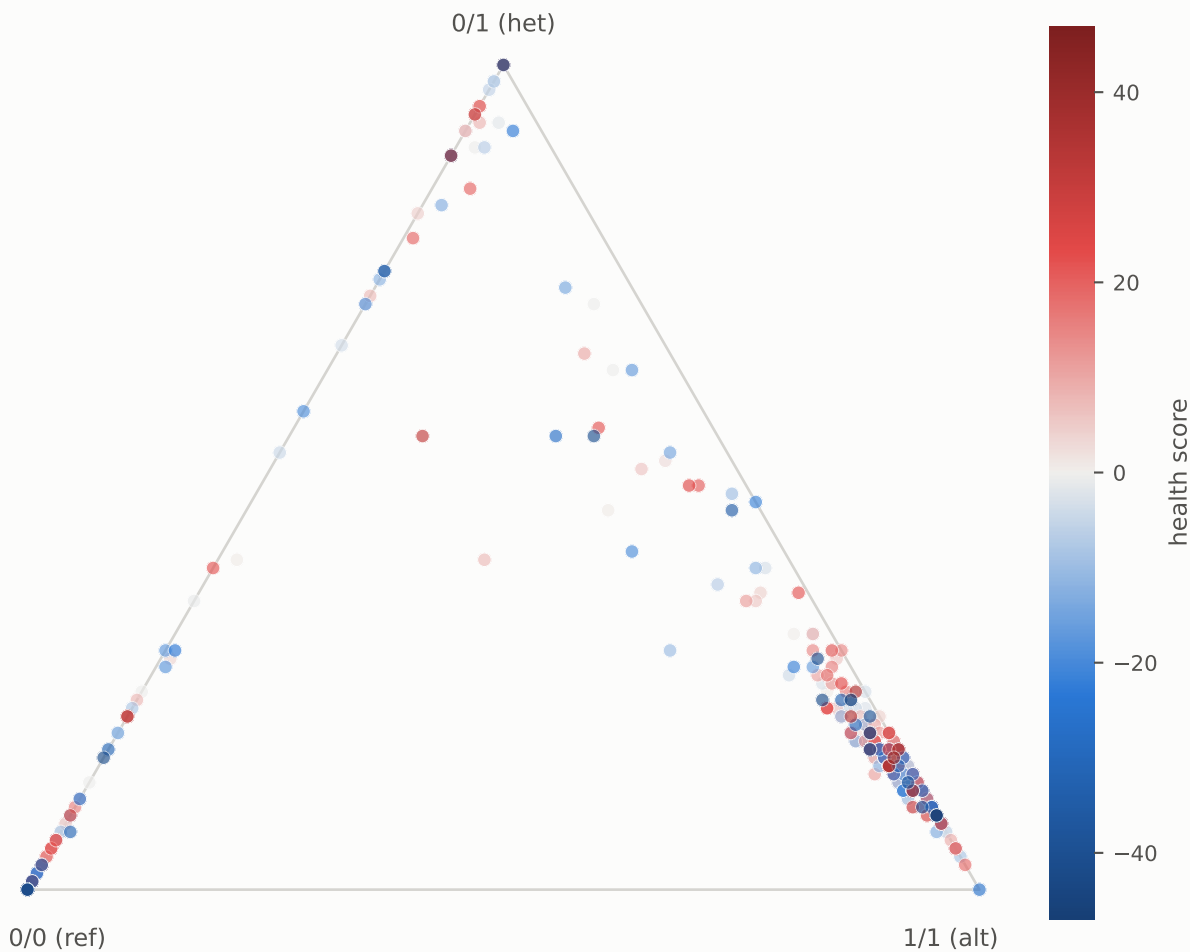
#54 by genotype uncertainty CHR_06:36,064,080 T>C
AF=0.53 DR2=0.82 $r=-0.032$ $\bar{H}=0.391$ F=2.4



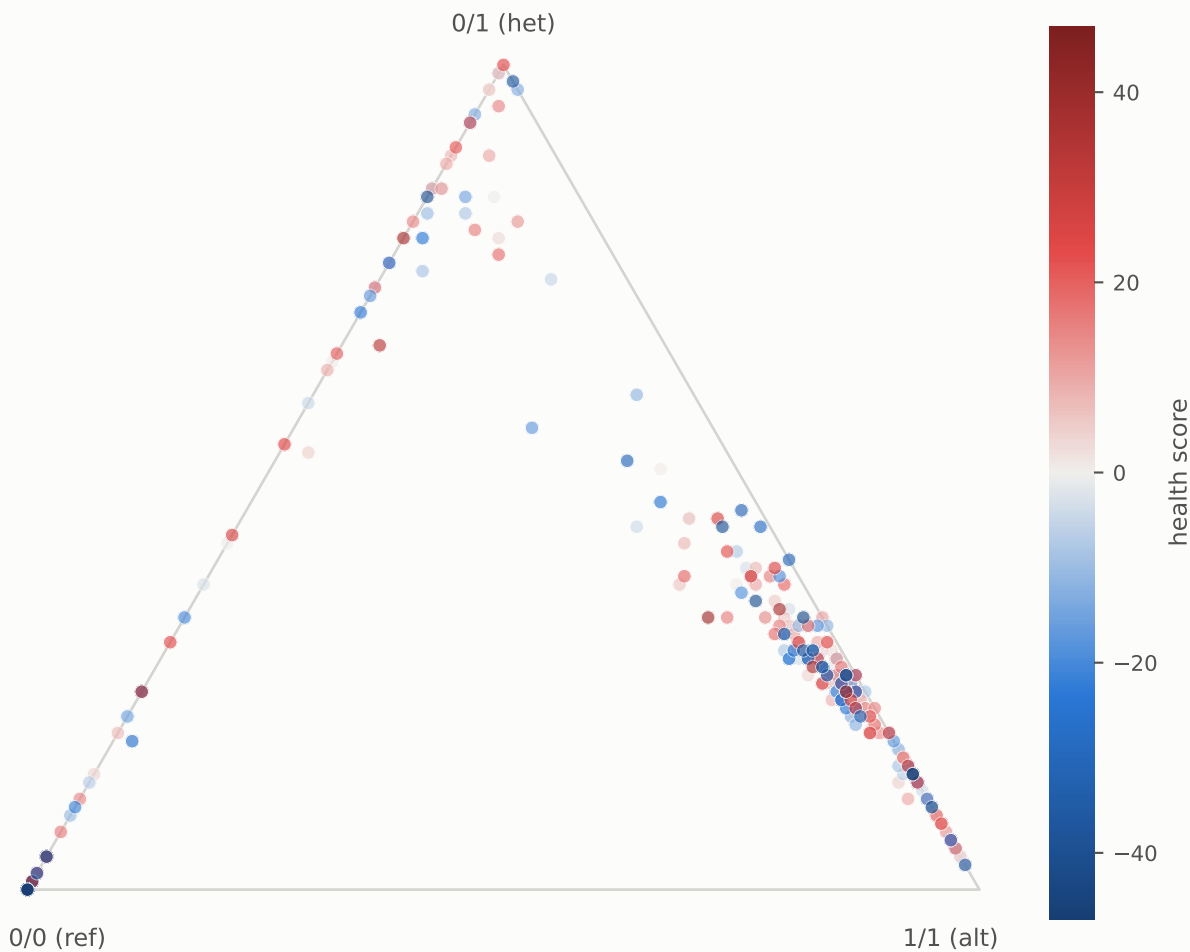
#55 by genotype uncertainty CHR_22:6,598,281 T>C
AF=0.51 DR2=0.81 $r=+0.002$ $\bar{H}=0.391$ F=2.2



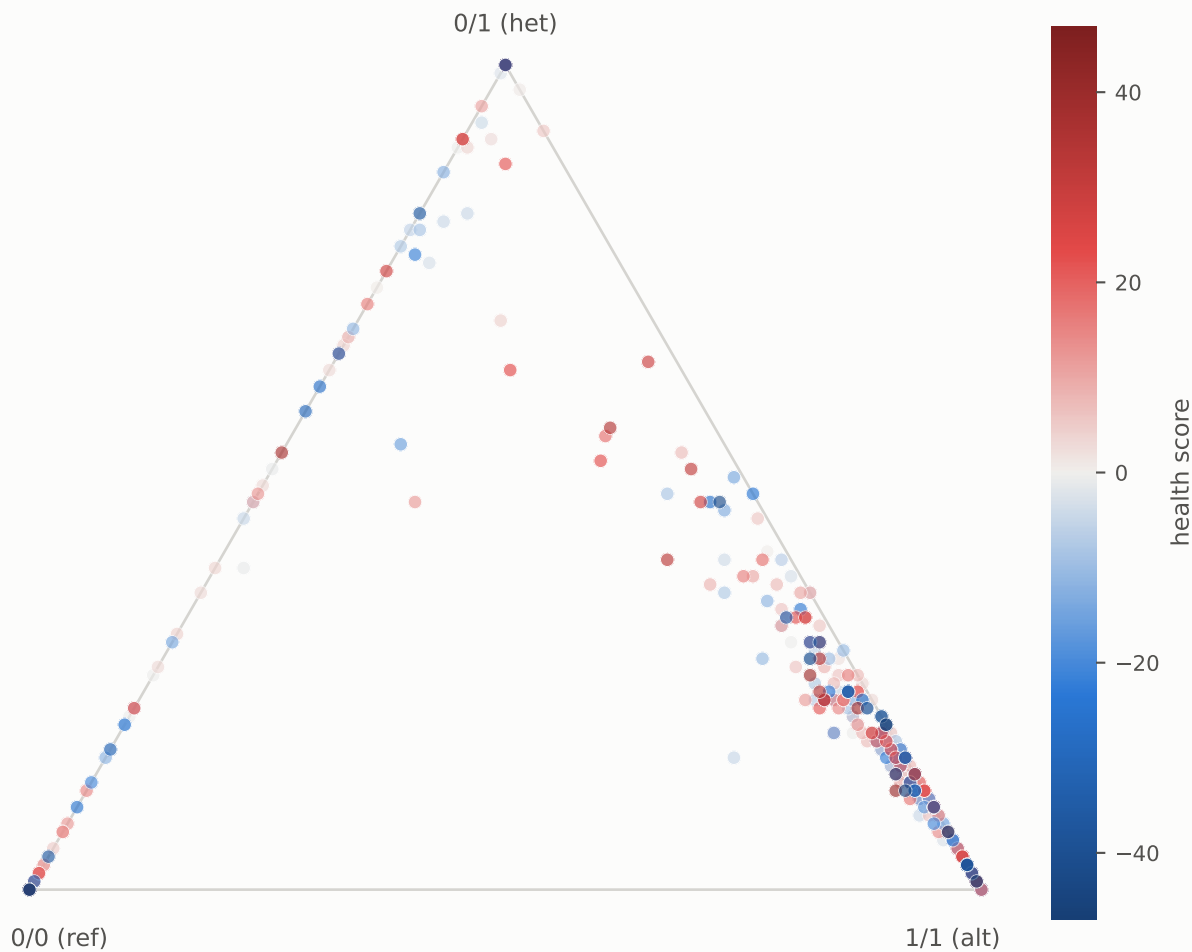
#56 by genotype uncertainty CHR_05:25,031,779 A>G
AF=0.58 DR2=0.81 $r=+0.051$ H=0.391 F=0.5



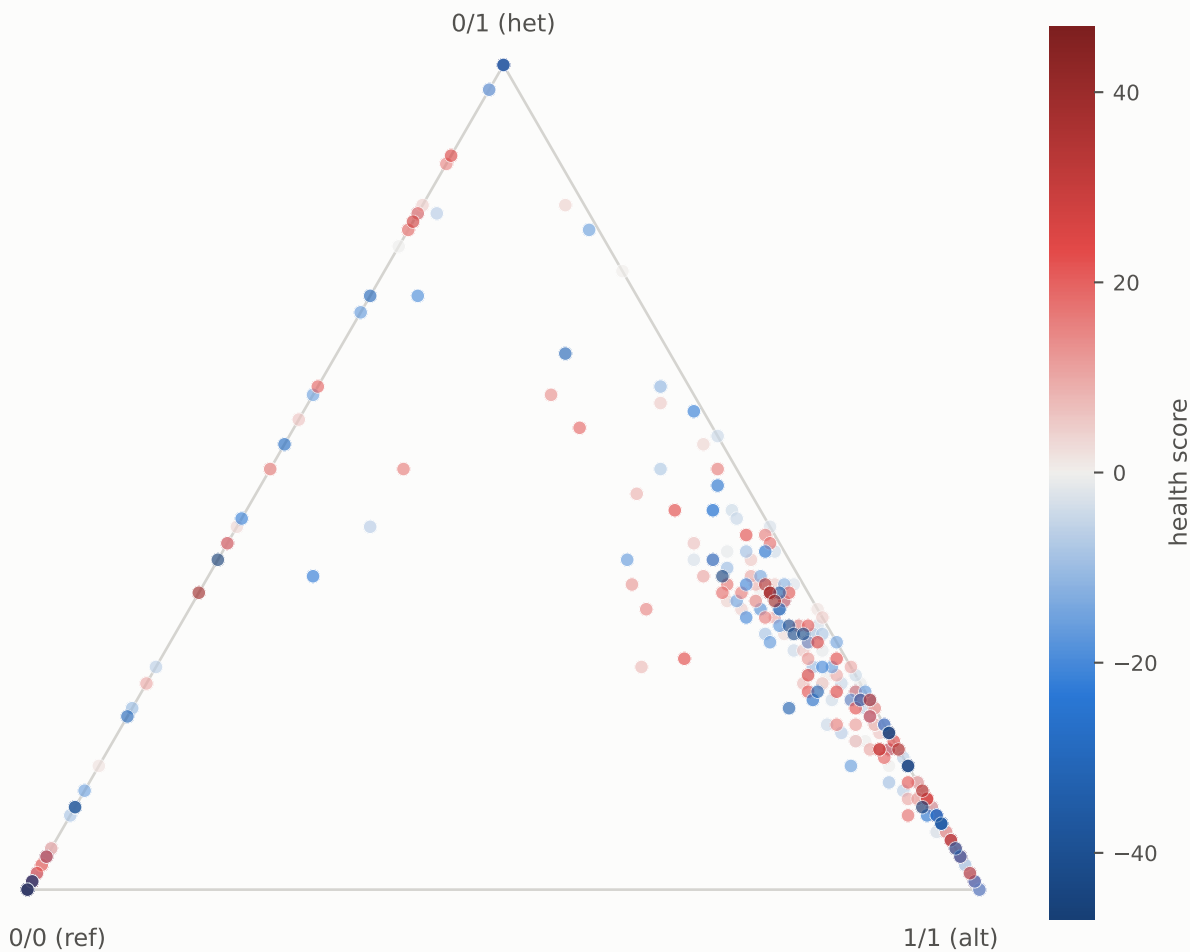
#57 by genotype uncertainty CHR_05:41,119,650 G>C
AF=0.44 DR2=0.82 $r=-0.024$ $\bar{H}=0.390$ $F=0.1$



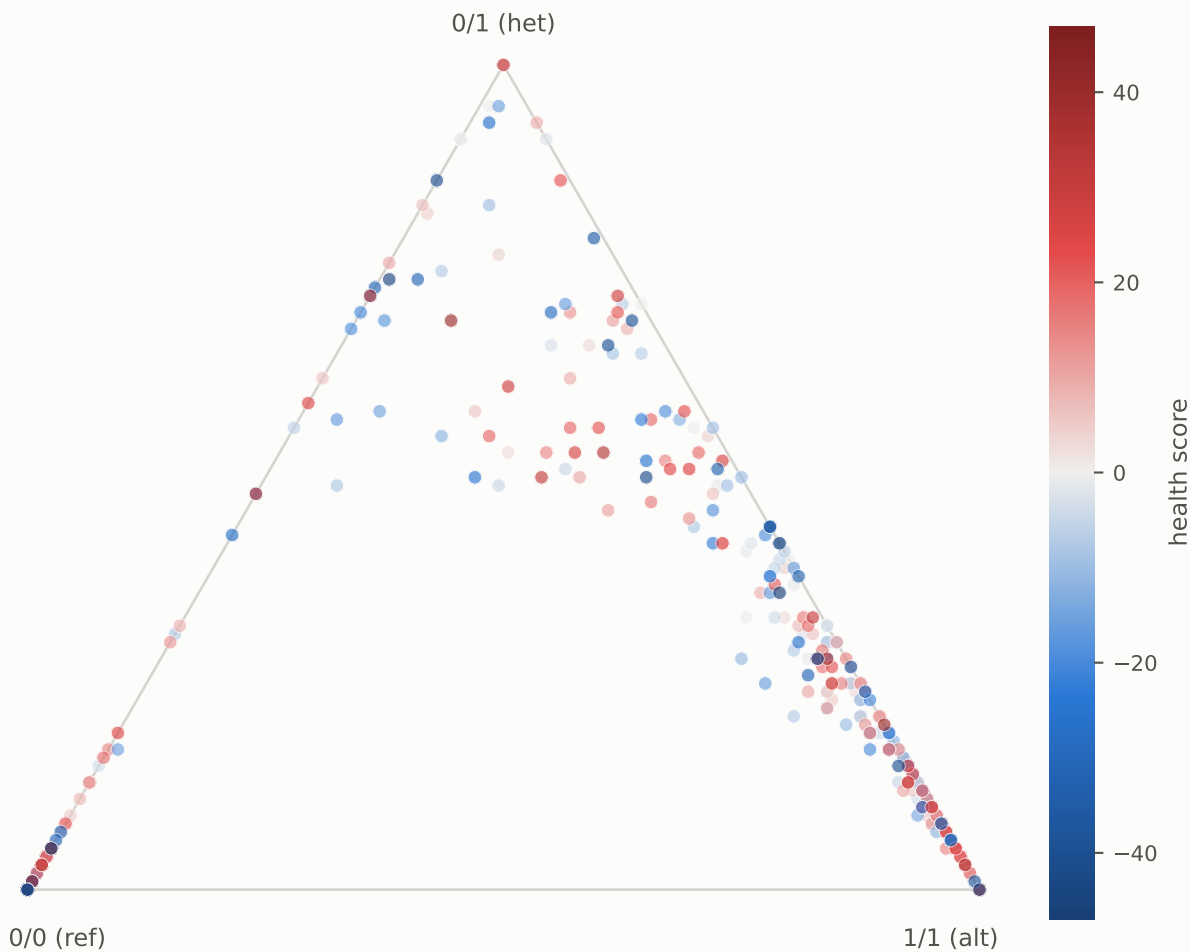
#58 by genotype uncertainty CHR_13:16,256,066 G>C
AF=0.62 DR2=0.81 $r=-0.042$ $\bar{H}=0.390$ $F=1.2$



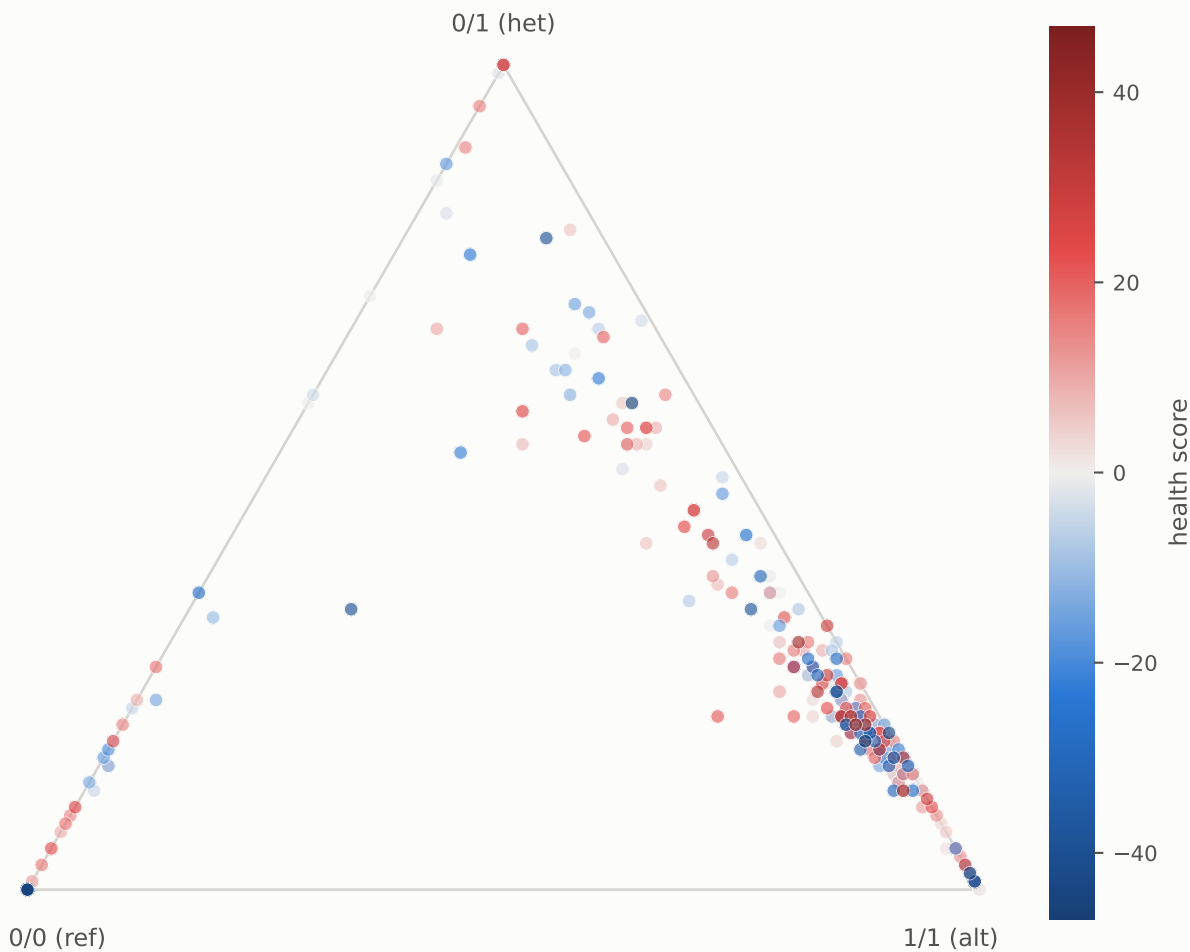
#59 by genotype uncertainty CHR_19:21,138,800 G>A
AF=0.51 DR2=0.81 $r=+0.011$ H=0.390 F=0.1



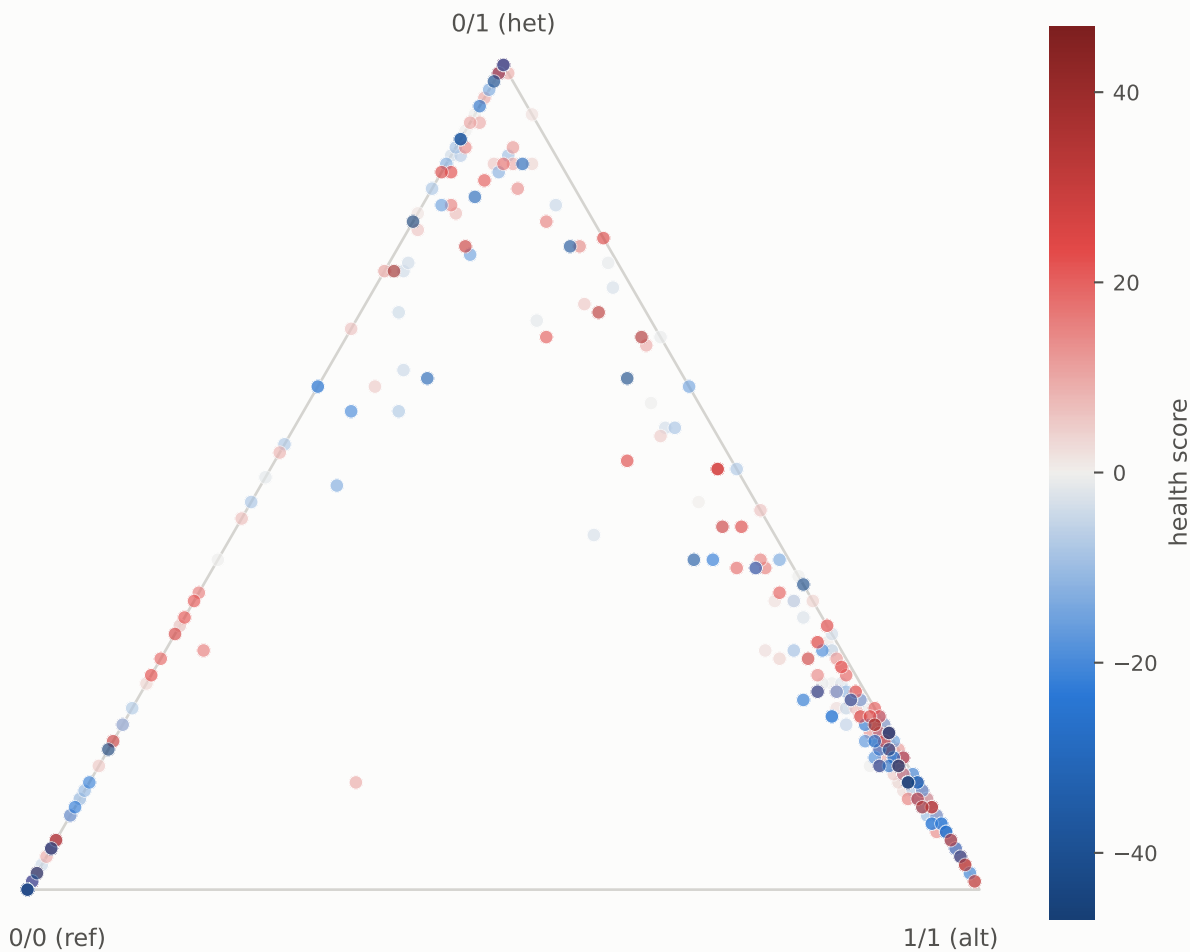
#60 by genotype uncertainty CHR_04:41,505,178 G>T
AF=0.54 DR2=0.81 $r=+0.031$ $H=0.390$ $F=0.0$



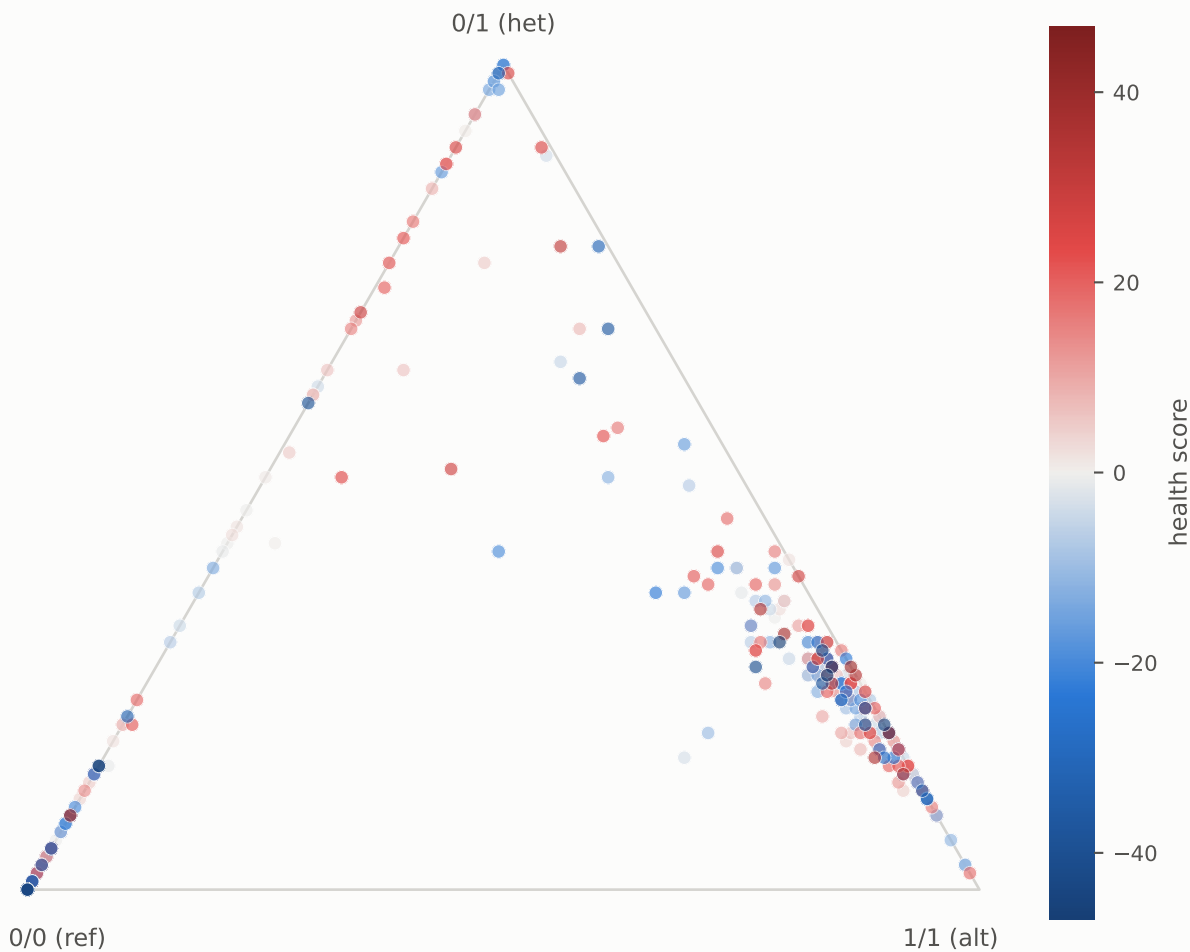
#61 by genotype uncertainty CHR_01:43,543,354 C>T
AF=0.54 DR2=0.81 r=+0.054 H=0.390 F=1.1



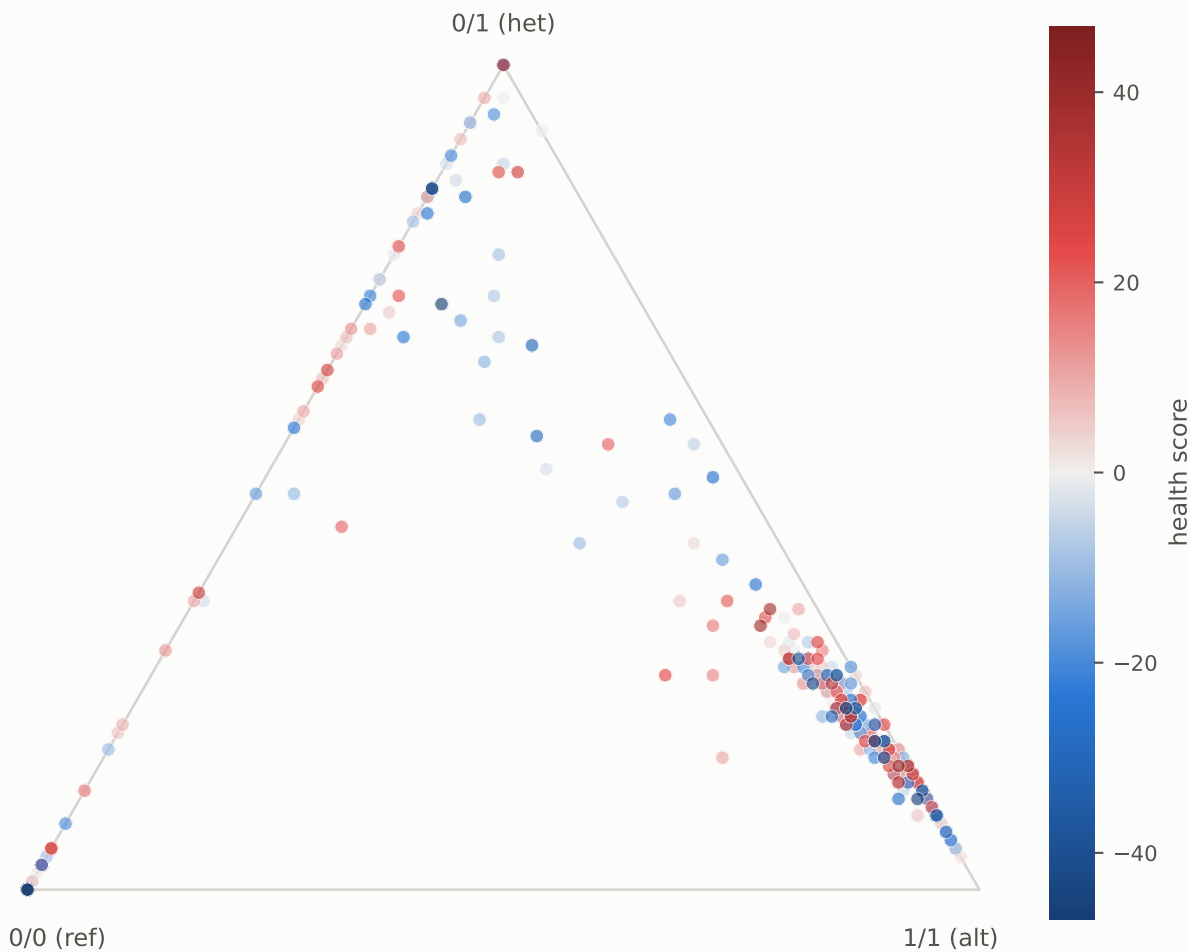
#62 by genotype uncertainty CHR_11:11,369,296 C>T
AF=0.54 DR2=0.81 $r=+0.006$ $\bar{H}=0.390$ F=0.0



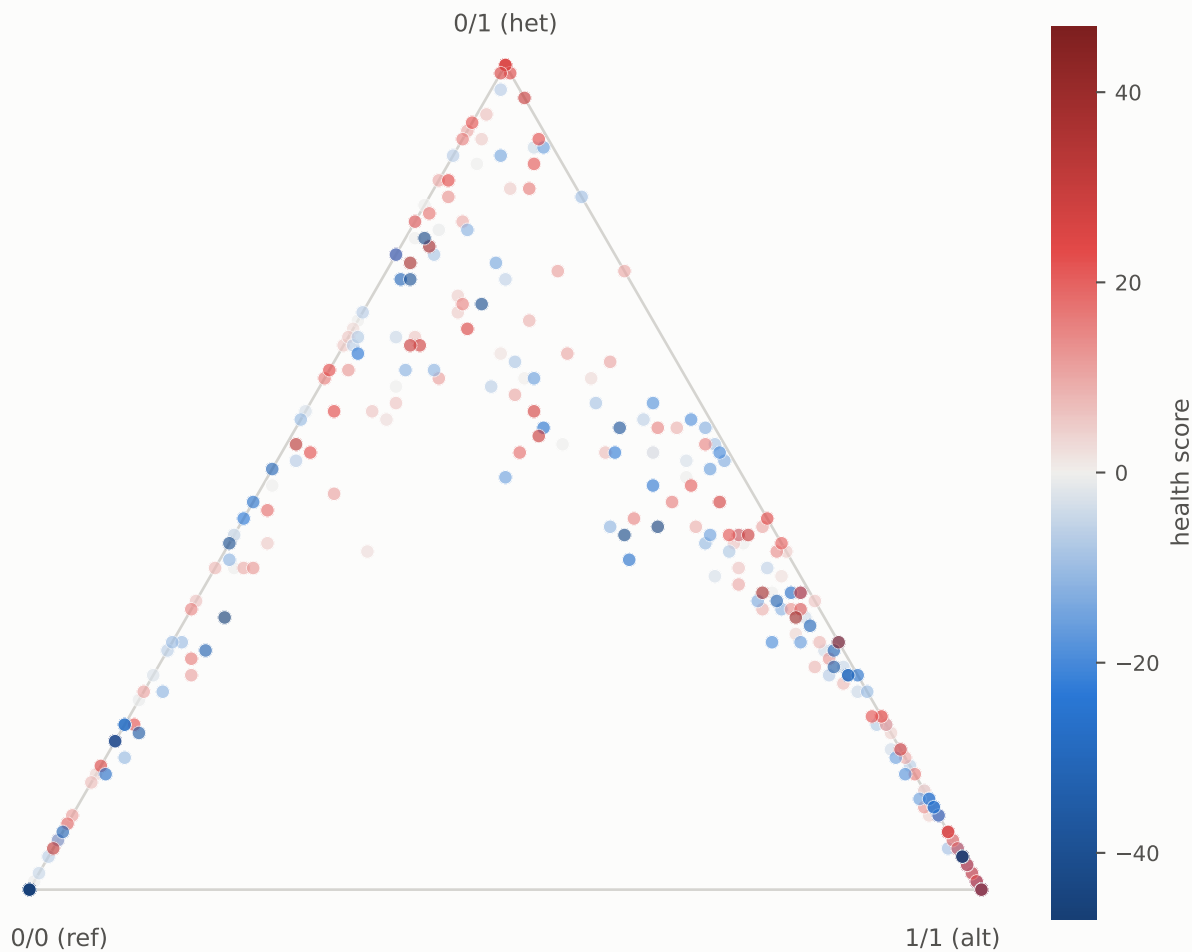
#63 by genotype uncertainty CHR_13:25,419,497 C>T
AF=0.44 DR2=0.81 $r=+0.057$ $\bar{H}=0.390$ $F=1.3$



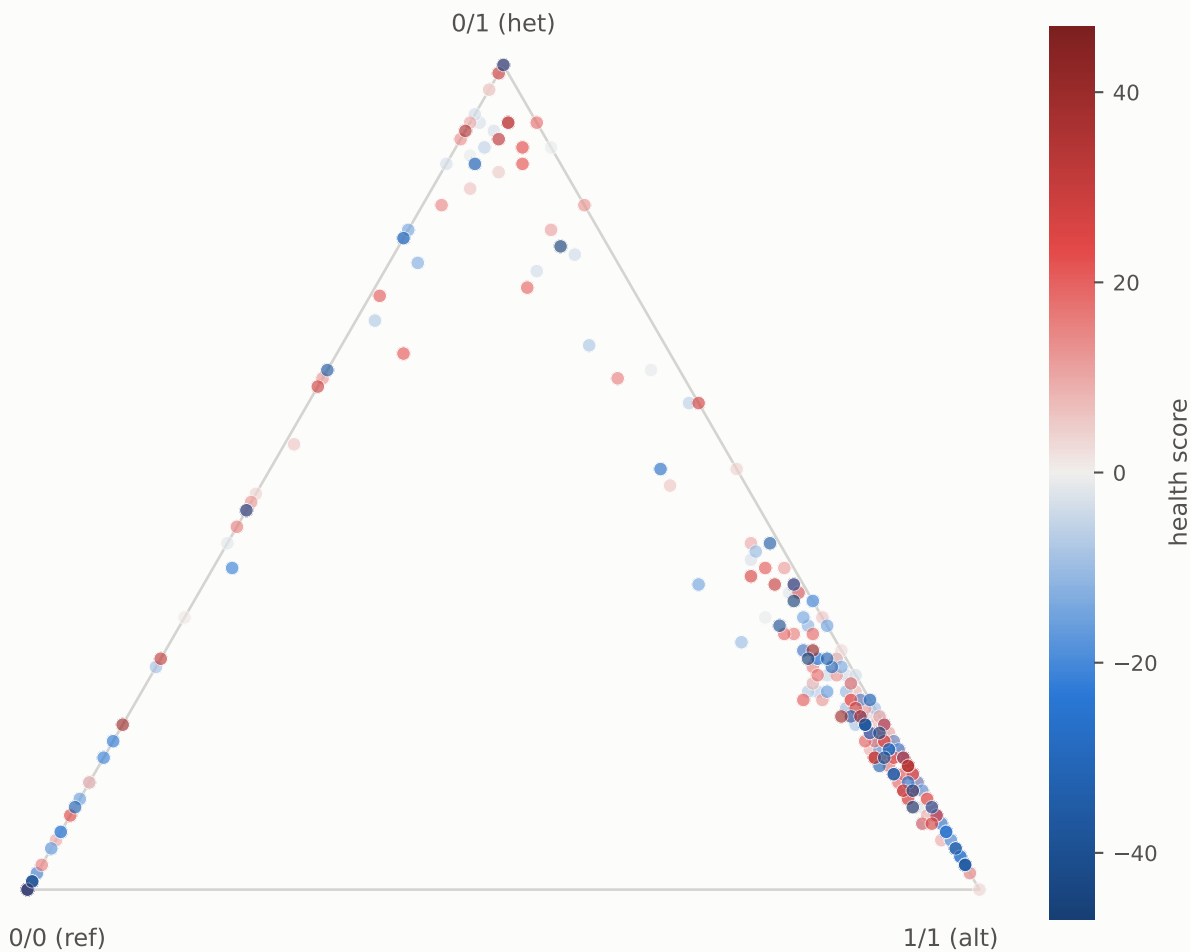
#64 by genotype uncertainty CHR_09:29,883,099 T>C
AF=0.49 DR2=0.81 $r=-0.013$ $\bar{H}=0.390$ F=1.9



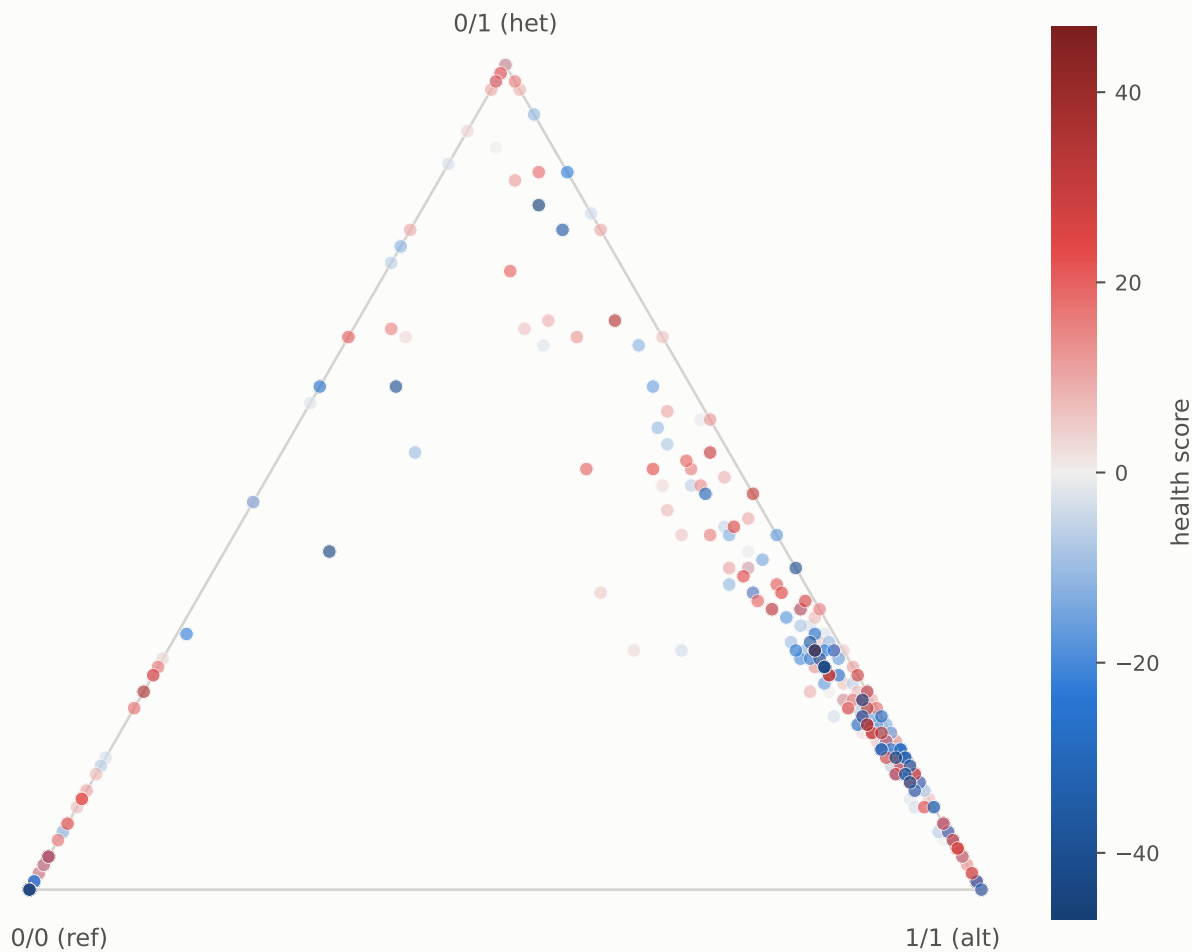
#65 by genotype uncertainty CHR_20:8,649,727 T>C
AF=0.47 DR2=0.81 $r=+0.038$ $\bar{H}=0.390$ F=1.8



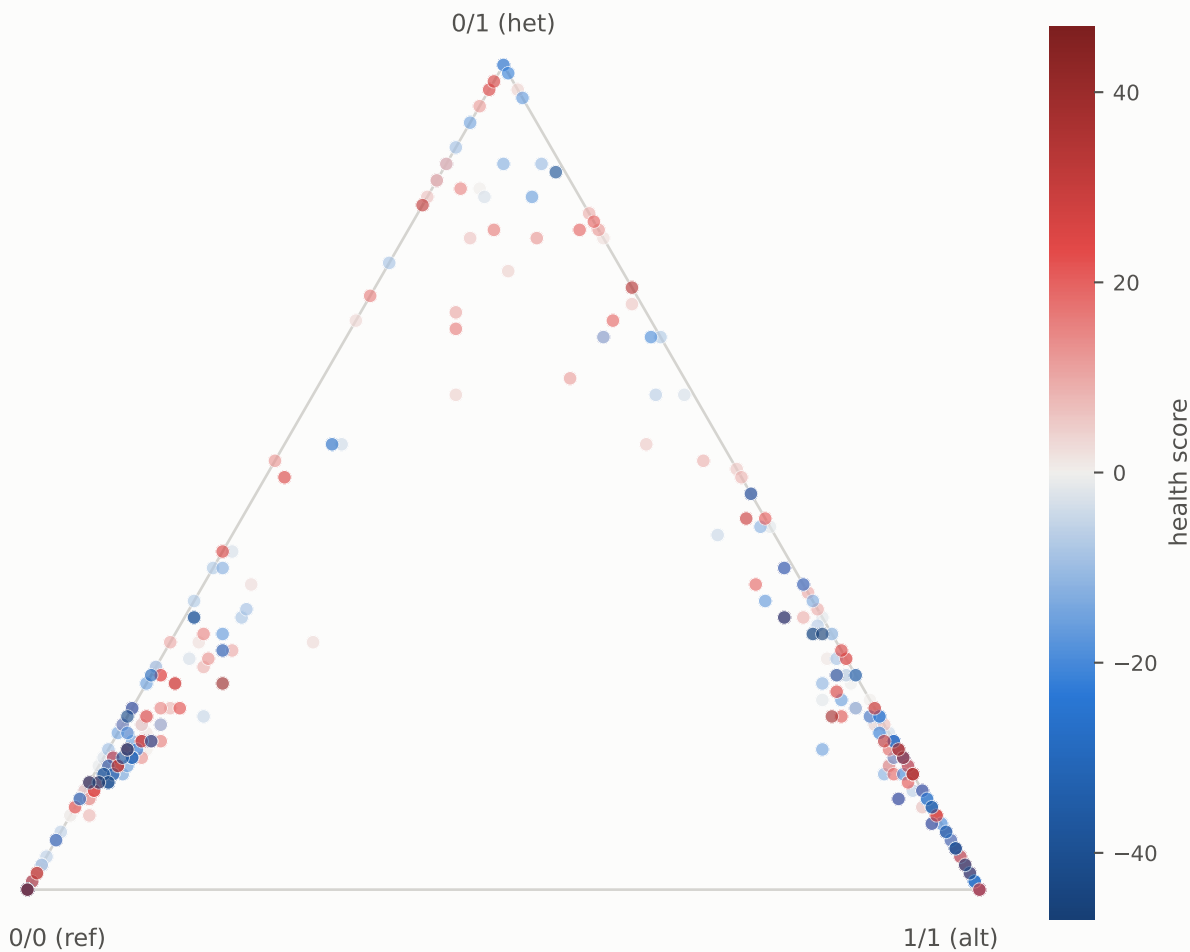
#66 by genotype uncertainty CHR_09:33,143,132 T>G
AF=0.62 DR2=0.81 $r=+0.027$ $H=0.390$ $F=1.2$



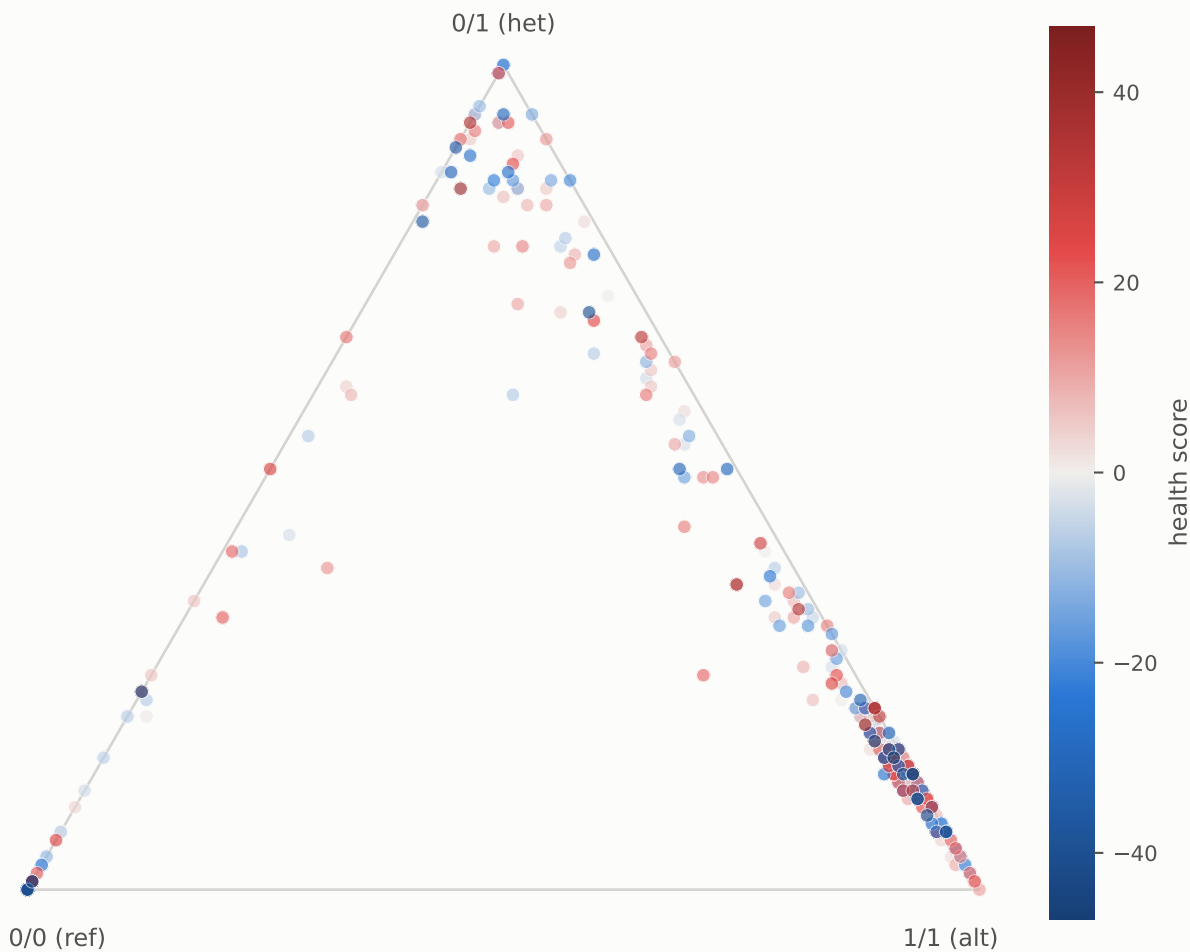
#67 by genotype uncertainty CHR_19:8,426,469 C>T
AF=0.53 DR2=0.81 $r=-0.036$ $\bar{H}=0.390$ $F=0.8$



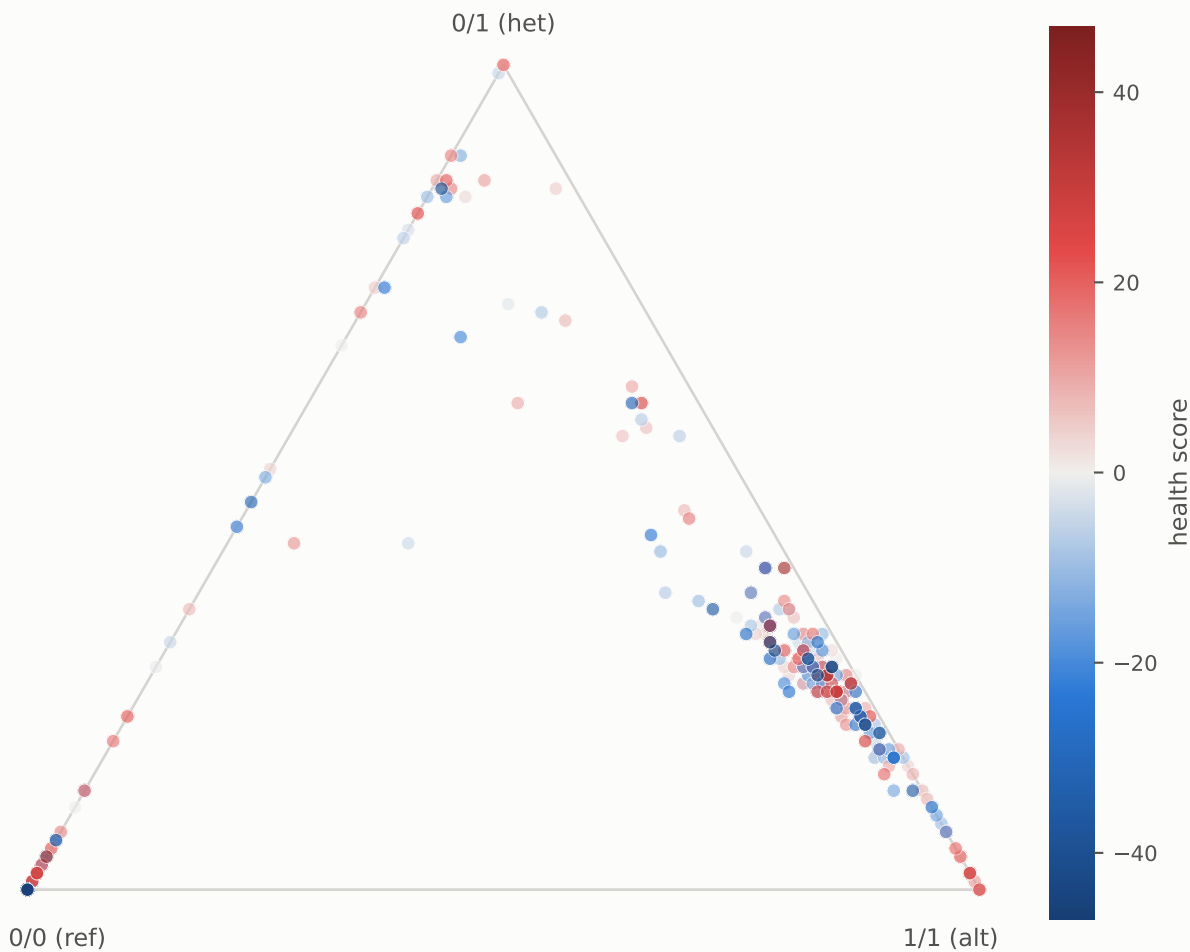
#68 by genotype uncertainty CHR_15:24,159,406 T>C
AF=0.44 DR2=0.81 $r=-0.014$ $\bar{H}=0.390$ F=1.0



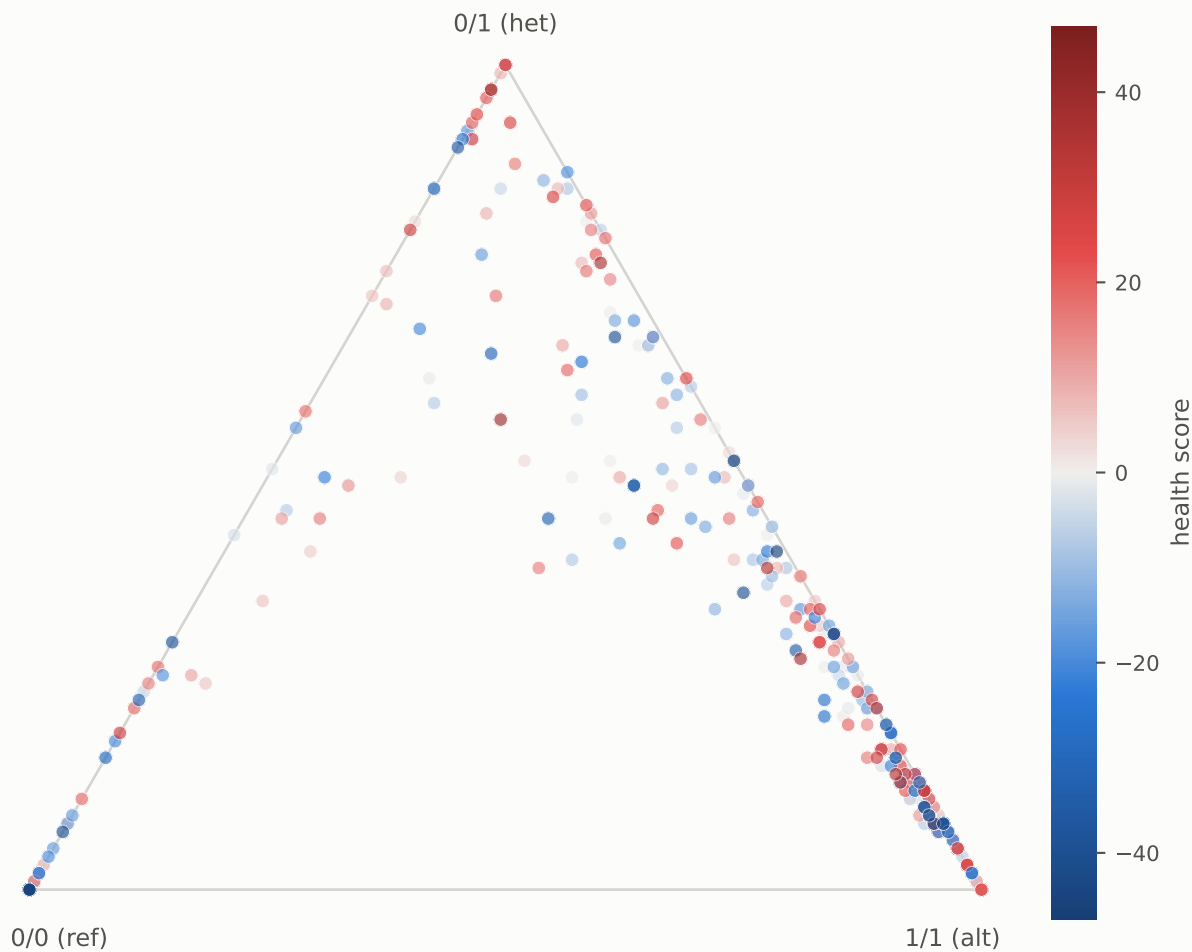
#69 by genotype uncertainty CHR_06:31,166,278 T>G
AF=0.6 DR2=0.81 r=+0.049 $\bar{H}$ =0.389 F=0.7



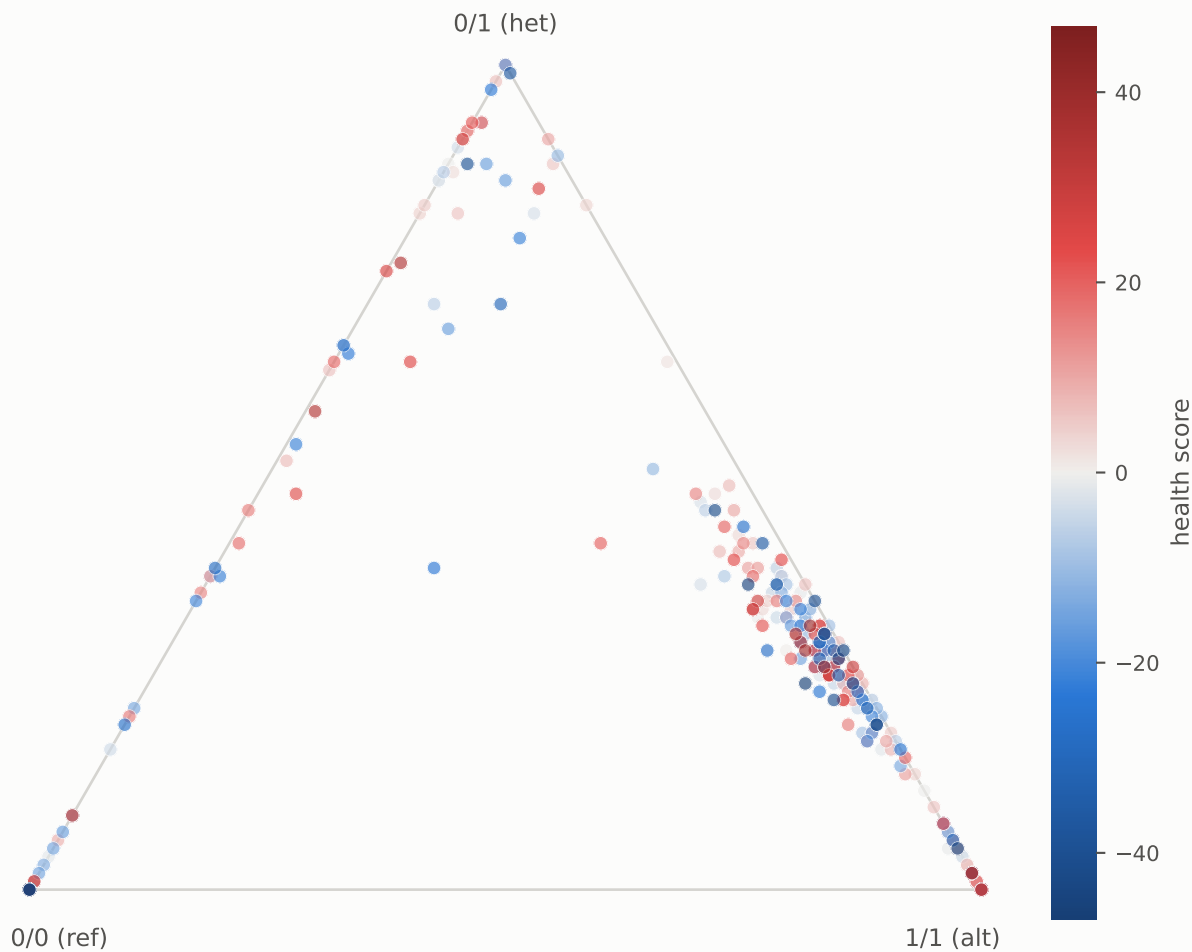
#70 by genotype uncertainty CHR_10:13,724,380 T>C
AF=0.45 DR2=0.81 $r=-0.057$ $\bar{H}=0.389$ F=1.0



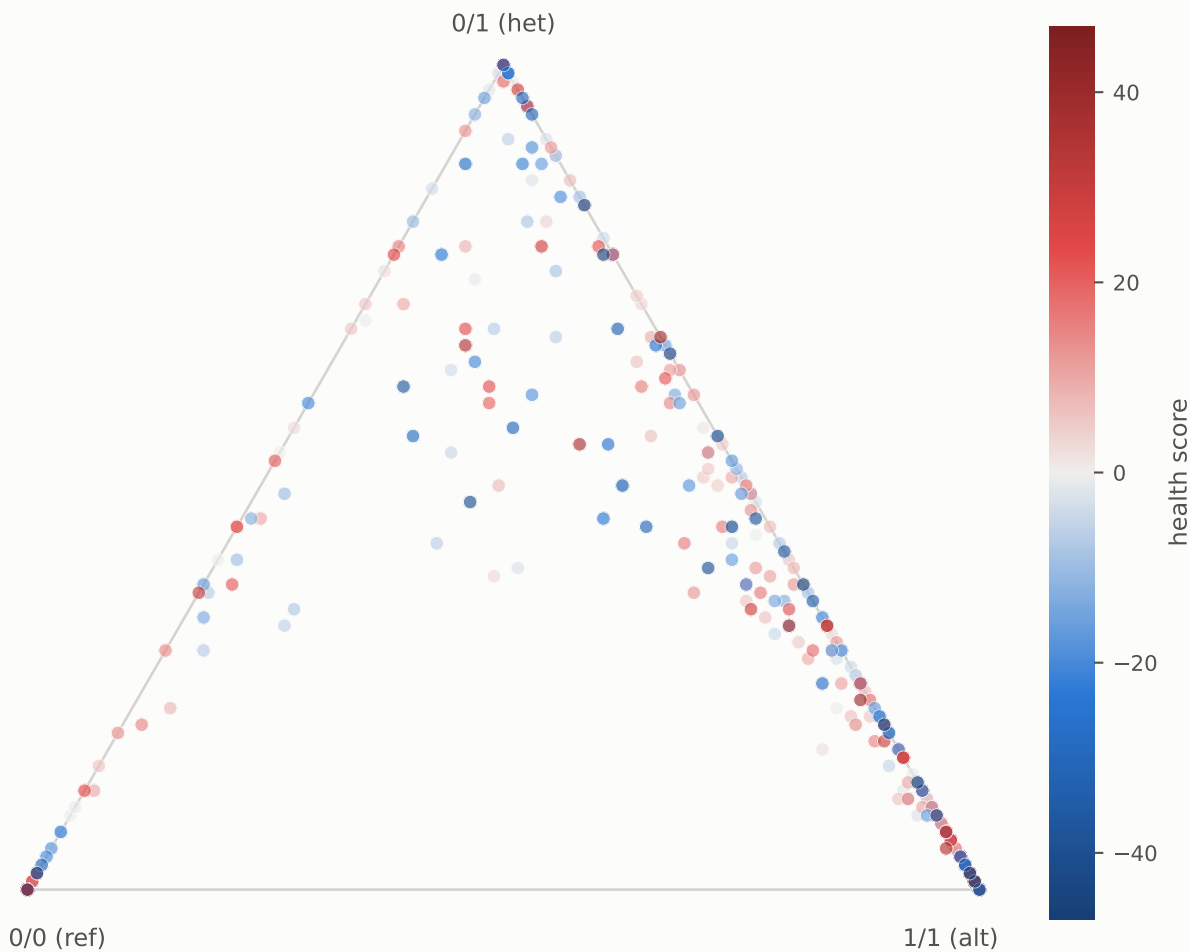
#71 by genotype uncertainty CHR_16:3,995,895 C>T
AF=0.54 DR2=0.81 $r=-0.013$ $\bar{H}=0.389$ F=0.5



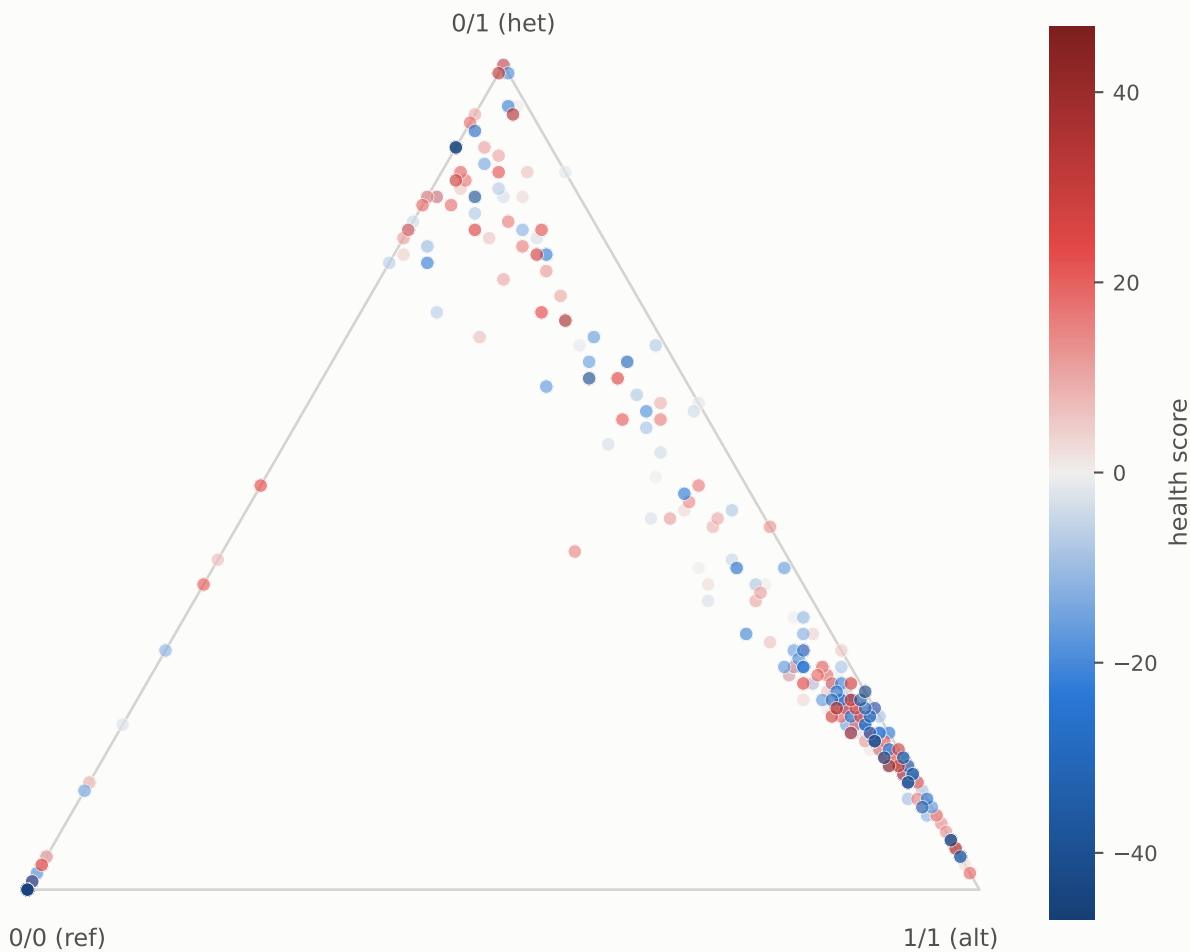
#72 by genotype uncertainty CHR_13:24,013,112 G>A
AF=0.53 DR2=0.81 $r=-0.032$ $\bar{H}=0.389$ $F=0.3$



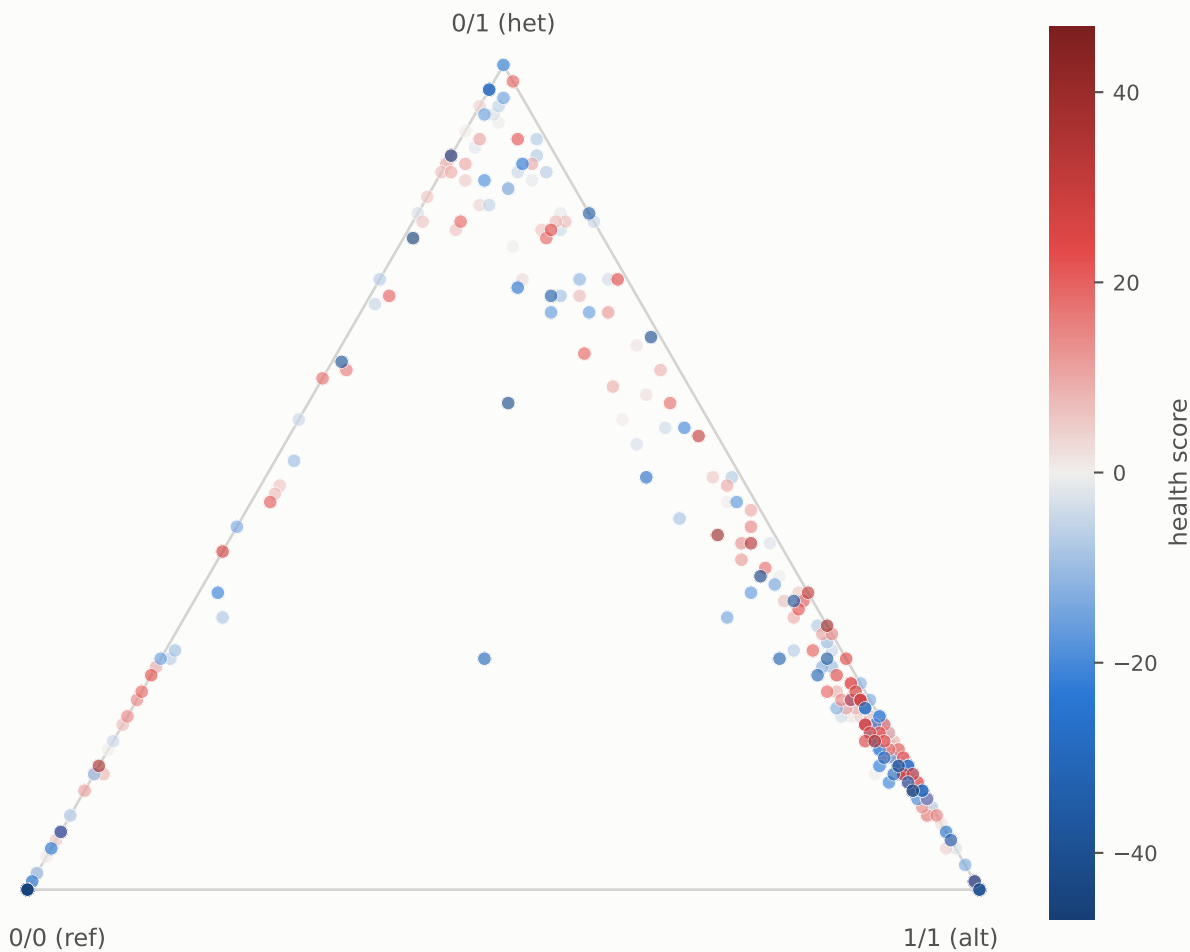
#73 by genotype uncertainty CHR_11:23,144,463 T>C
AF=0.57 DR2=0.81 $r=-0.036$ $\bar{H}=0.389$ F=3.2



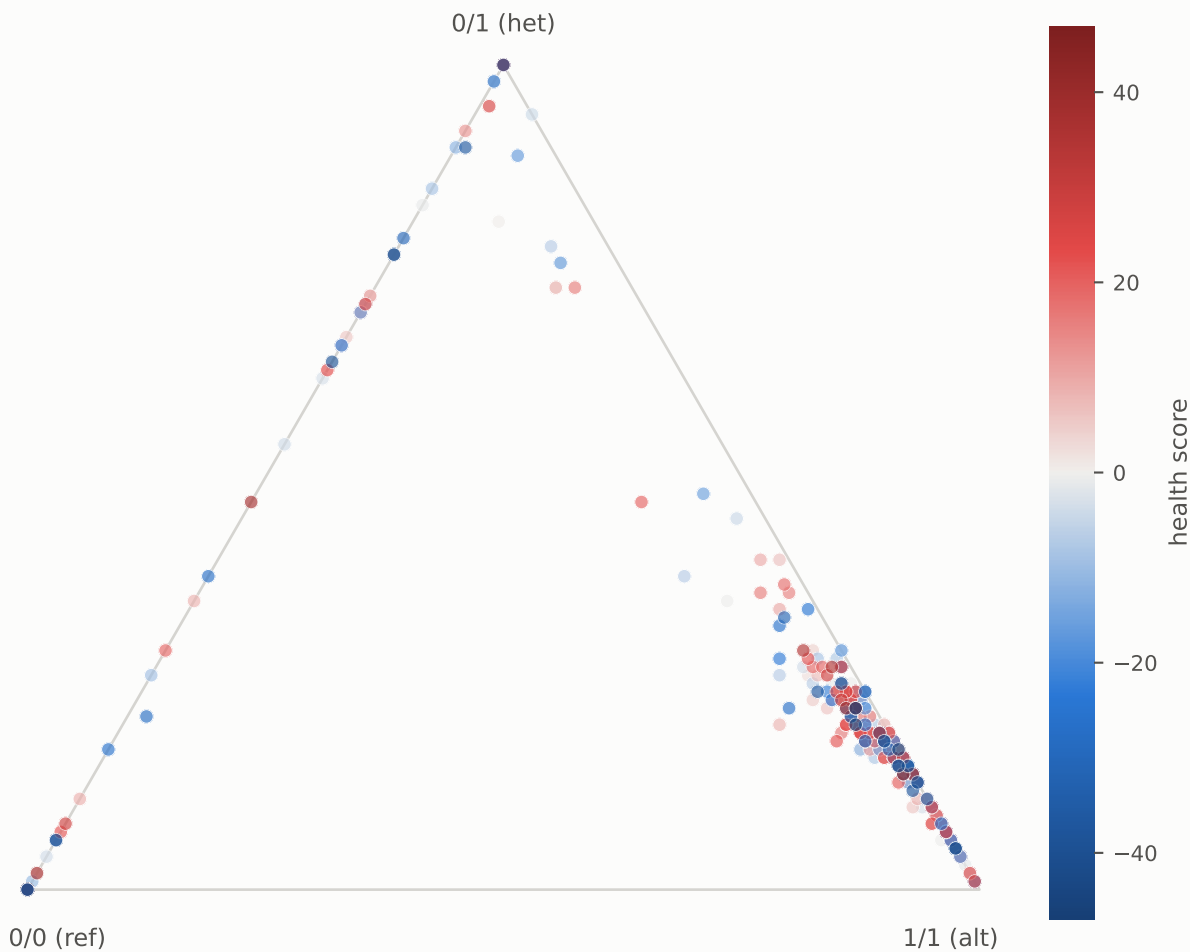
#74 by genotype uncertainty CHR_05:27,375,172 C>G
AF=0.46 DR2=0.82 $r=-0.073$ $\bar{H}=0.389$ F=1.9



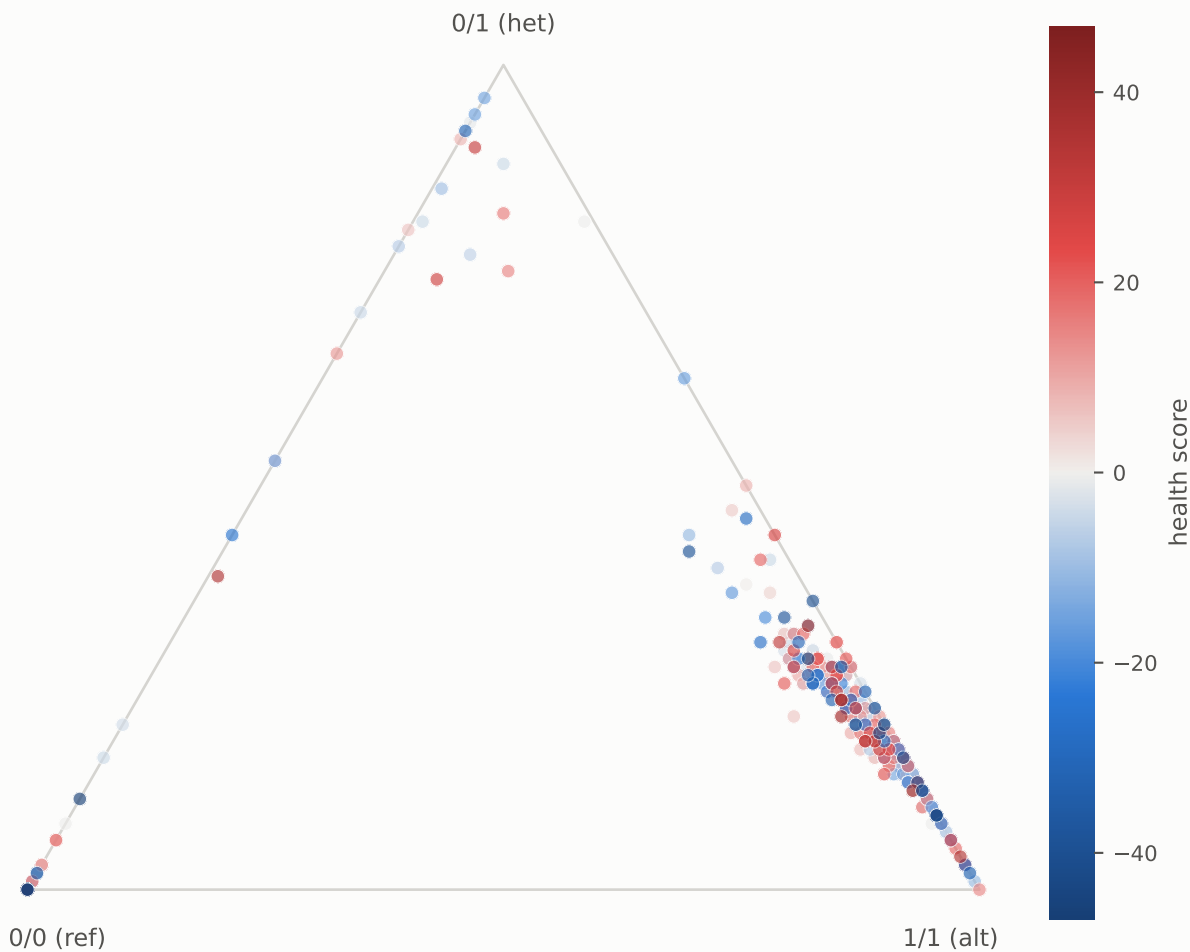
#75 by genotype uncertainty CHR_17:3,296,326 T>C
AF=0.53 DR2=0.81 $r=-0.023$ $\bar{H}=0.389$ F=1.3



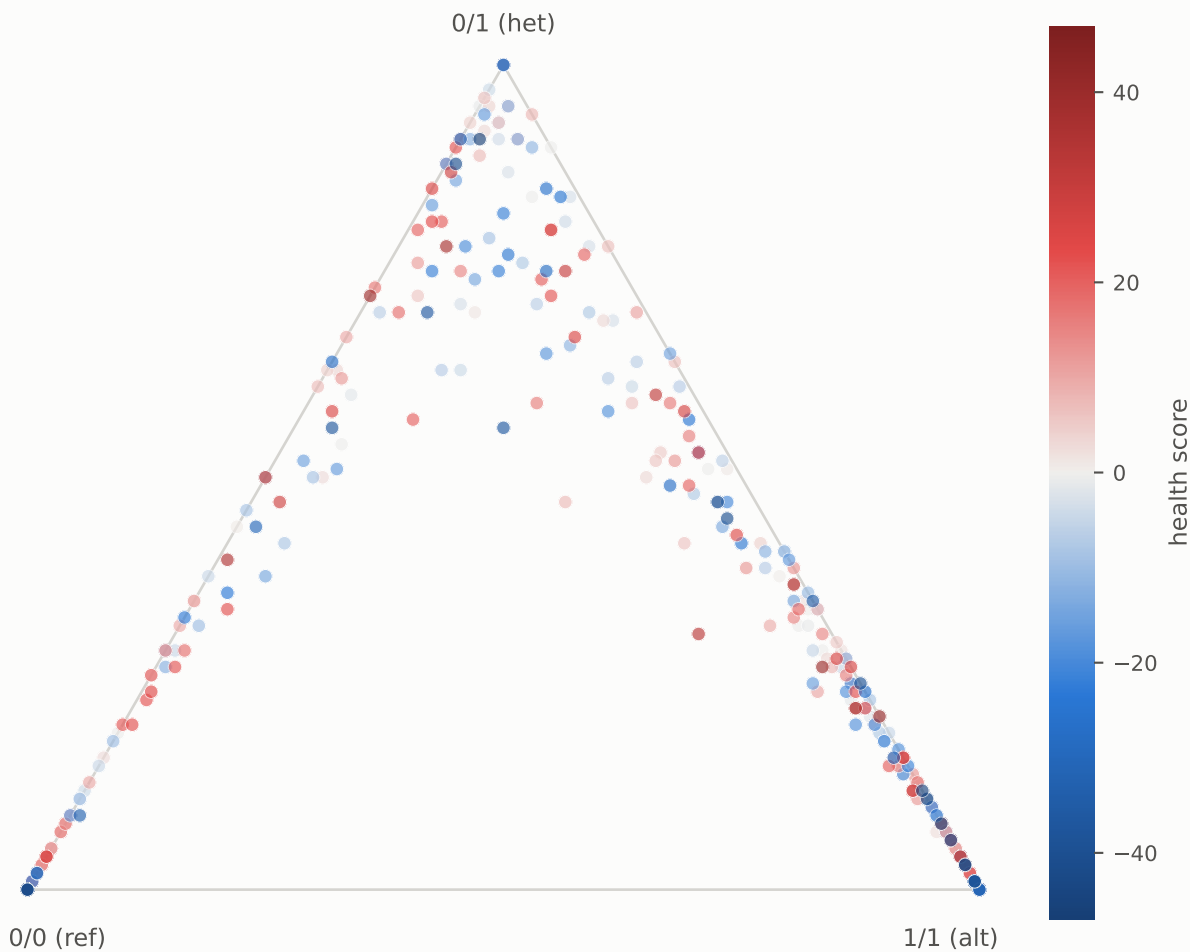
#76 by genotype uncertainty CHR_01:33,942,262 C>T
AF=0.63 DR2=0.81 $r=-0.015$ $\bar{H}=0.389$ F=1.4



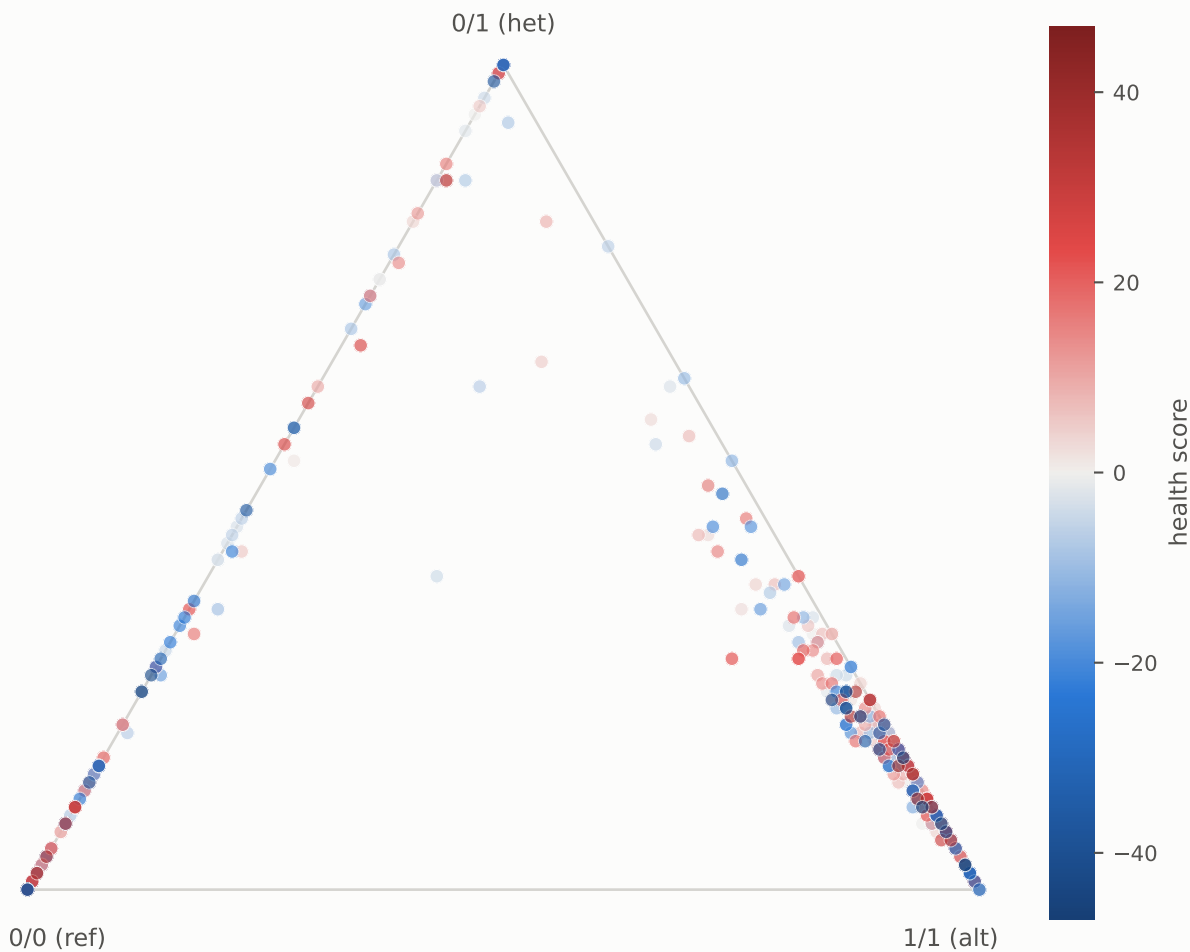
#77 by genotype uncertainty CHR_08:30,205,147 C>T
AF=0.56 DR2=0.81 $r=+0.010$ $\bar{H}=0.389$ F=0.0



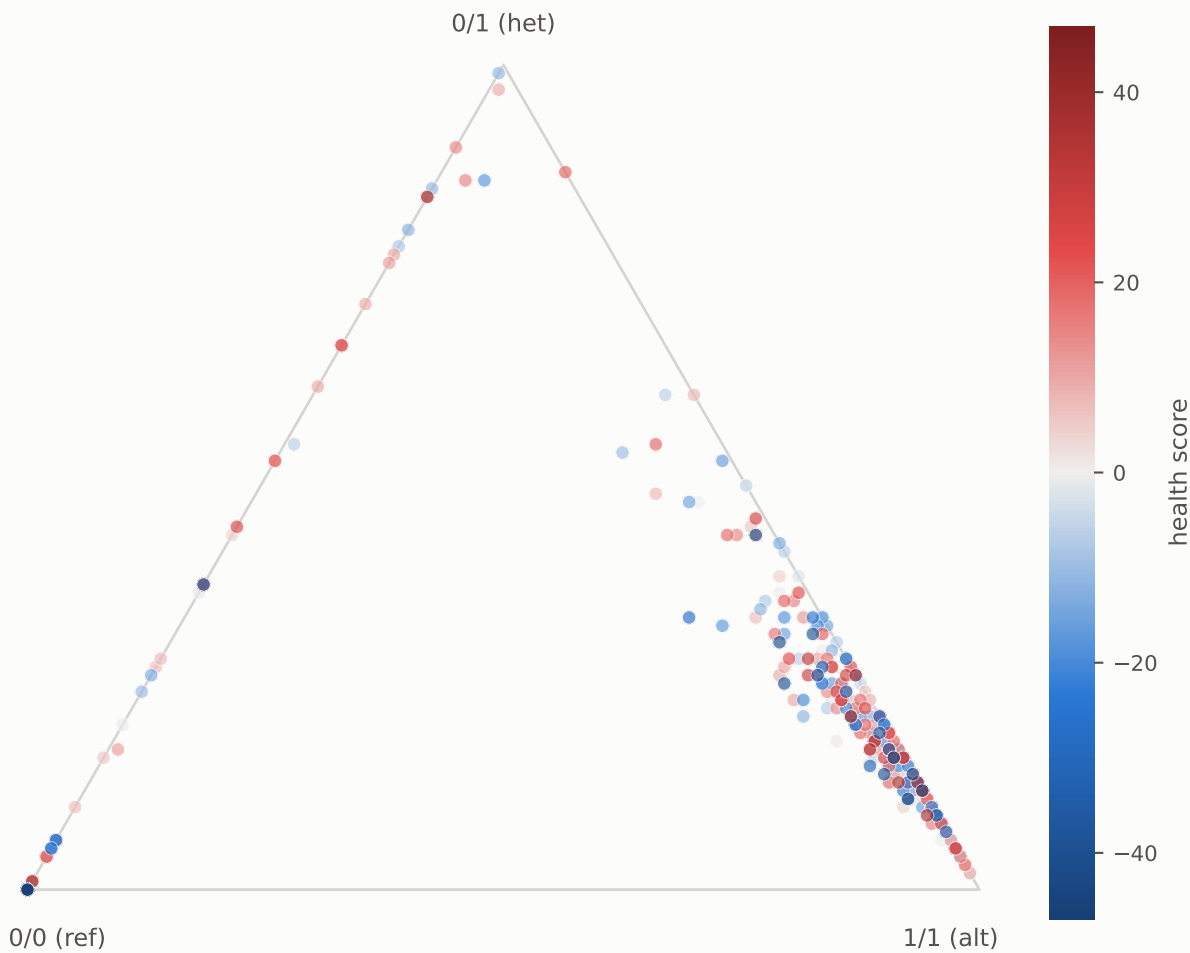
#78 by genotype uncertainty CHR_07:10,883,182 G>A
AF=0.46 DR2=0.81 r=-0.062 H=0.388 F=1.1



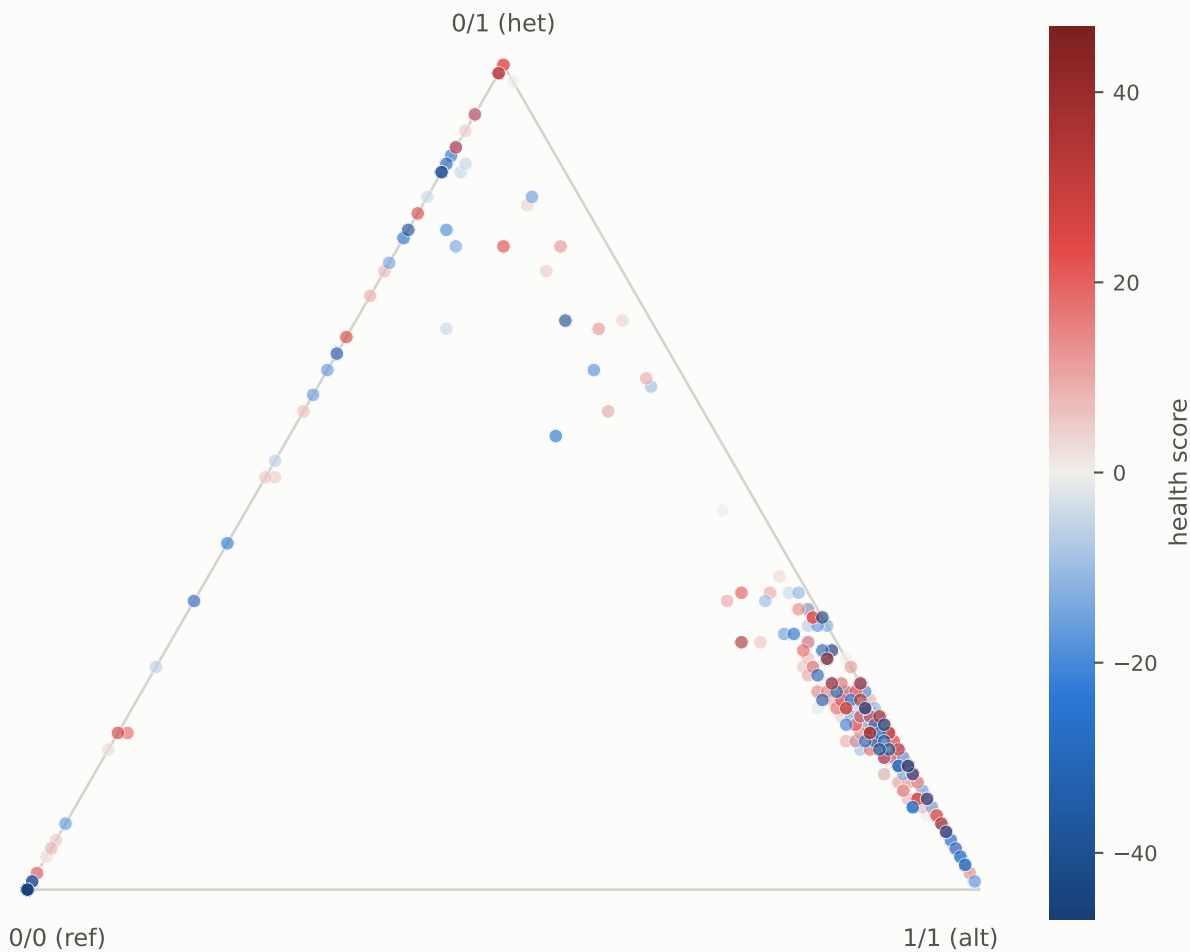
#79 by genotype uncertainty CHR_02:7,023,339 A>T
AF=0.59 DR2=0.81 $r=+0.041$ $\bar{H}=0.388$ F=0.7



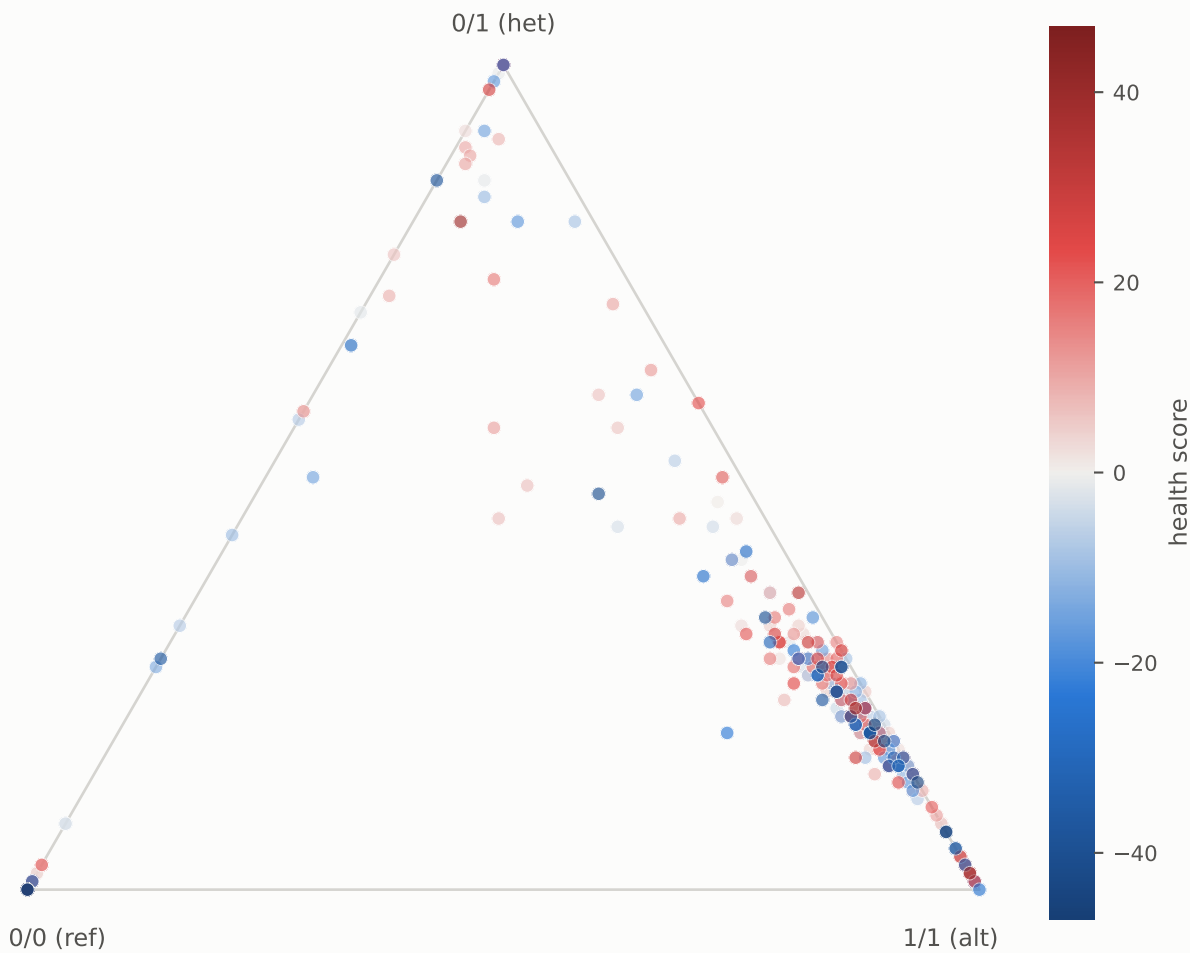
#80 by genotype uncertainty CHR_11:30,749,733 T>A
AF=0.6 DR2=0.81 r=+0.081 $\bar{H}$ =0.388 F=2.9



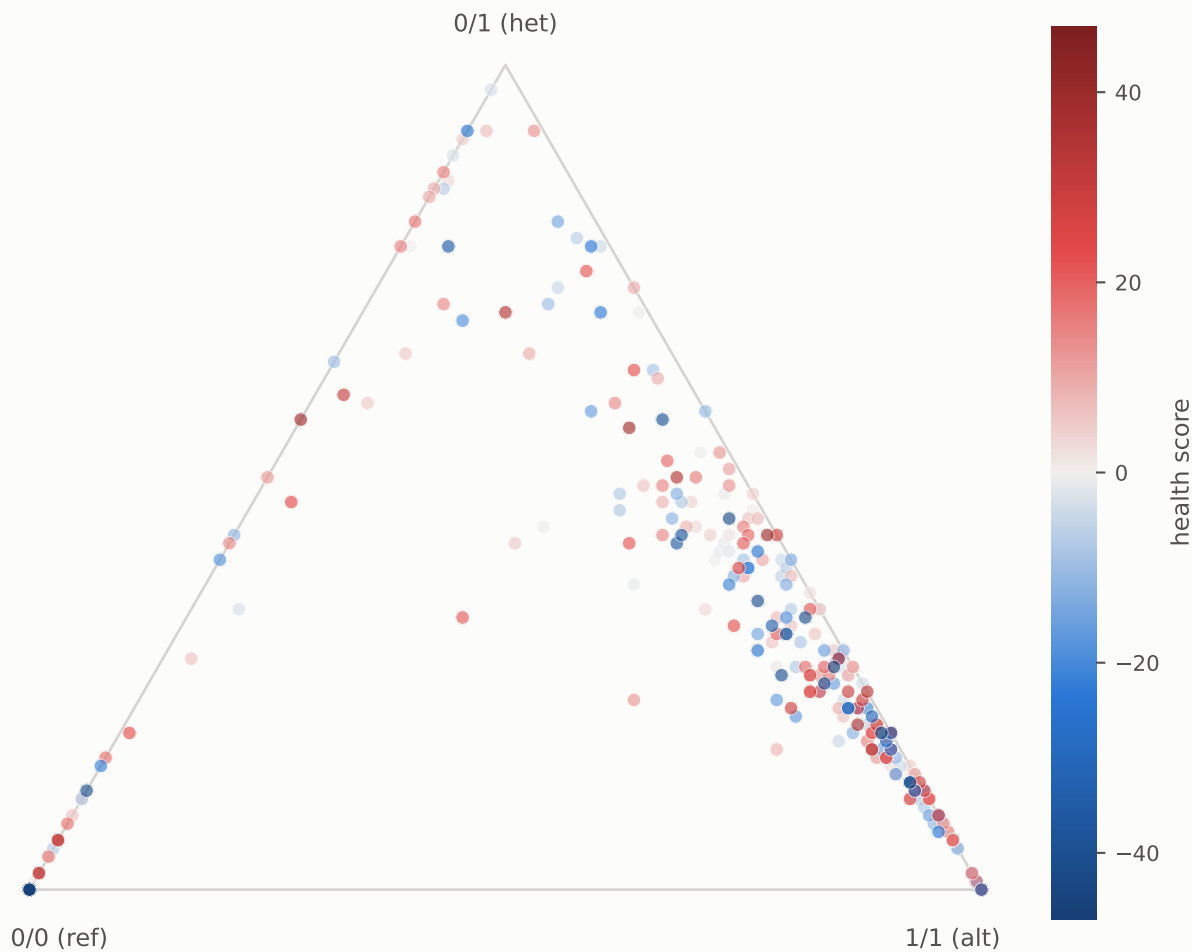
#81 by genotype uncertainty CHR_18:19,947,767 T>A
AF=0.59 DR2=0.81 r=+0.007 H=0.388 F=0.9



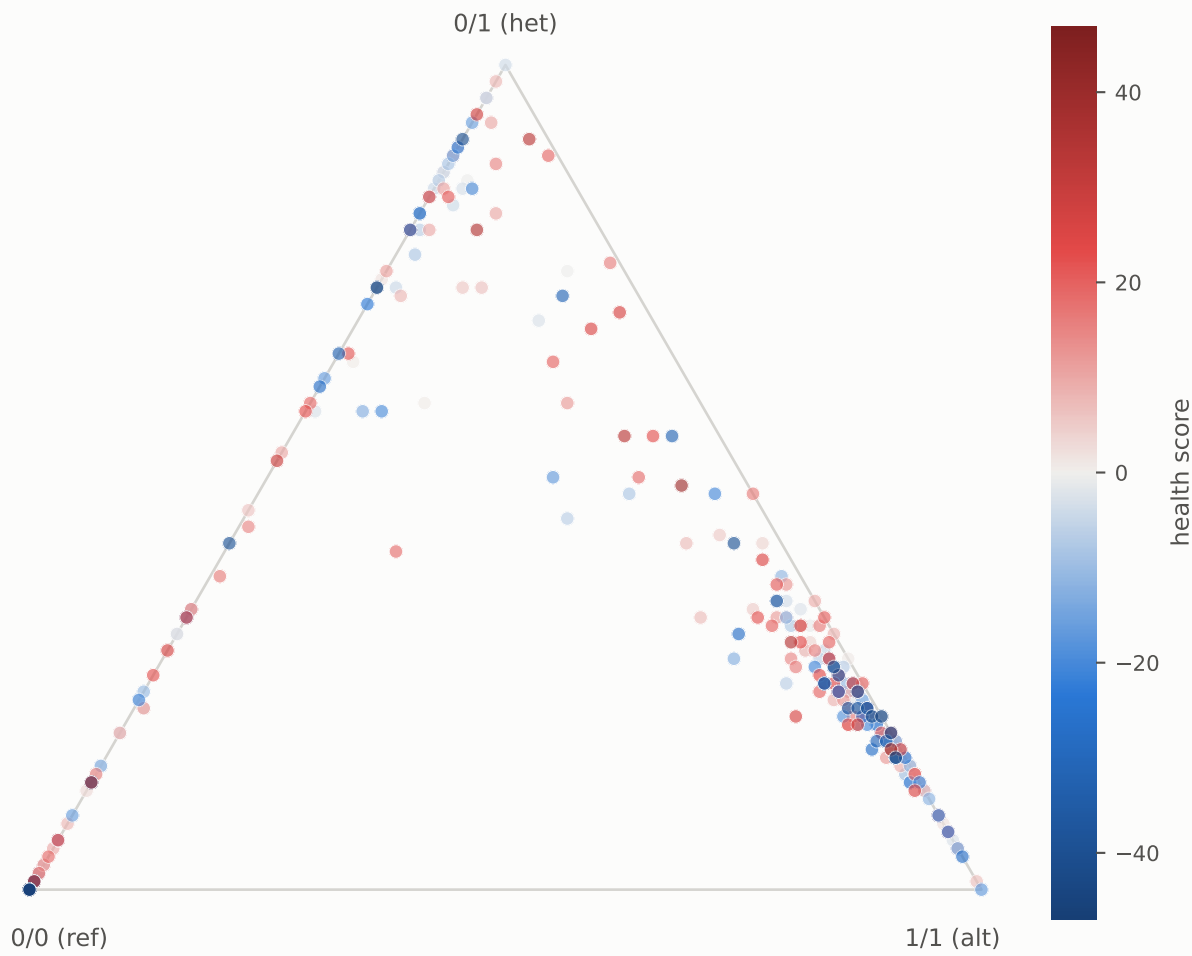
#82 by genotype uncertainty CHR_05:10,541,229 G>A
AF=0.54 DR2=0.81 $r=-0.080$ $\bar{H}=0.388$ $F=1.4$



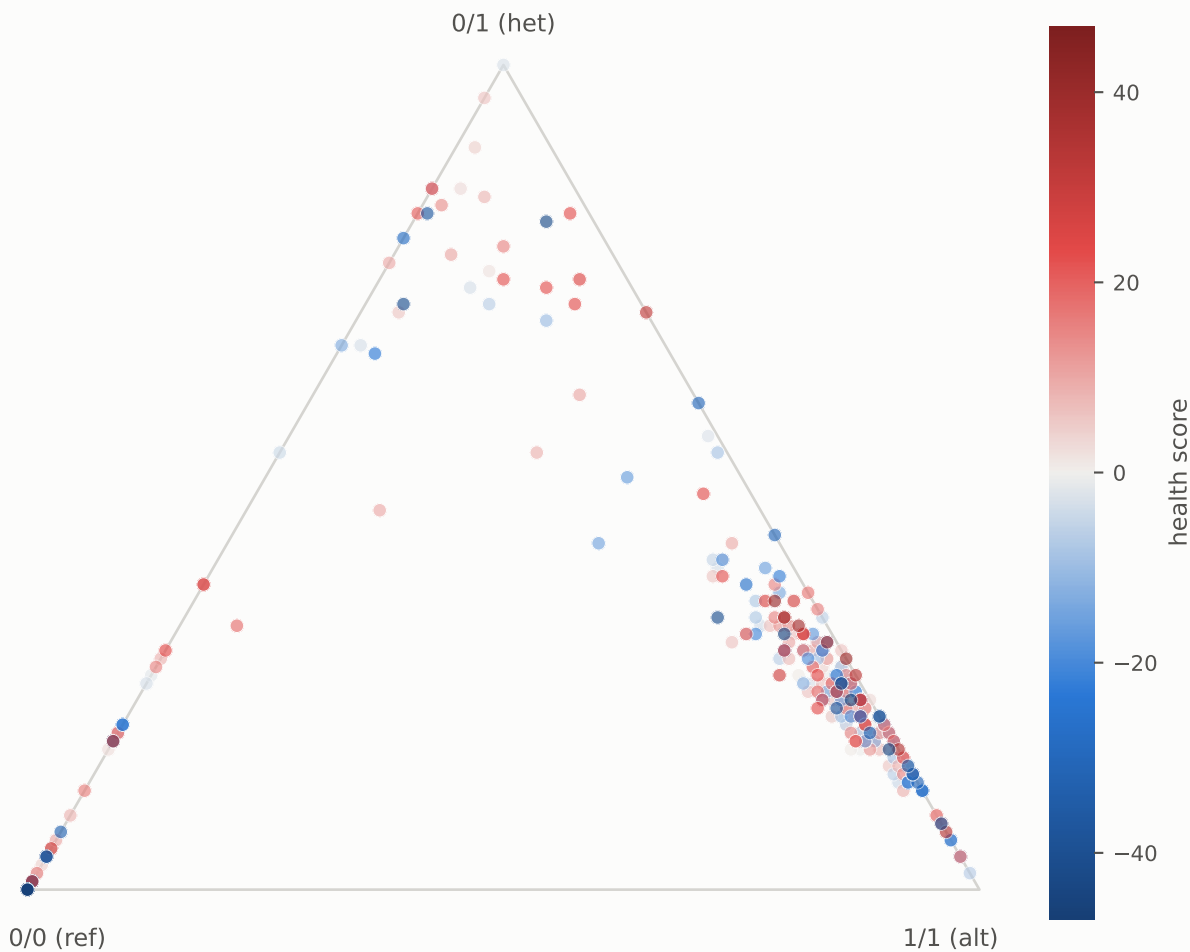
#83 by genotype uncertainty CHR_03:36,292,404 A>G
AF=0.49 DR2=0.81 $r=+0.058$ $H=0.388$ $F=1.8$



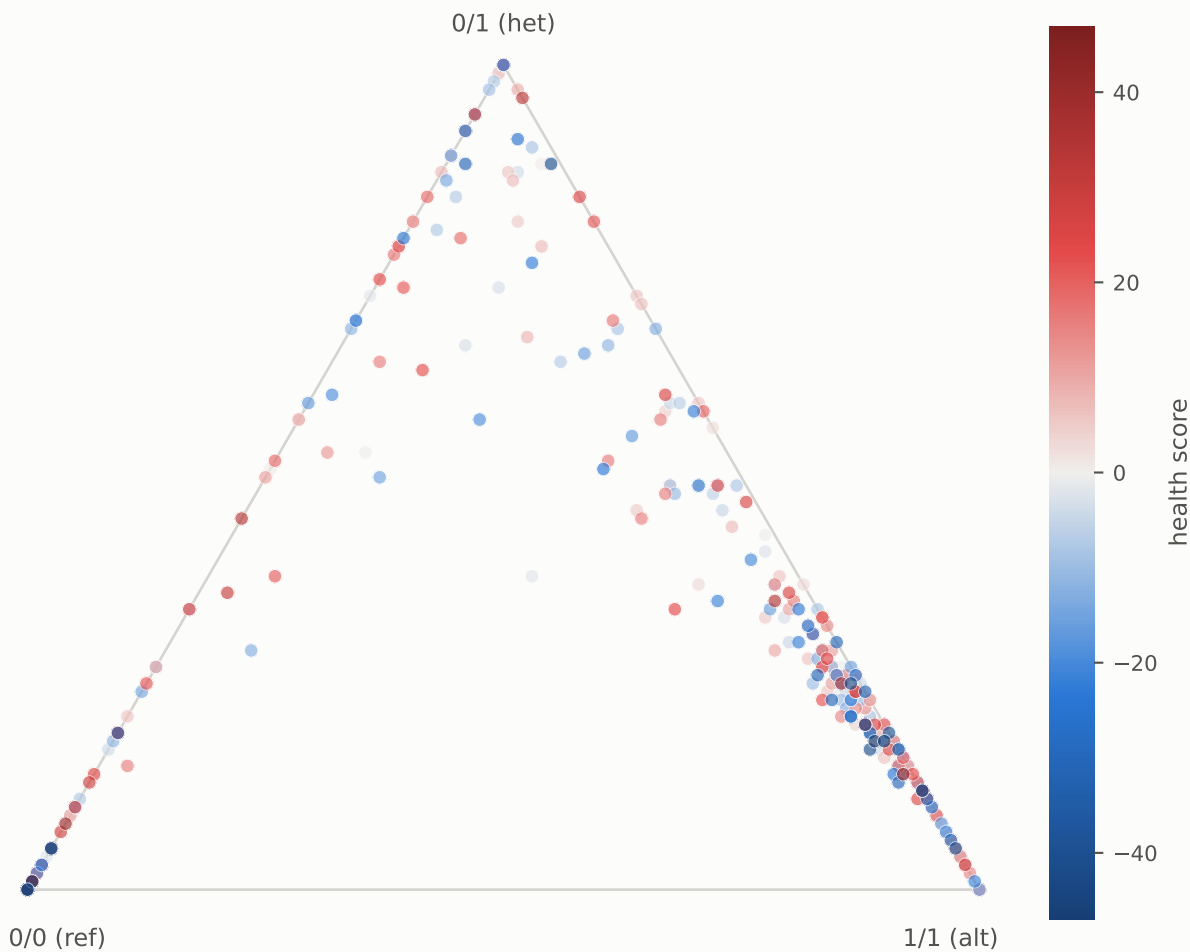
#84 by genotype uncertainty CHR_12:10,270,073 G>A
AF=0.45 DR2=0.81 $r=-0.020$ $\bar{H}=0.388$ F=0.2



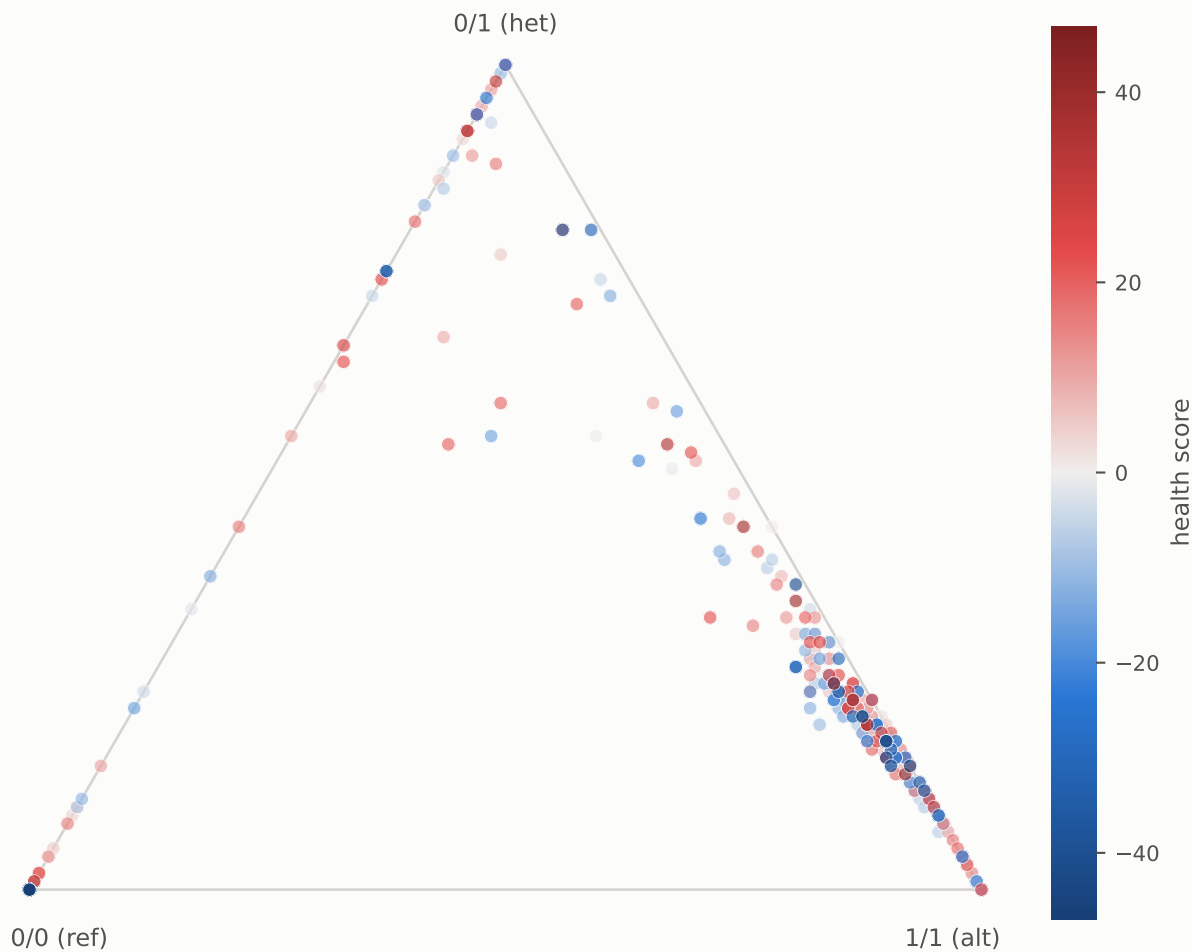
#85 by genotype uncertainty CHR_17:16,778,254 T>C
AF=0.46 DR2=0.81 $r=+0.046$ $\bar{H}=0.388$ F=0.5



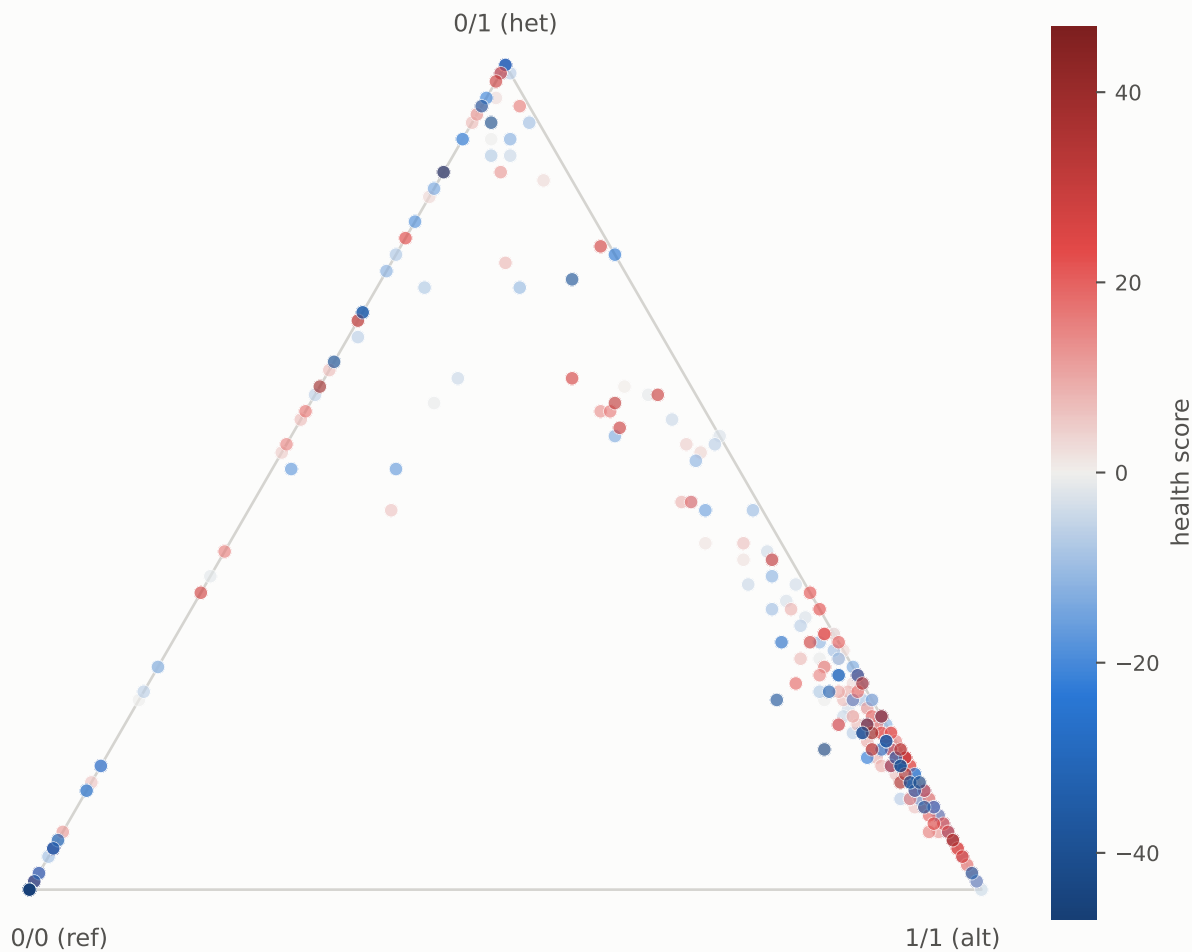
#86 by genotype uncertainty CHR_10:26,911,806 A>G
AF=0.5 DR2=0.81 $r=-0.039$ $\bar{H}=0.388$ F=0.5



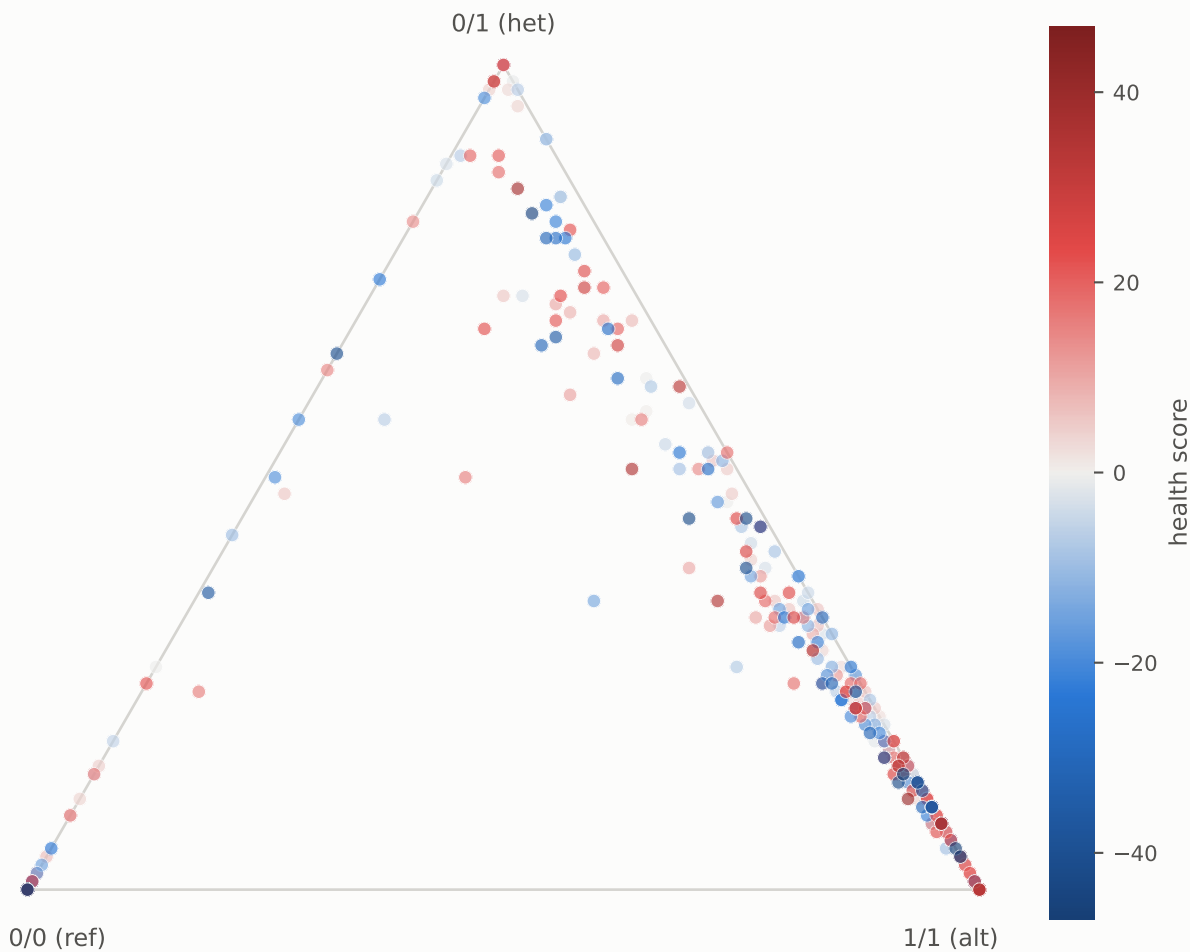
#87 by genotype uncertainty CHR_03:8,506,914 A>T
AF=0.56 DR2=0.81 $r=-0.010$ $\bar{H}=0.388$ F=0.7



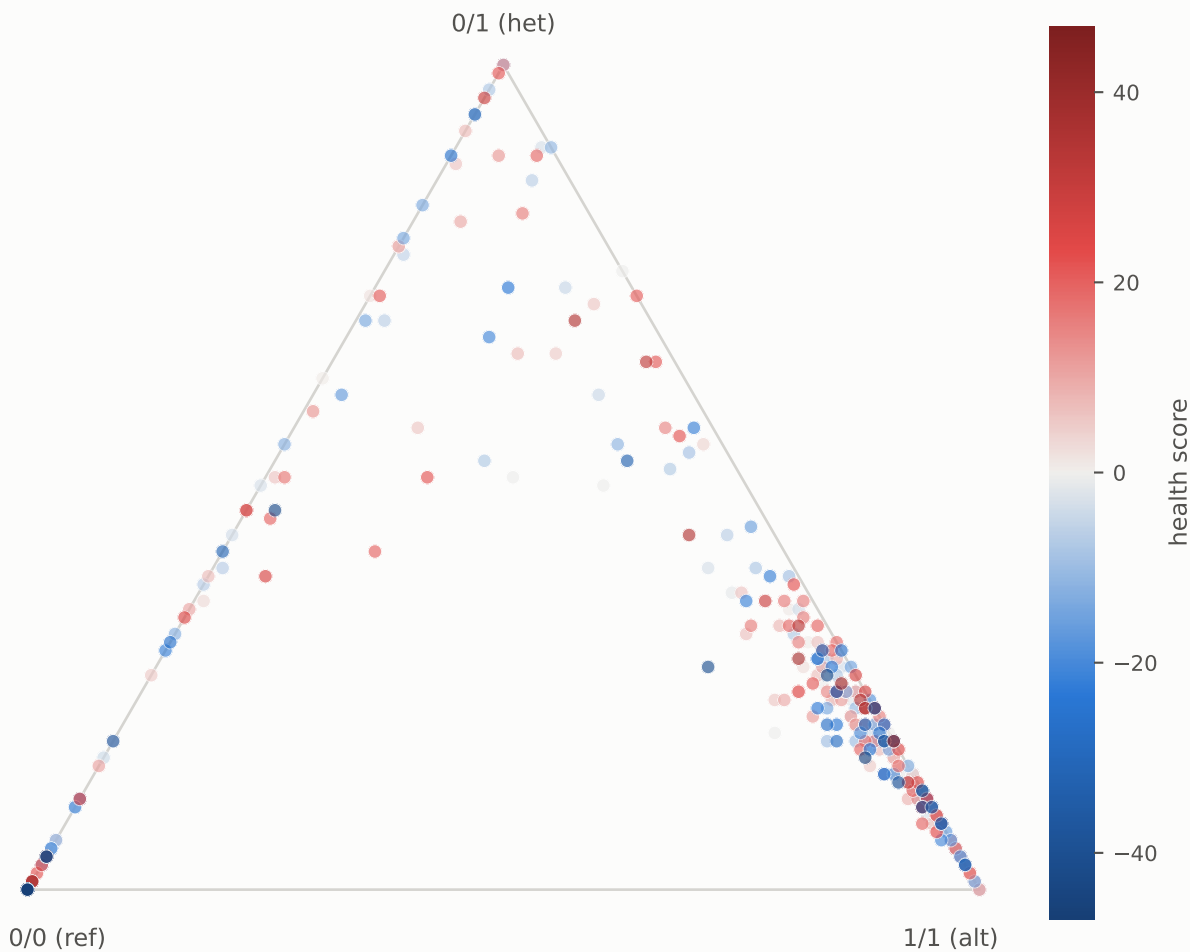
#88 by genotype uncertainty CHR_21:9,273,358 T>A
AF=0.6 DR2=0.81 r=+0.169 H=0.388 F=5.7



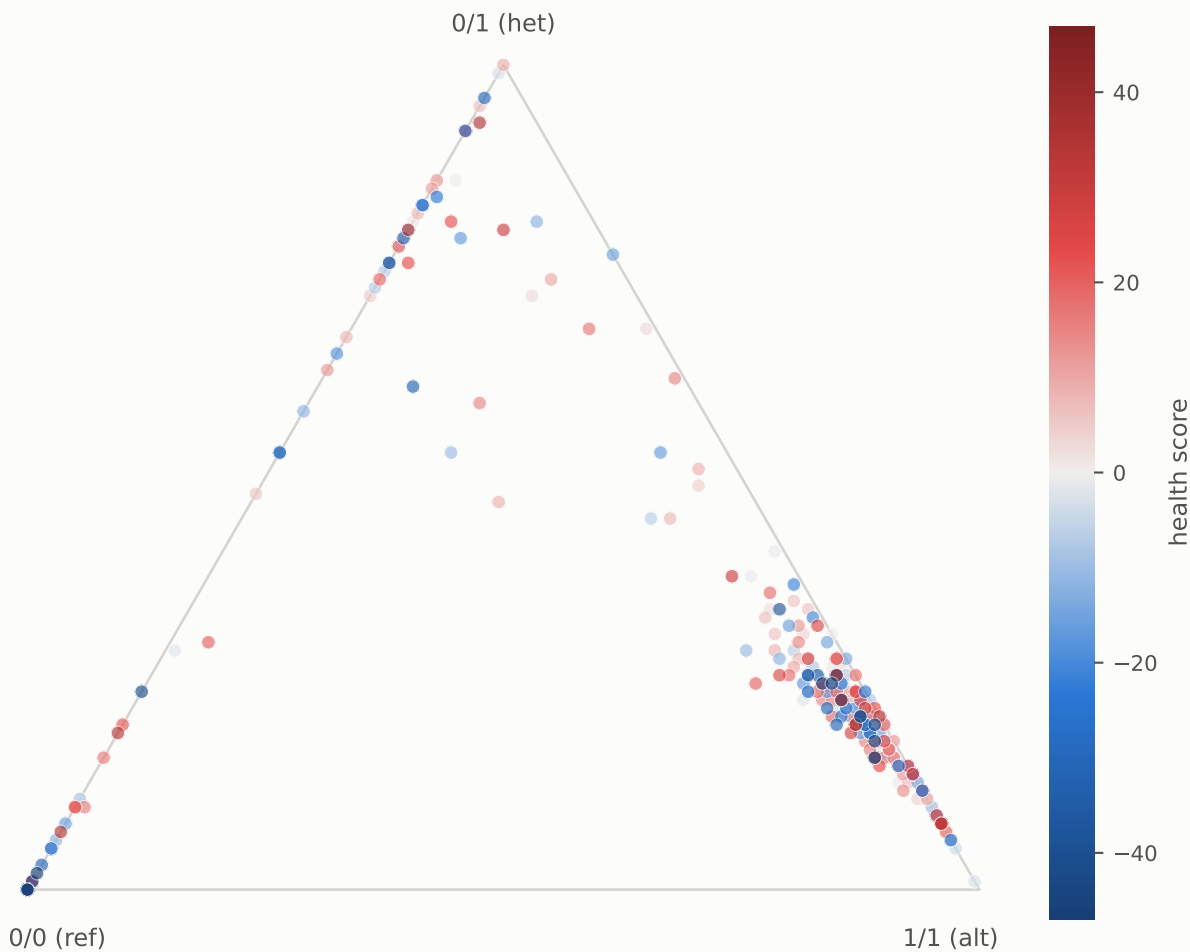
#89 by genotype uncertainty CHR_08:28,061,043 A>G
AF=0.59 DR2=0.81 $r=+0.048$ H=0.388 F=0.3



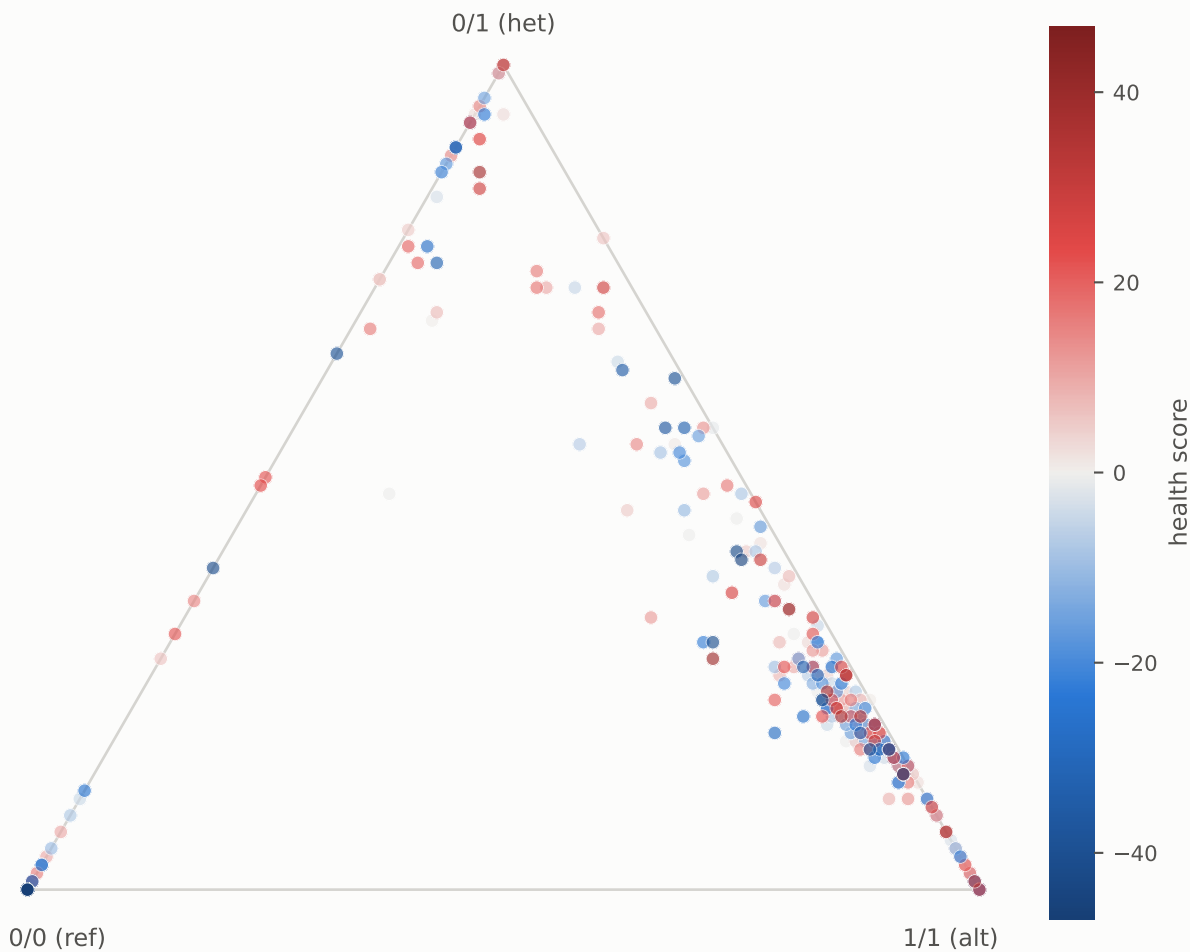
#90 by genotype uncertainty CHR_20:11,736,747 A>G
AF=0.55 DR2=0.82 $r=+0.037$ H=0.387 F=0.7



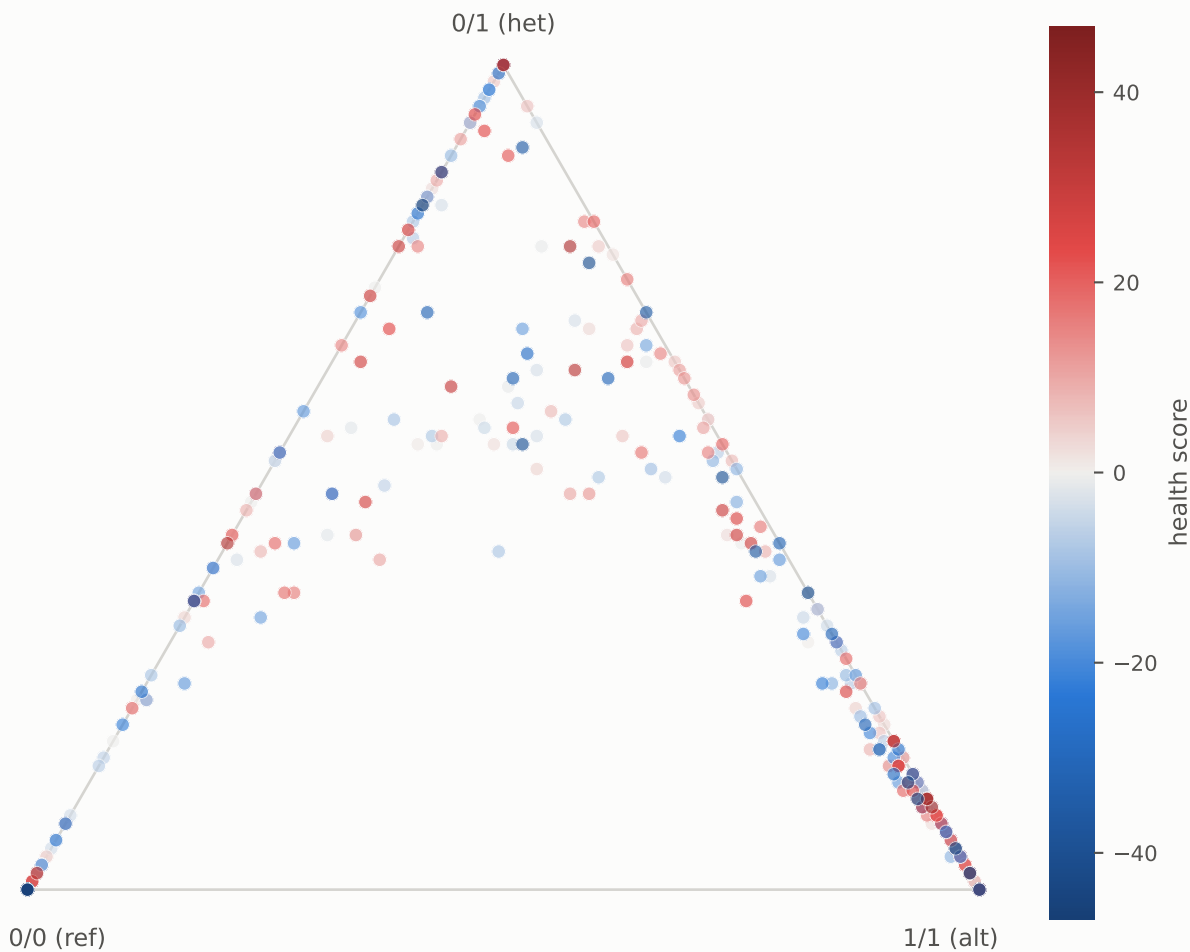
#91 by genotype uncertainty CHR_07:12,130,925 C>T
AF=0.49 DR2=0.81 $r=+0.074$ $\bar{H}=0.387$ F=0.8



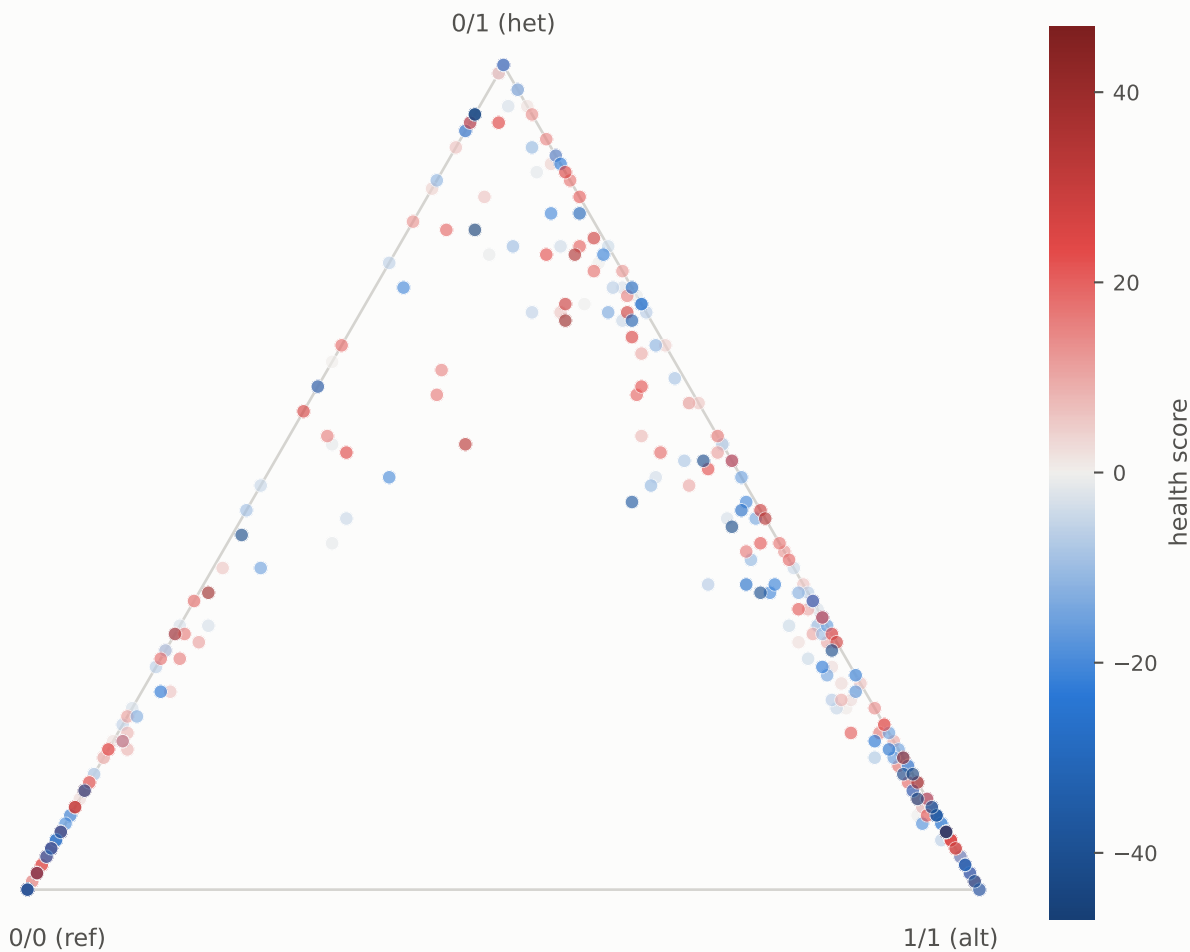
#92 by genotype uncertainty CHR_16:27,978,366 C>T
AF=0.49 DR2=0.81 r=+0.001 H=0.387 F=0.0



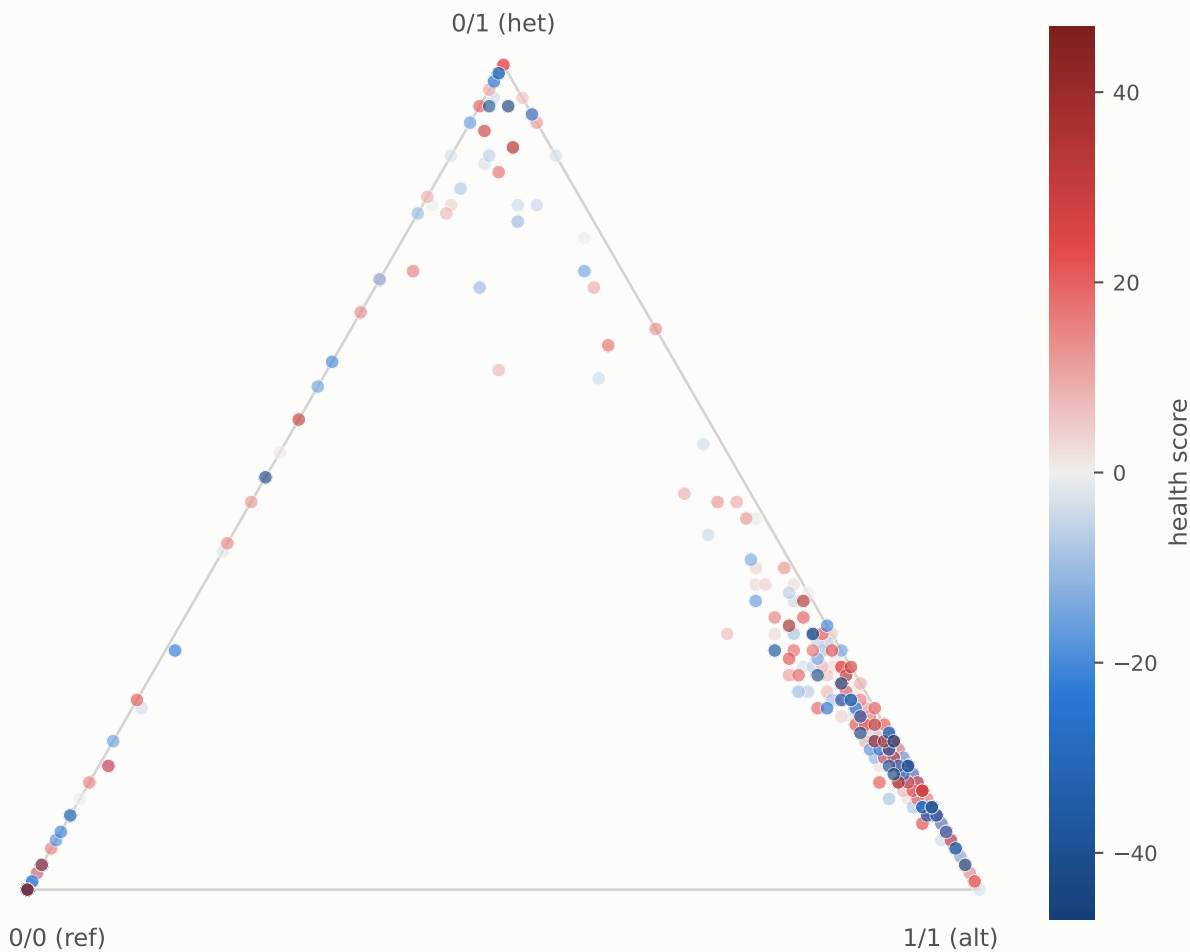
#93 by genotype uncertainty CHR_04:14,854,259 A>G
AF=0.54 DR2=0.81 $r=+0.053$ H=0.387 F=0.4



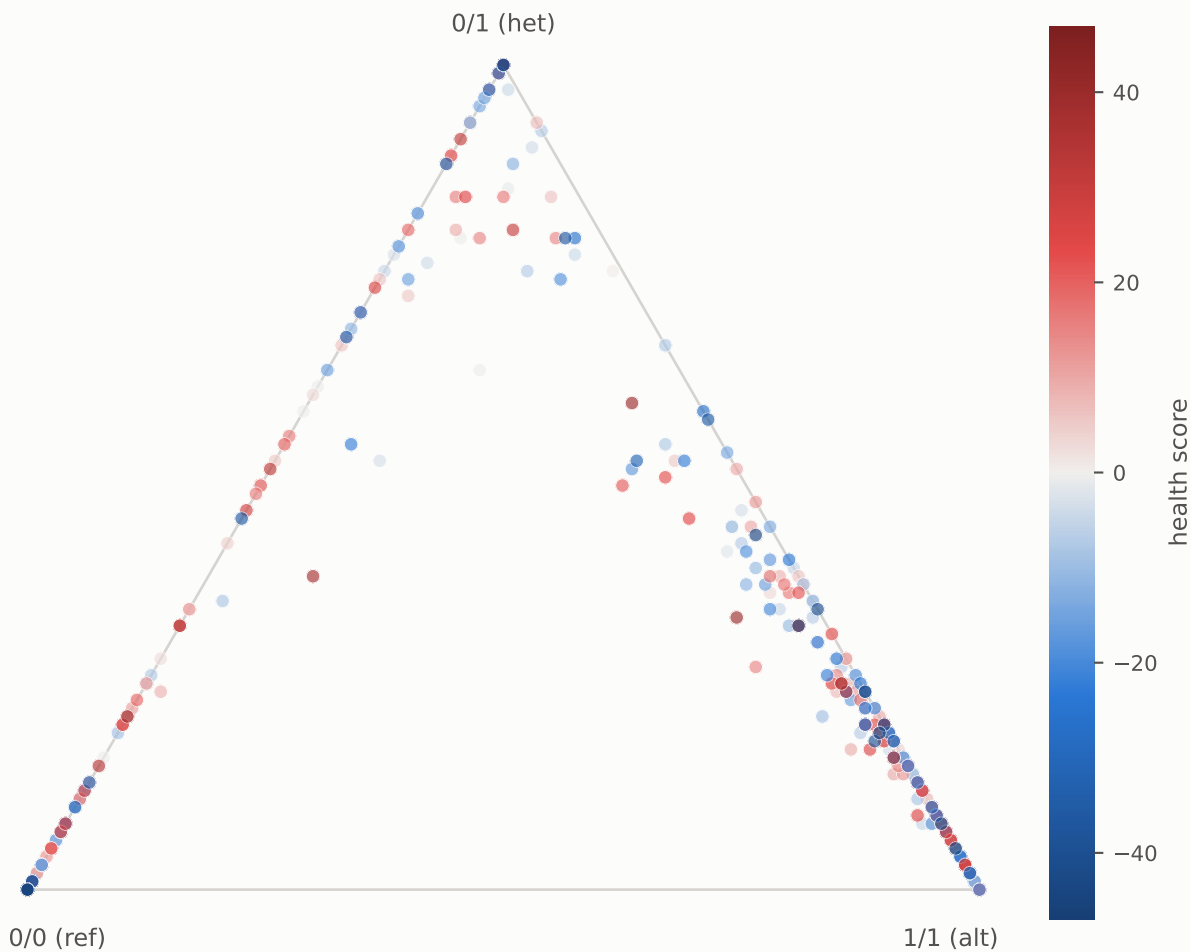
#94 by genotype uncertainty CHR_09:30,445,997 A>G
AF=0.51 DR2=0.81 $r=-0.072$ $\bar{H}=0.387$ F=1.5



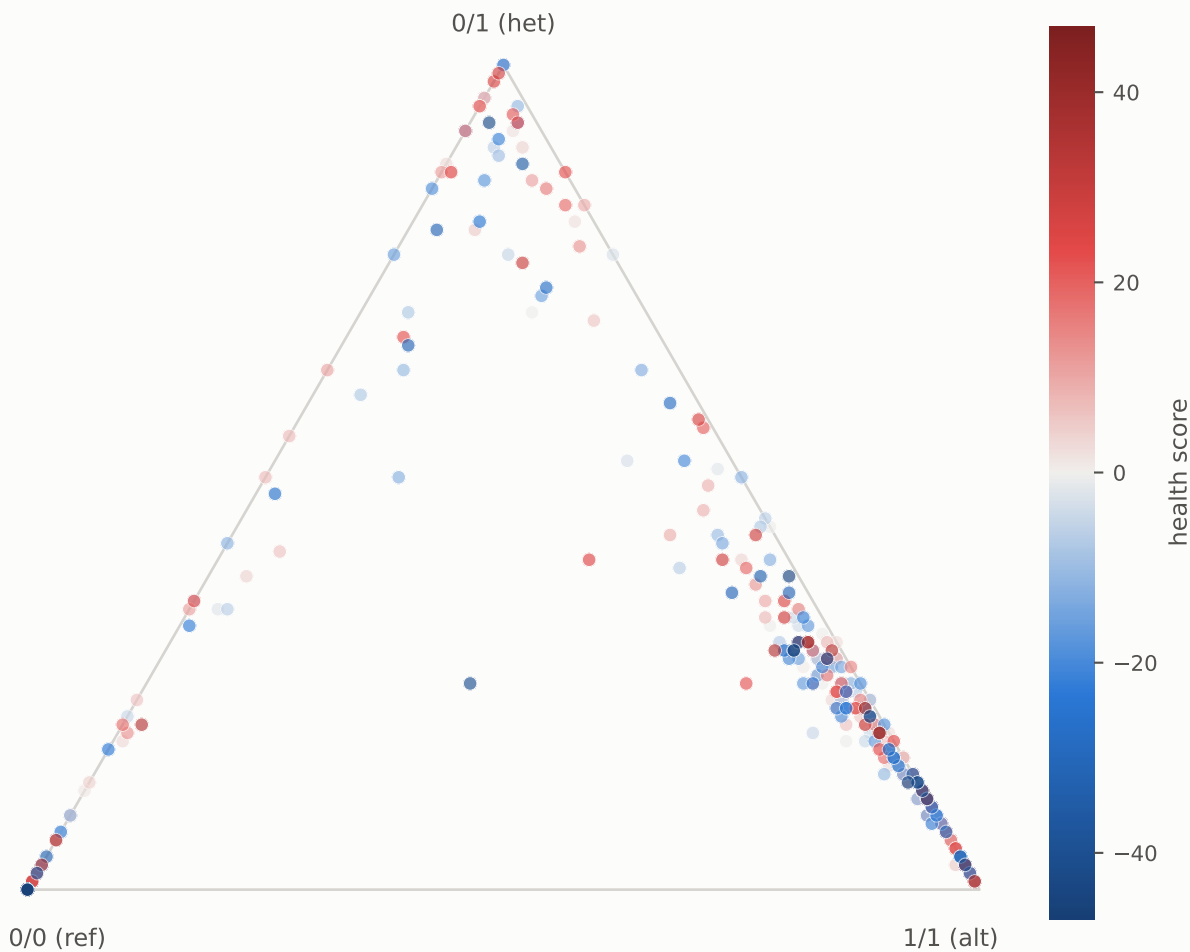
#95 by genotype uncertainty CHR_09:33,141,307 T>C
AF=0.61 DR2=0.81 $r=+0.009$ $\bar{H}=0.387$ F=0.1



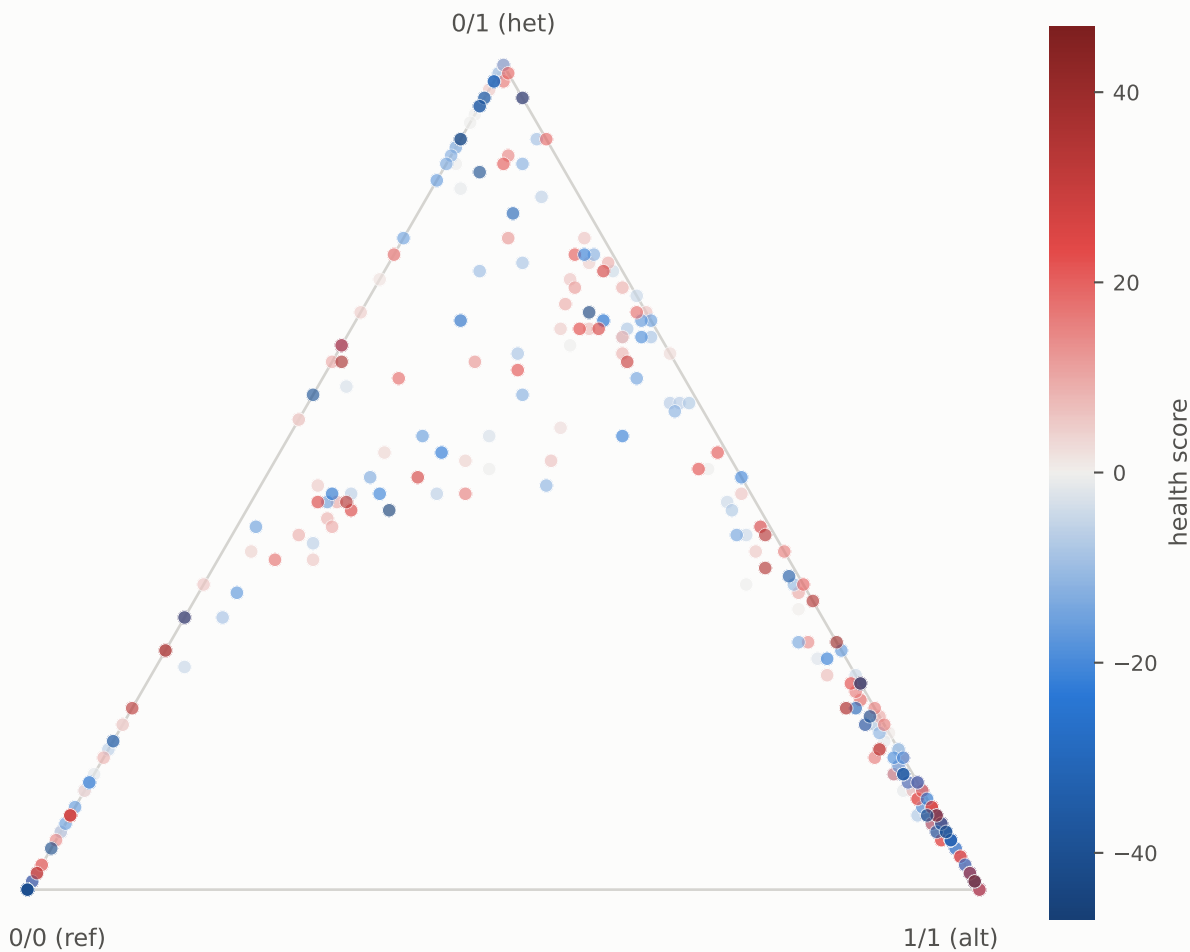
#96 by genotype uncertainty CHR_17:18,499,692 C>G
AF=0.57 DR2=0.81 $r=-0.024$ $\bar{H}=0.387$ F=0.4



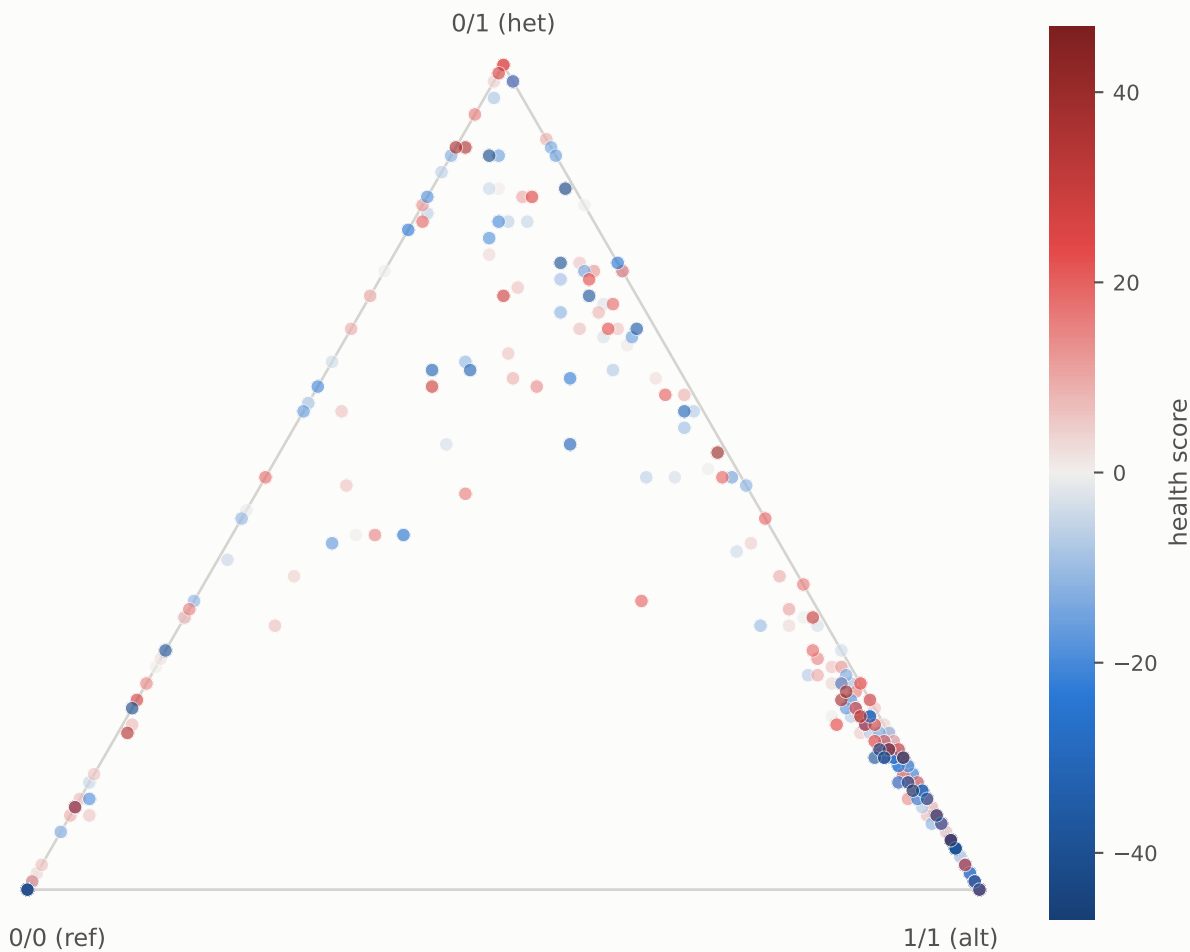
#97 by genotype uncertainty CHR_04:34,910,279 C>A
AF=0.52 DR2=0.81 $r=-0.071$ $\bar{H}=0.387$ F=1.0



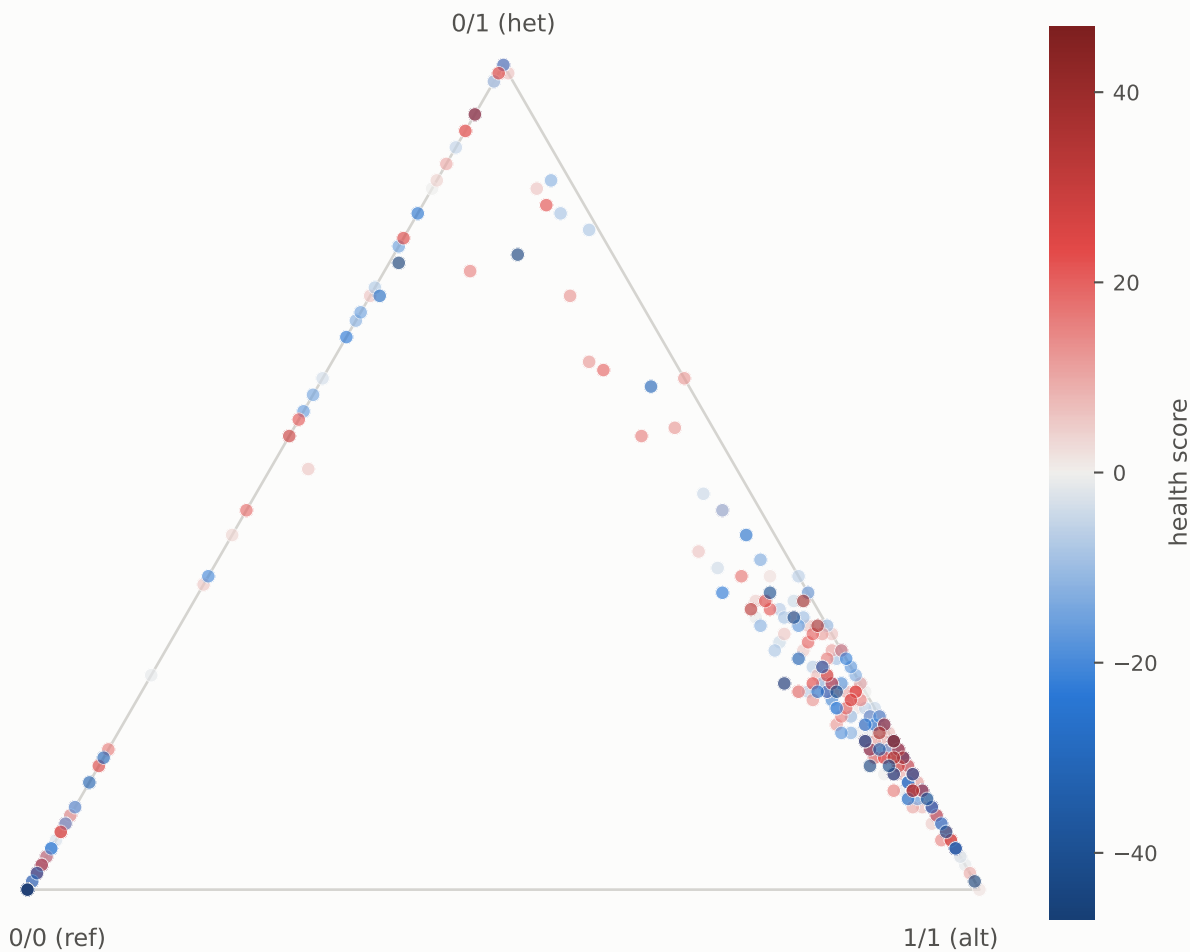
#98 by genotype uncertainty CHR_18:2,566,863 C>T
AF=0.54 DR2=0.81 $r=-0.050$ $\bar{H}=0.387$ F=2.3



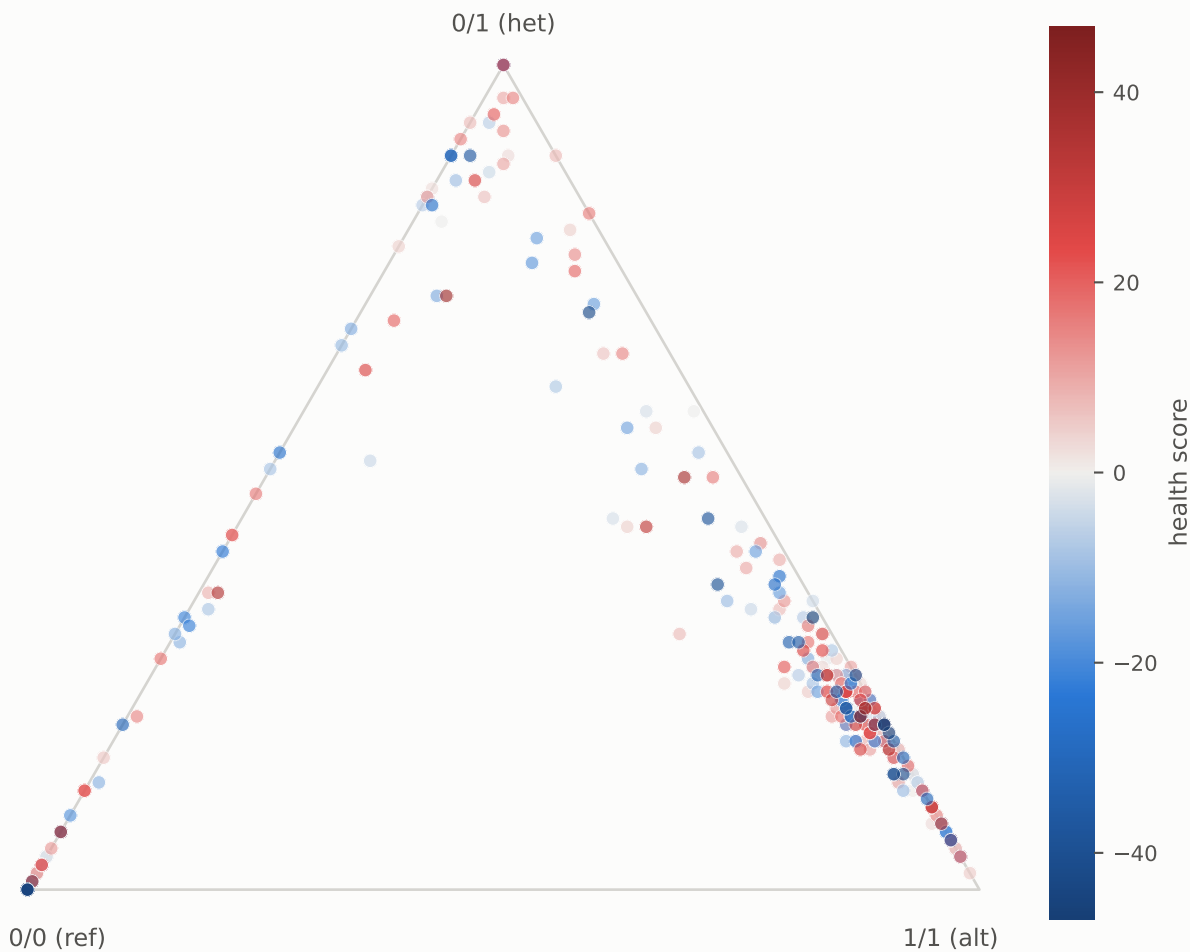
#99 by genotype uncertainty CHR_19:19,079,659 G>T
AF=0.61 DR2=0.81 $r=-0.046$ $\bar{H}=0.387$ F=0.7



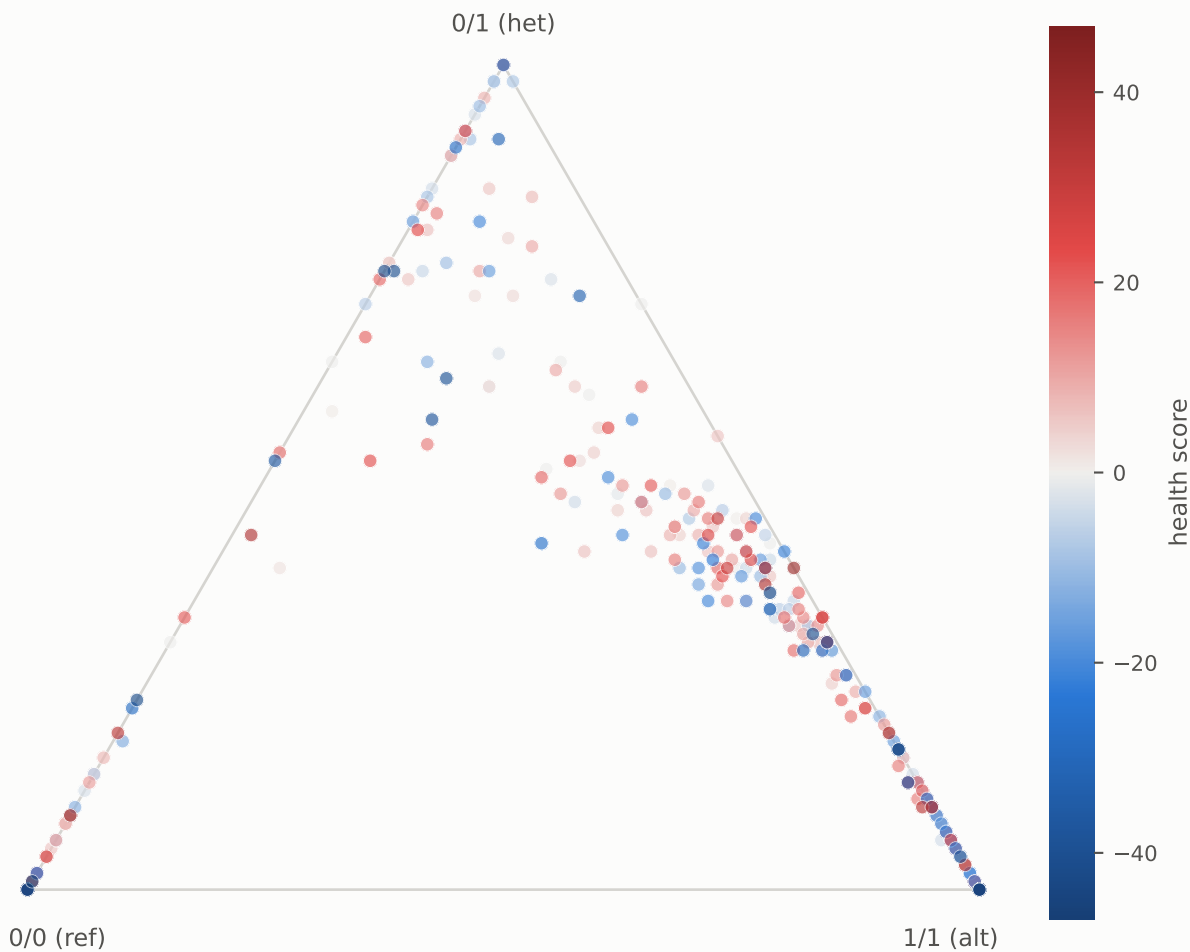
#100 by genotype uncertainty CHR_13:24,042,353 T>C
AF=0.57 DR2=0.81 $r=-0.037$ $\bar{H}=0.387$ F=0.4



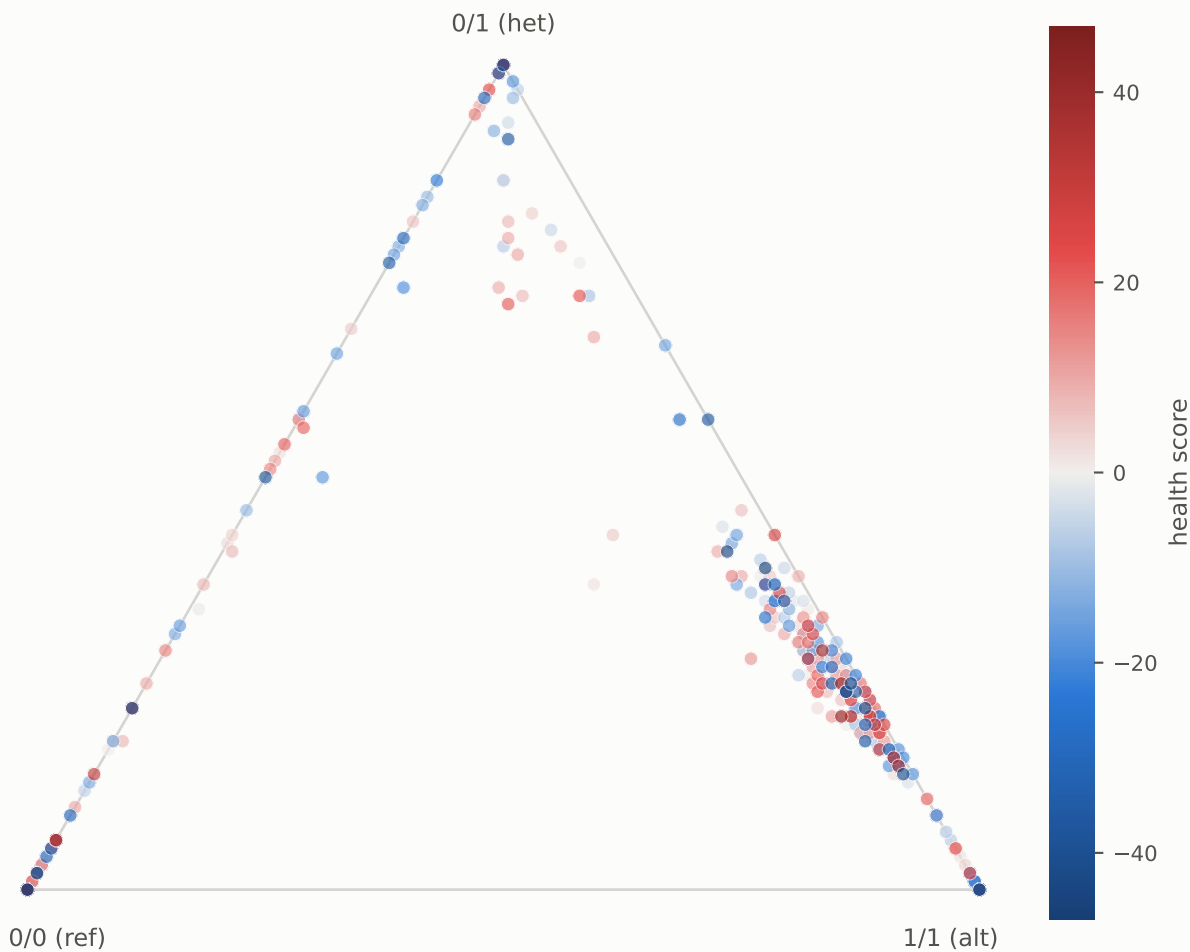
#101 by genotype uncertainty CHR_15:19,399,221 G>A
AF=0.5 DR2=0.81 r=+0.011 $\bar{H}$ =0.386 F=0.0



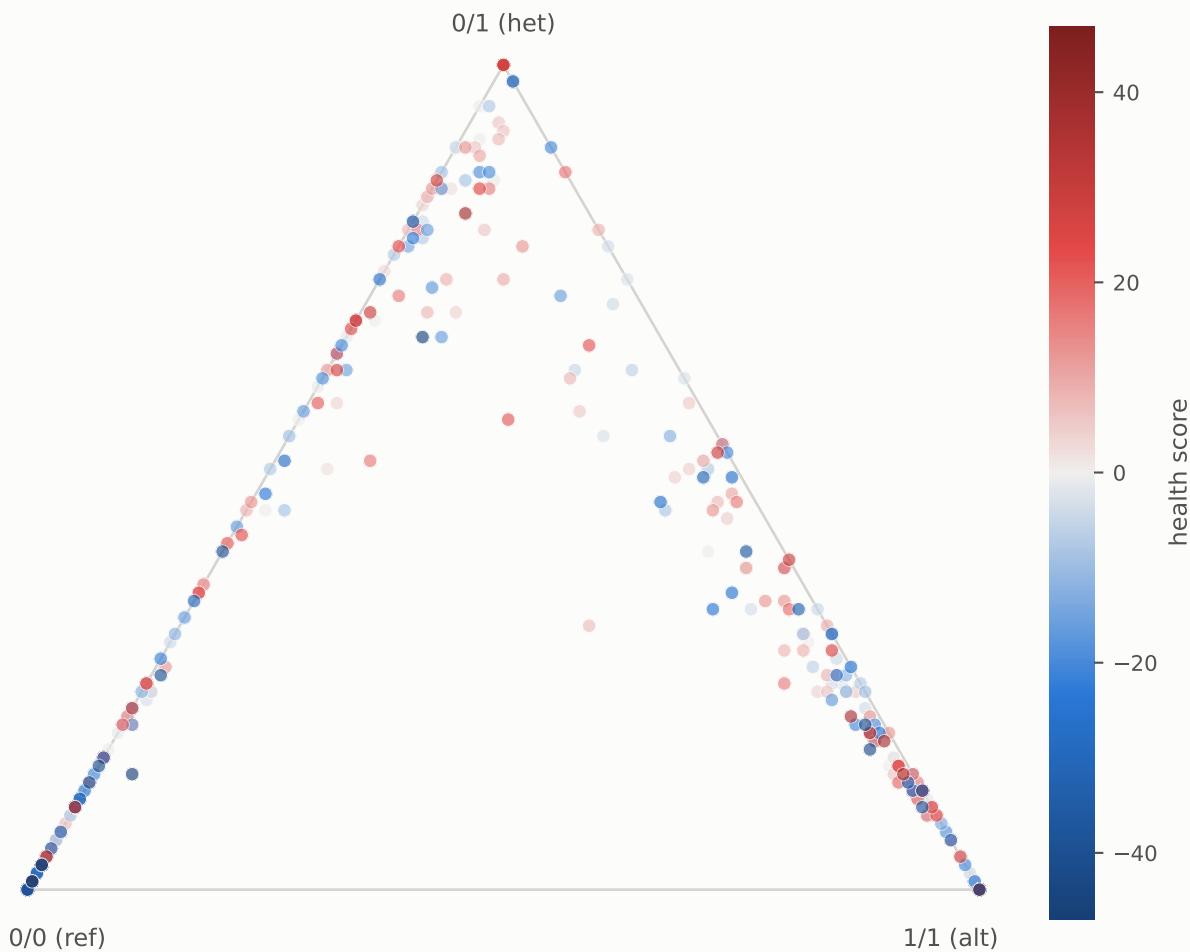
#102 by genotype uncertainty CHR_19:6,678,612 A>C
AF=0.49 DR2=0.82 r=-0.006 H=0.386 F=0.2



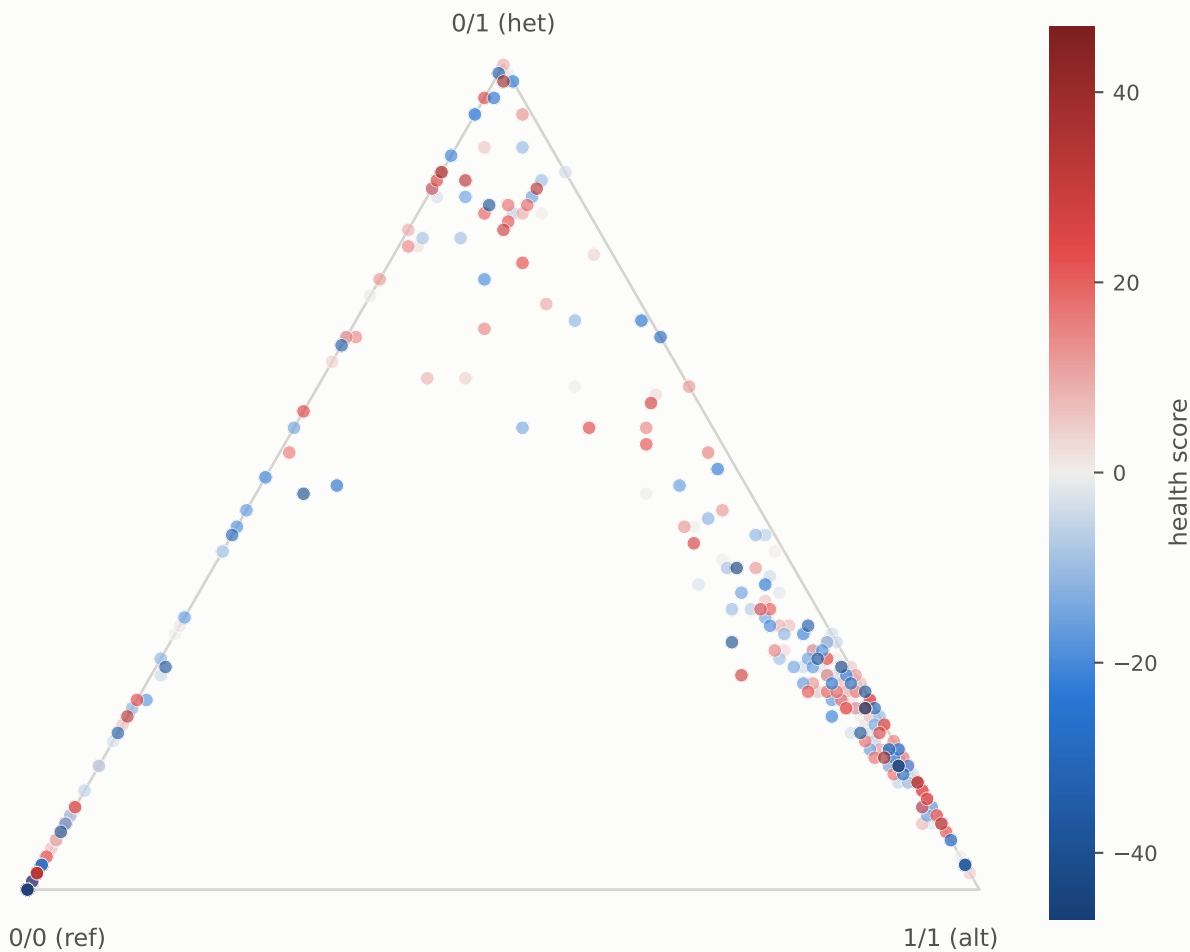
#103 by genotype uncertainty CHR_19:2,011,290 T>C
AF=0.57 DR2=0.81 $r=-0.070$ $H=0.386$ $F=0.9$



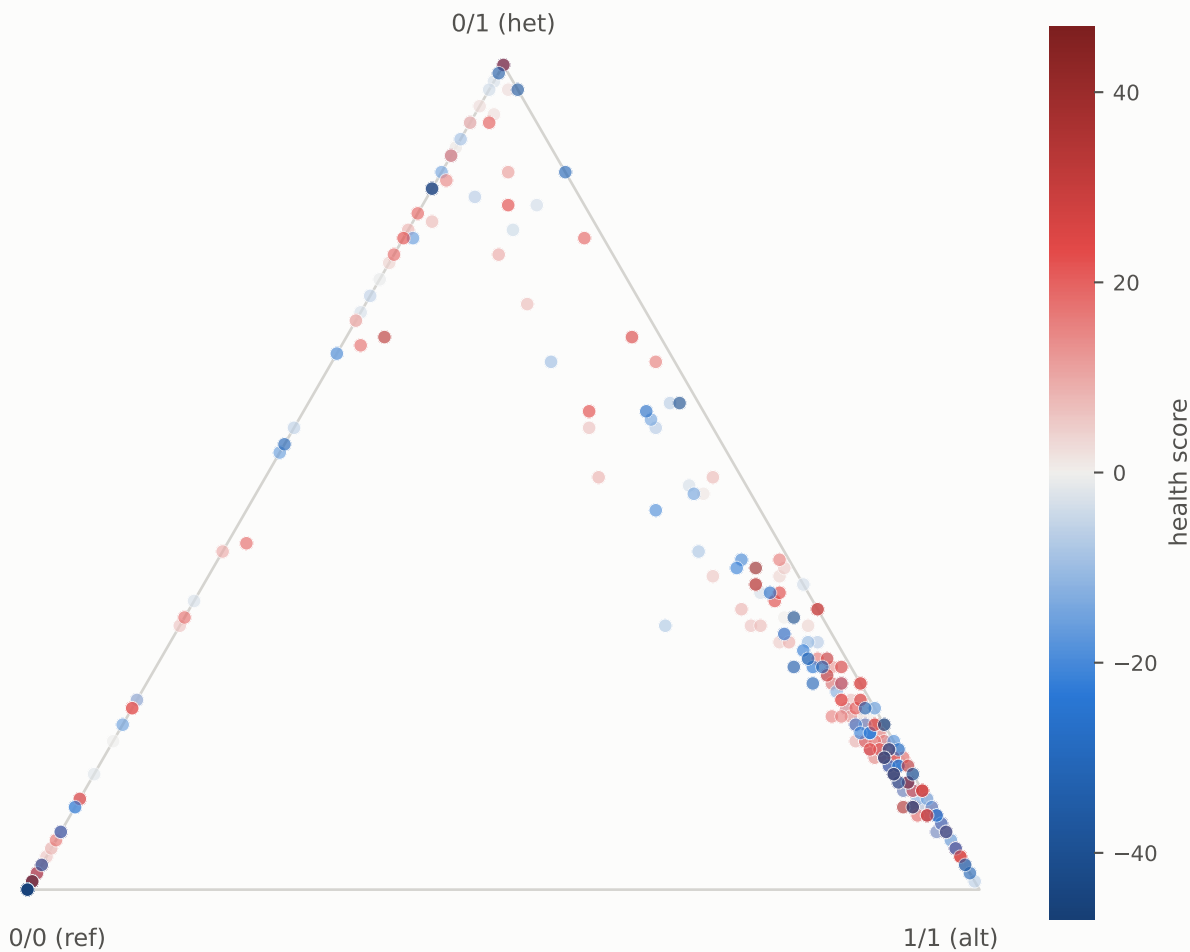
#104 by genotype uncertainty CHR_19:19,897,021 G>A
AF=0.41 DR2=0.81 $r=+0.056$ $\bar{H}=0.386$ F=1.1



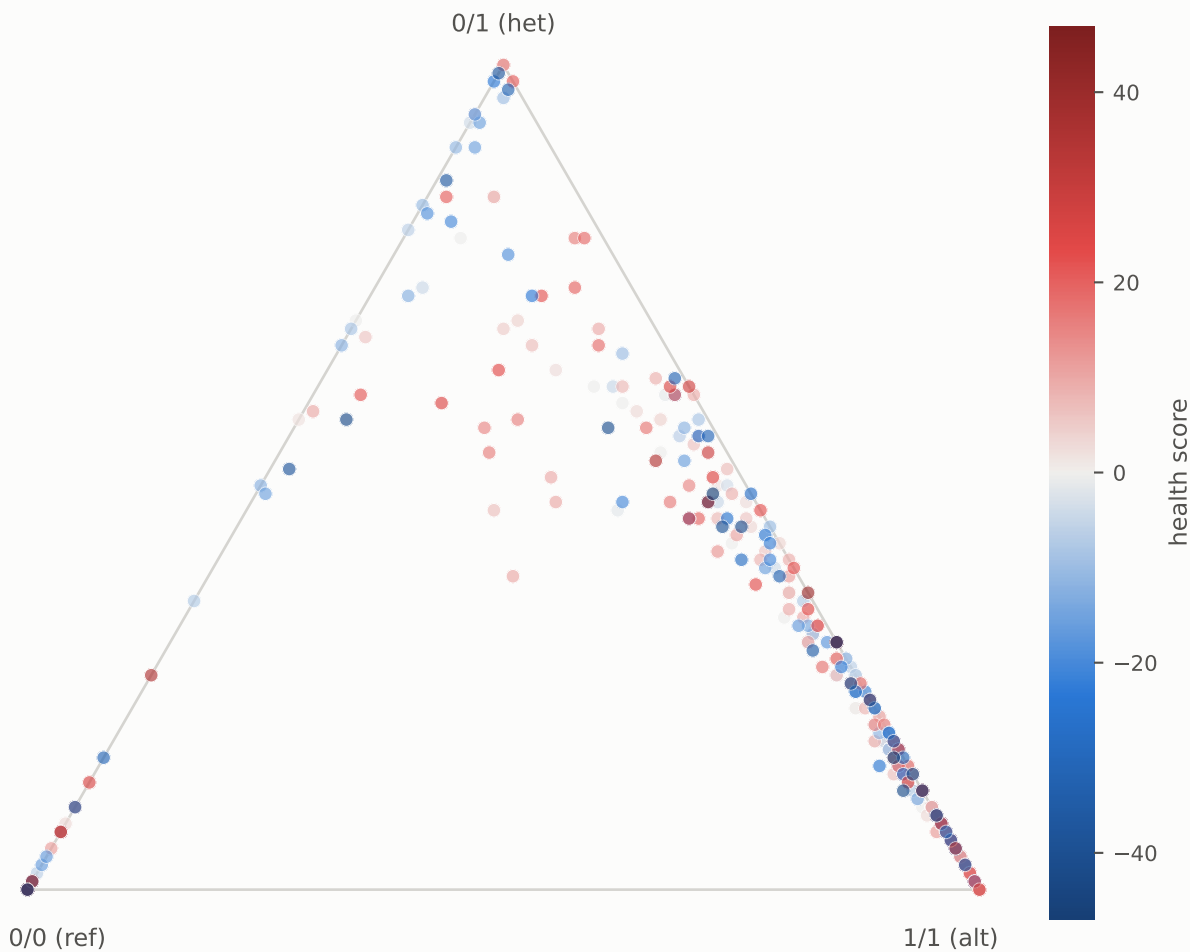
#105 by genotype uncertainty CHR_22:15,229,005 T>A
AF=0.47 DR2=0.81 r=-0.032 $\bar{H}$ =0.386 F=0.8



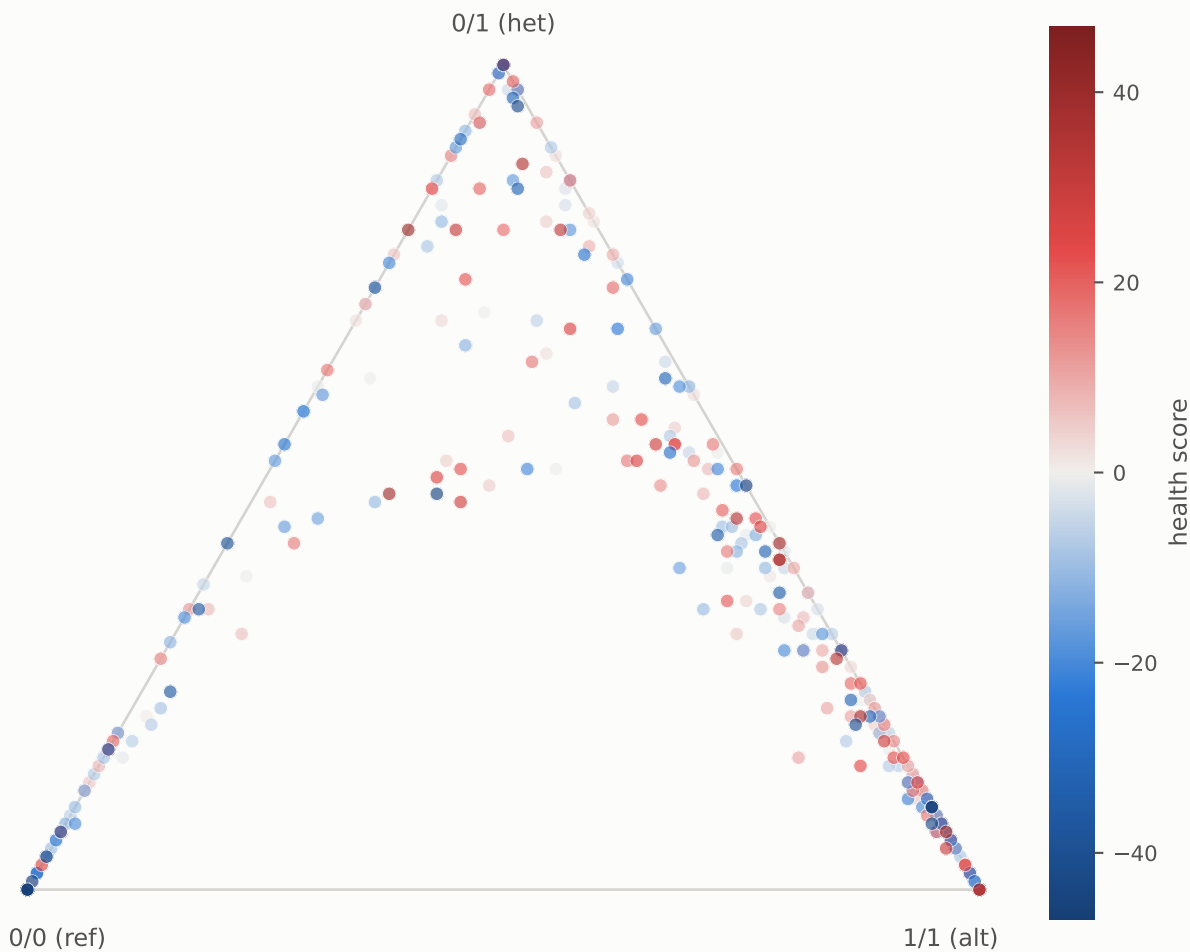
#106 by genotype uncertainty CHR_10:24,374,503 G>A
AF=0.54 DR2=0.82 $r=+0.011$ $\bar{H}=0.386$ F=0.1



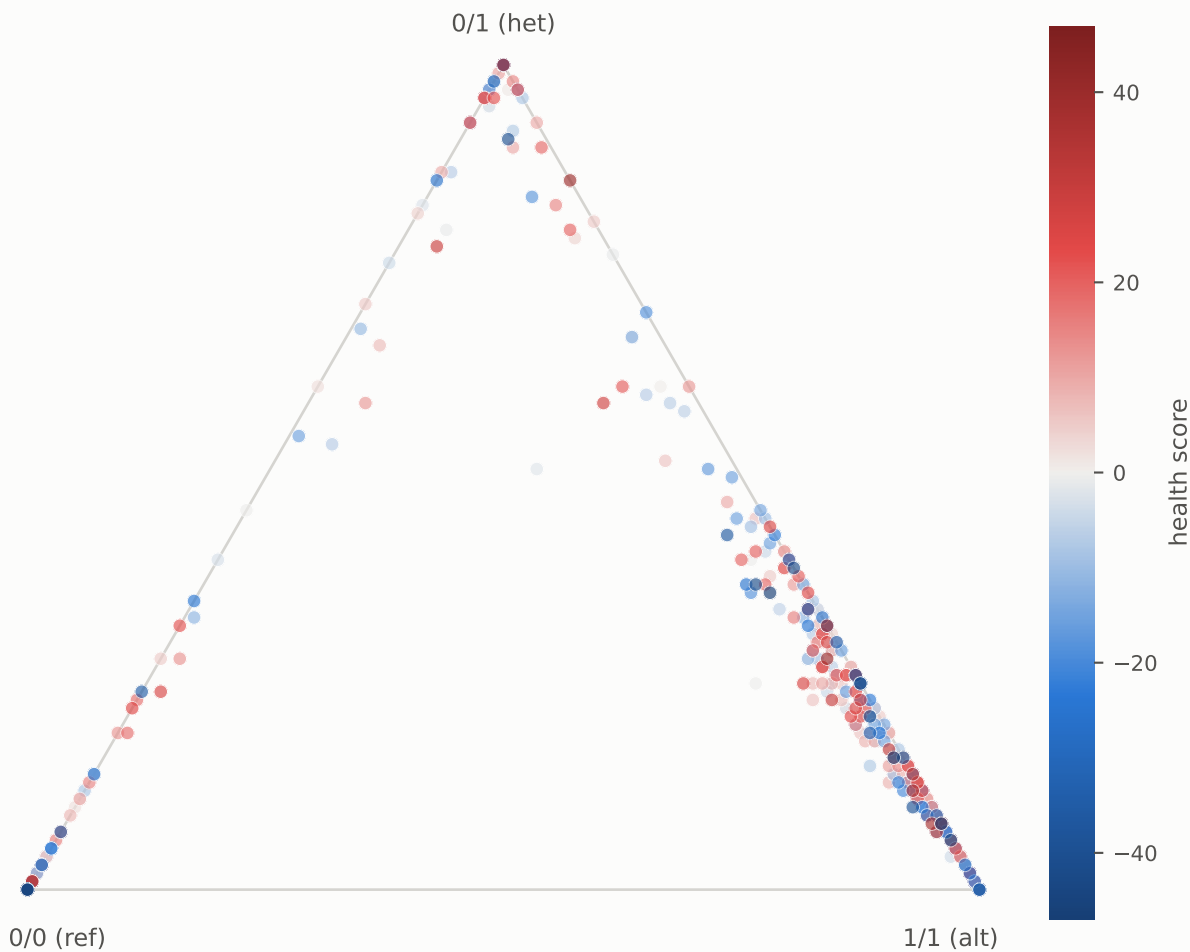
#107 by genotype uncertainty CHR_05:36,913,351 G>A
AF=0.54 DR2=0.81 r=-0.047 $\bar{H}$ =0.386 F=0.9



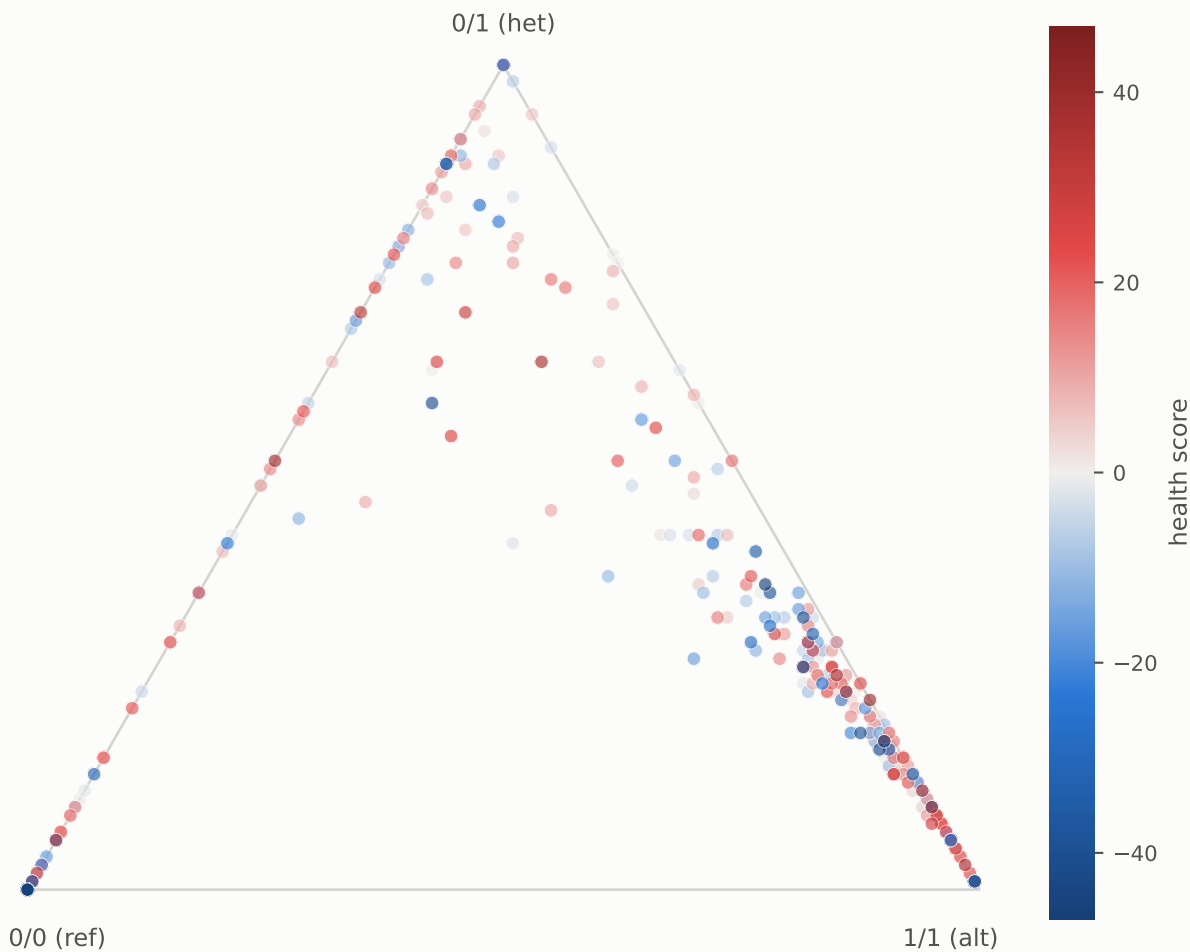
#108 by genotype uncertainty CHR_15:9,978,206 C>T
AF=0.5 DR2=0.81 r=+0.074 H=0.386 F=1.5



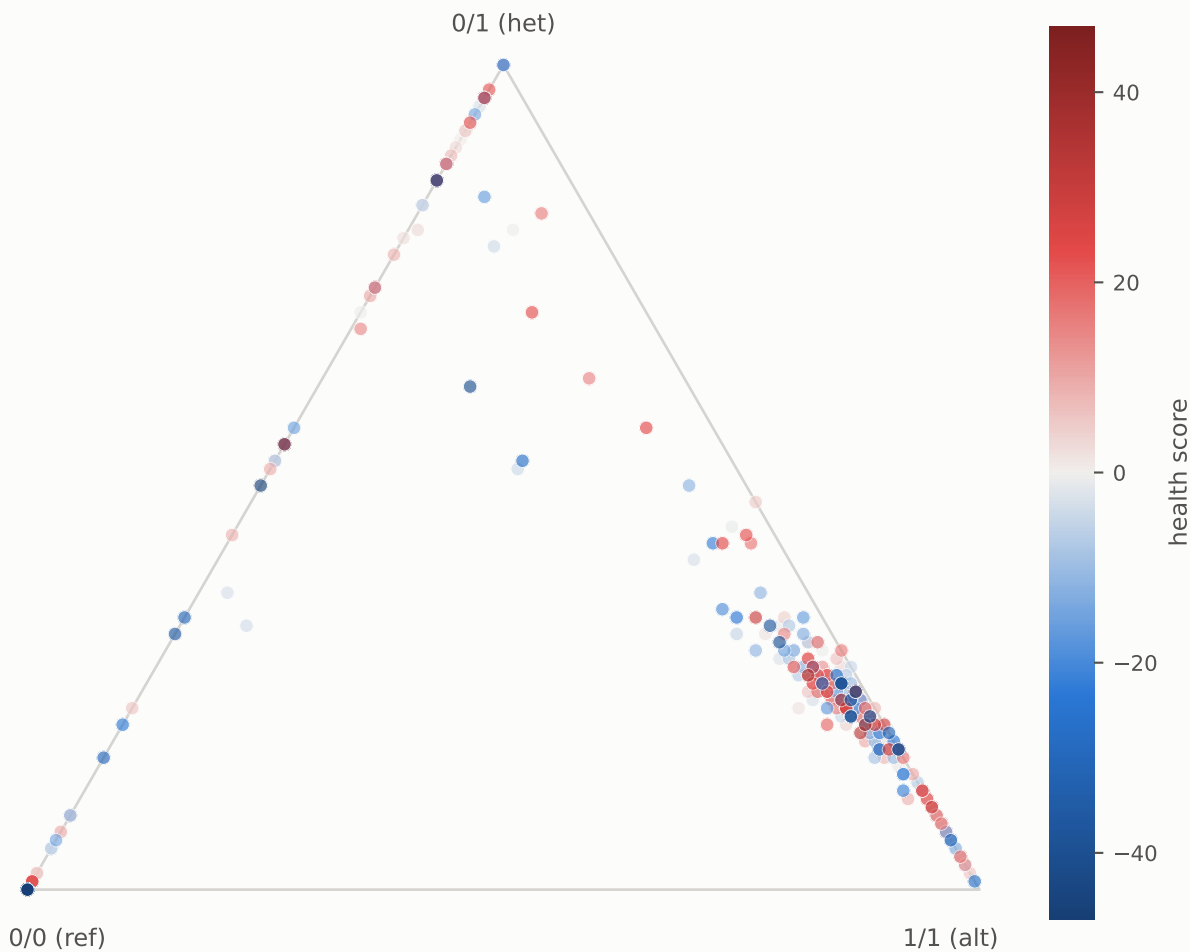
#109 by genotype uncertainty CHR_17:18,529,328 G>A
AF=0.6 DR2=0.81 $r=+0.018$ $\bar{H}=0.386$ F=0.4



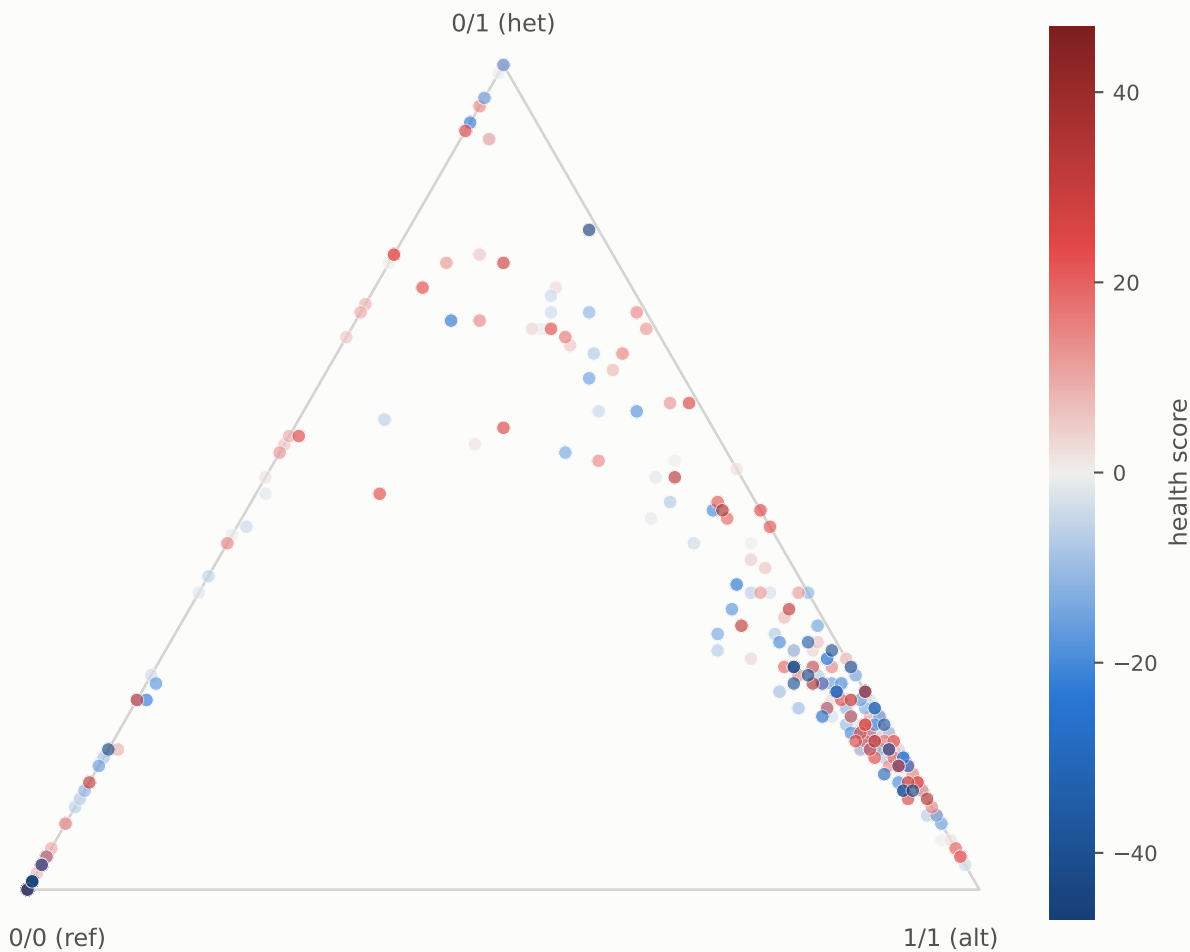
#110 by genotype uncertainty CHR_23:5,327,011 T>C
AF=0.49 DR2=0.81 $r=+0.113$ $\bar{H}=0.386$ F=4.8



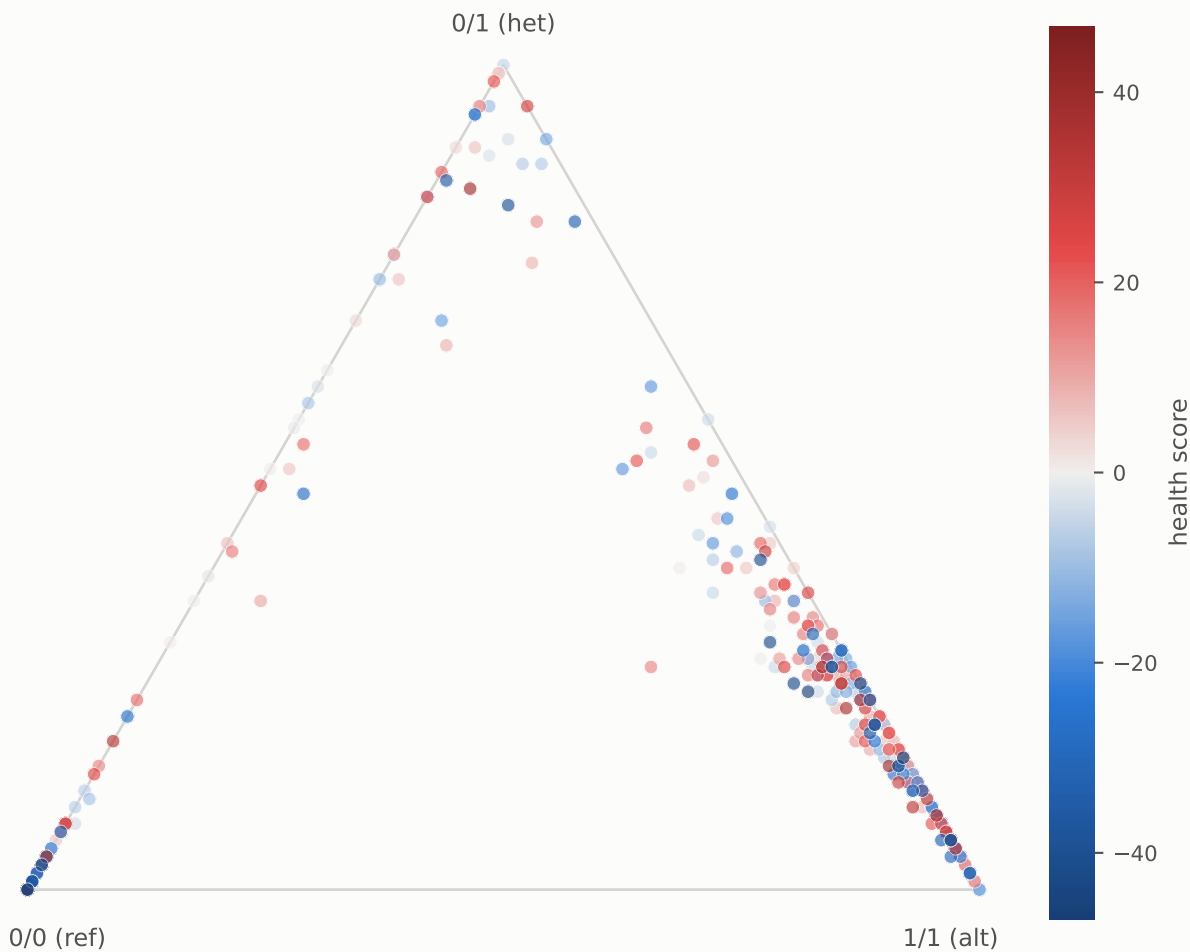
#111 by genotype uncertainty CHR_11:23,423,062 C>T
AF=0.49 DR2=0.82 $r=+0.059$ $\bar{H}=0.386$ F=1.0



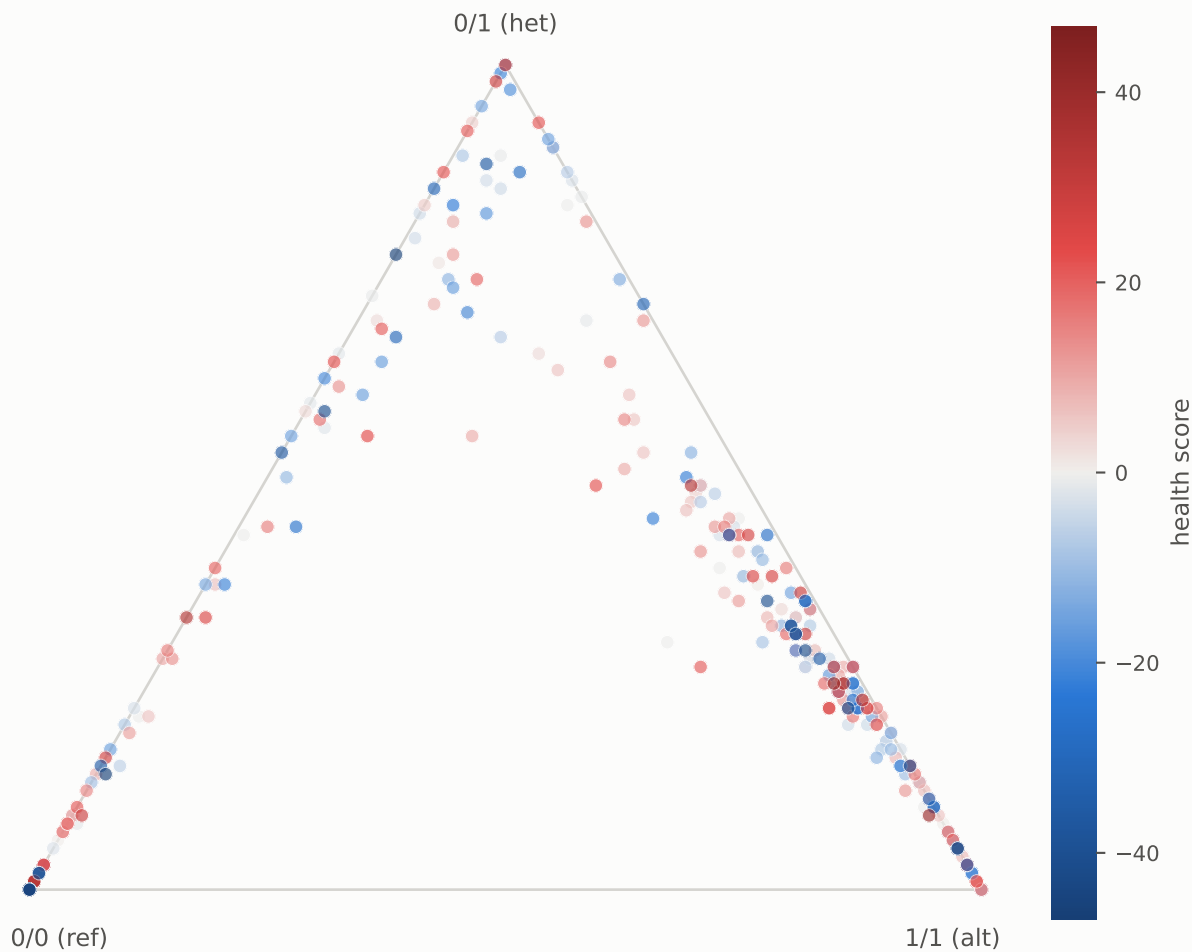
#112 by genotype uncertainty CHR_14:1,109,544 C>T
AF=0.48 DR2=0.81 $r=+0.004$ $\bar{H}=0.386$ $F=2.6$



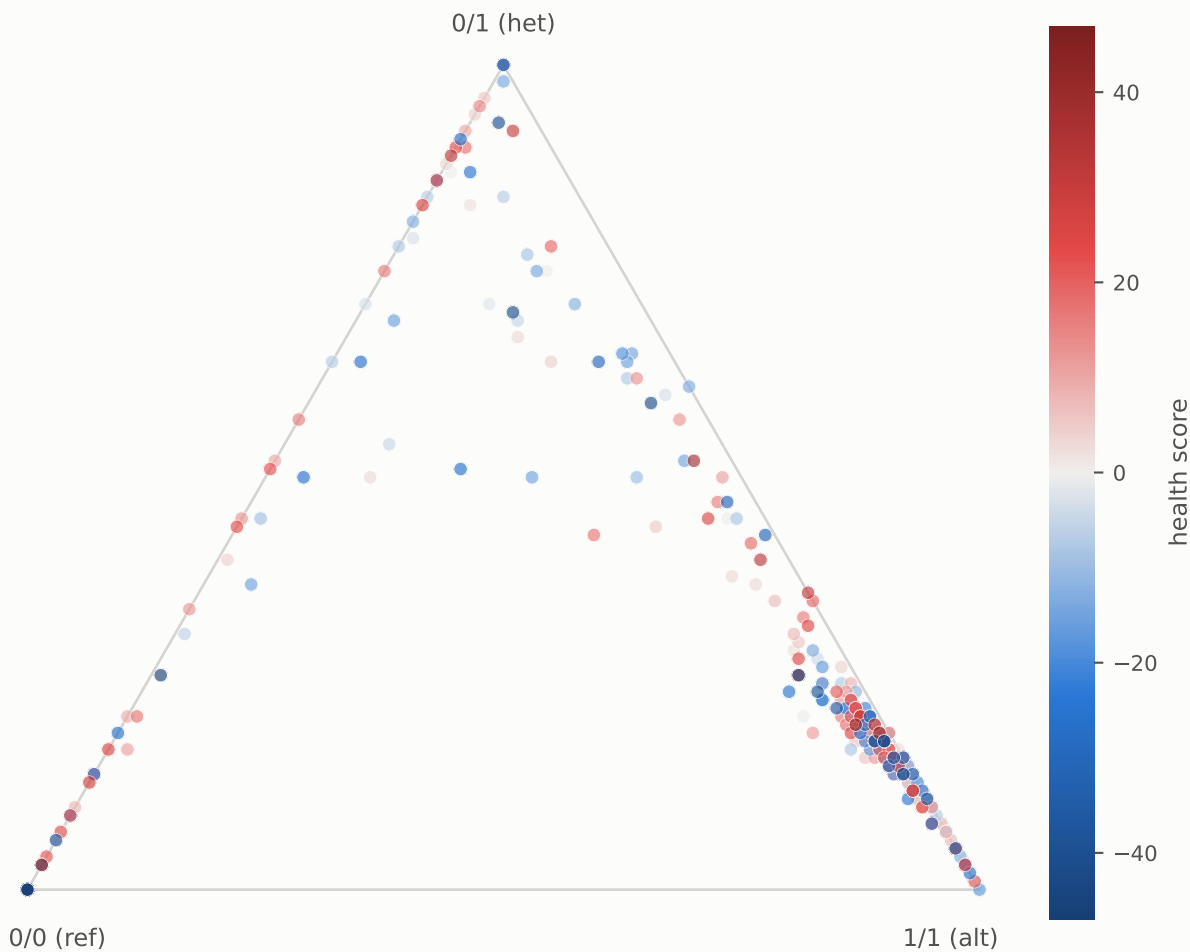
#113 by genotype uncertainty CHR_07:1,191,742 C>A
AF=0.58 DR2=0.81 $r=+0.048$ $\bar{H}=0.386$ F=0.4



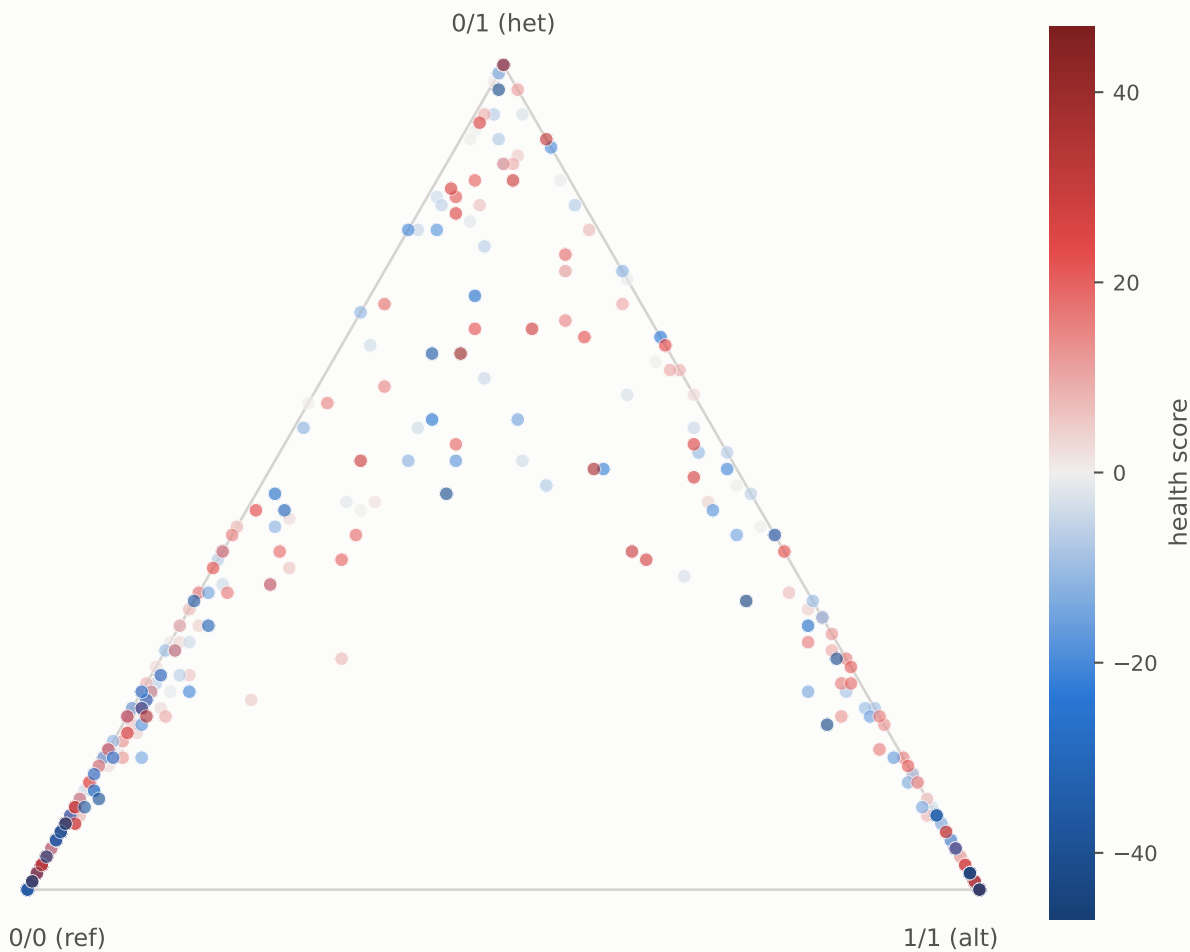
#114 by genotype uncertainty CHR_10:8,136,493 A>G
AF=0.46 DR2=0.81 $r=+0.007$ $\bar{H}=0.386$ F=0.7



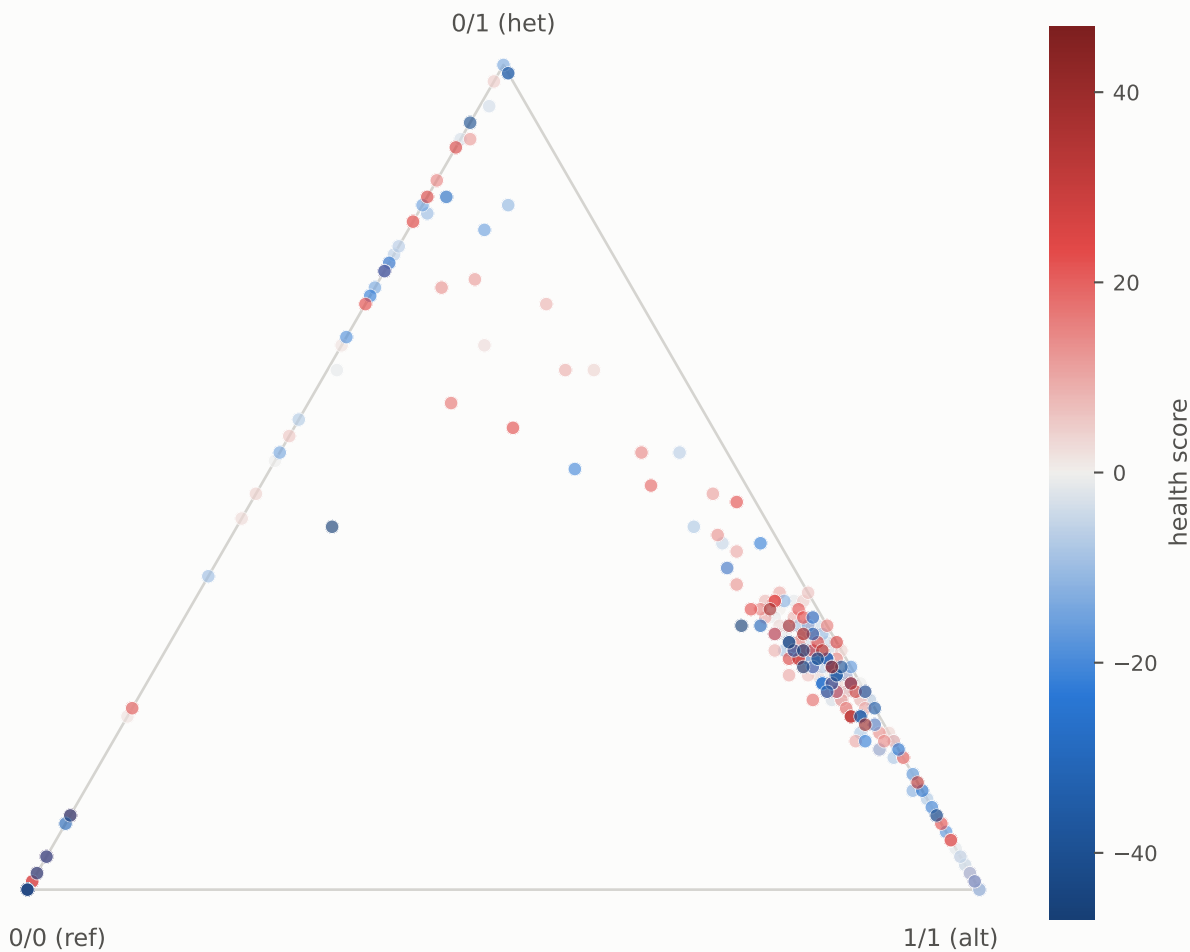
#115 by genotype uncertainty CHR_22:2,873,106 A>G
AF=0.53 DR2=0.82 r=-0.032 H=0.386 F=0.9



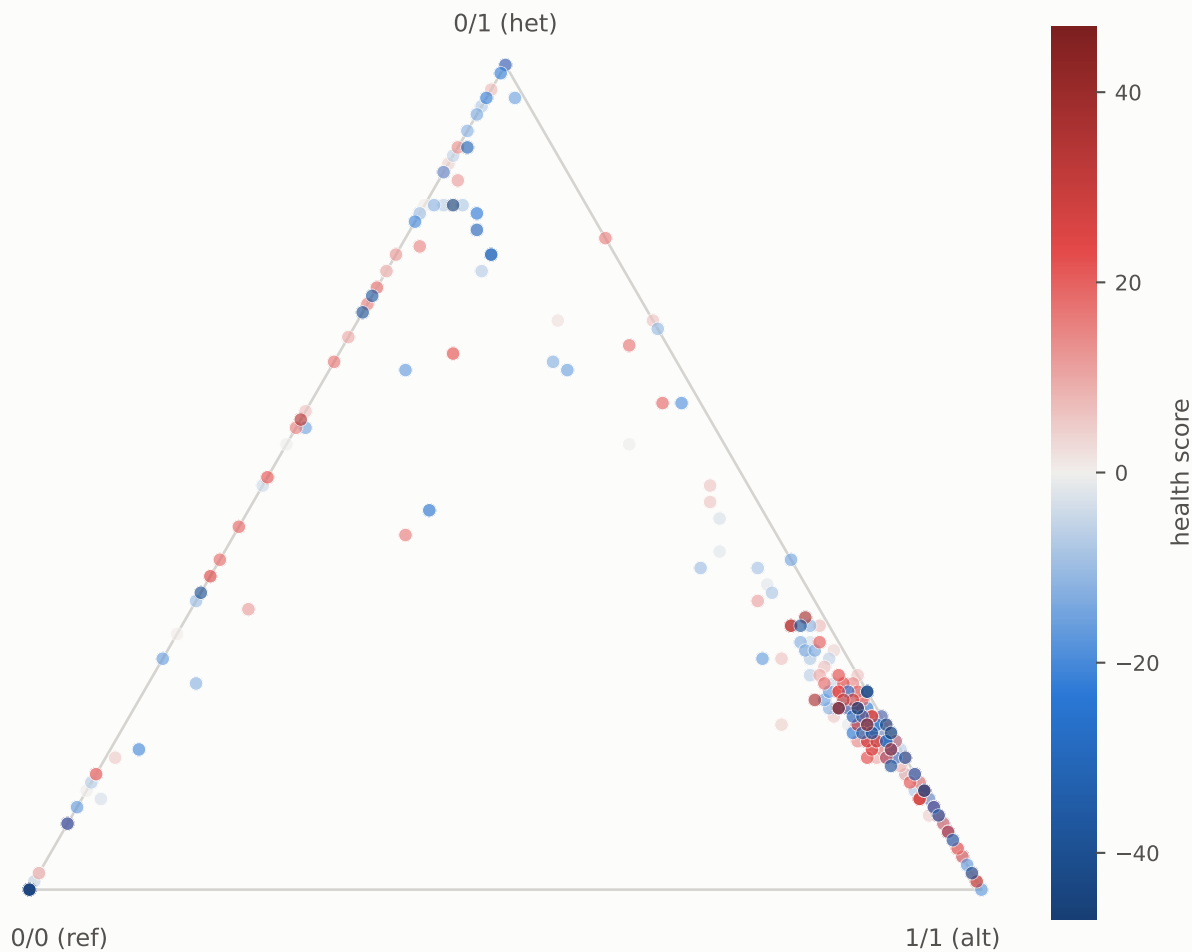
#116 by genotype uncertainty CHR_05:9,174,661 C>T
AF=0.4 DR2=0.81 r=-0.019 H=0.386 F=0.9



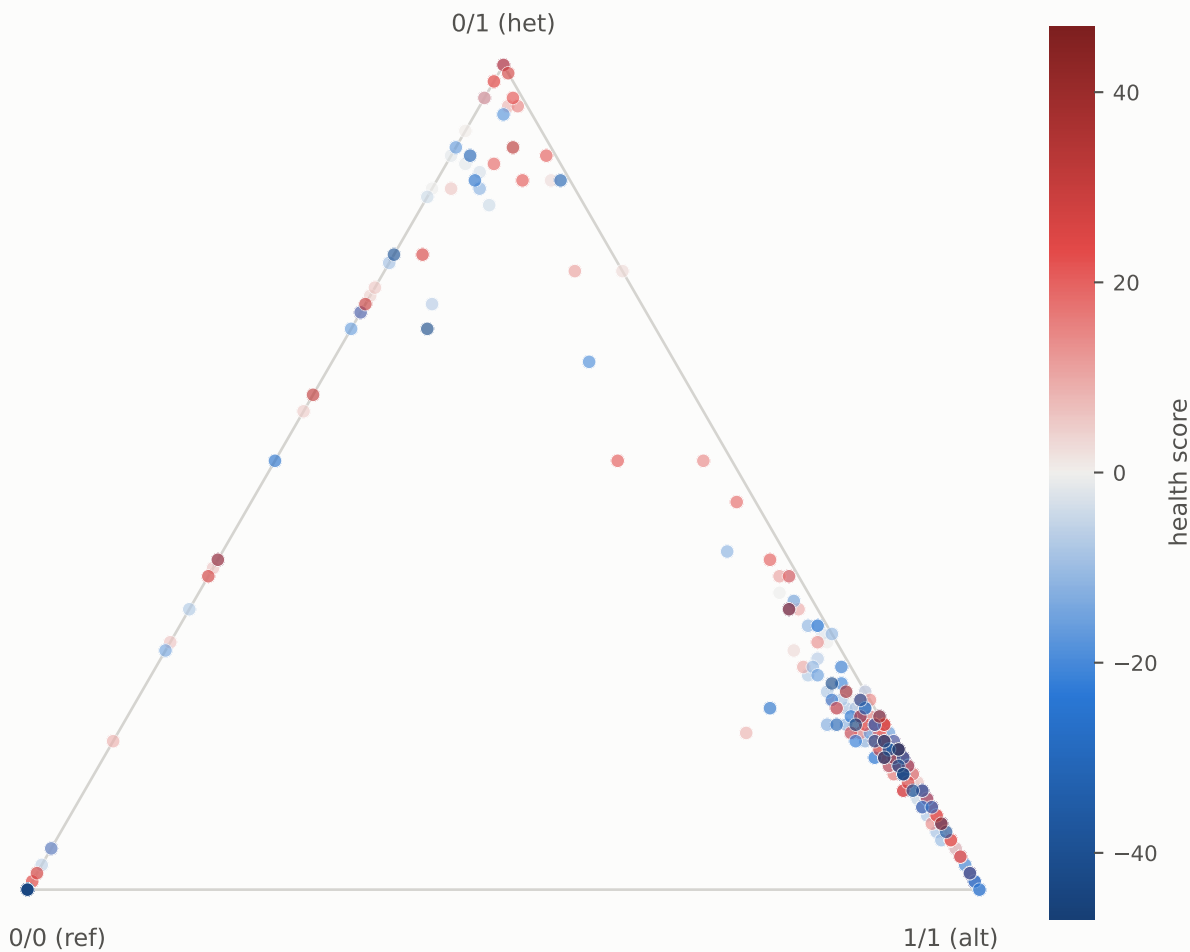
#117 by genotype uncertainty CHR_11:588,700 C>T
AF=0.45 DR2=0.81 $r=+0.007$ H=0.386 F=0.1



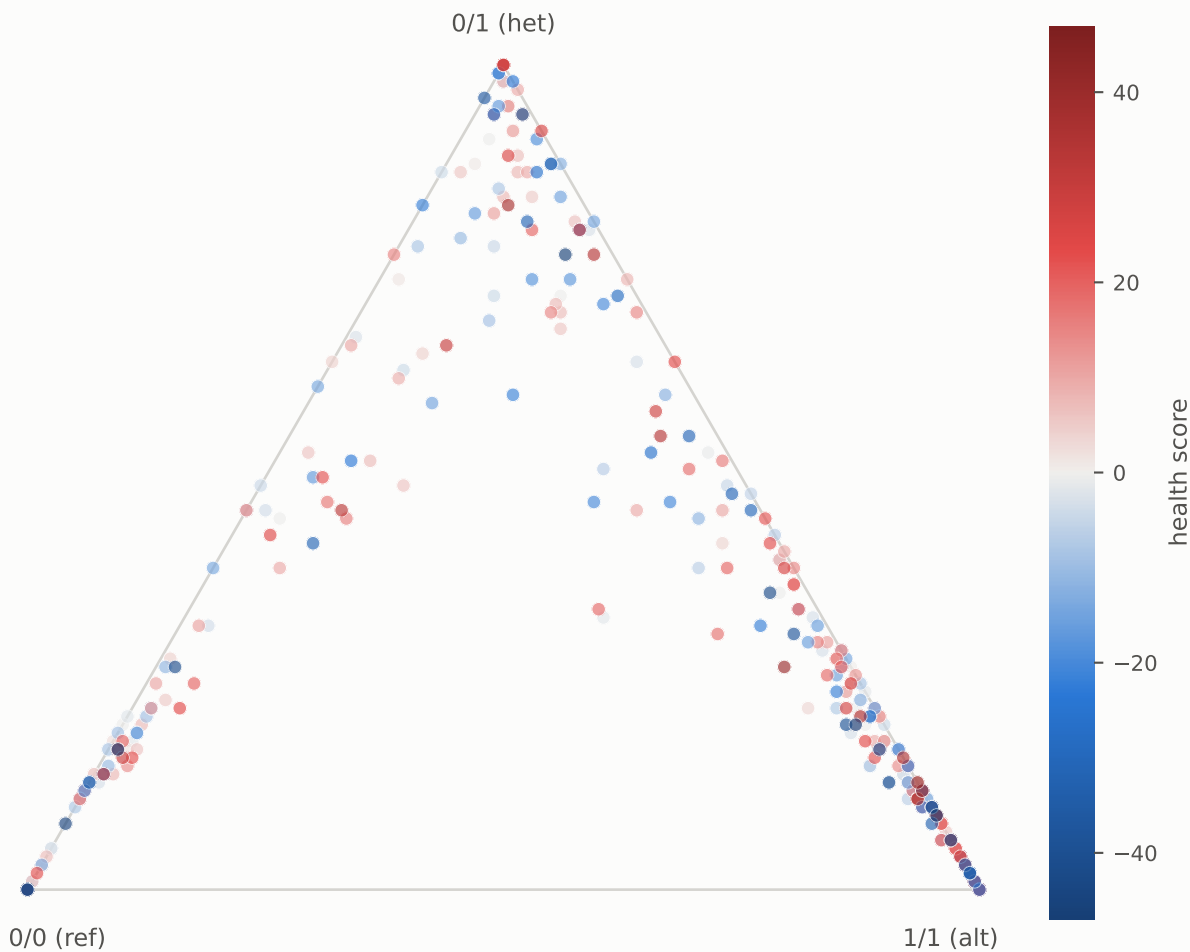
#118 by genotype uncertainty CHR_04:23,286,659 G>A
AF=0.52 DR2=0.82 $r=+0.017$ $\bar{H}=0.386$ F=1.9



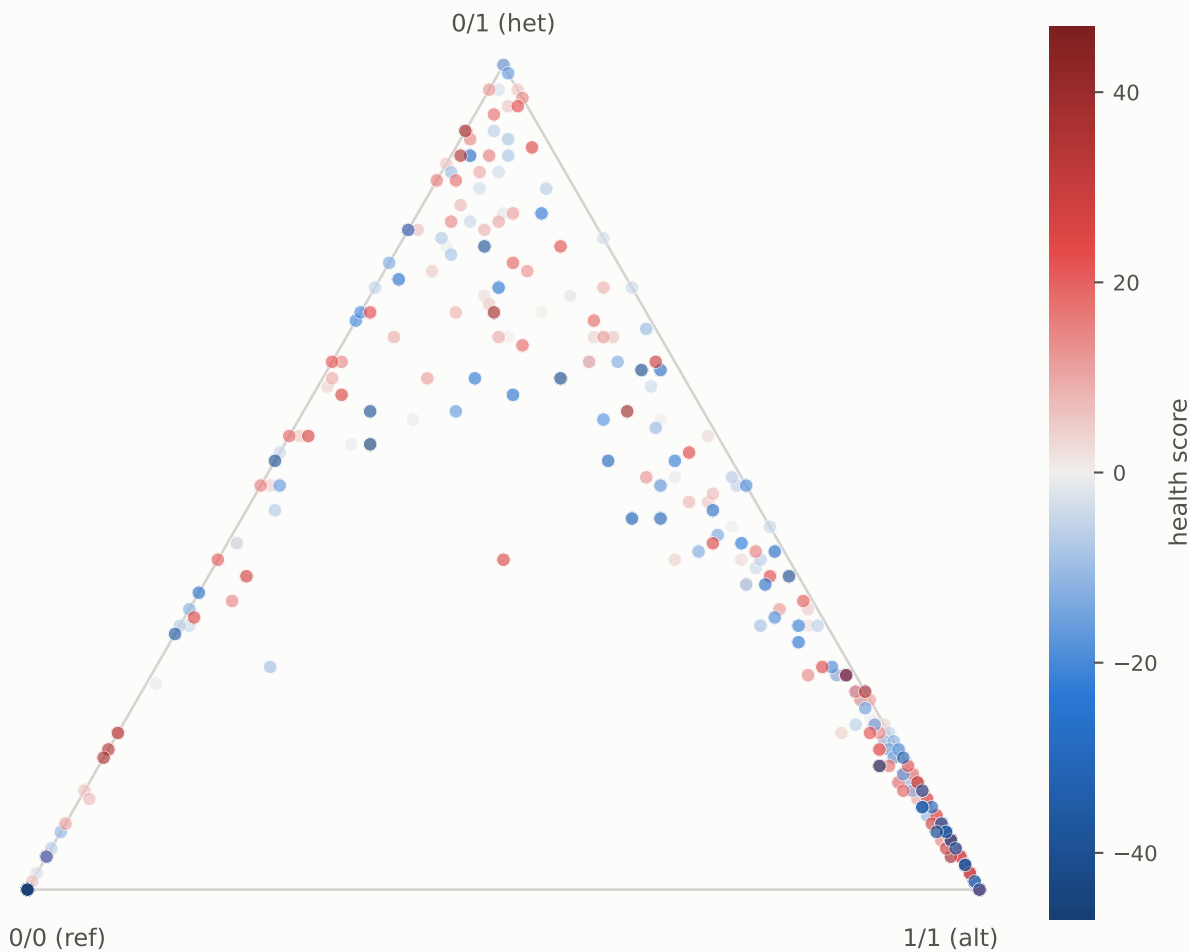
#119 by genotype uncertainty CHR_17:18,543,935 C>T
AF=0.66 DR2=0.81 $r=+0.007$ $\bar{H}=0.385$ $F=0.2$



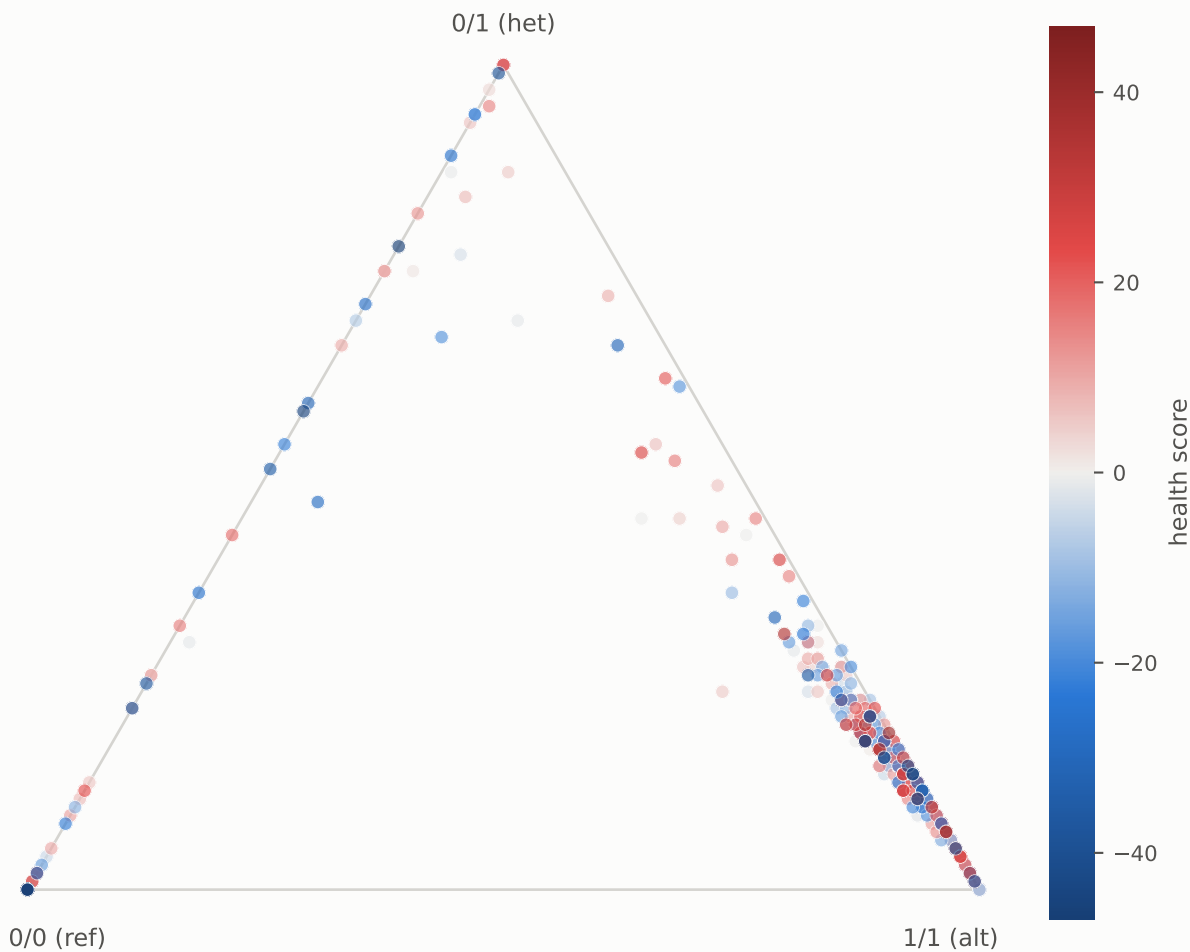
#120 by genotype uncertainty CHR_08:34,676,568 C>T
AF=0.55 DR2=0.81 $r=+0.061$ $\bar{H}=0.385$ F=0.9



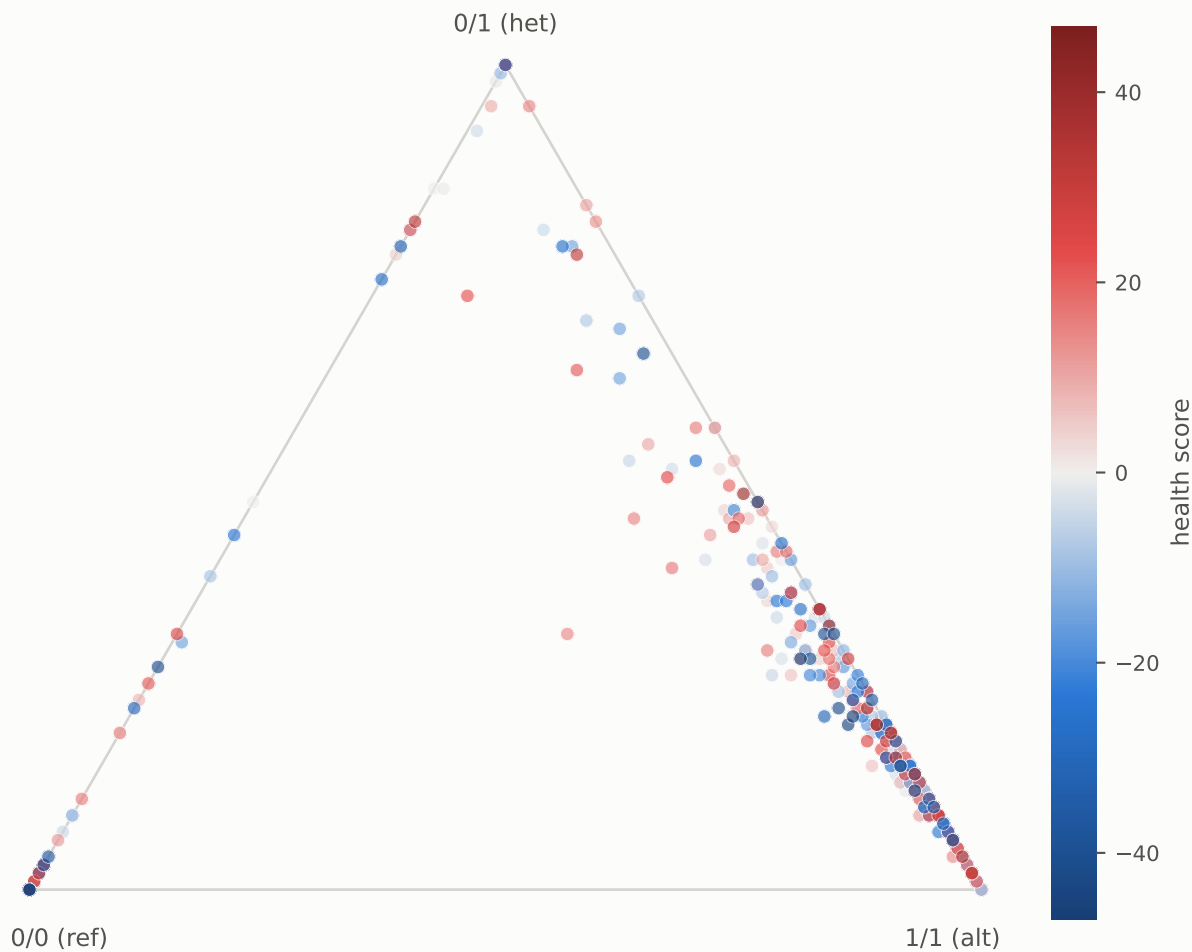
#121 by genotype uncertainty CHR_15:13,304,291 A>C
AF=0.57 DR2=0.81 $r=-0.031$ $\bar{H}=0.385$ F=0.3



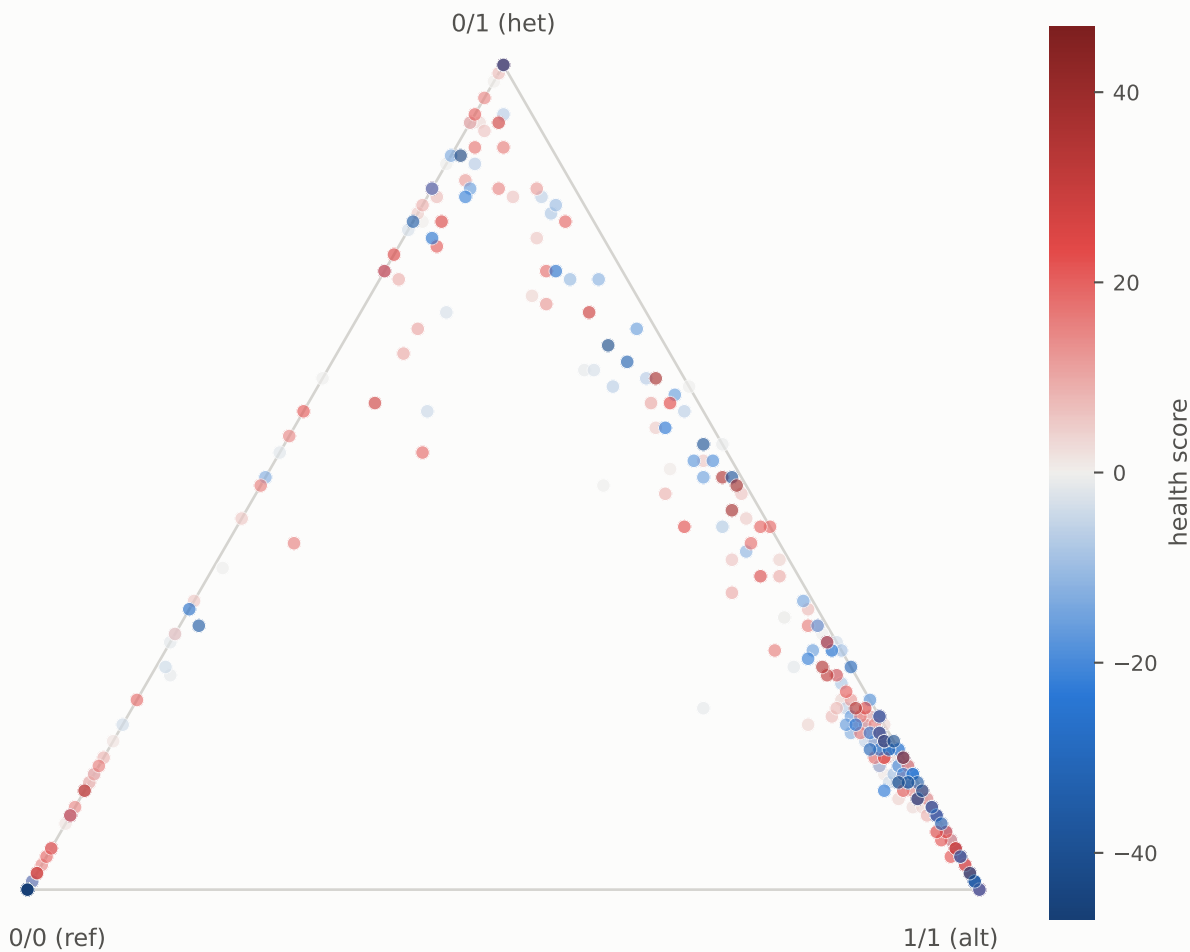
#122 by genotype uncertainty CHR_22:6,645,129 G>A
AF=0.63 DR2=0.81 $r=+0.028$ $\bar{H}=0.385$ F=2.0



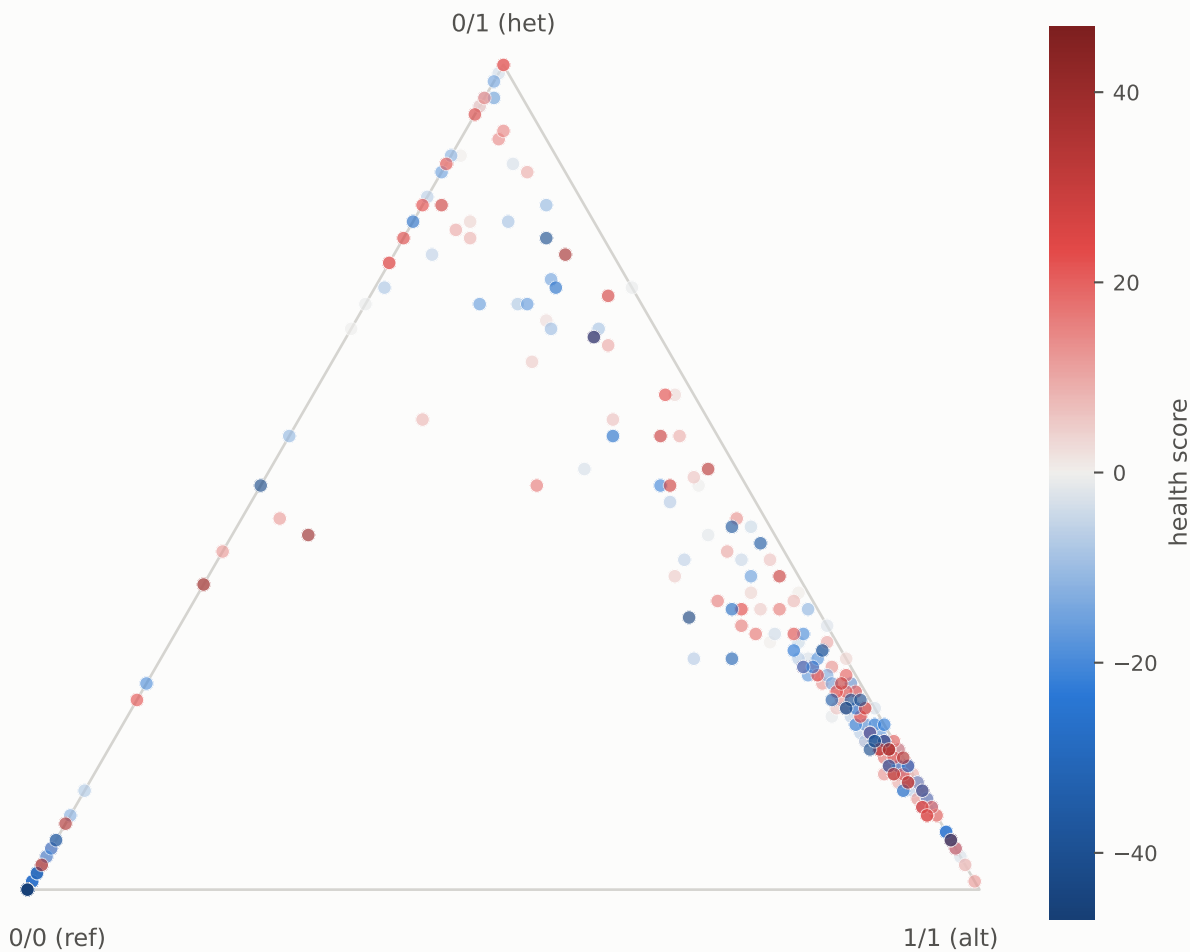
#123 by genotype uncertainty CHR_05:5,896,446 G>A
AF=0.6 DR2=0.81 r=-0.015 H=0.385 F=0.1



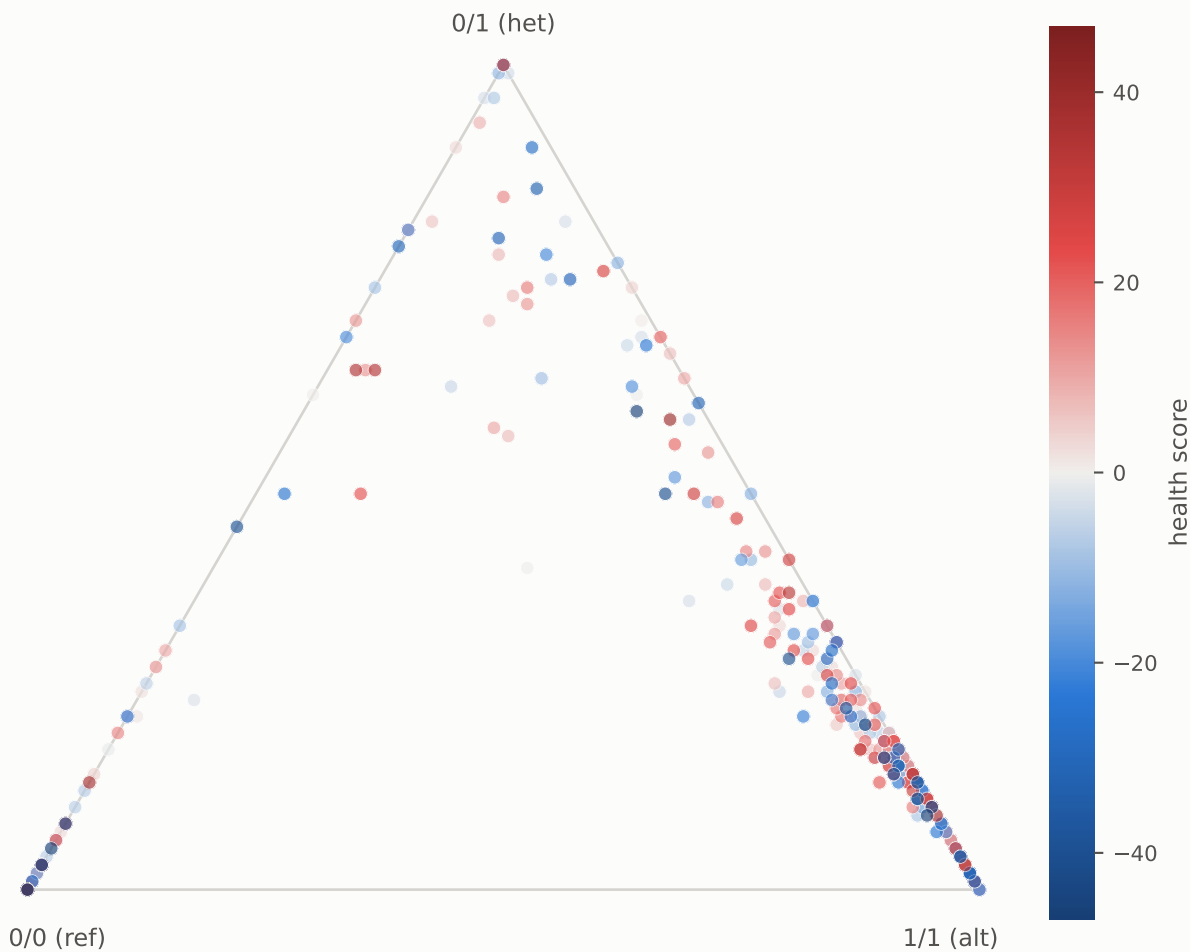
#124 by genotype uncertainty CHR_18:19,607,250 G>C
AF=0.56 DR2=0.81 $r=-0.048$ $\bar{H}=0.385$ F=0.2



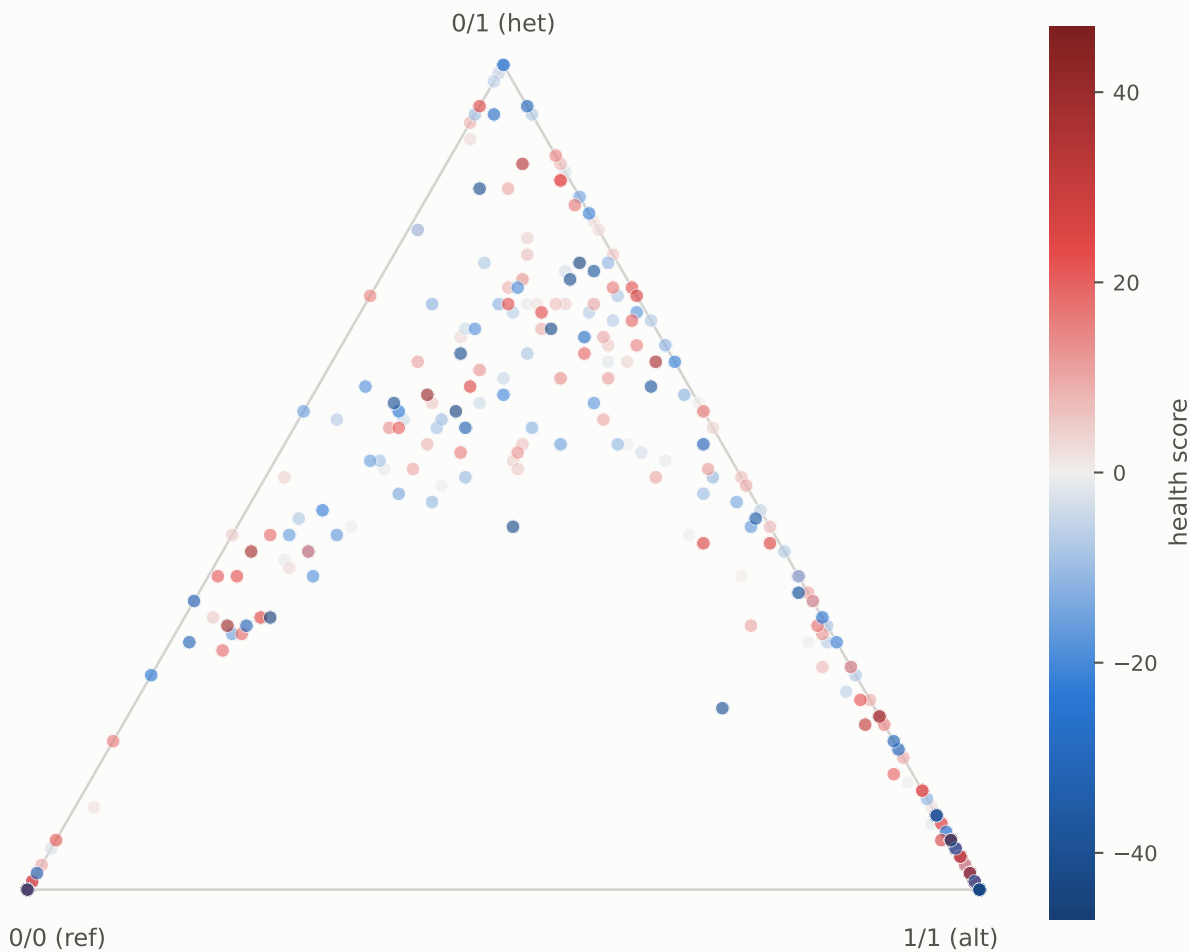
#125 by genotype uncertainty CHR_17:11,395,593 G>A
AF=0.49 DR2=0.82 $r=+0.072$ $\bar{H}=0.385$ $F=1.5$



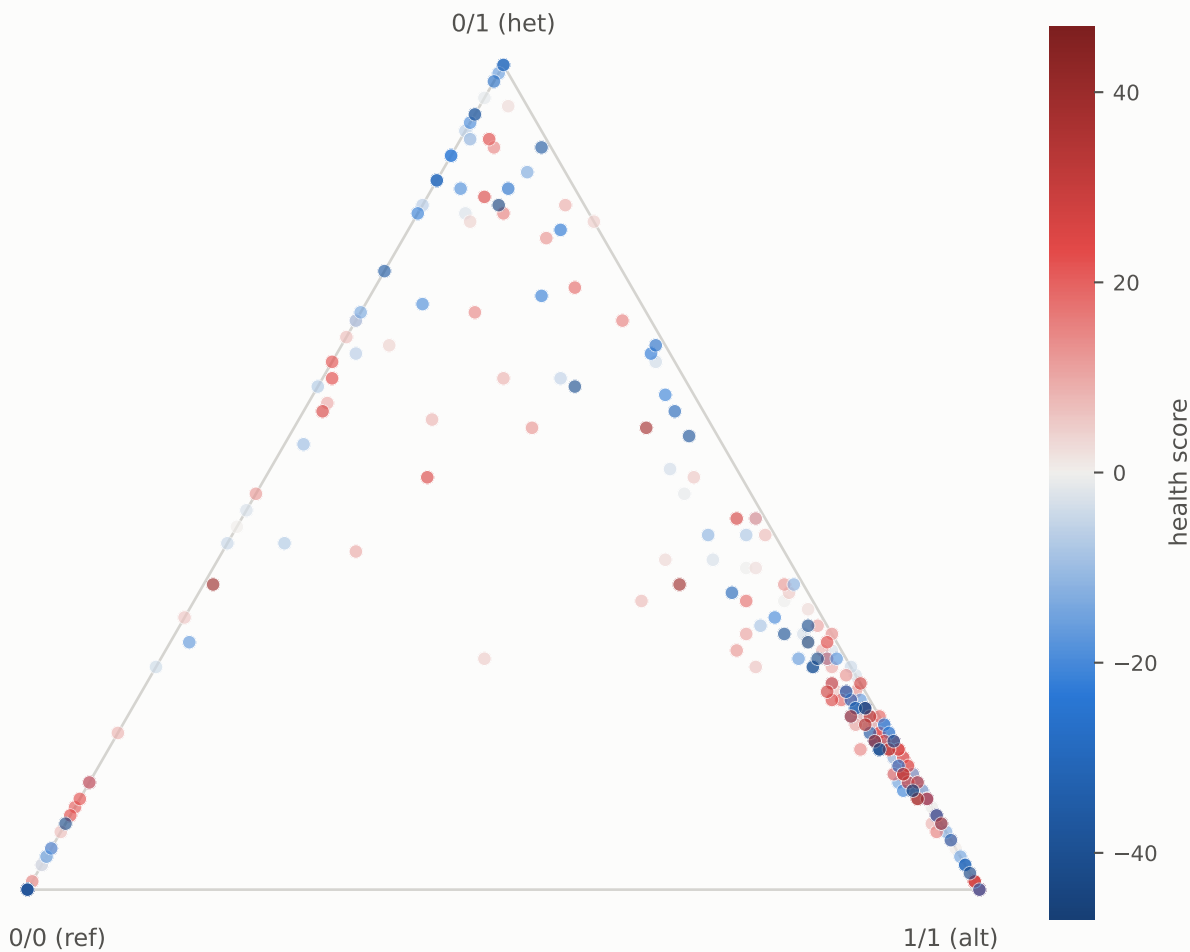
#126 by genotype uncertainty CHR_14:27,842,593 C>A
AF=0.57 DR2=0.81 $r=+0.004$ $\bar{H}=0.385$ F=0.2



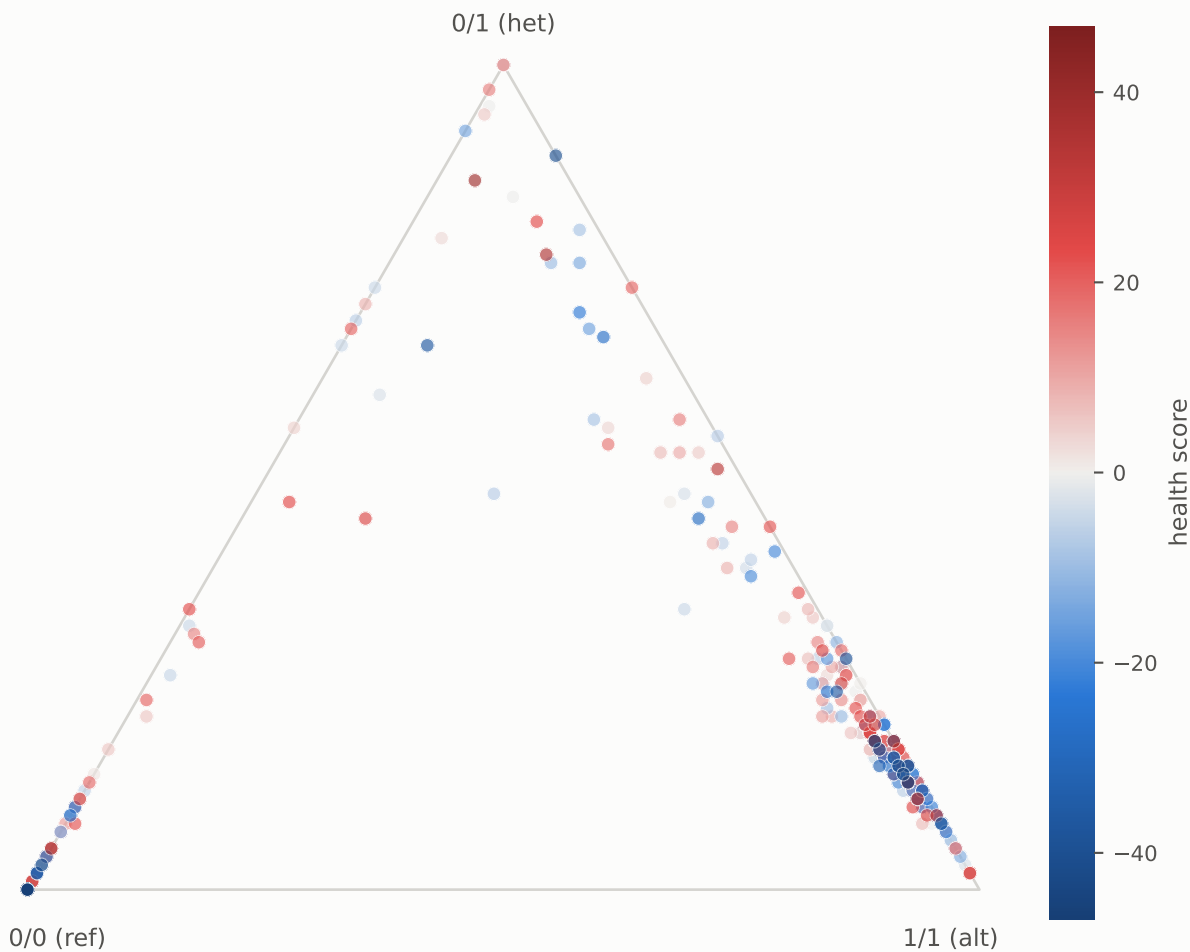
#127 by genotype uncertainty CHR_03:14,839,673 A>G
AF=0.52 DR2=0.81 $r=-0.052$ $\bar{H}=0.385$ F=2.5



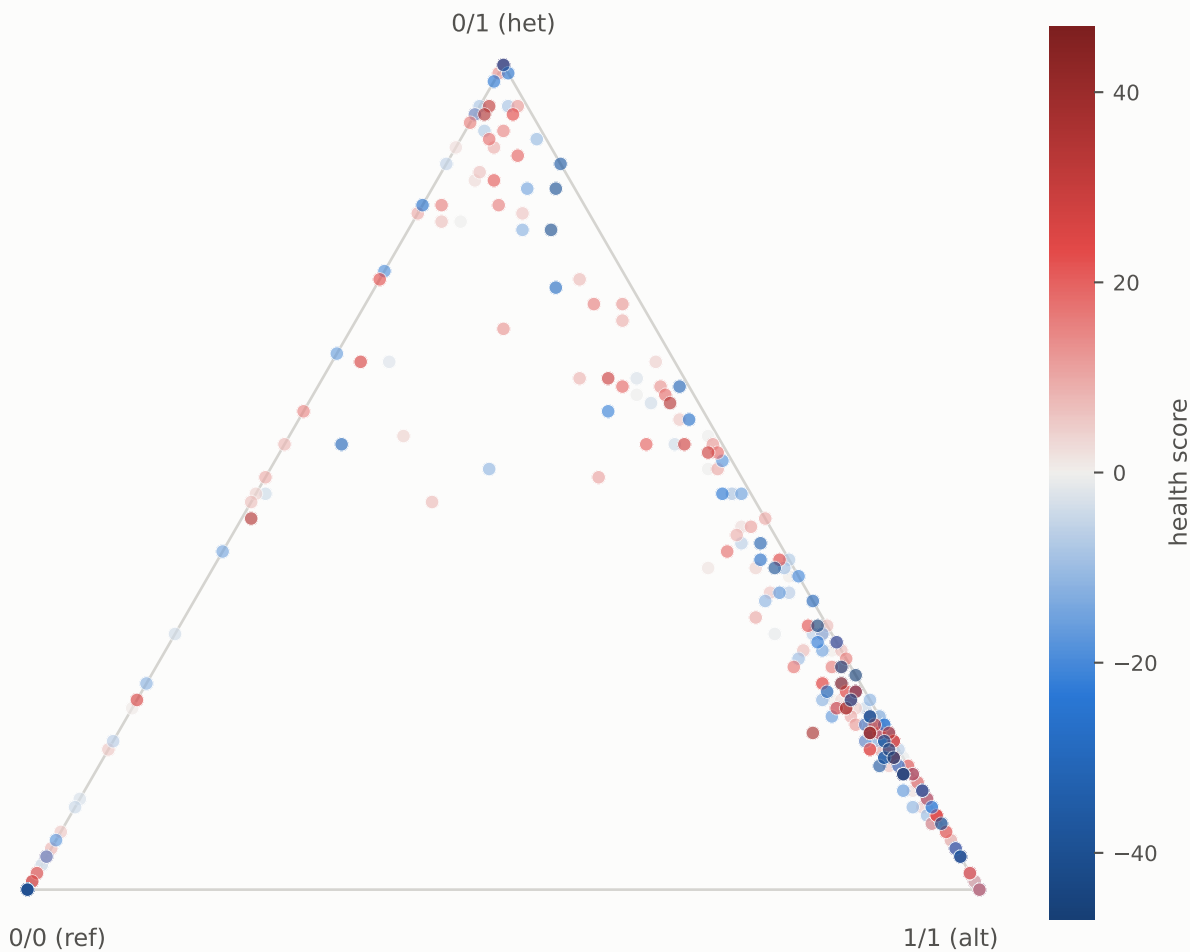
#128 by genotype uncertainty CHR_12:18,909,371 G>A
AF=0.58 DR2=0.81 $r=-0.027$ $\bar{H}=0.385$ F=5.5



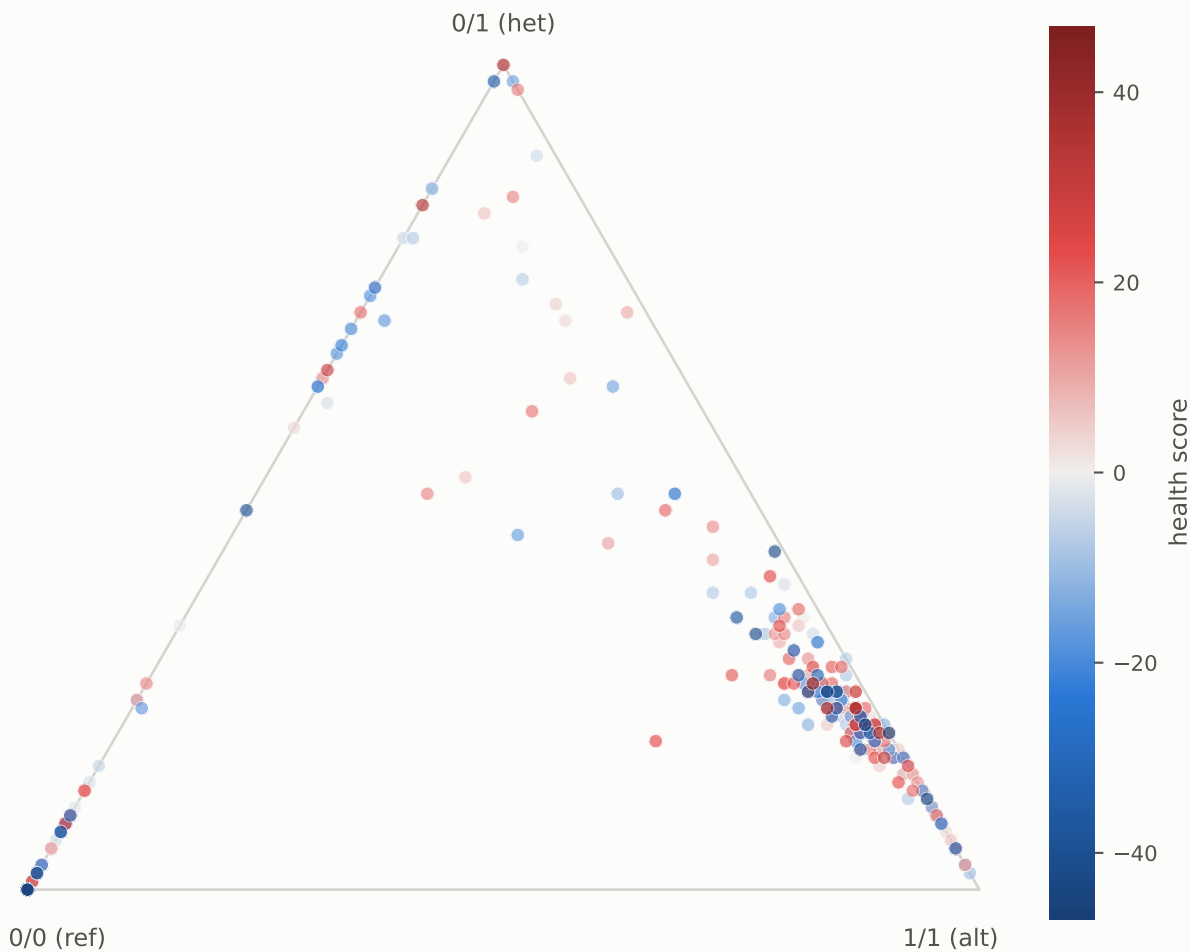
#129 by genotype uncertainty CHR_17:1,317,188 G>A
AF=0.6 DR2=0.81 r=+0.027 H=0.385 F=0.4



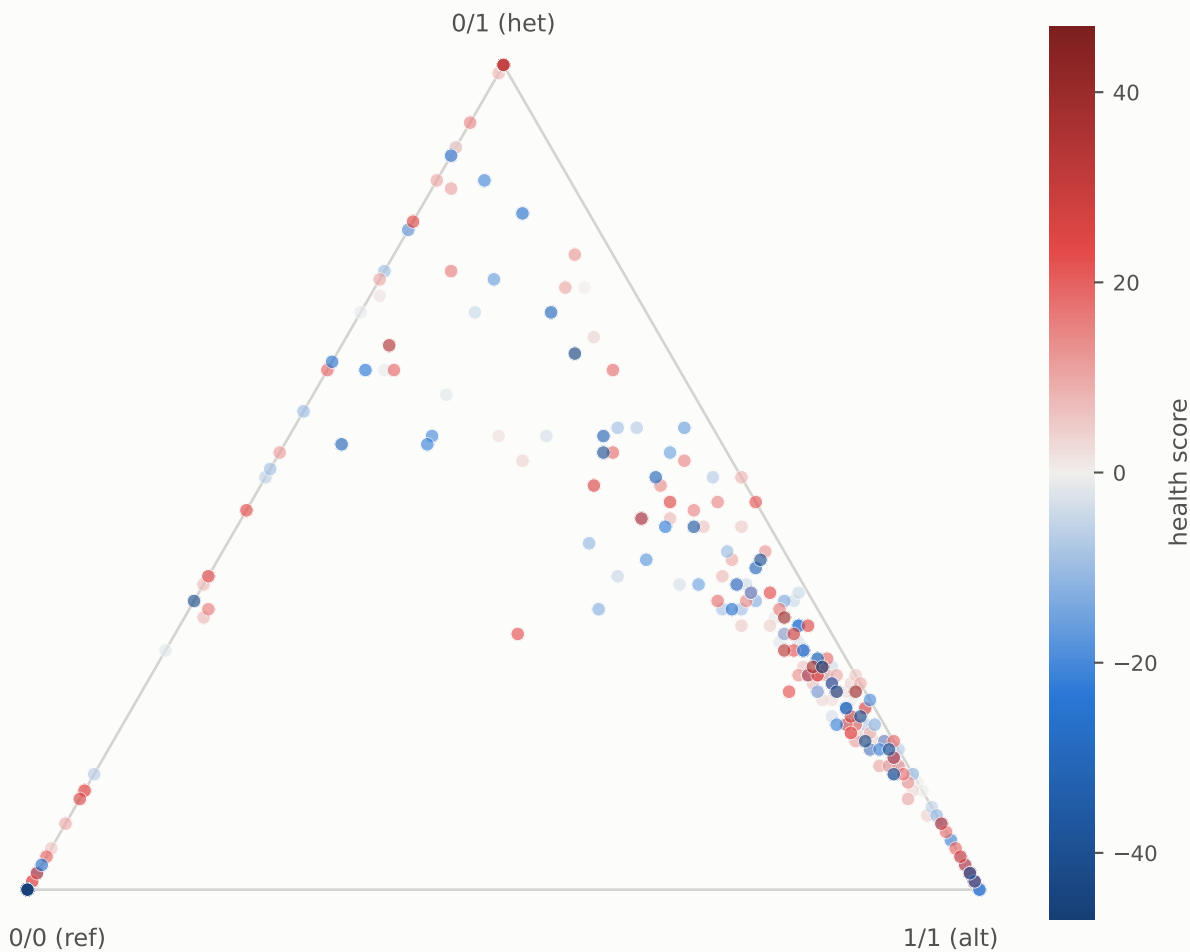
#130 by genotype uncertainty CHR_11:31,647,320 G>A
AF=0.54 DR2=0.81 $r=-0.060$ $\bar{H}=0.385$ F=1.9



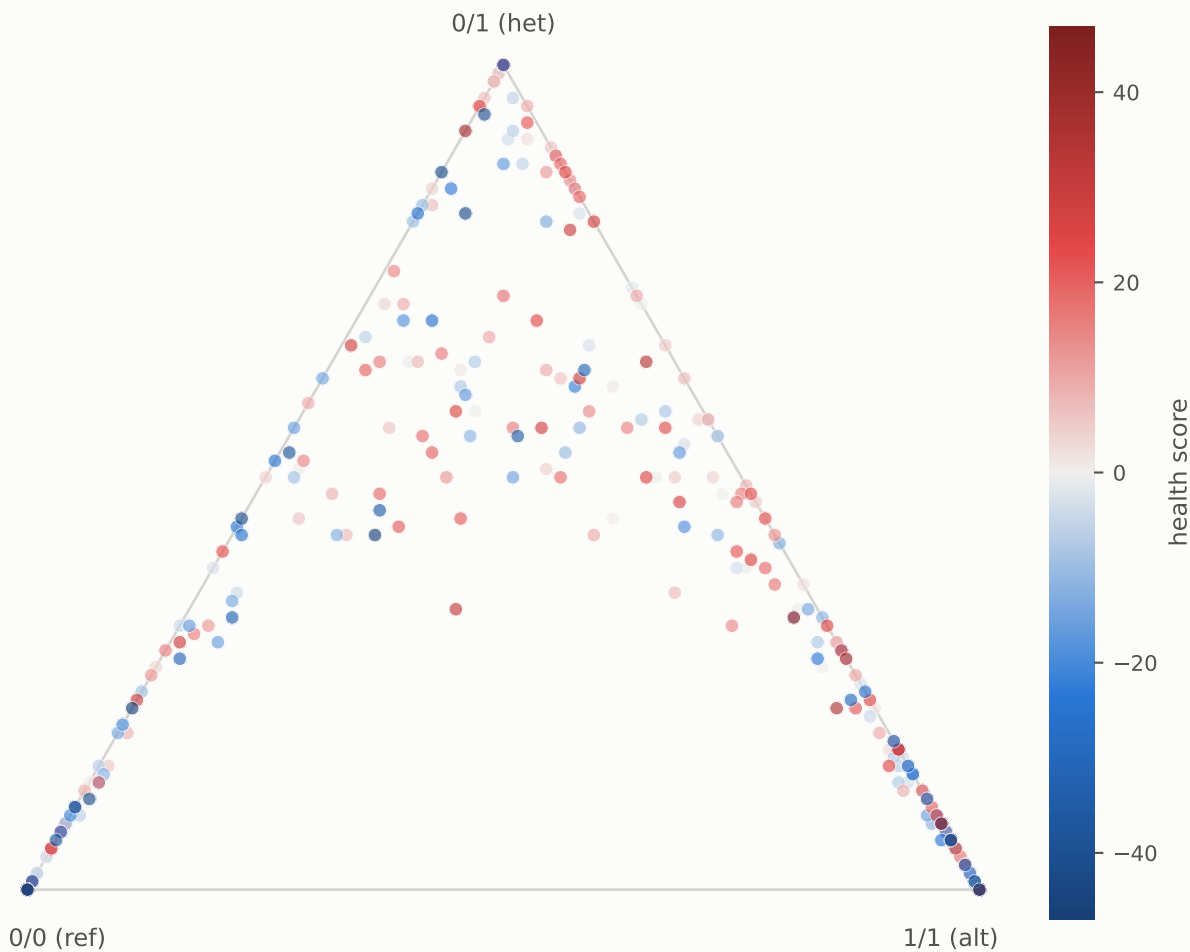
#131 by genotype uncertainty CHR_04:23,285,258 G>A
AF=0.46 DR2=0.81 $r=+0.044$ $\bar{H}=0.384$ F=0.5



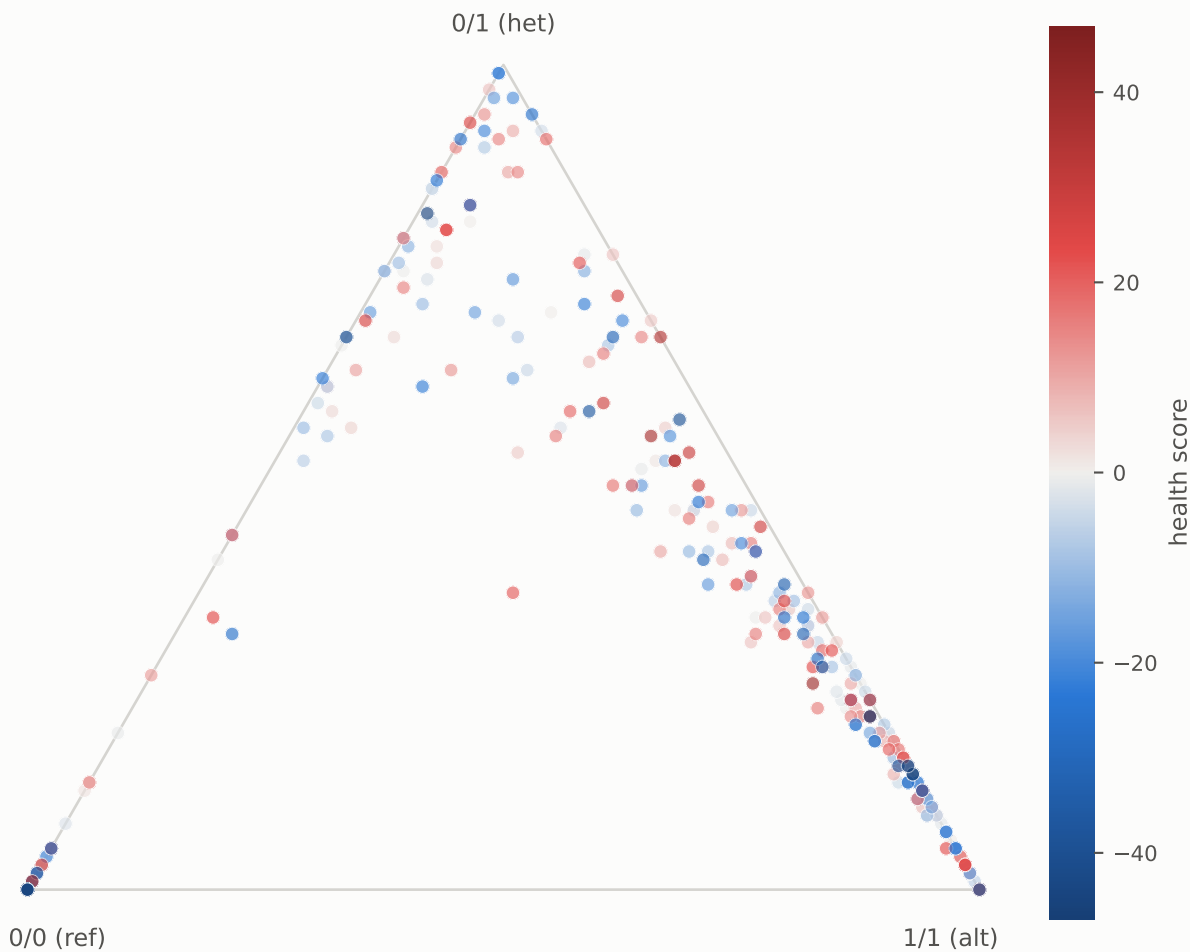
#132 by genotype uncertainty CHR_13:4,541,870 T>C
AF=0.44 DR2=0.81 $r=-0.002$ H=0.384 F=0.1



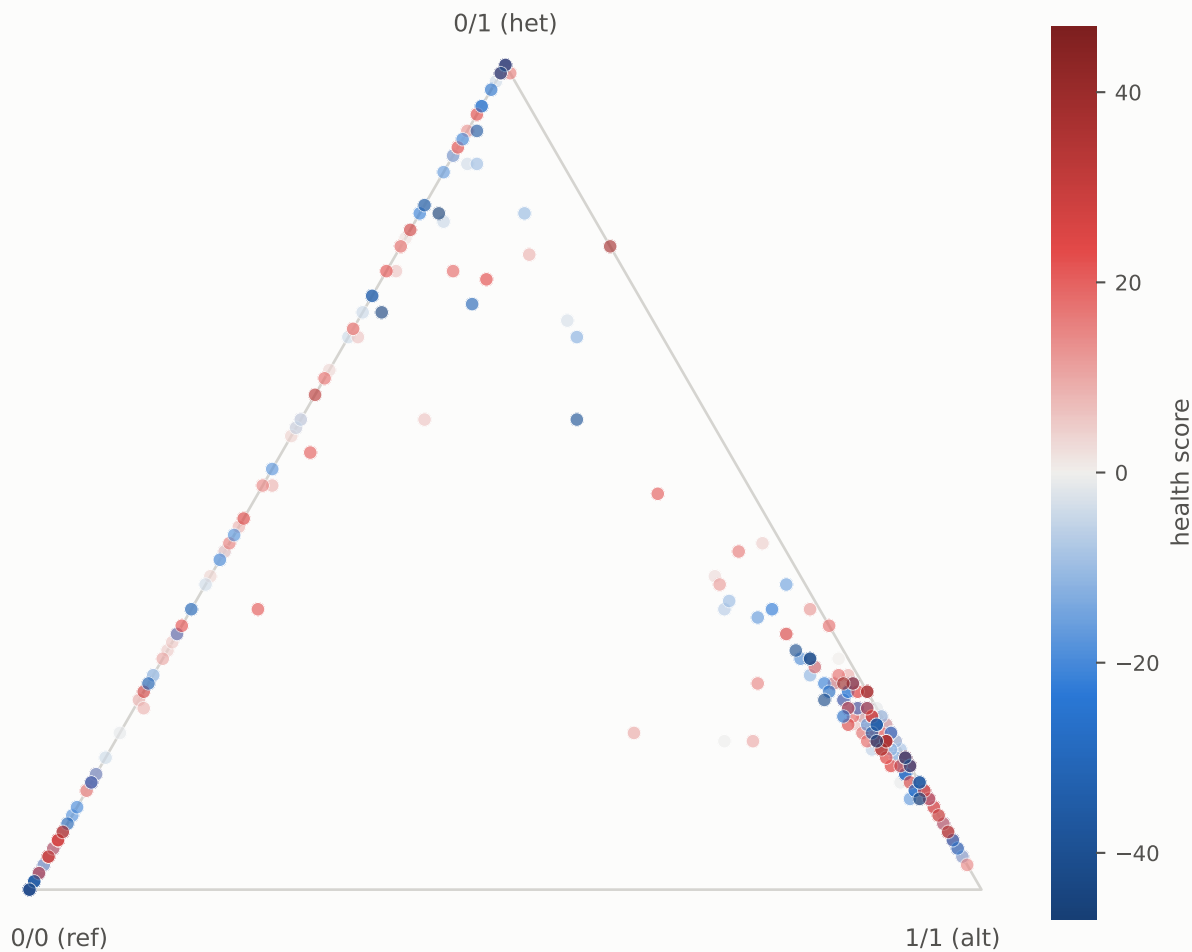
#133 by genotype uncertainty CHR_06:12,540,558 C>T
AF=0.46 DR2=0.81 $r=+0.093$ $\bar{H}=0.384$ F=4.0



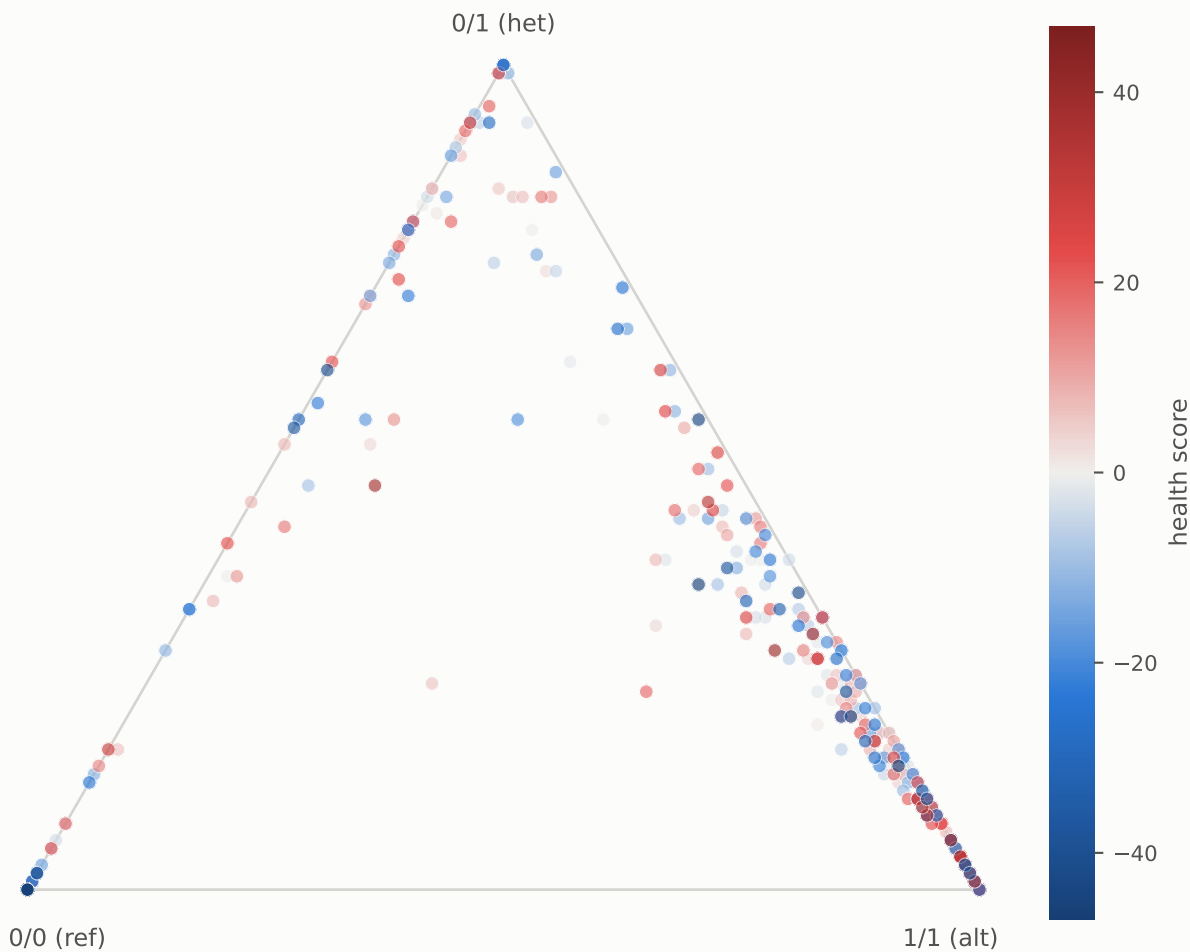
#134 by genotype uncertainty CHR_07:7,421,215 A>G
AF=0.46 DR2=0.81 $r=-0.035$ $\bar{H}=0.384$ $F=0.4$



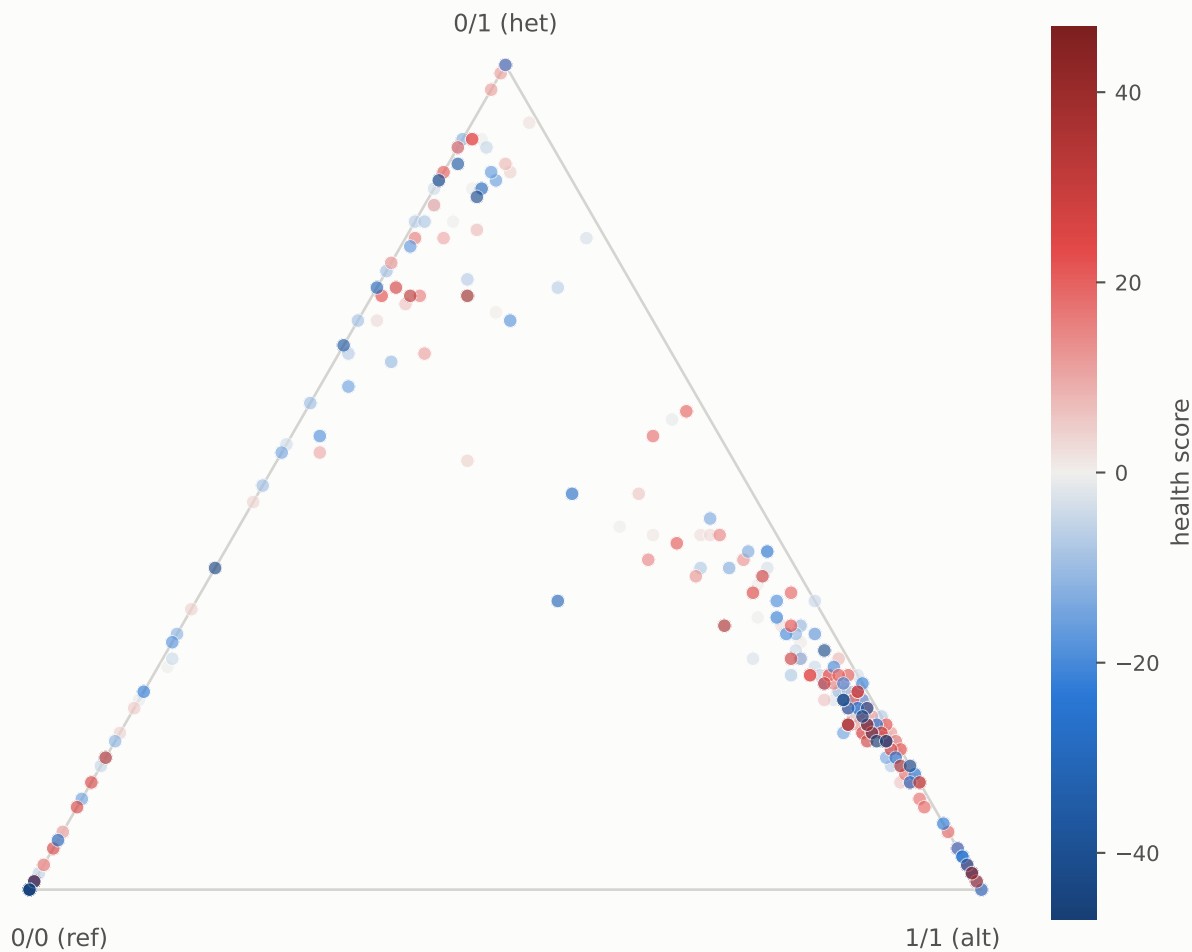
#135 by genotype uncertainty CHR_09:1,017,085 A>G
AF=0.52 DR2=0.81 $r=+0.013$ $\bar{H}=0.384$ F=0.9



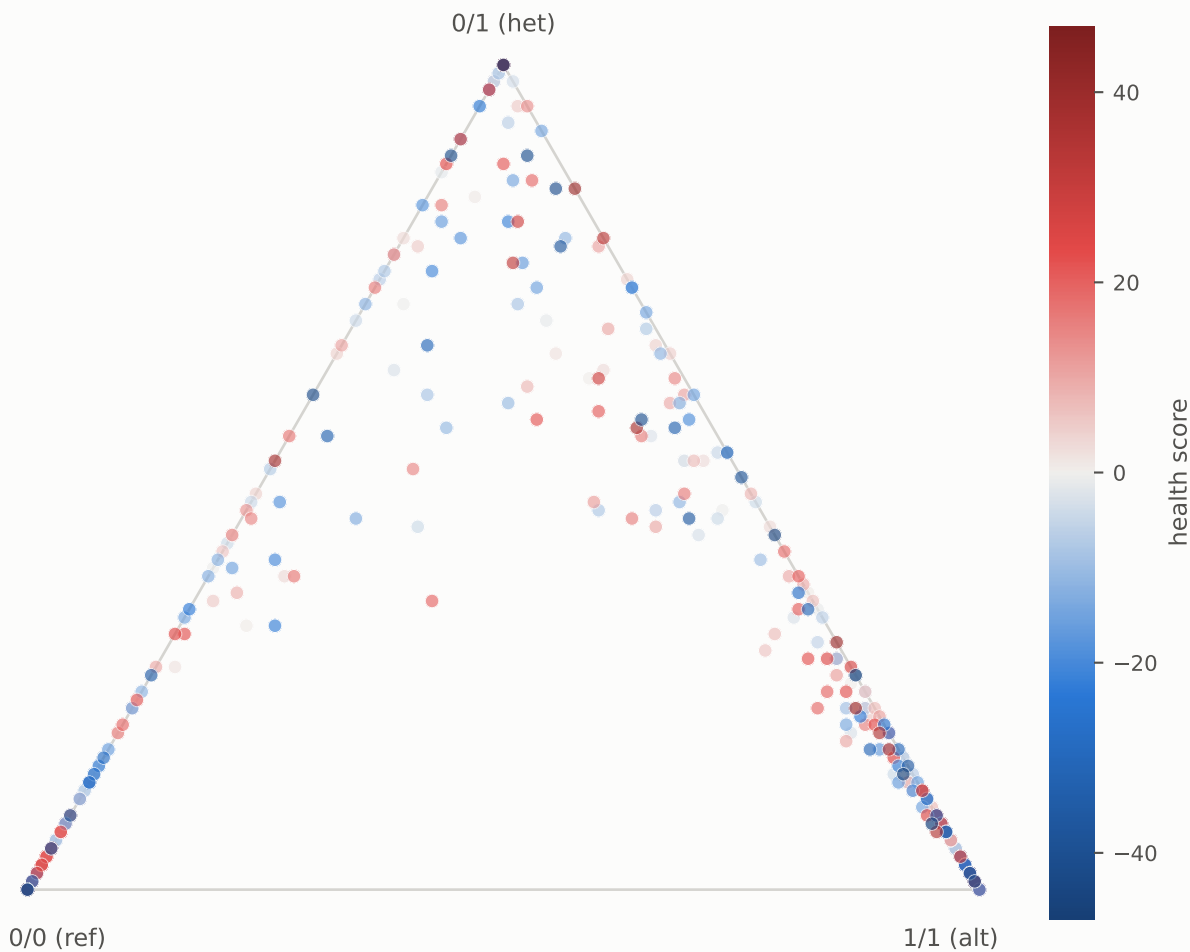
#136 by genotype uncertainty CHR_22:15,423,170 C>T
AF=0.58 DR2=0.81 $r=+0.011$ $\bar{H}=0.384$ $F=0.4$



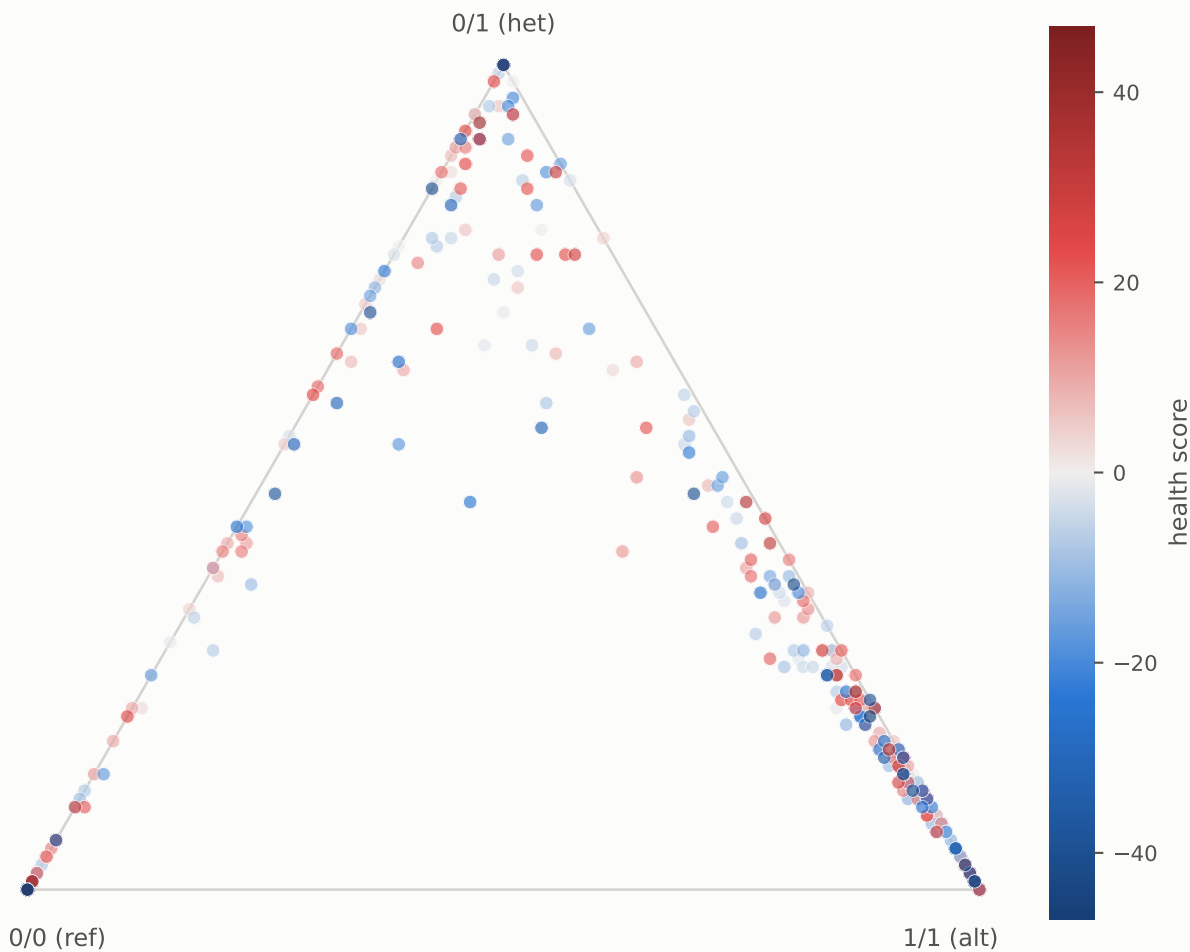
#137 by genotype uncertainty CHR_01:3,253,977 G>A
AF=0.47 DR2=0.81 $r=+0.018$ $\bar{H}=0.384$ F=0.1



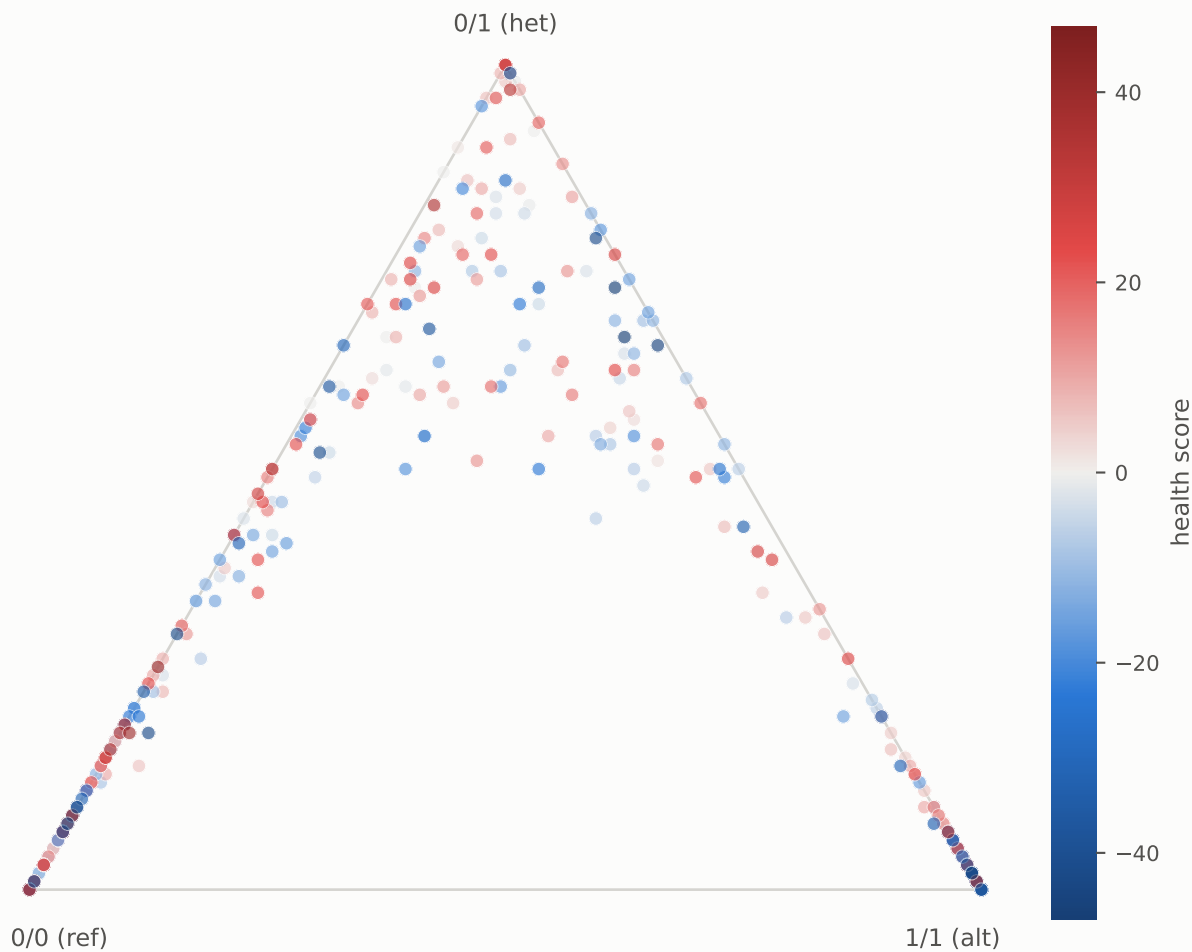
#138 by genotype uncertainty CHR_10:28,626,291 T>C
AF=0.51 DR2=0.81 $r=-0.041$ $\bar{H}=0.384$ F=1.0



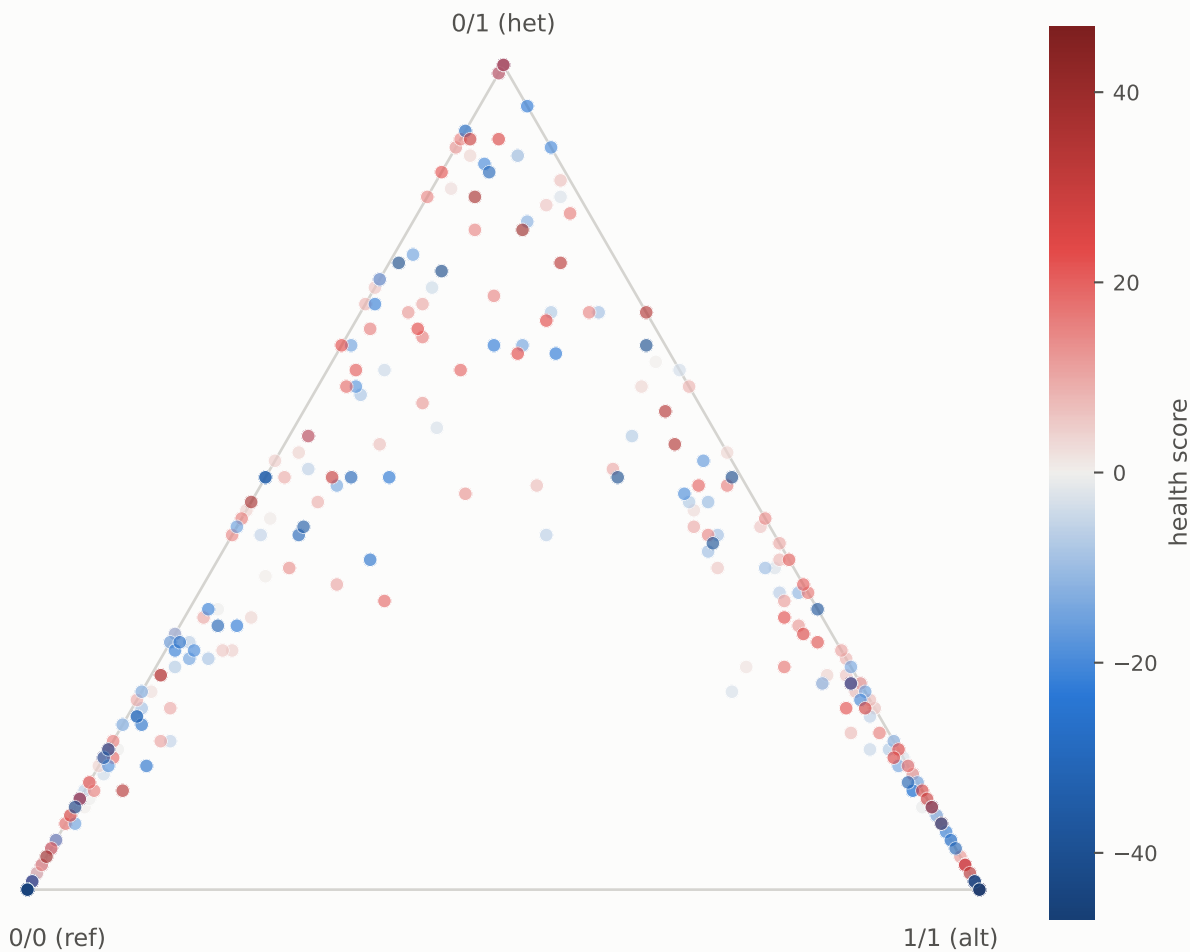
#139 by genotype uncertainty CHR_13:22,747,602 T>C
AF=0.51 DR2=0.81 r=-0.007 $\bar{H}$ =0.384 F=0.3



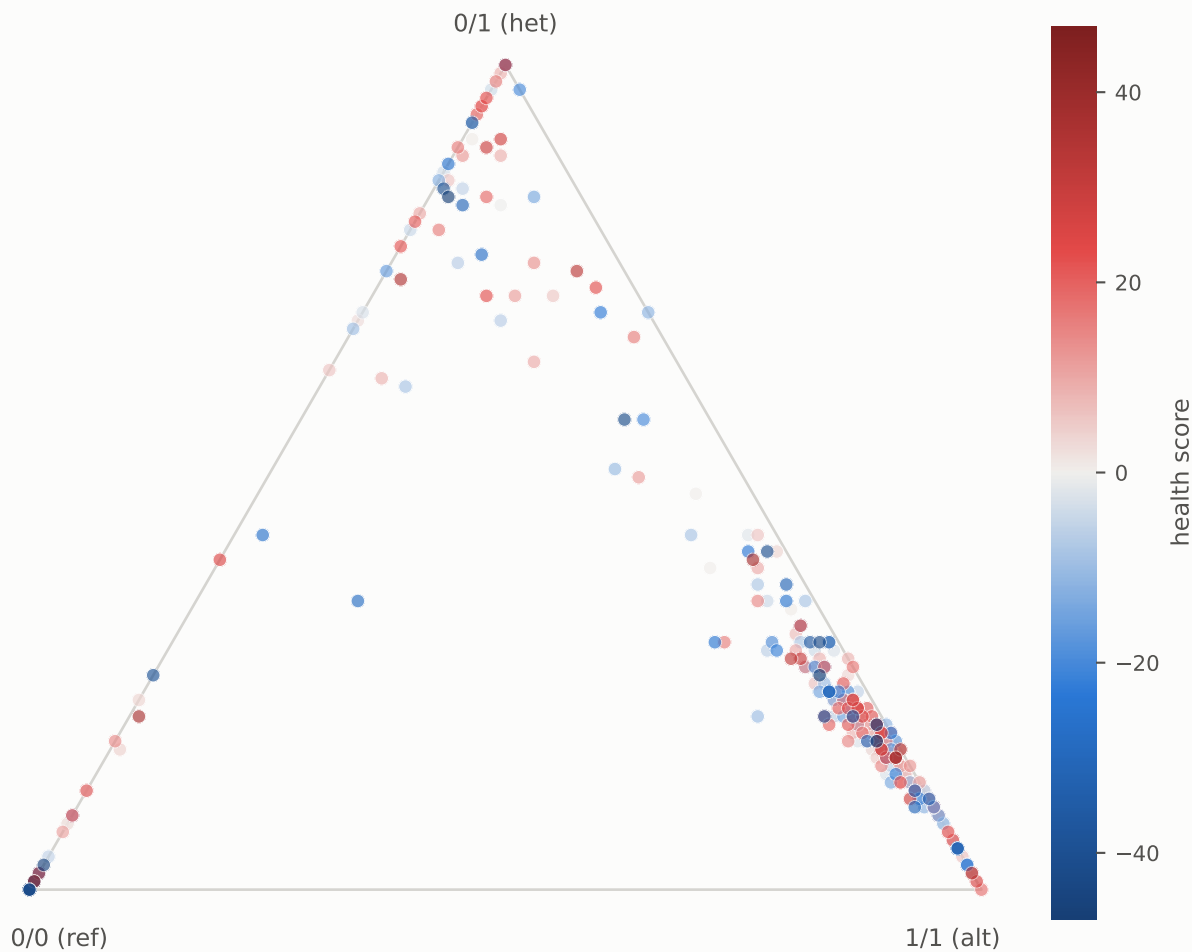
#140 by genotype uncertainty CHR_04:244,756 A>C
AF=0.51 DR2=0.81 $r=-0.099$ H=0.384 F=1.4



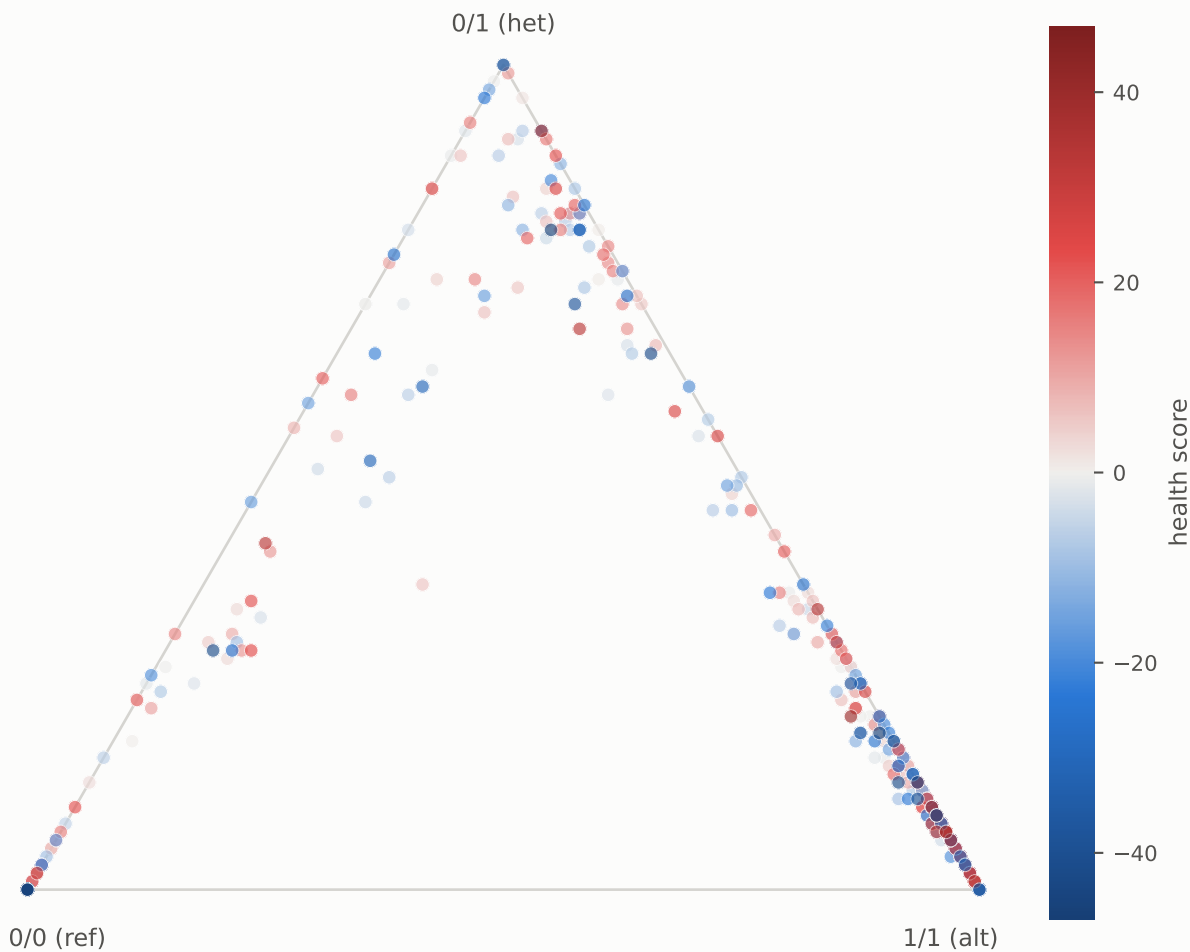
#141 by genotype uncertainty CHR_15:25,686,908 A>T
AF=0.48 DR2=0.81 $r=-0.024$ $\bar{H}=0.384$ F=0.1



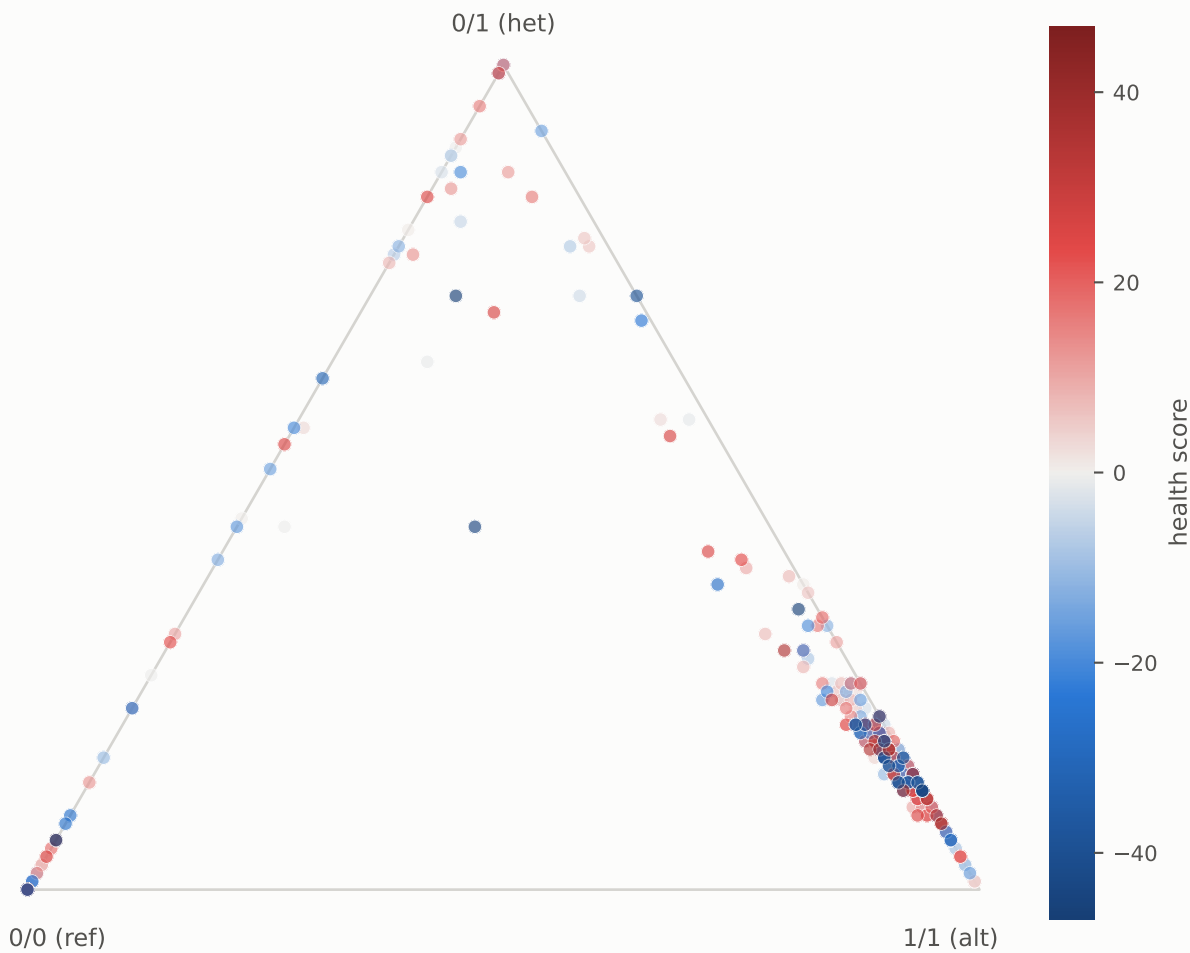
#142 by genotype uncertainty CHR_07:13,331,262 C>G
AF=0.51 DR2=0.82 $r=+0.067$ $\bar{H}=0.384$ F=1.1



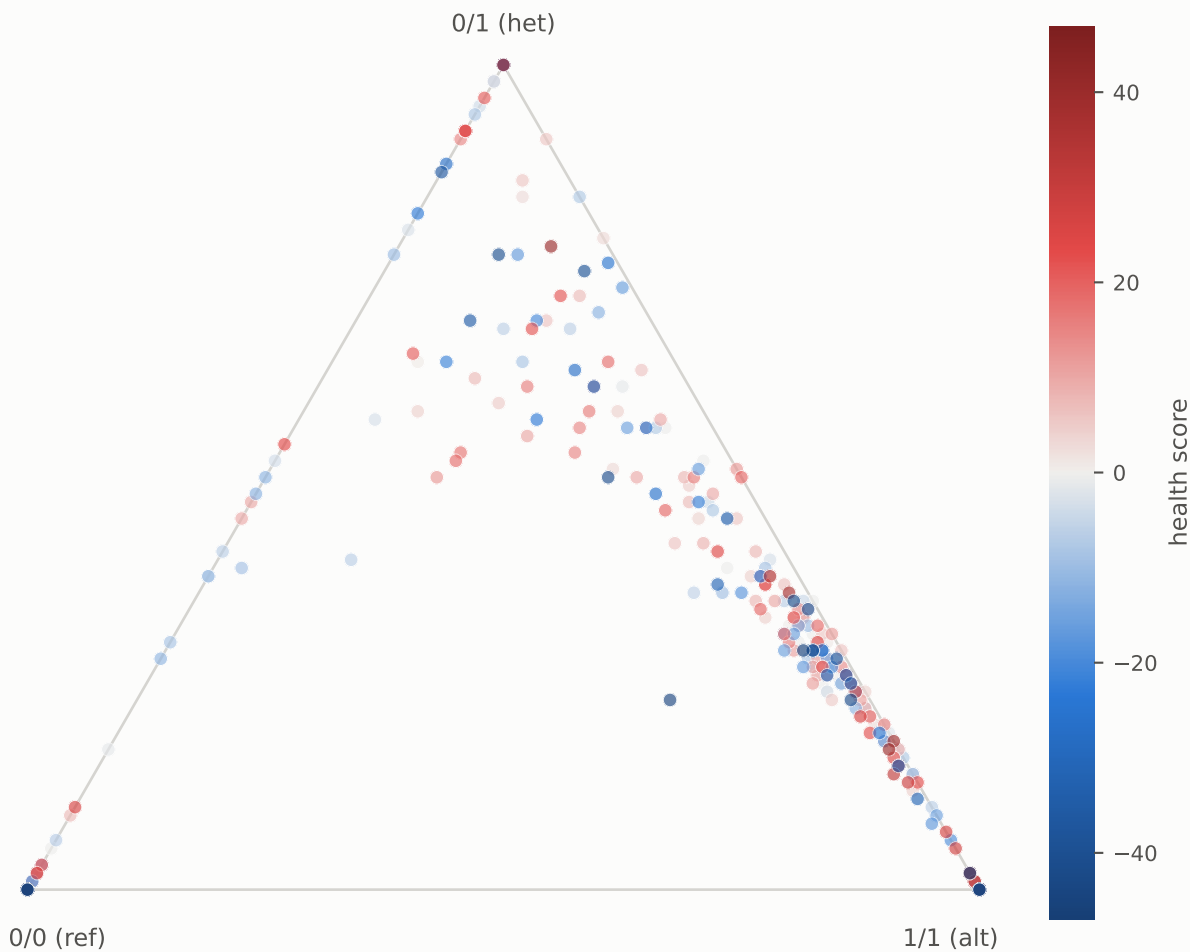
#143 by genotype uncertainty CHR_04:17,150,160 G>T
AF=0.65 DR2=0.81 $r=+0.002$ $\bar{H}=0.384$ F=0.5



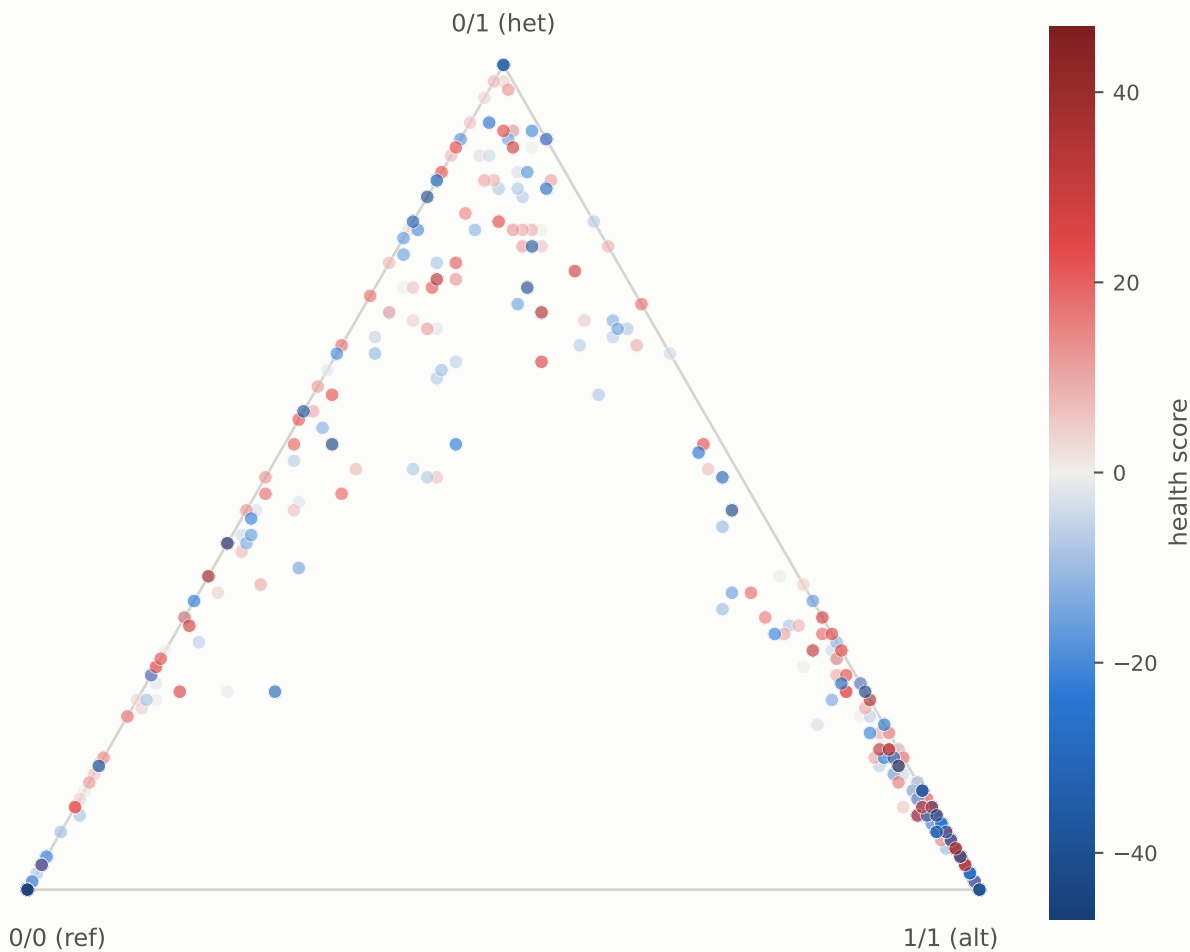
#144 by genotype uncertainty CHR_19:9,139,367 A>C
AF=0.65 DR2=0.81 $r=+0.029$ $\bar{H}=0.384$ F=0.4



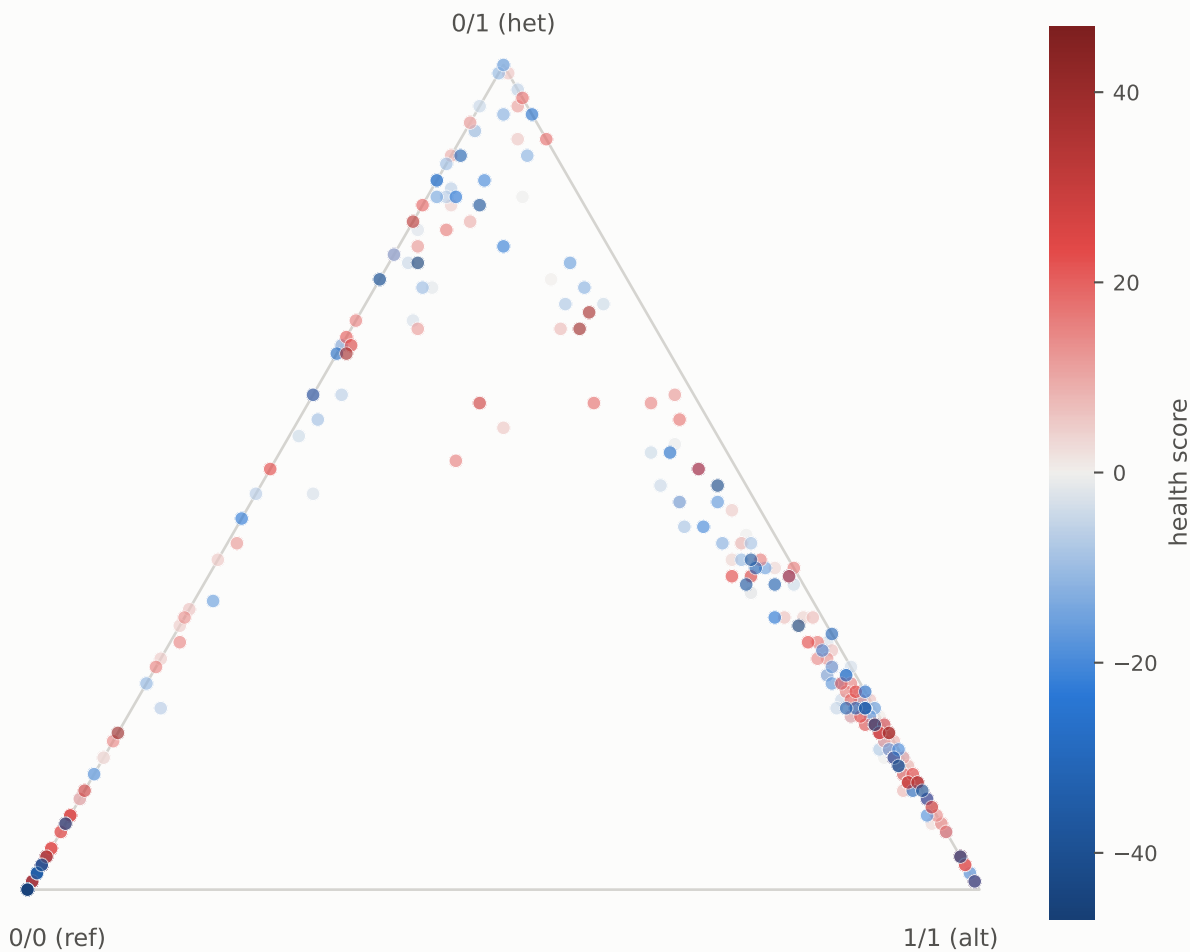
#145 by genotype uncertainty CHR_15:19,383,838 A>C
AF=0.51 DR2=0.81 $r=+0.016$ $\bar{H}=0.384$ F=0.1



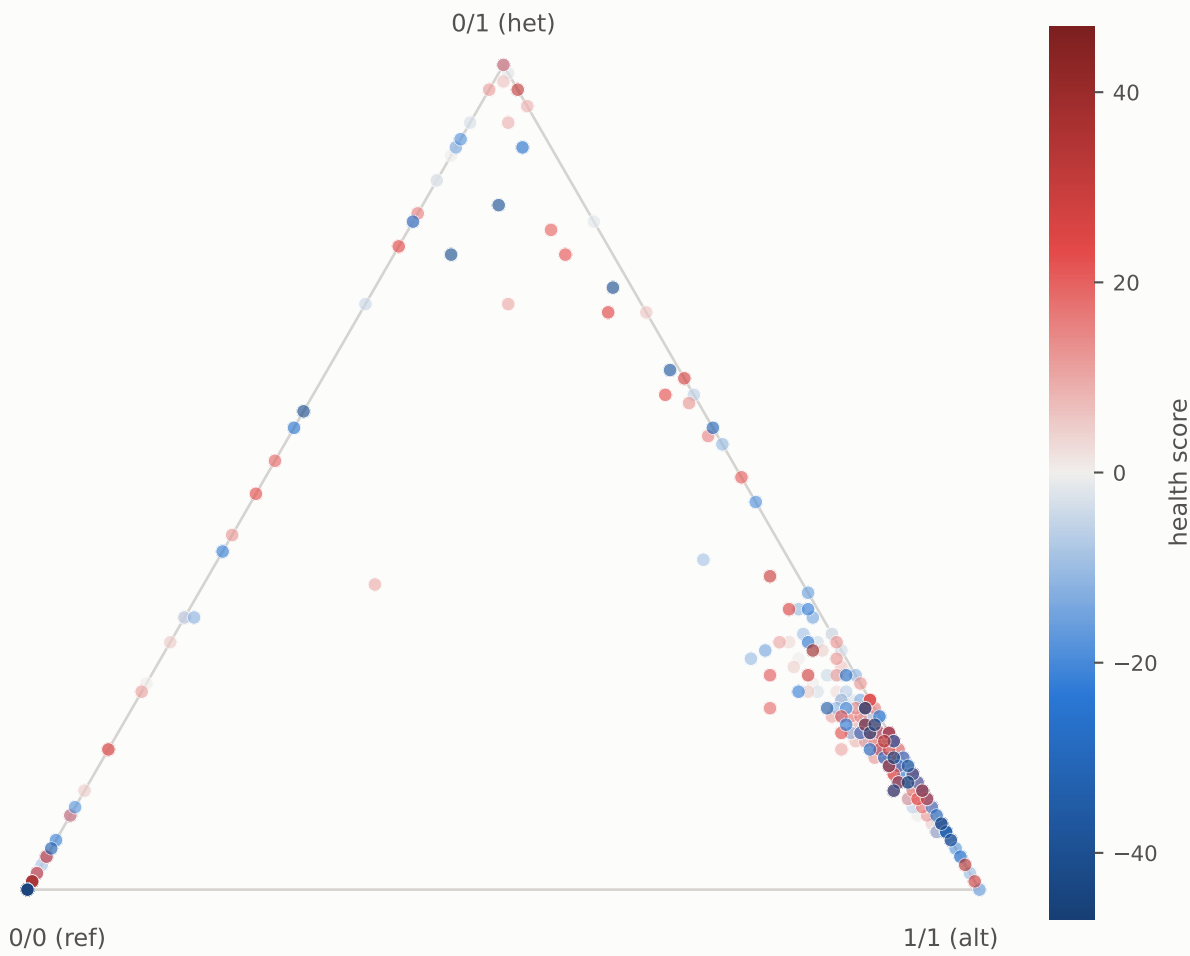
#146 by genotype uncertainty CHR_18:12,273,861 A>T
AF=0.51 DR2=0.81 r=-0.008 $\bar{H}$ =0.384 F=0.3



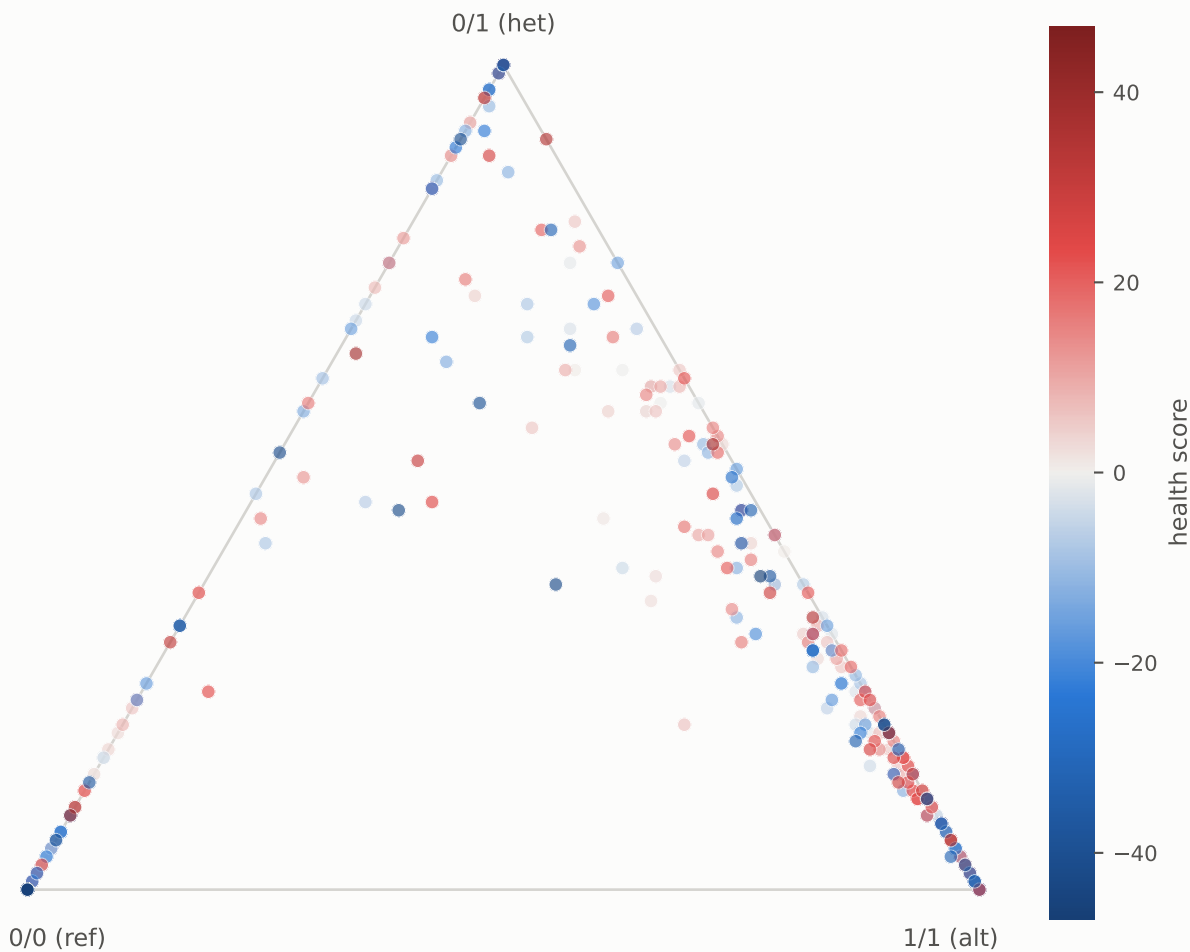
#147 by genotype uncertainty CHR_01:43,554,159 T>C
AF=0.47 DR2=0.82 $r=+0.028$ $\bar{H}=0.384$ F=0.4



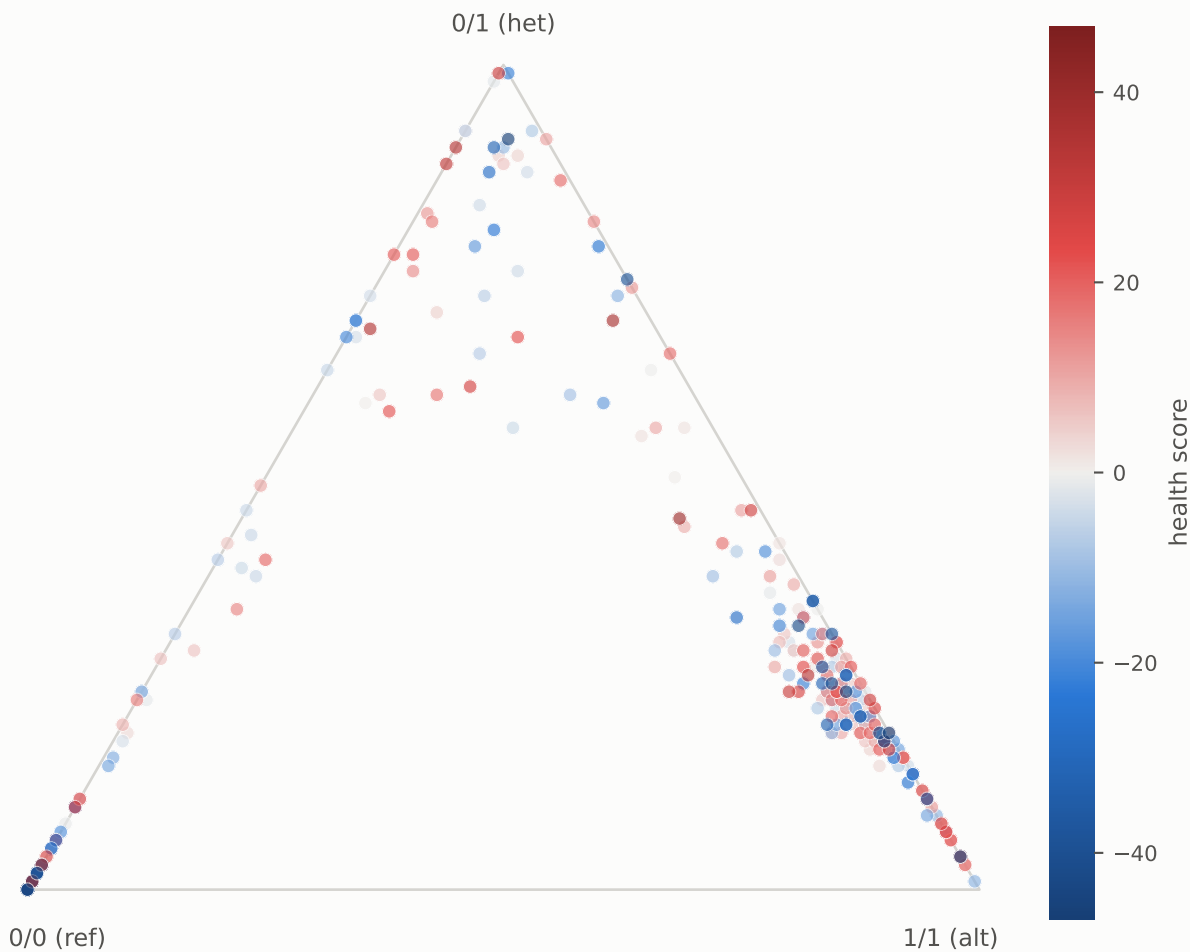
#148 by genotype uncertainty CHR_03:4,506,172 C>T
AF=0.62 DR2=0.82 $r=-0.003$ H=0.384 F=0.1



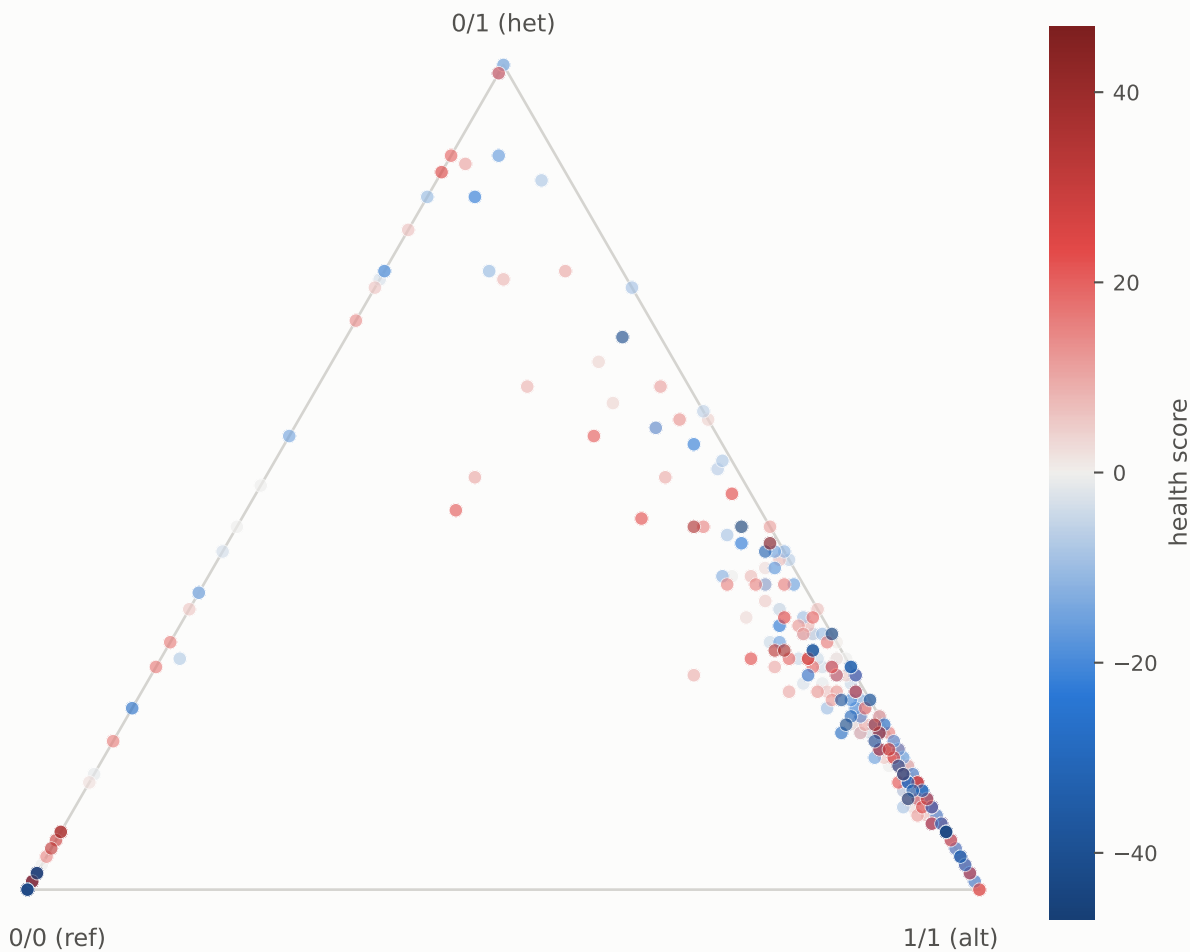
#149 by genotype uncertainty CHR_16:13,314,171 G>T
AF=0.55 DR2=0.81 $r=+0.031$ $\bar{H}=0.384$ F=0.1



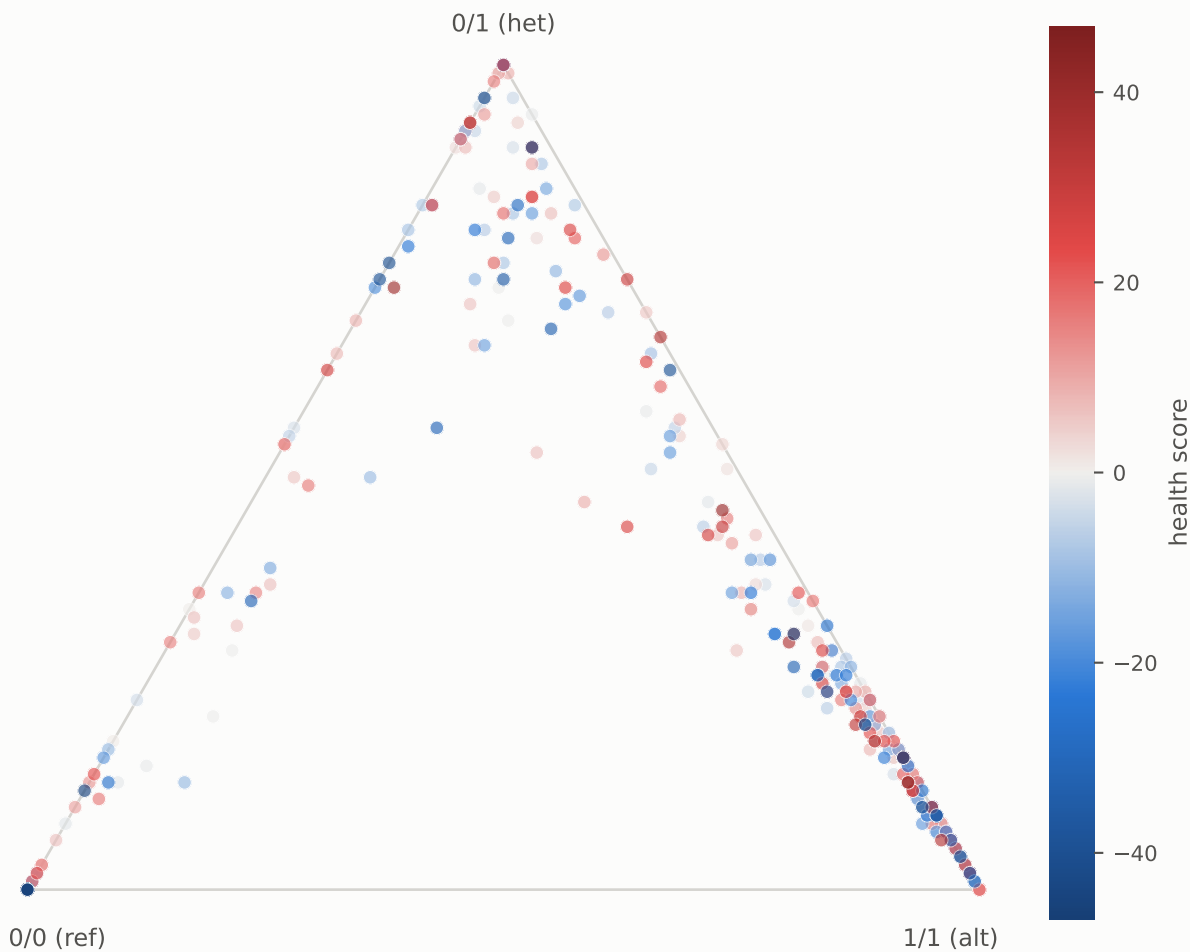
#150 by genotype uncertainty CHR_09:33,148,314 A>C
AF=0.47 DR2=0.81 $r=+0.015$ $\bar{H}=0.383$ F=0.2



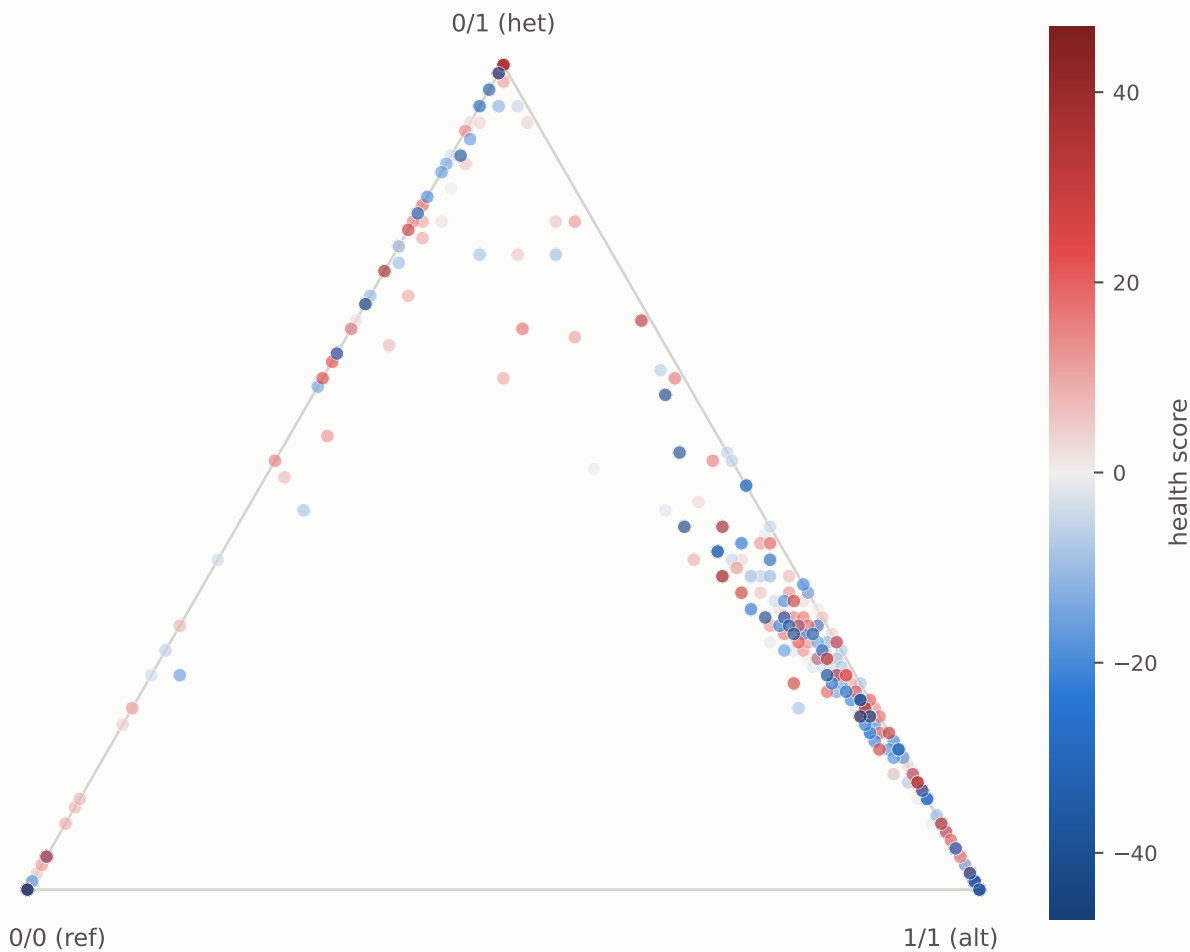
#151 by genotype uncertainty CHR_19:718,190 A>T
AF=0.55 DR2=0.82 $r=-0.087$ H=0.383 F=1.4



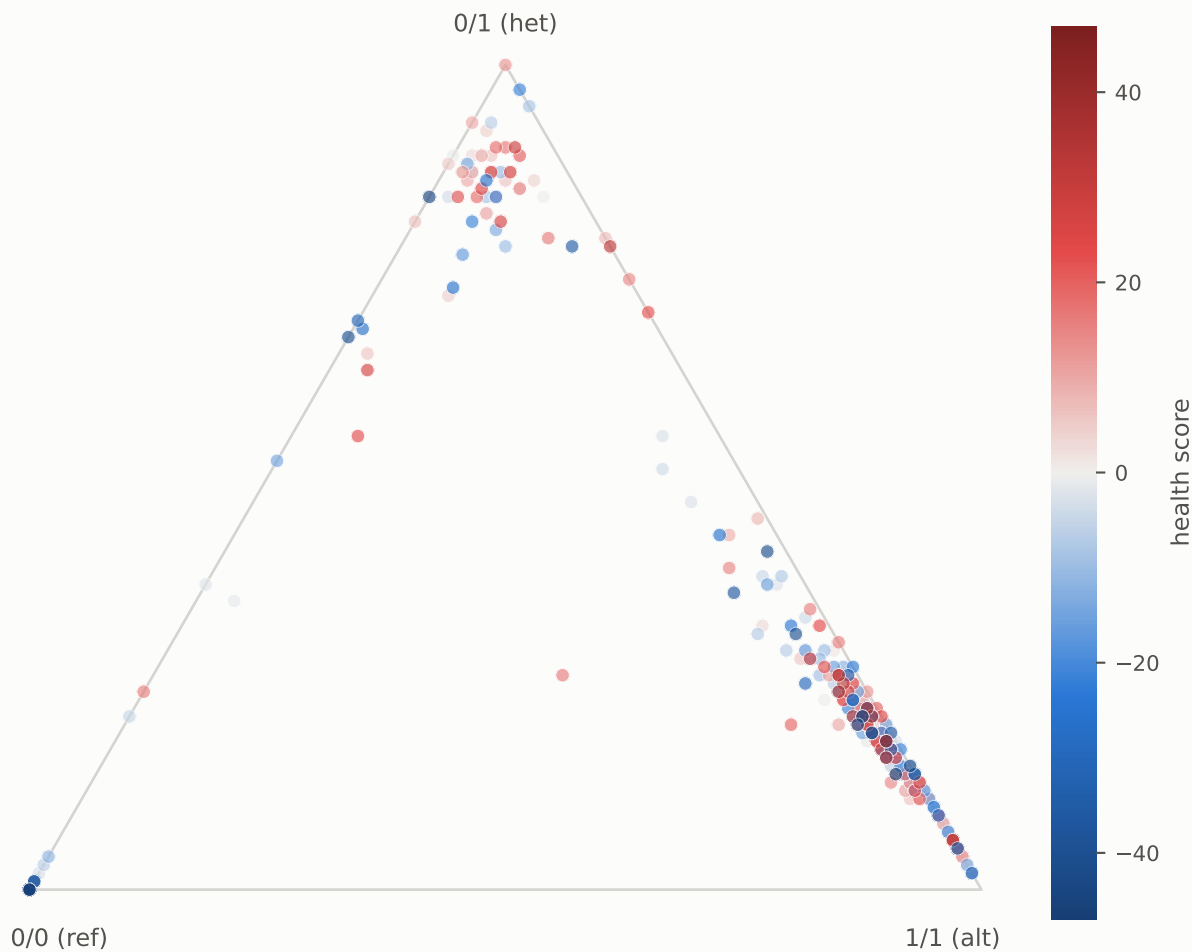
#152 by genotype uncertainty CHR_01:51,545,915 A>C
AF=0.52 DR2=0.81 $r=-0.001$ $\bar{H}=0.383$ F=0.0



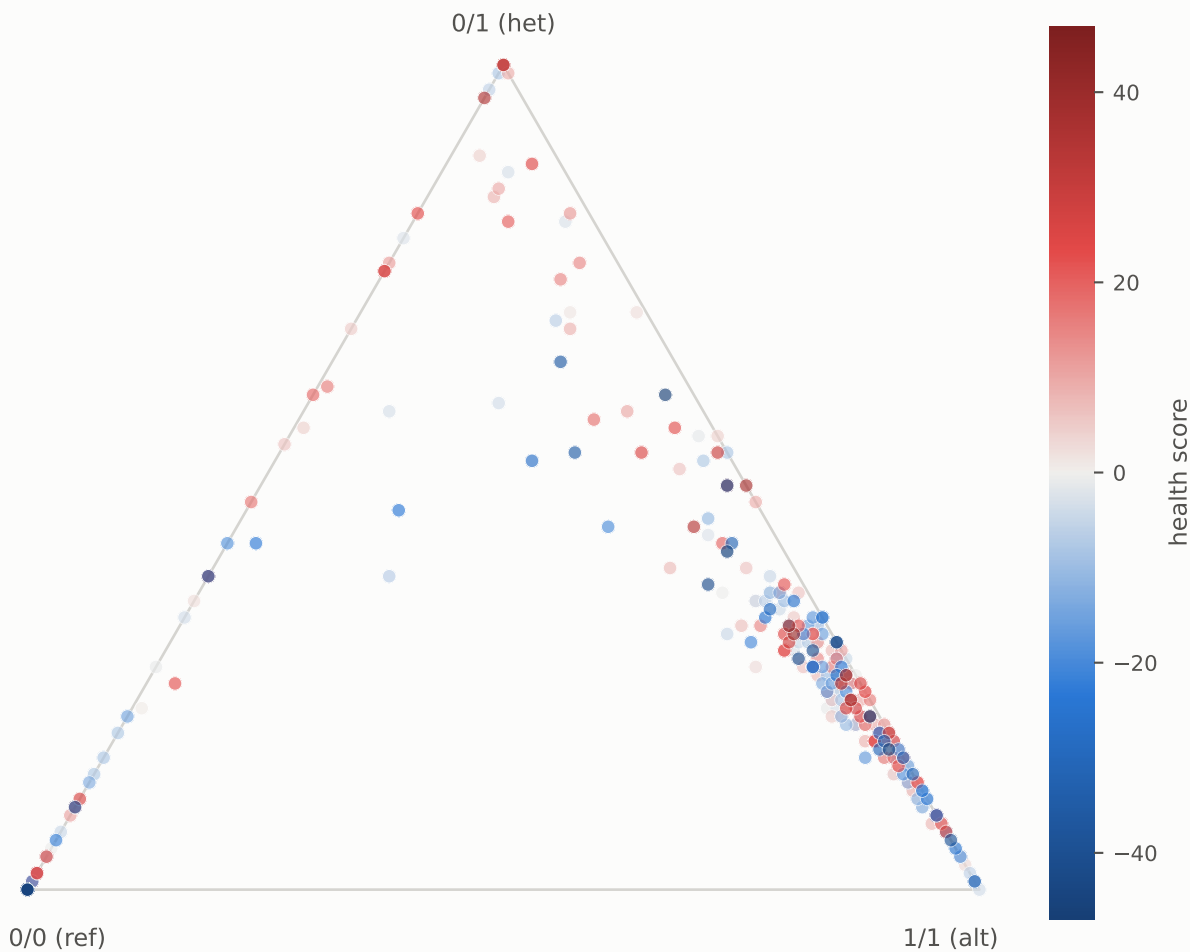
#153 by genotype uncertainty CHR_09:24,824,042 A>G
AF=0.55 DR2=0.81 $r=-0.075$ $\bar{H}=0.383$ F=1.4



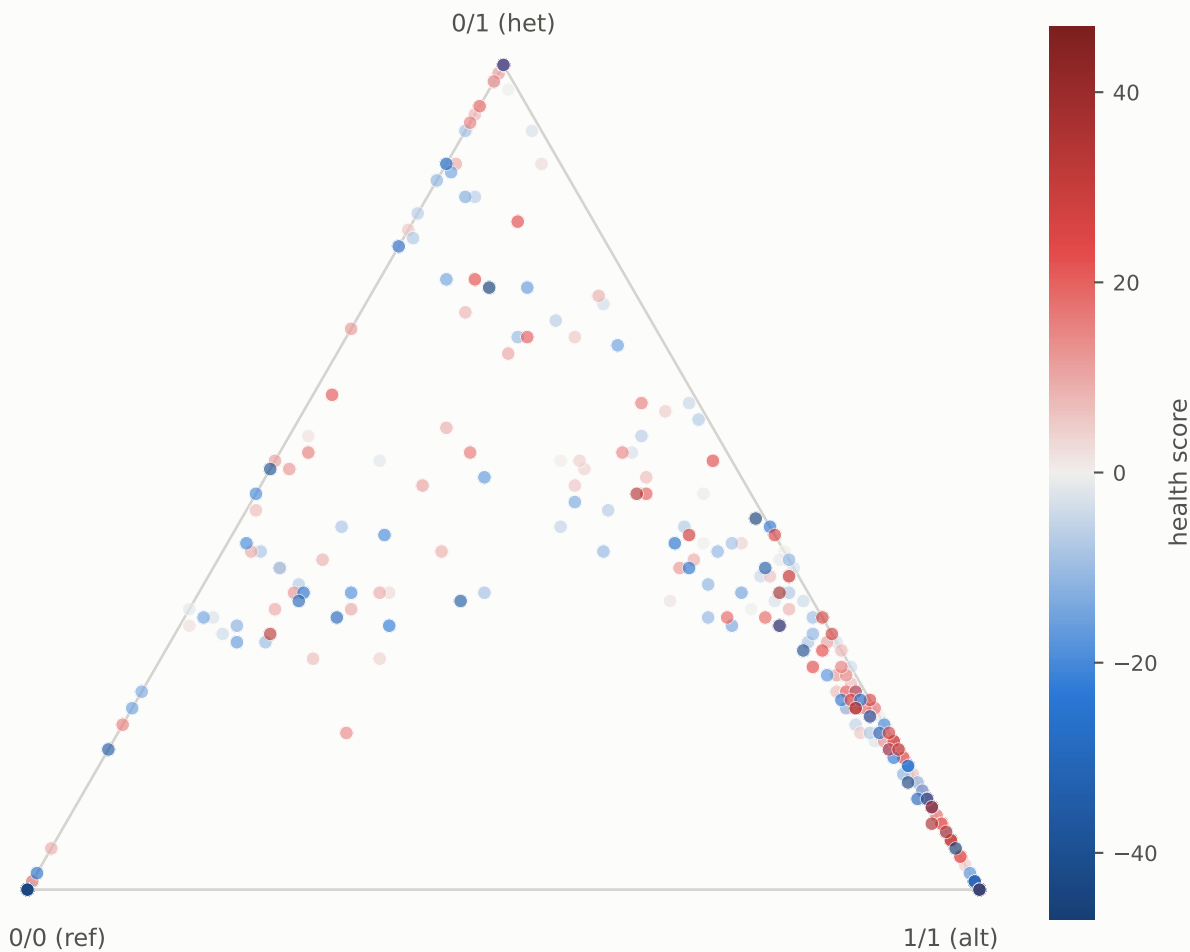
#154 by genotype uncertainty CHR_17:16,506,024 A>G
AF=0.59 DR2=0.81 $r=+0.057$ $\bar{H}=0.383$ F=1.1



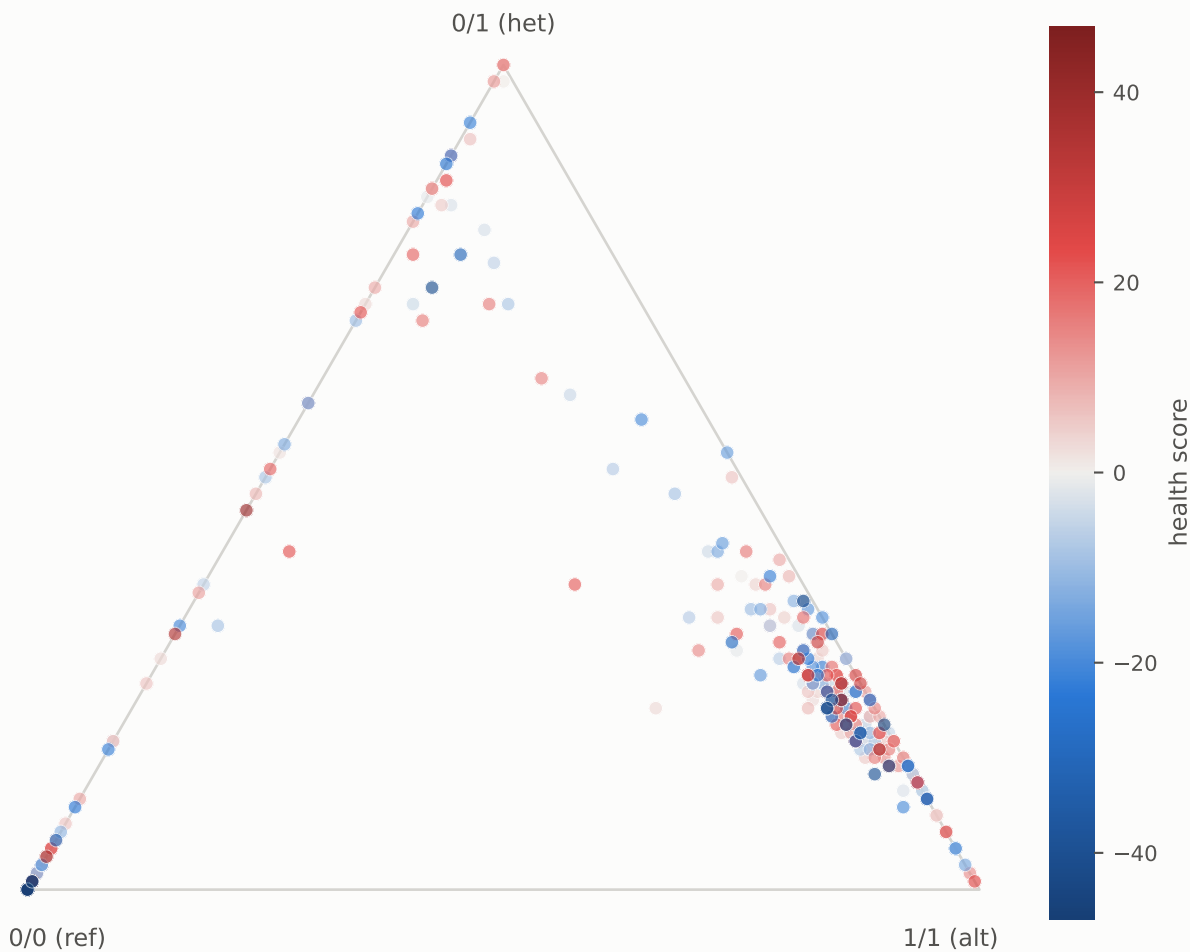
#155 by genotype uncertainty CHR_17:18,674,393 C>T
AF=0.48 DR2=0.81 $r=+0.007$ $\bar{H}=0.383$ F=1.9



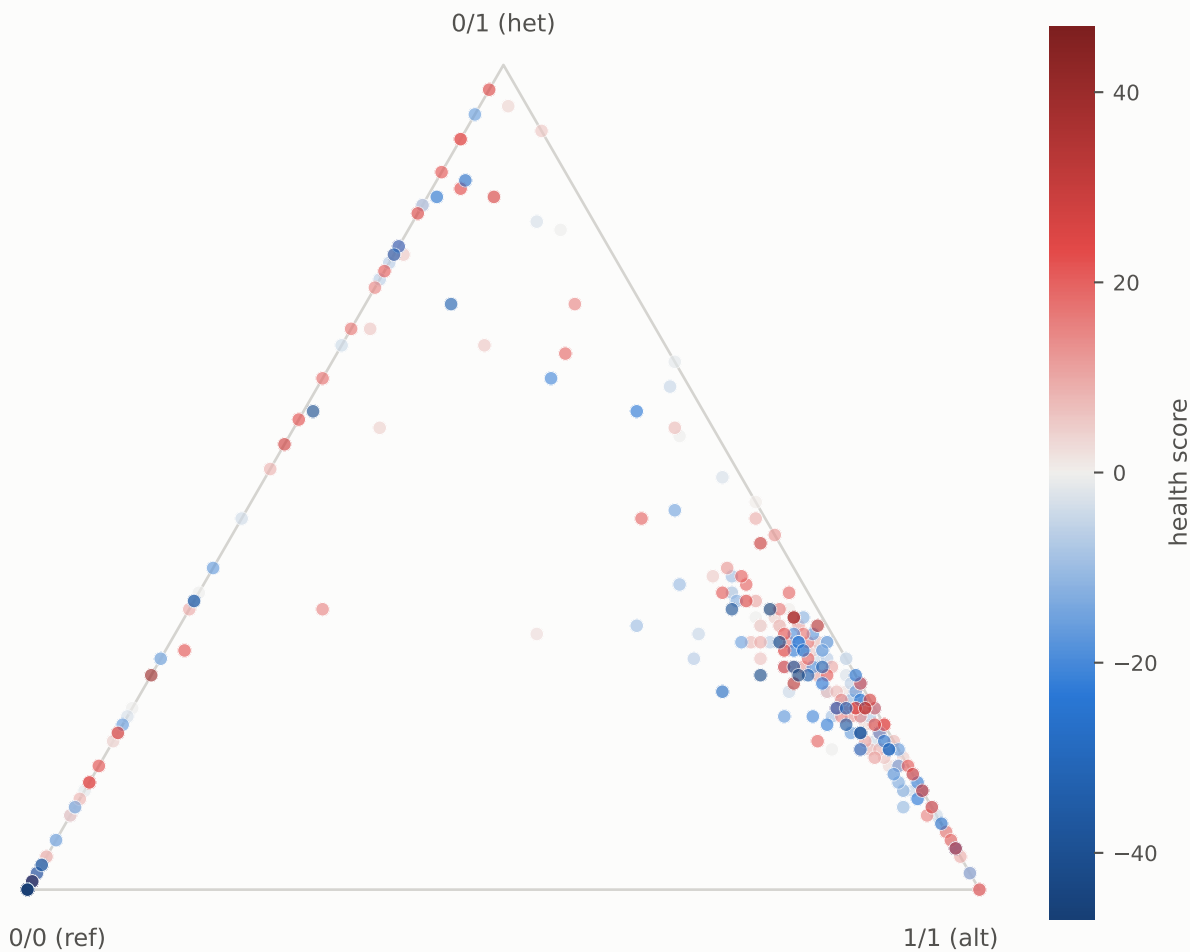
#156 by genotype uncertainty CHR_13:27,862,867 G>C
AF=0.48 DR2=0.82 $r=+0.021$ $\bar{H}=0.383$ F=0.5



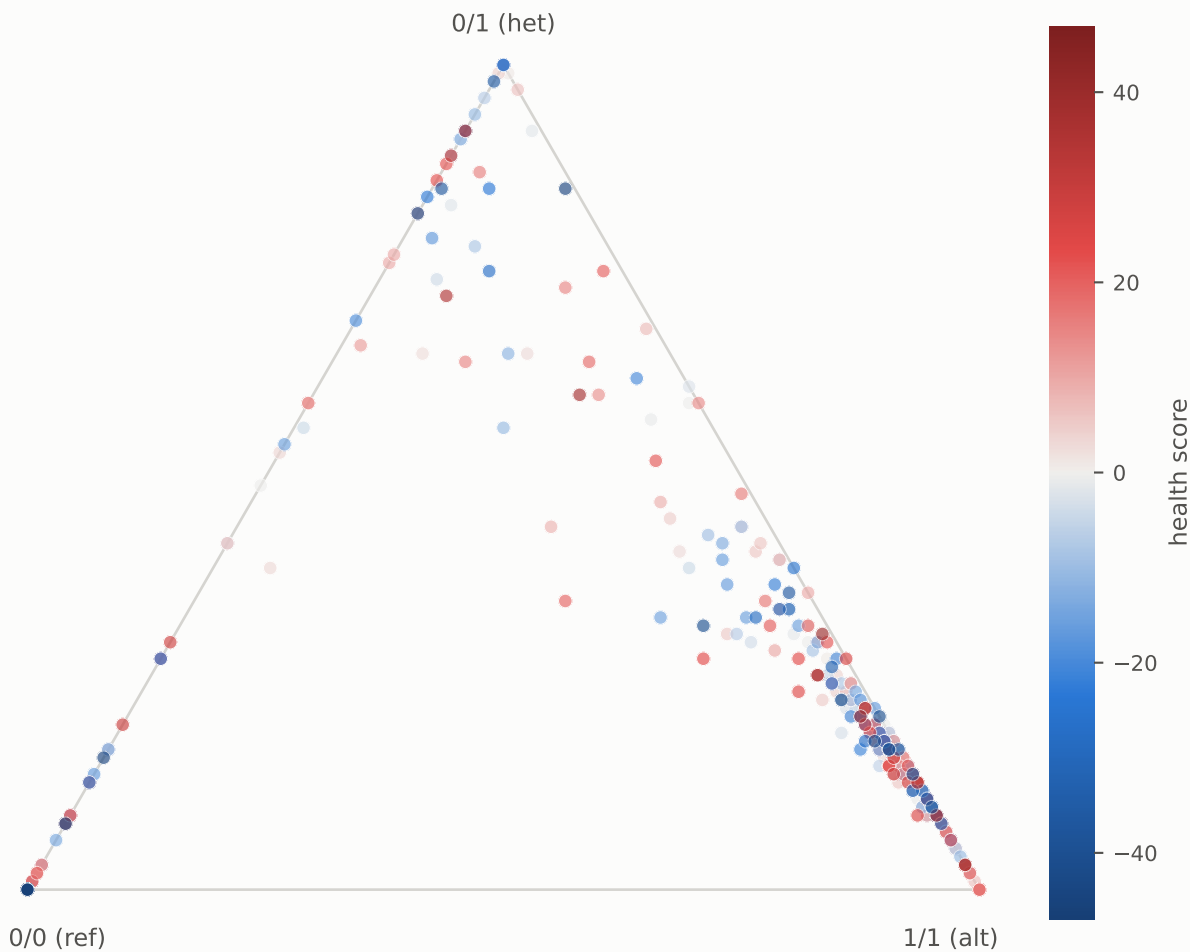
#157 by genotype uncertainty CHR_12:12,457,297 C>T
AF=0.44 DR2=0.81 $r=+0.039$ $\bar{H}=0.383$ F=0.3



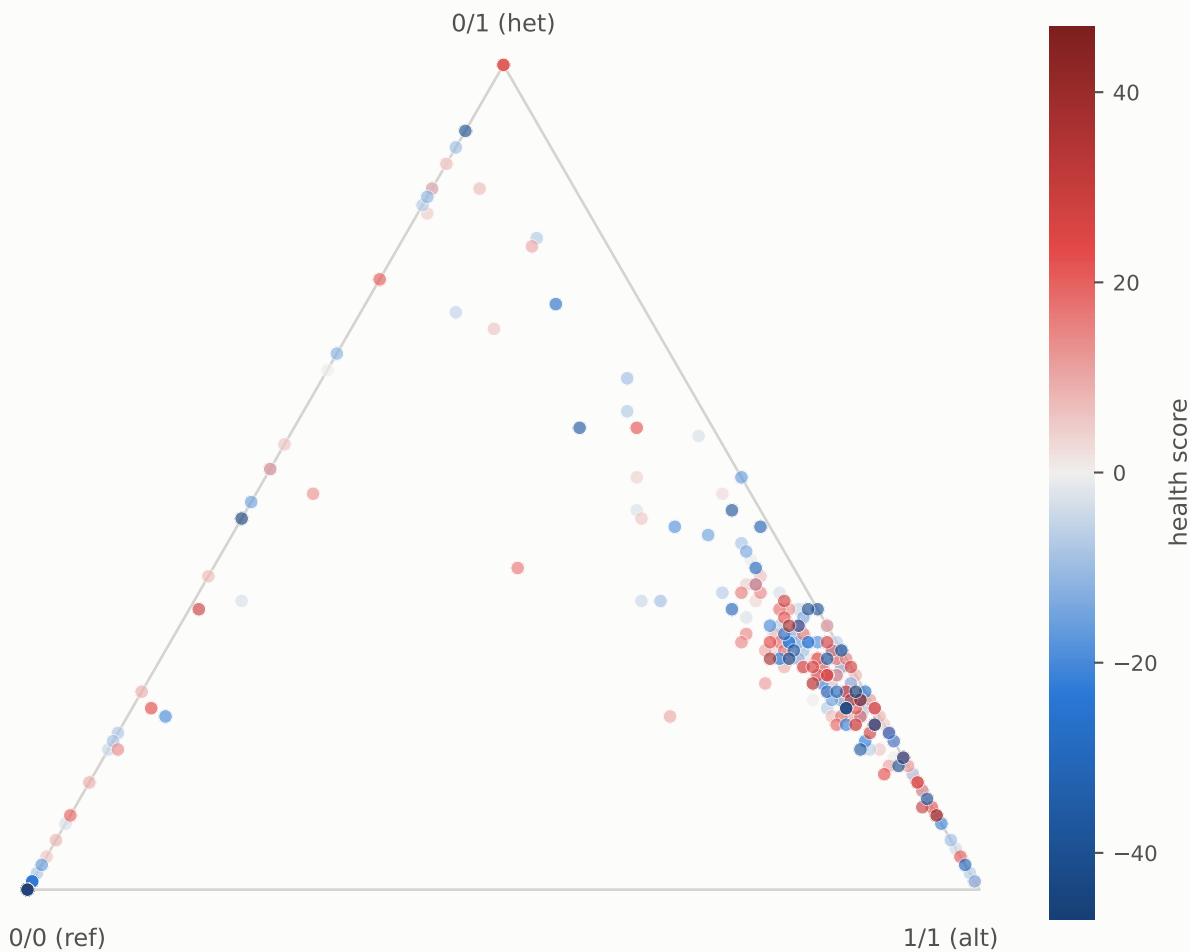
#158 by genotype uncertainty CHR_06:35,231,983 A>G
AF=0.43 DR2=0.81 $r=-0.005$ $\bar{H}=0.383$ F=0.6



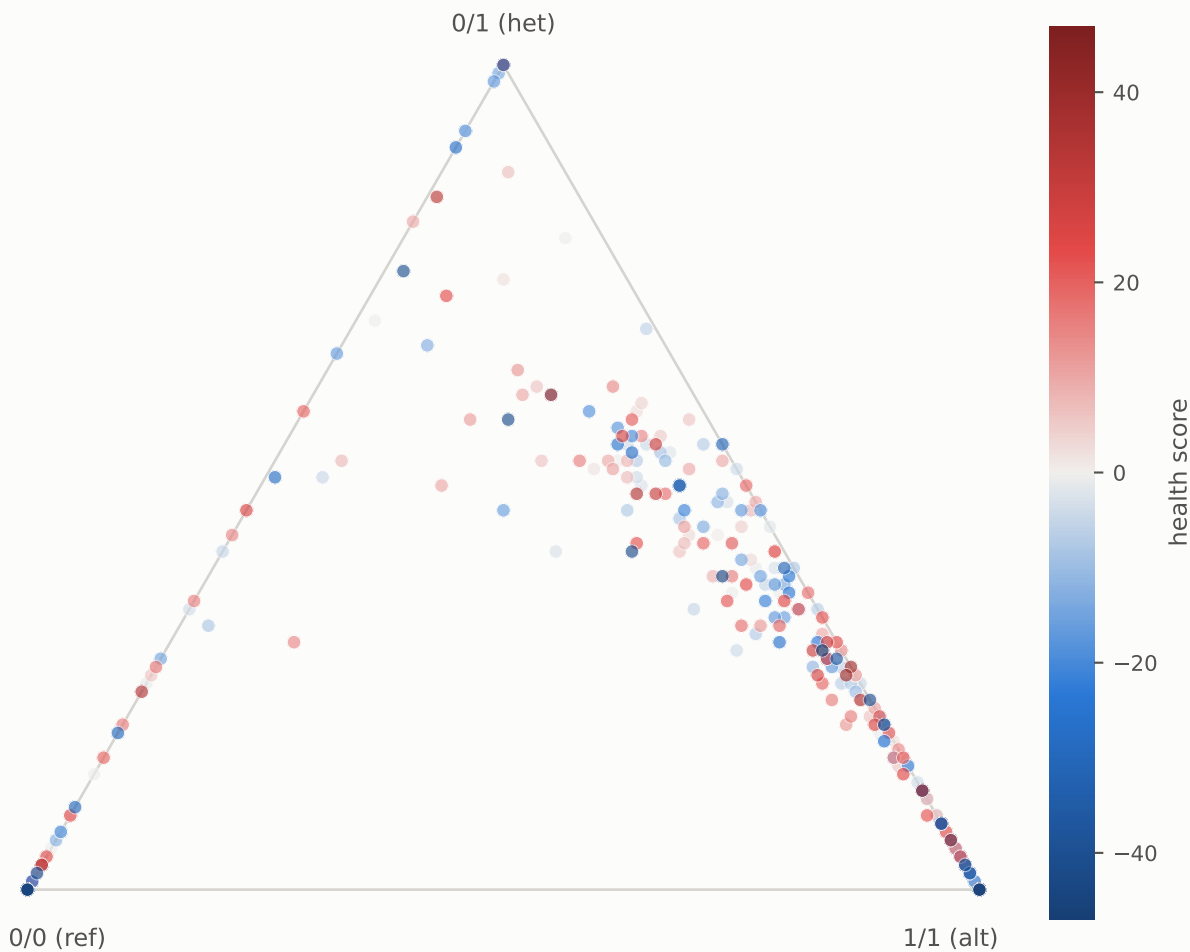
#159 by genotype uncertainty CHR_17:28,539,925 A>C
AF=0.54 DR2=0.82 $r=+0.042$ $\bar{H}=0.383$ $F=0.2$



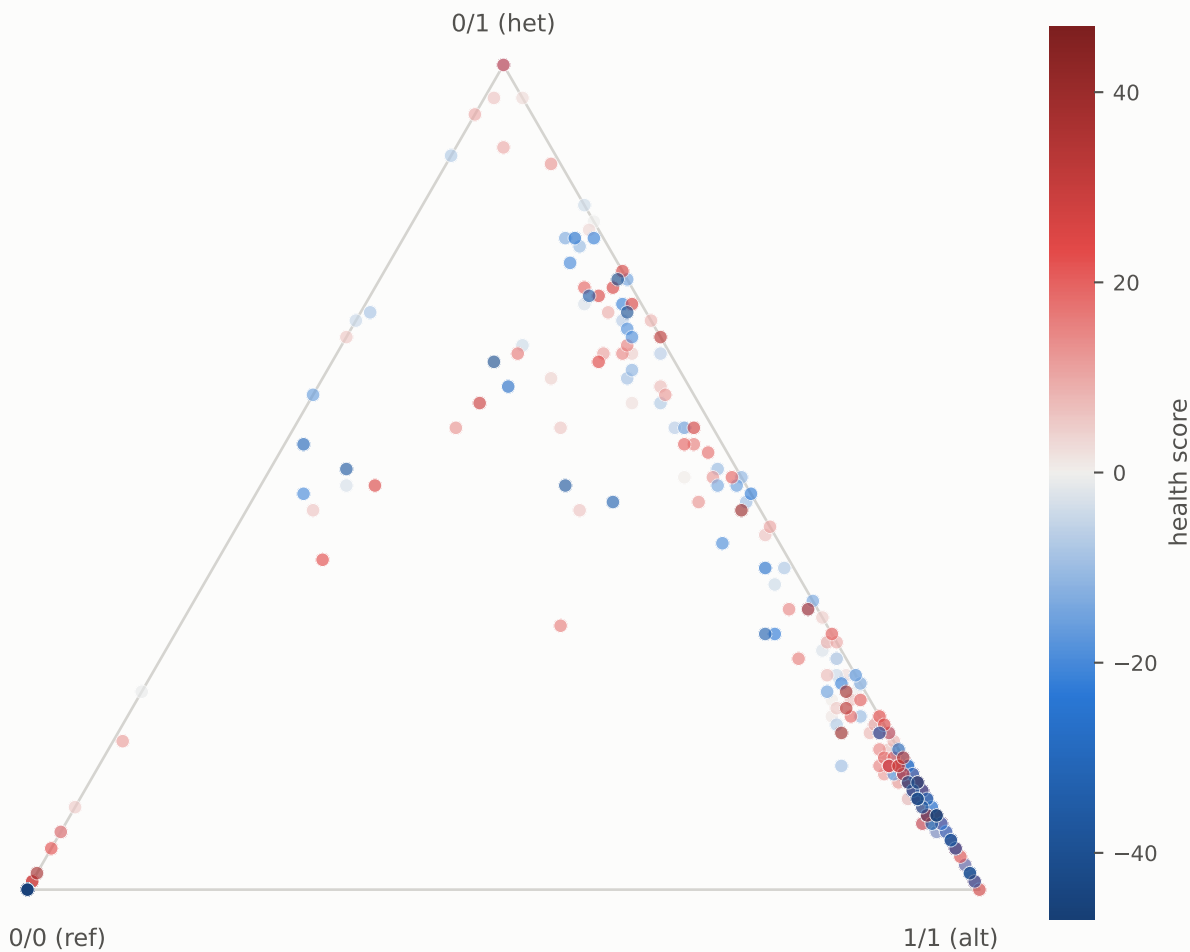
#160 by genotype uncertainty CHR_18:5,967,962 T>C
AF=0.45 DR2=0.81 r=-0.025 H=0.383 F=0.1



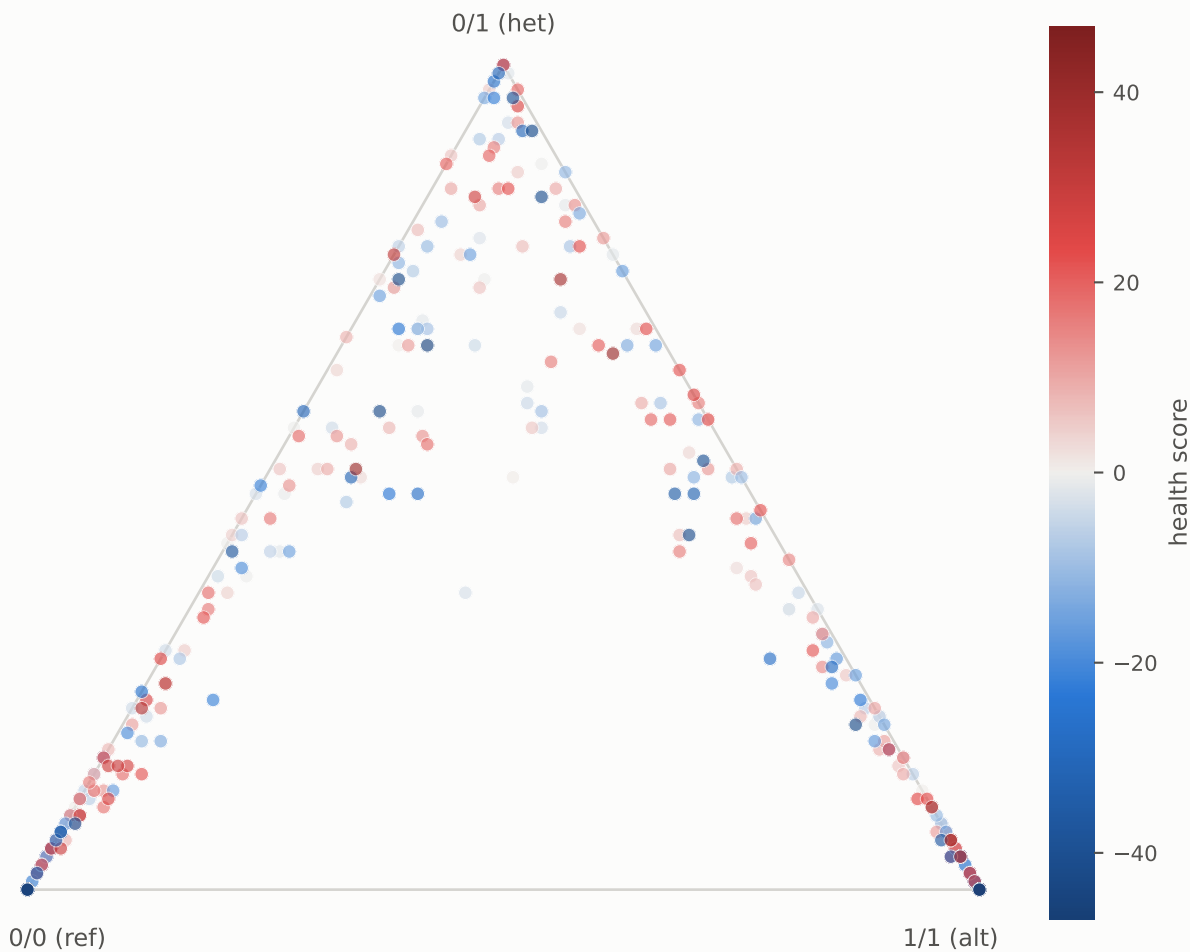
#161 by genotype uncertainty CHR_17:18,712,687 A>T
AF=0.52 DR2=0.81 $r=+0.020$ $\bar{H}=0.383$ F=0.2



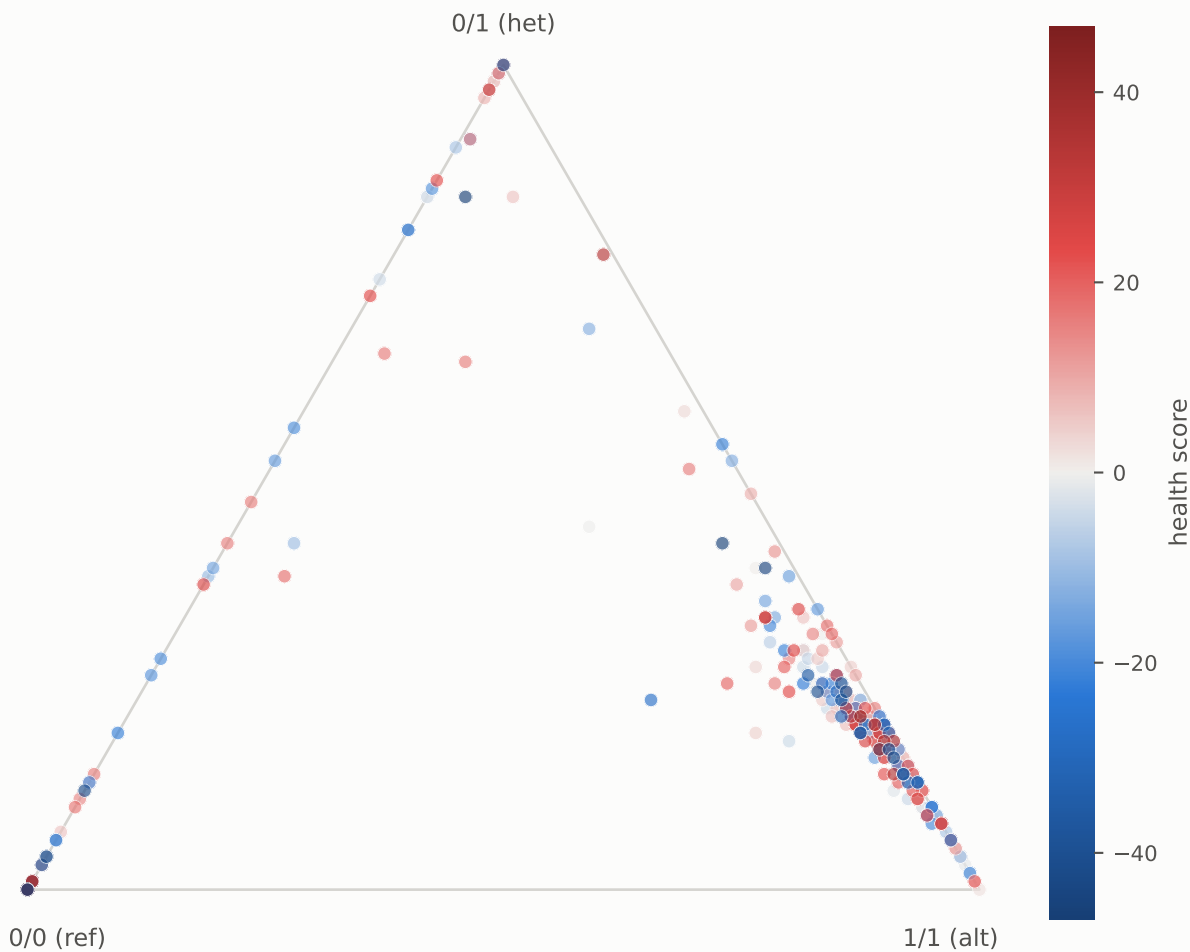
#162 by genotype uncertainty CHR_22:6,638,503 C>T
AF=0.63 DR2=0.81 $r=-0.034$ H=0.383 F=0.5



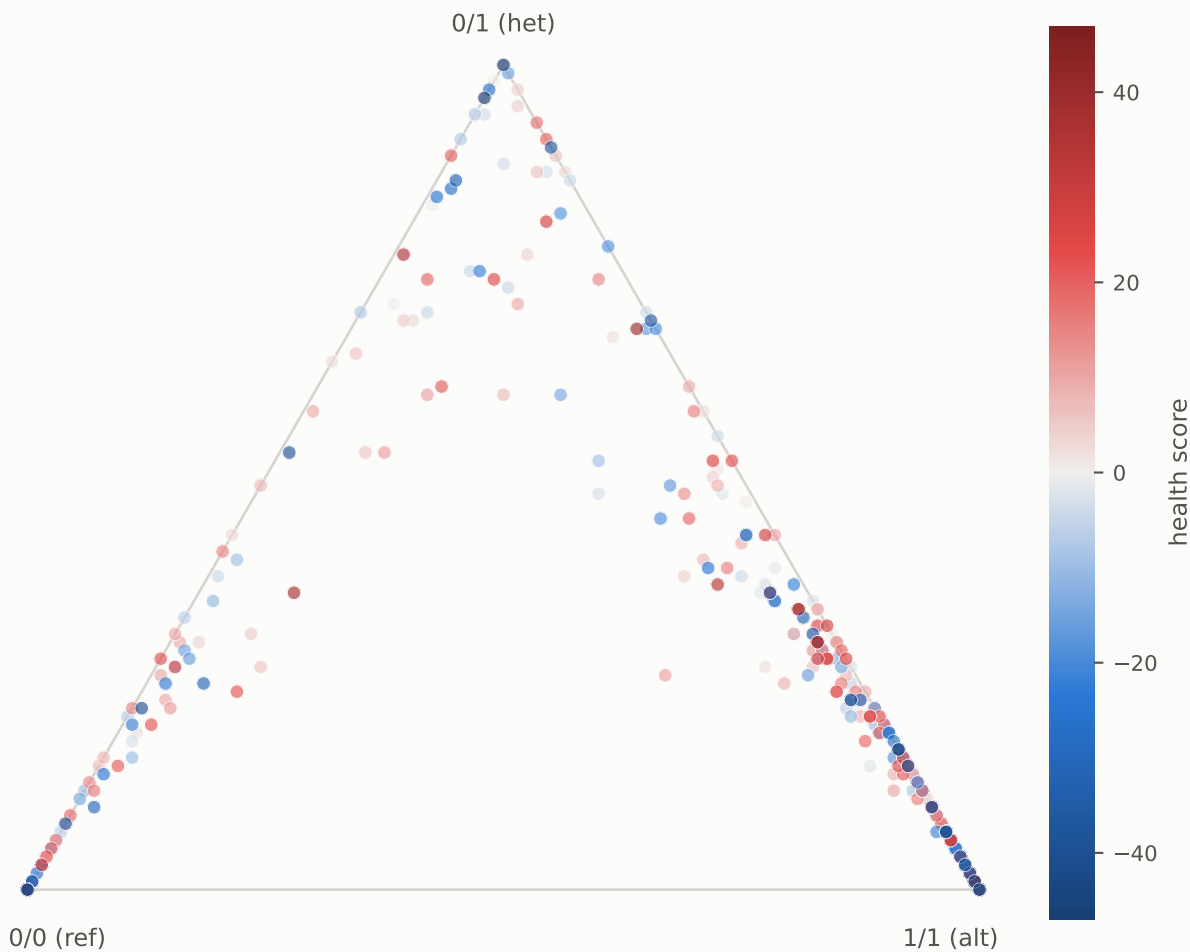
#163 by genotype uncertainty CHR_15:26,905,864 G>A
AF=0.51 DR2=0.81 $r=+0.013$ $\bar{H}=0.383$ F=0.0



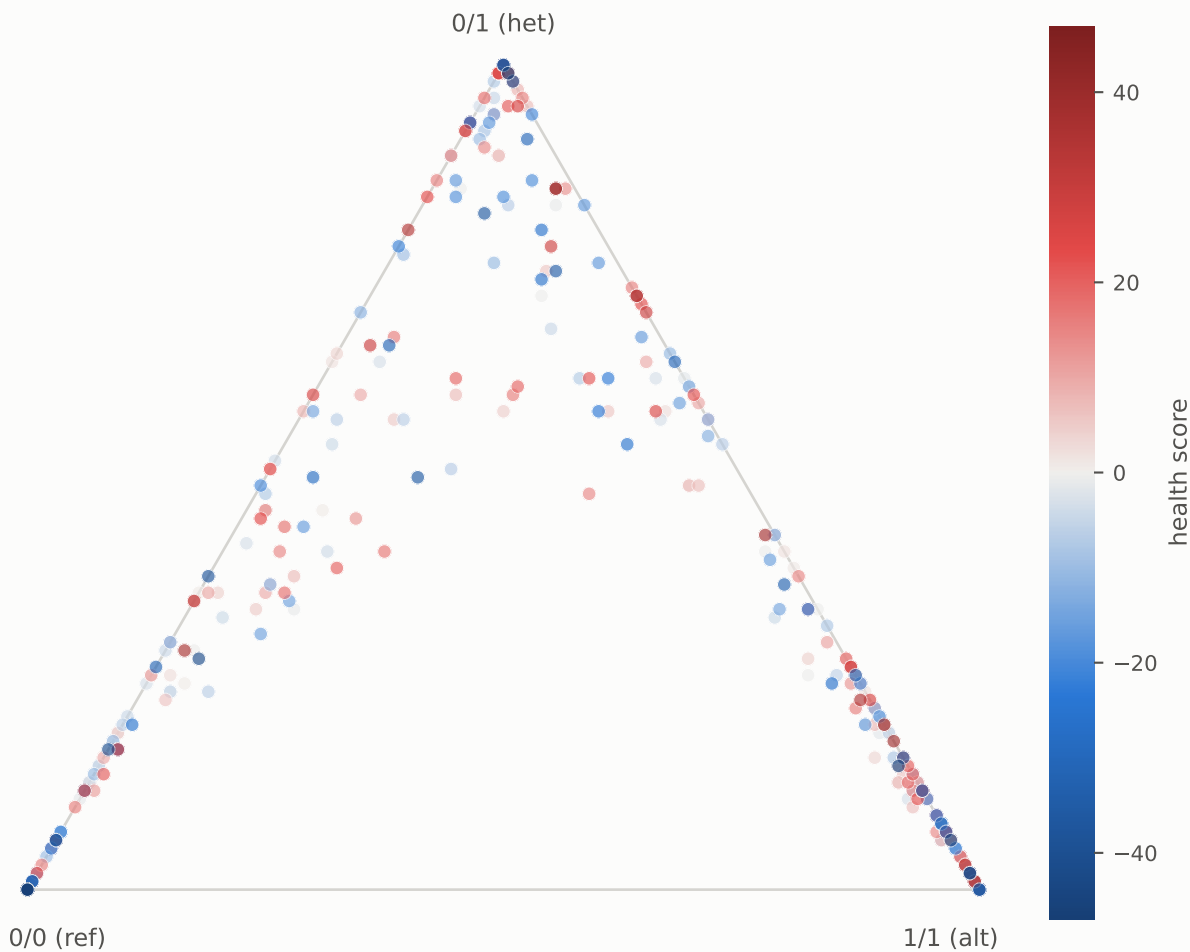
#164 by genotype uncertainty CHR_20:780,995 A>G
AF=0.56 DR2=0.81 $r=+0.006$ $H=0.383$ $F=0.0$



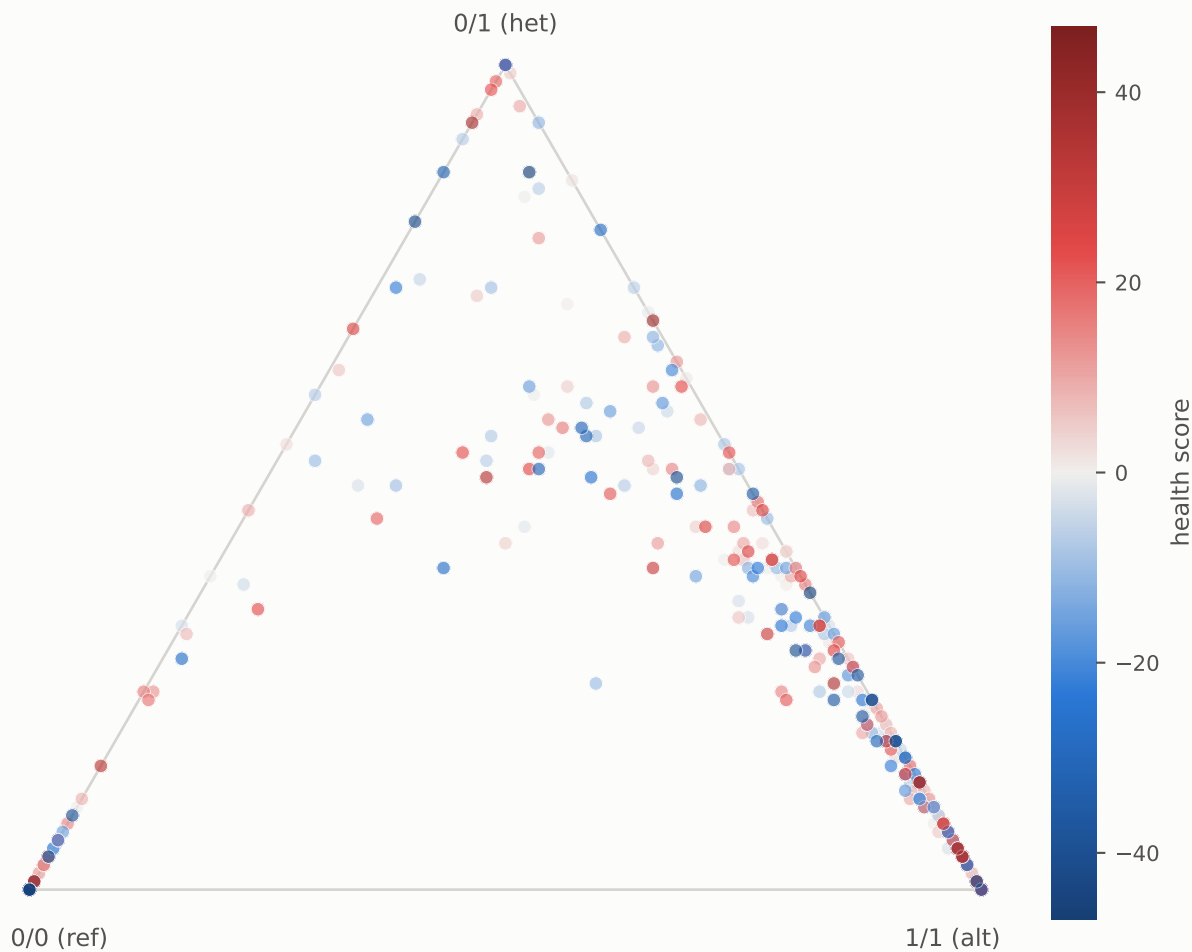
#165 by genotype uncertainty CHR_06:18,185,922 G>A
AF=0.53 DR2=0.82 $r=-0.003$ $\bar{H}=0.383$ $F=0.2$



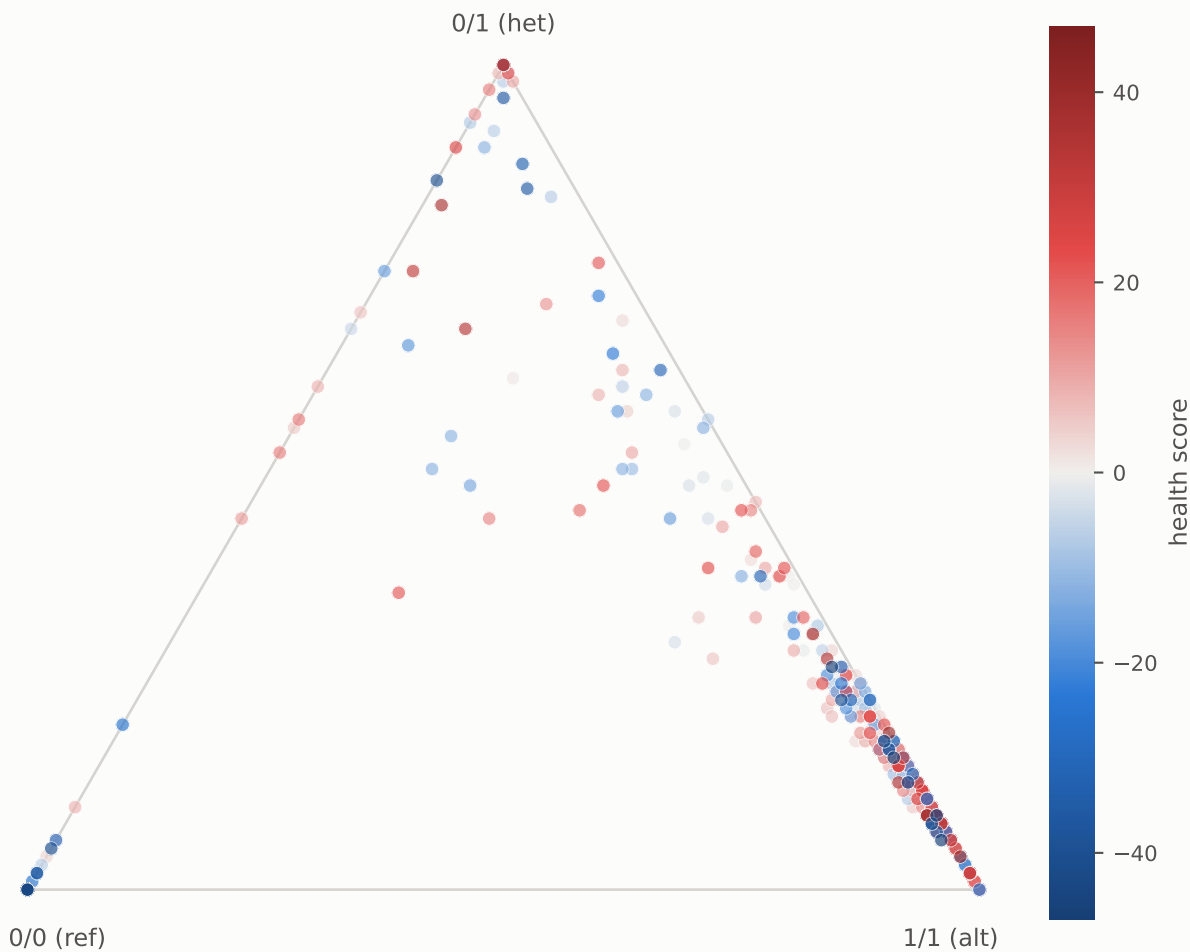
#166 by genotype uncertainty CHR_07:19,197,176 A>G
AF=0.46 DR2=0.81 $r=+0.024$ $\bar{H}=0.383$ F=0.2



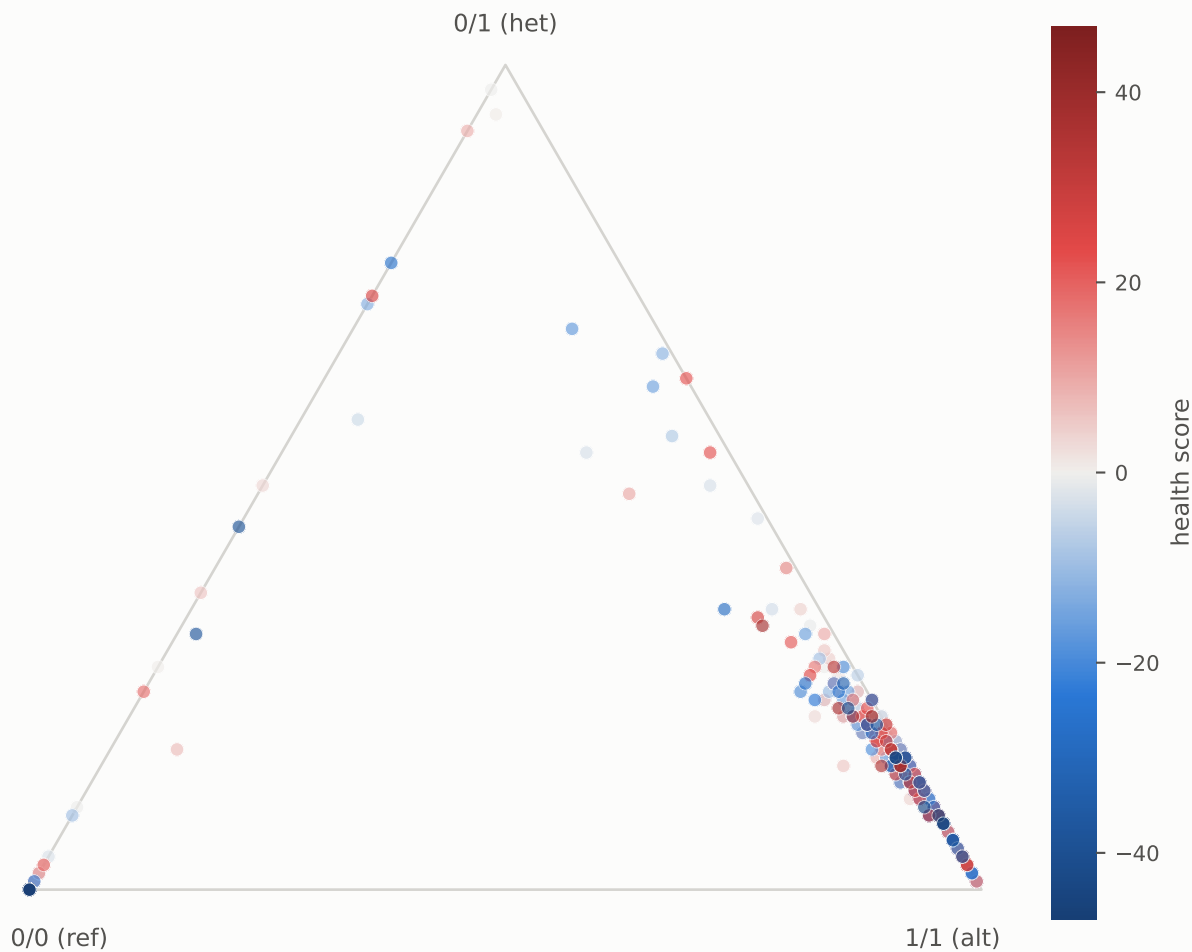
#167 by genotype uncertainty CHR_22:15,422,169 G>A
AF=0.57 DR2=0.81 $r=+0.010$ $\bar{H}=0.383$ F=0.4



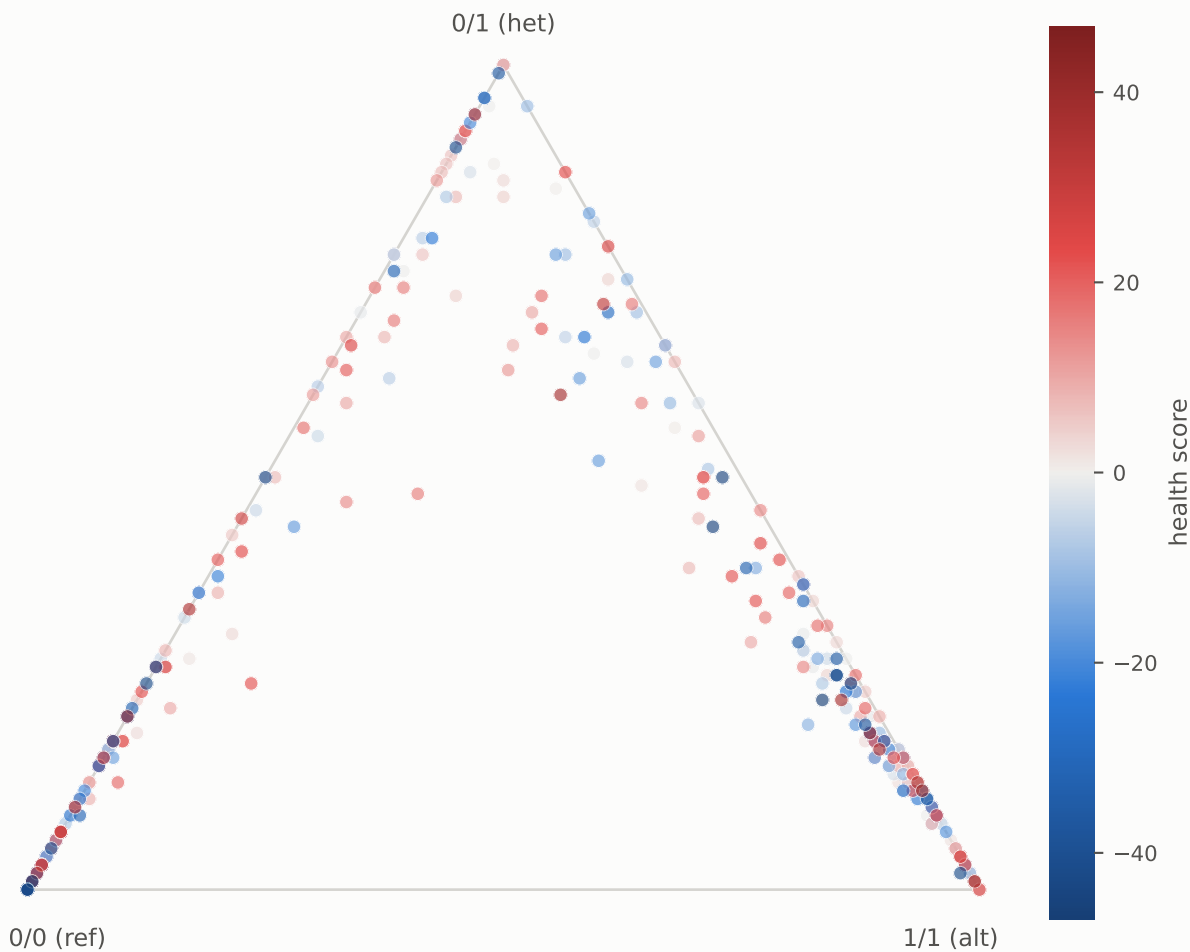
#168 by genotype uncertainty CHR_17:3,774,130 A>C
AF=0.67 DR2=0.81 $r=+0.158$ $\bar{H}=0.383$ F=6.3



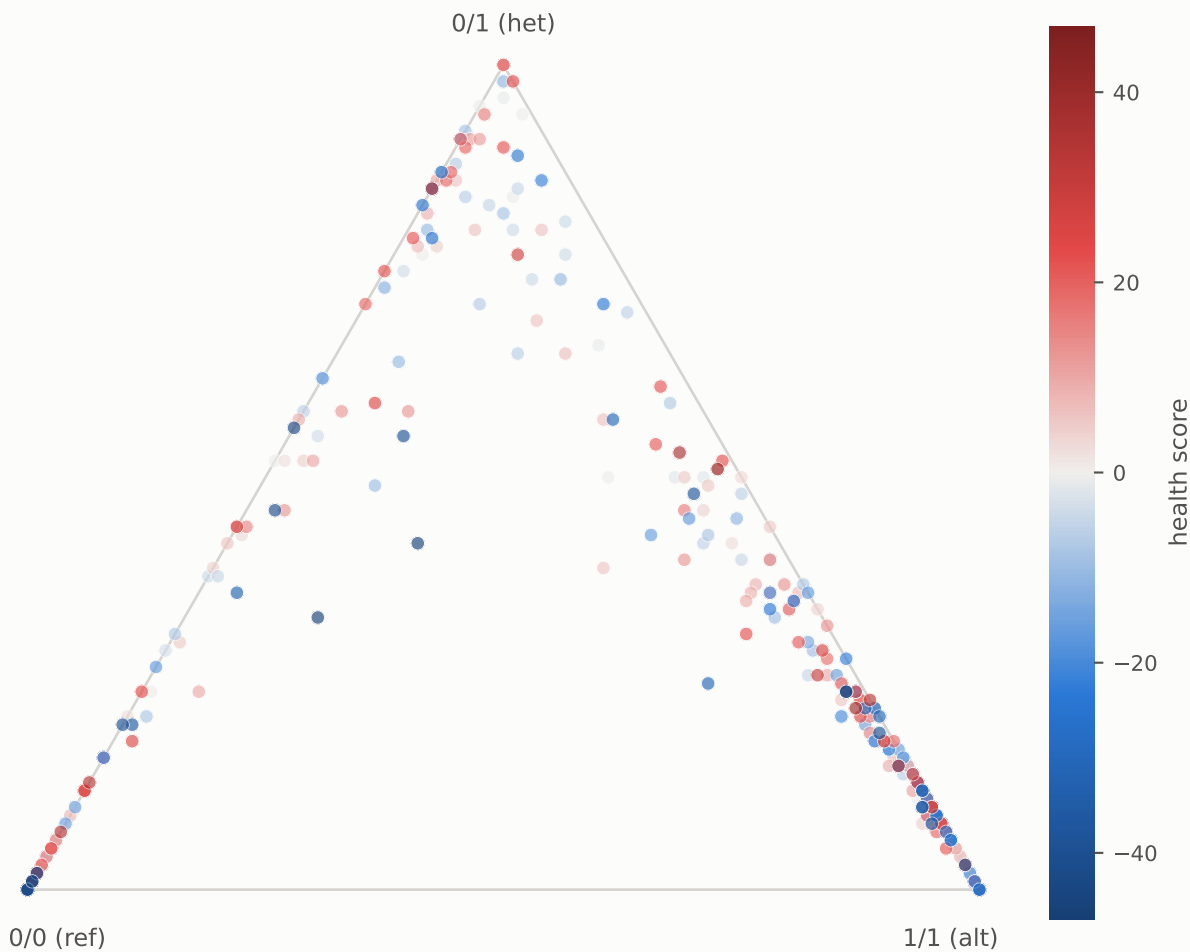
#169 by genotype uncertainty CHR_01:5,800,312 A>G
AF=0.68 DR2=0.82 $r=+0.010$ $\bar{H}=0.383$ F=0.1



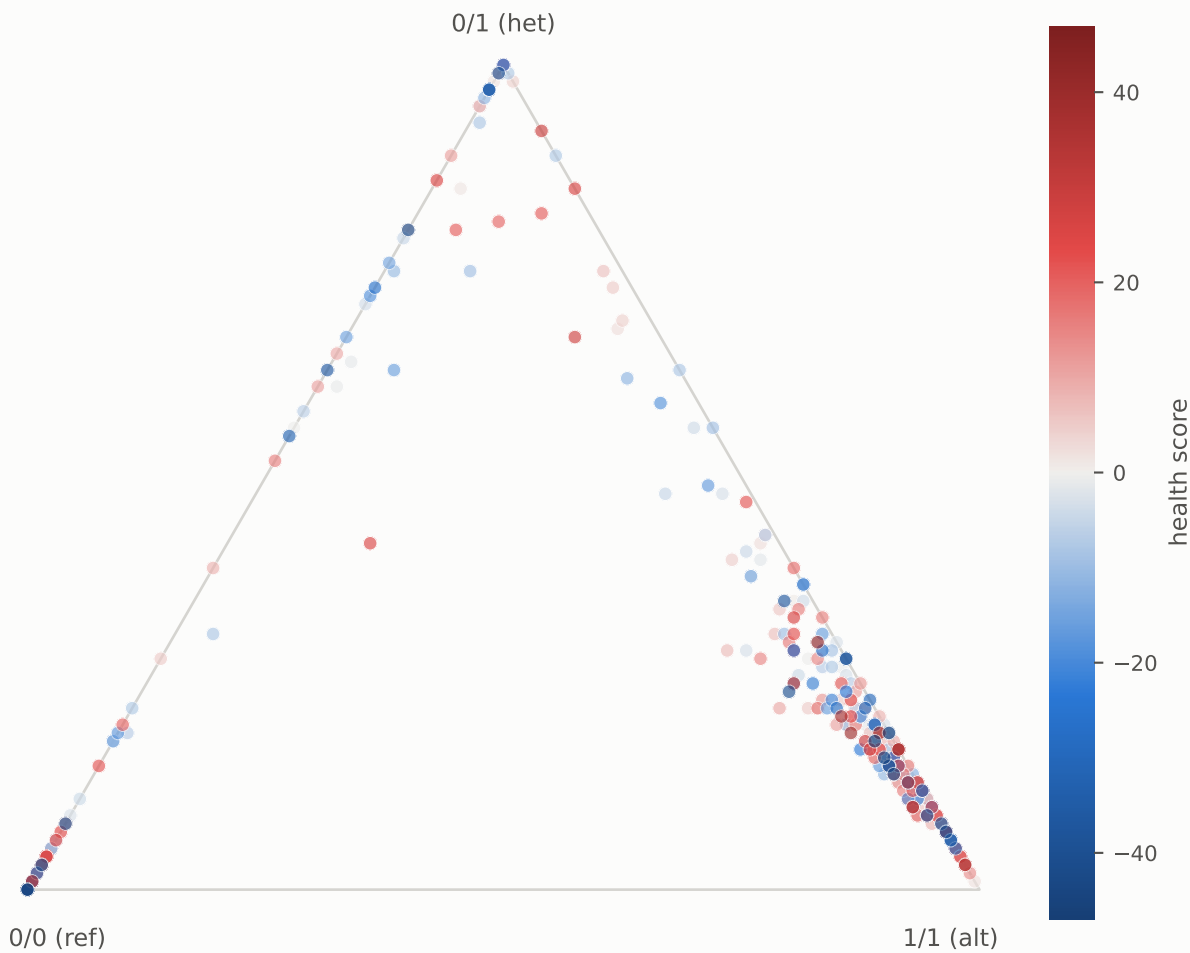
#170 by genotype uncertainty CHR_07:131,954 T>C
AF=0.42 DR2=0.82 $r=-0.013$ H=0.383 F=0.5



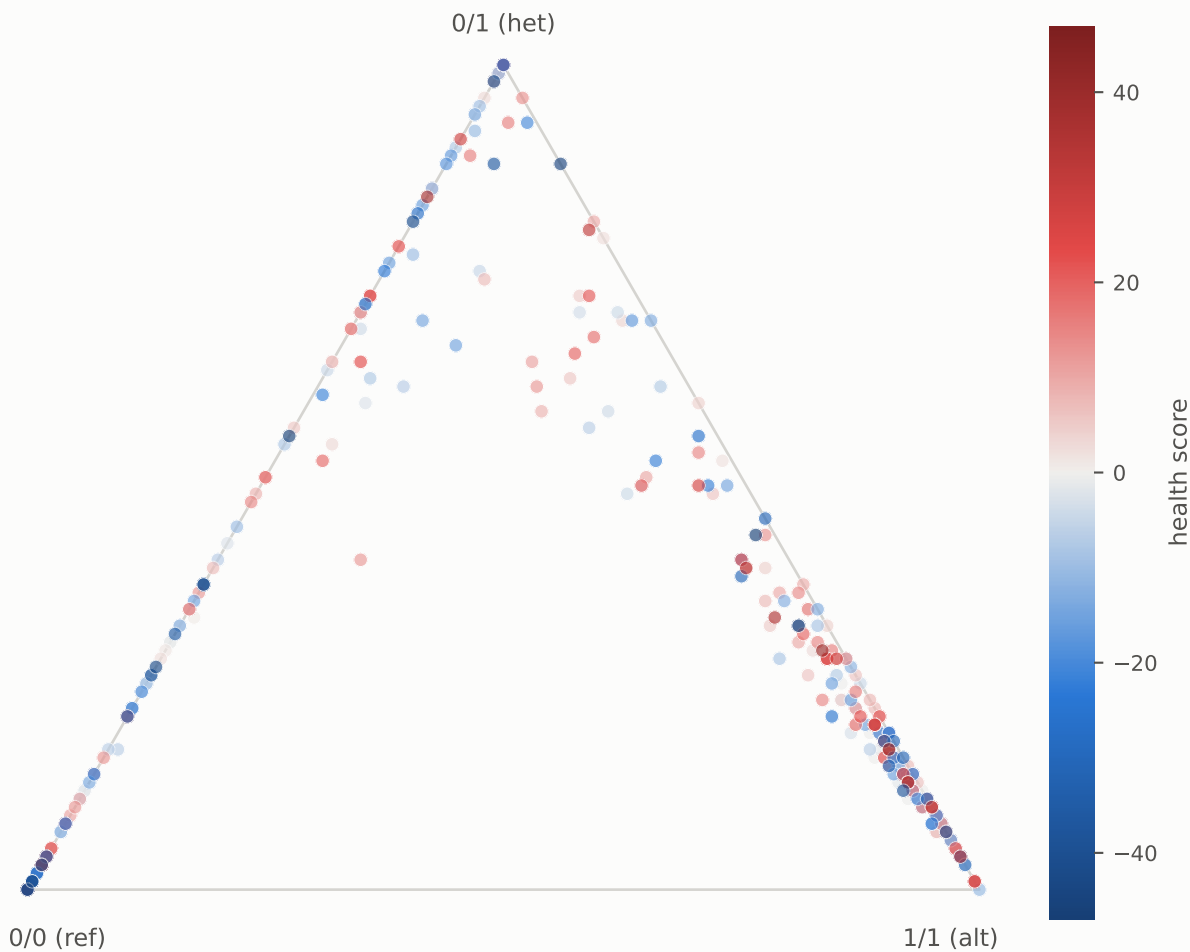
#171 by genotype uncertainty CHR_17:24,931,582 C>T
AF=0.47 DR2=0.82 $r=-0.068$ $\bar{H}=0.382$ $F=1.1$



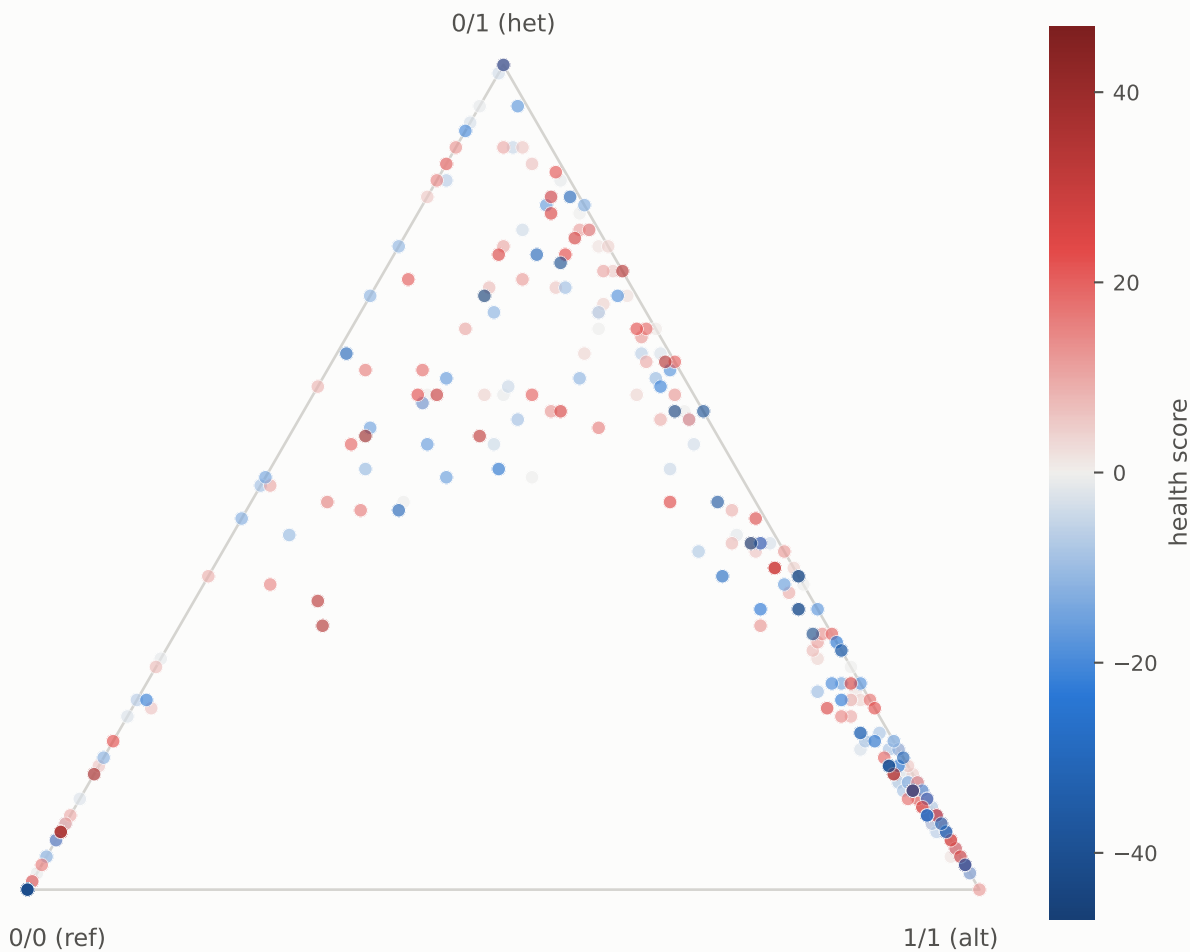
#172 by genotype uncertainty CHR_07:32,526,067 A>T
AF=0.58 DR2=0.81 $r=+0.035$ $\bar{H}=0.382$ F=1.3



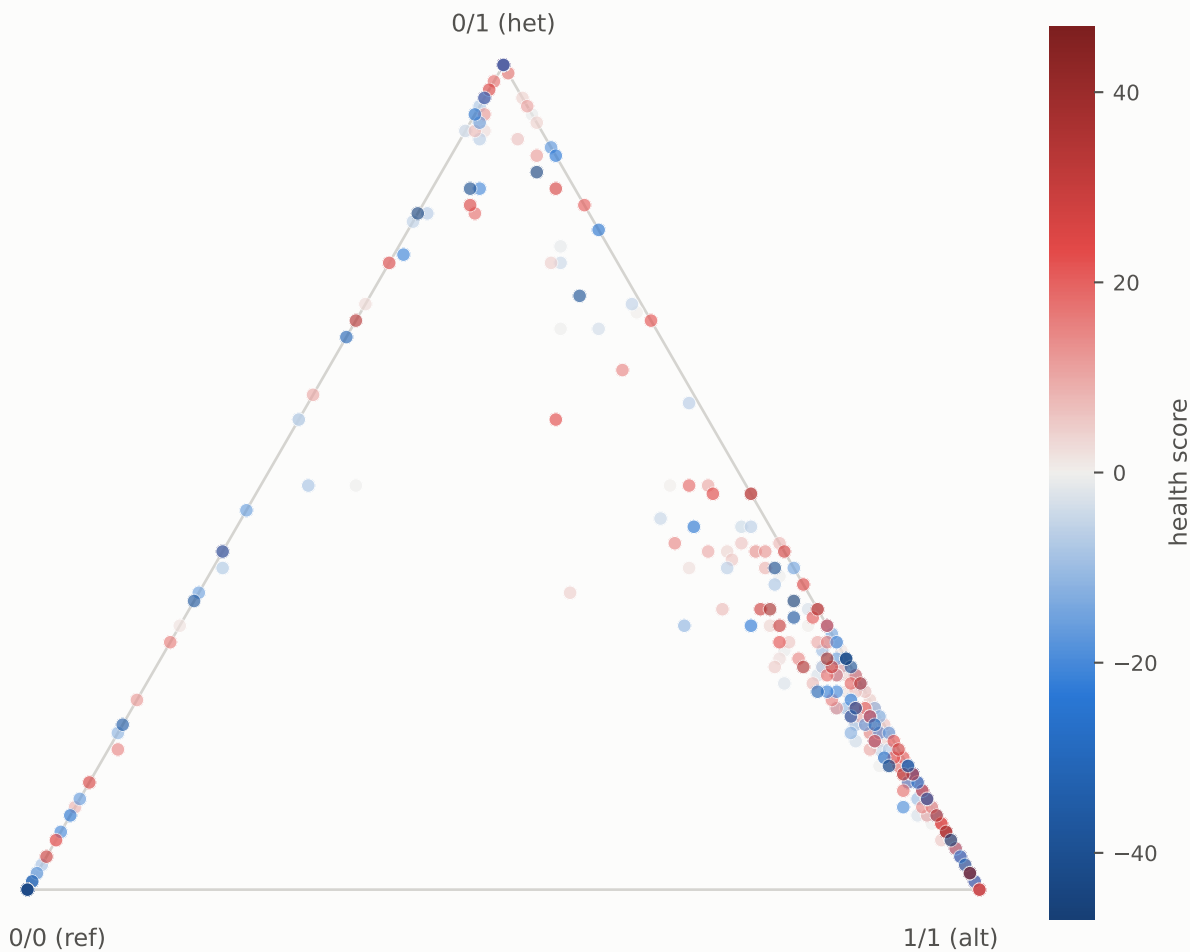
#173 by genotype uncertainty CHR_19:3,483,003 A>T
AF=0.45 DR2=0.81 $r=+0.043$ $\bar{H}=0.382$ F=1.1



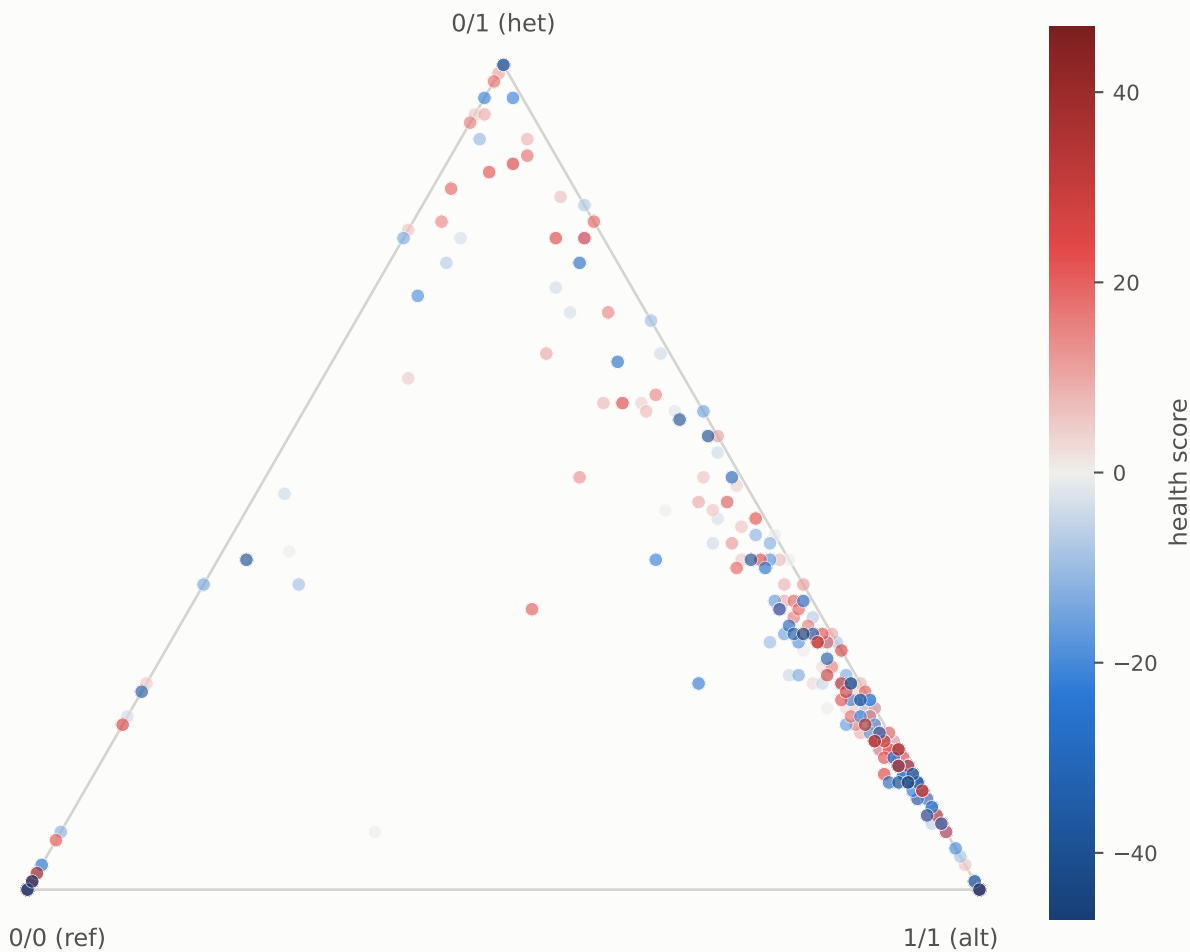
#174 by genotype uncertainty CHR_10:11,749,189 A>G
AF=0.48 DR2=0.81 $r=-0.071$ $\bar{H}=0.382$ F=2.4



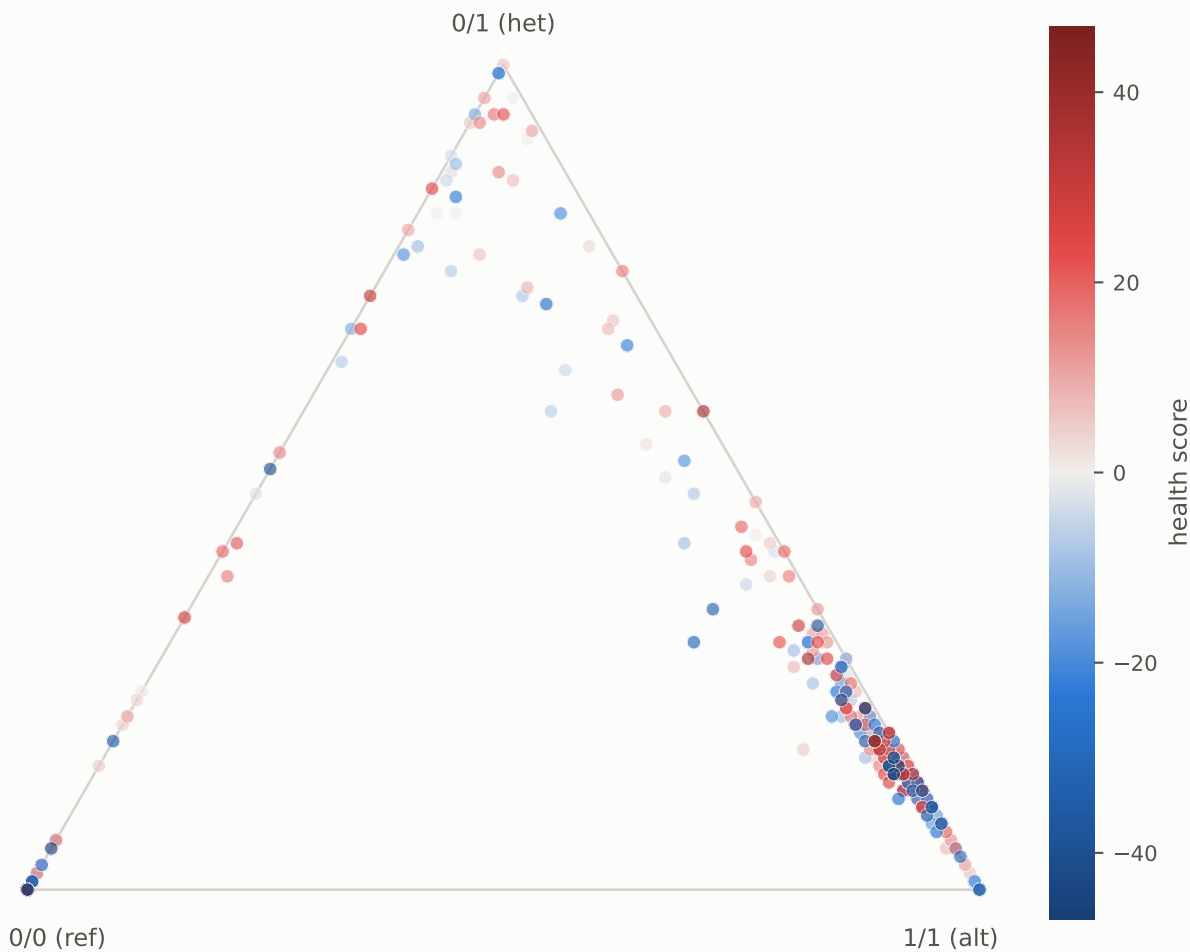
#175 by genotype uncertainty CHR_19:3,028,841 T>G
AF=0.57 DR2=0.82 $r=+0.079$ $\bar{H}=0.382$ F=1.5



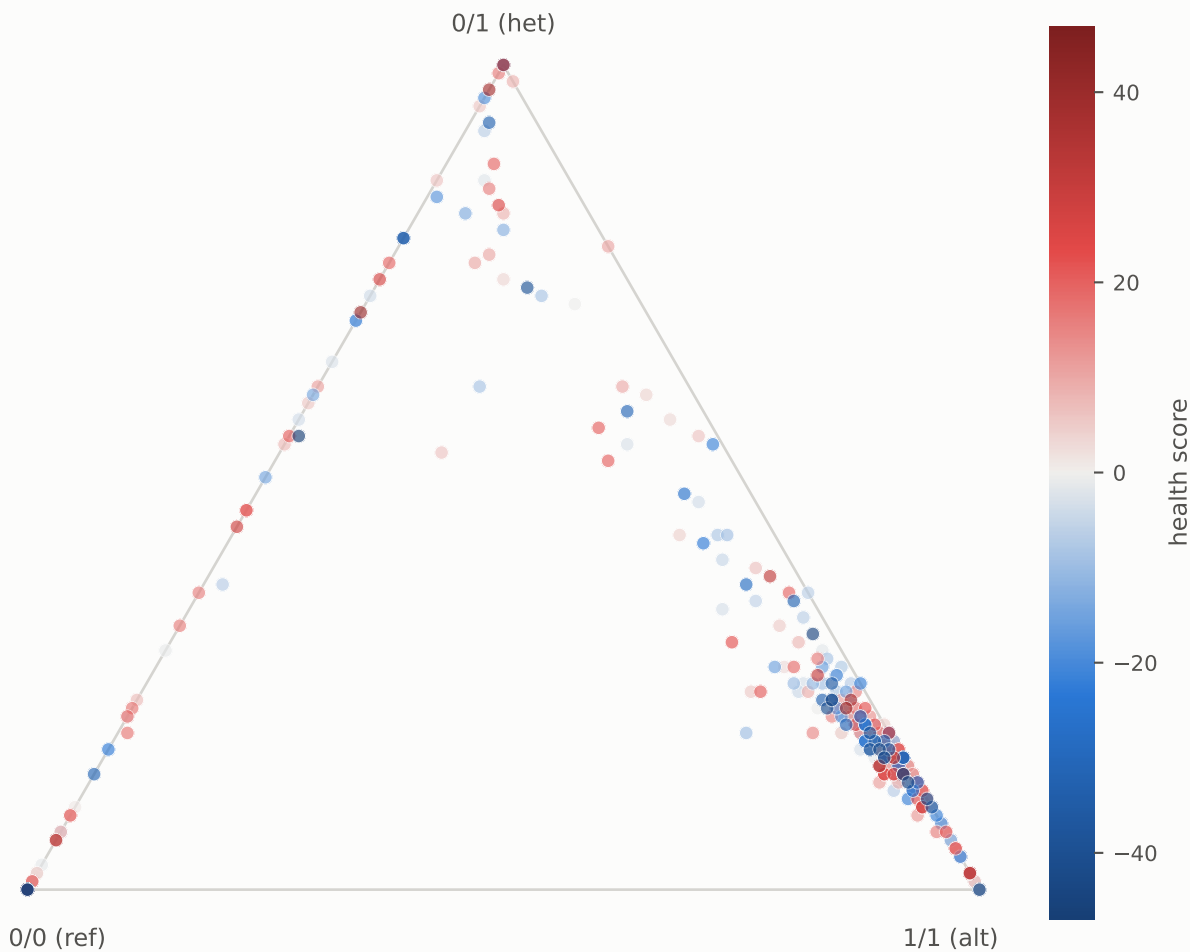
#176 by genotype uncertainty CHR_03:43,490,151 T>A
AF=0.6 DR2=0.81 r=-0.068 H=0.382 F=0.6



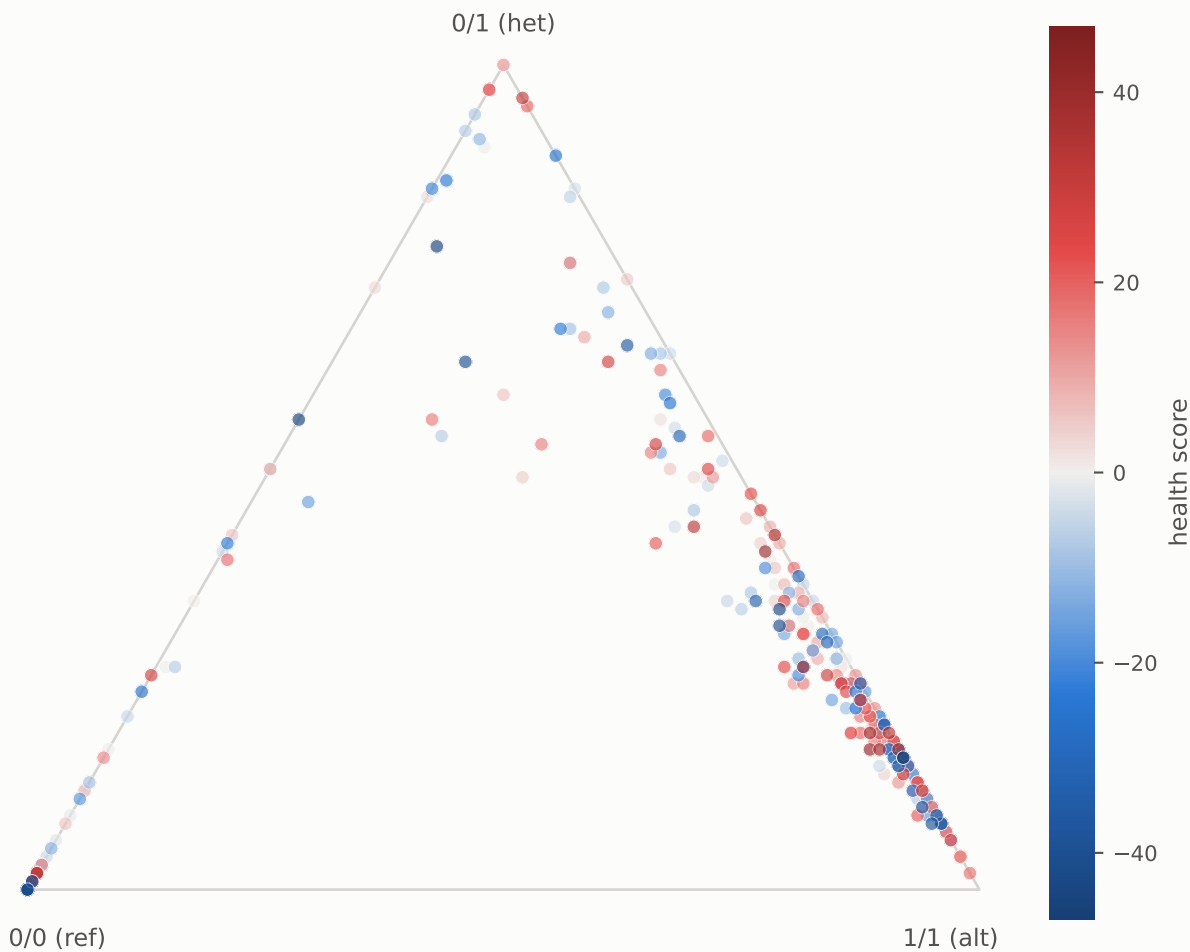
#177 by genotype uncertainty CHR_18:23,816,142 A>C
AF=0.57 DR2=0.82 $r=+0.024$ $\bar{H}=0.382$ F=0.2



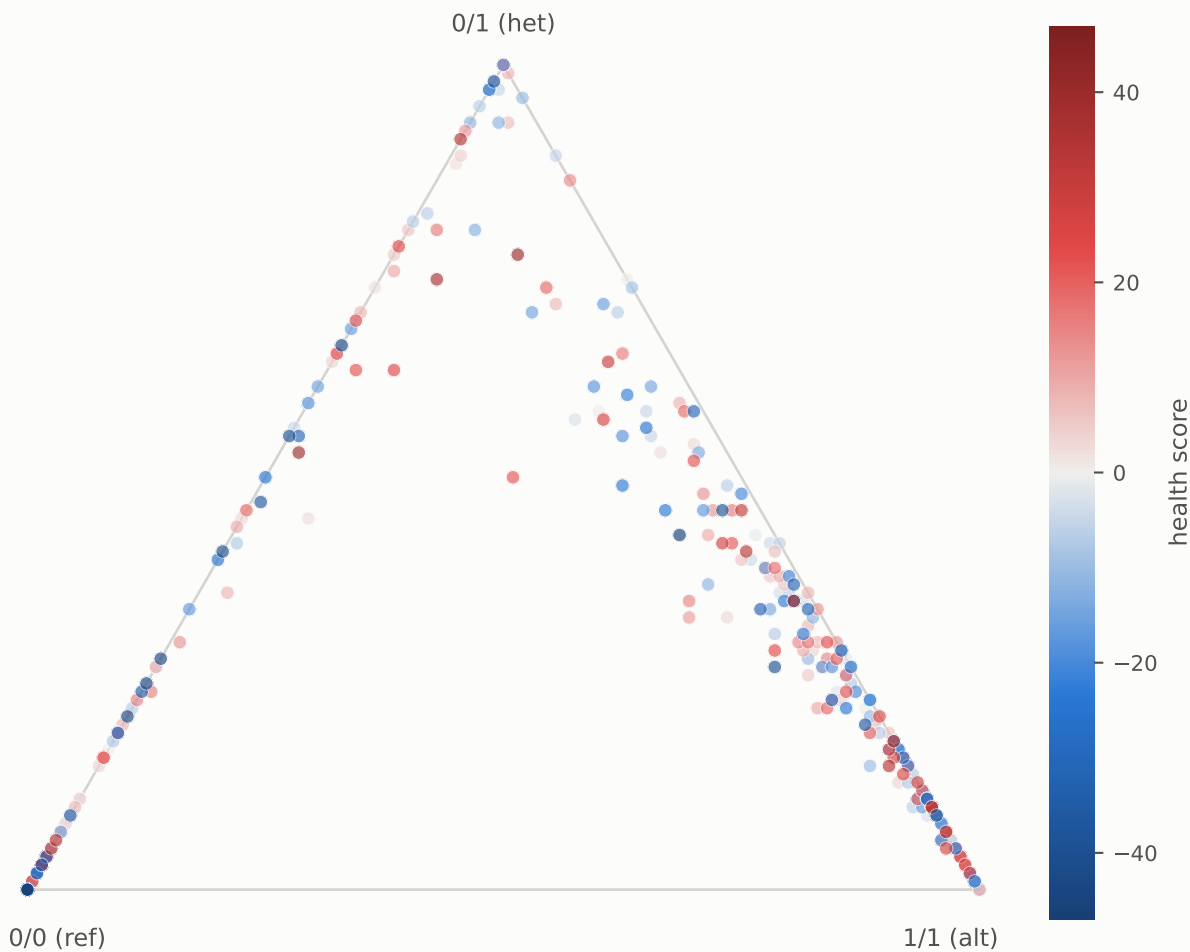
#178 by genotype uncertainty CHR_05:19,182,793 A>C
AF=0.56 DR2=0.81 $r=-0.049$ $\bar{H}=0.382$ F=0.8



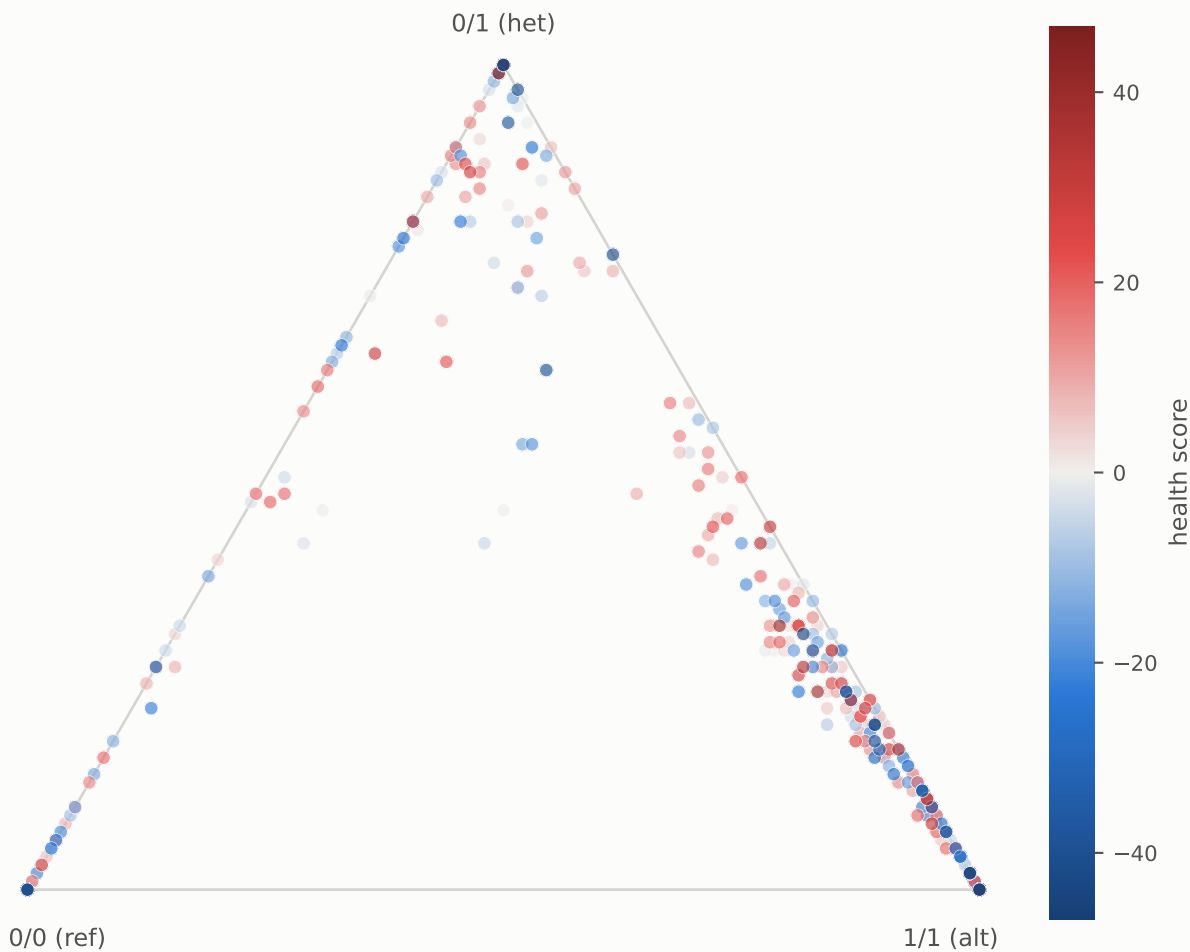
#179 by genotype uncertainty CHR_01:43,537,156 C>T
AF=0.54 DR2=0.81 $r=+0.065$ $\bar{H}=0.382$ F=1.4



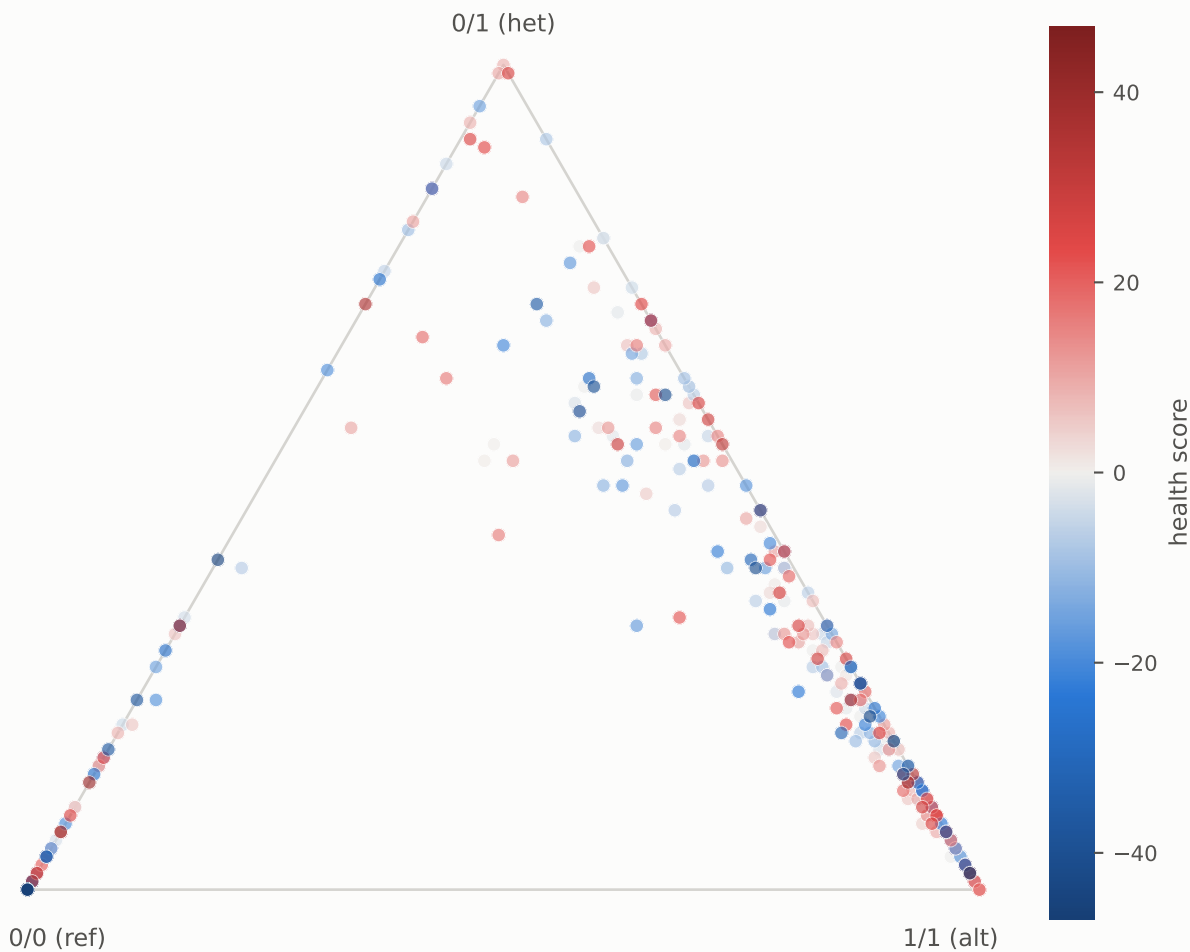
#180 by genotype uncertainty CHR_13:4,622,780 T>C
AF=0.49 DR2=0.81 $r=+0.032$ $\bar{H}=0.382$ F=0.4



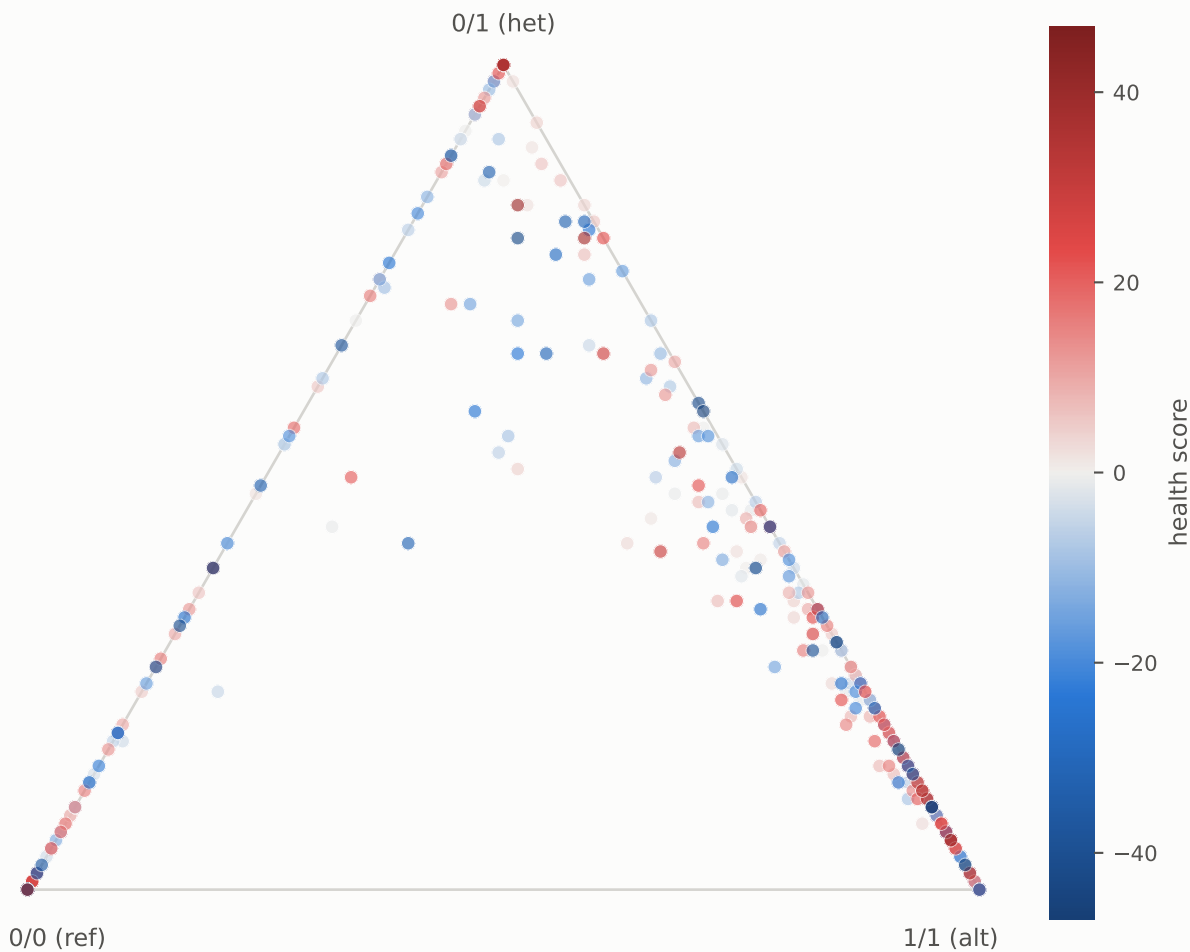
#181 by genotype uncertainty CHR_09:19,495,387 A>G
AF=0.58 DR2=0.81 $r=-0.027$ $\bar{H}=0.382$ F=0.1



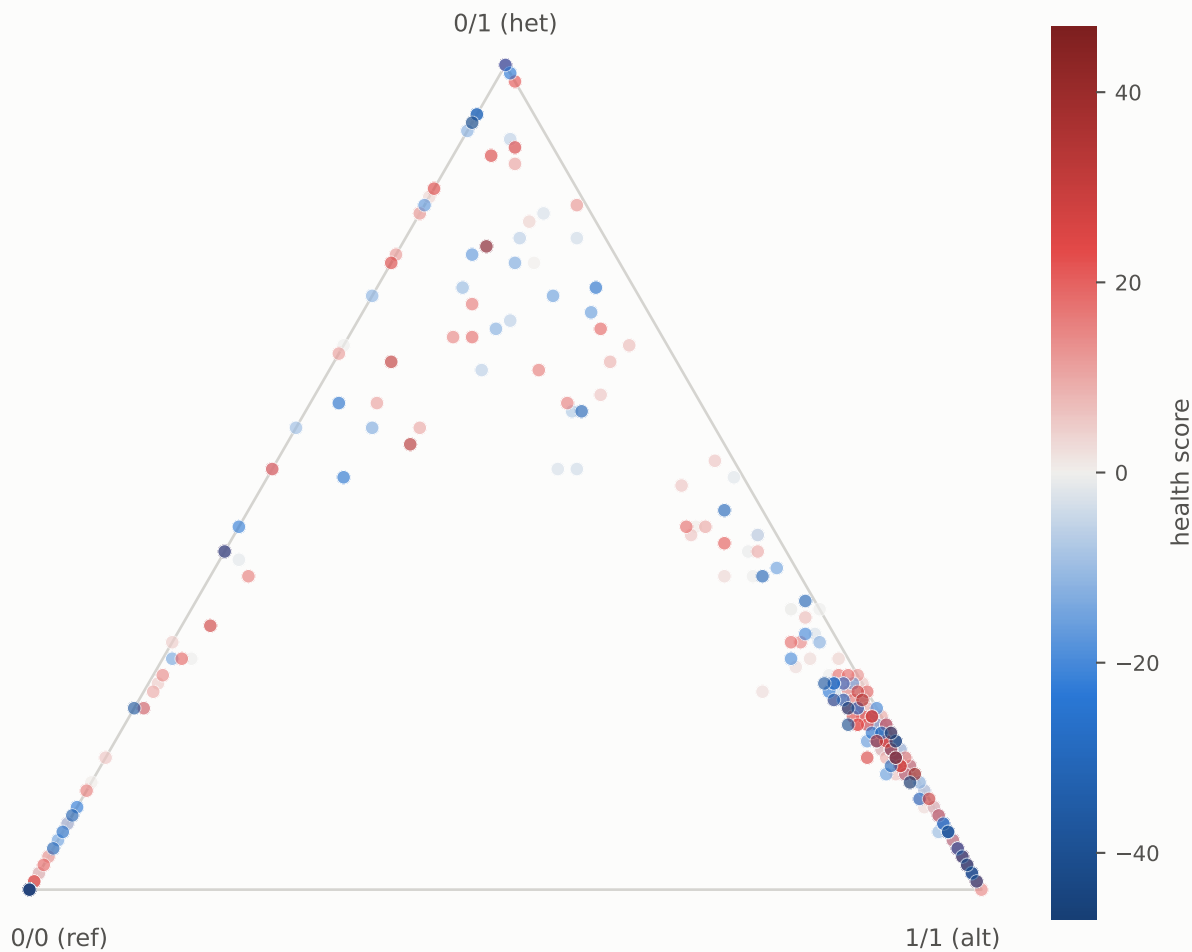
#182 by genotype uncertainty CHR_17:3,106,189 T>C
AF=0.51 DR2=0.81 $r=+0.046$ $\bar{H}=0.382$ F=0.5



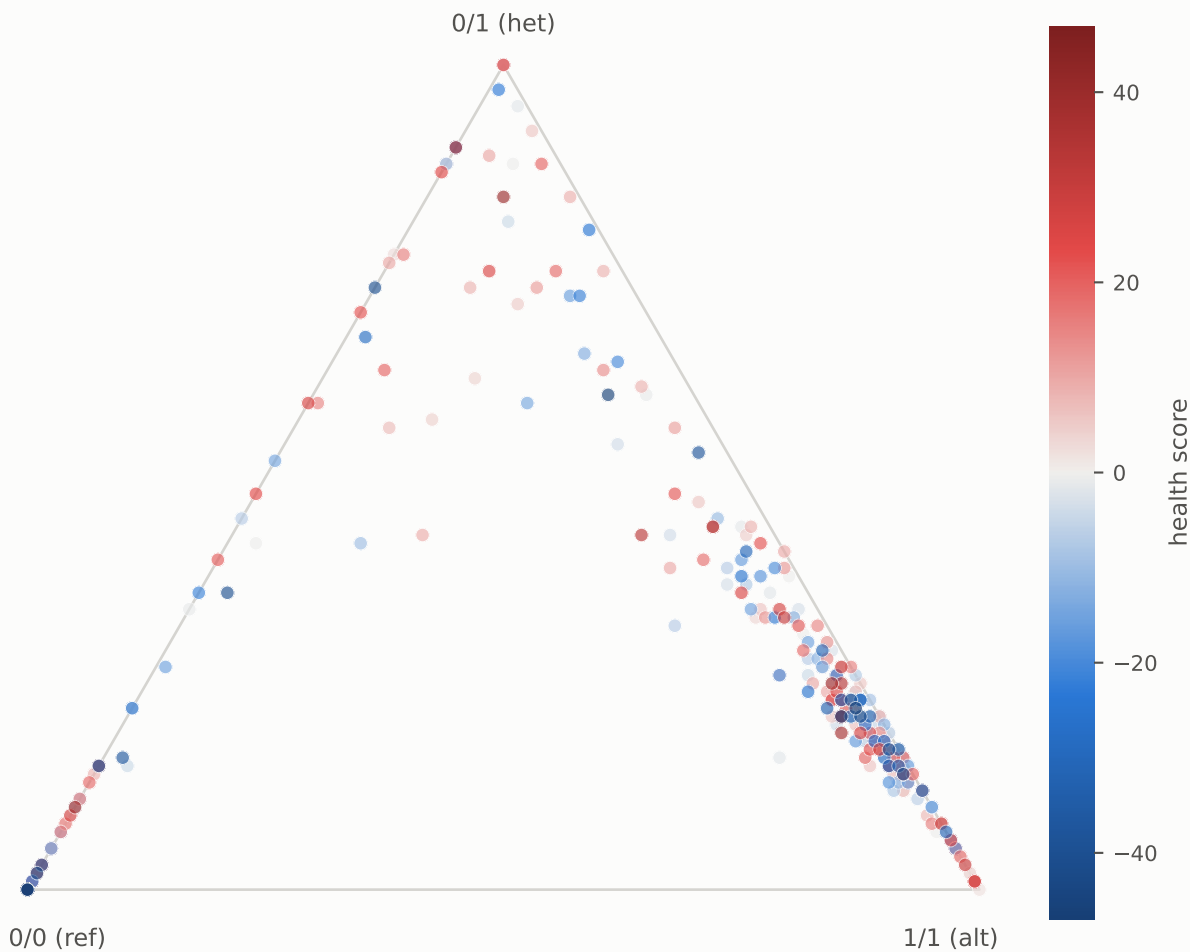
#183 by genotype uncertainty CHR_18:14,623,919 A>C
AF=0.54 DR2=0.81 $r=-0.001$ $\bar{H}=0.382$ F=0.6



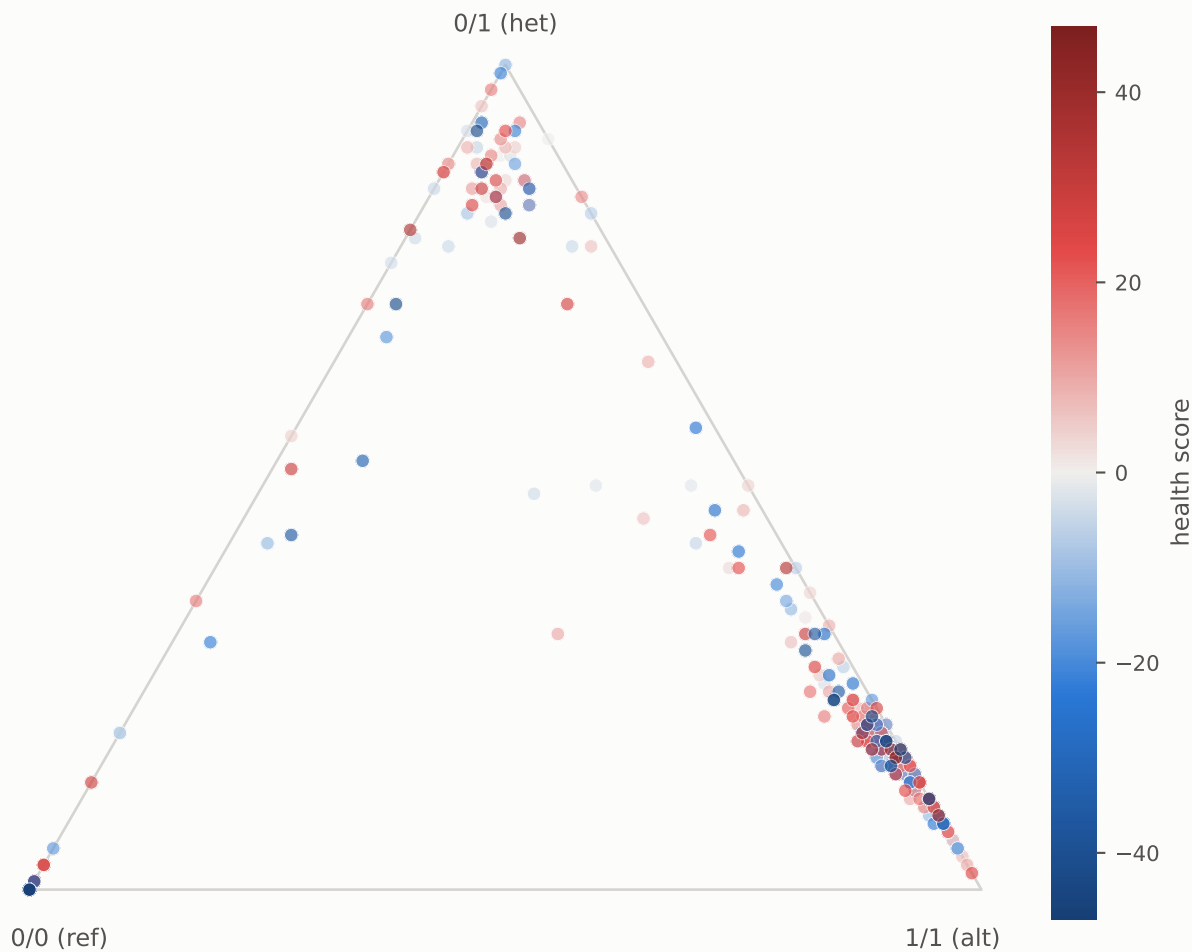
#184 by genotype uncertainty CHR_08:15,214,584 G>C
AF=0.53 DR2=0.81 $r=-0.012$ $\bar{H}=0.382$ F=0.1



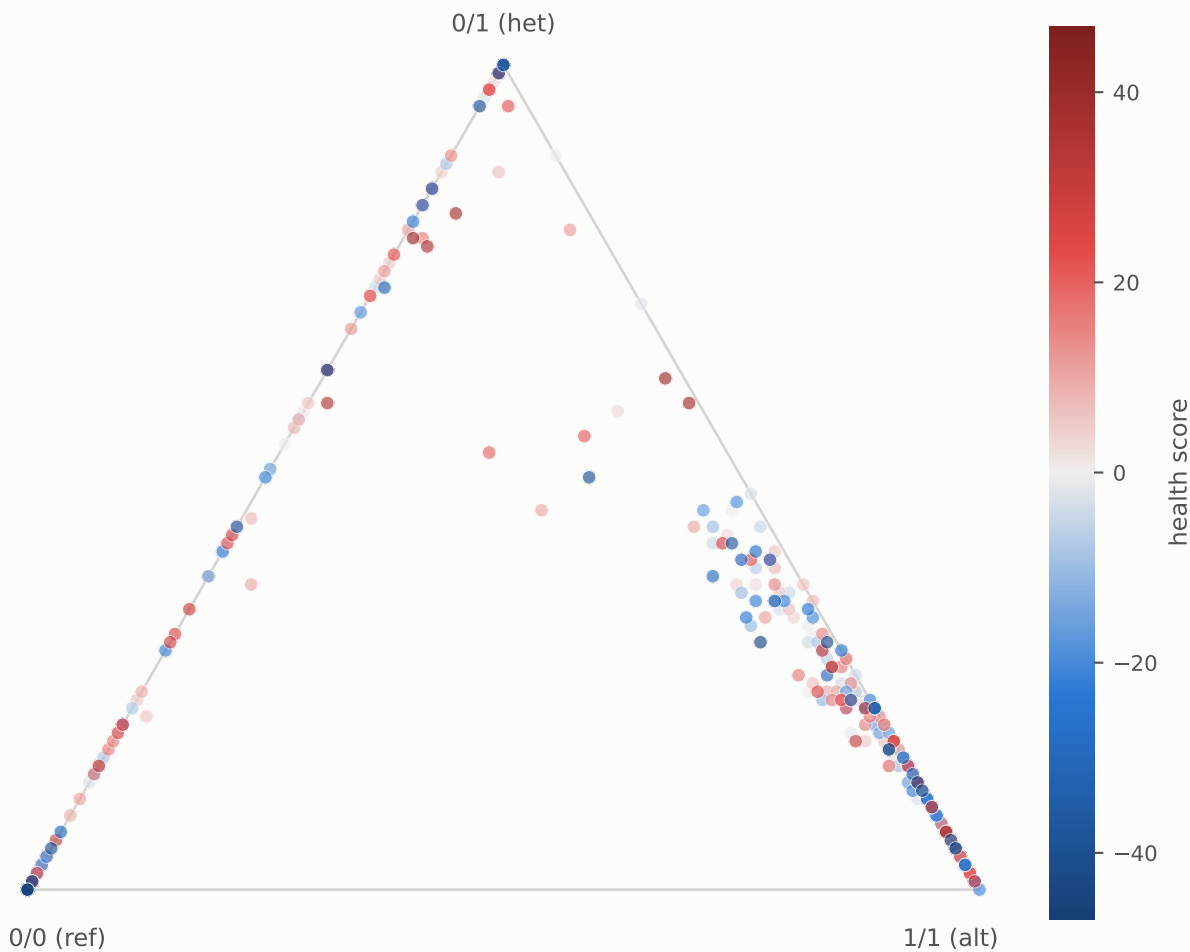
#185 by genotype uncertainty CHR_08:10,934,513 T>C
AF=0.51 DR2=0.81 $r=+0.022$ $\bar{H}=0.382$ F=0.8



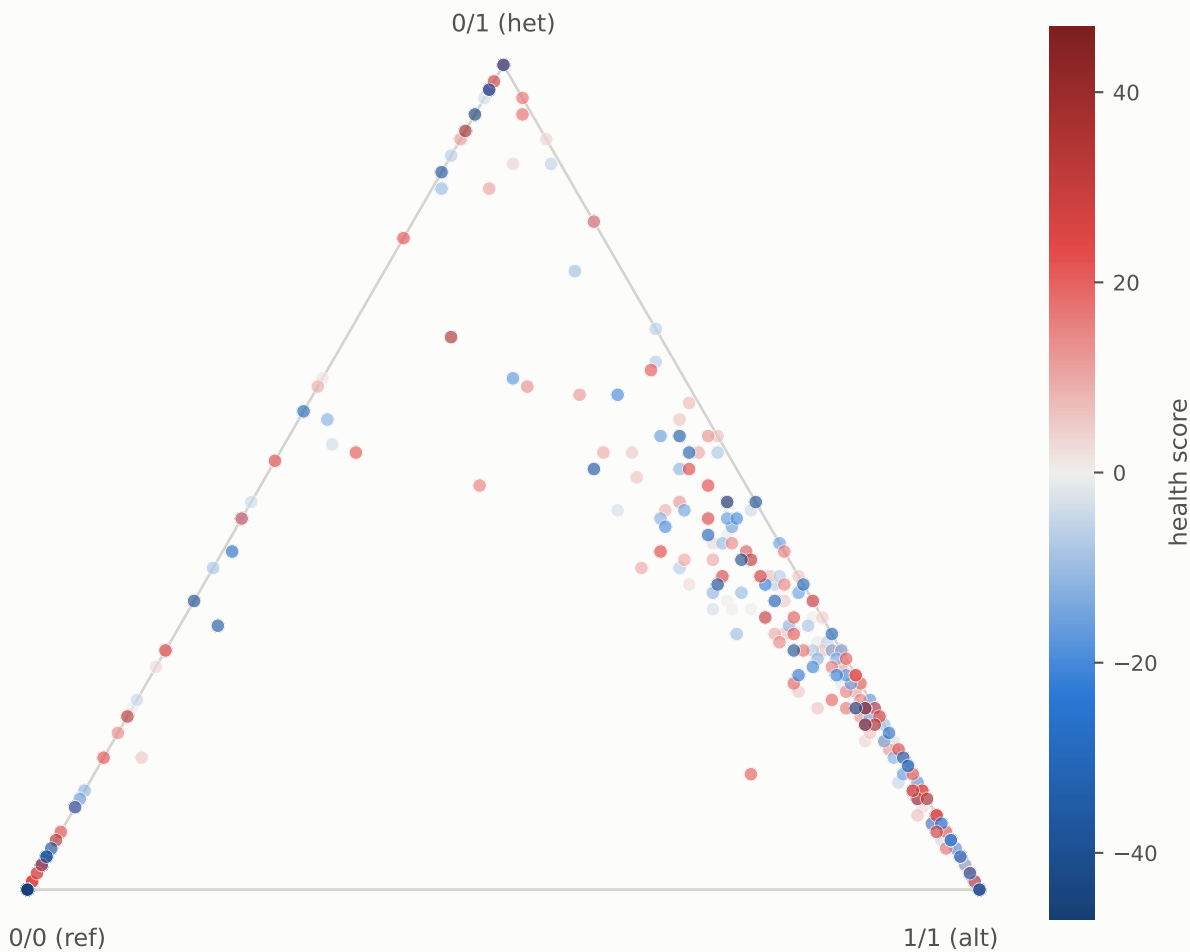
#186 by genotype uncertainty CHR_17:16,516,985 A>G
AF=0.61 DR2=0.81 $r=+0.037$ $\bar{H}=0.382$ F=1.1



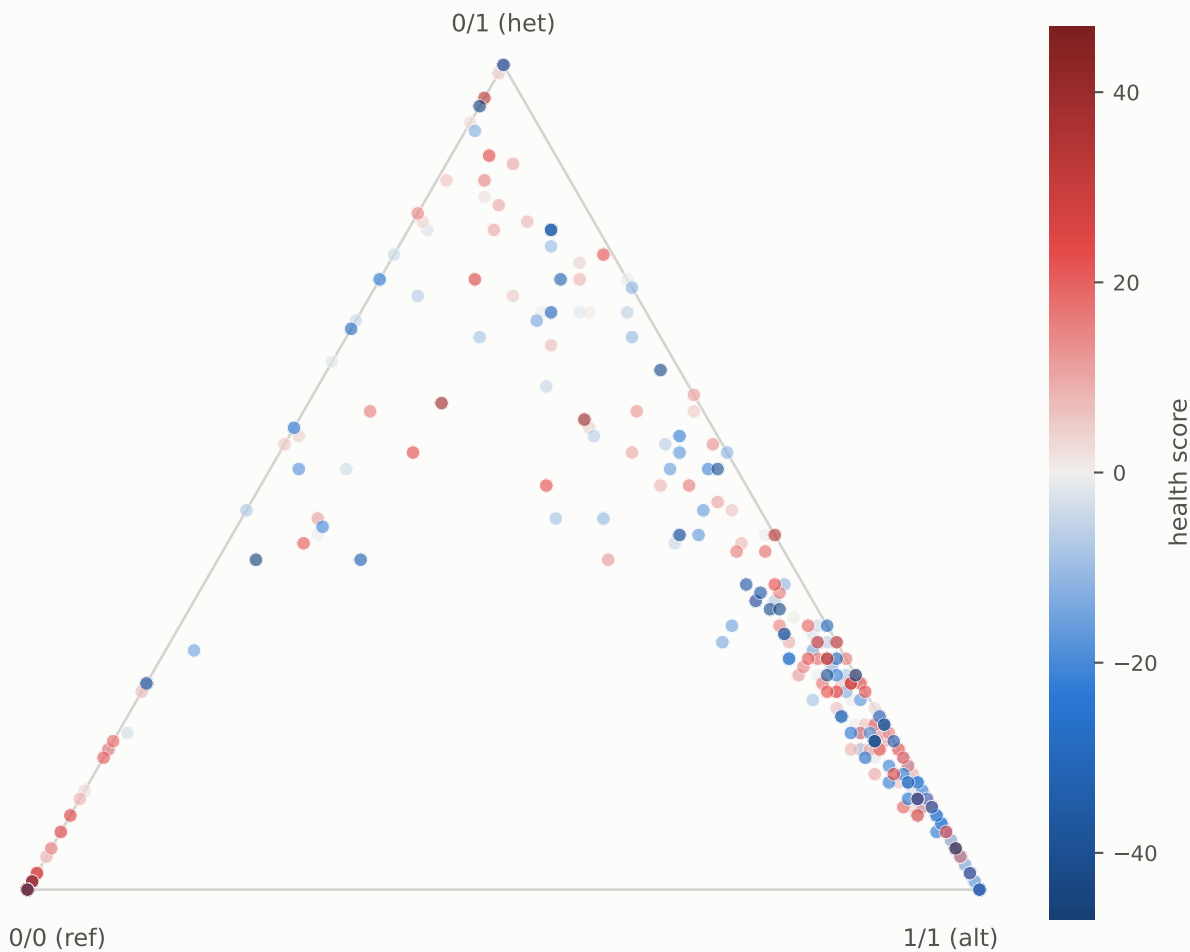
#187 by genotype uncertainty CHR_15:2,008,082 G>A
AF=0.54 DR2=0.81 $r=-0.087$ $\bar{H}=0.382$ $F=3.2$



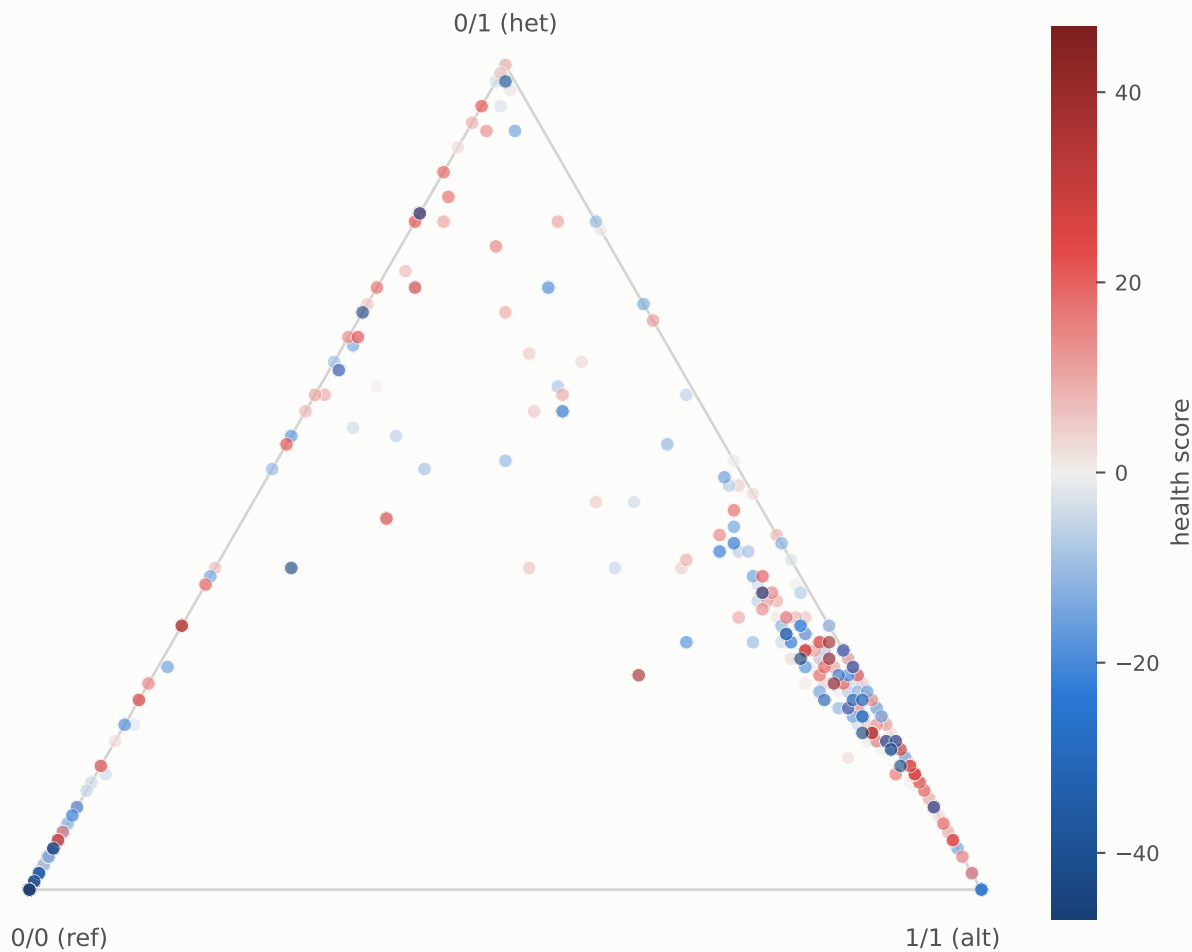
#188 by genotype uncertainty CHR_02:20,540,796 T>C
AF=0.5 DR2=0.81 $r=+0.035$ $\bar{H}=0.382$ F=0.3



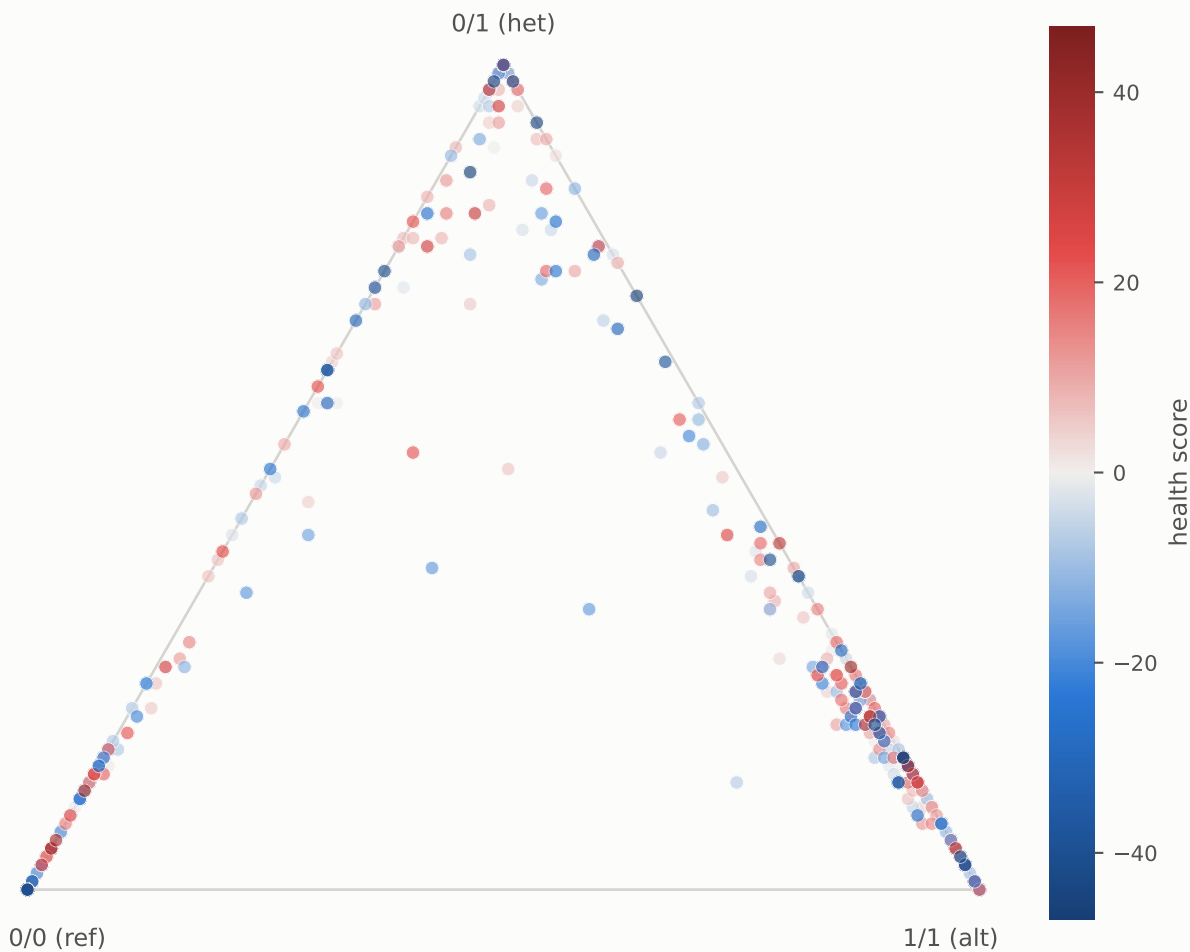
#189 by genotype uncertainty CHR_05:31,715,271 A>C
AF=0.48 DR2=0.81 $r=-0.194$ $\bar{H}=0.382$ F=7.7



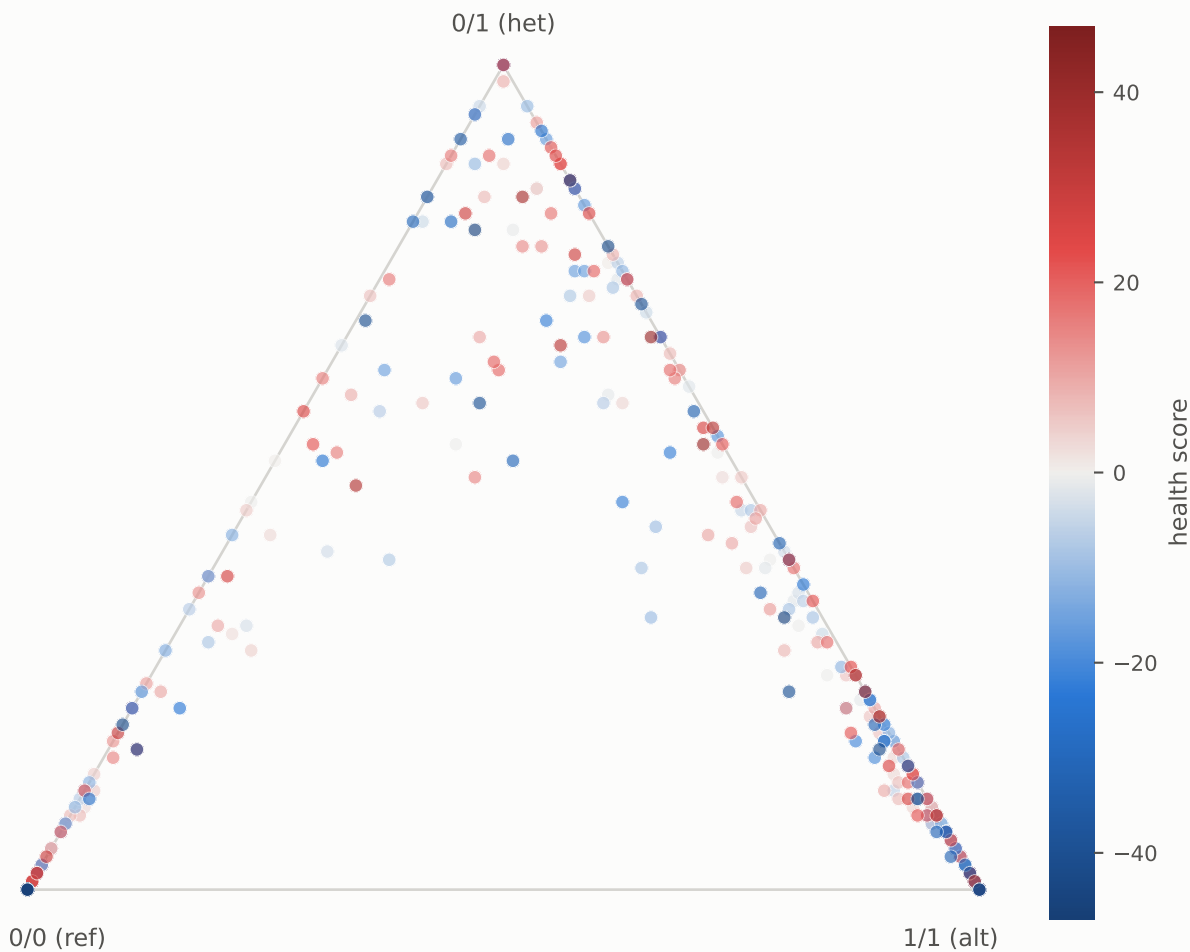
#190 by genotype uncertainty CHR_13:8,004,021 A>G
AF=0.44 DR2=0.81 $r=+0.032$ $\bar{H}=0.382$ F=0.4



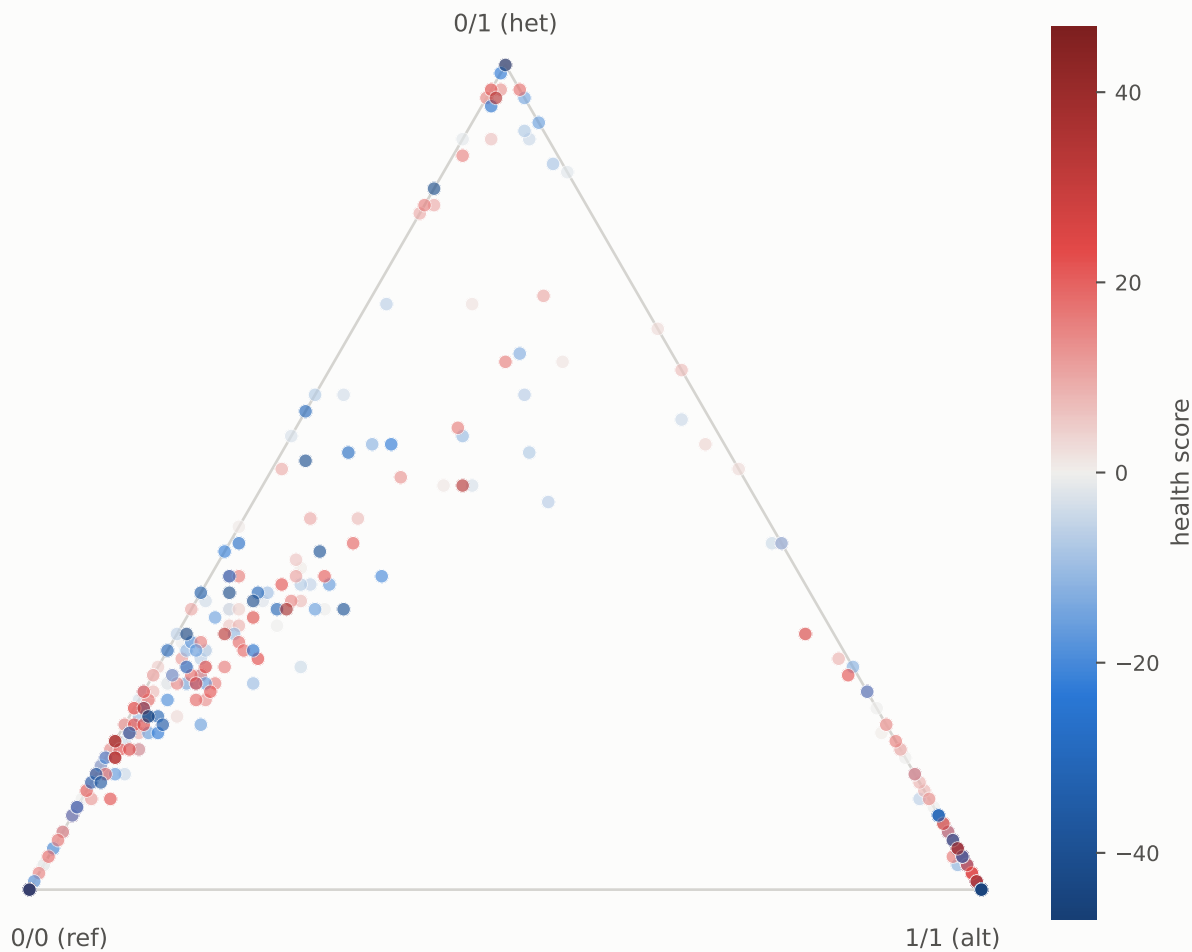
#191 by genotype uncertainty CHR_17:24,068,839 G>T
AF=0.56 DR2=0.81 $r=-0.031$ $\bar{H}=0.381$ F=2.6



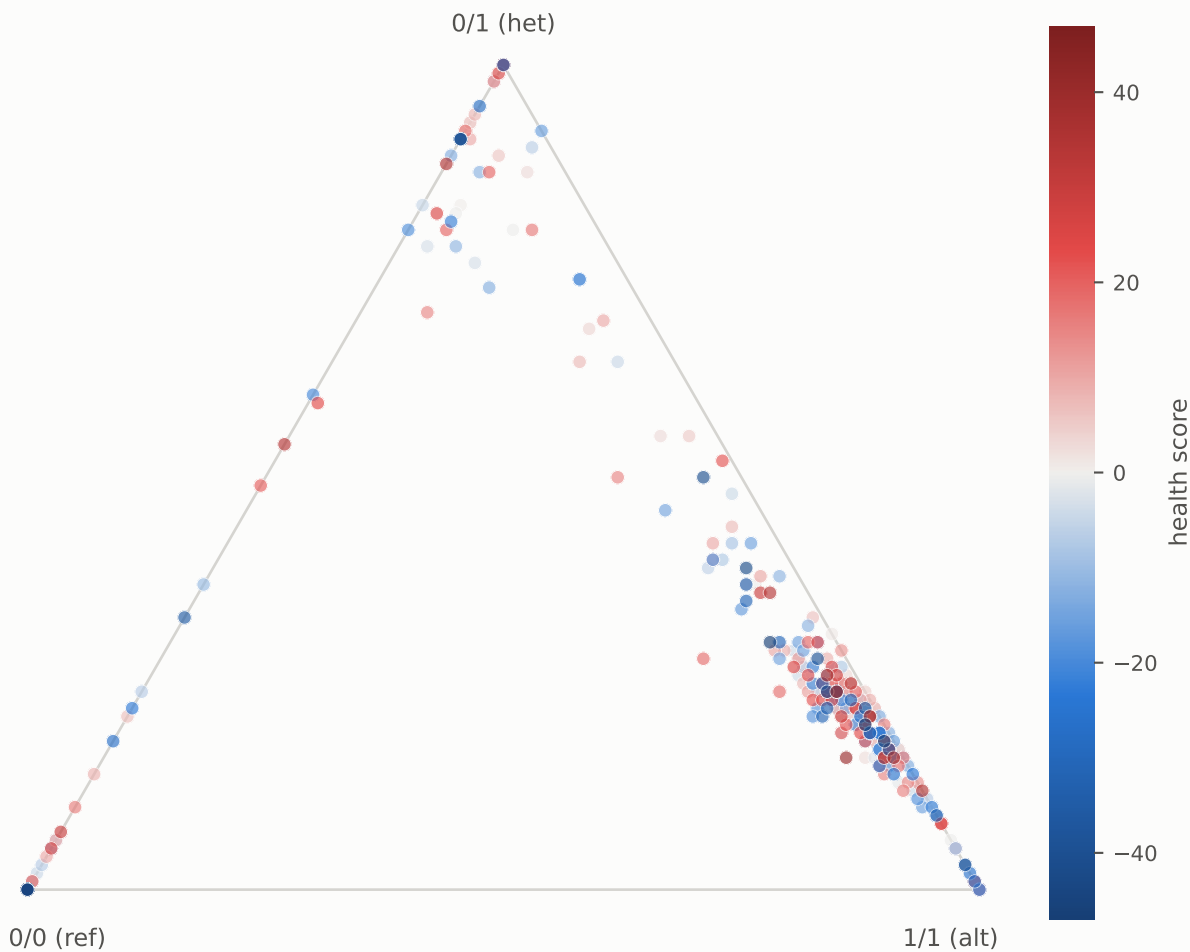
#192 by genotype uncertainty CHR_06:27,138,794 A>T
AF=0.53 DR2=0.81 r=-0.033 $\bar{H}$ =0.381 F=0.4



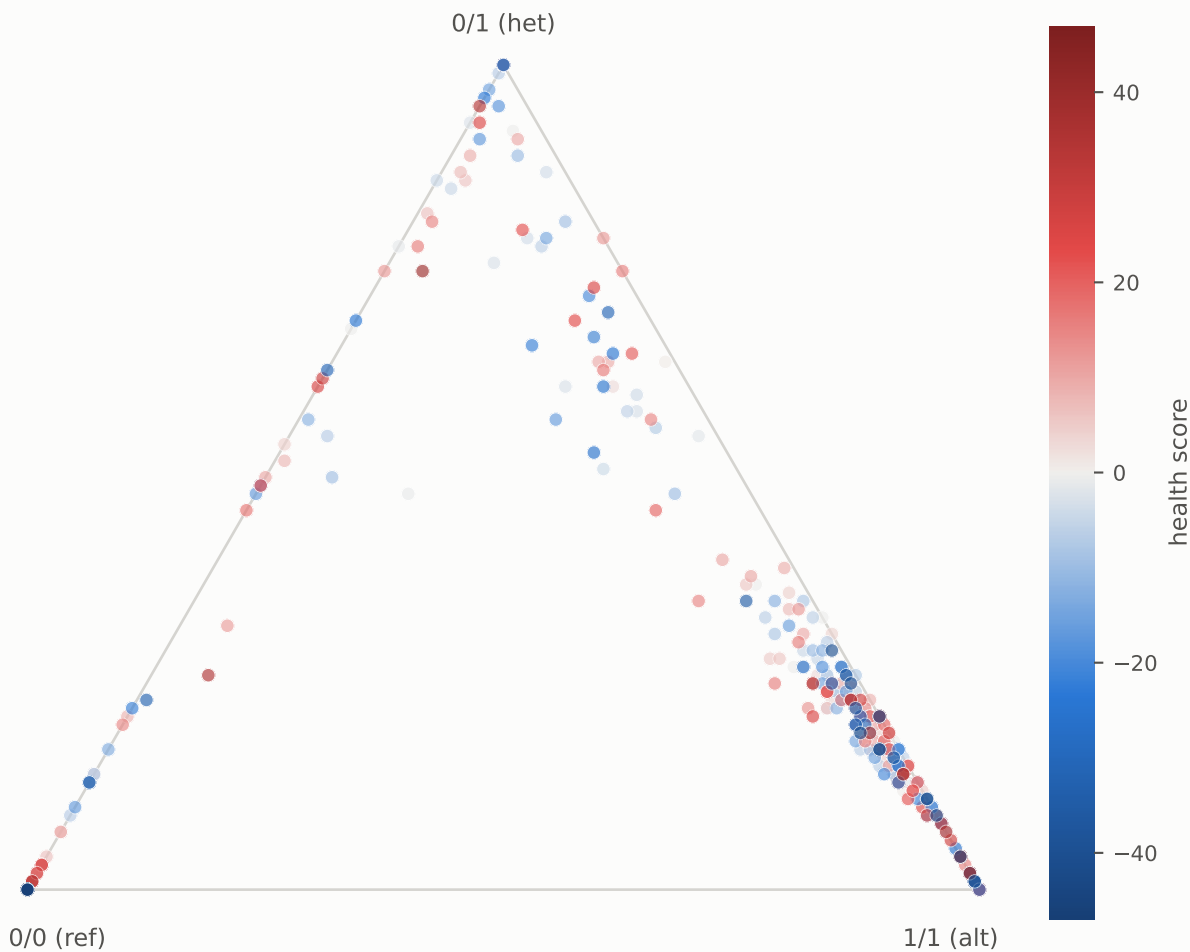
#193 by genotype uncertainty CHR_07:6,733,907 A>G
AF=0.43 DR2=0.81 $r=+0.055$ $\bar{H}=0.381$ F=1.0



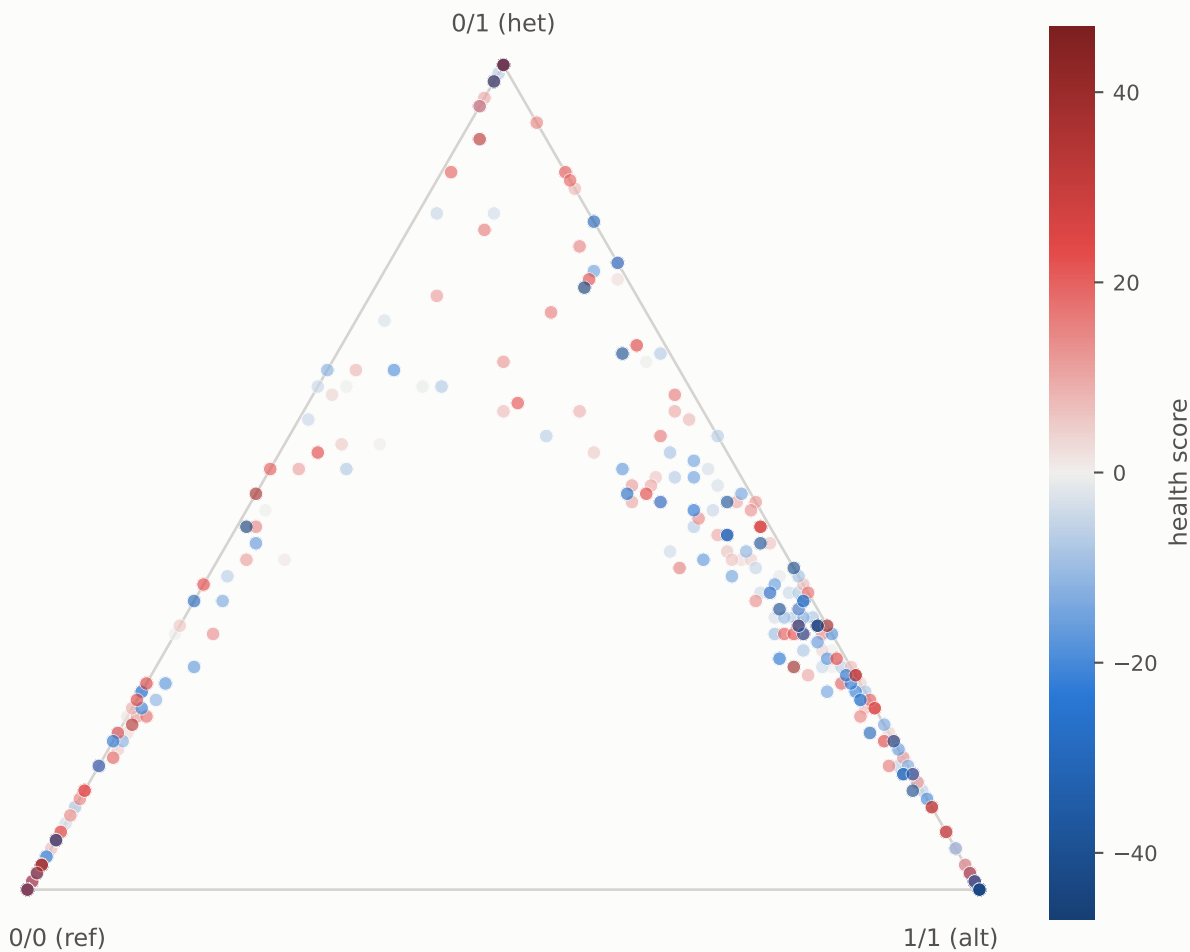
#194 by genotype uncertainty CHR_11:23,581,648 G>A
AF=0.51 DR2=0.81 $r=-0.049$ $\bar{H}=0.381$ F=0.4



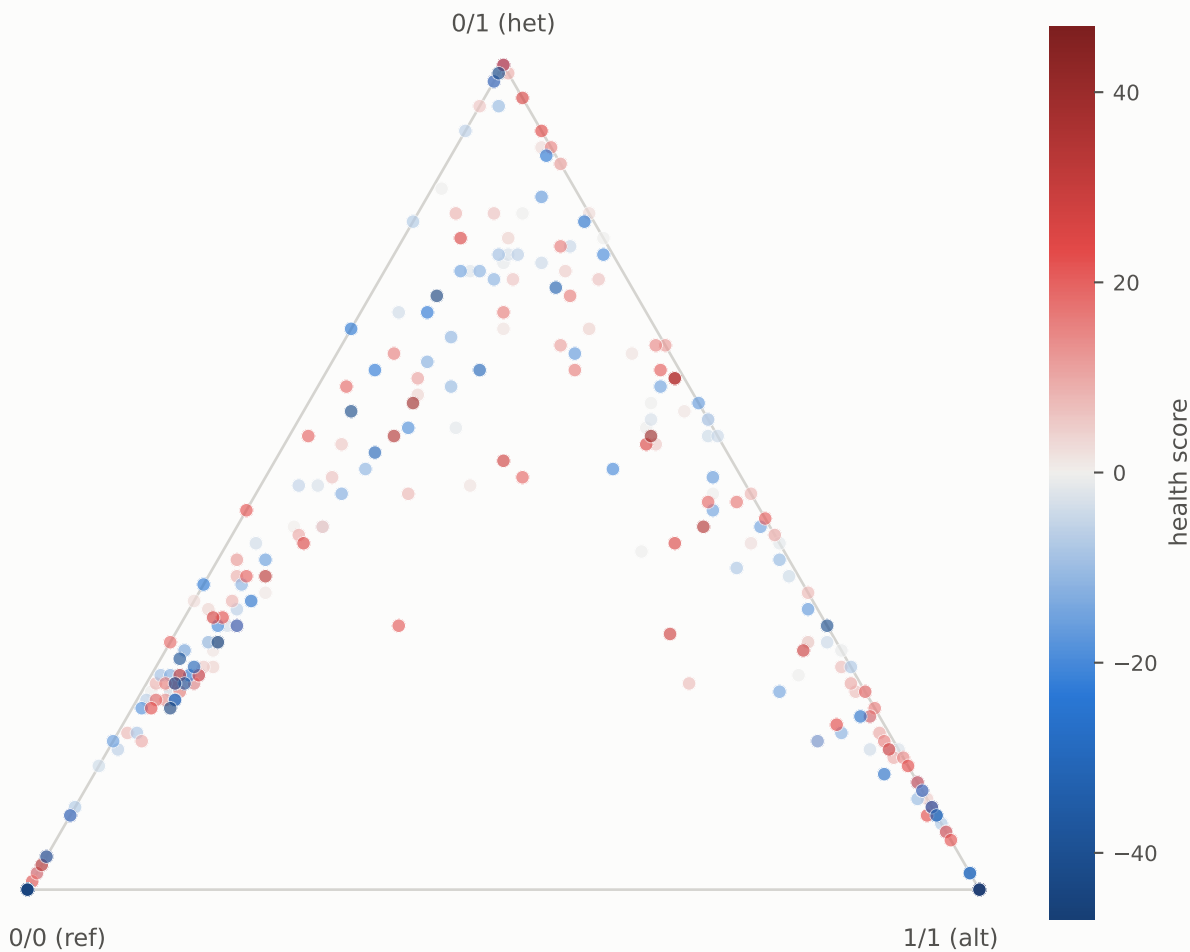
#195 by genotype uncertainty CHR_12:8,284,482 C>T
AF=0.51 DR2=0.81 $r=-0.026$ $H=0.381$ $F=0.1$



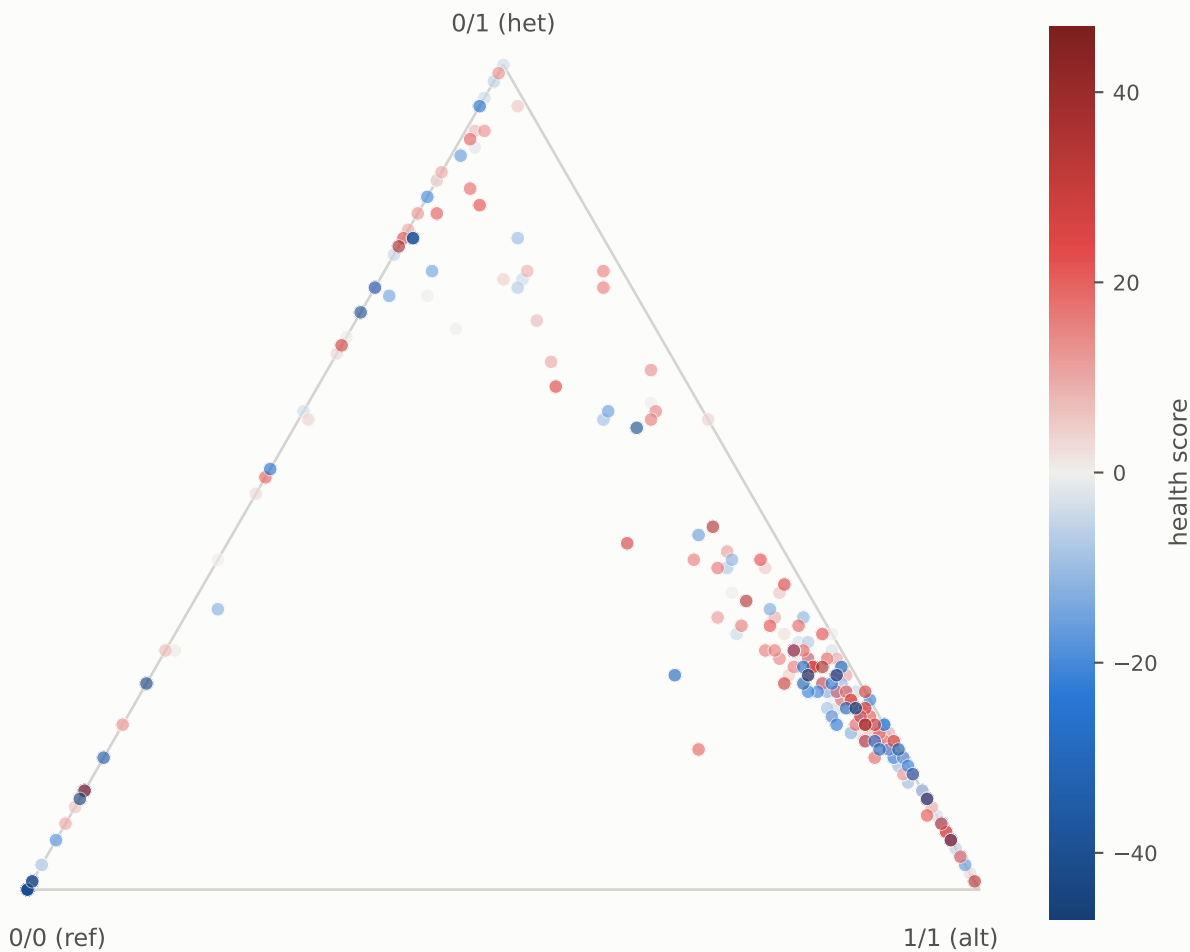
#196 by genotype uncertainty CHR_08:35,928,371 T>C
AF=0.51 DR2=0.81 $r=-0.086$ $\bar{H}=0.381$ F=1.9



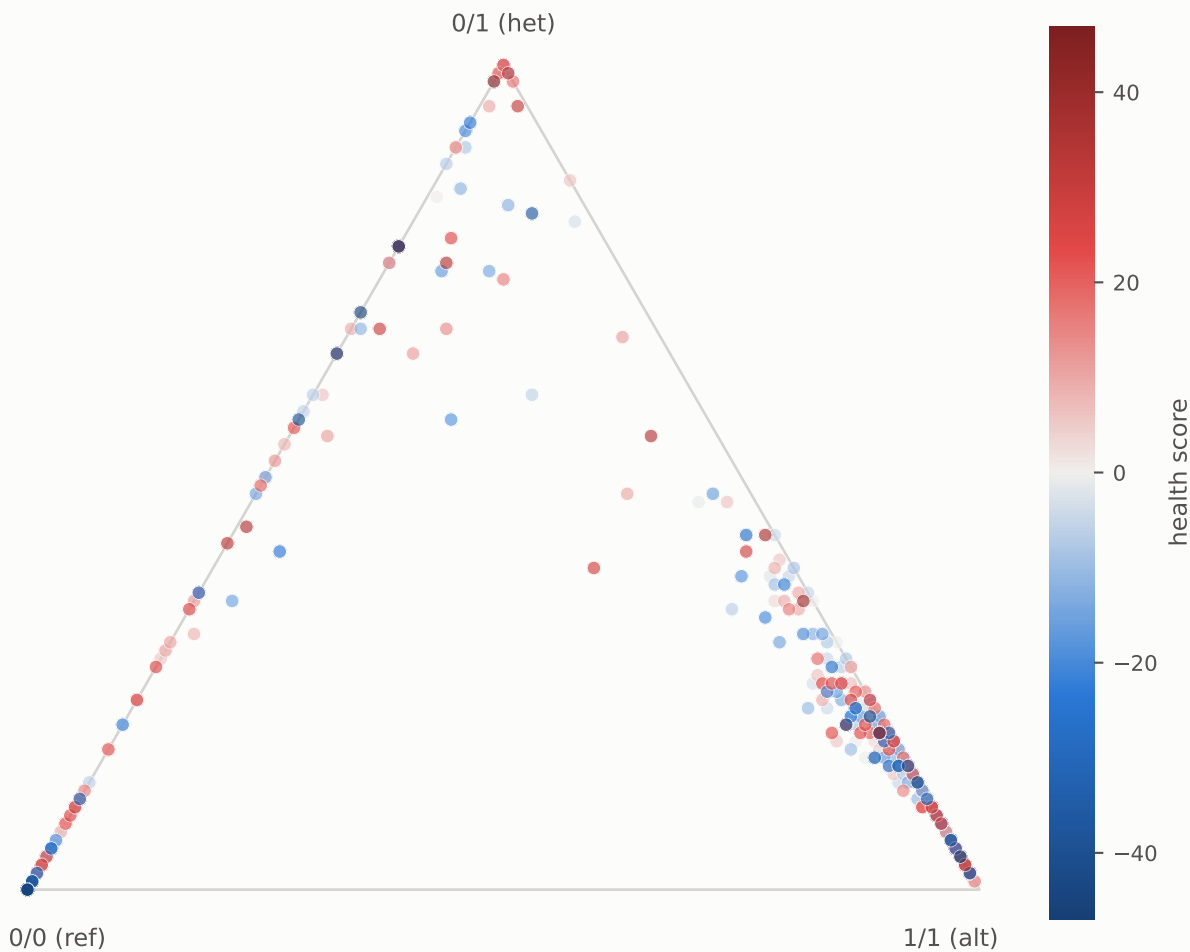
#197 by genotype uncertainty CHR_02:33,607,381 C>T
AF=0.51 DR2=0.81 $r=+0.081$ $\bar{H}=0.381$ F=1.3



#198 by genotype uncertainty CHR_04:34,782,342 A>G
AF=0.46 DR2=0.81 $r=+0.129$ $\bar{H}=0.381$ F=3.9



#199 by genotype uncertainty CHR_15:17,605,276 G>A
AF=0.57 DR2=0.81 $r=+0.013$ $\bar{H}=0.381$ F=0.6



#200 by genotype uncertainty CHR_01:50,610,753 C>G
AF=0.66 DR2=0.81 $r=+0.004$ $\bar{H}=0.381$ $F=0.2$

