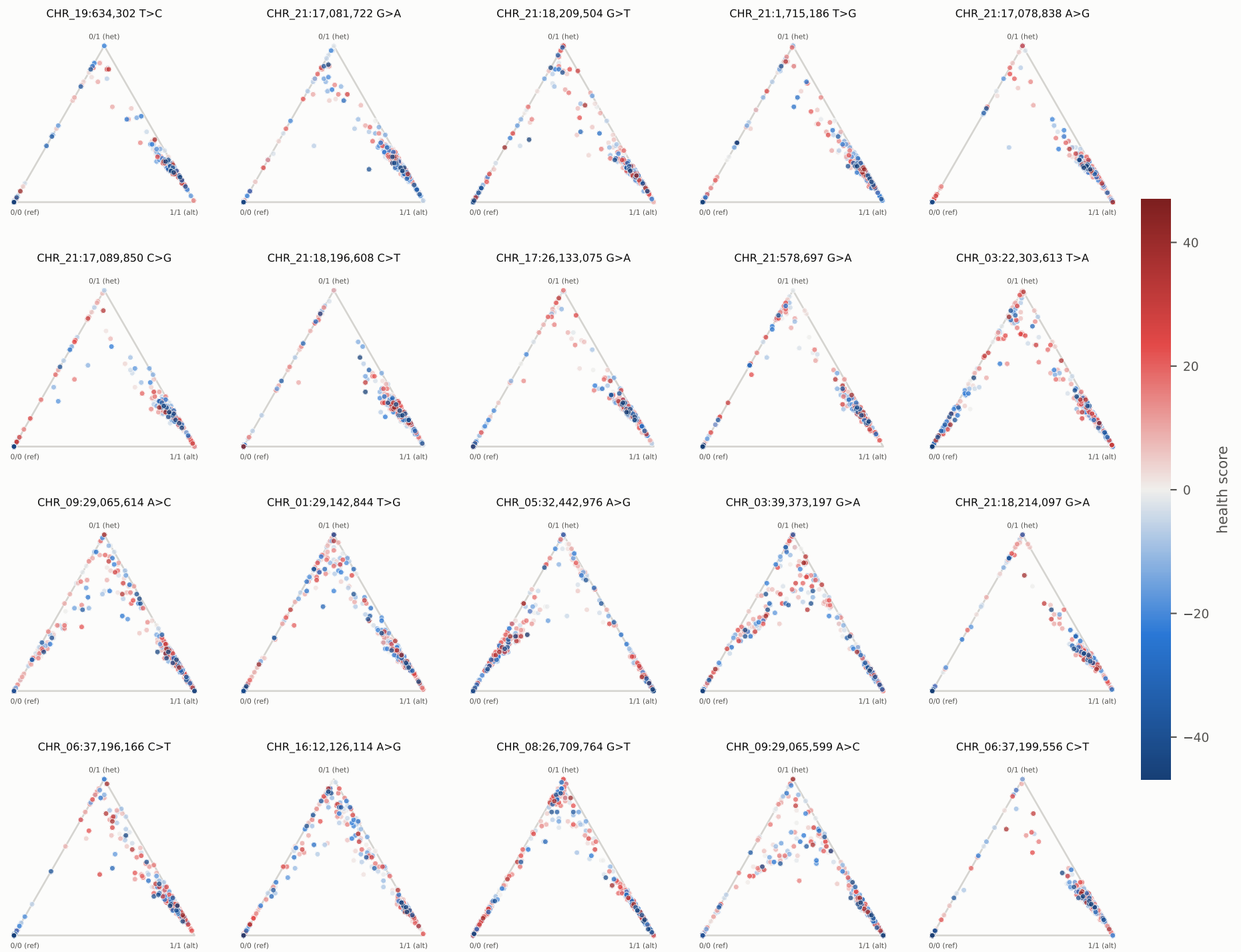
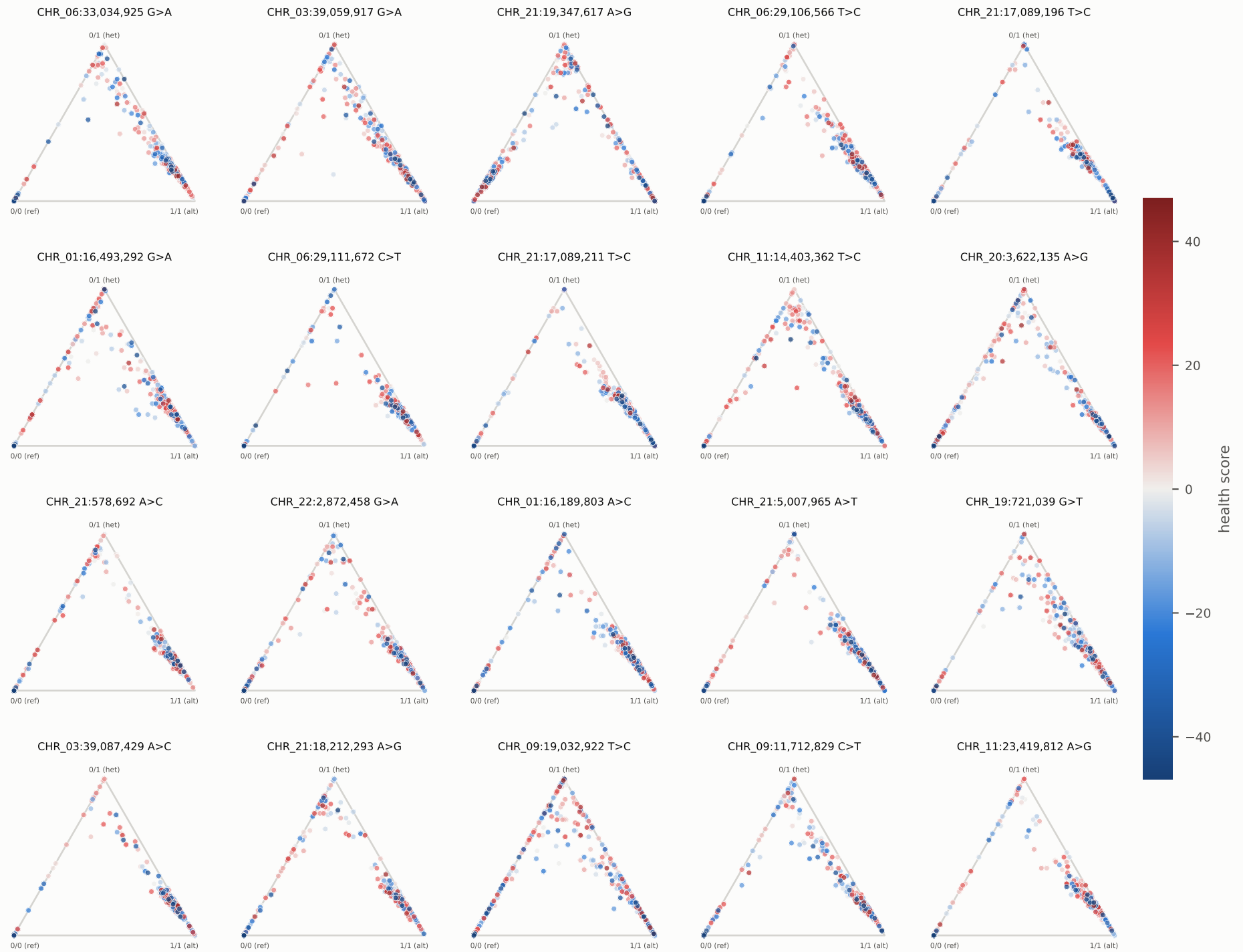


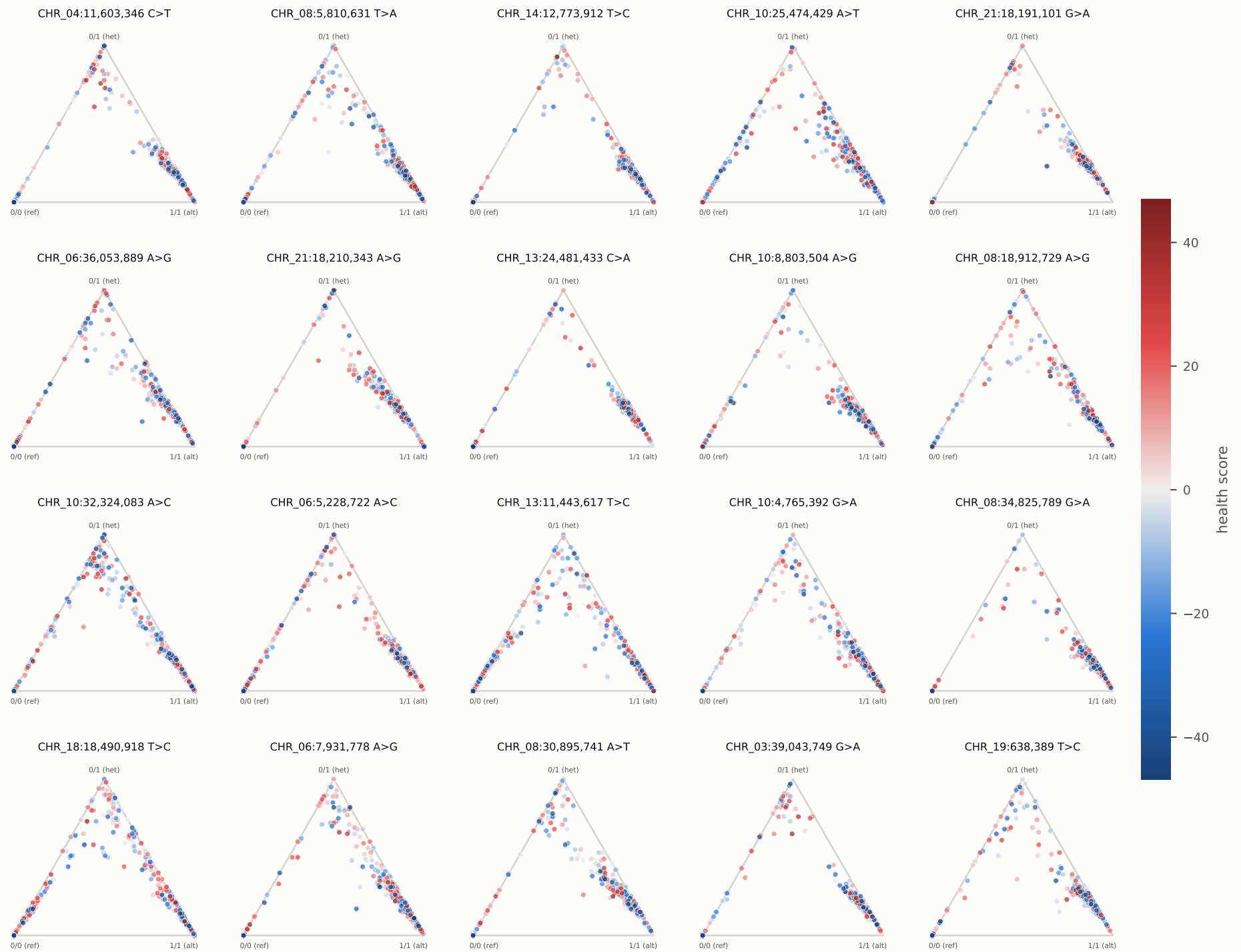
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 1/10



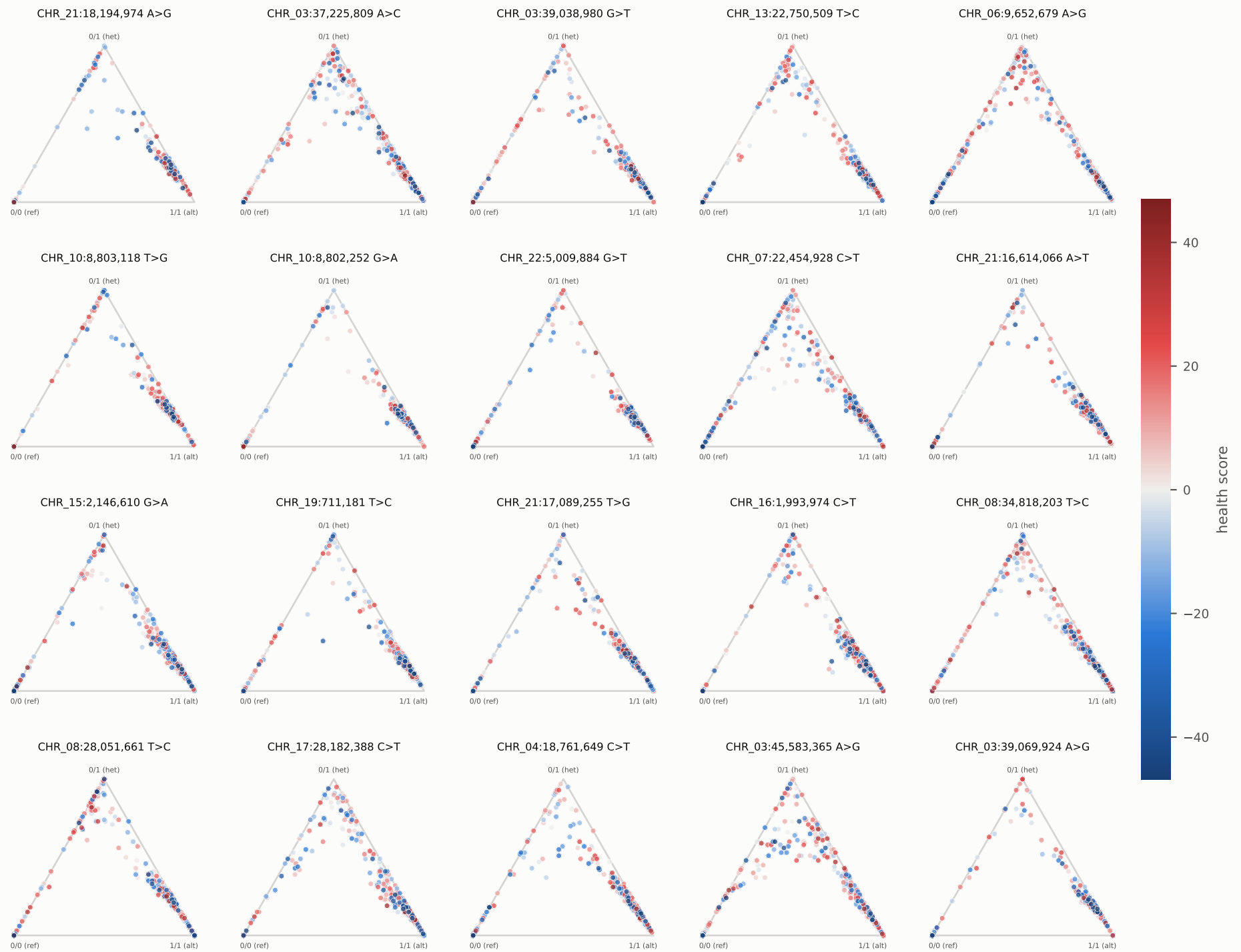
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 2/10



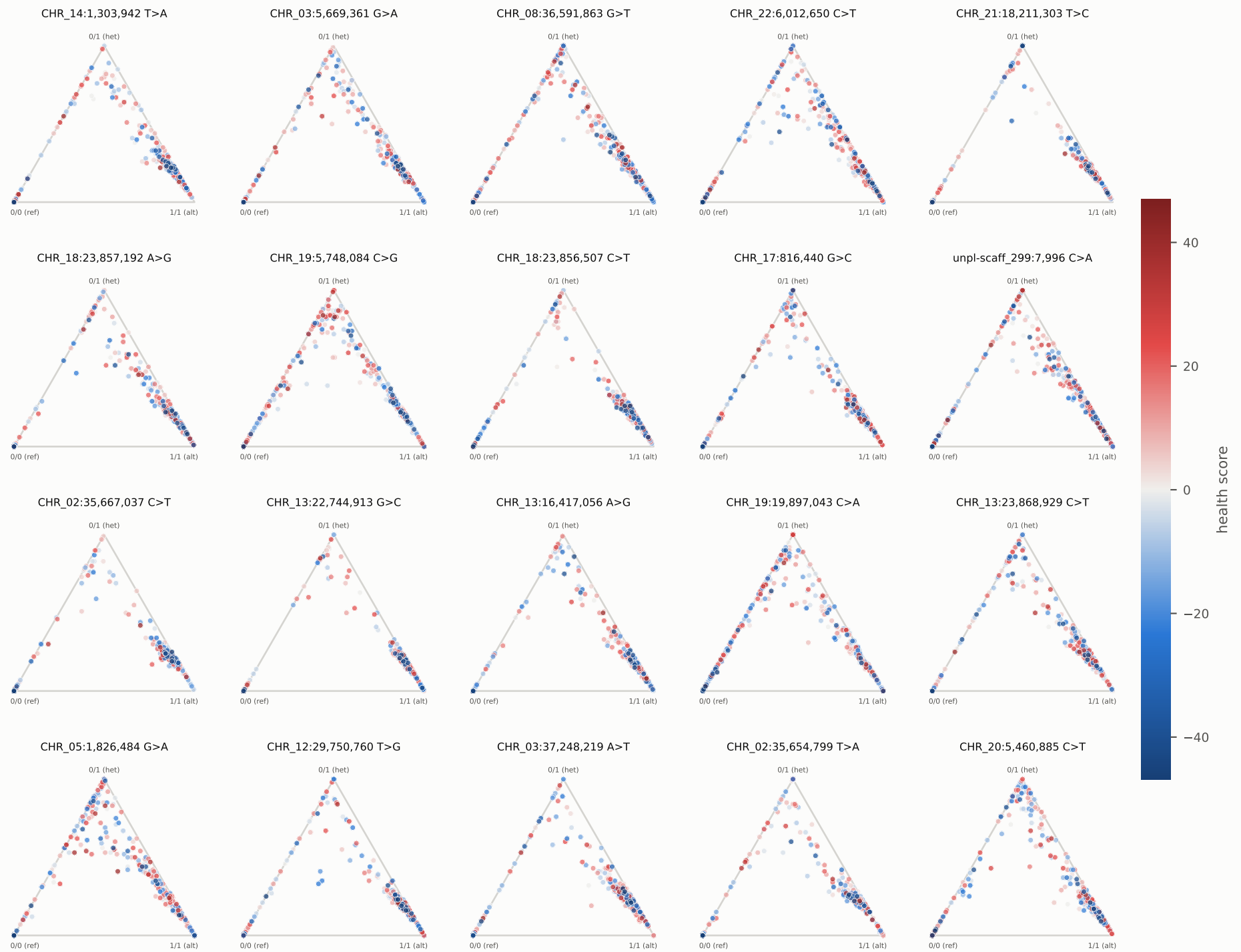
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 3/10



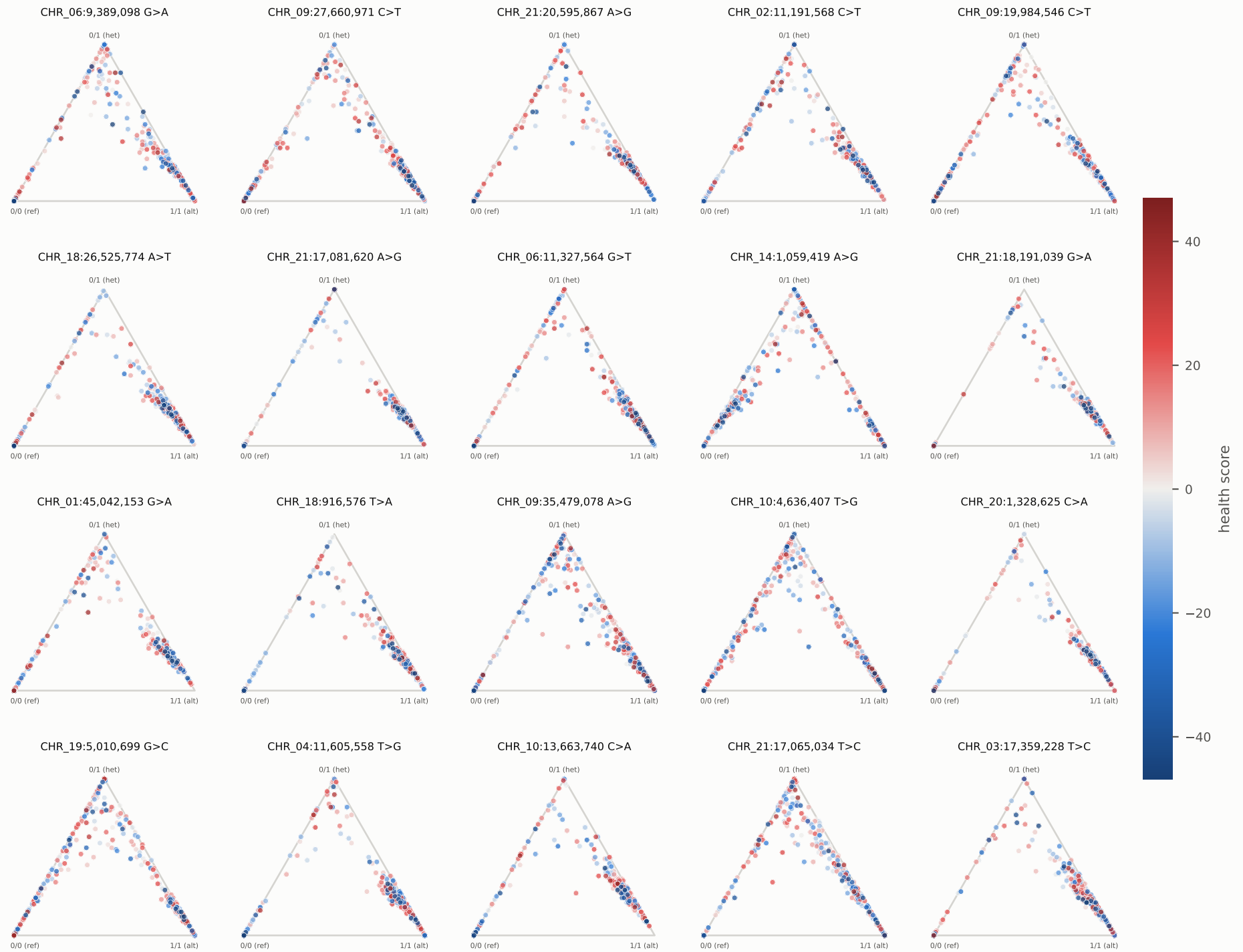
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 4/10



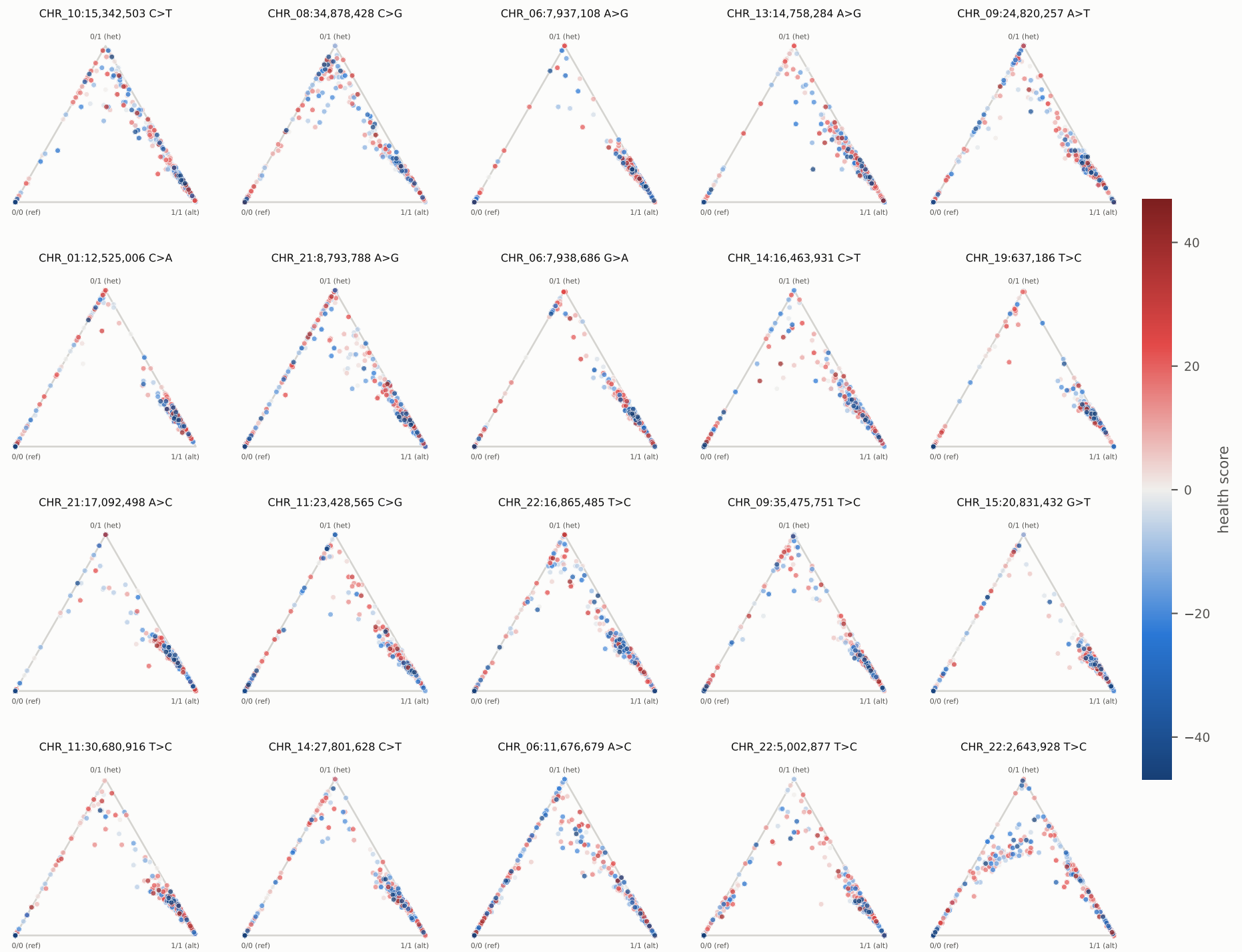
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 5/10



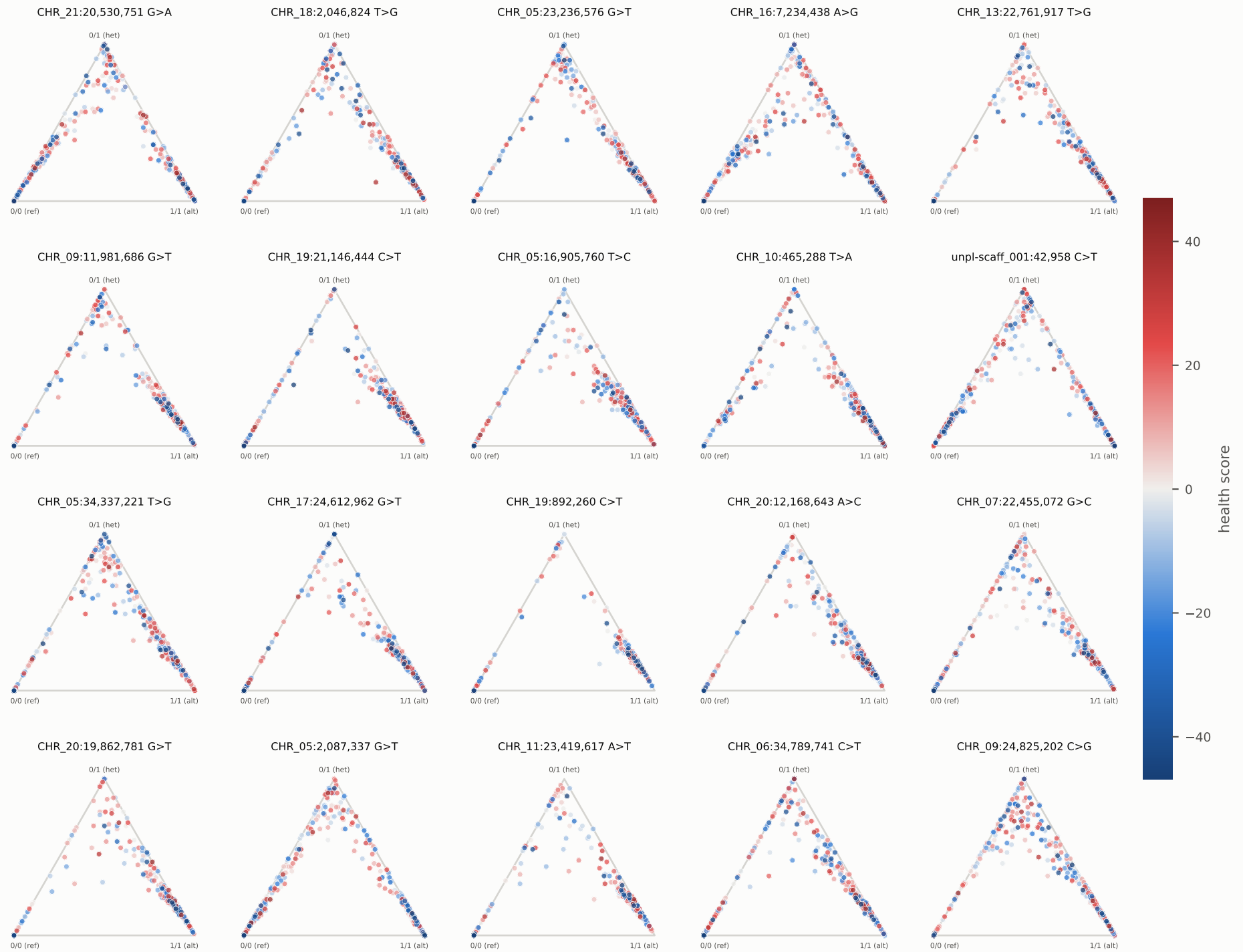
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 6/10

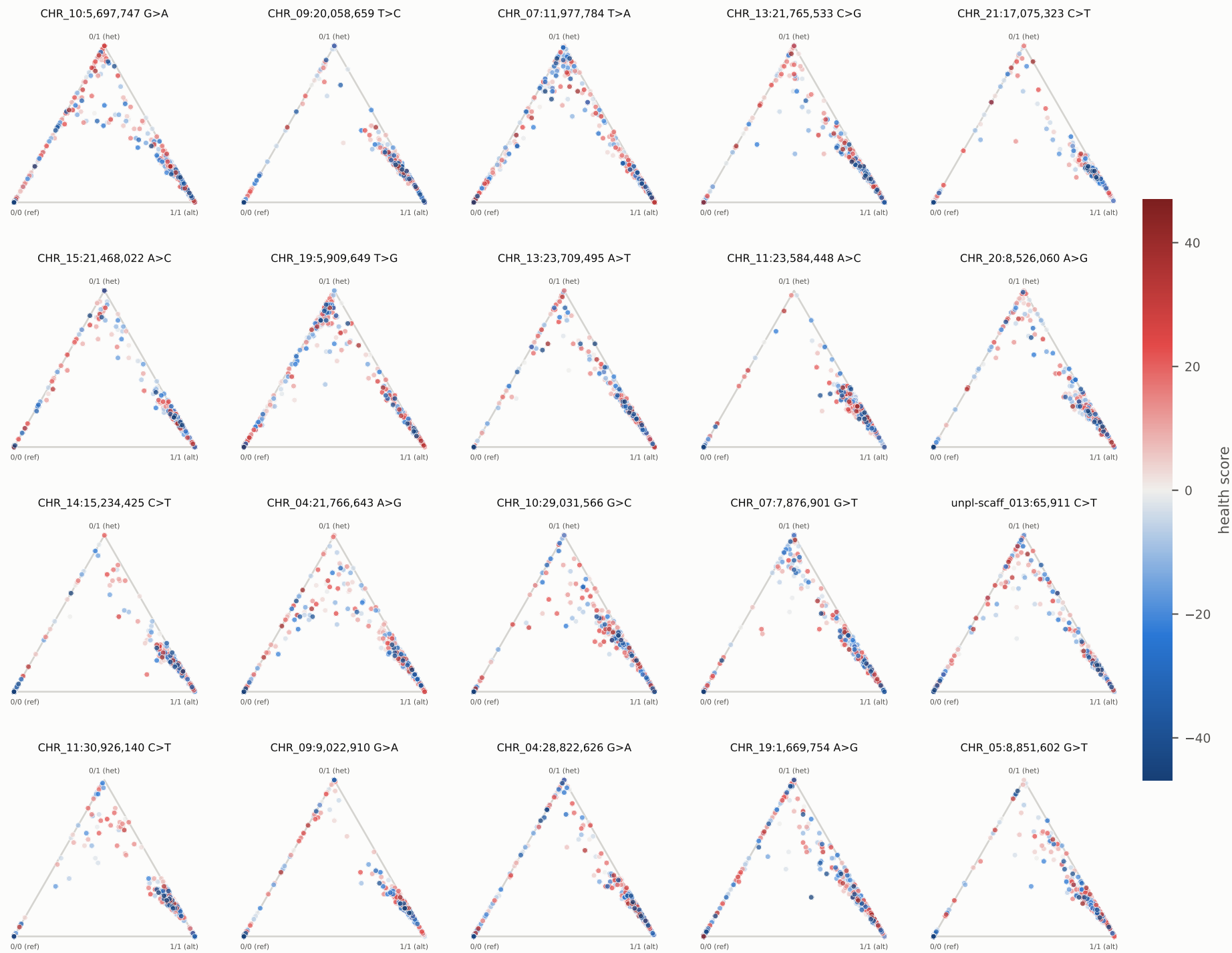


full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 7/10

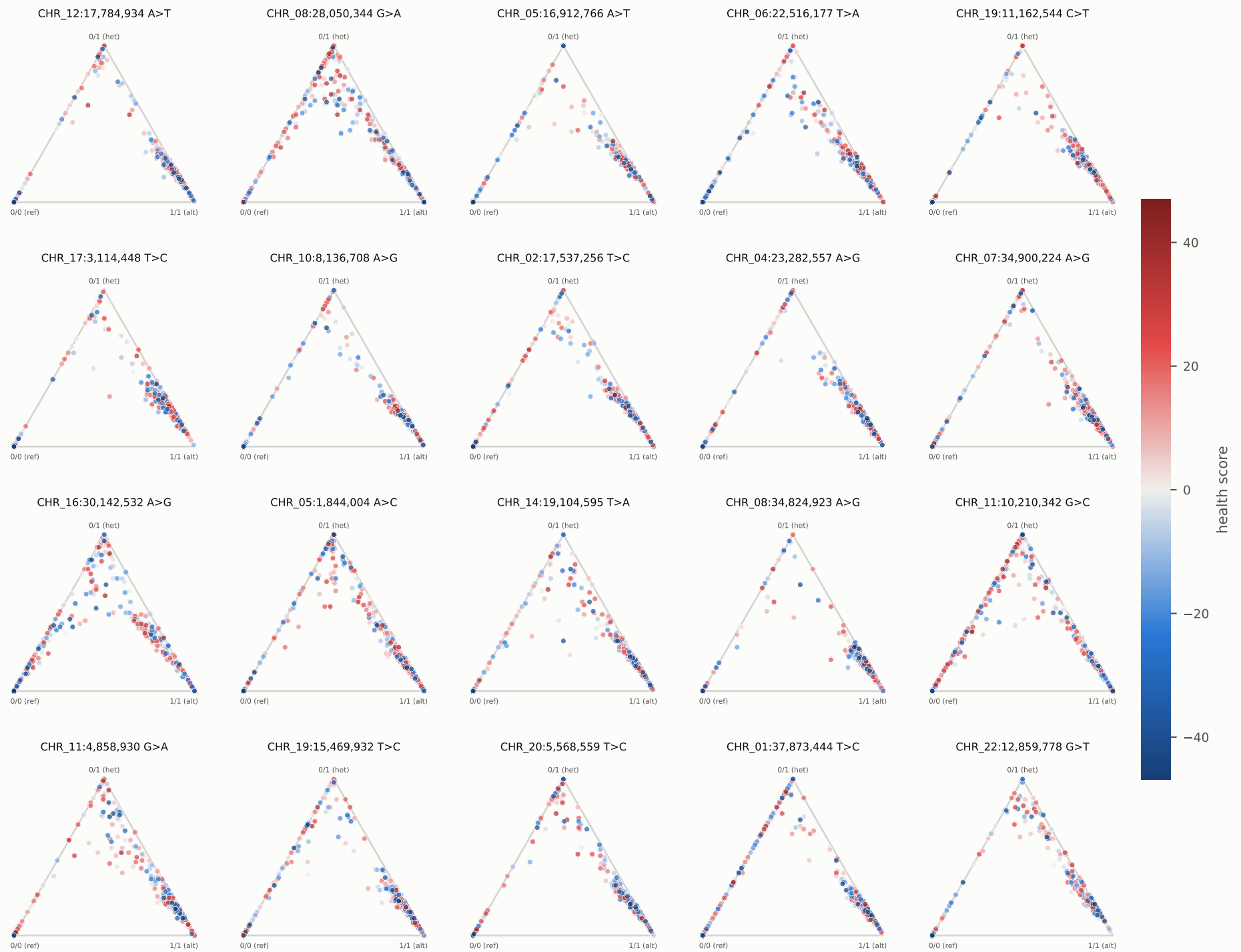


full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 8/10

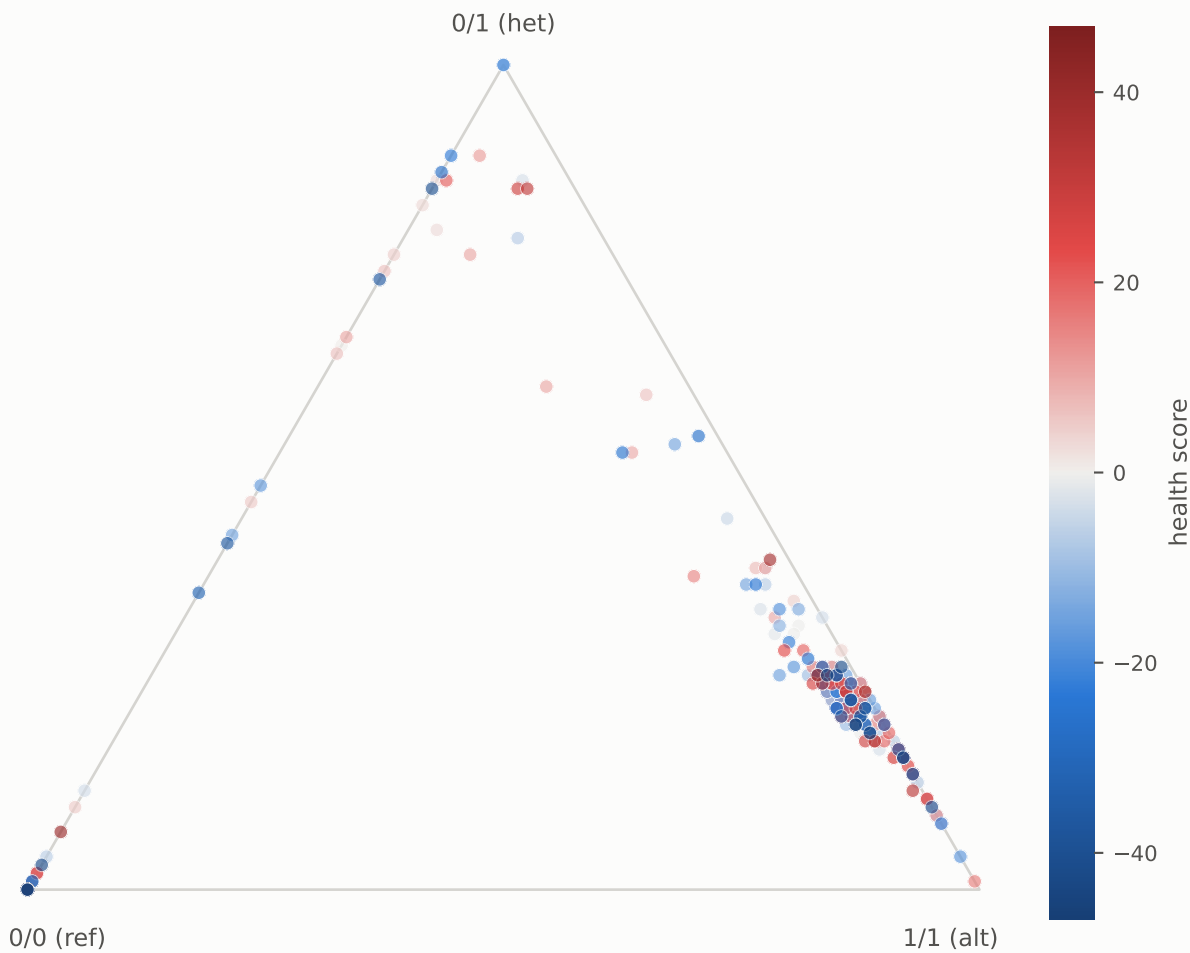




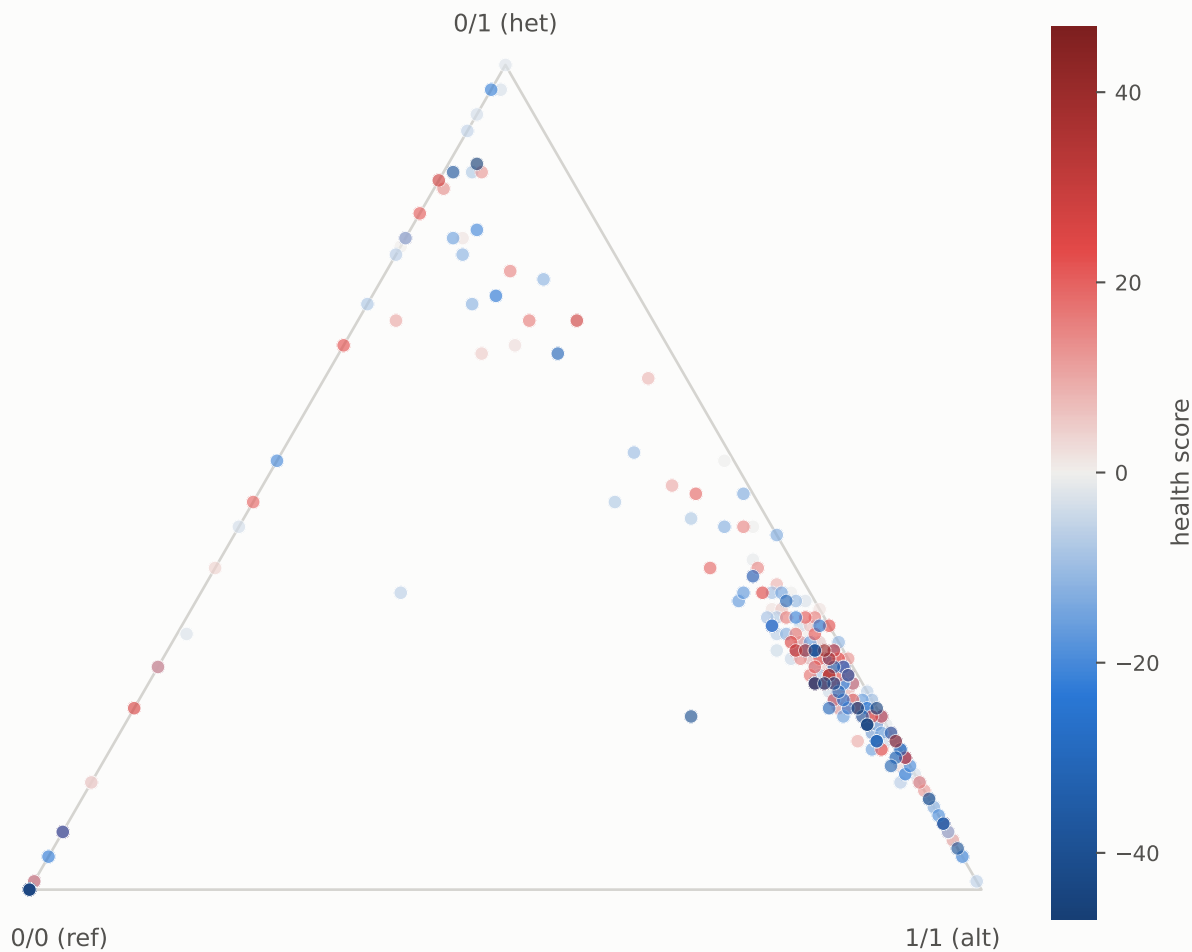
full — top 200 SNPs by genotype uncertainty (mean GP entropy) — overview 10/10



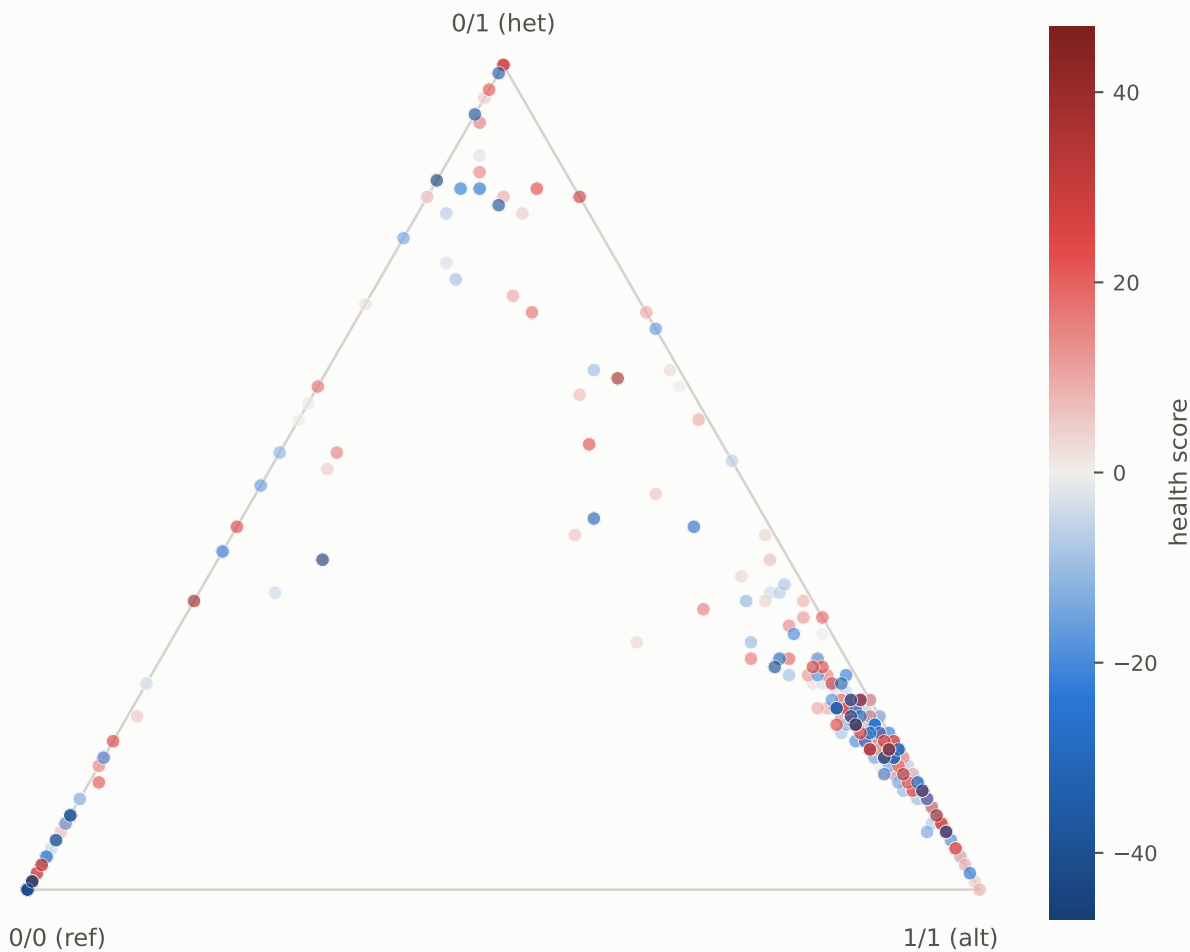
#1 by genotype uncertainty CHR_19:634,302 T>C
AF=0.52 DR2=0.81 $r=-0.095$ $\bar{H}=0.426$ $F=2.0$



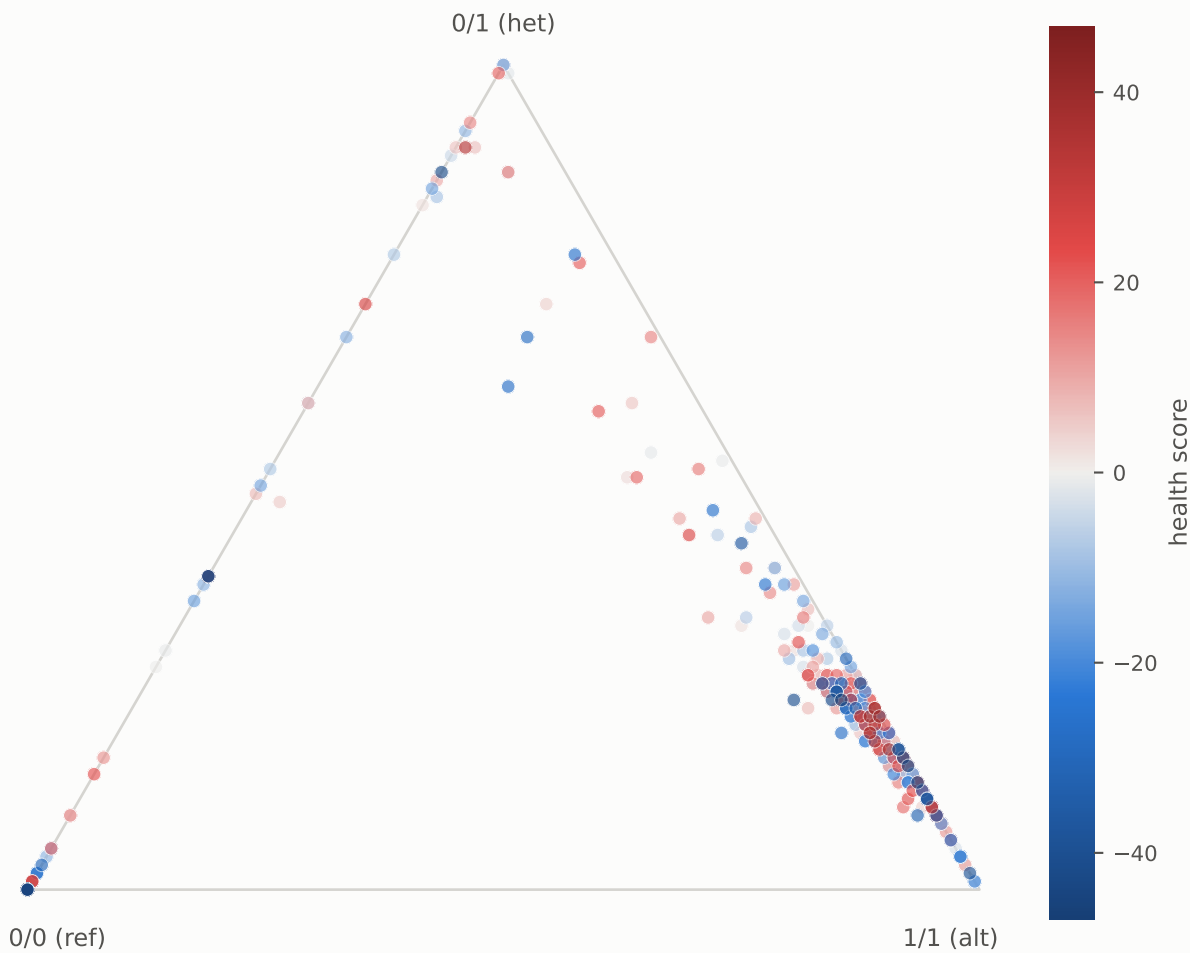
#2 by genotype uncertainty CHR_21:17,081,722 G>A
AF=0.49 DR2=0.81 $r=-0.156$ H=0.425 F=5.7



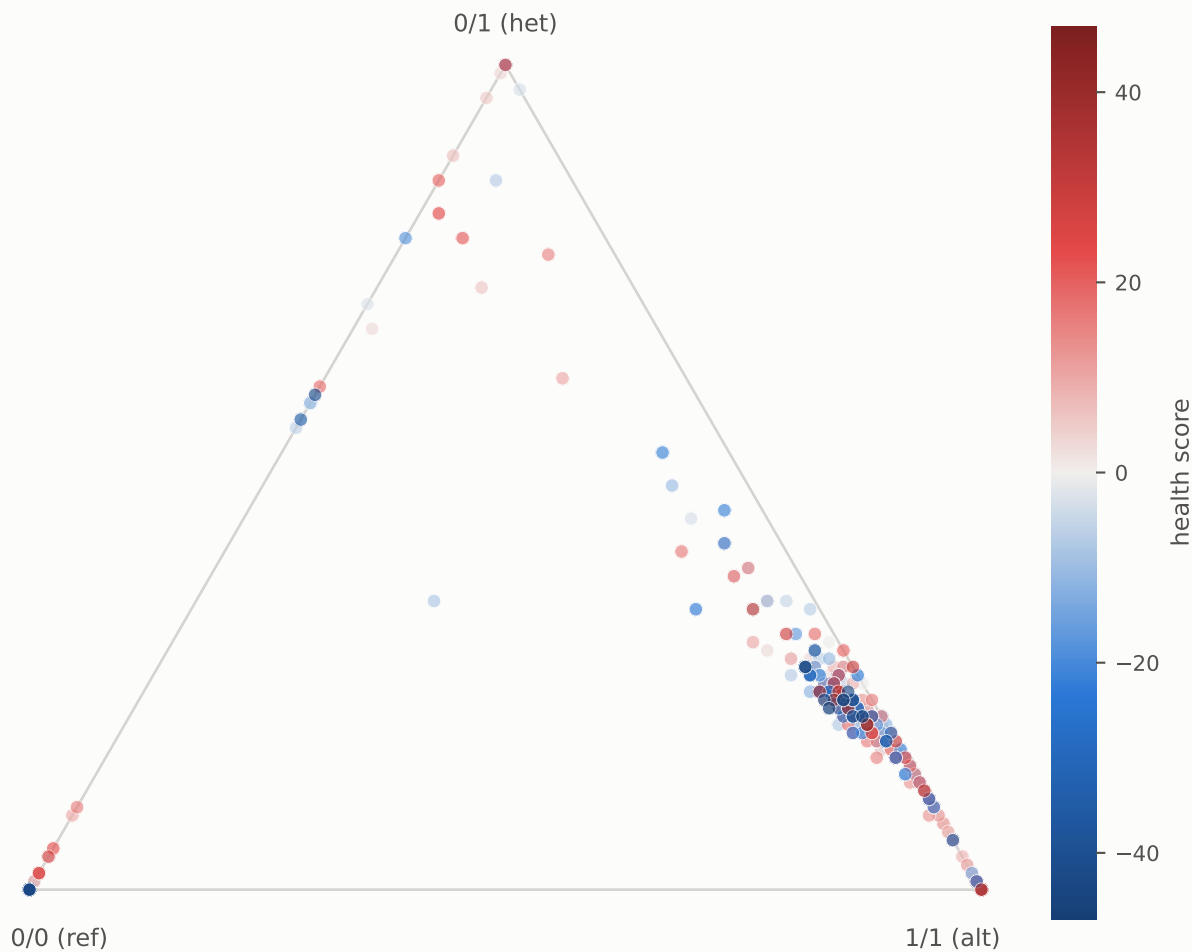
#3 by genotype uncertainty CHR_21:18,209,504 G>T
AF=0.55 DR2=0.81 r=+0.049 H=0.417 F=0.6



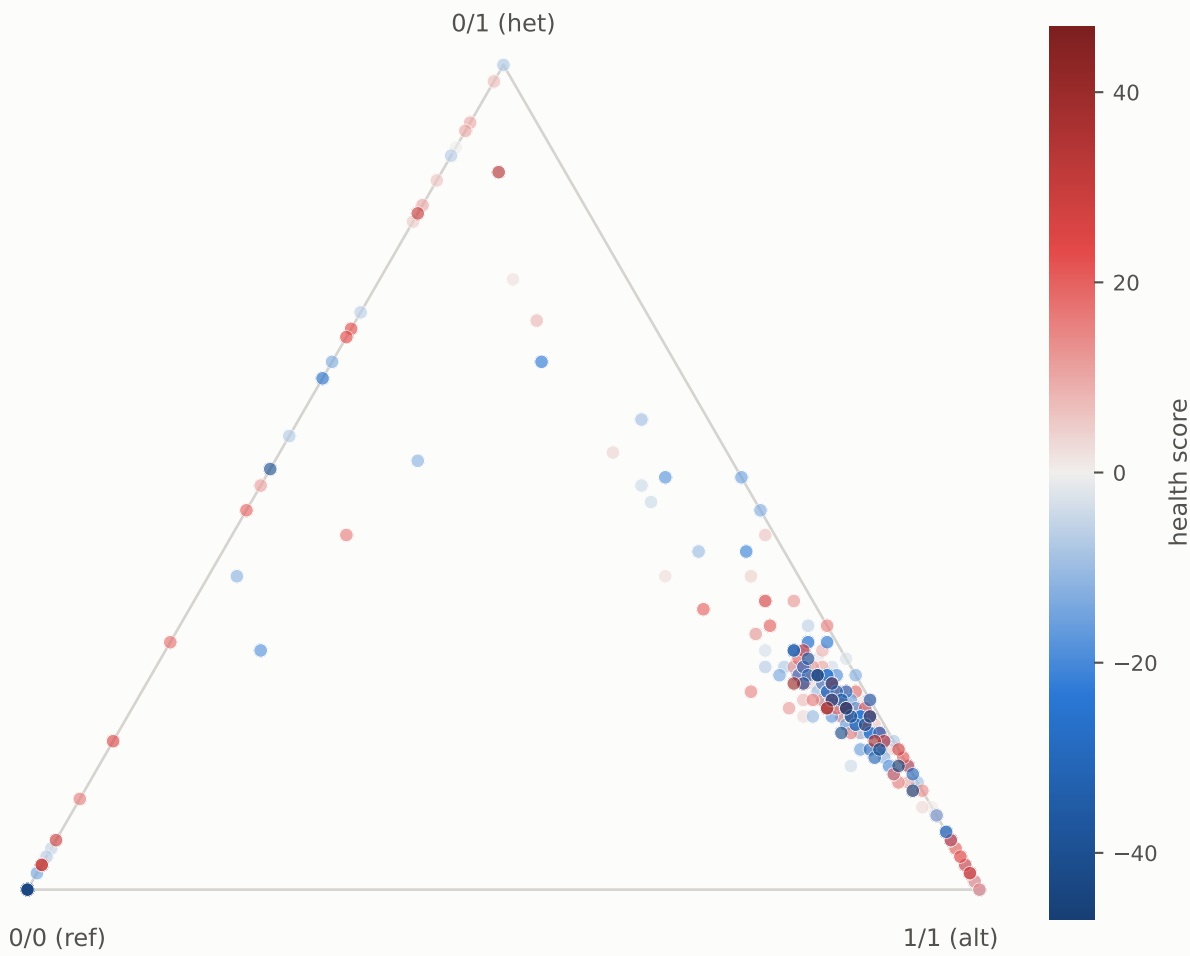
#4 by genotype uncertainty CHR_21:1,715,186 T>G
AF=0.57 DR2=0.82 $r=-0.040$ $\bar{H}=0.417$ F=0.4



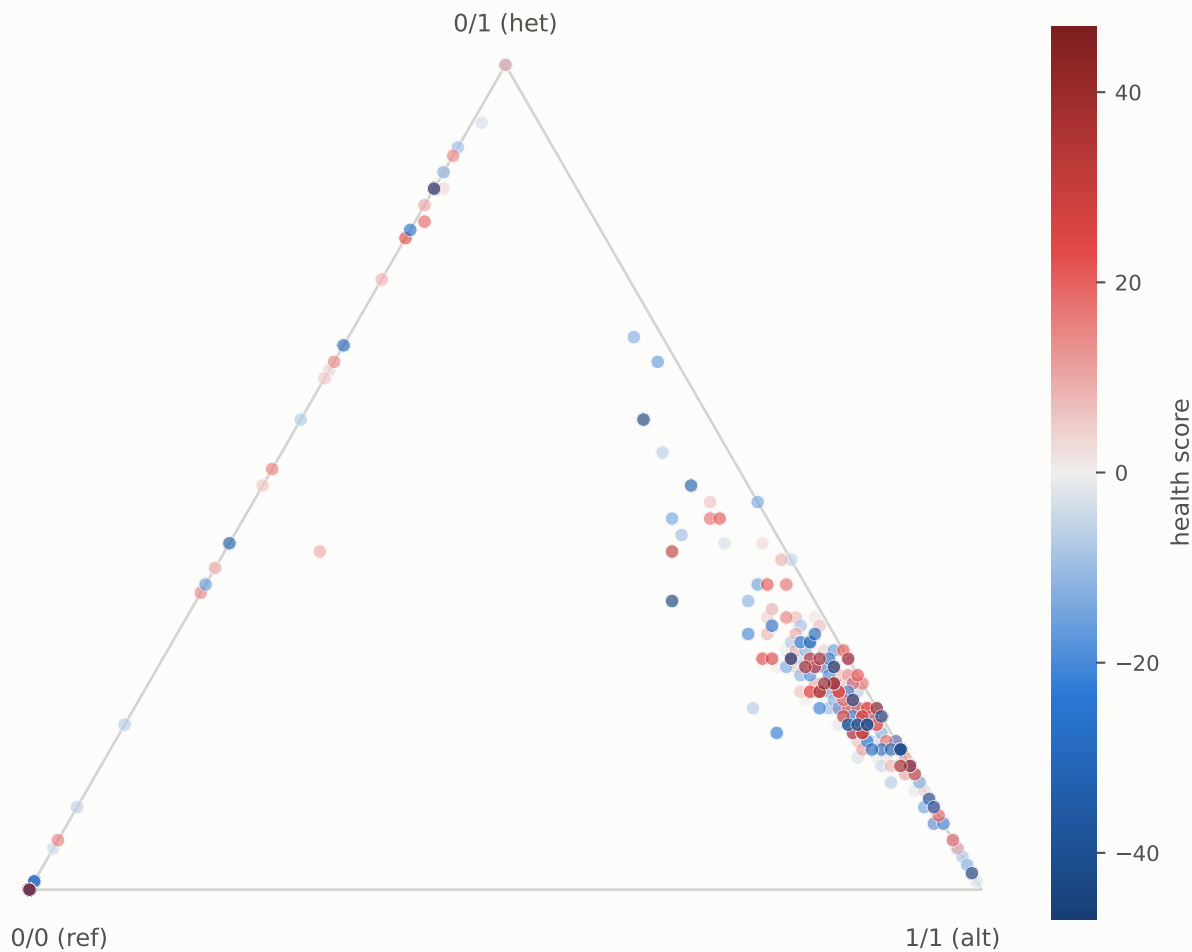
#5 by genotype uncertainty CHR_21:17,078,838 A>G
AF=0.56 DR2=0.81 r=-0.094 H=0.416 F=2.7



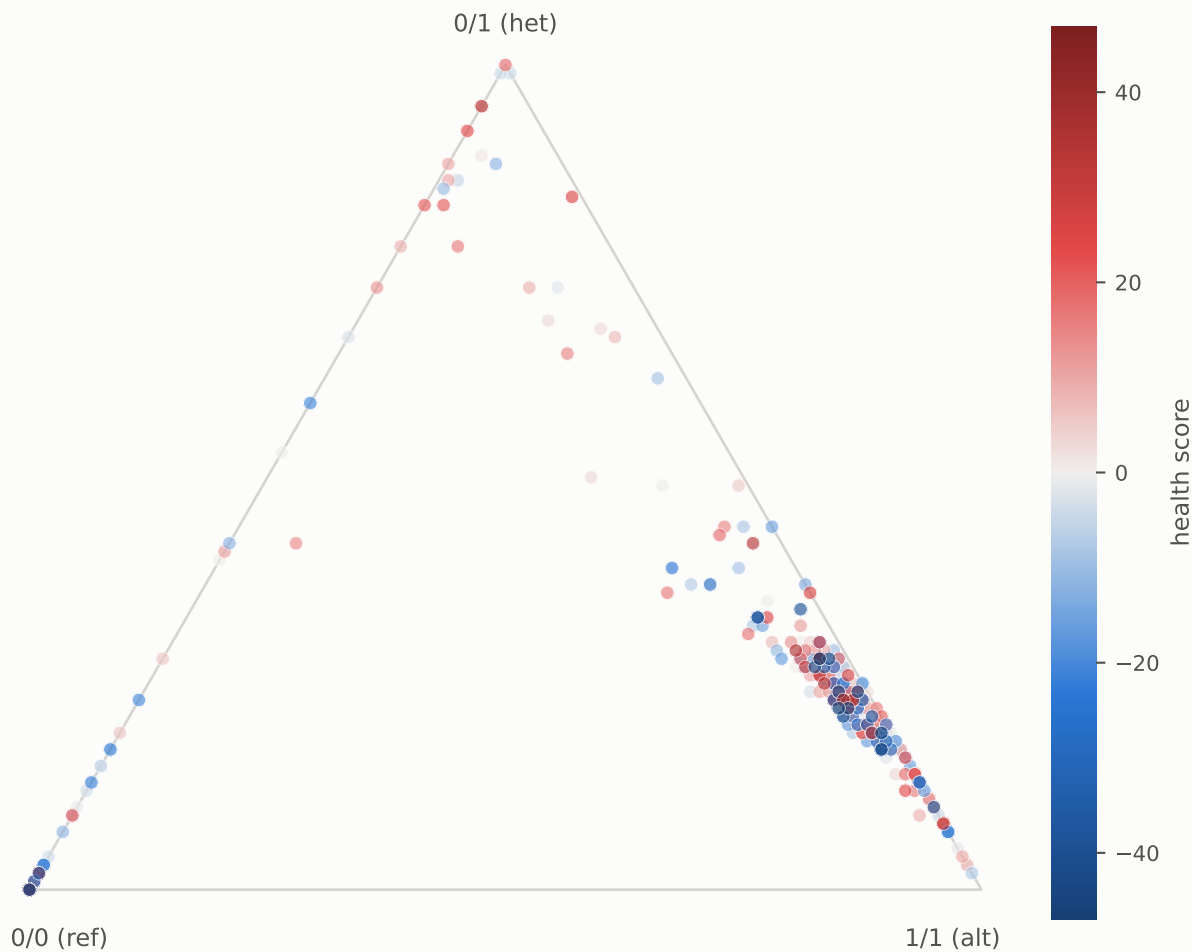
#6 by genotype uncertainty CHR_21:17,089,850 C>G
AF=0.52 DR2=0.81 $r=-0.154$ H=0.415 F=5.9



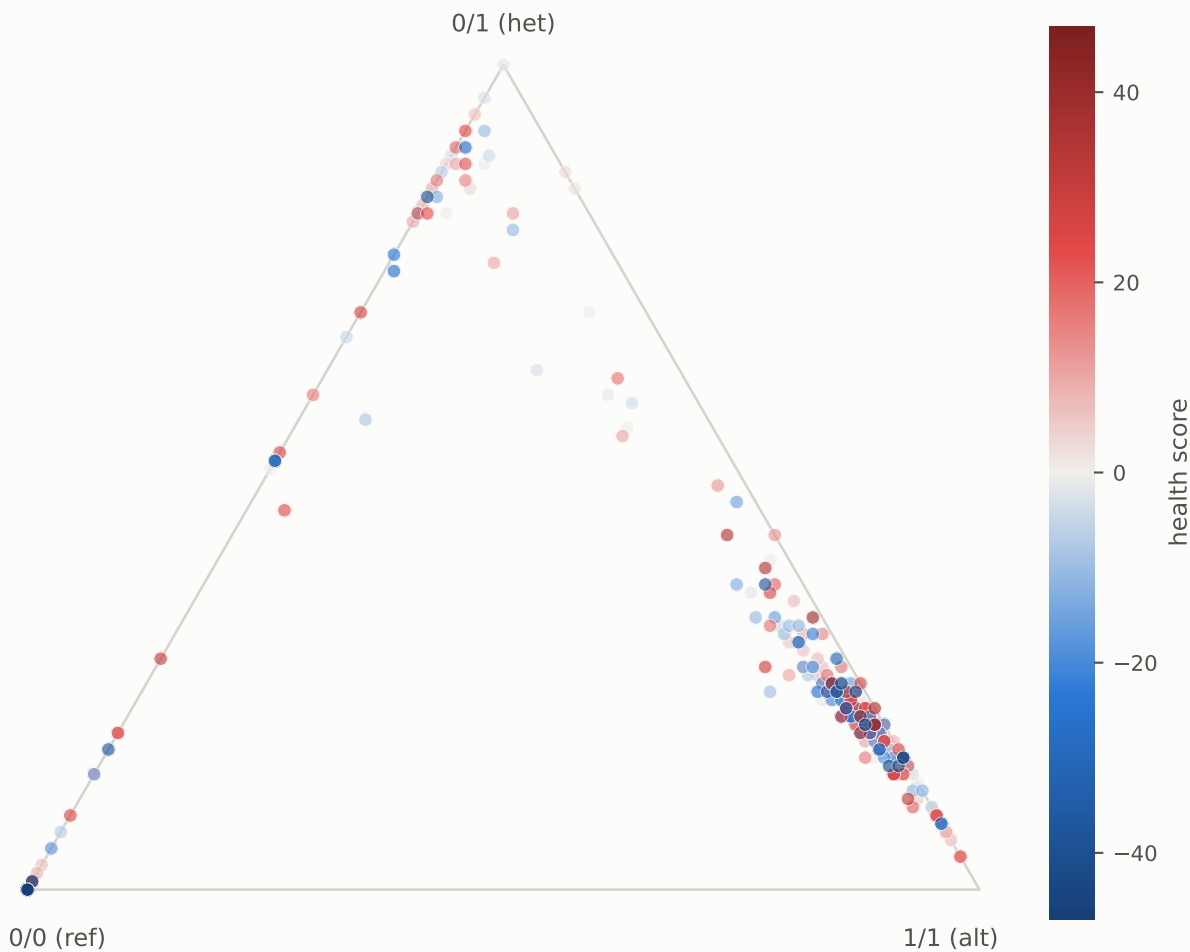
#7 by genotype uncertainty CHR_21:18,196,608 C>T
AF=0.51 DR2=0.81 $r=-0.021$ $H=0.415$ $F=0.8$



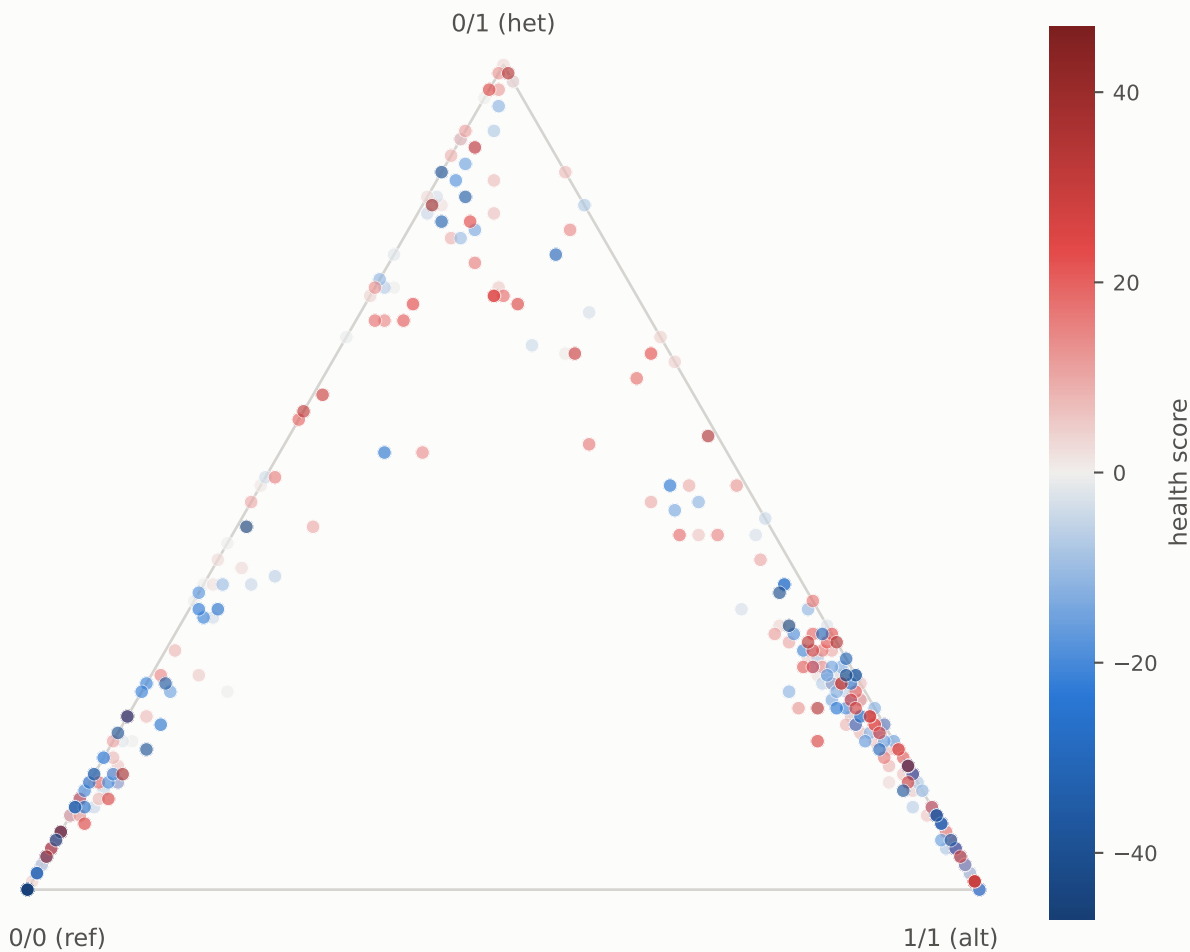
#8 by genotype uncertainty CHR_17:26,133,075 G>A
AF=0.52 DR2=0.81 r=+0.020 H=0.414 F=2.0



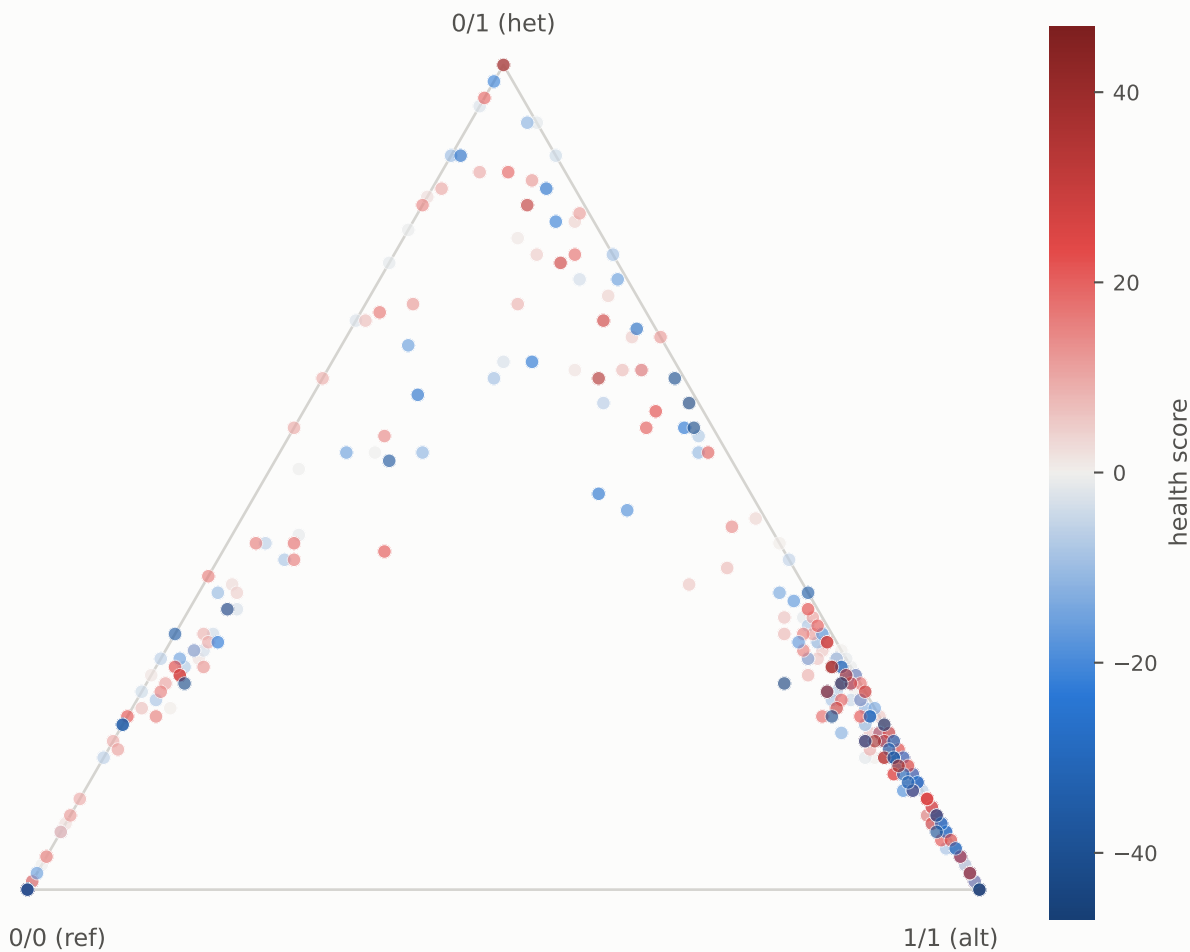
#9 by genotype uncertainty CHR_21:578,697 G>A
AF=0.53 DR2=0.81 $r=+0.023$ $\bar{H}=0.414$ F=0.2



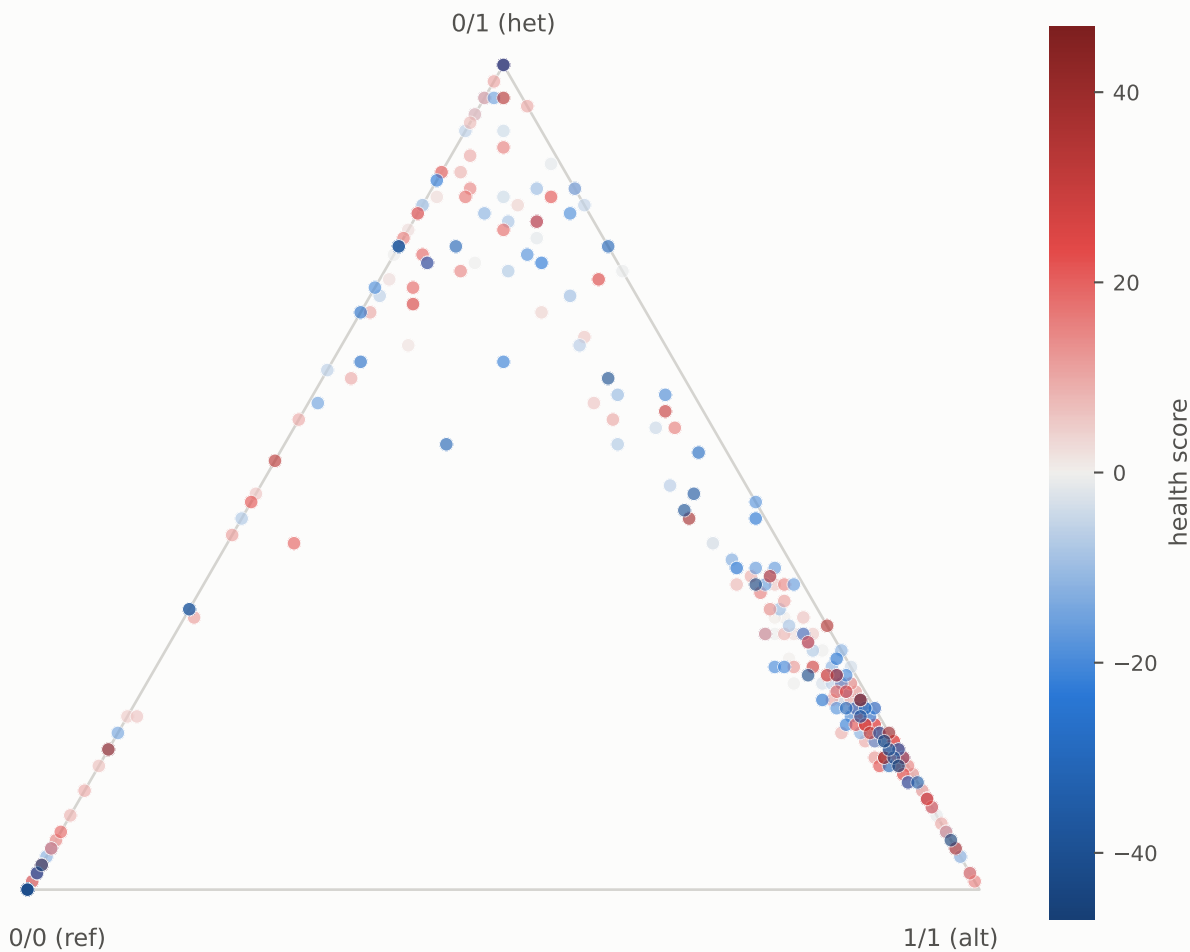
#10 by genotype uncertainty CHR_03:22,303,613 T>A
AF=0.48 DR2=0.81 r=+0.076 H=0.414 F=5.7



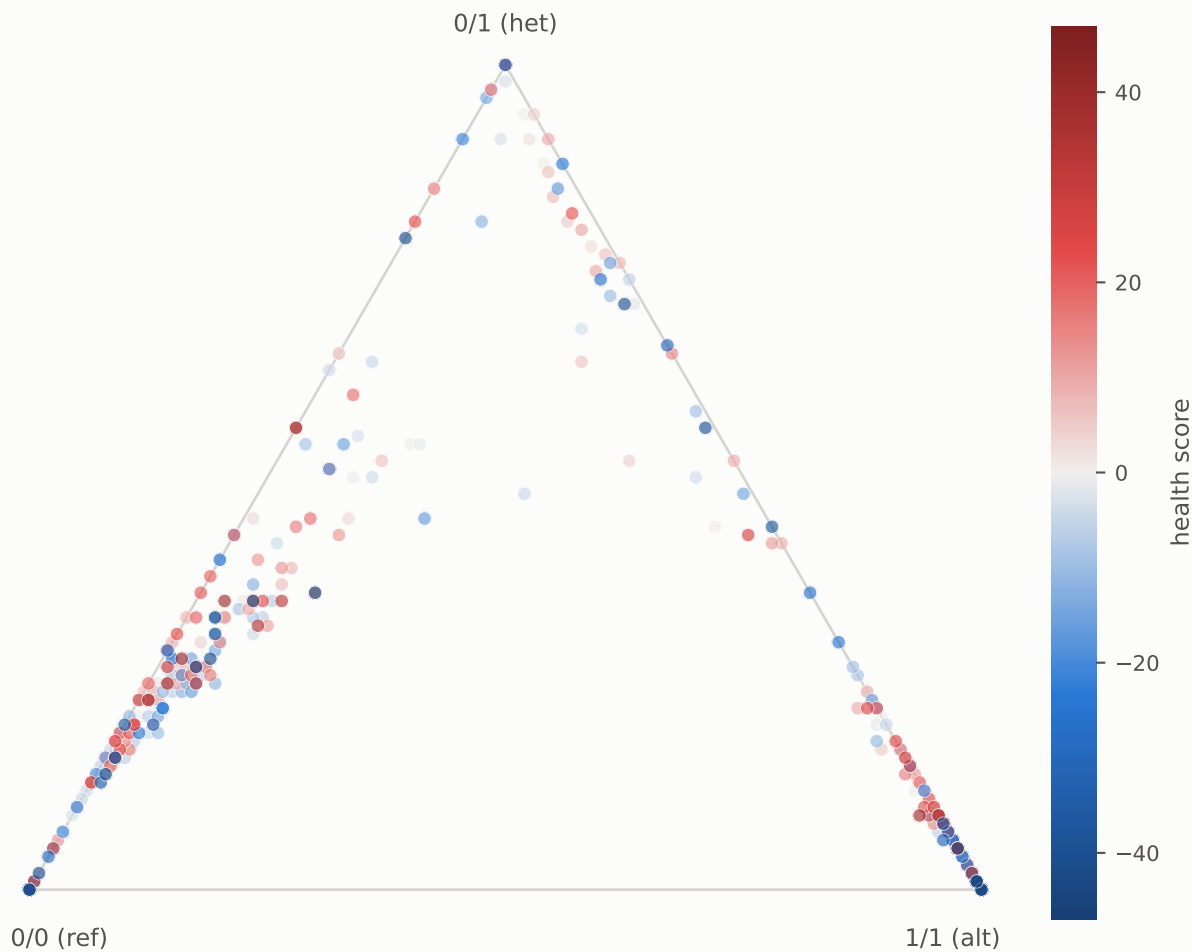
#11 by genotype uncertainty CHR_09:29,065,614 A>C
AF=0.54 DR2=0.81 $r=-0.015$ $\bar{H}=0.413$ F=0.1



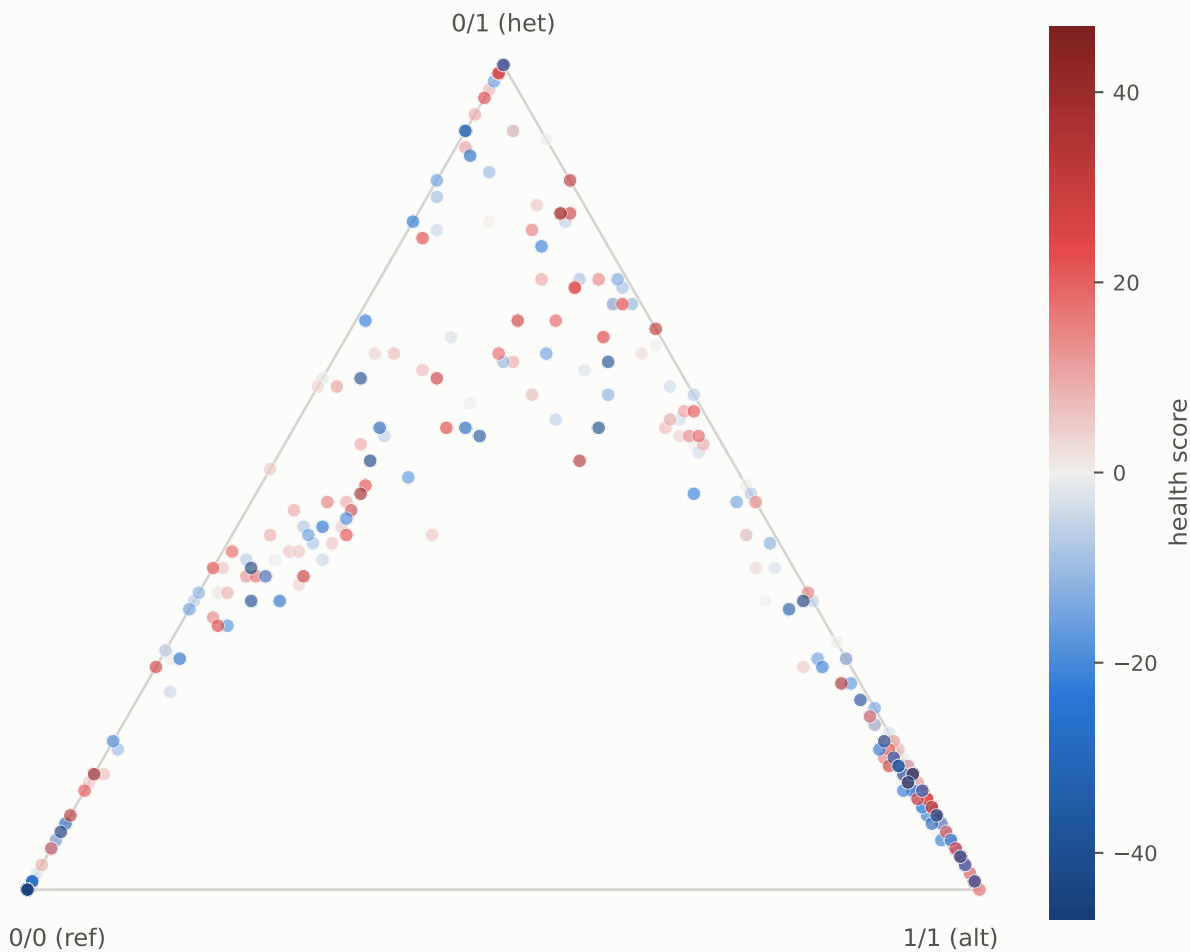
#12 by genotype uncertainty CHR_01:29,142,844 T>G
AF=0.47 DR2=0.81 $r=-0.014$ $\bar{H}=0.411$ F=1.1



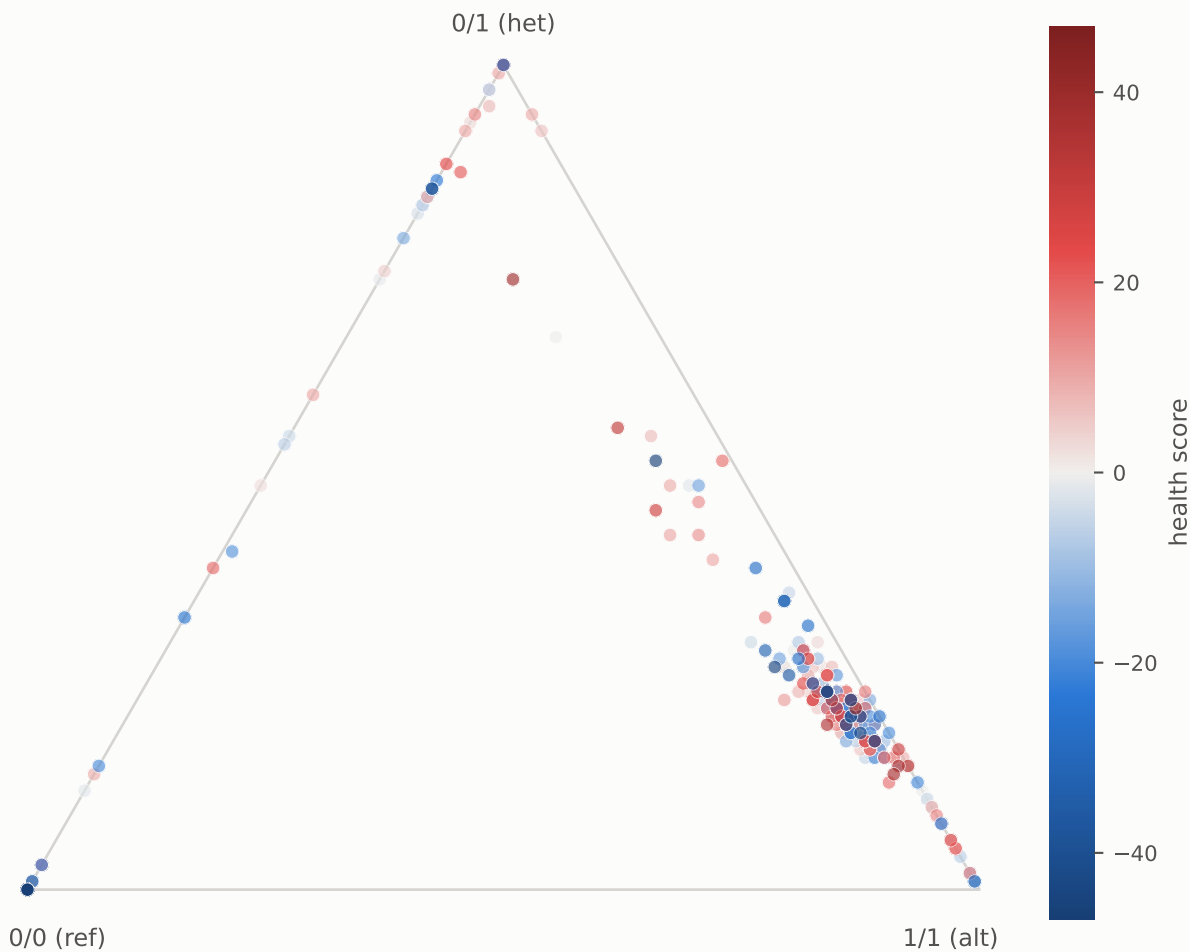
#13 by genotype uncertainty CHR_05:32,442,976 A>G
AF=0.47 DR2=0.81 $r=+0.009$ H=0.411 F=0.5



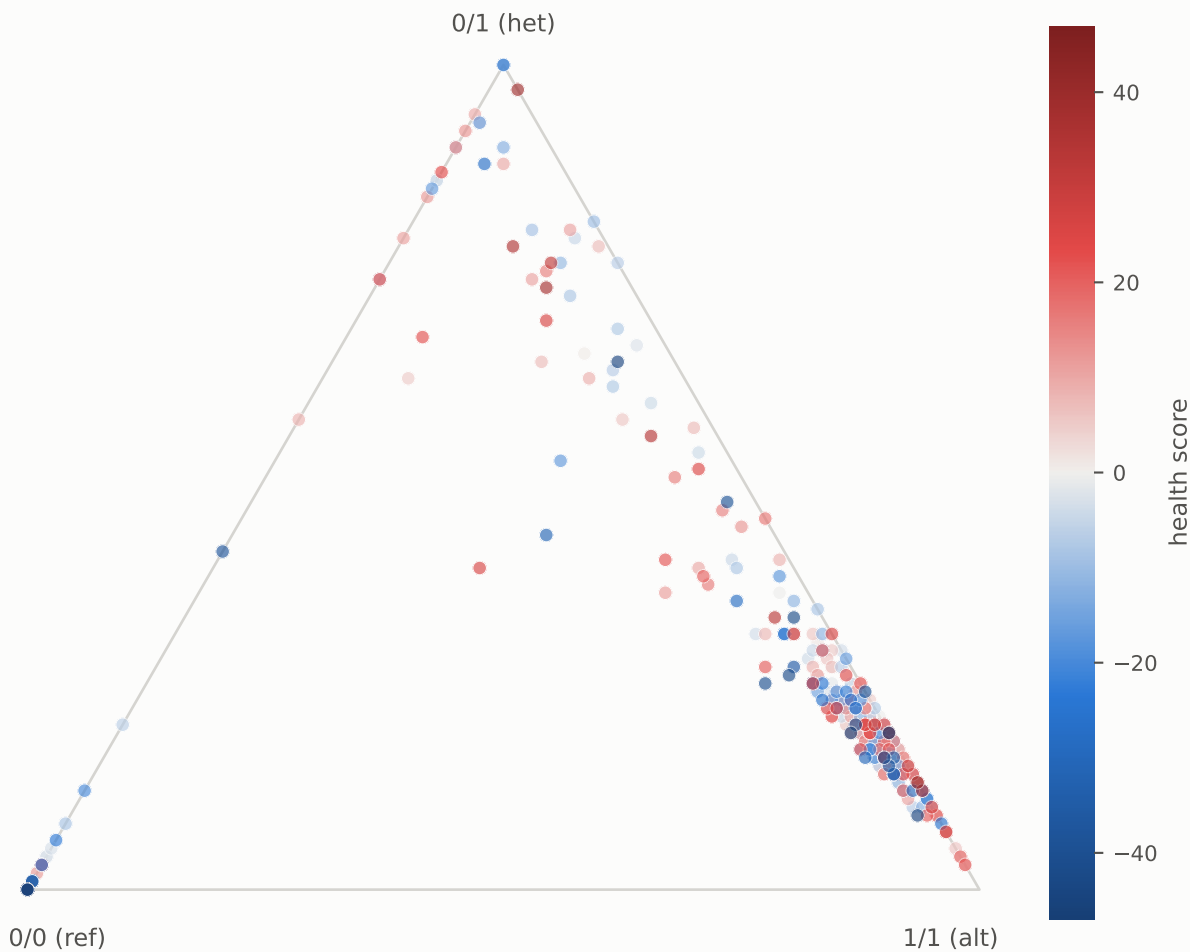
#14 by genotype uncertainty CHR_03:39,373,197 G>A
AF=0.53 DR2=0.81 $r=+0.016$ H=0.411 F=0.7



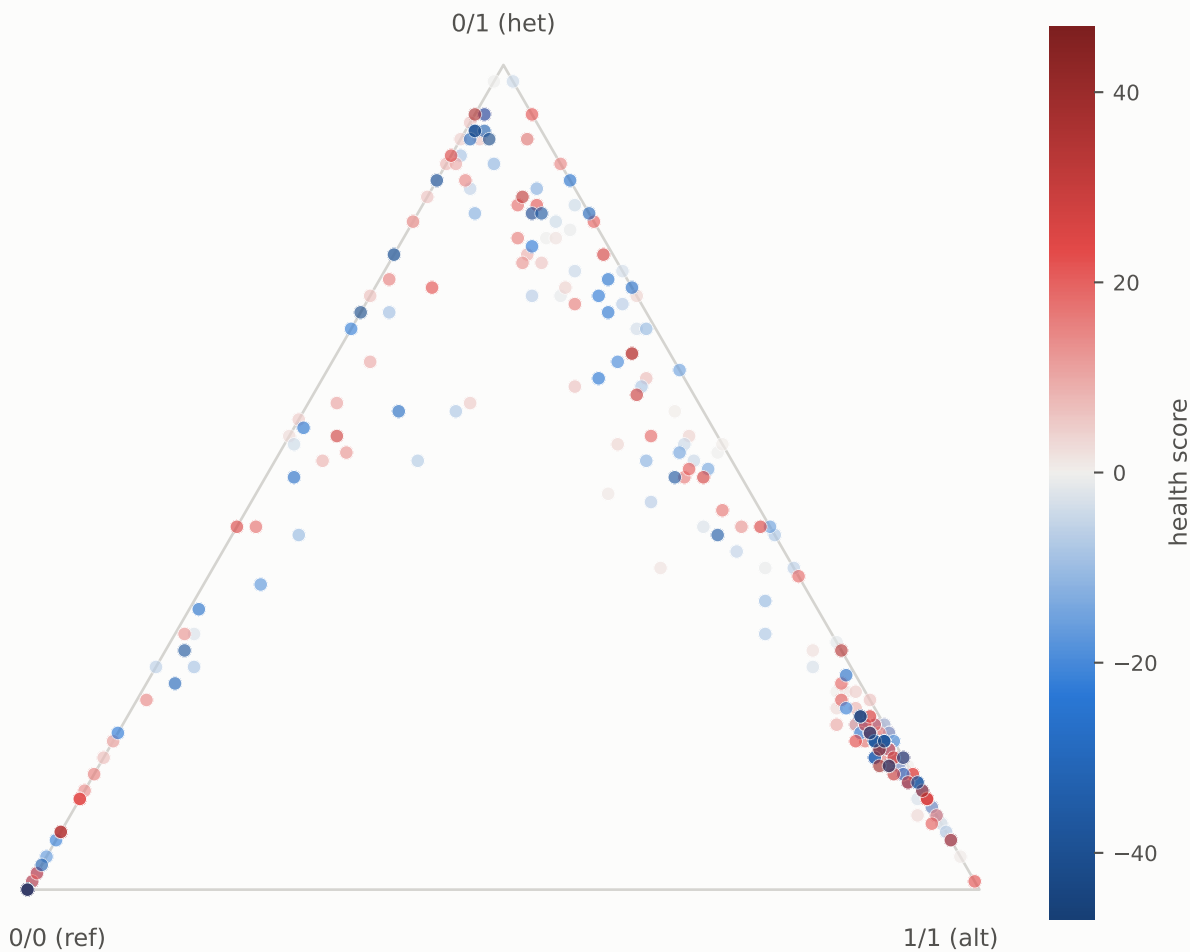
#15 by genotype uncertainty CHR_21:18,214,097 G>A
AF=0.5 DR2=0.81 r=+0.056 H=0.411 F=0.8



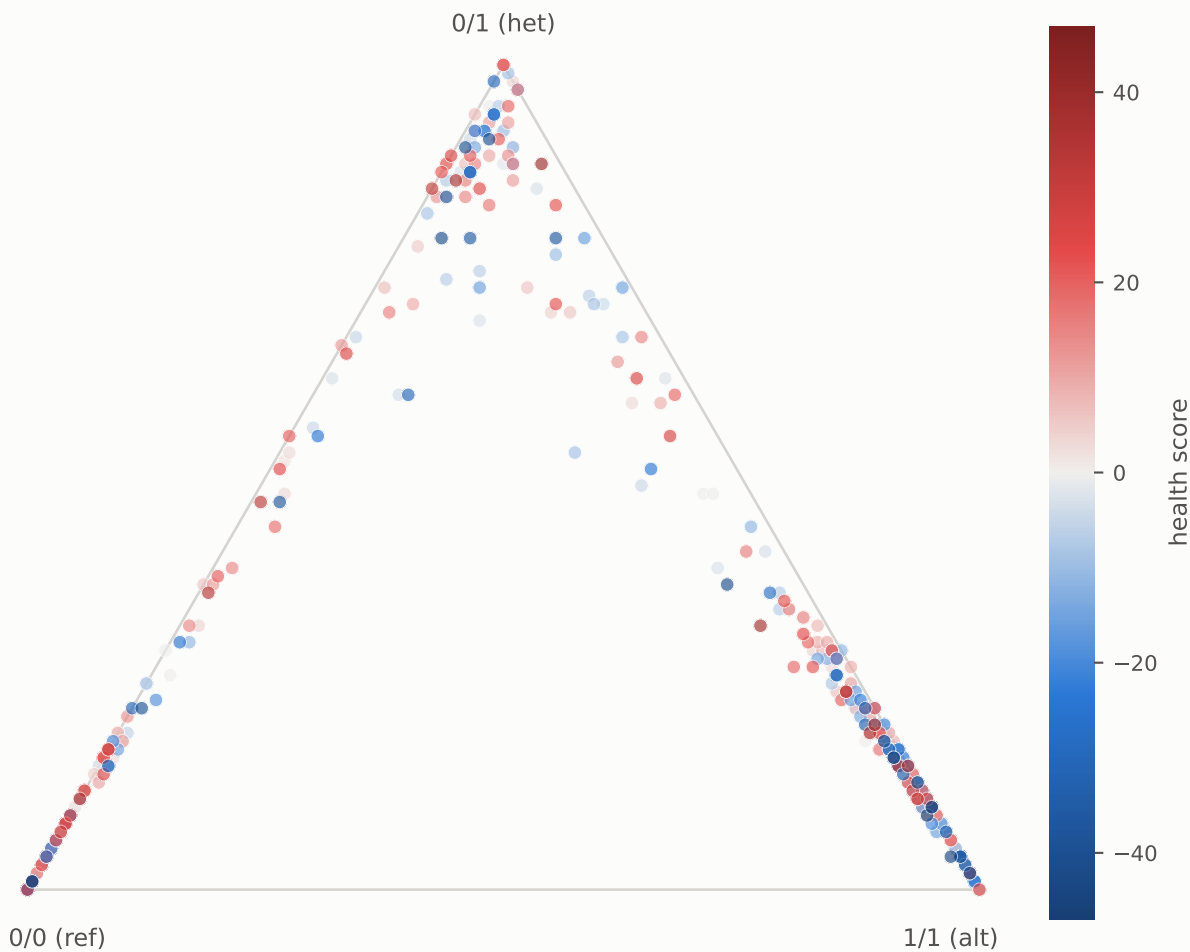
#16 by genotype uncertainty CHR_06:37,196,166 C>T
AF=0.53 DR2=0.81 $r=+0.049$ $H=0.410$ $F=2.0$



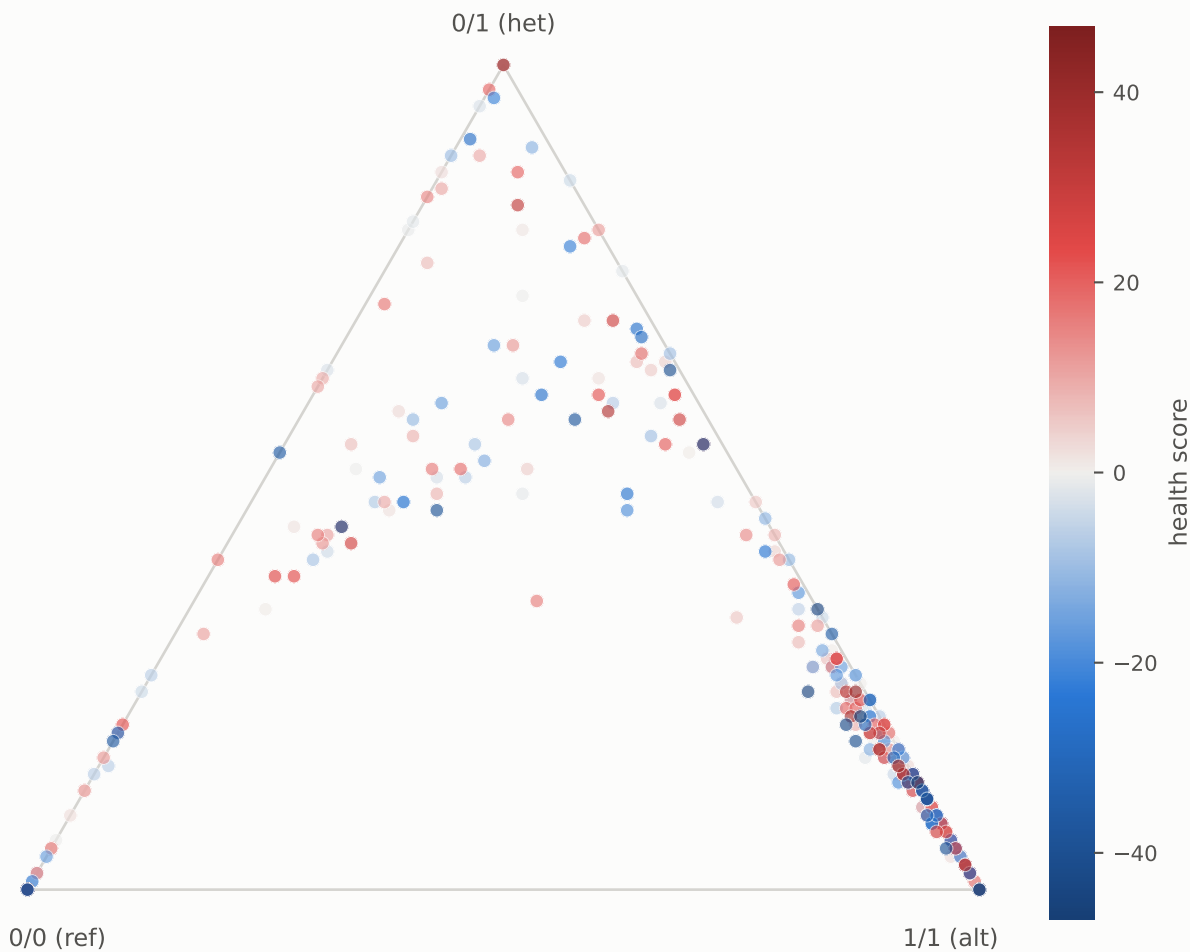
#17 by genotype uncertainty CHR_16:12,126,114 A>G
AF=0.51 DR2=0.81 $r=+0.001$ H=0.410 F=1.2



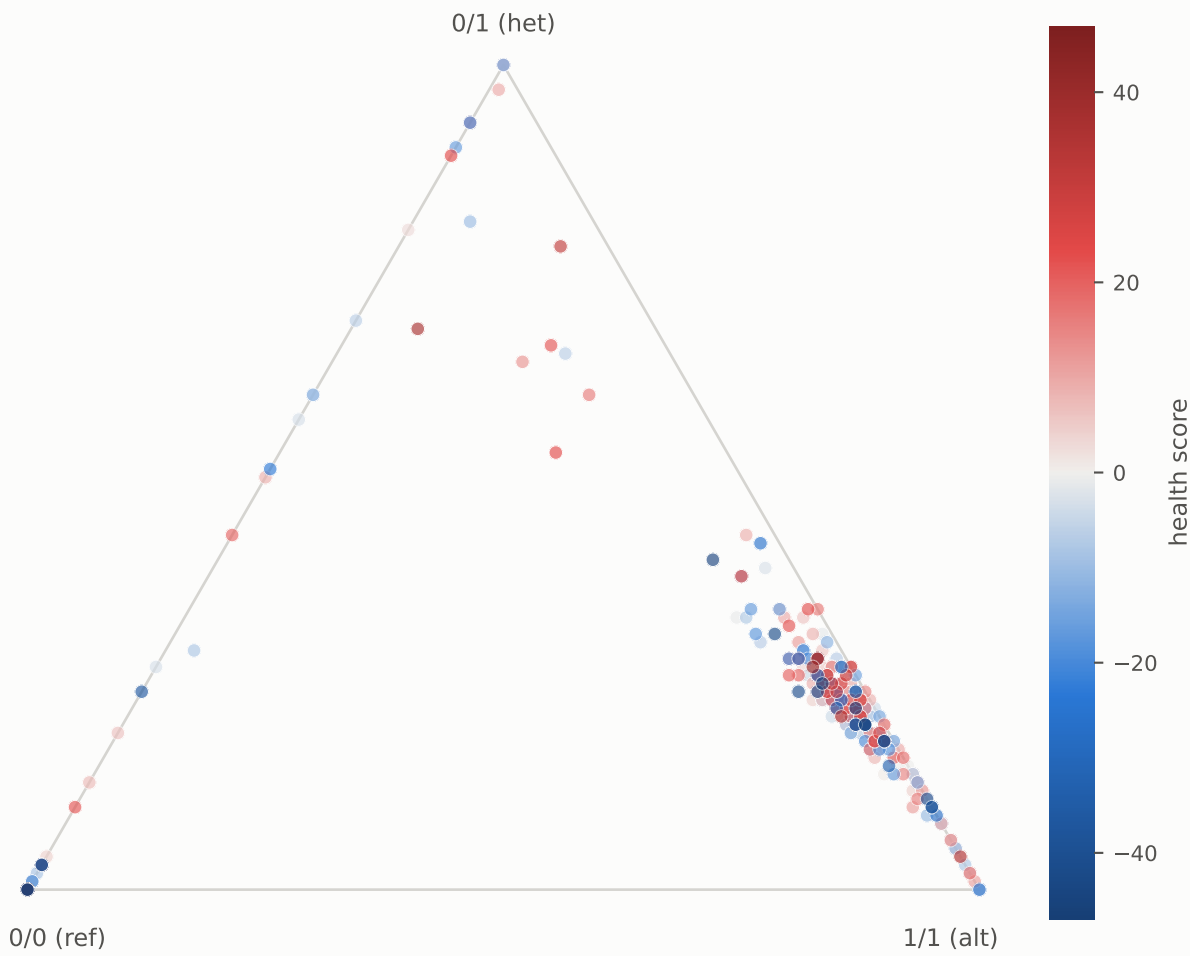
#18 by genotype uncertainty CHR_08:26,709,764 G>T
AF=0.53 DR2=0.81 $r=-0.098$ $\bar{H}=0.410$ F=1.9



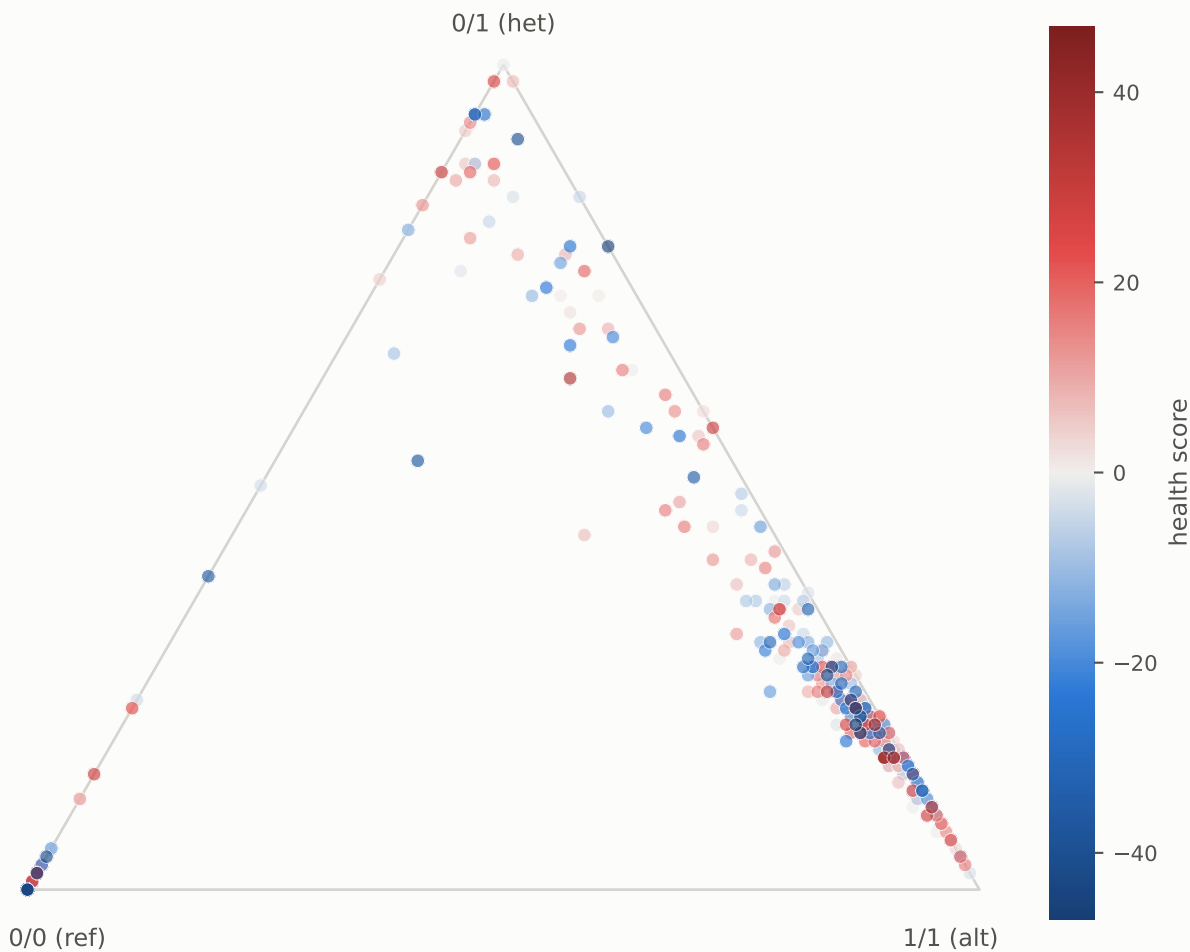
#19 by genotype uncertainty CHR_09:29,065,599 A>C
AF=0.57 DR2=0.81 $r=-0.019$ $\bar{H}=0.410$ F=0.2



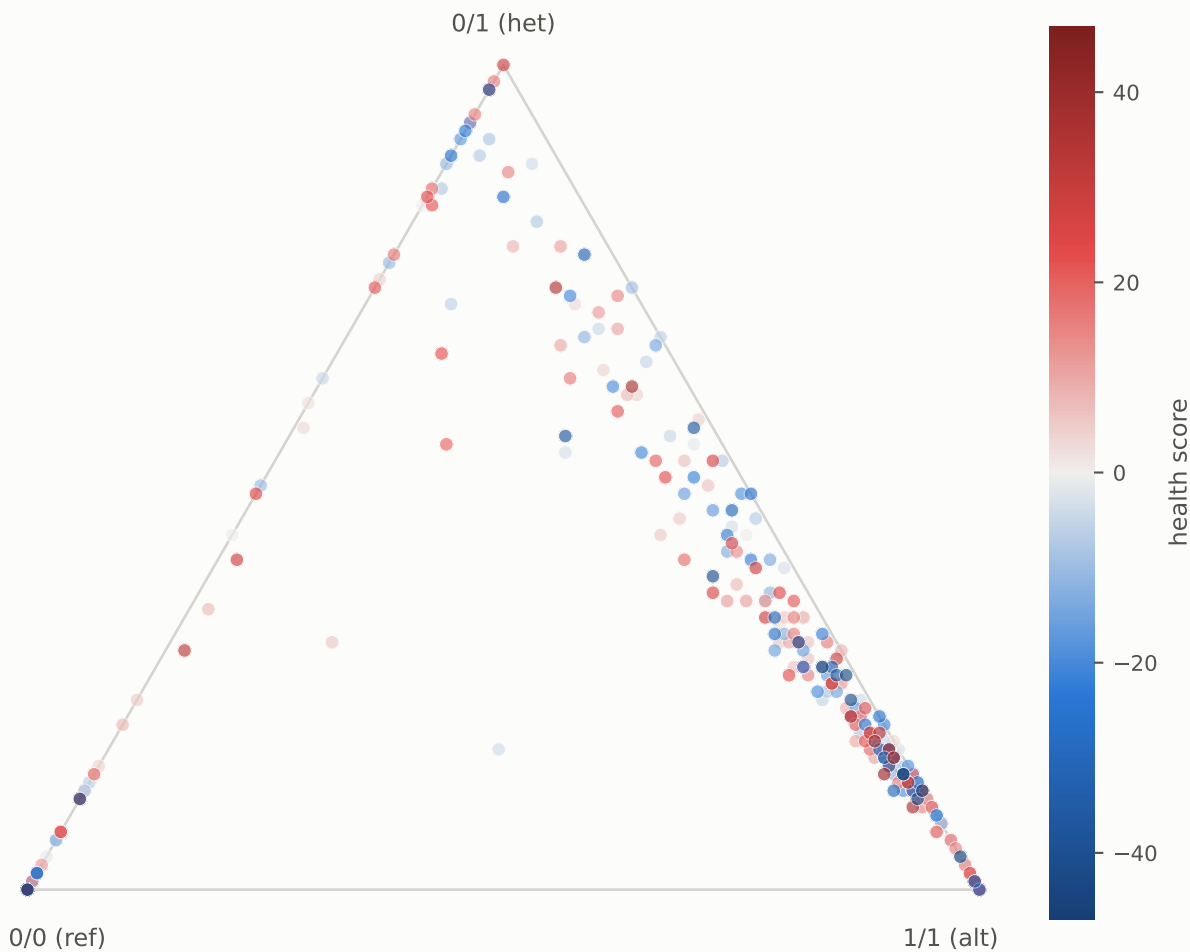
#20 by genotype uncertainty CHR_06:37,199,556 C>T
AF=0.54 DR2=0.81 r=+0.067 H=0.410 F=1.4



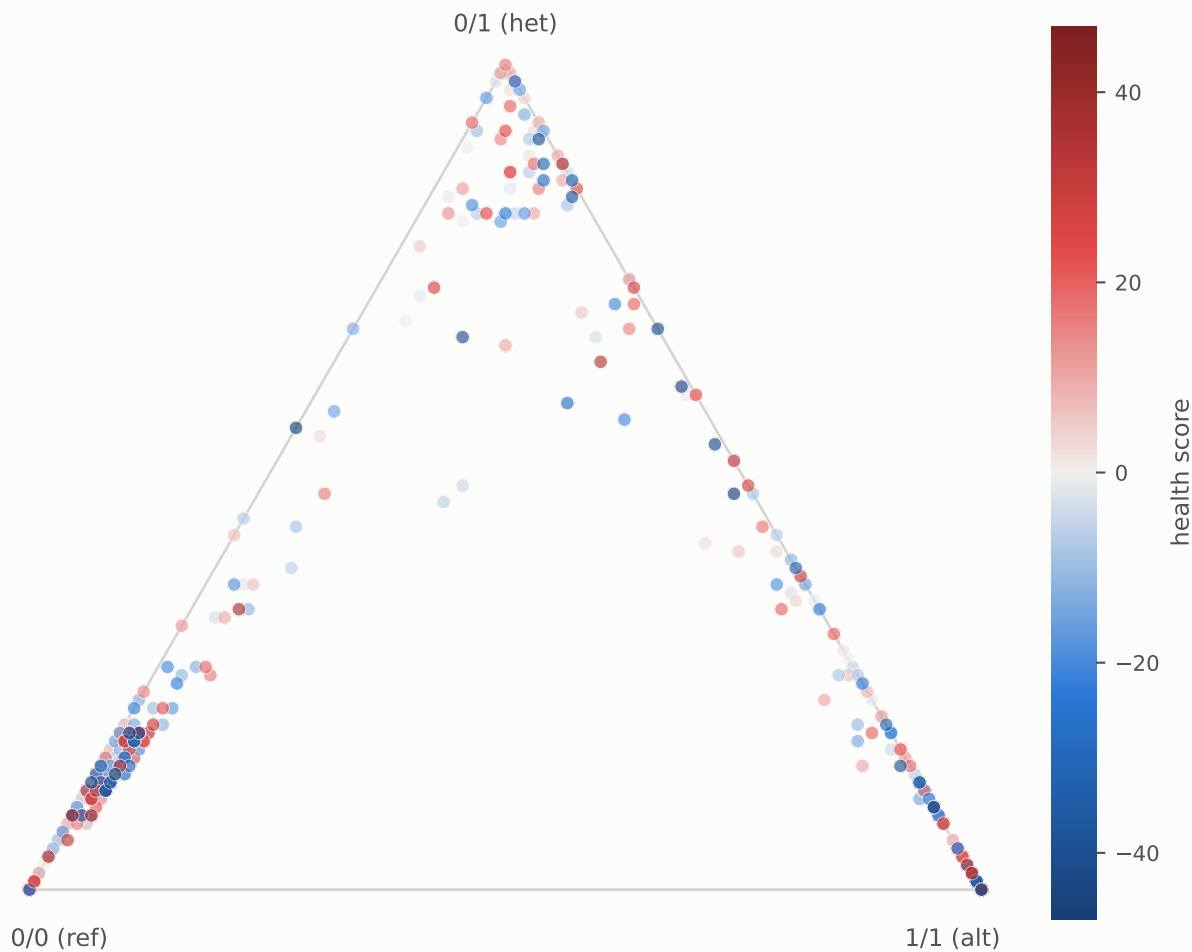
#21 by genotype uncertainty CHR_06:33,034,925 G>A
AF=0.55 DR2=0.81 $r=-0.034$ $\bar{H}=0.409$ F=0.4



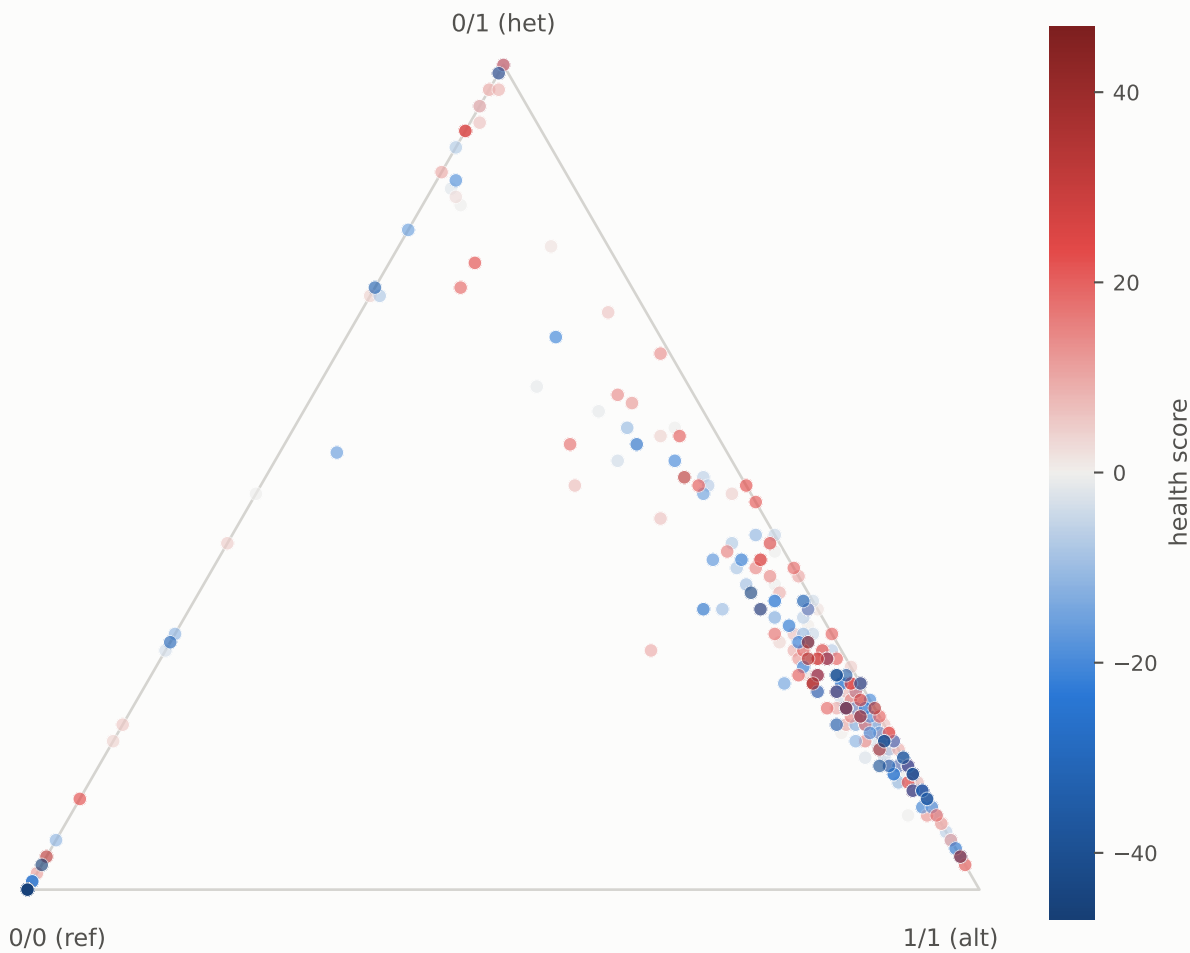
#22 by genotype uncertainty CHR_03:39,059,917 G>A
AF=0.52 DR2=0.81 $r=+0.011$ H=0.409 F=0.2



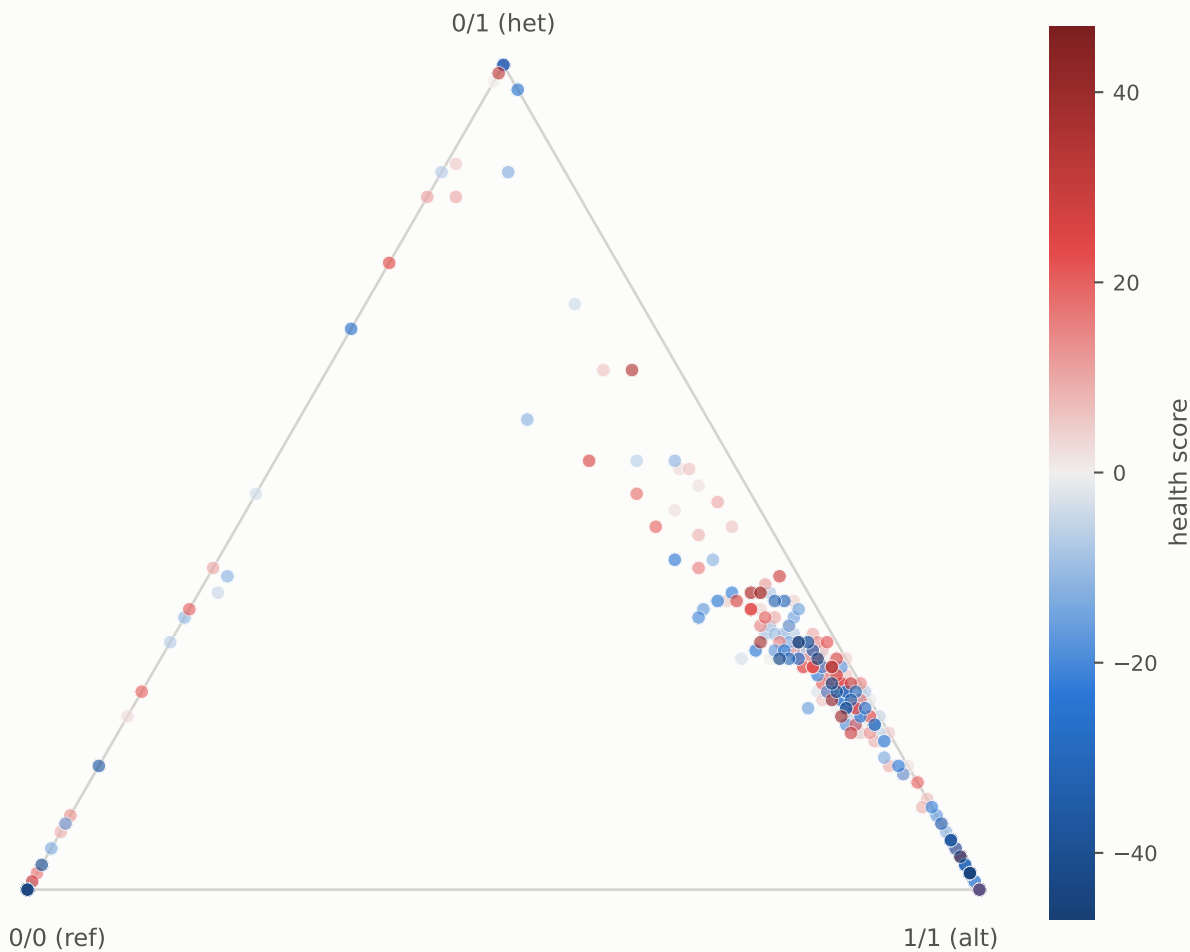
#23 by genotype uncertainty CHR_21:19,347,617 A>G
AF=0.47 DR2=0.81 $r=-0.009$ $\bar{H}=0.408$ F=0.2



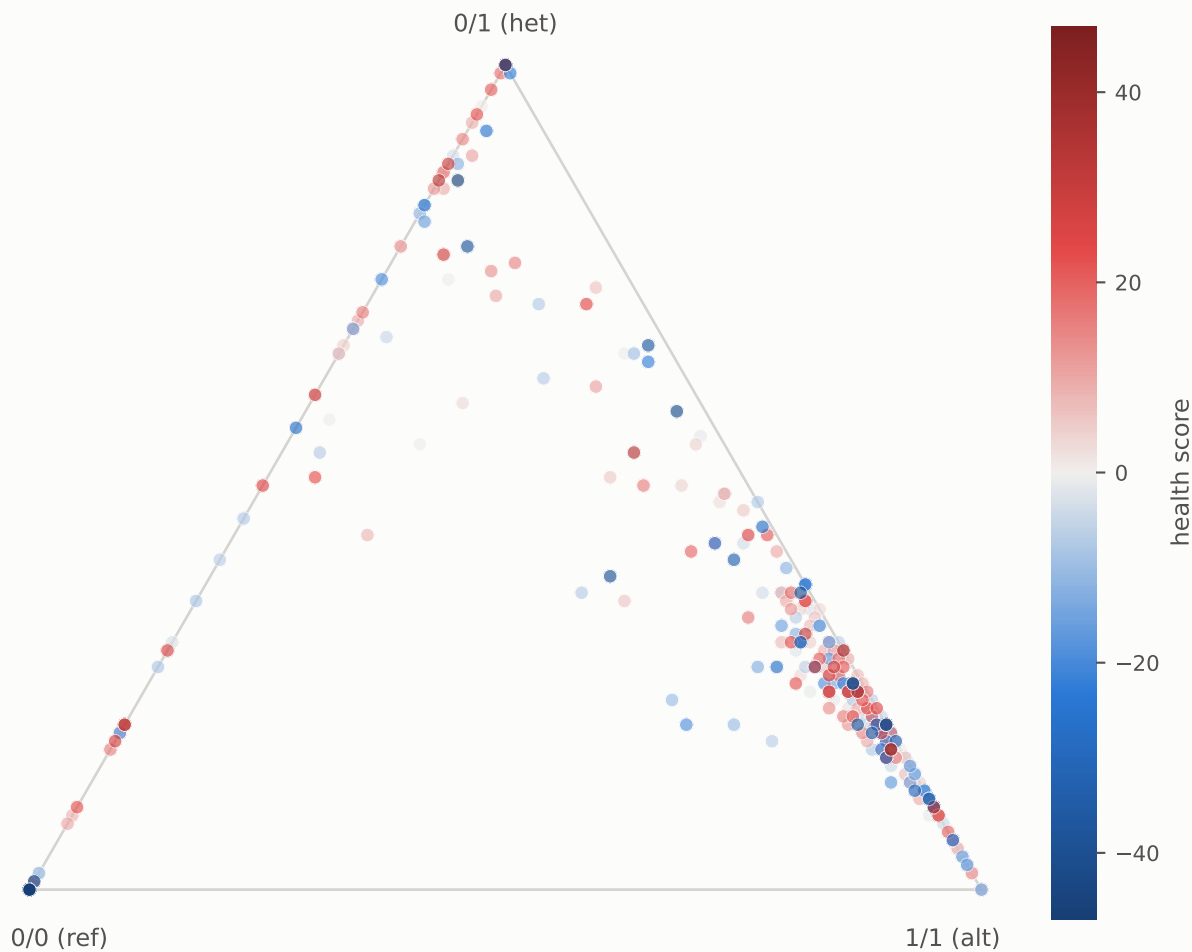
#24 by genotype uncertainty CHR_06:29,106,566 T>C
AF=0.54 DR2=0.81 $r=-0.013$ $\bar{H}=0.408$ F=0.2



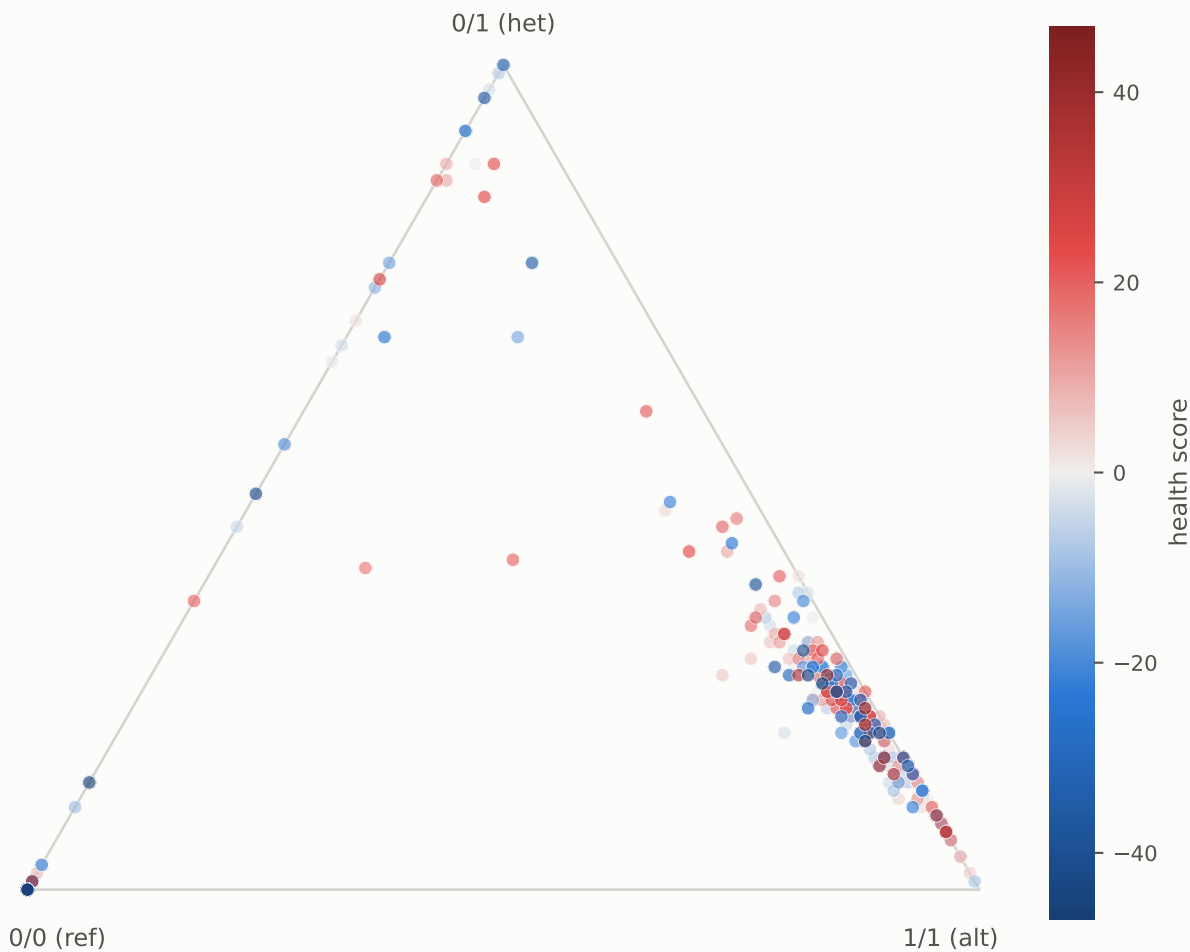
#25 by genotype uncertainty CHR_21:17,089,196 T>C
AF=0.53 DR2=0.81 r=-0.130 H=0.408 F=3.8



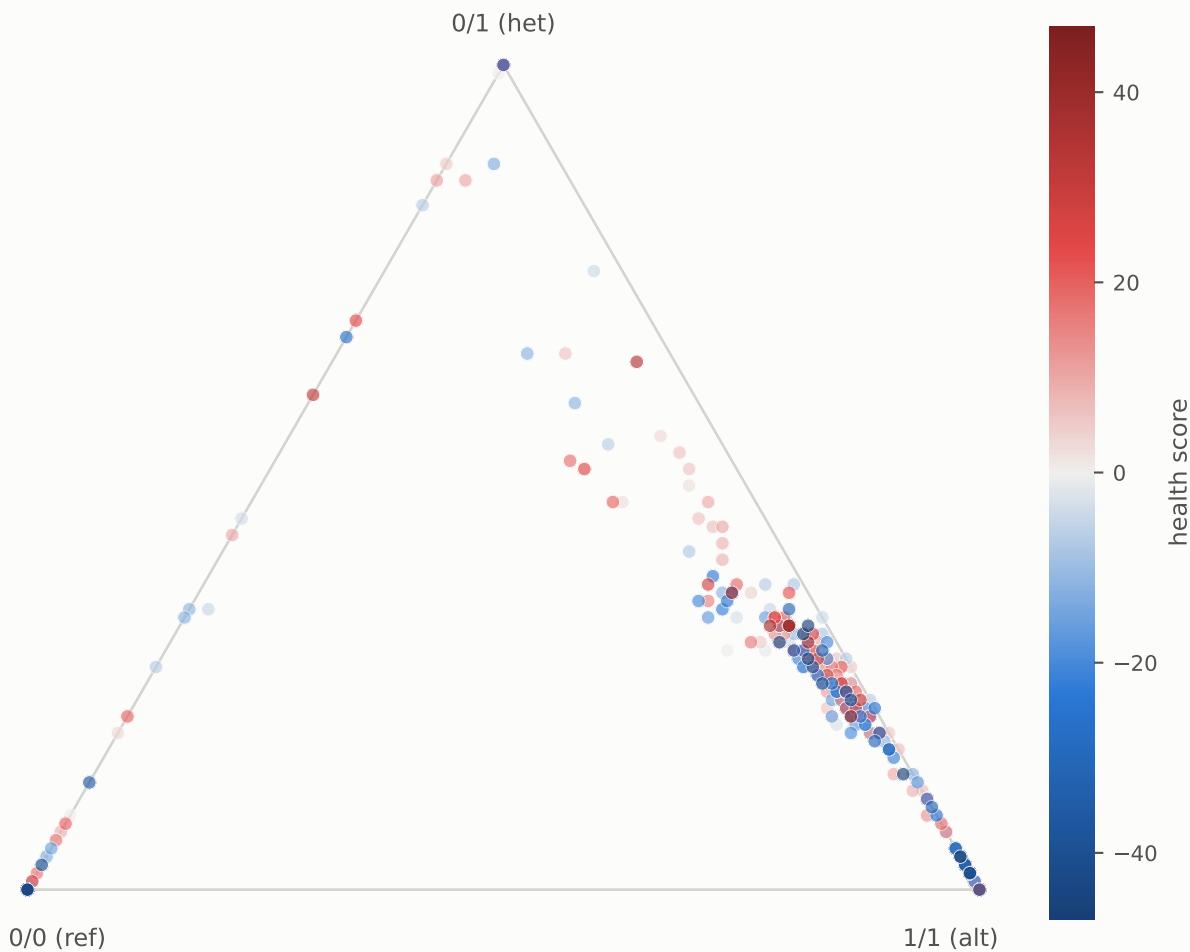
#26 by genotype uncertainty CHR_01:16,493,292 G>A
AF=0.5 DR2=0.81 $r=+0.065$ $\bar{H}=0.408$ F=1.0



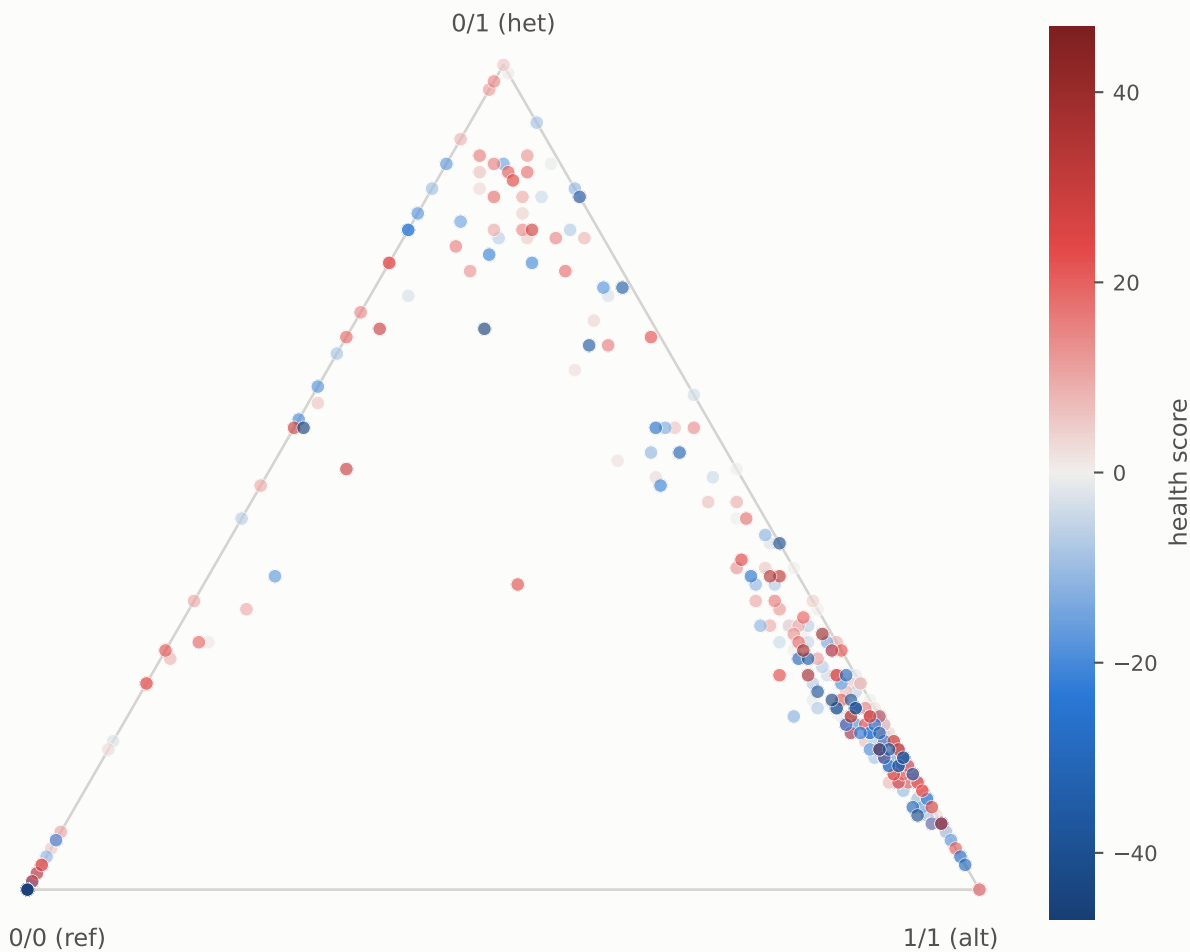
#27 by genotype uncertainty CHR_06:29,111,672 C>T
AF=0.54 DR2=0.81 $r=+0.006$ $\bar{H}=0.408$ F=0.5



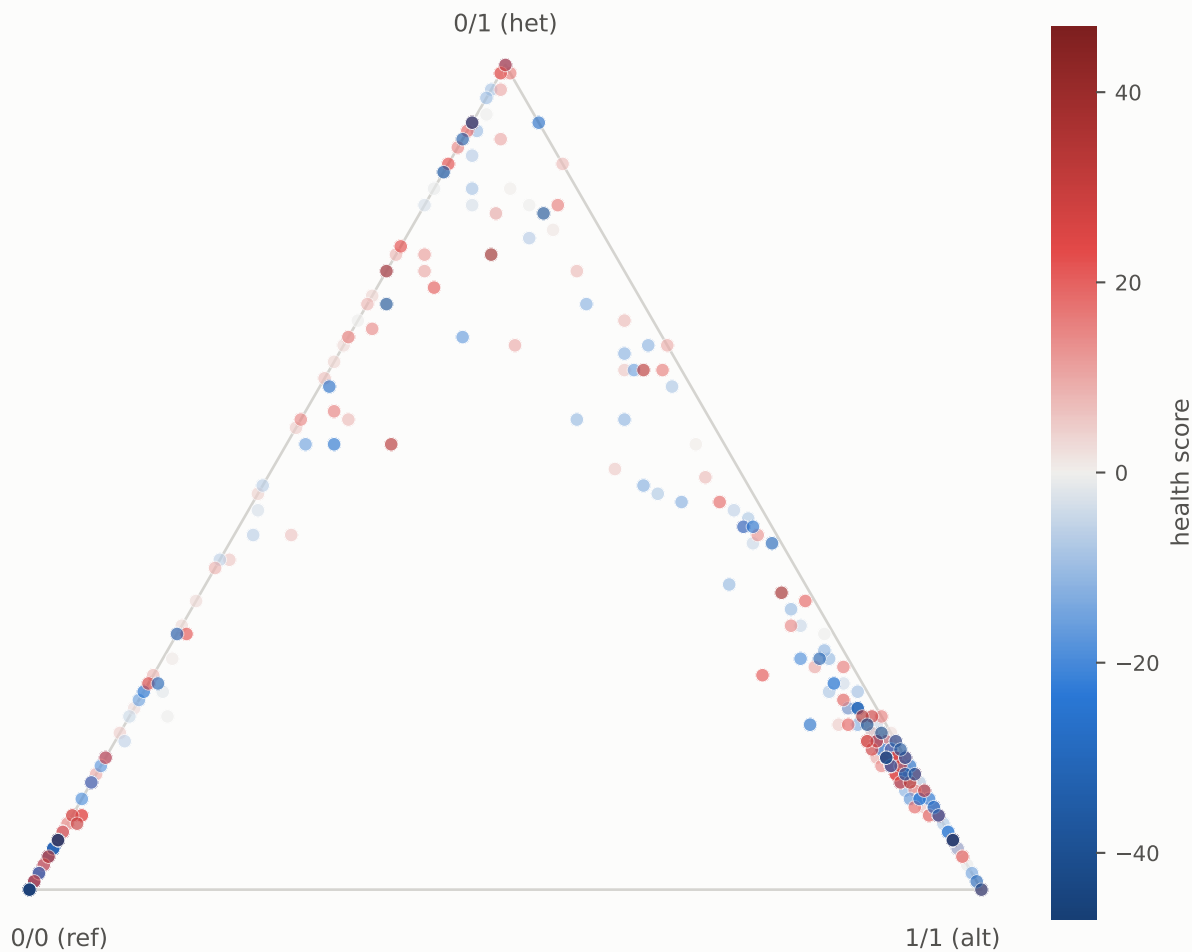
#28 by genotype uncertainty CHR_21:17,089,211 T>C
AF=0.53 DR2=0.81 r=-0.143 H=0.407 F=5.0



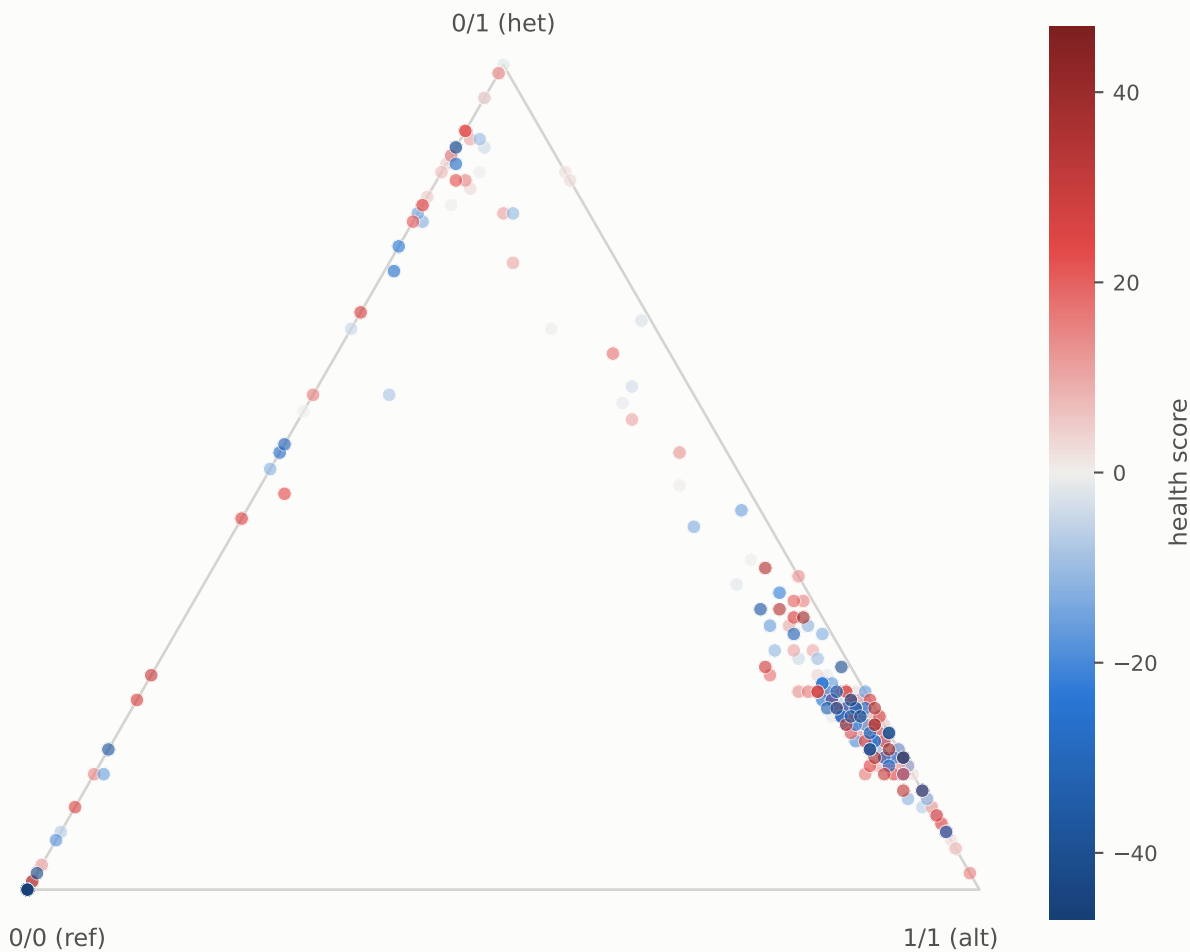
#29 by genotype uncertainty CHR_11:14,403,362 T>C
AF=0.52 DR2=0.81 $r=-0.016$ $\bar{H}=0.407$ F=0.0



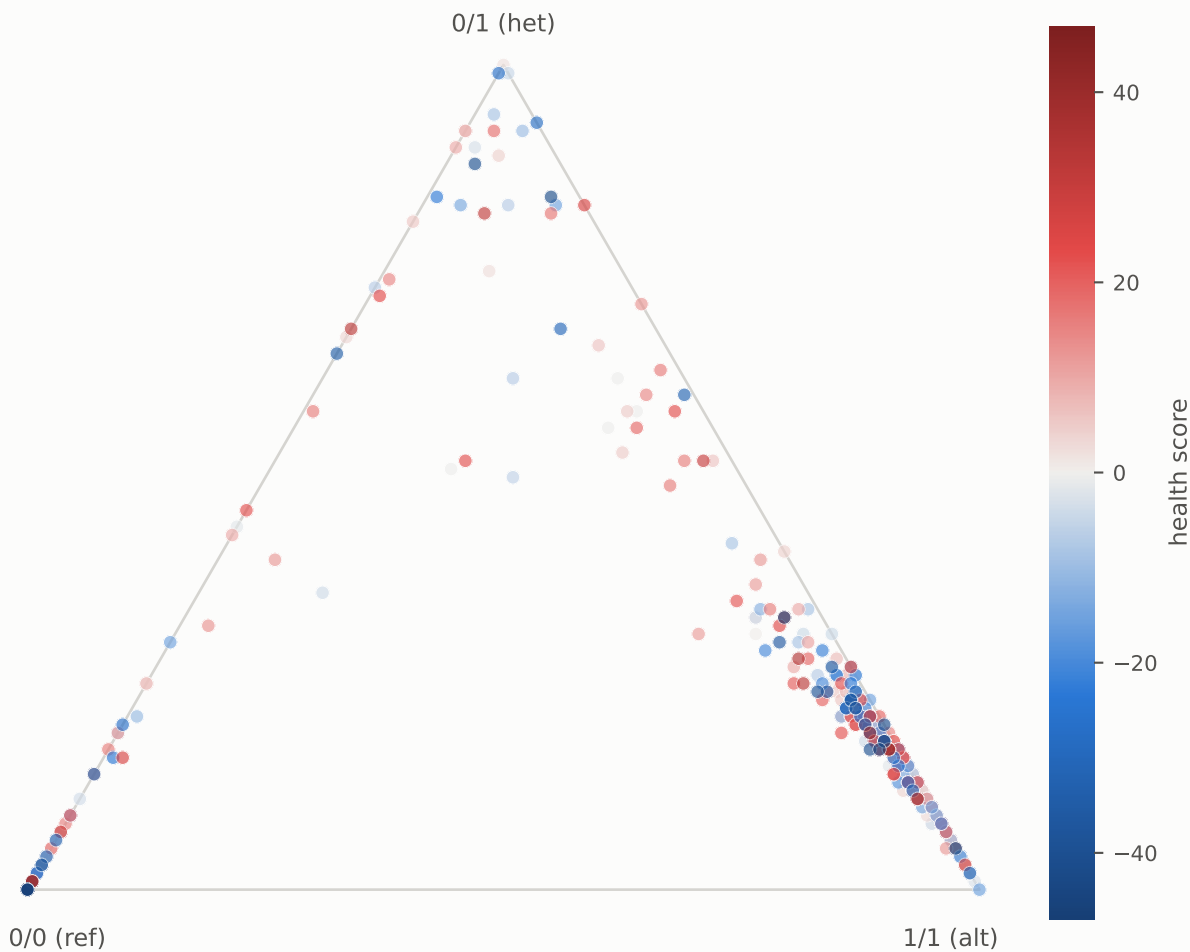
#30 by genotype uncertainty CHR_20:3,622,135 A>G
AF=0.51 DR2=0.81 $r=-0.029$ $\bar{H}=0.407$ F=0.5



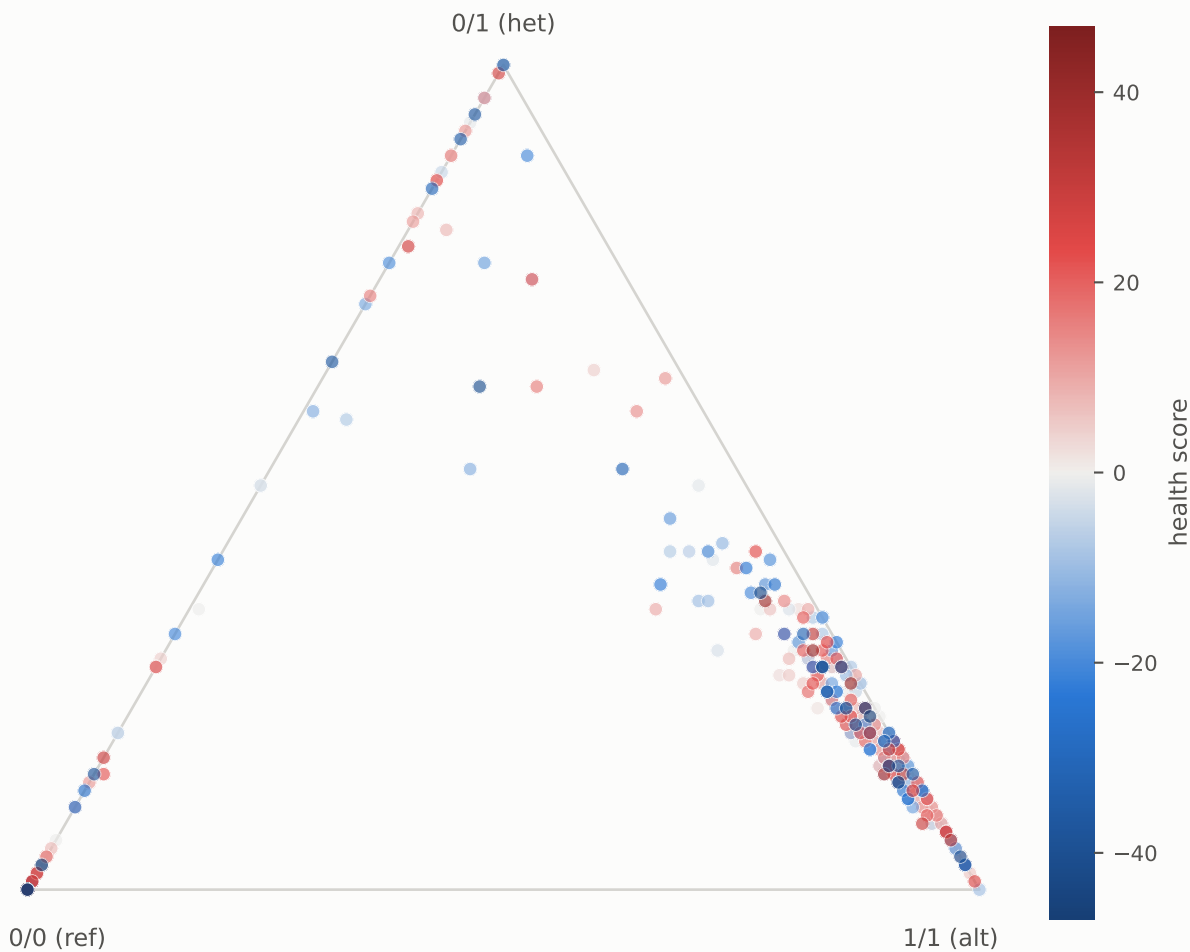
#31 by genotype uncertainty CHR_21:578,692 A>C
AF=0.53 DR2=0.81 $r=+0.023$ $\bar{H}=0.407$ F=0.1



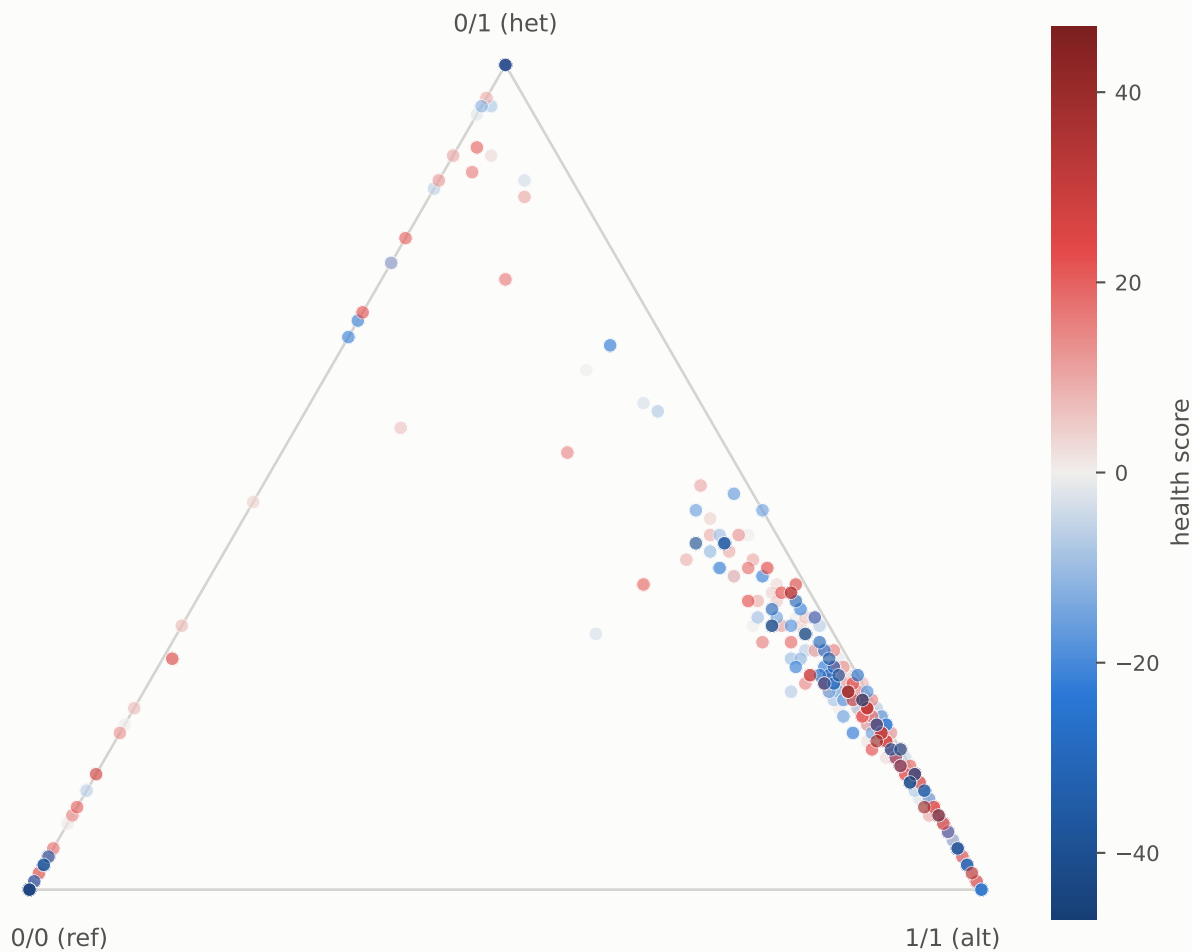
#32 by genotype uncertainty CHR_22:2,872,458 G>A
AF=0.57 DR2=0.81 r=-0.054 $\bar{H}$ =0.406 F=1.0



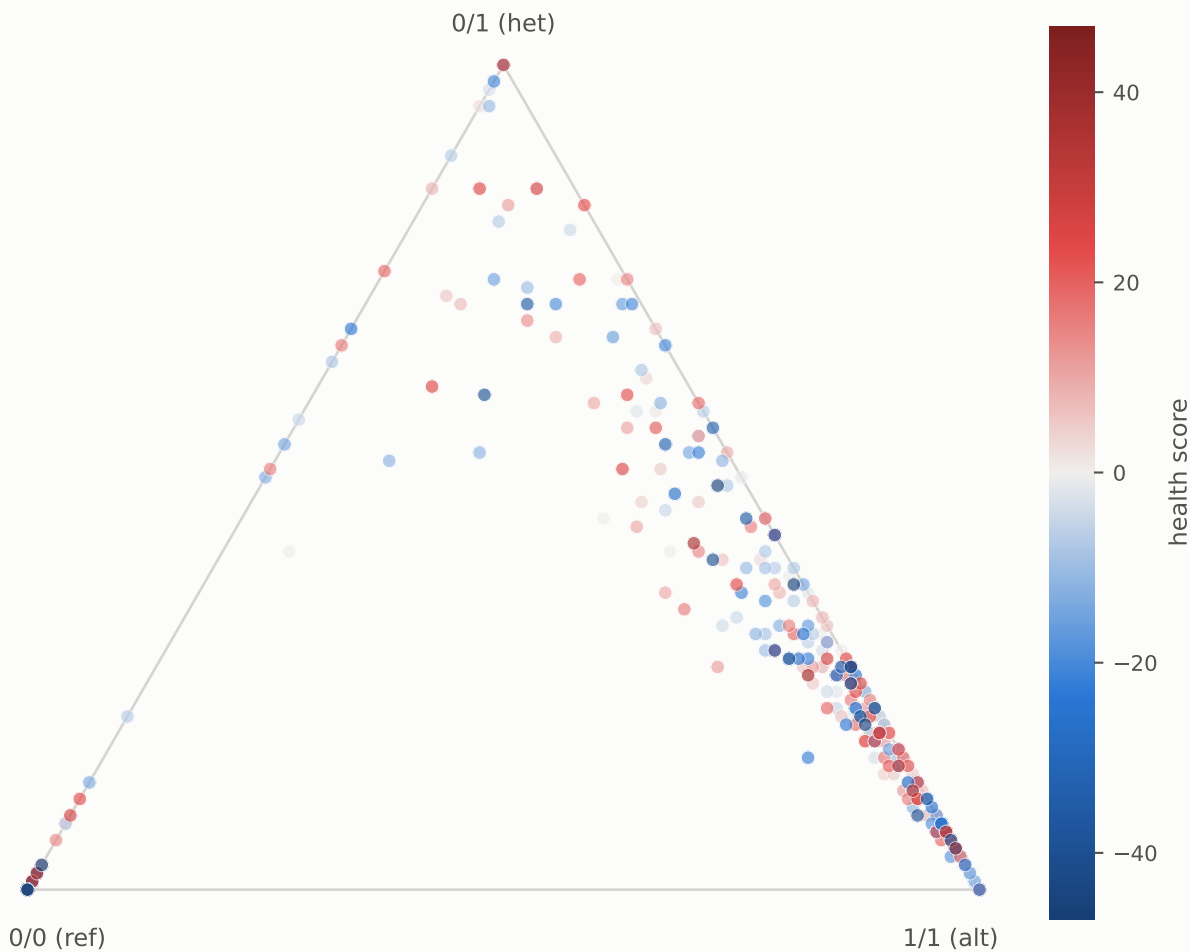
#33 by genotype uncertainty CHR_01:16,189,803 A>C
AF=0.55 DR2=0.81 $r=-0.035$ $\bar{H}=0.406$ F=1.5



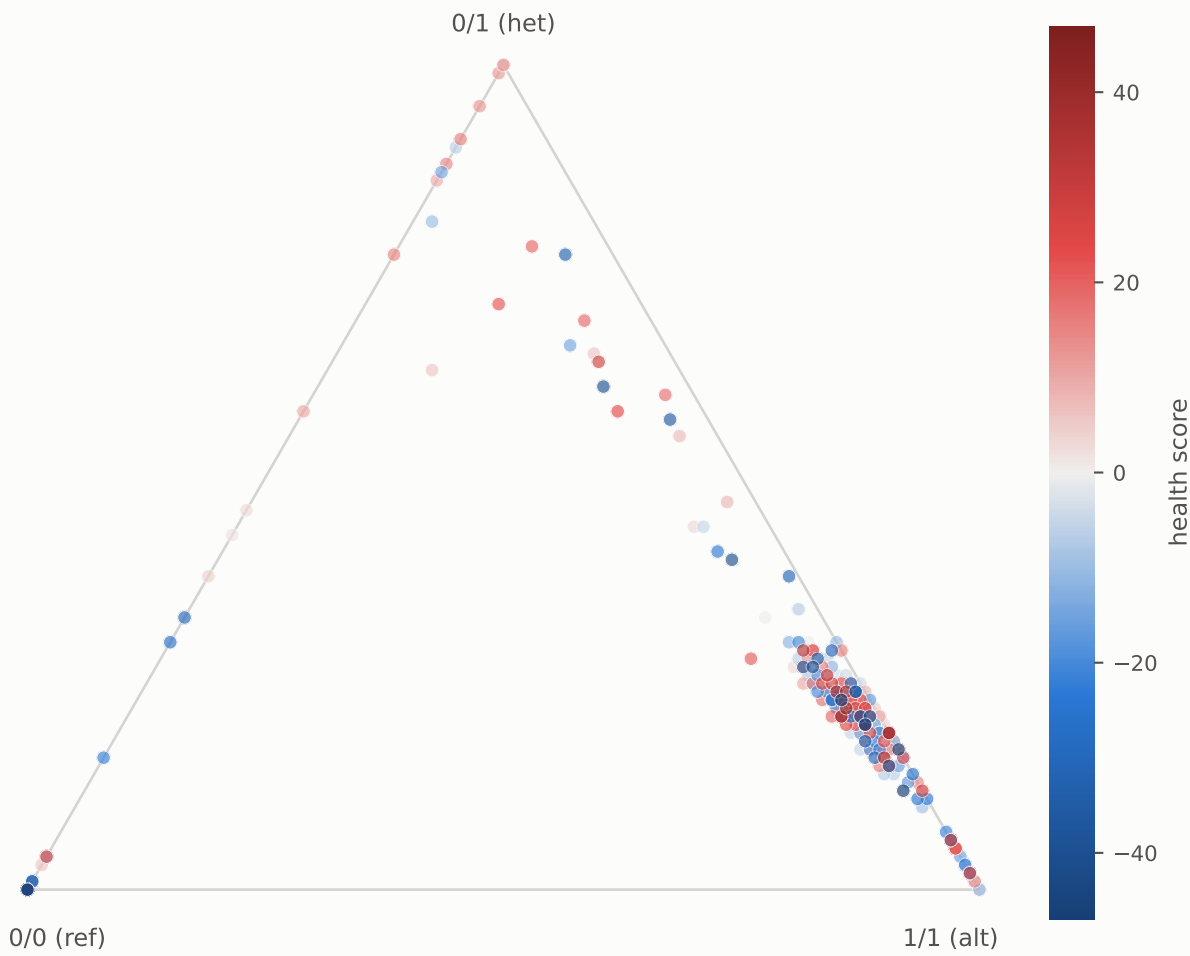
#34 by genotype uncertainty CHR_21:5,007,965 A>T
AF=0.57 DR2=0.81 $r=+0.019$ $\bar{H}=0.406$ F=0.1



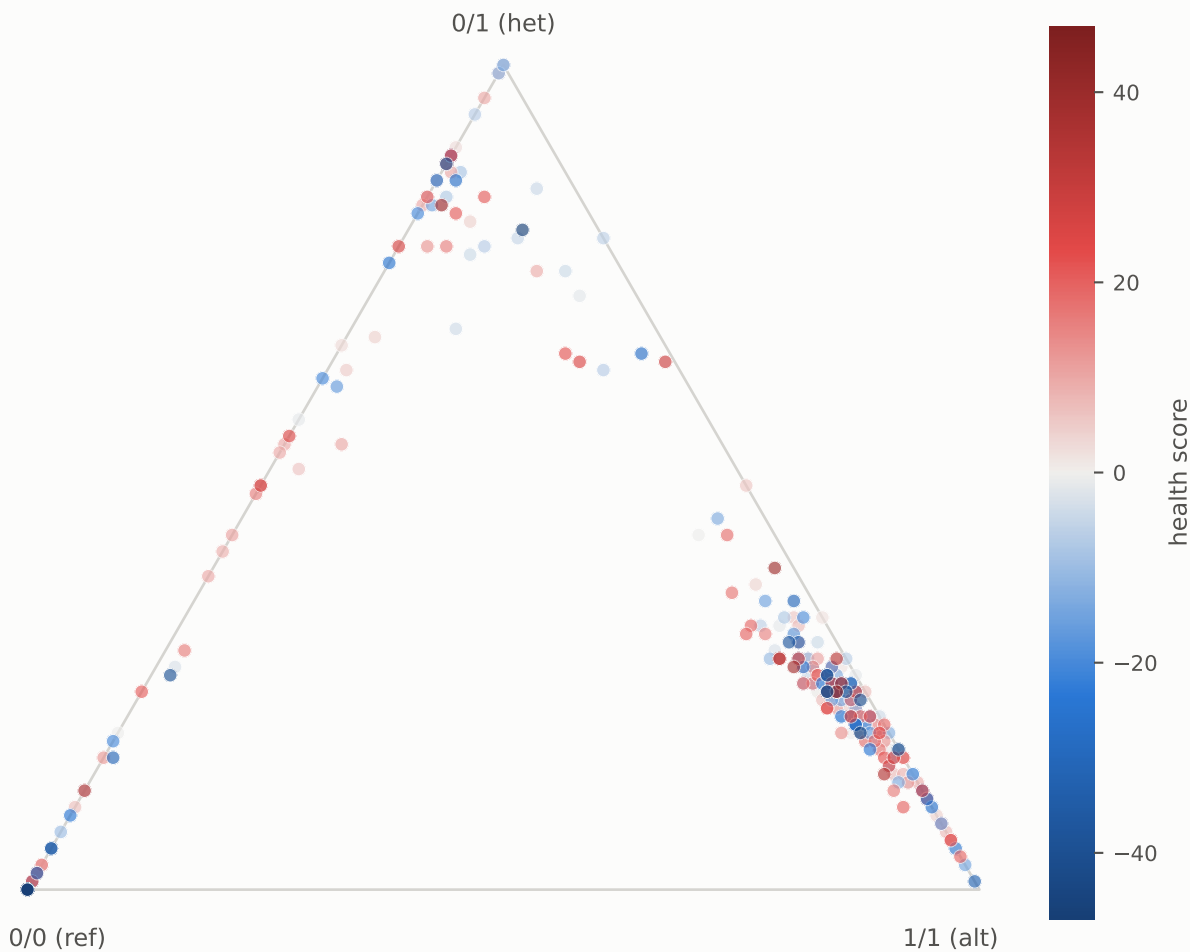
#35 by genotype uncertainty CHR_19:721,039 G>T
AF=0.53 DR2=0.81 $r=-0.065$ H=0.405 F=1.0



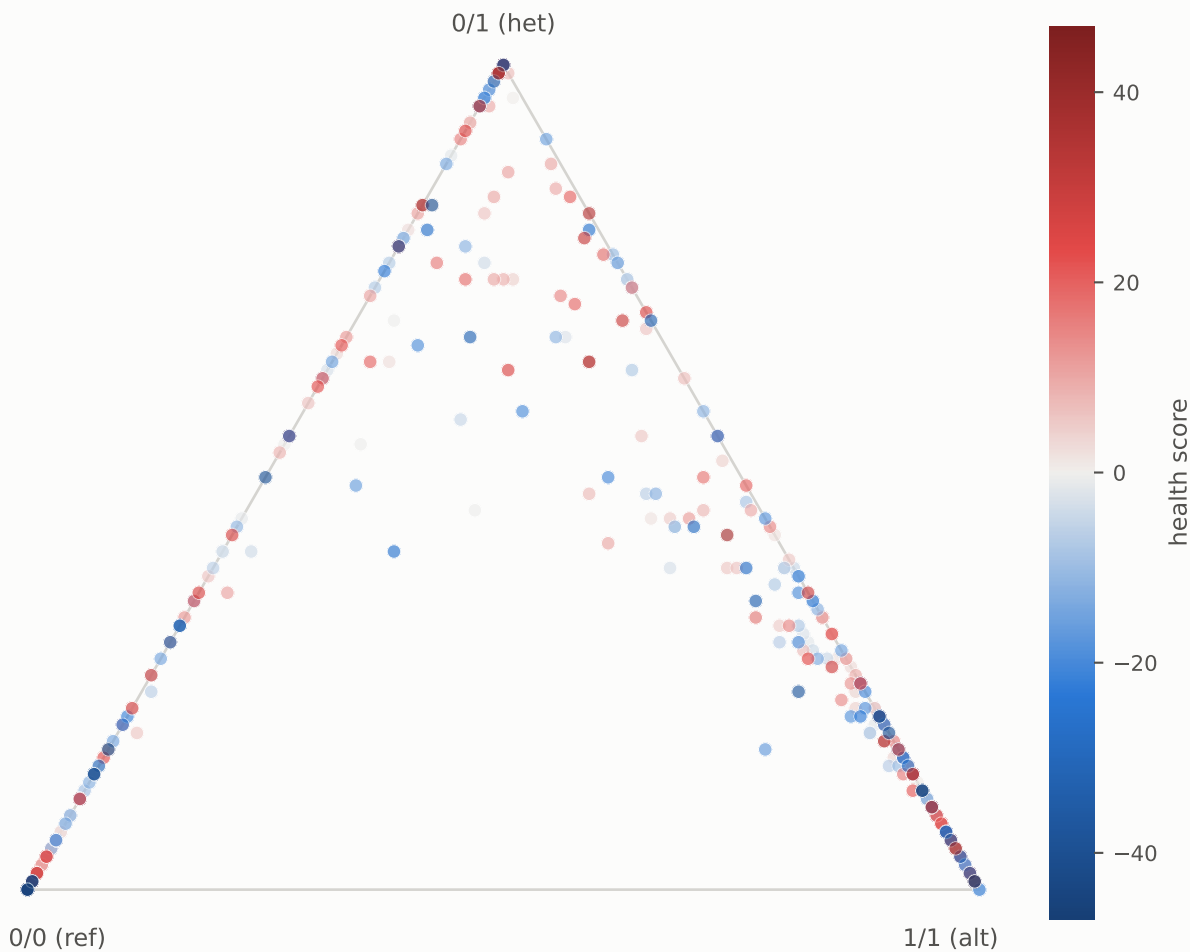
#36 by genotype uncertainty CHR_03:39,087,429 A>C
AF=0.54 DR2=0.81 $r=+0.030$ $H=0.405$ $F=0.9$



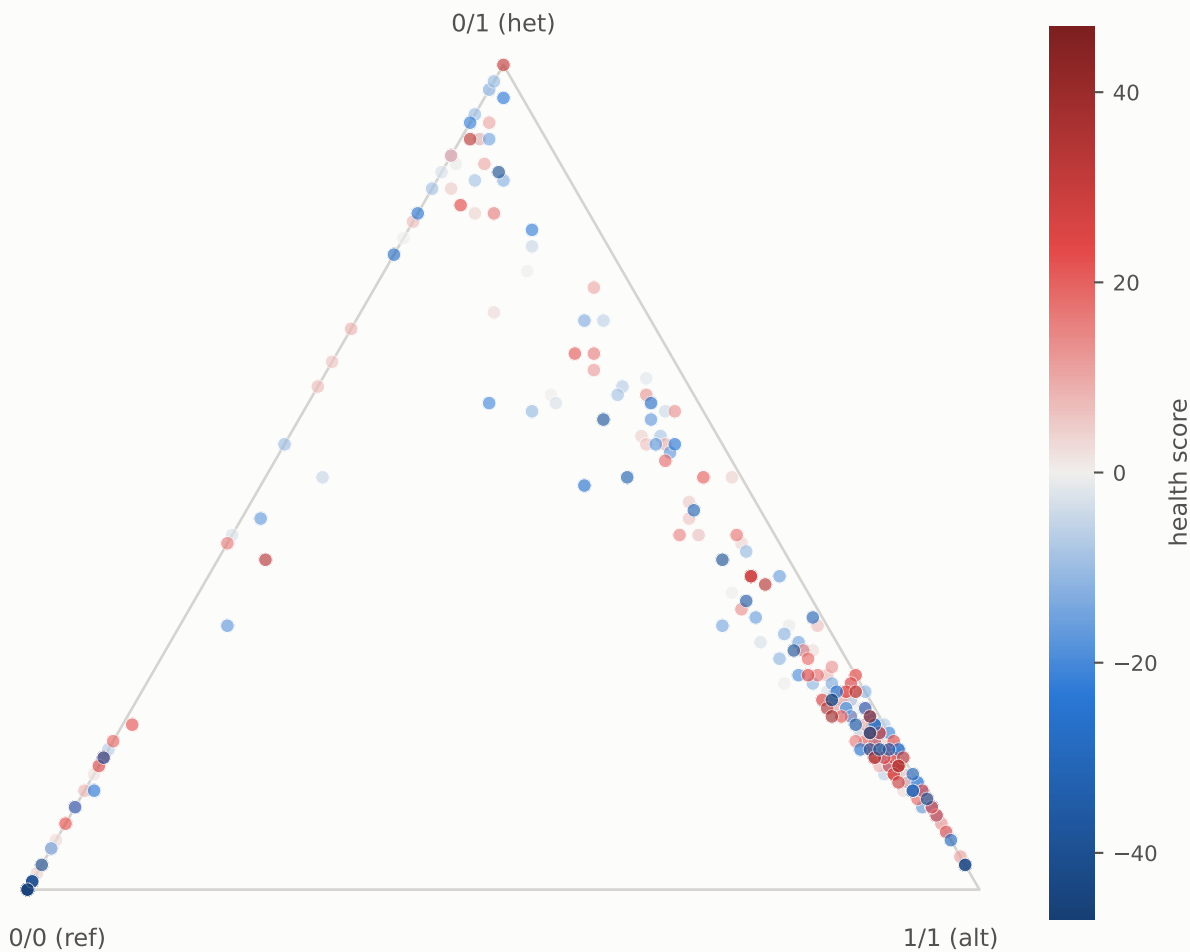
#37 by genotype uncertainty CHR_21:18,212,293 A>G
AF=0.46 DR2=0.82 $r=+0.016$ H=0.405 F=0.1



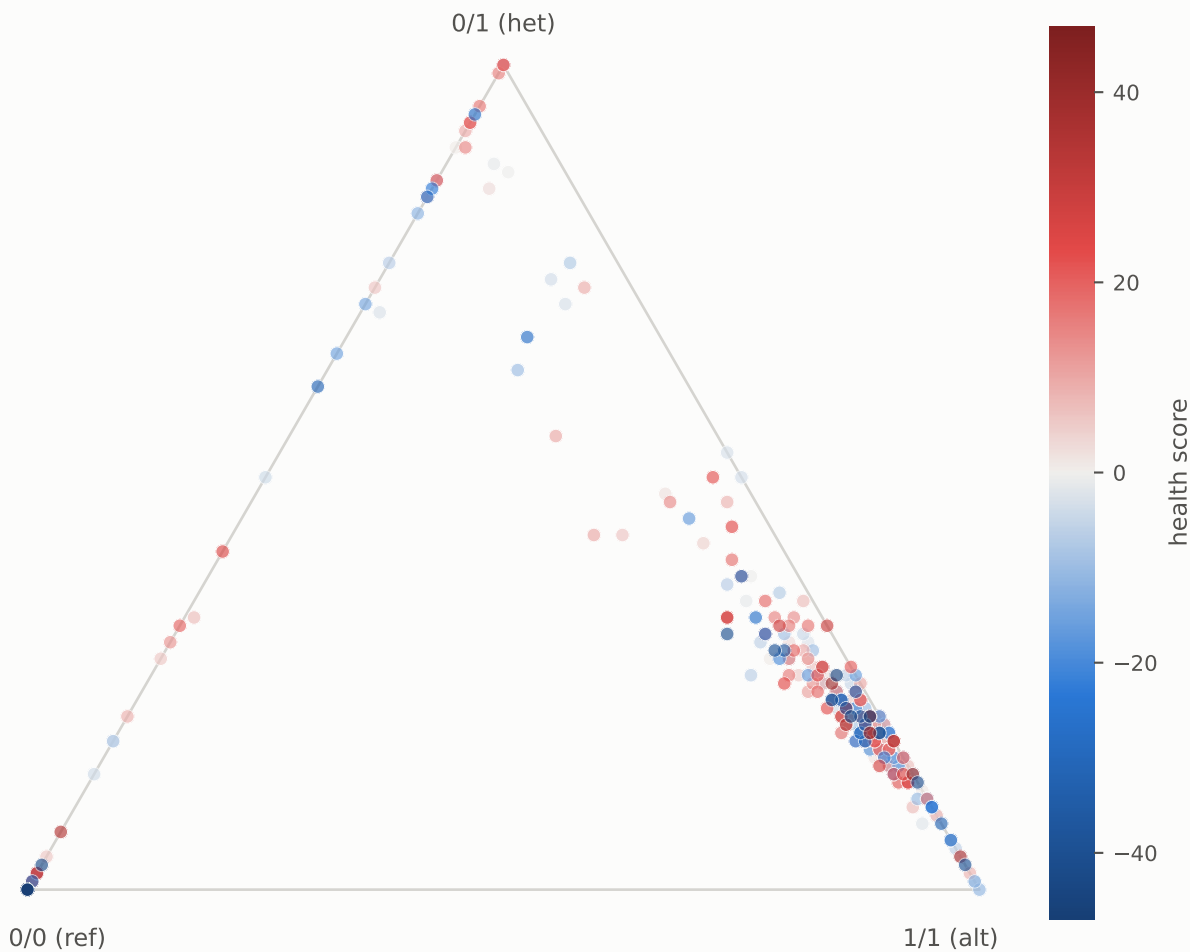
#38 by genotype uncertainty CHR_09:19,032,922 T>C
AF=0.48 DR2=0.81 r=+0.001 H=0.404 F=1.2



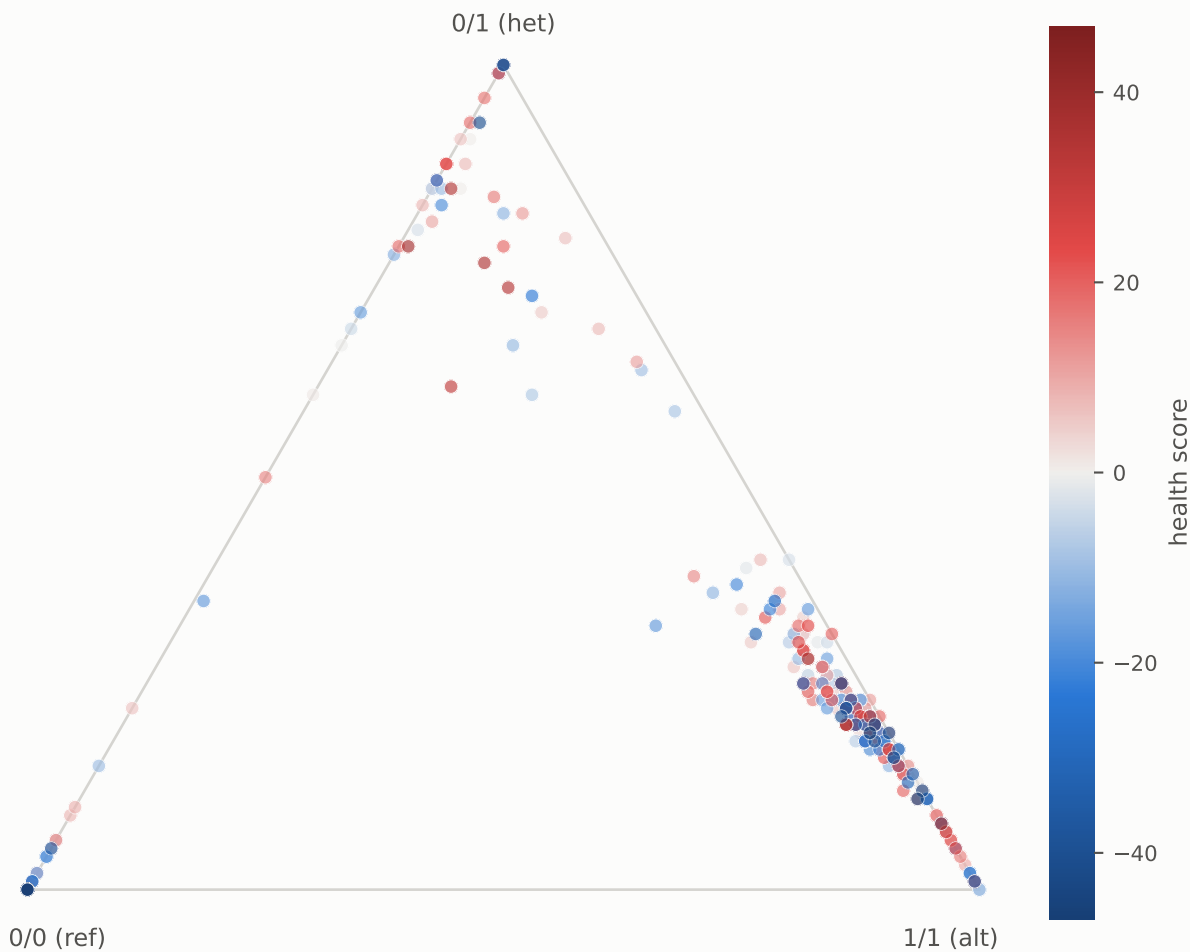
#39 by genotype uncertainty CHR_09:11,712,829 C>T
AF=0.5 DR2=0.81 r=+0.020 $\bar{H}$ =0.404 F=1.3



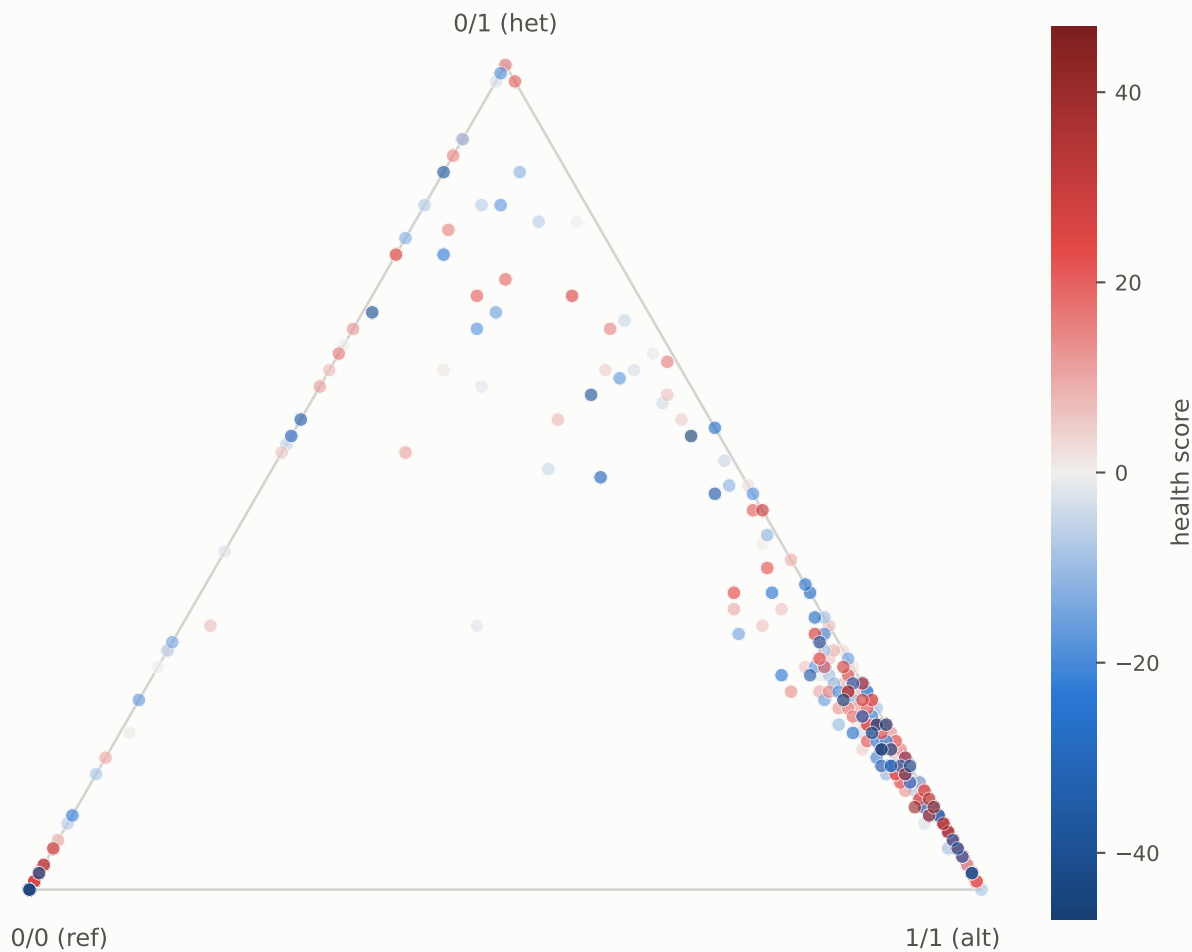
#40 by genotype uncertainty CHR_11:23,419,812 A>G
AF=0.53 DR2=0.81 $r=+0.044$ $H=0.404$ $F=0.4$



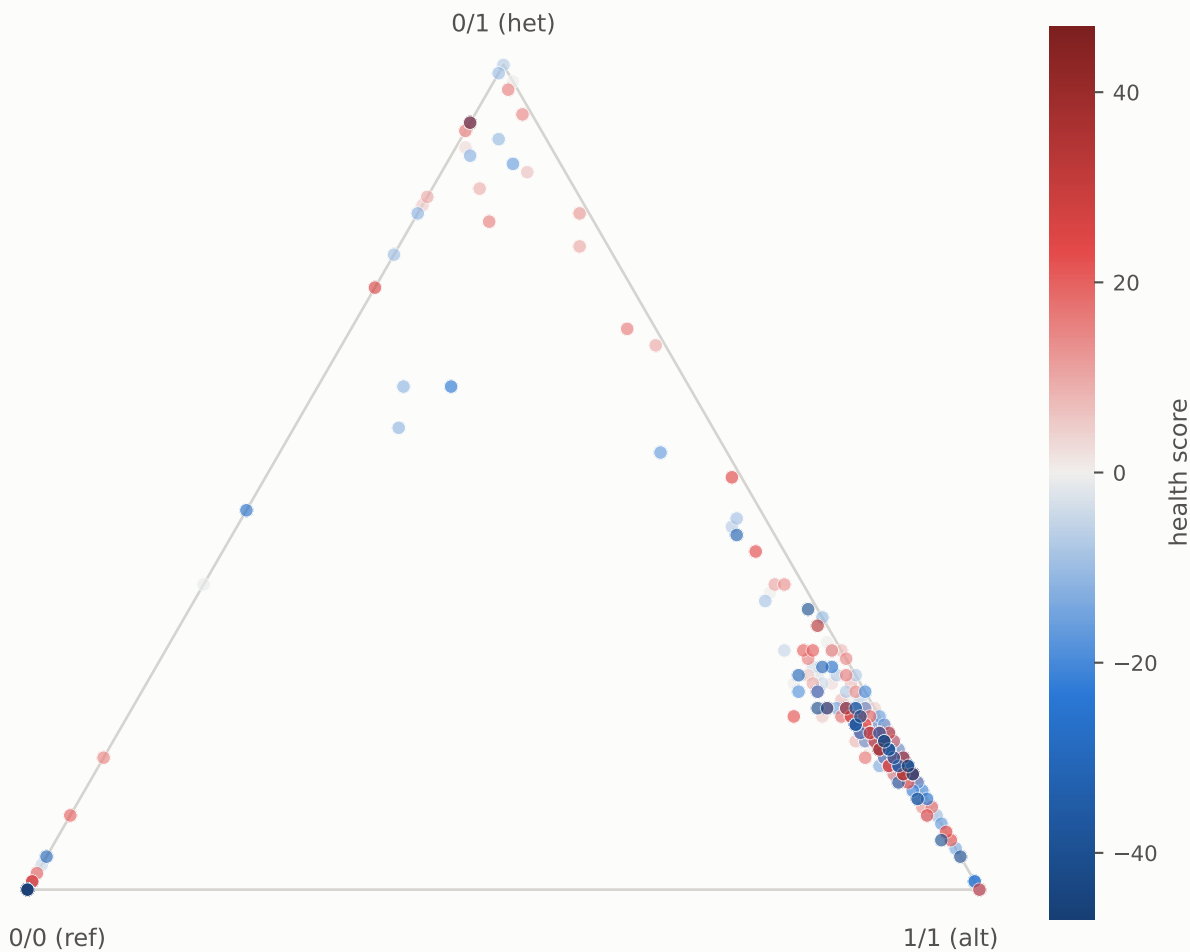
#41 by genotype uncertainty CHR_04:11,603,346 C>T
AF=0.54 DR2=0.81 $r=+0.034$ $\bar{H}=0.404$ F=1.2



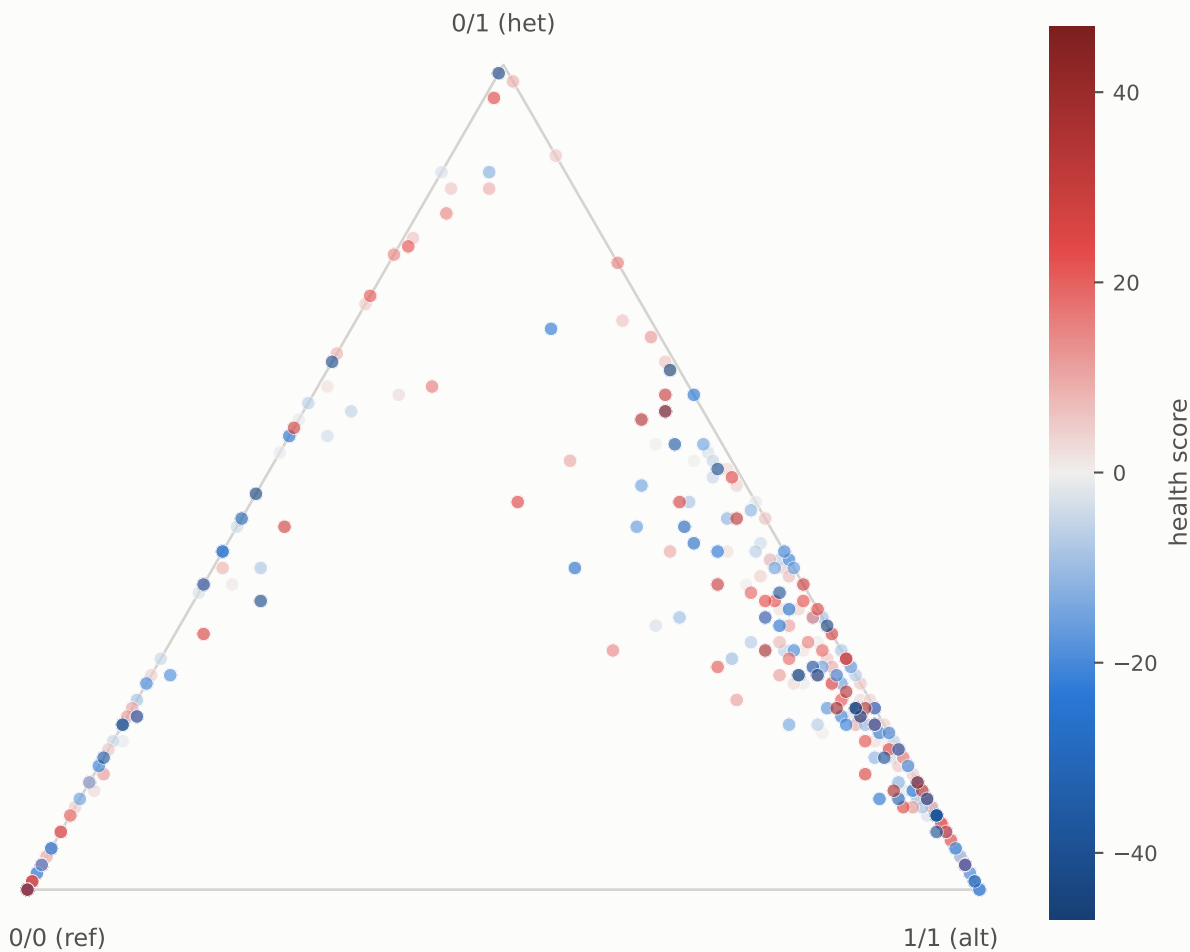
#42 by genotype uncertainty CHR_08:5,810,631 T>A
AF=0.61 DR2=0.81 $r=+0.059$ $\bar{H}=0.404$ F=2.2



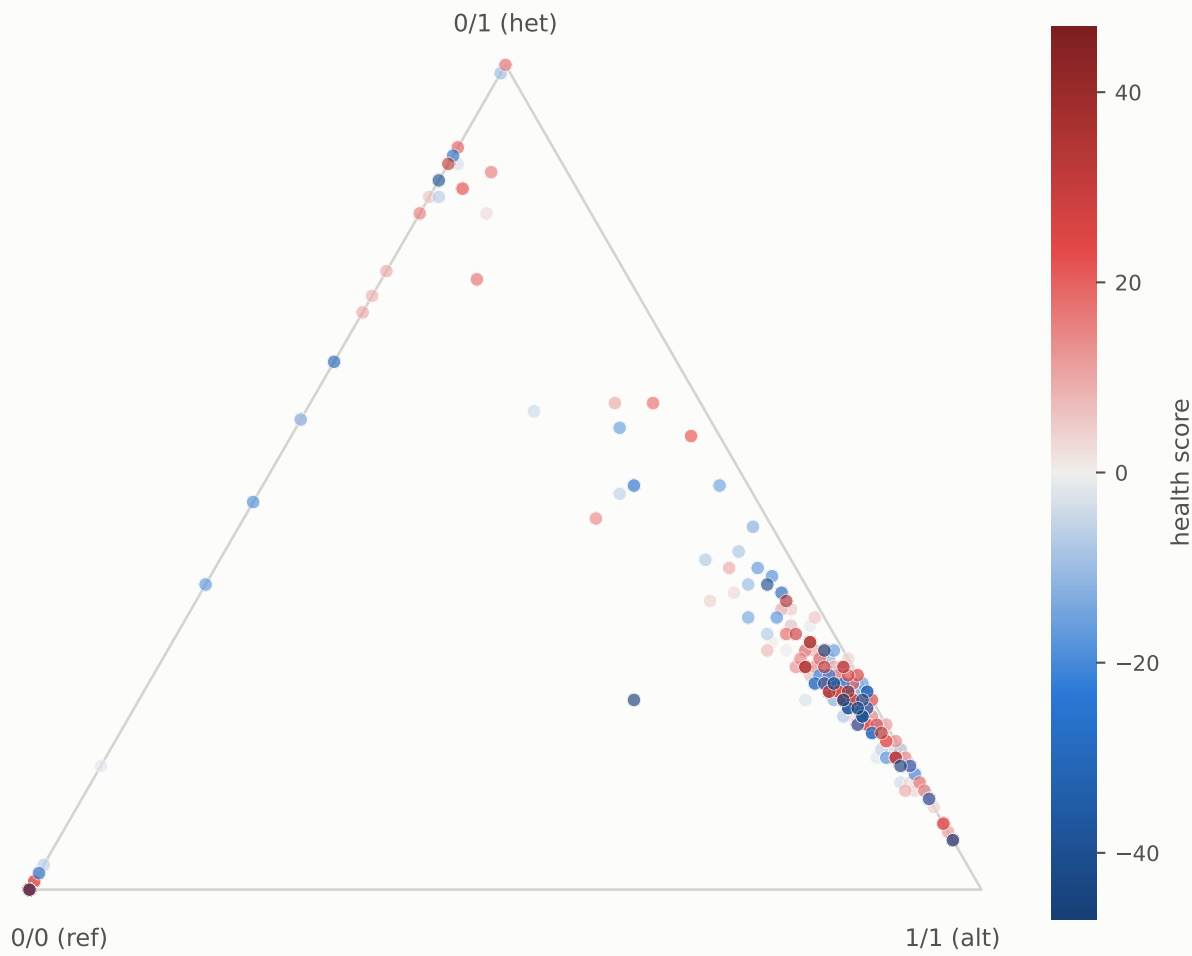
#43 by genotype uncertainty CHR_14:12,773,912 T>C
AF=0.64 DR2=0.81 $r=-0.041$ $\bar{H}=0.404$ F=0.7



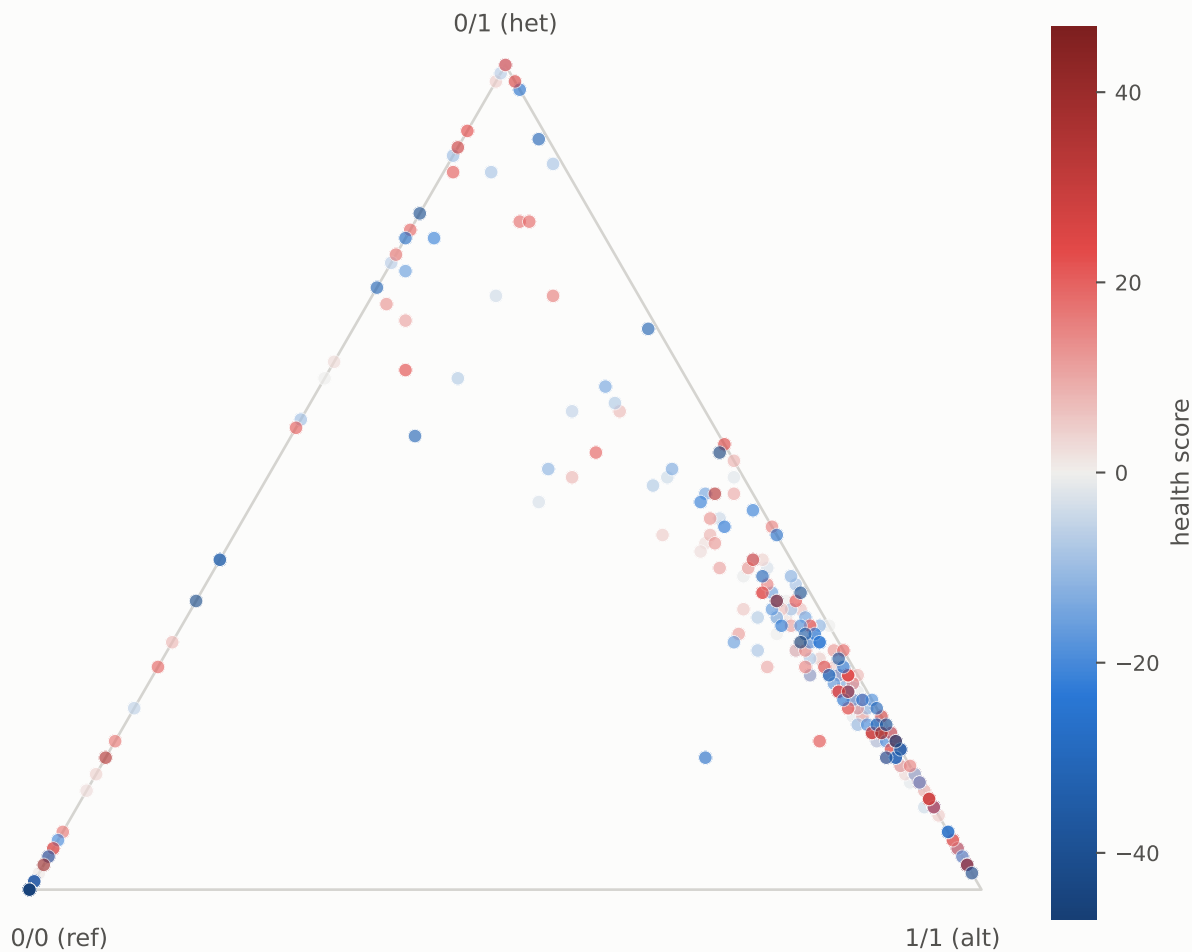
#44 by genotype uncertainty CHR_10:25,474,429 A>T
AF=0.48 DR2=0.81 $r=-0.101$ $\bar{H}=0.404$ F=1.4



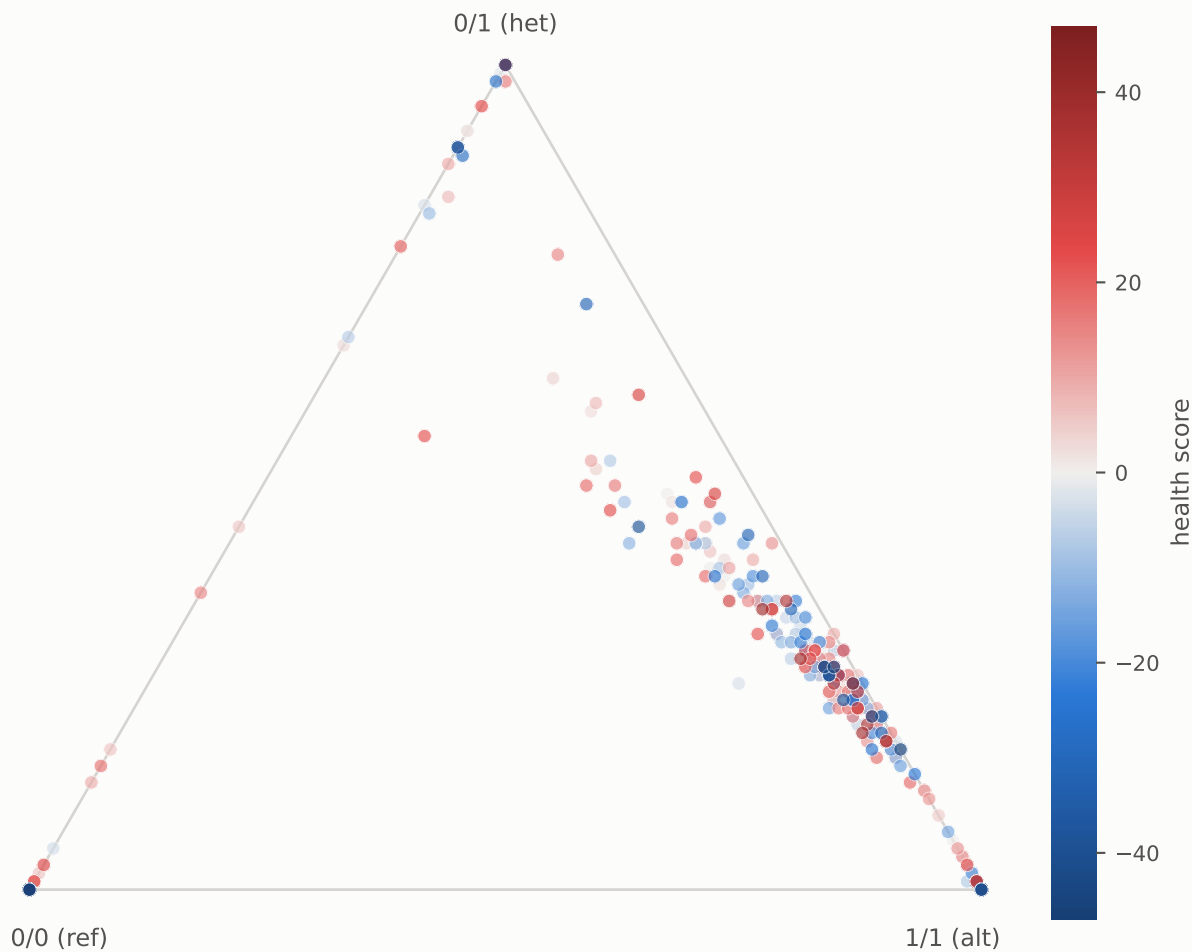
#45 by genotype uncertainty CHR_21:18,191,101 G>A
AF=0.5 DR2=0.82 r=+0.009 H=0.404 F=0.2



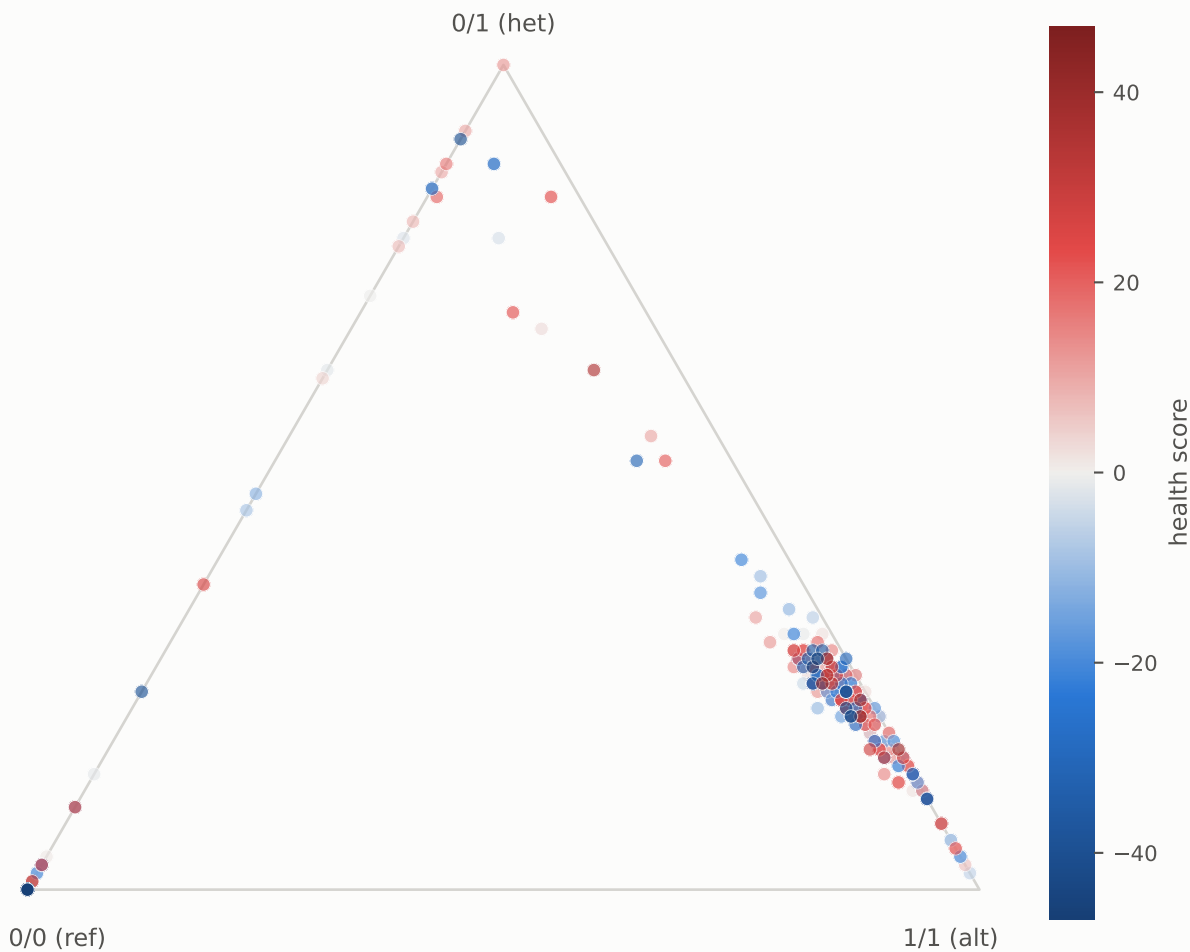
#46 by genotype uncertainty CHR_06:36,053,889 A>G
AF=0.48 DR2=0.81 $r=-0.031$ $\bar{H}=0.404$ $F=0.4$



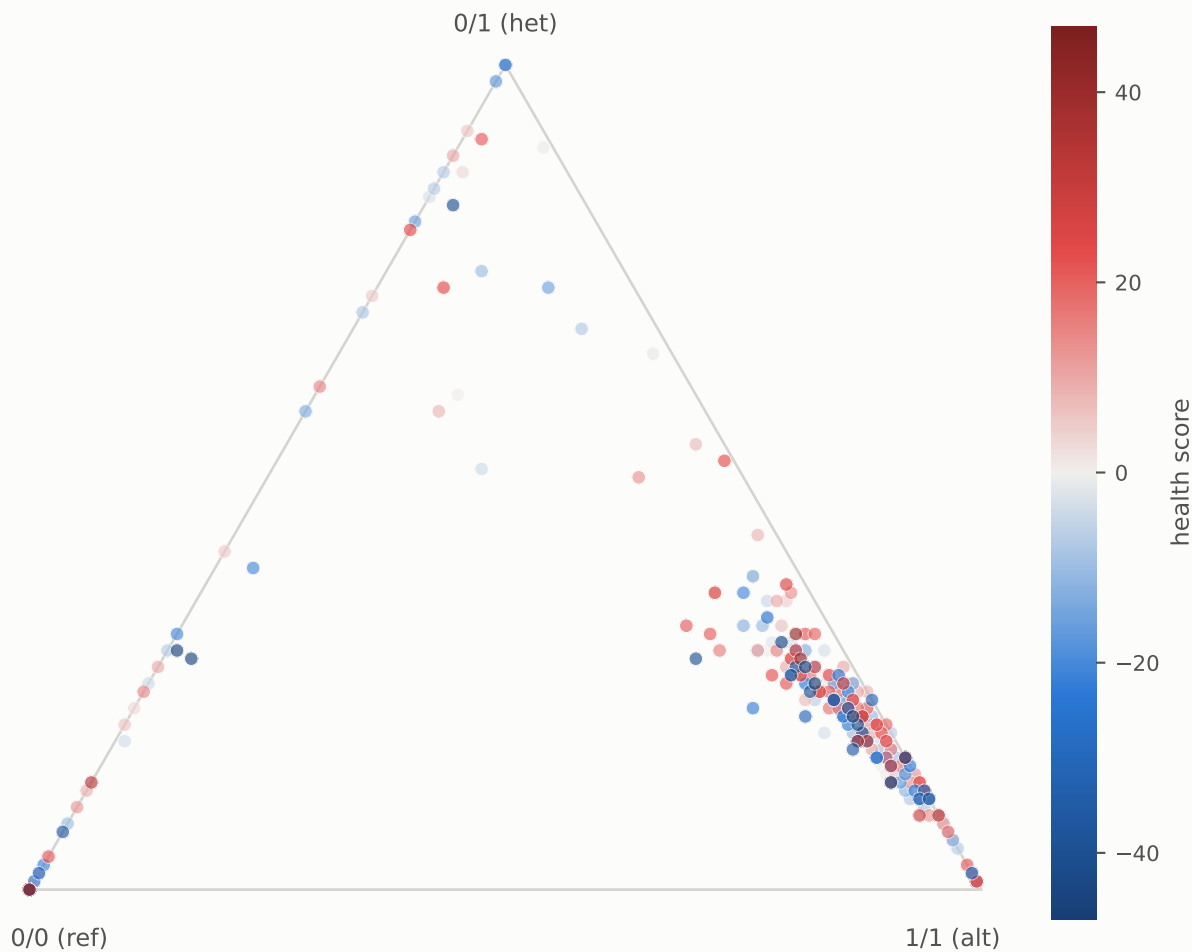
#47 by genotype uncertainty CHR_21:18,210,343 A>G
AF=0.52 DR2=0.81 $r=+0.031$ $H=0.404$ $F=0.2$



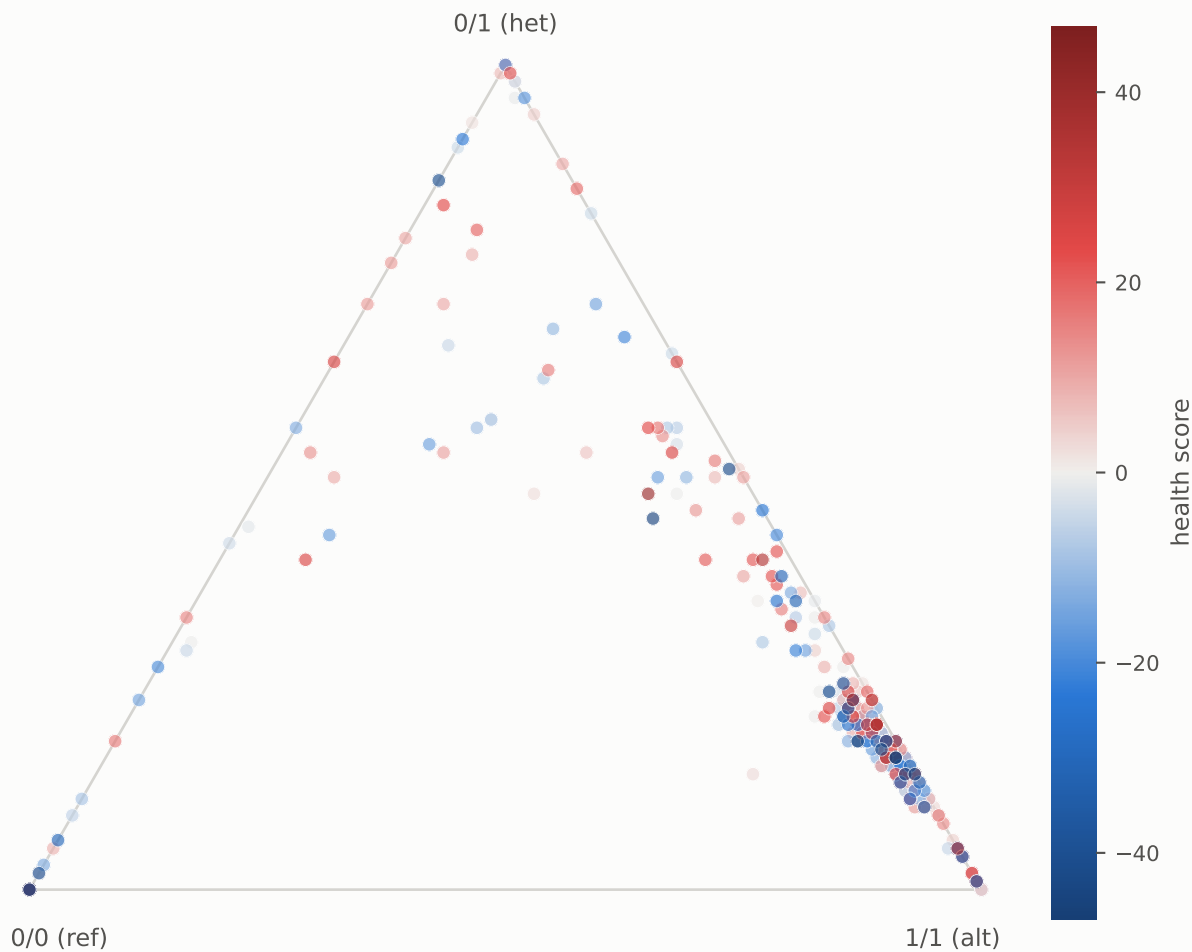
#48 by genotype uncertainty CHR_13:24,481,433 C>A
AF=0.53 DR2=0.81 $r=+0.022$ $H=0.404$ $F=0.3$



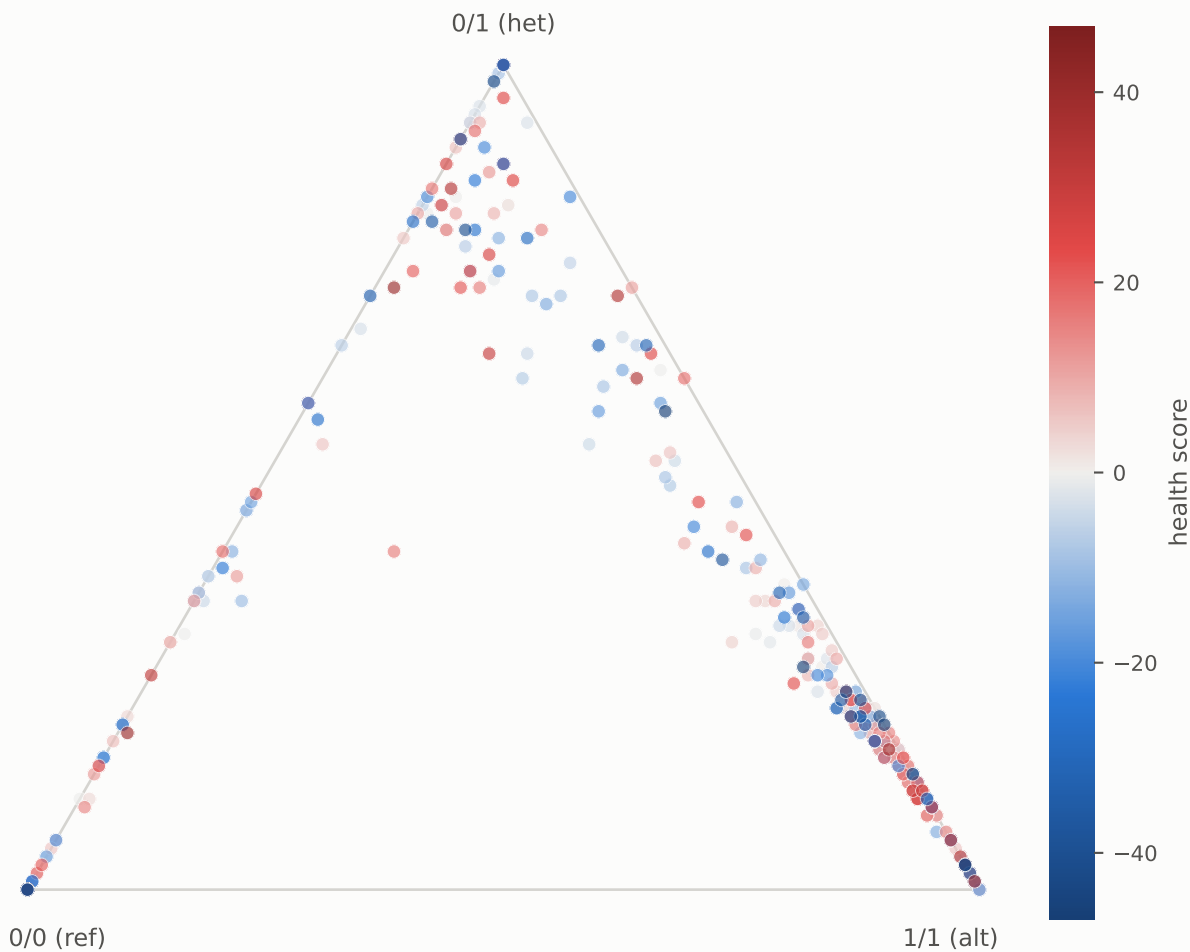
#49 by genotype uncertainty CHR_10:8,803,504 A>G
AF=0.51 DR2=0.81 $r=+0.016$ $\bar{H}=0.404$ F=0.1



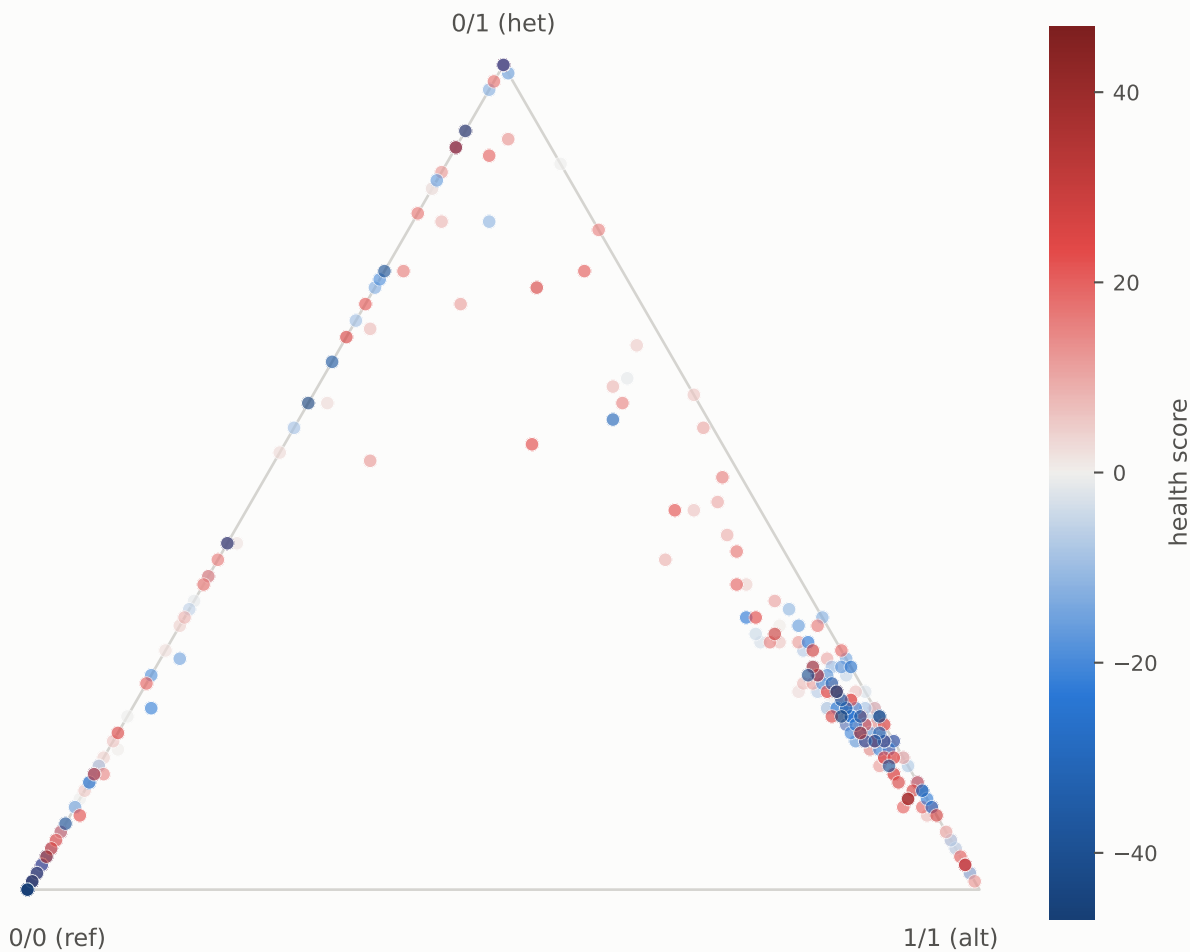
#50 by genotype uncertainty CHR_08:18,912,729 A>G
AF=0.57 DR2=0.81 $r=+0.038$ H=0.403 F=0.6



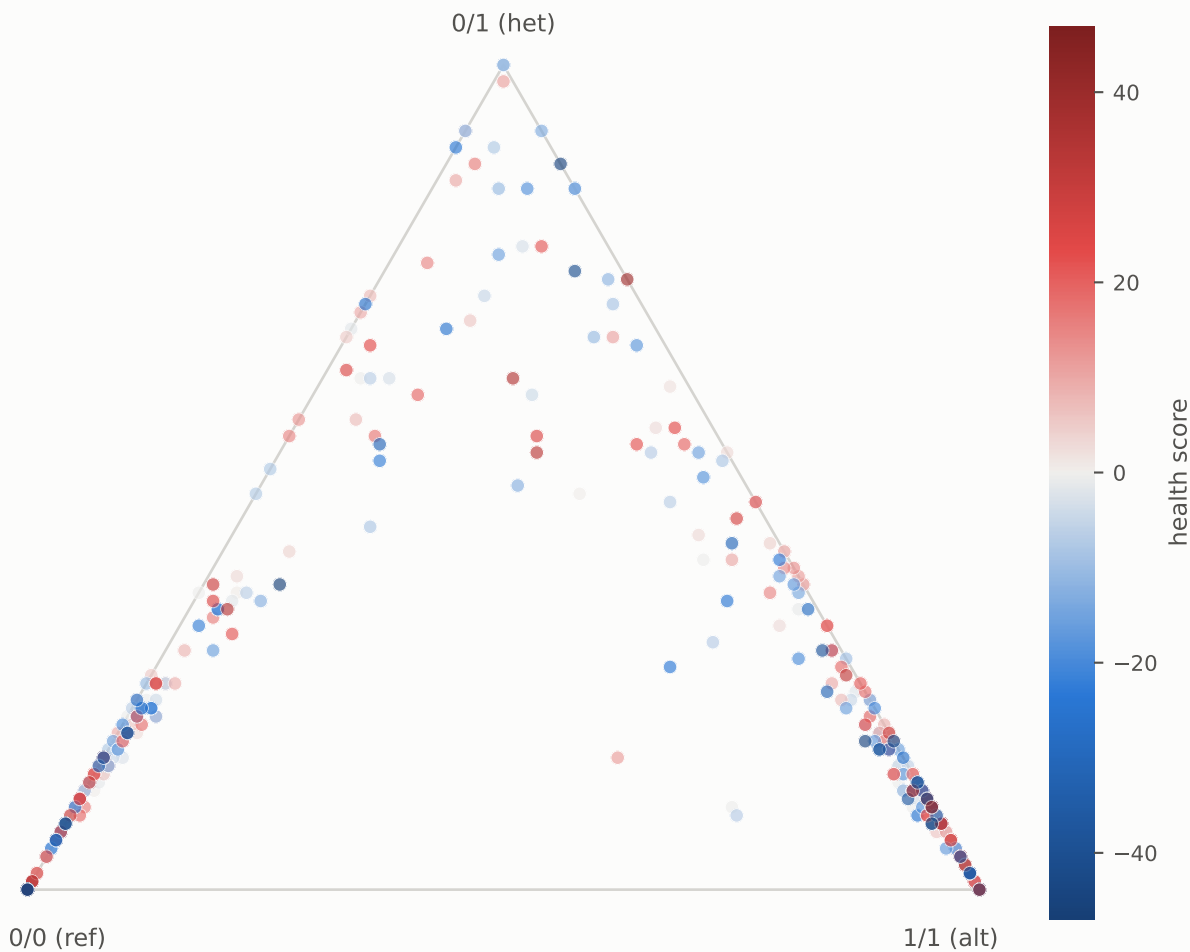
#51 by genotype uncertainty CHR_10:32,324,083 A>C
AF=0.47 DR2=0.81 $r=-0.049$ $\bar{H}=0.403$ F=0.8



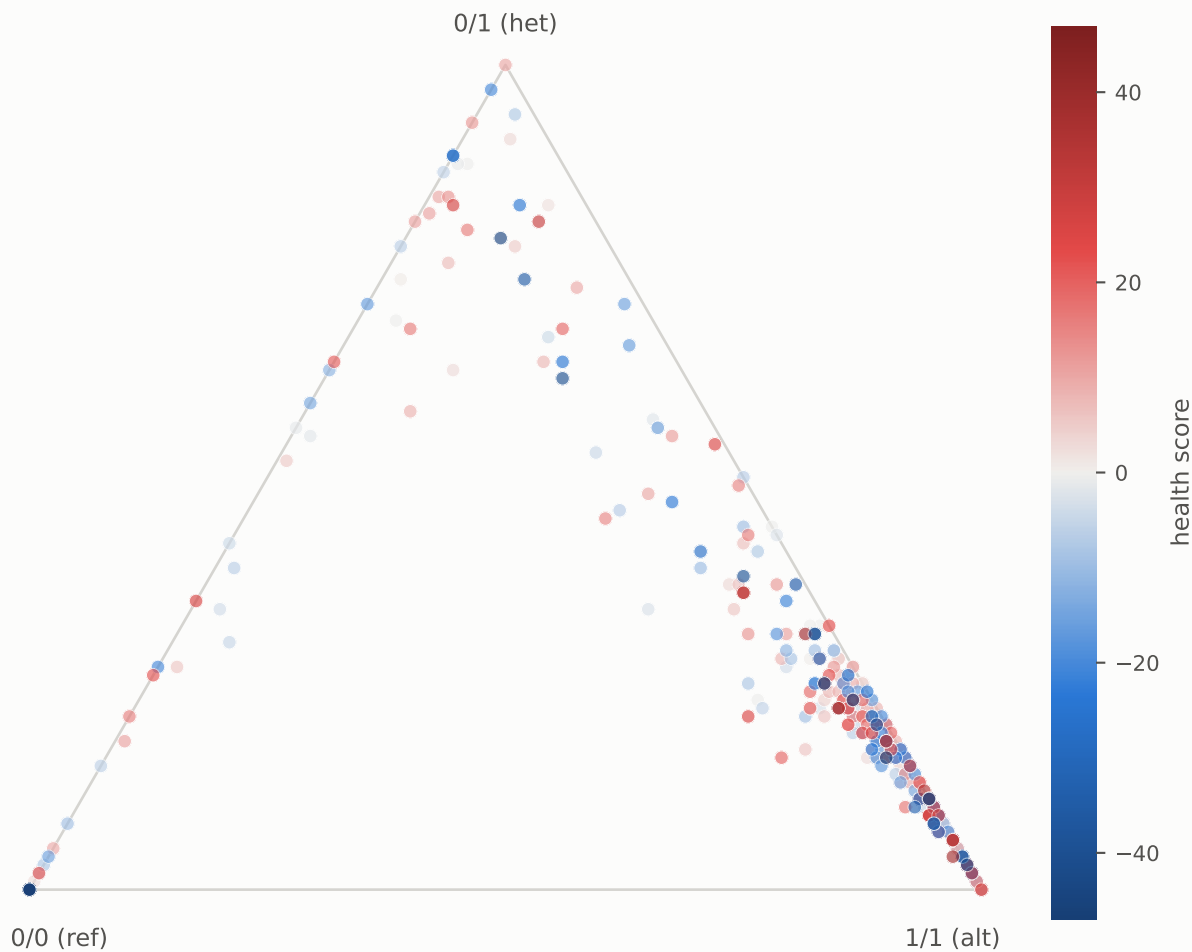
#52 by genotype uncertainty CHR_06:5,228,722 A>C
AF=0.5 DR2=0.81 $r=+0.022$ $\bar{H}=0.403$ F=0.9



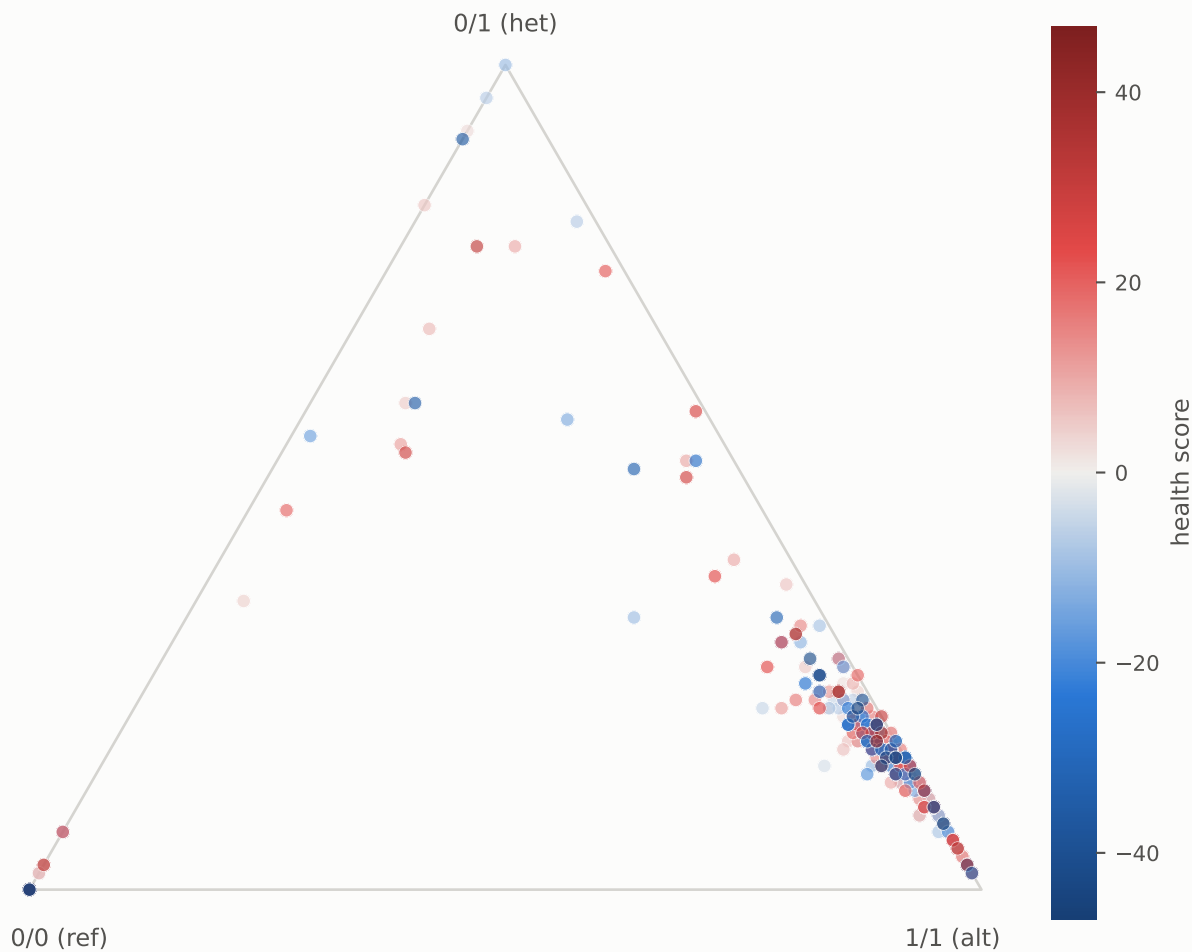
#53 by genotype uncertainty CHR_13:11,443,617 T>C
AF=0.5 DR2=0.81 r=+0.005 $\bar{H}$ =0.403 F=0.1



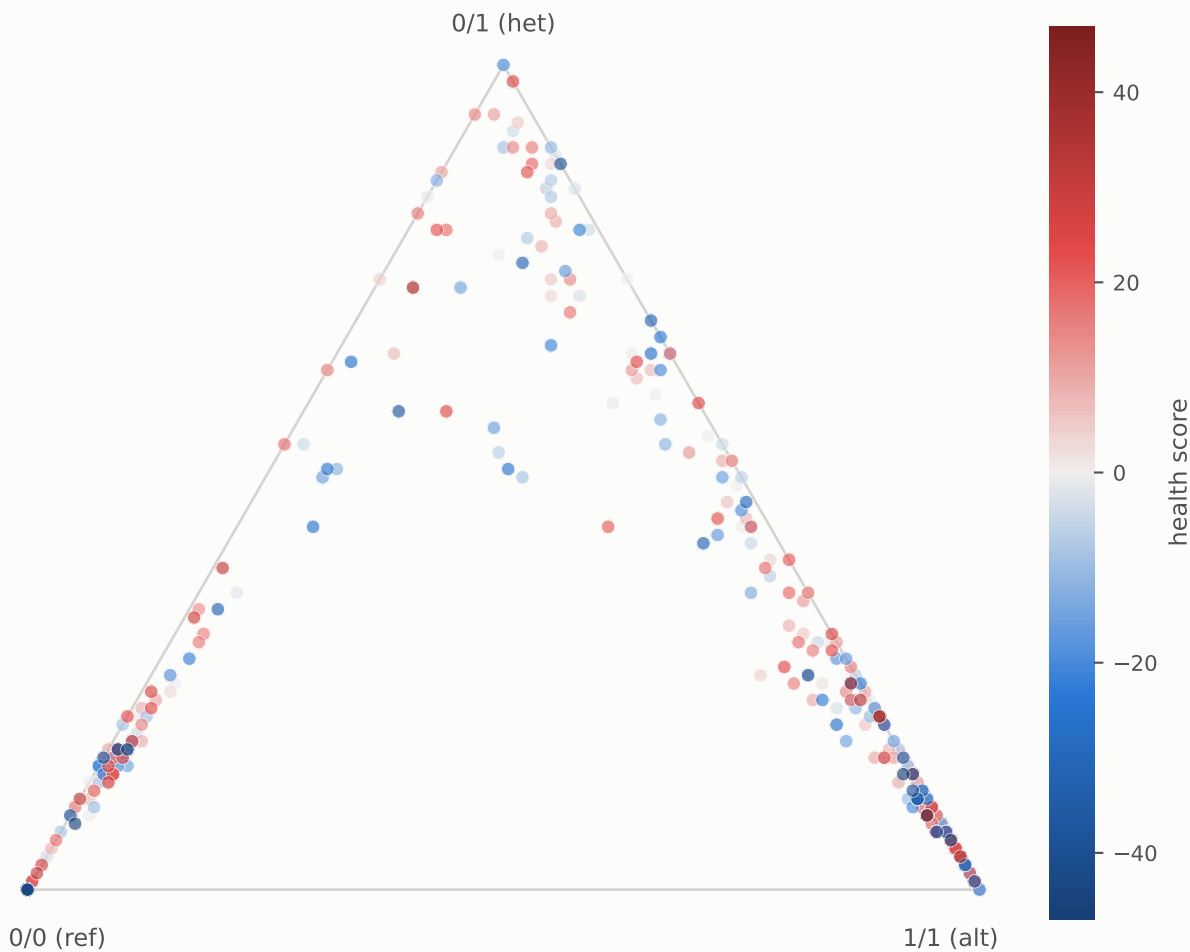
#54 by genotype uncertainty CHR_10:4,765,392 G>A
AF=0.56 DR2=0.82 $r=+0.027$ $\bar{H}=0.403$ F=0.4



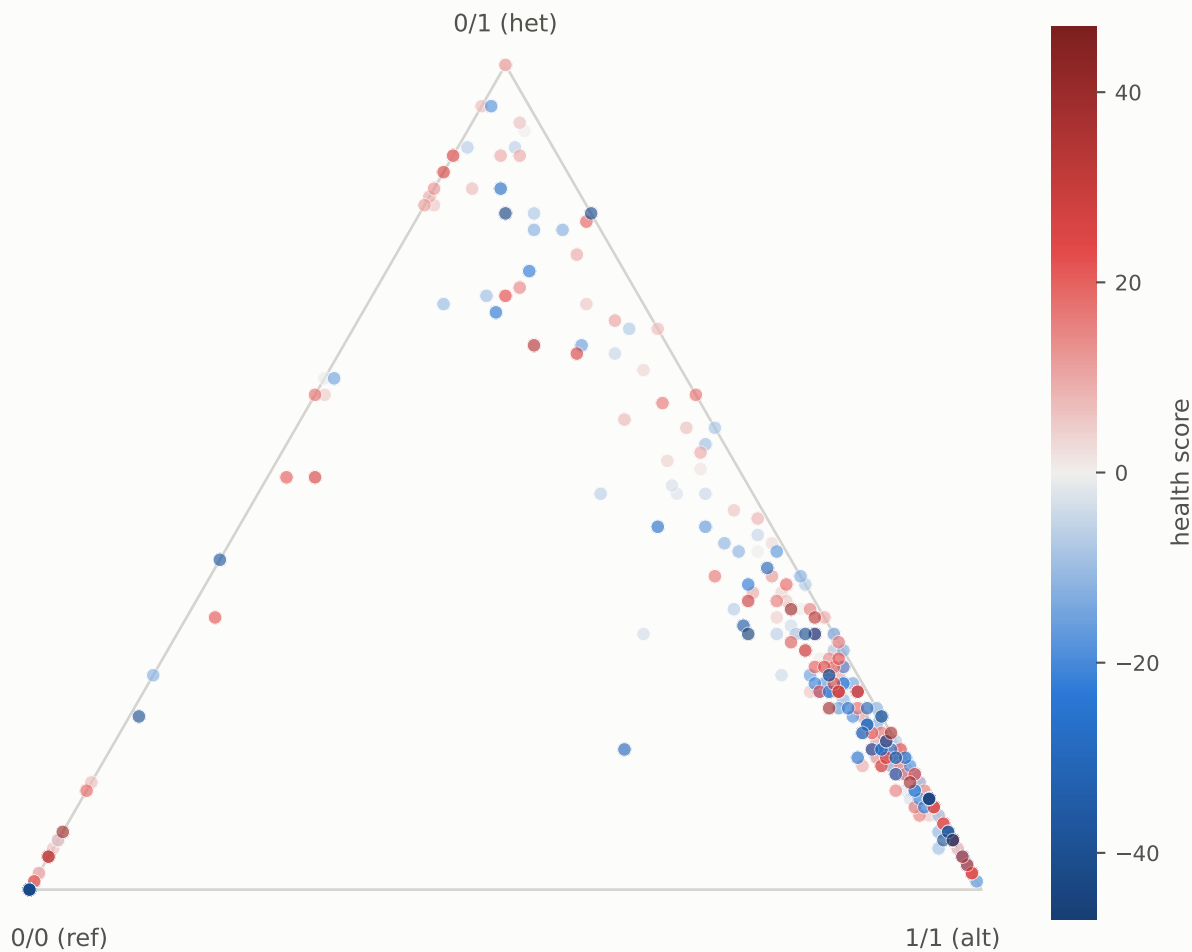
#55 by genotype uncertainty CHR_08:34,825,789 G>A
AF=0.6 DR2=0.82 $r=-0.079$ $\bar{H}=0.403$ F=1.5



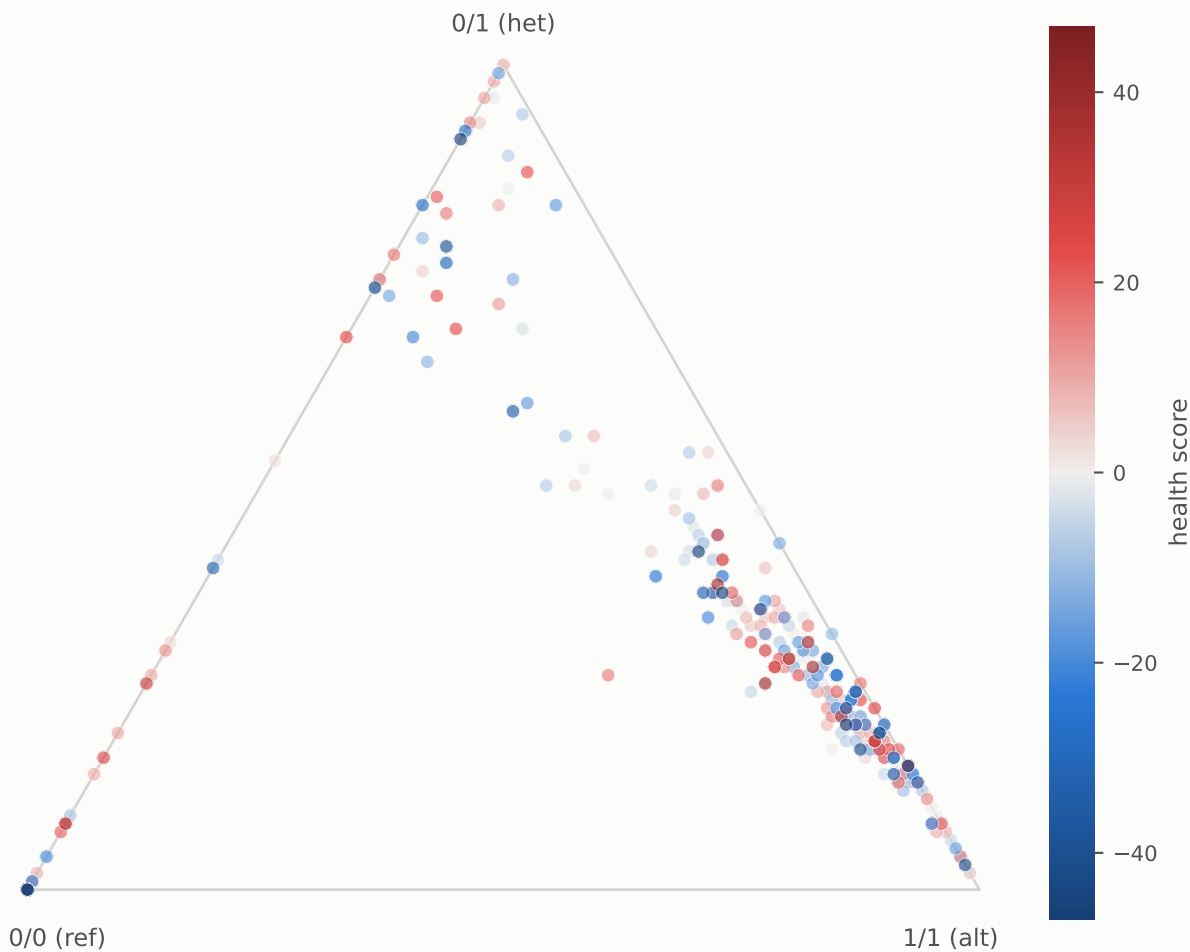
#56 by genotype uncertainty CHR_18:18,490,918 T>C
AF=0.52 DR2=0.81 $r=-0.006$ $\bar{H}=0.403$ $F=0.0$



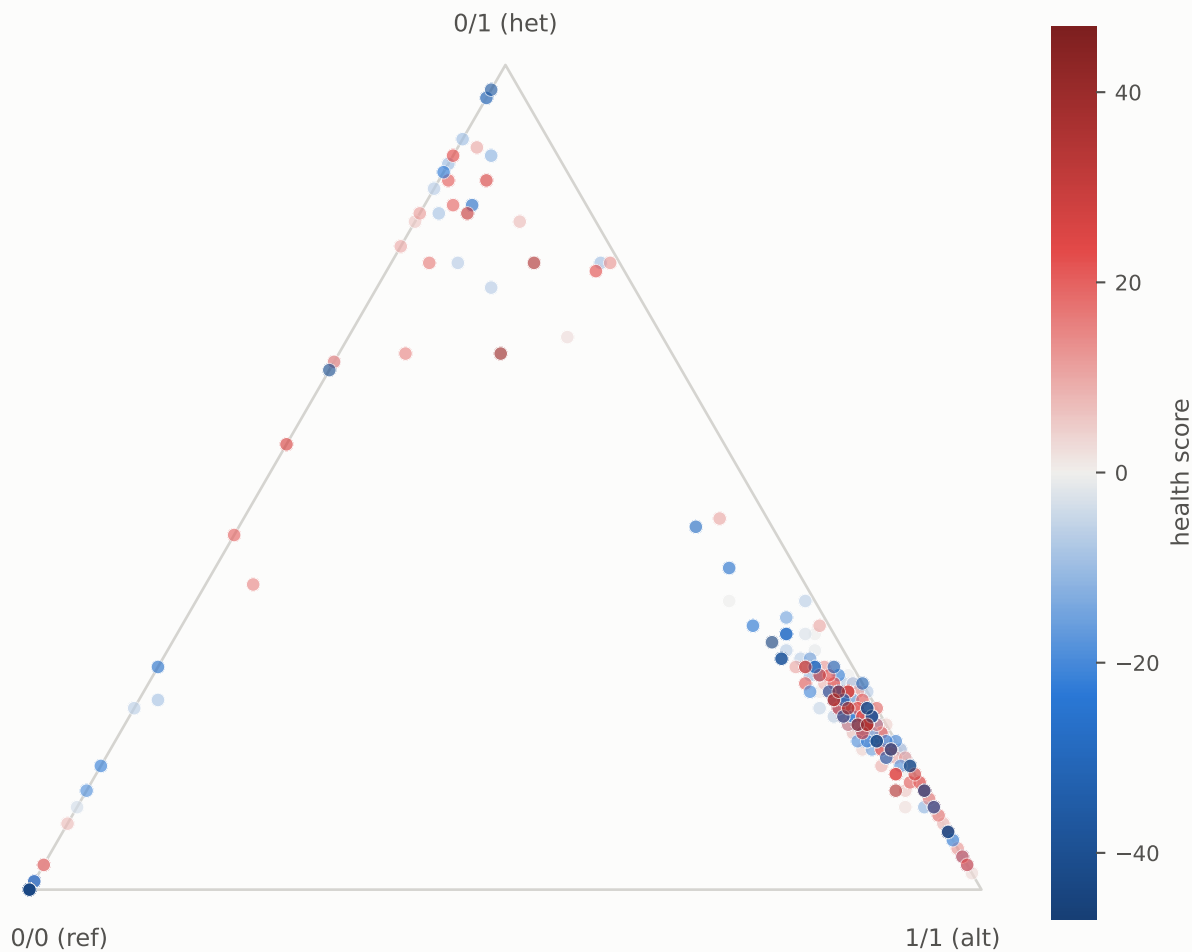
#57 by genotype uncertainty CHR_06:7,931,778 A>G
AF=0.56 DR2=0.81 $r=-0.073$ $\bar{H}=0.402$ F=1.4



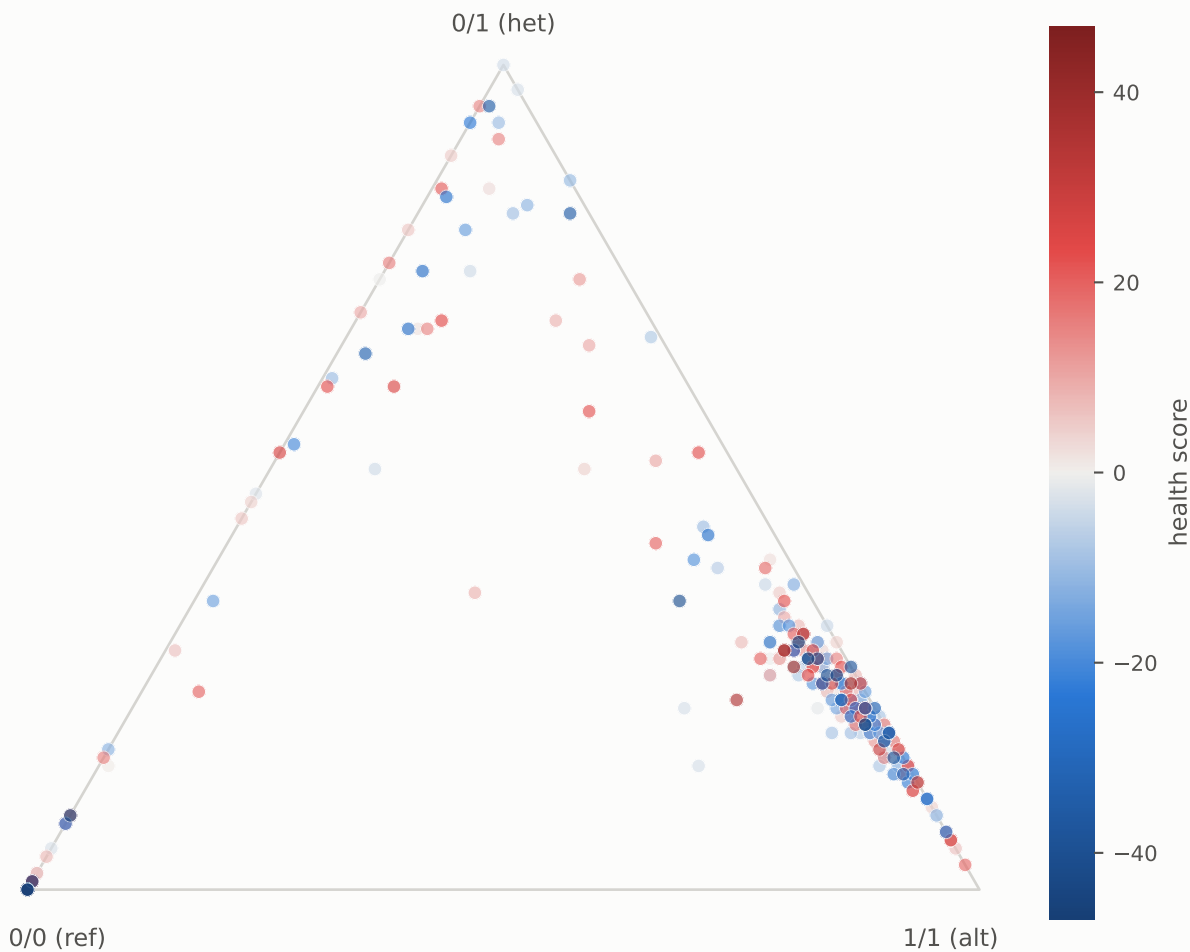
#58 by genotype uncertainty CHR_08:30,895,741 A>T
AF=0.43 DR2=0.81 $r=-0.053$ $\bar{H}=0.402$ F=1.2



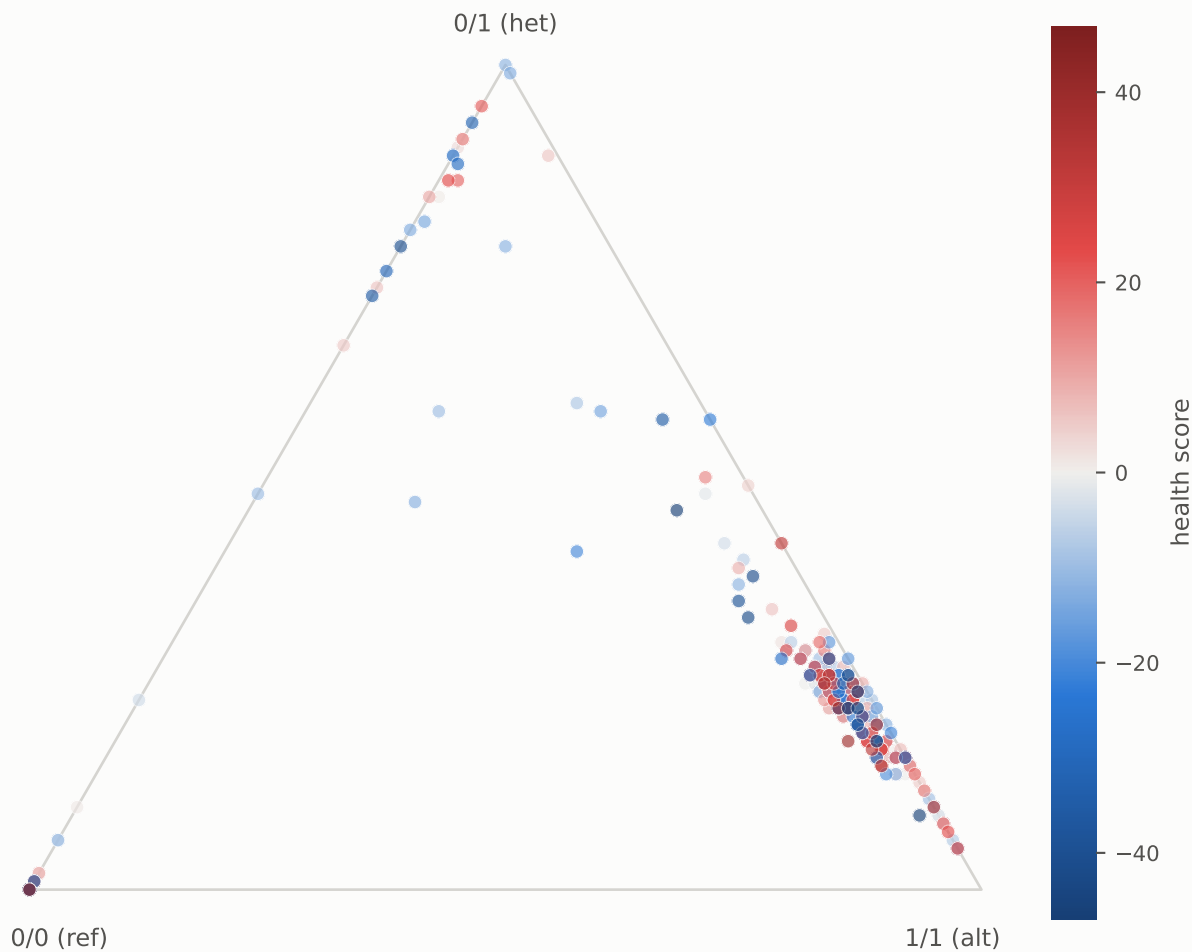
#59 by genotype uncertainty CHR_03:39,043,749 G>A
AF=0.53 DR2=0.82 $r=+0.021$ H=0.402 F=0.8



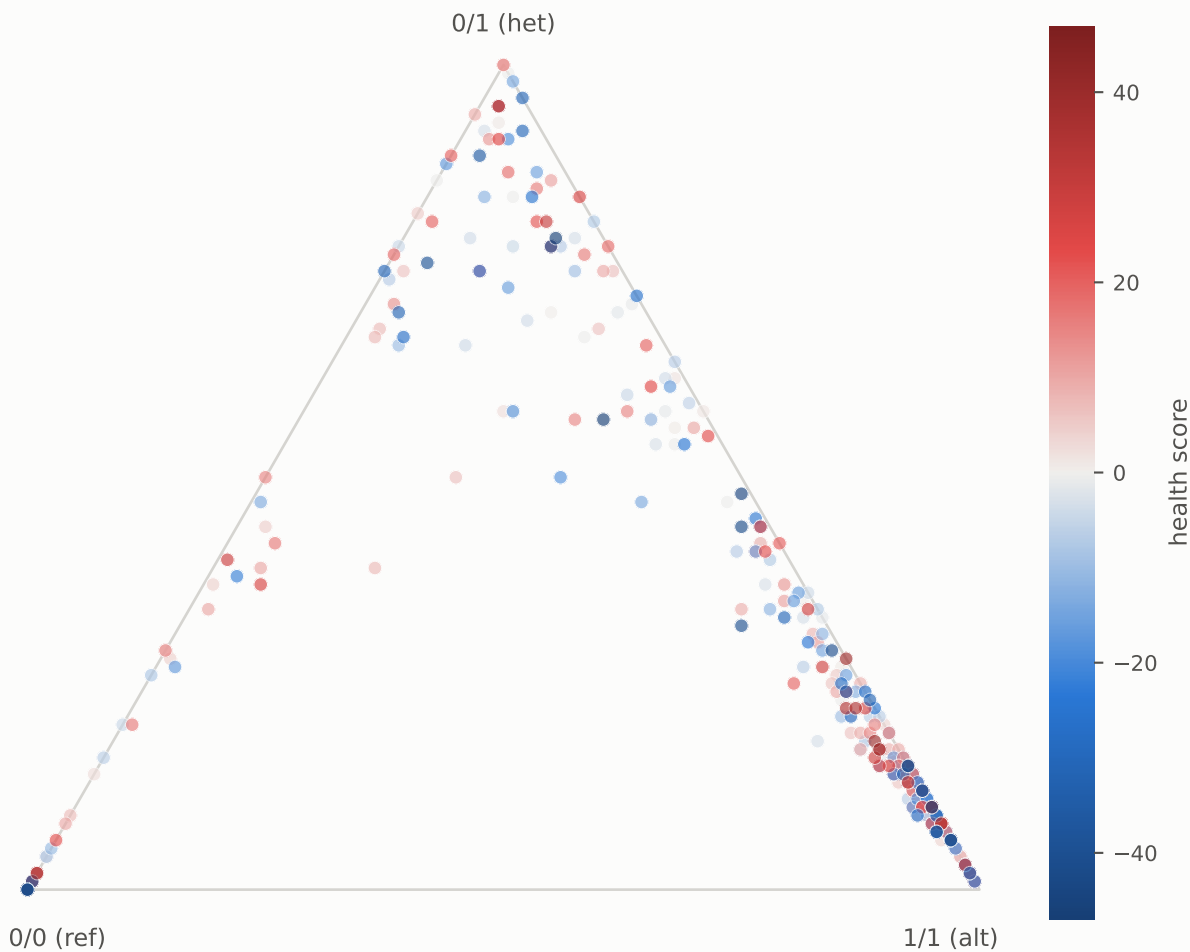
#60 by genotype uncertainty CHR_19:638,389 T>C
AF=0.45 DR2=0.81 $r=-0.057$ $H=0.402$ $F=0.8$



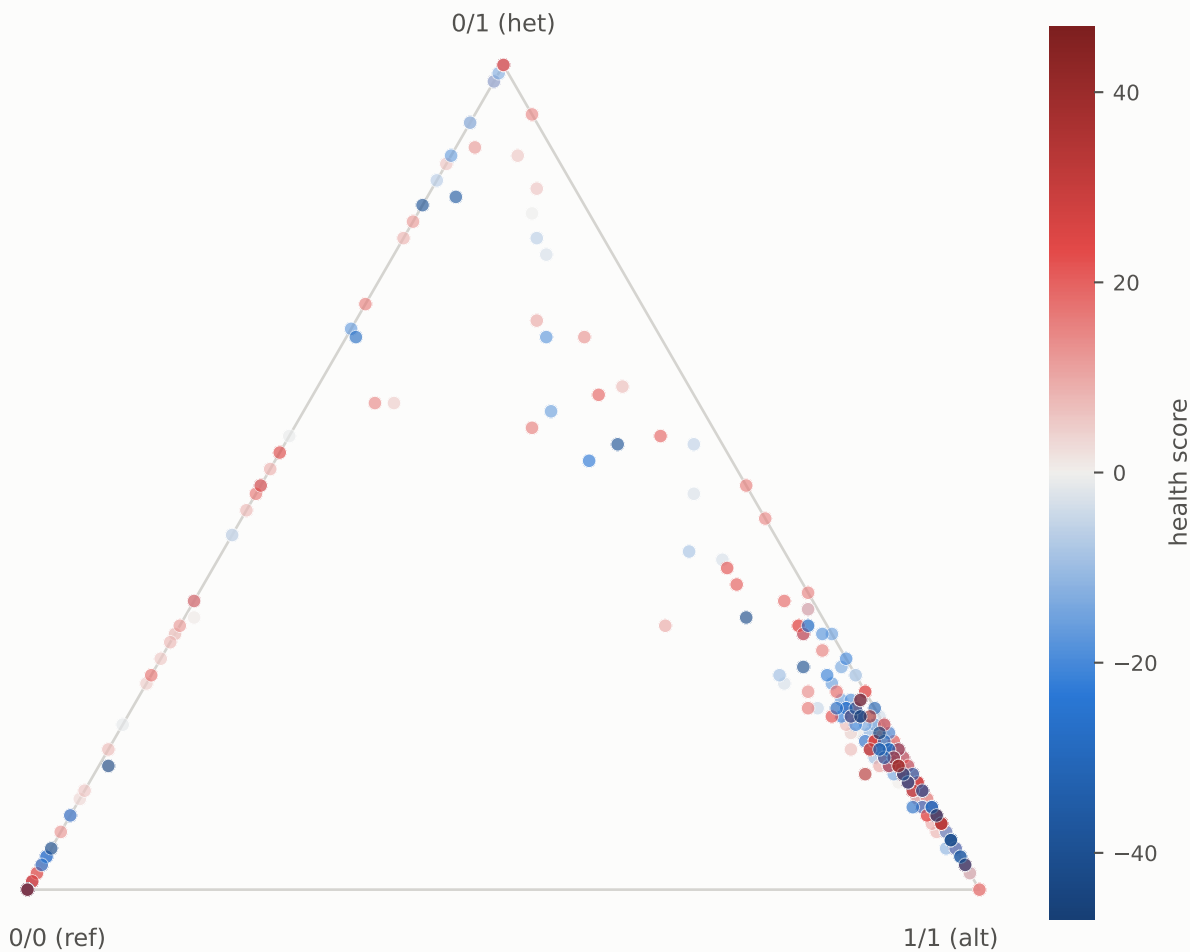
#61 by genotype uncertainty CHR_21:18,194,974 A>G
AF=0.51 DR2=0.81 $r=+0.007$ H=0.402 F=4.6



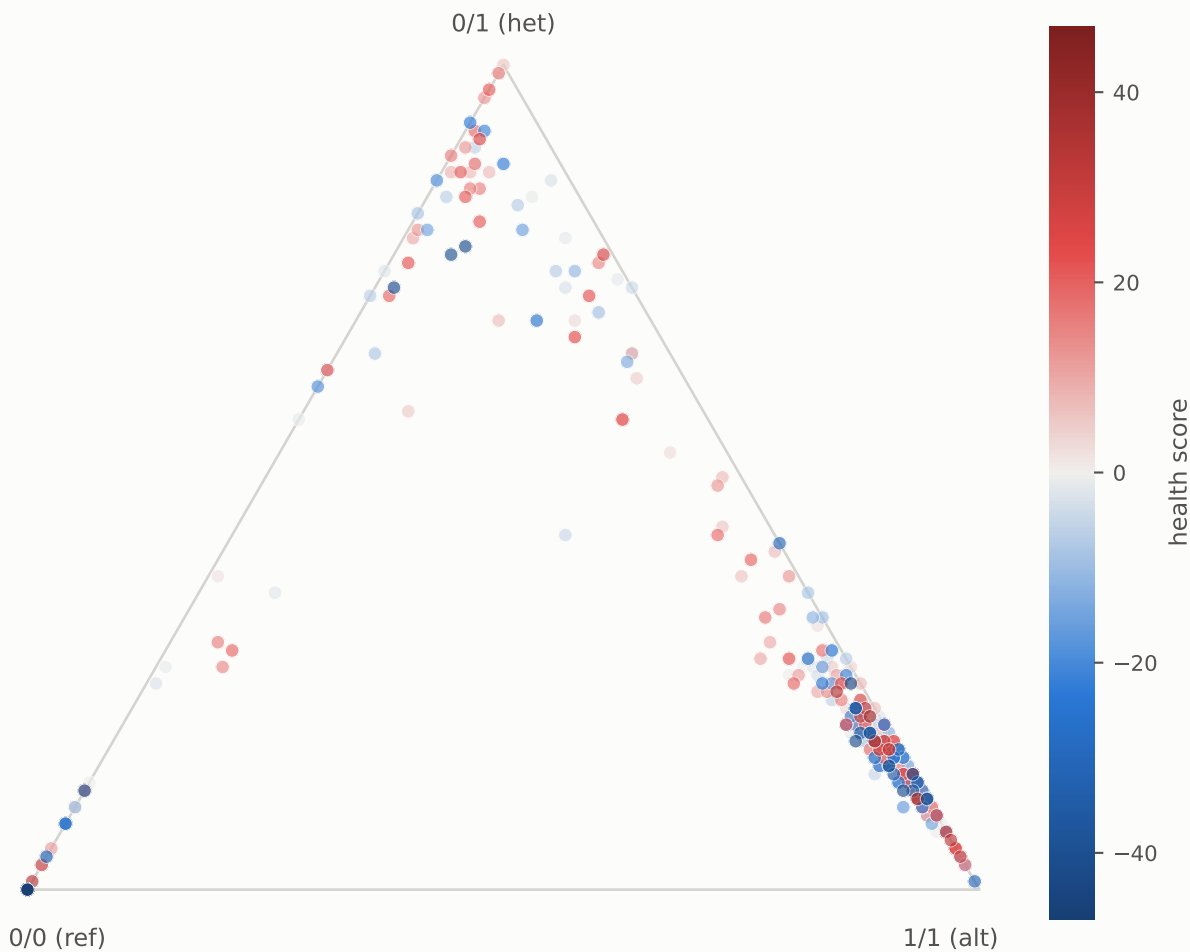
#62 by genotype uncertainty CHR_03:37,225,809 A>C
AF=0.58 DR2=0.81 r=-0.040 H=0.402 F=1.3



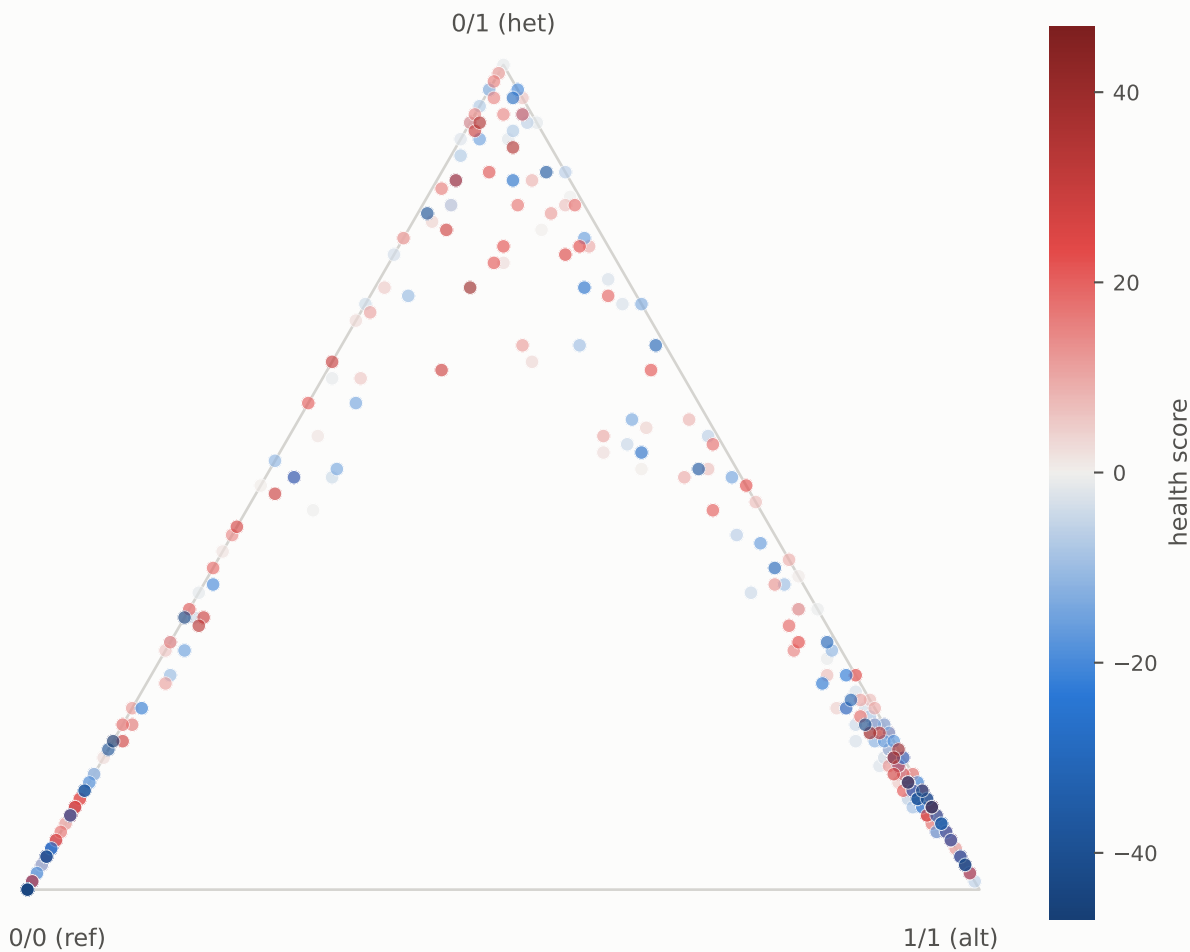
#63 by genotype uncertainty CHR_03:39,038,980 G>T
AF=0.64 DR2=0.81 $r=+0.025$ $H=0.402$ $F=0.1$



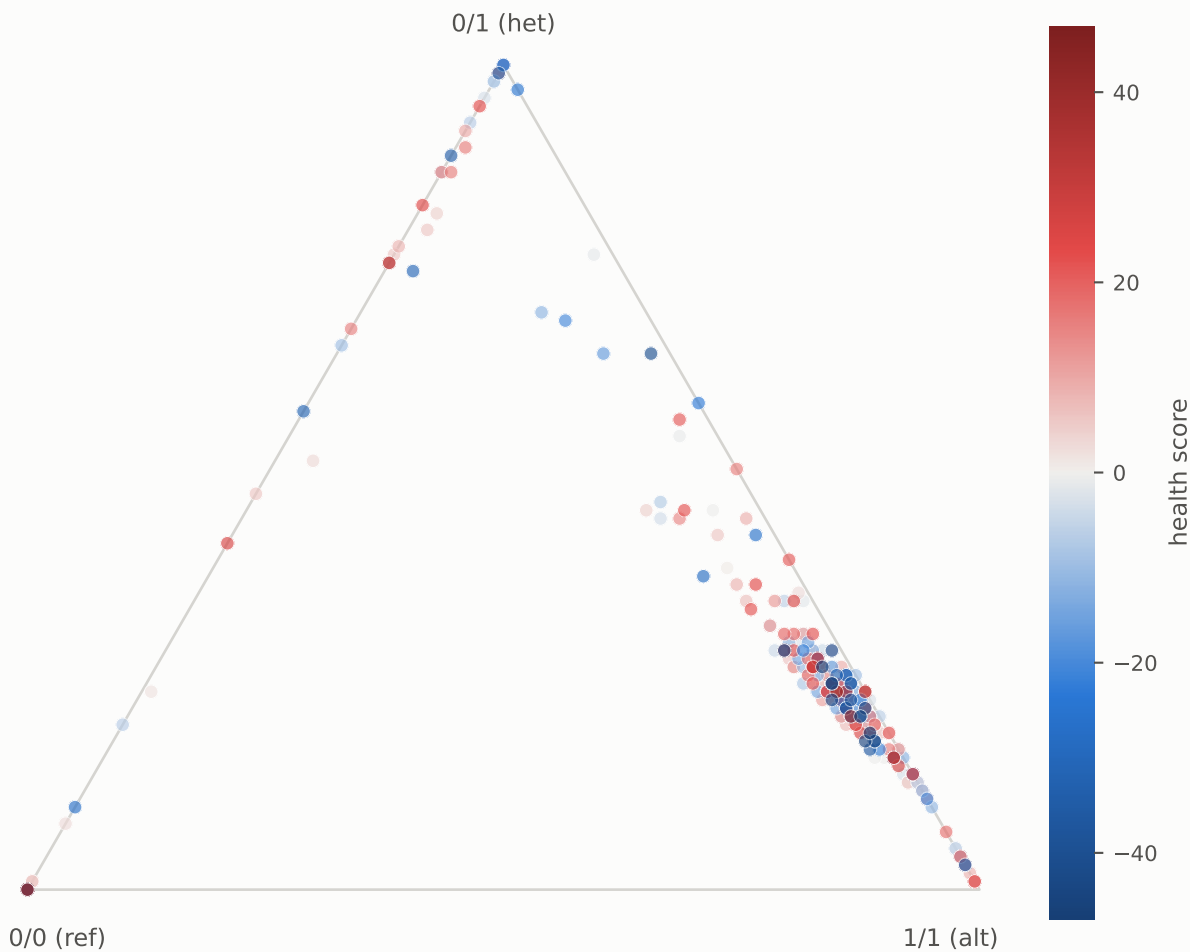
#64 by genotype uncertainty CHR_13:22,750,509 T>C
AF=0.57 DR2=0.82 $r=-0.012$ $\bar{H}=0.402$ F=0.6



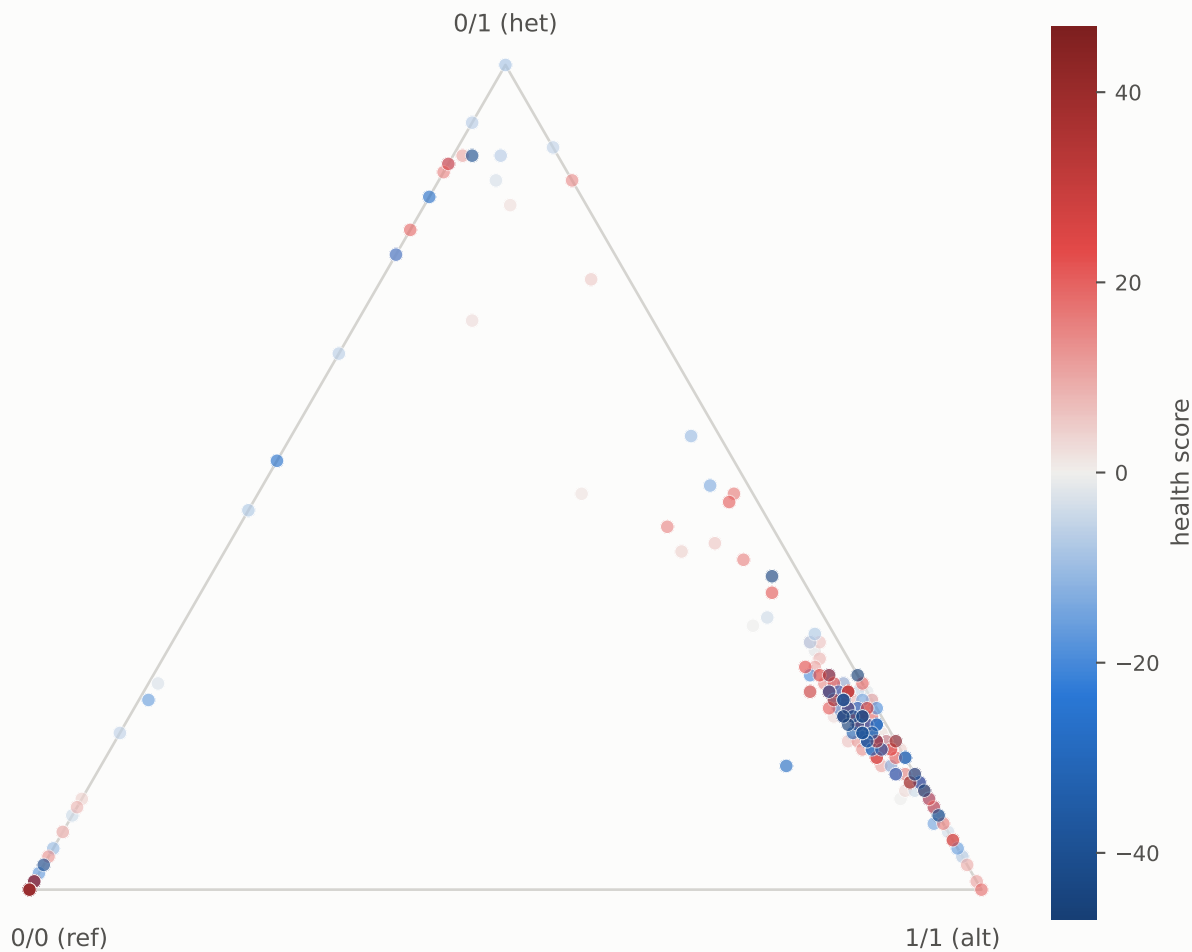
#65 by genotype uncertainty CHR_06:9,652,679 A>G
AF=0.55 DR2=0.81 $r=-0.014$ $\bar{H}=0.401$ F=1.2



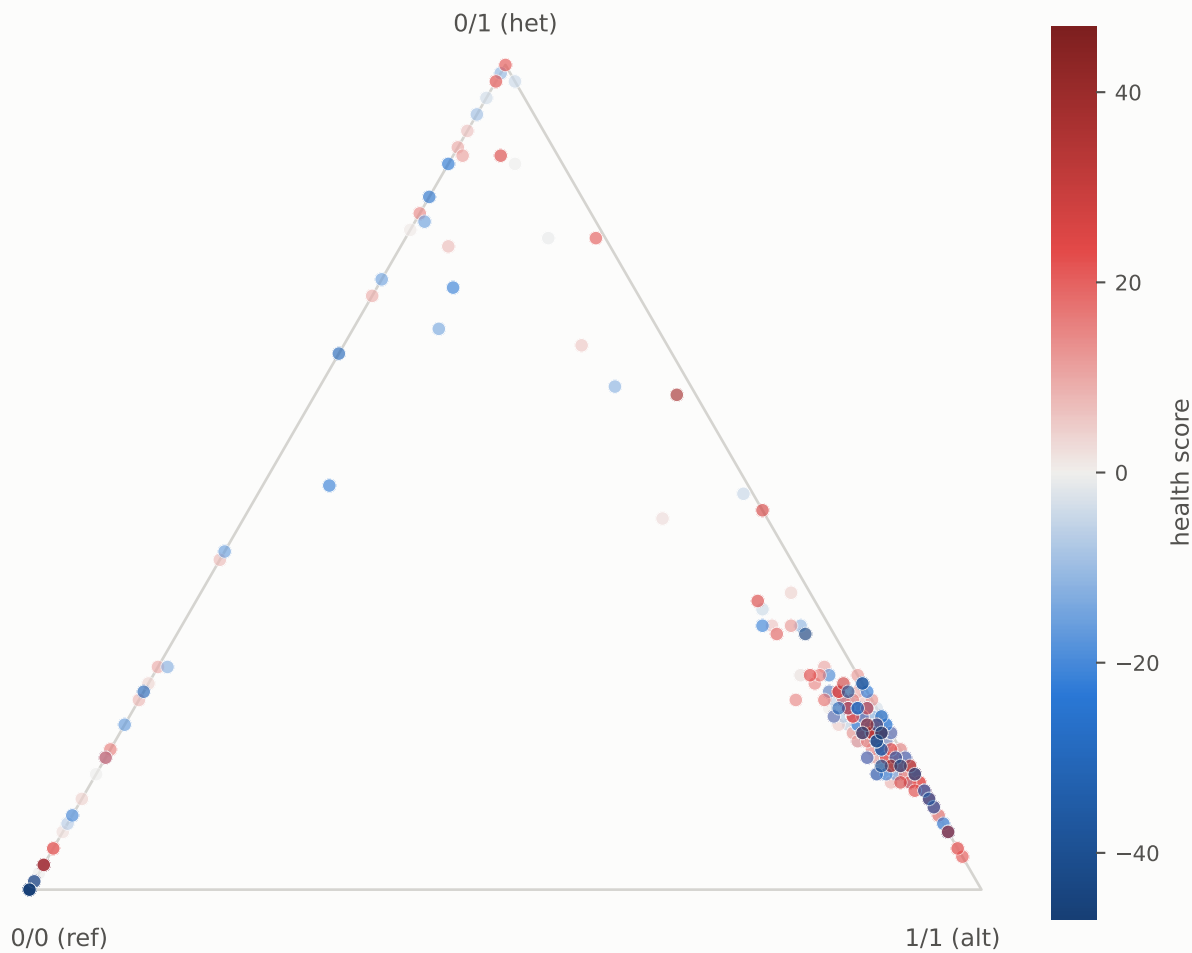
#66 by genotype uncertainty CHR_10:8,803,118 T>G
AF=0.51 DR2=0.81 r=-0.011 $\bar{H}$ =0.401 F=0.2



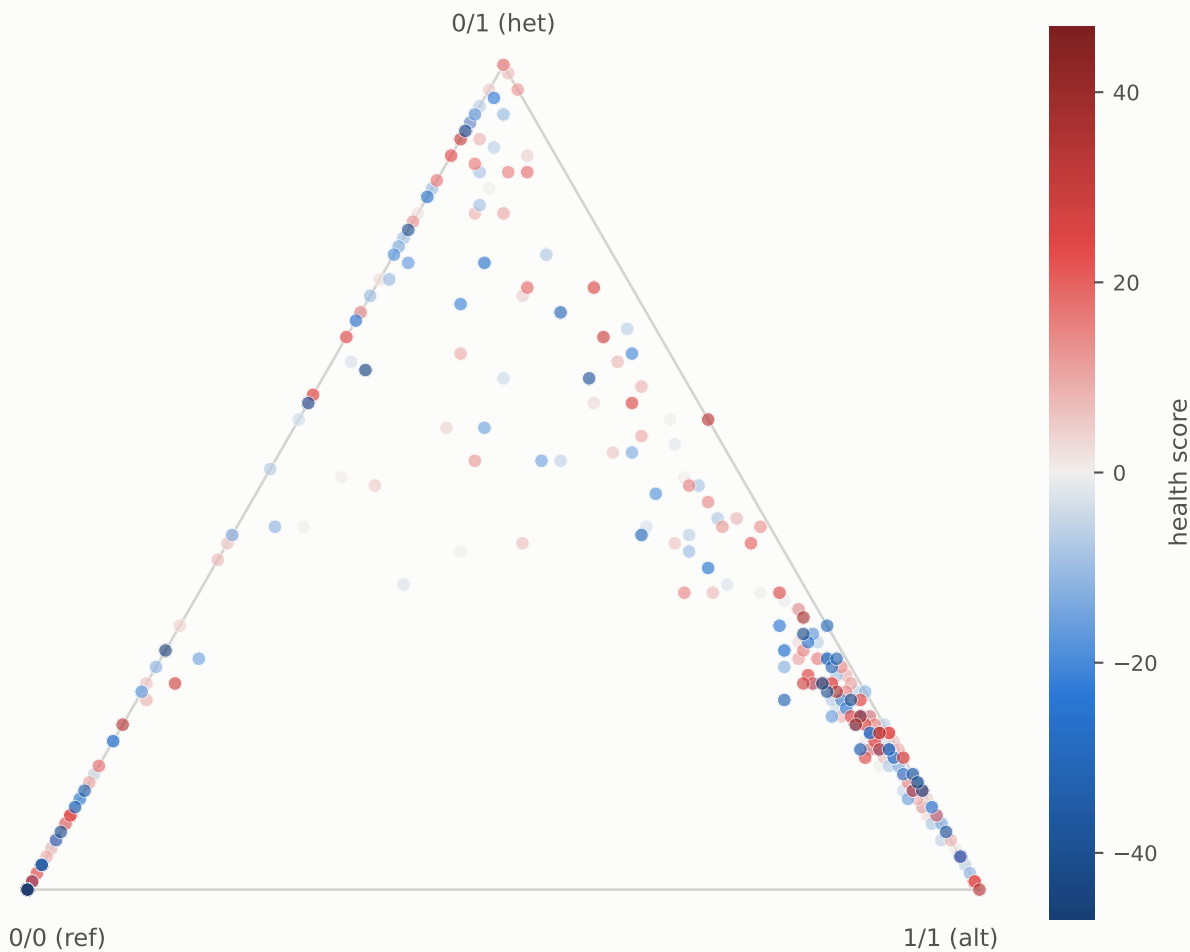
#67 by genotype uncertainty CHR_10:8,802,252 G>A
AF=0.55 DR2=0.82 $r=+0.004$ $\bar{H}=0.401$ $F=0.4$



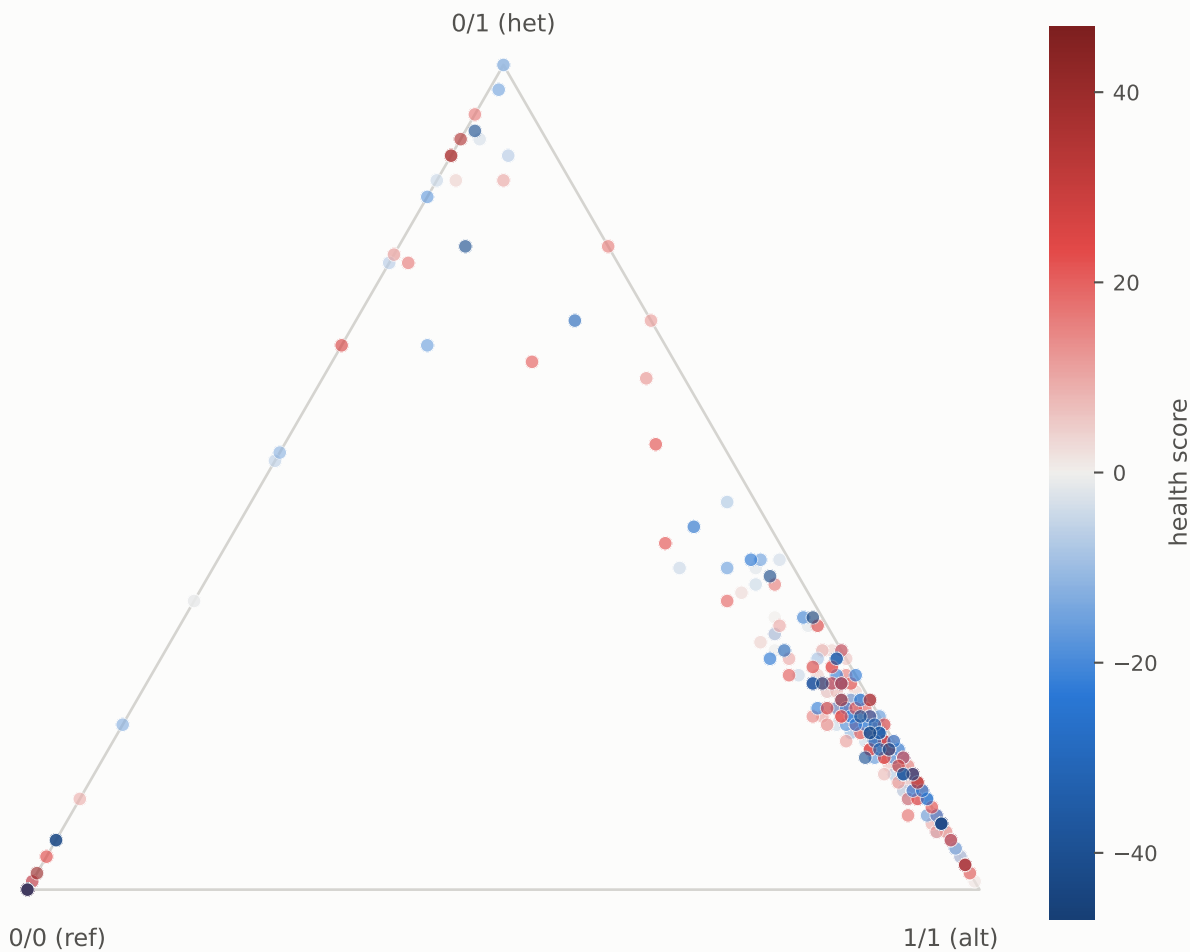
#68 by genotype uncertainty CHR_22:5,009,884 G>T
AF=0.58 DR2=0.81 $r=+0.066$ $\bar{H}=0.401$ F=0.8



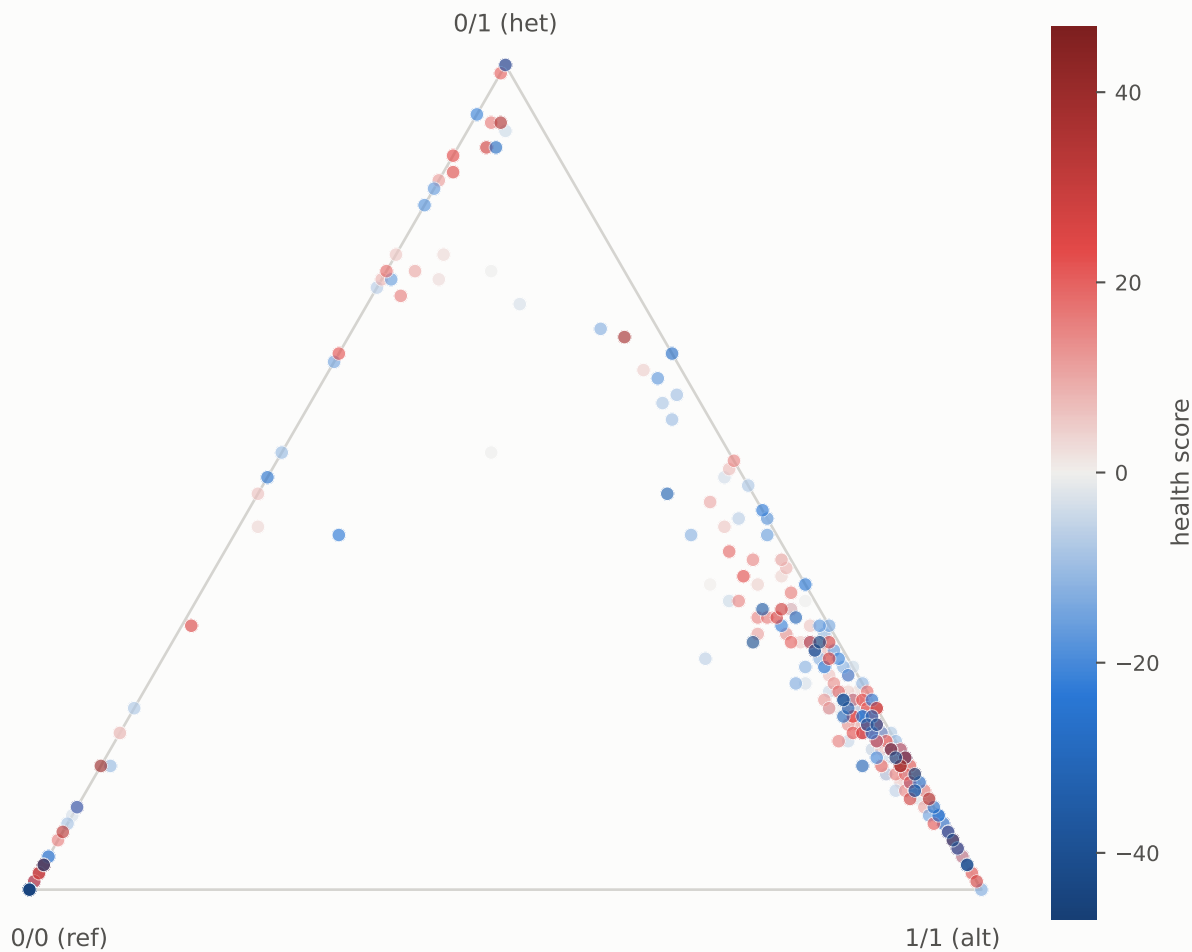
#69 by genotype uncertainty CHR_07:22,454,928 C>T
AF=0.45 DR2=0.81 $r=-0.008$ $\bar{H}=0.401$ $F=0.3$



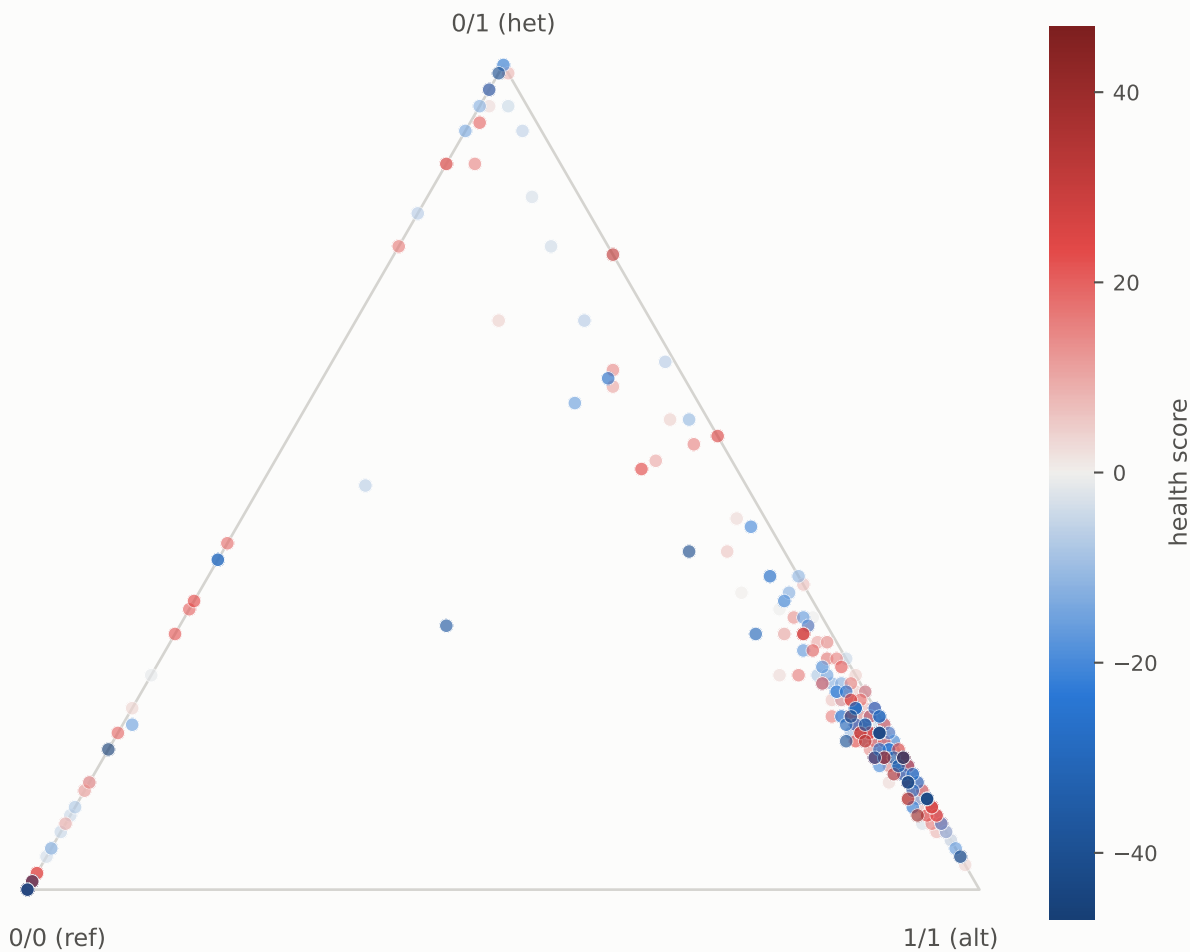
#70 by genotype uncertainty CHR_21:16,614,066 A>T
AF=0.6 DR2=0.81 r=-0.097 $\bar{H}$ =0.401 F=2.5



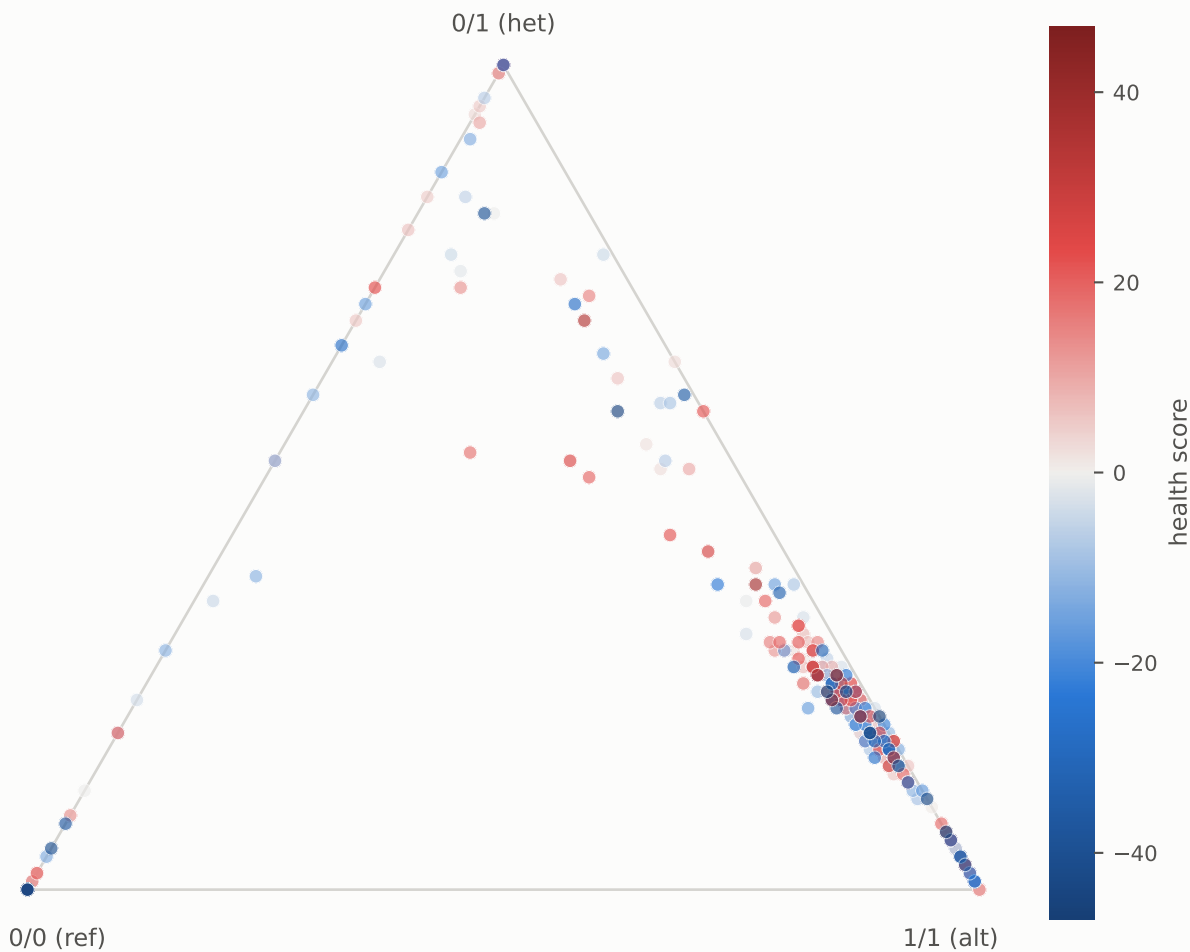
#71 by genotype uncertainty CHR_15:2,146,610 G>A
AF=0.57 DR2=0.81 $r=+0.008$ $\bar{H}=0.401$ F=0.1



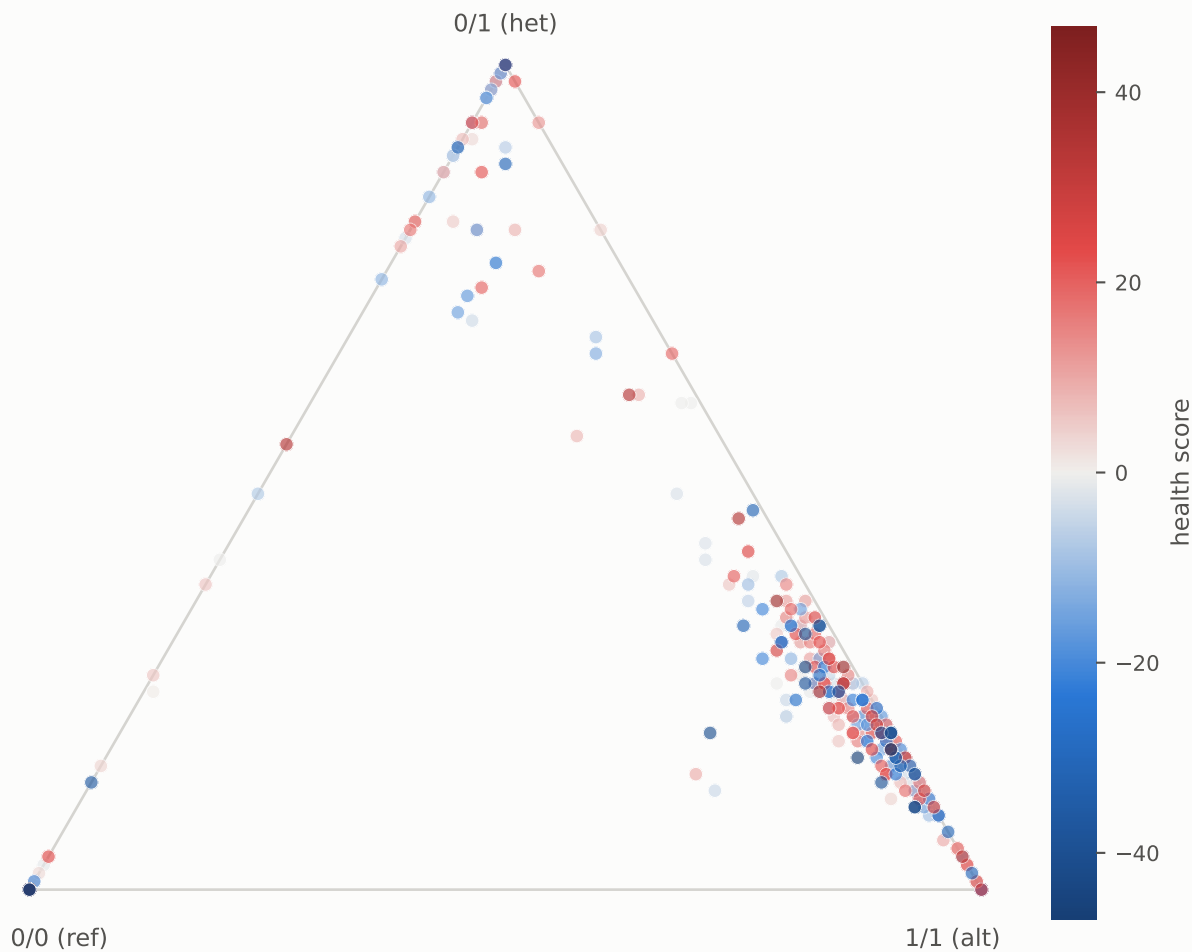
#72 by genotype uncertainty CHR_19:711,181 T>C
AF=0.56 DR2=0.83 $r=-0.098$ $H=0.401$ $F=2.2$



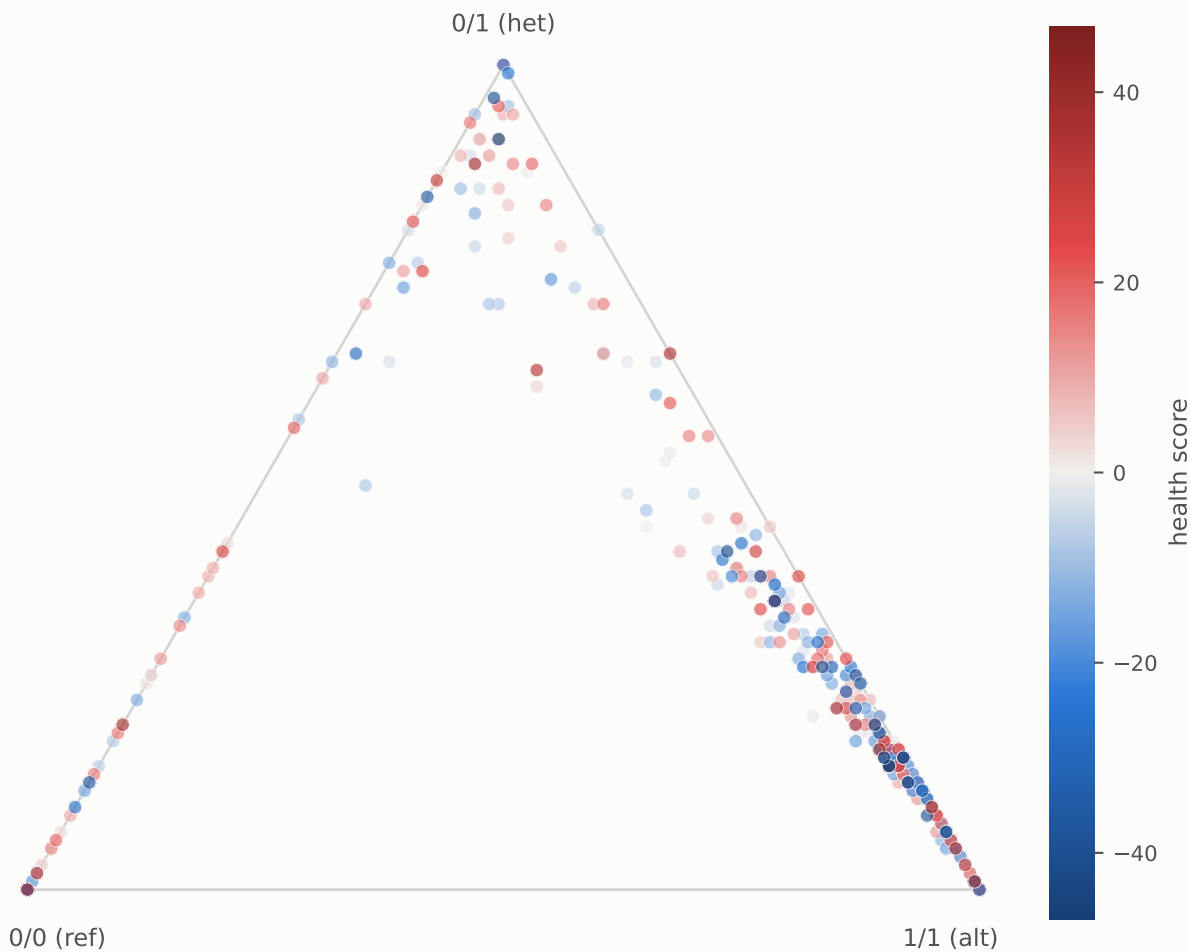
#73 by genotype uncertainty CHR_21:17,089,255 T>G
AF=0.52 DR2=0.82 $r=-0.133$ $\bar{H}=0.400$ F=3.3



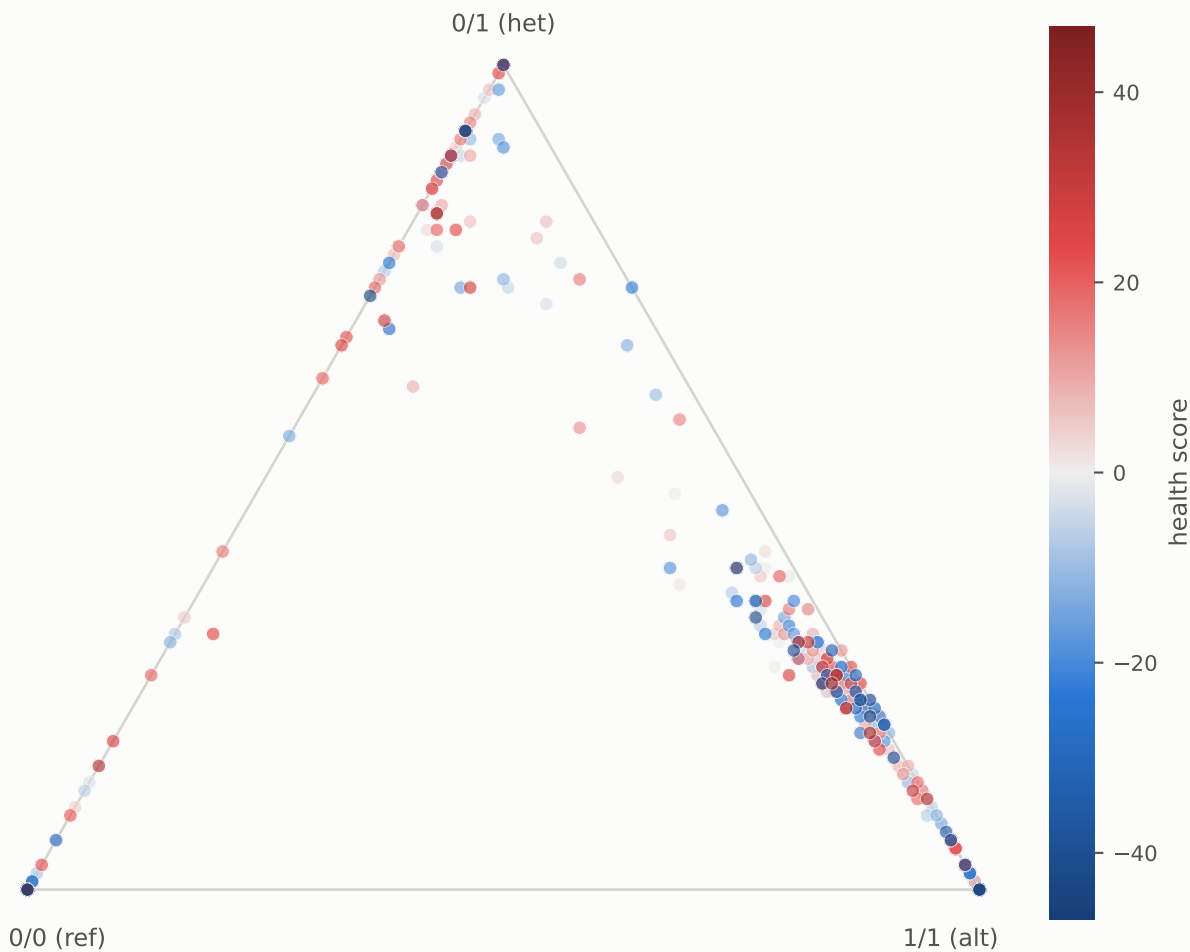
#74 by genotype uncertainty CHR_16:1,993,974 C>T
AF=0.57 DR2=0.81 $r=+0.005$ $\bar{H}=0.400$ F=0.0



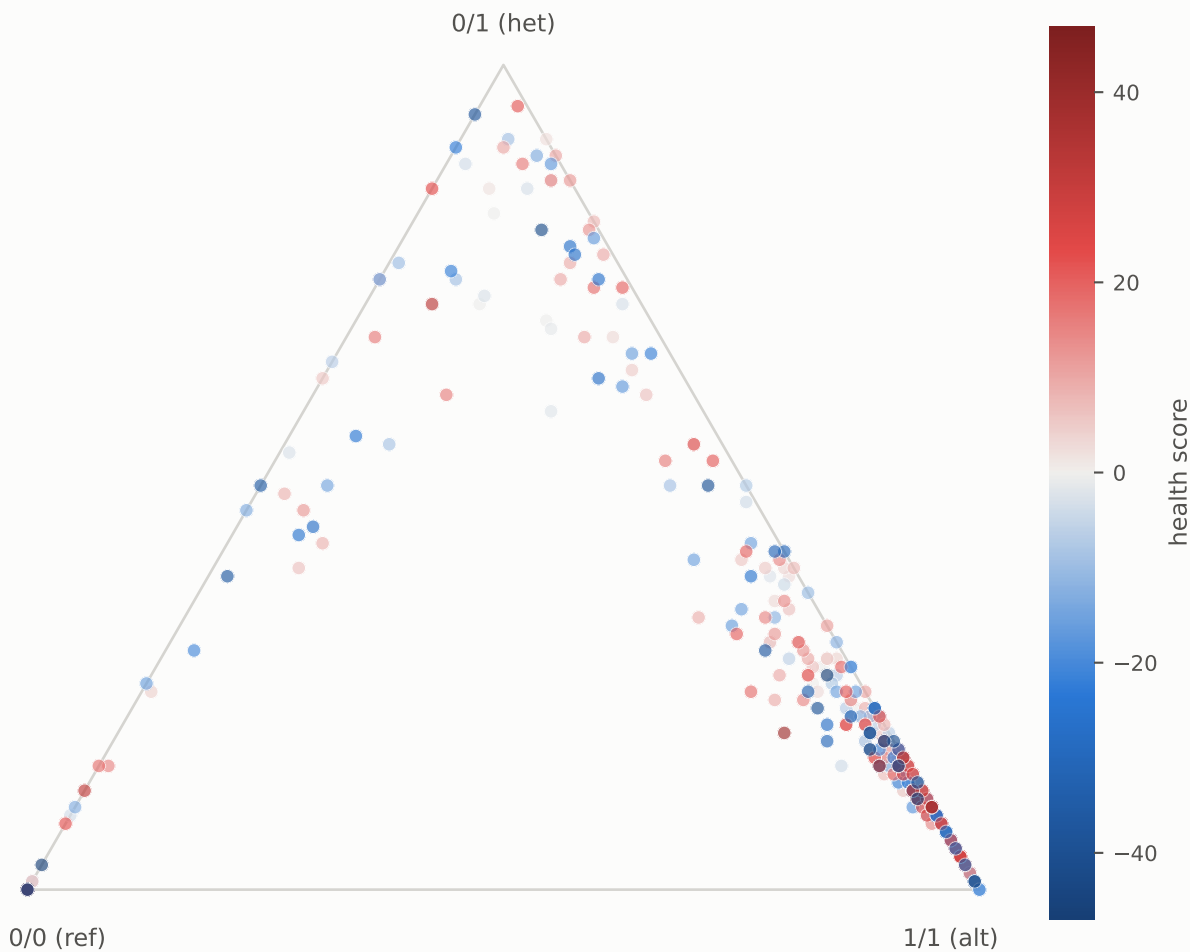
#75 by genotype uncertainty CHR_08:34,818,203 T>C
AF=0.52 DR2=0.82 $r=-0.147$ $\bar{H}=0.400$ F=5.9



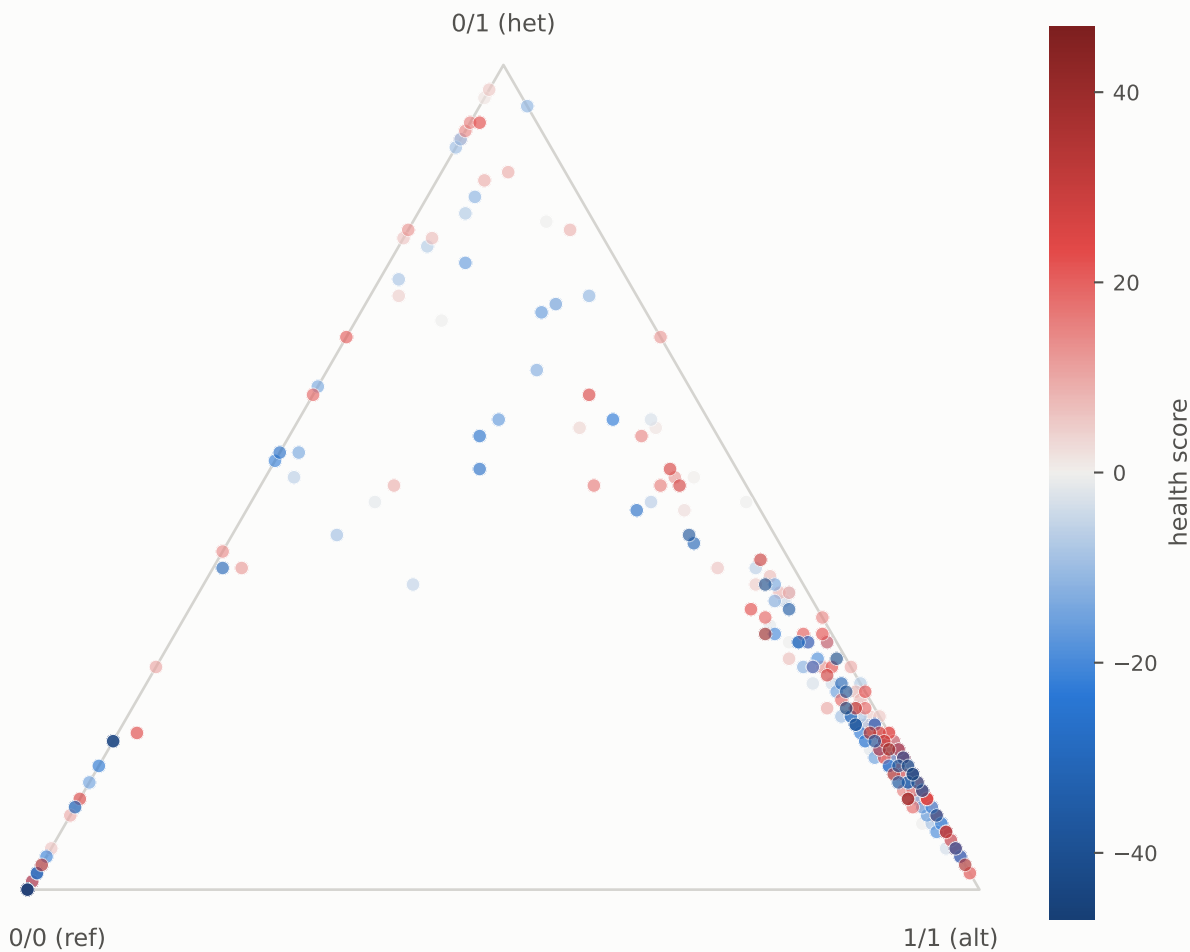
#76 by genotype uncertainty CHR_08:28,051,661 T>C
AF=0.51 DR2=0.81 $r=-0.022$ $\bar{H}=0.400$ F=1.5



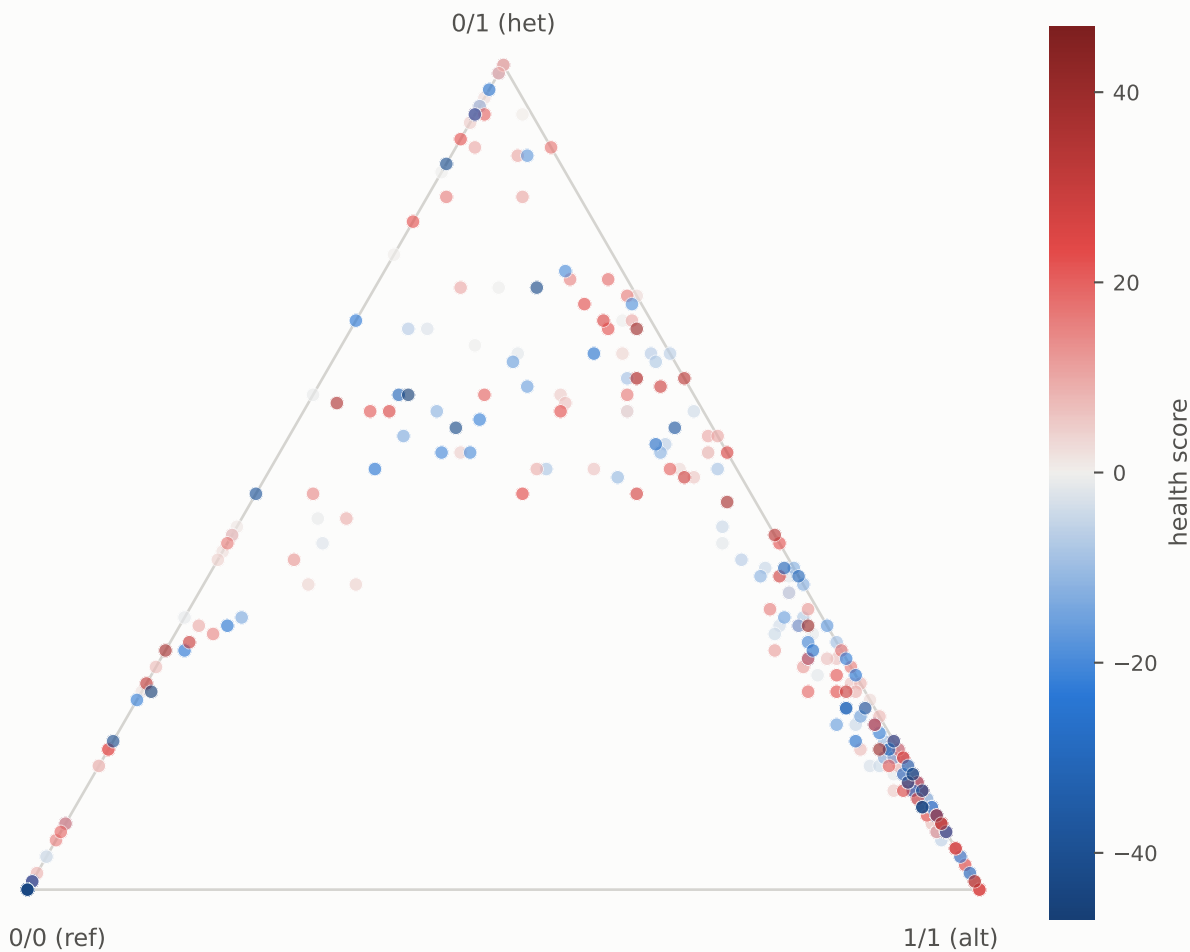
#77 by genotype uncertainty CHR_17:28,182,388 C>T
AF=0.59 DR2=0.81 $r=-0.022$ $\bar{H}=0.400$ F=0.6



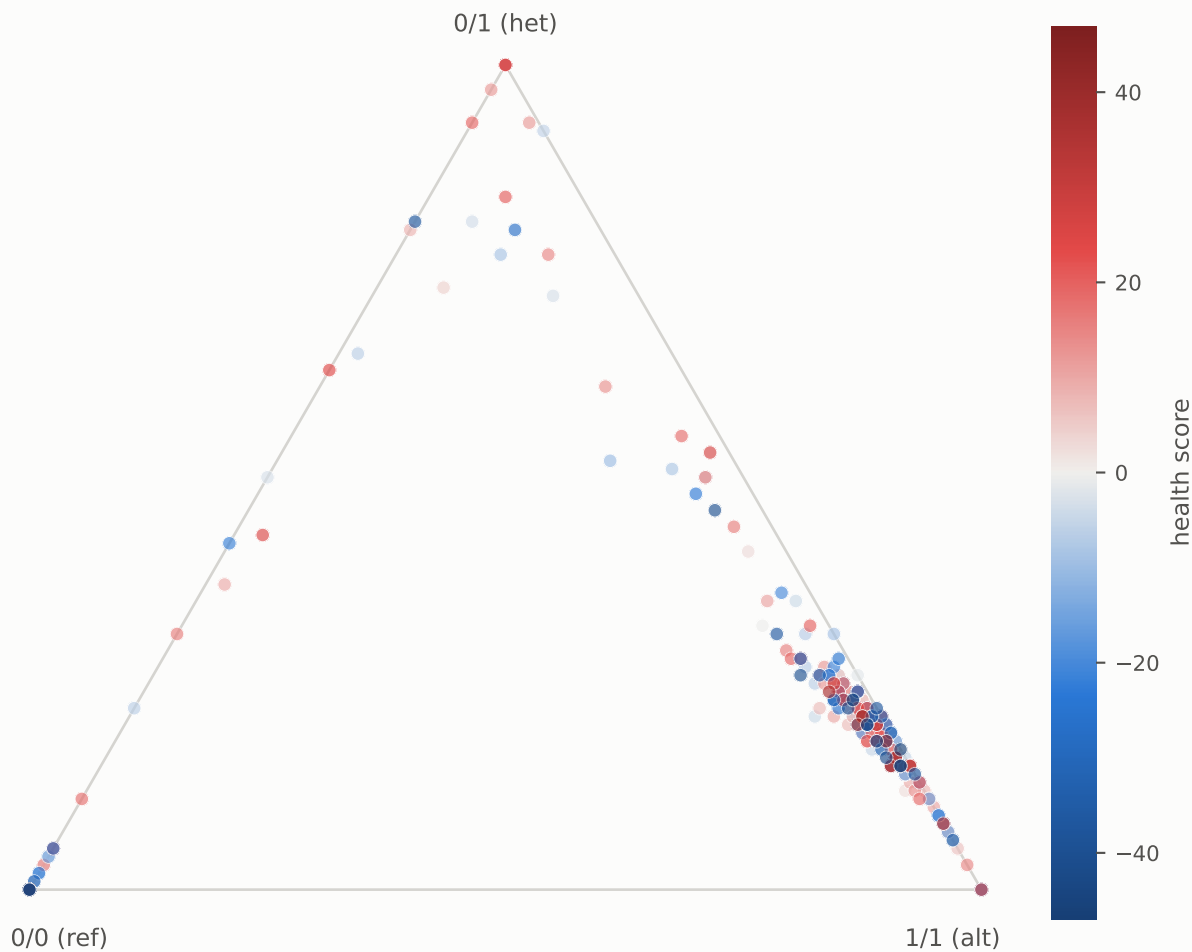
#78 by genotype uncertainty CHR_04:18,761,649 C>T
AF=0.59 DR2=0.81 $r=+0.040$ $\bar{H}=0.400$ $F=0.2$



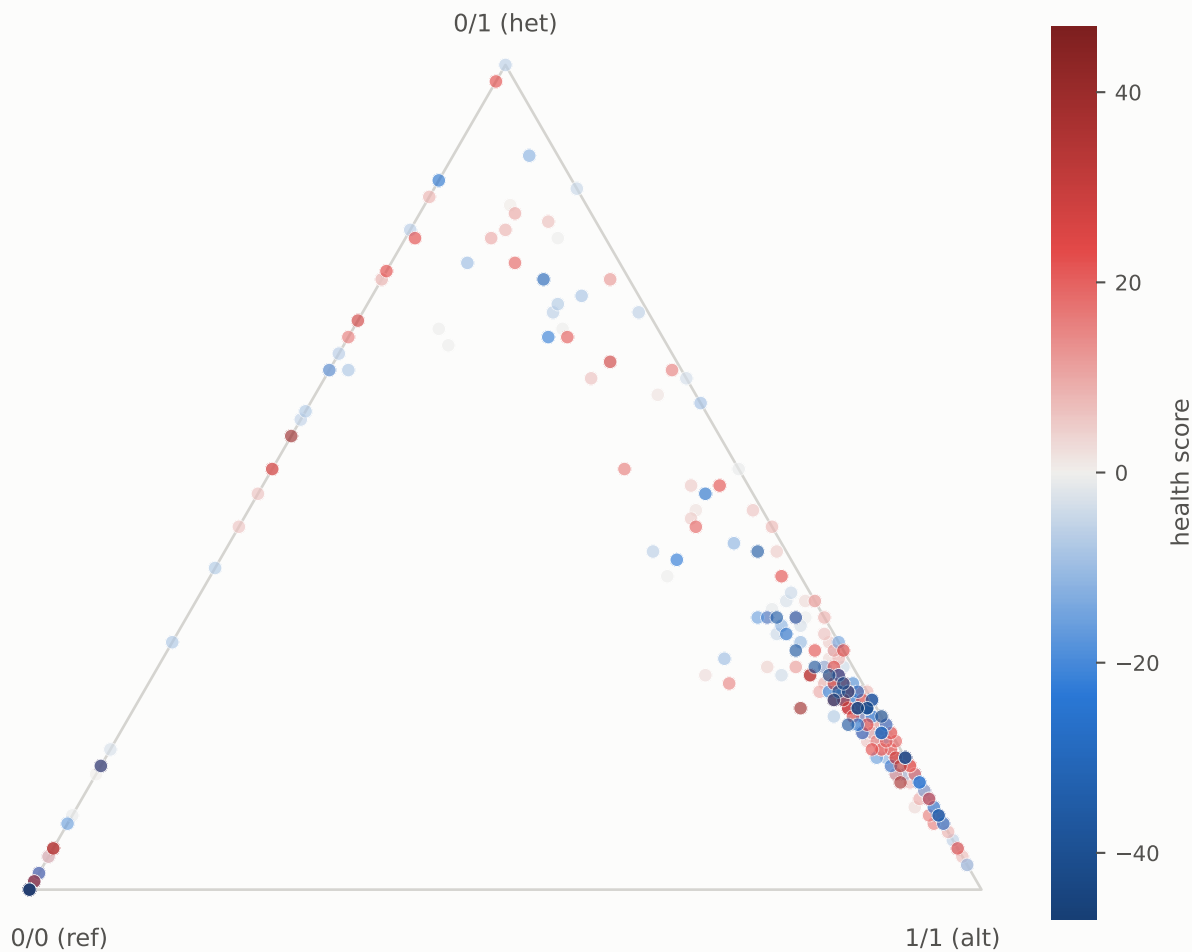
#79 by genotype uncertainty CHR_03:45,583,365 A>G
AF=0.5 DR2=0.81 r=+0.066 H=0.400 F=1.1



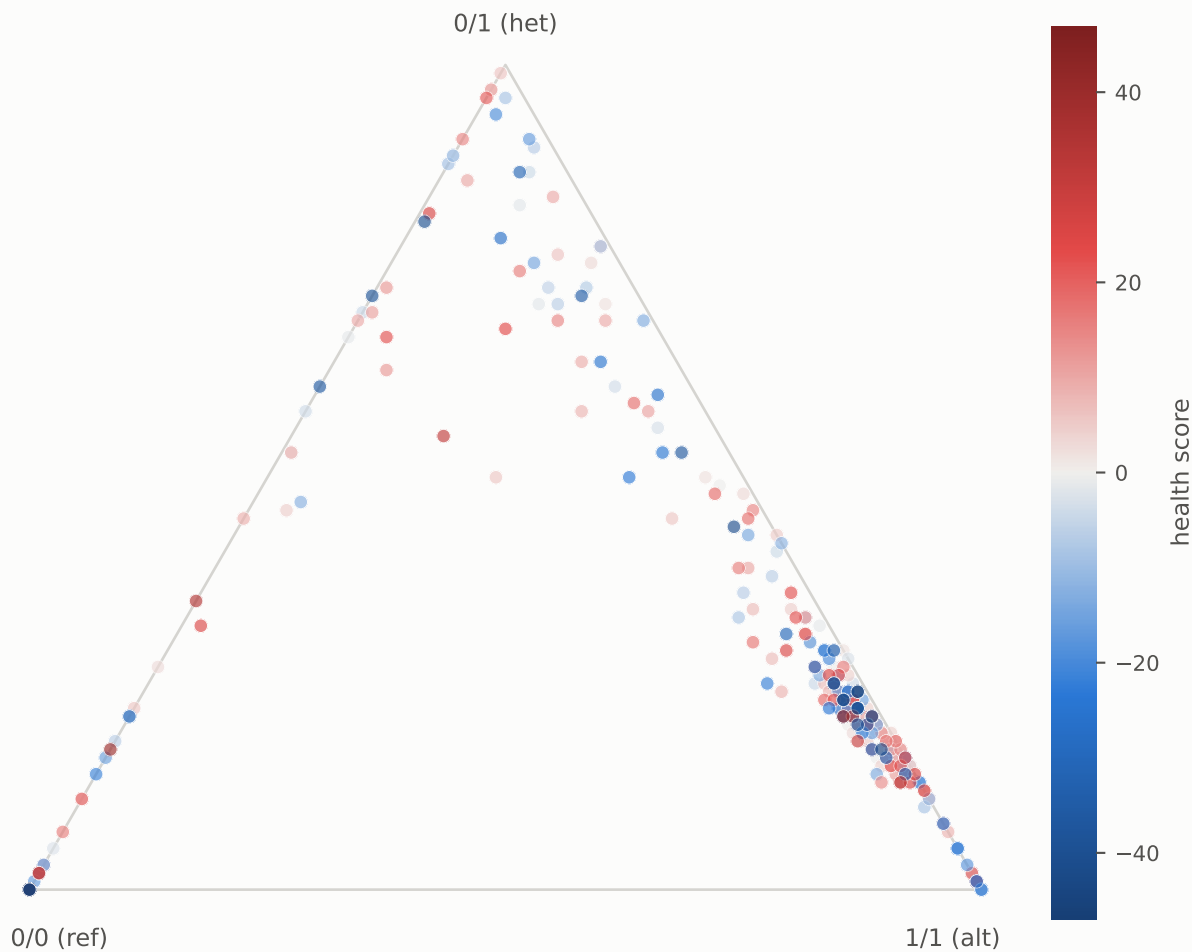
#80 by genotype uncertainty CHR_03:39,069,924 A>G
AF=0.58 DR2=0.81 $r=+0.016$ H=0.400 F=1.1



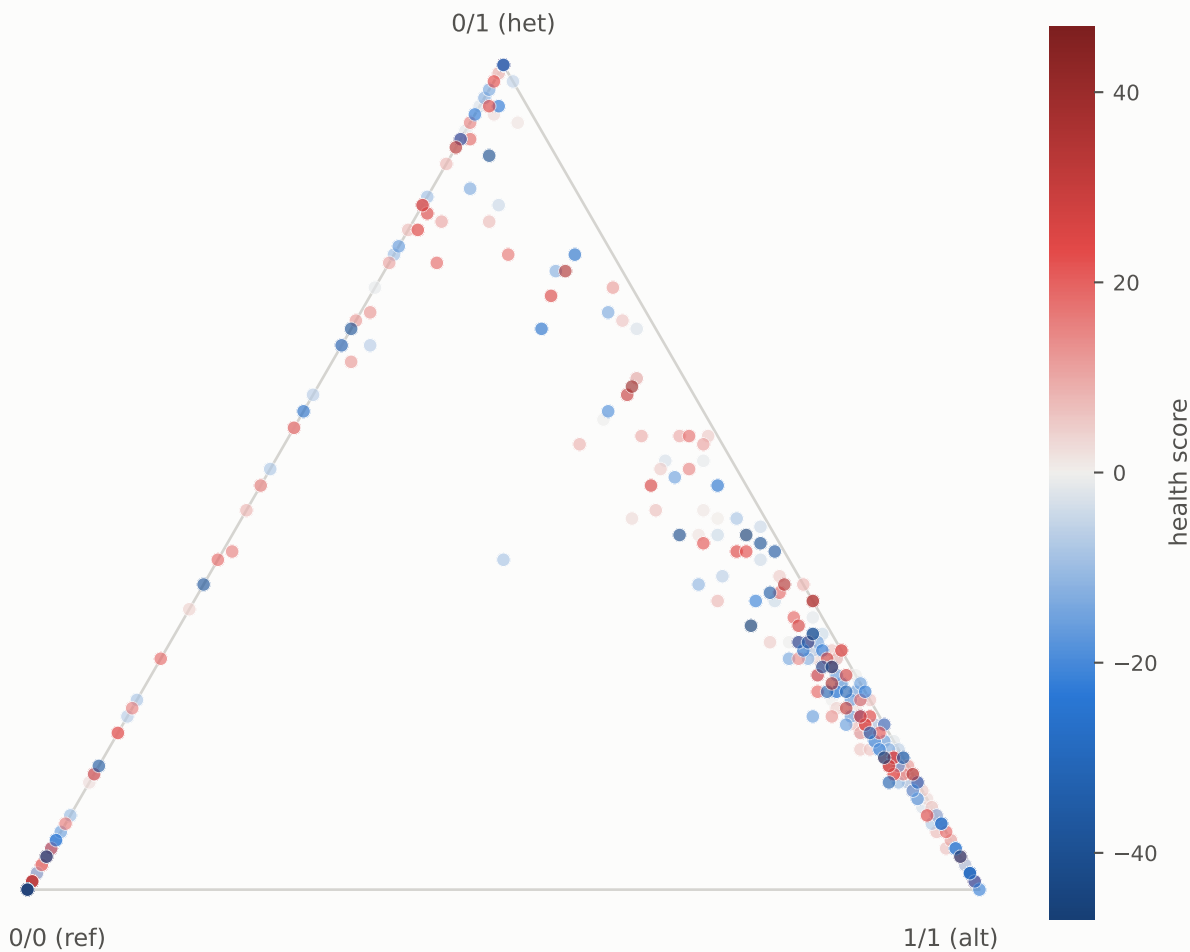
#81 by genotype uncertainty CHR_14:1,303,942 T>A
AF=0.49 DR2=0.81 $r=-0.055$ $\bar{H}=0.400$ $F=1.7$



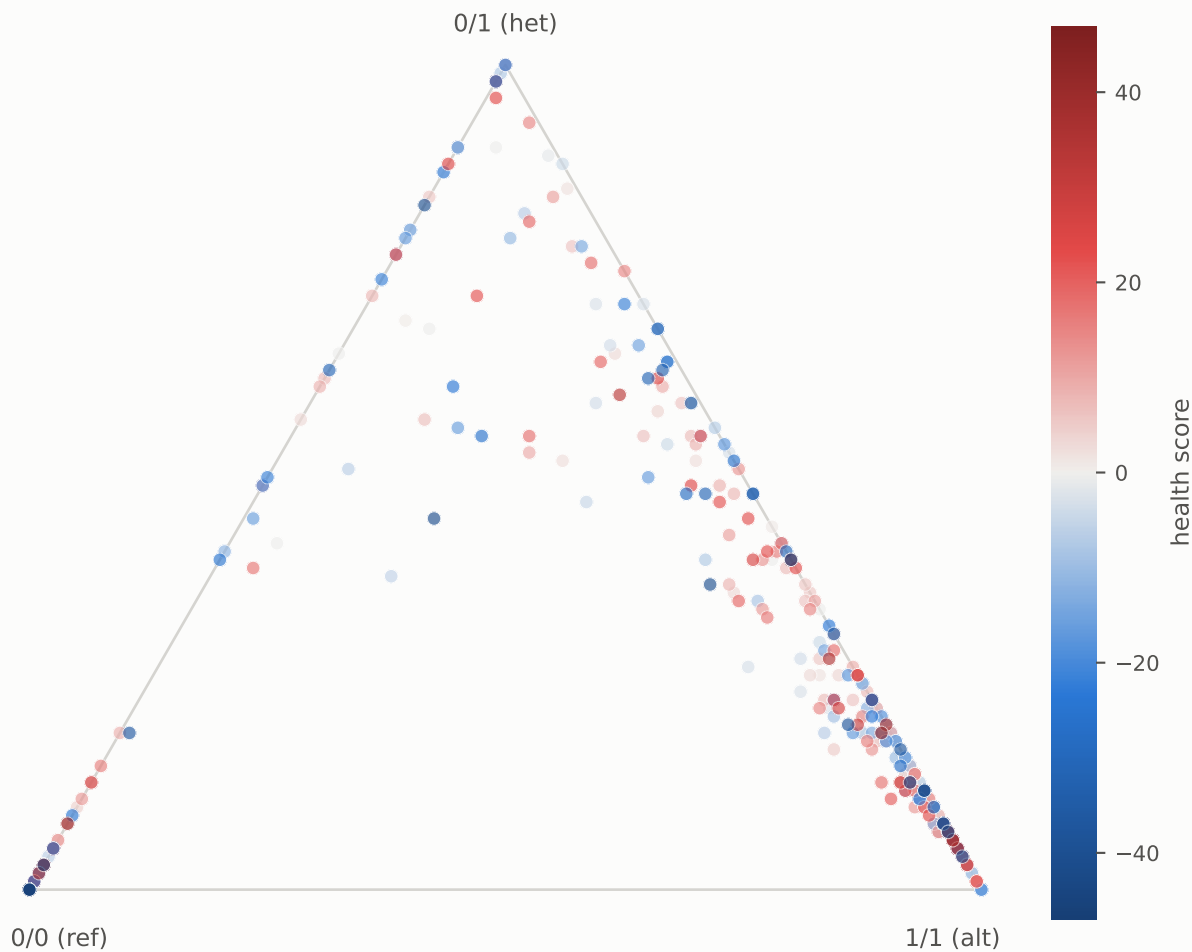
#82 by genotype uncertainty CHR_03:5,669,361 G>A
AF=0.53 DR2=0.81 r=-0.109 $\bar{H}$ =0.400 F=3.1



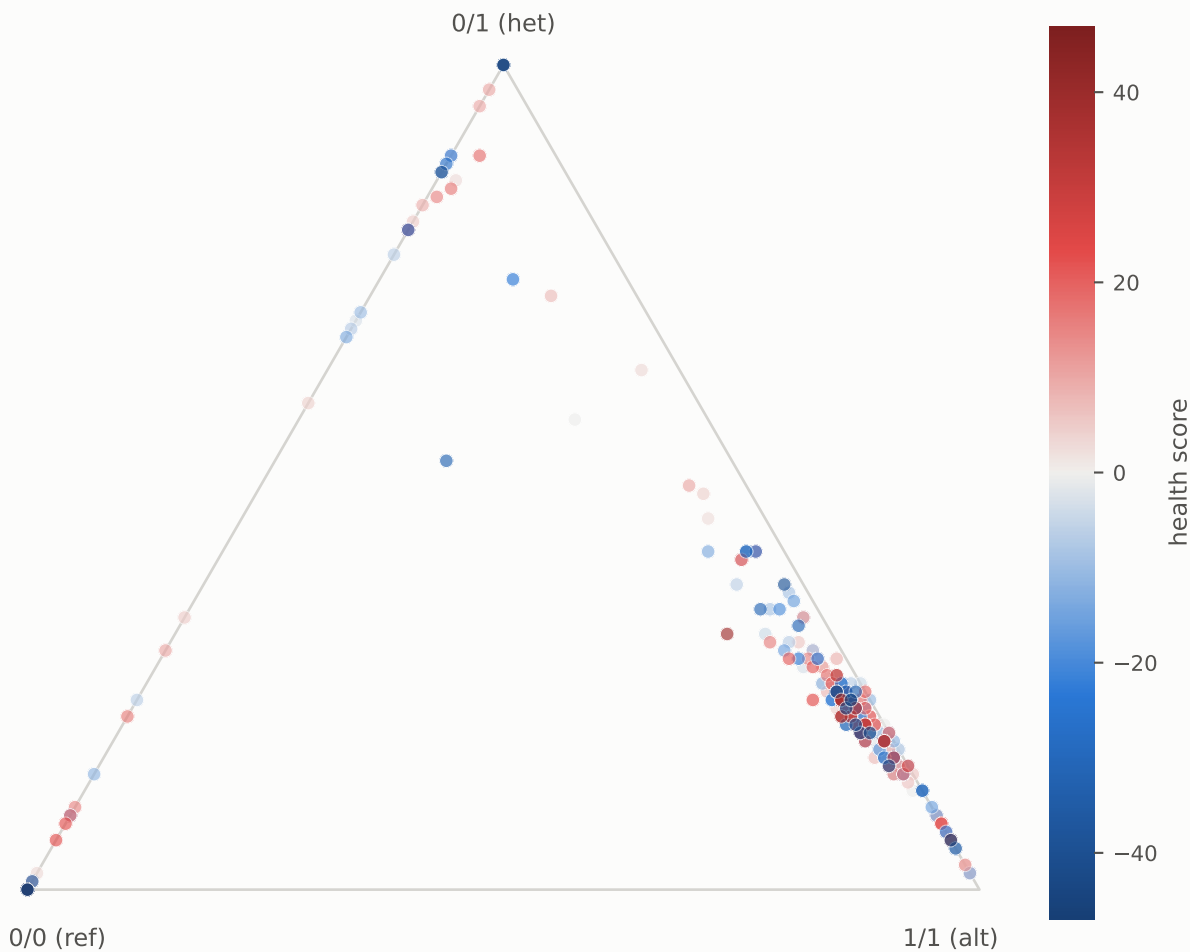
#83 by genotype uncertainty CHR_08:36,591,863 G>T
AF=0.49 DR2=0.81 $r=-0.050$ $\bar{H}=0.400$ F=2.2



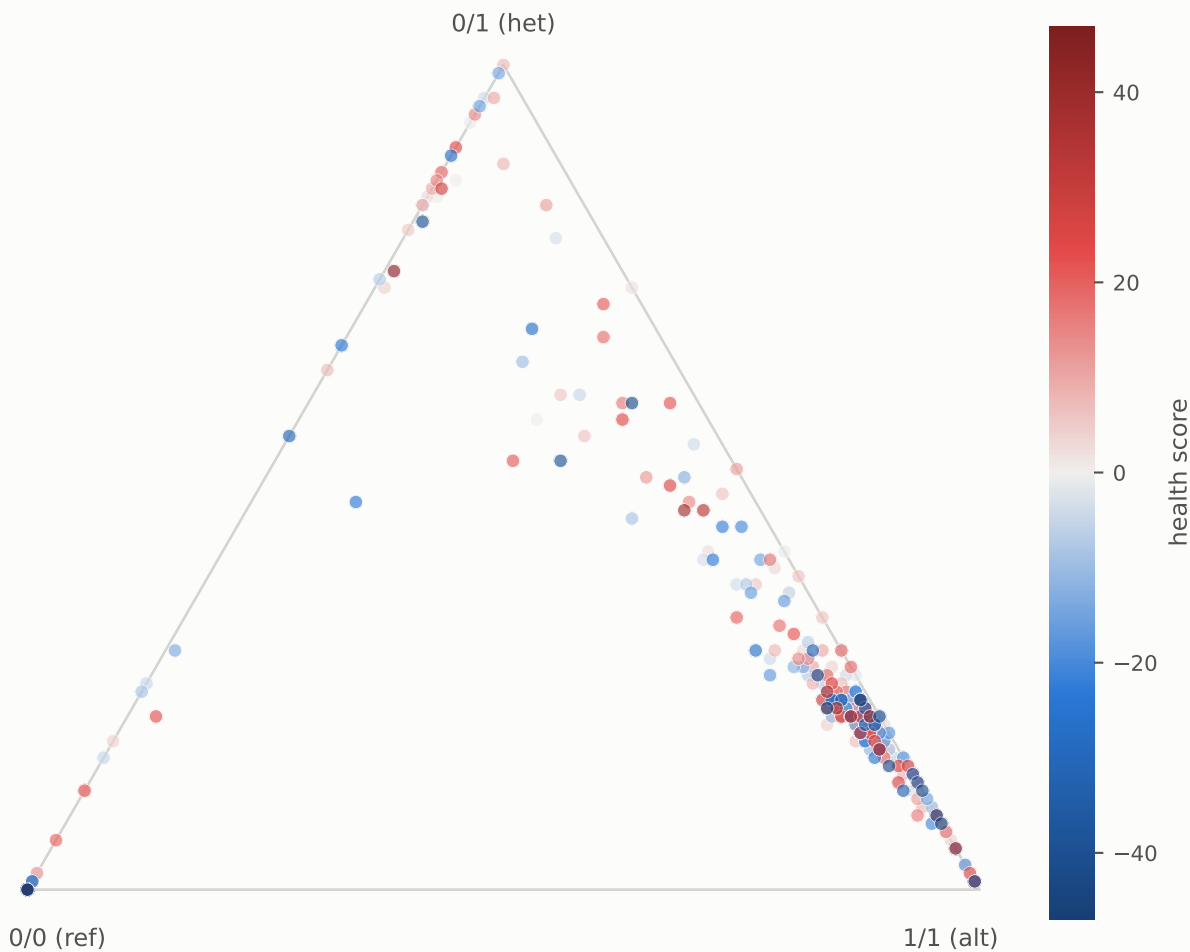
#84 by genotype uncertainty CHR_22:6,012,650 C>T
AF=0.58 DR2=0.81 $r=+0.013$ $\bar{H}=0.399$ F=2.1



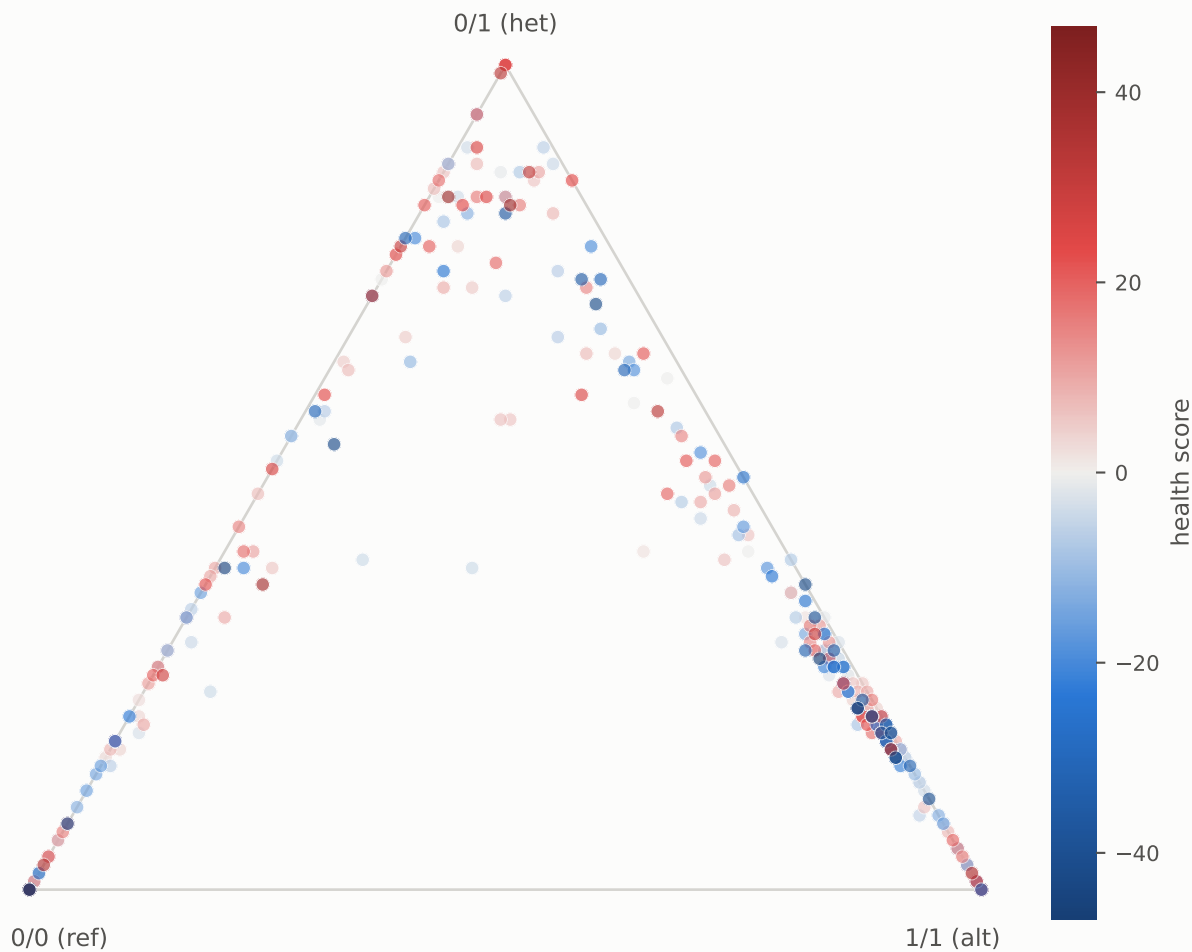
#85 by genotype uncertainty CHR_21:18,211,303 T>C
AF=0.52 DR2=0.83 r=+0.043 H=0.399 F=2.1



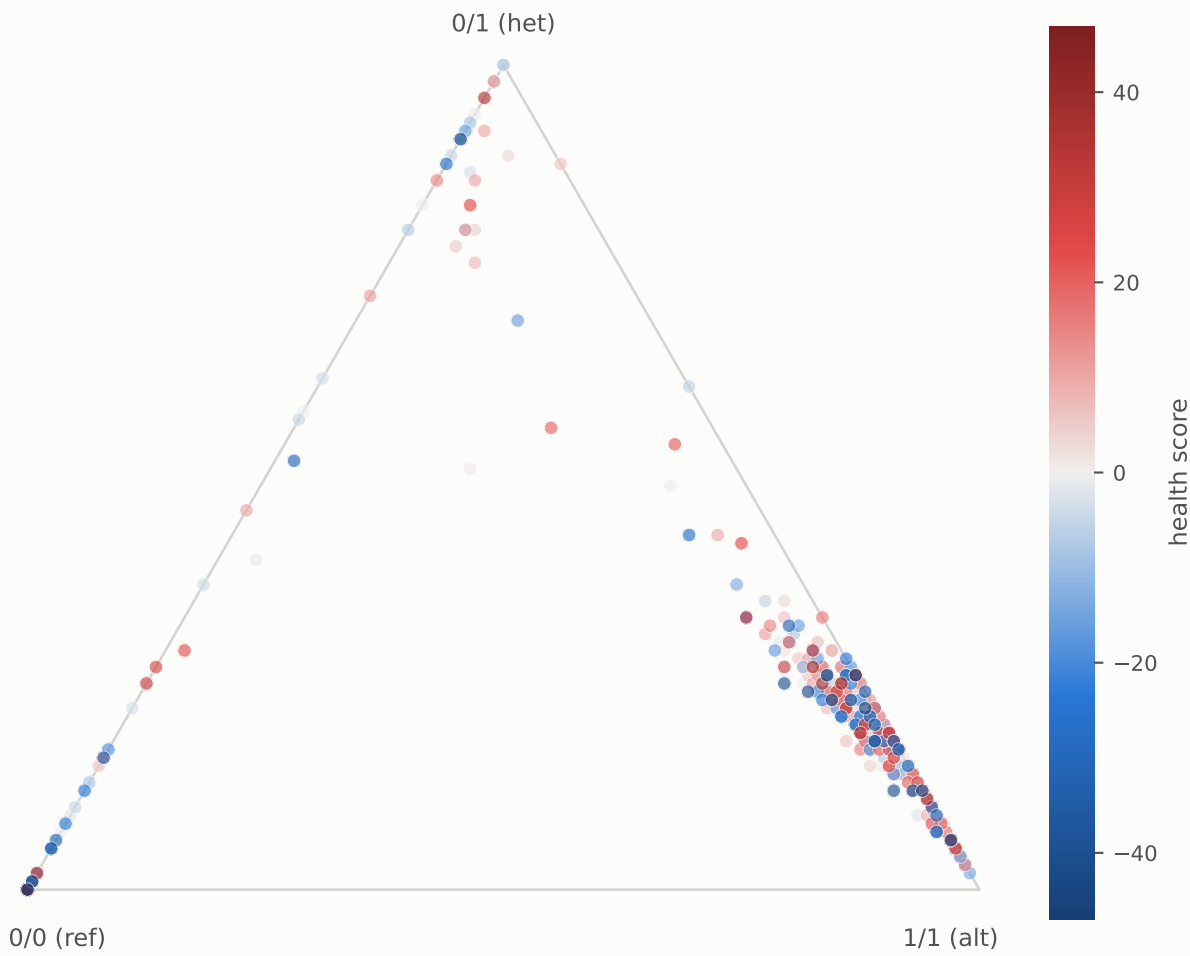
#86 by genotype uncertainty CHR_18:23,857,192 A>G
AF=0.49 DR2=0.81 $r=-0.000$ $\bar{H}=0.399$ $F=0.5$



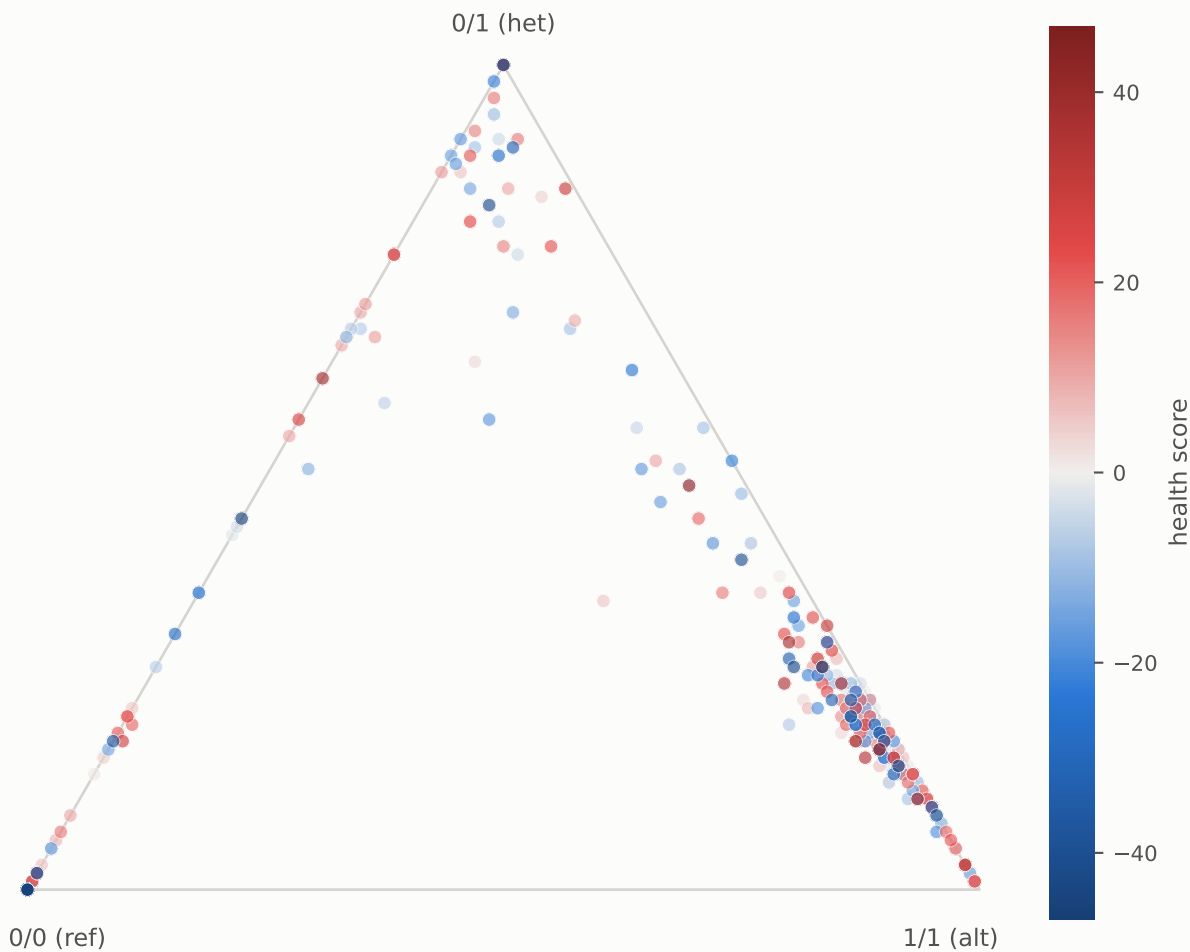
#87 by genotype uncertainty CHR_19:5,748,084 C>G
AF=0.45 DR2=0.81 $r=-0.105$ $\bar{H}=0.399$ F=5.6



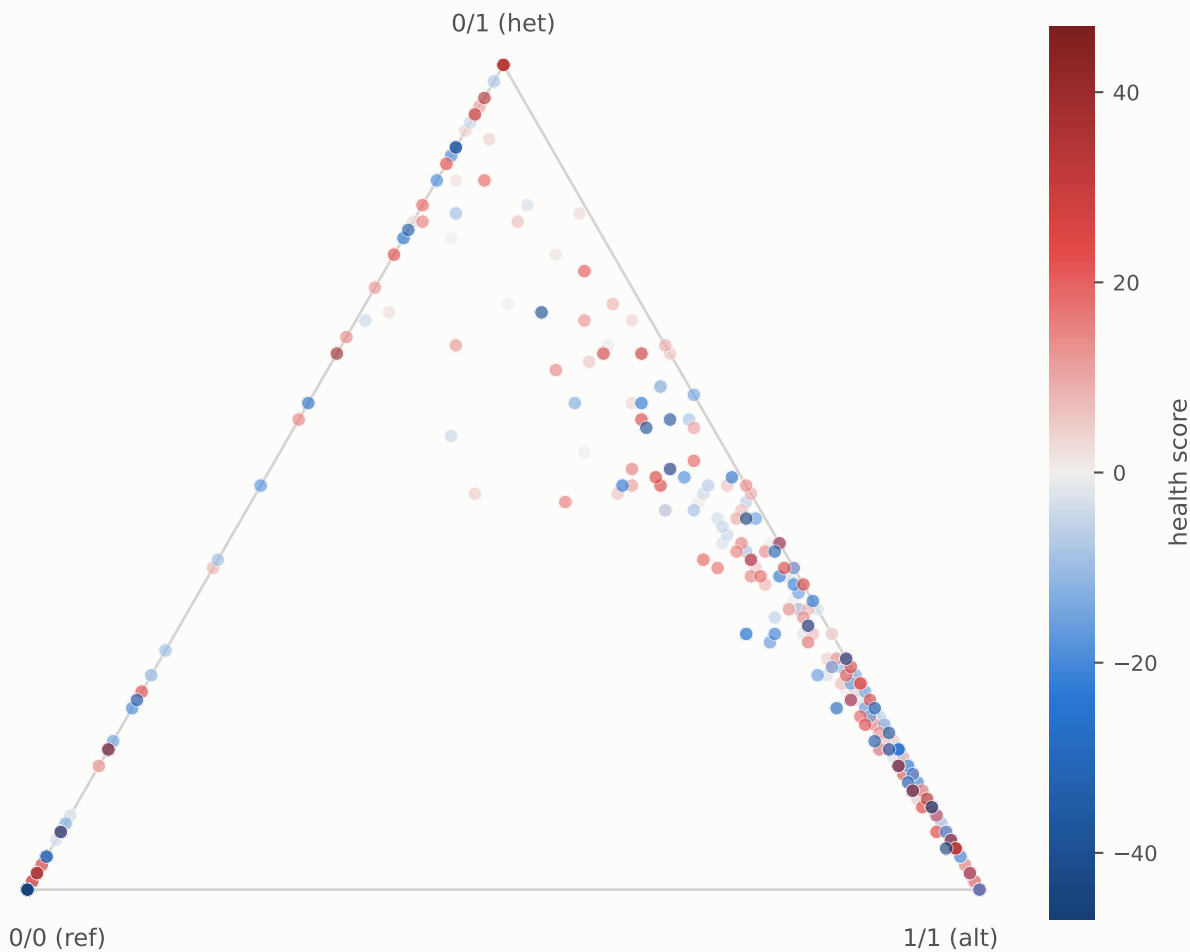
#88 by genotype uncertainty CHR_18:23,856,507 C>T
AF=0.55 DR2=0.81 r=+0.010 H=0.399 F=0.0



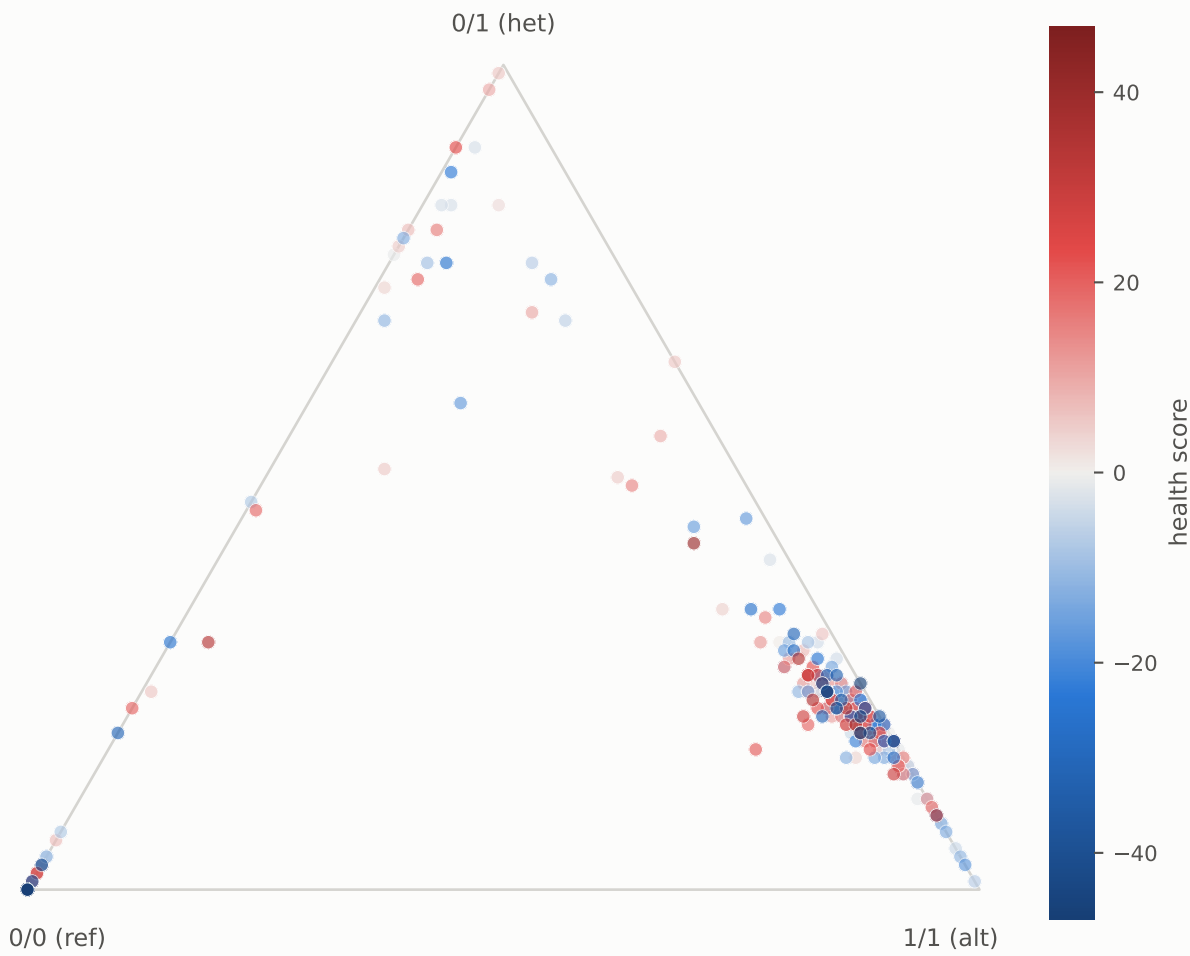
#89 by genotype uncertainty CHR_17:816,440 G>C
AF=0.53 DR2=0.81 $r=+0.041$ $\bar{H}=0.399$ F=0.6



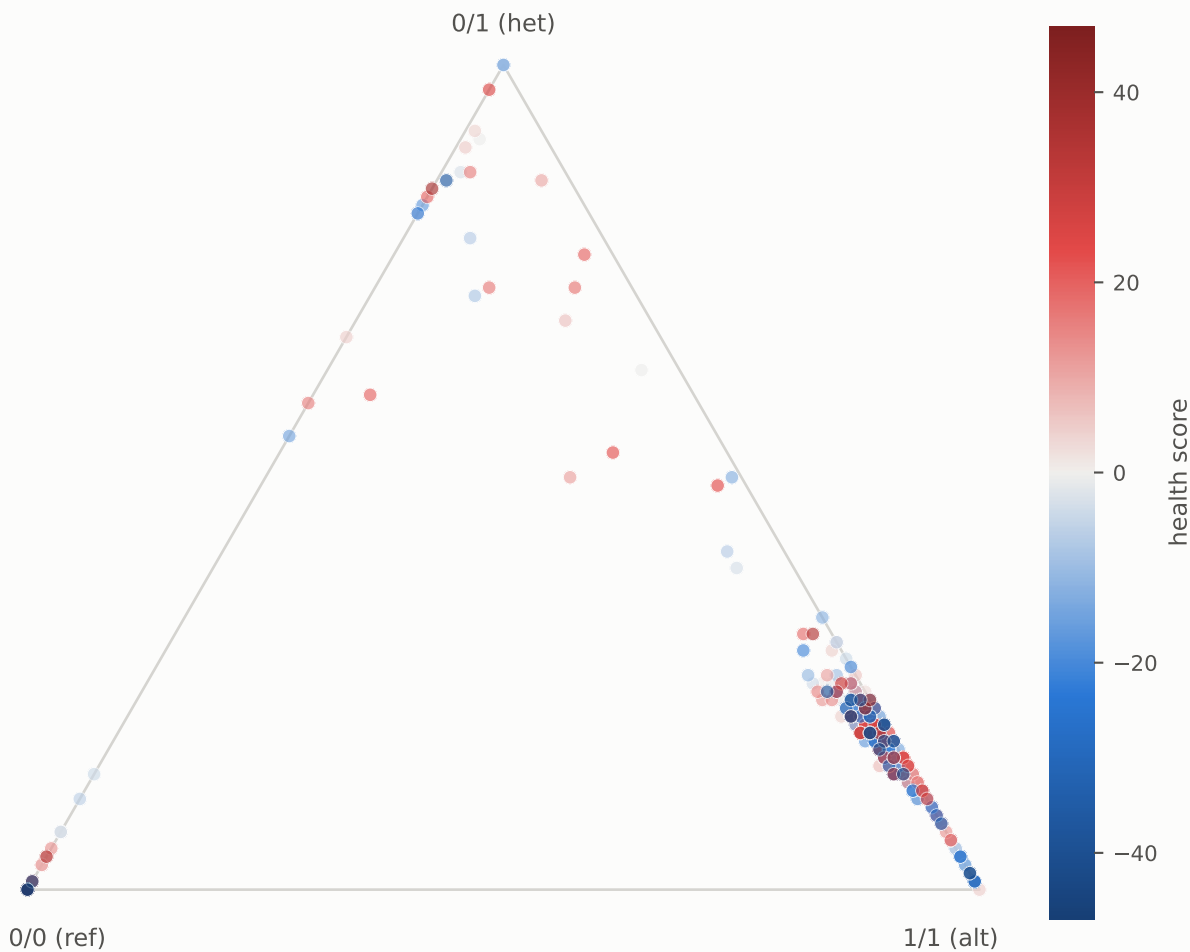
#90 by genotype uncertainty unpl-scaff_299:7,996 C>A
AF=0.52 DR2=0.81 $r=+0.013$ H=0.399 F=0.9



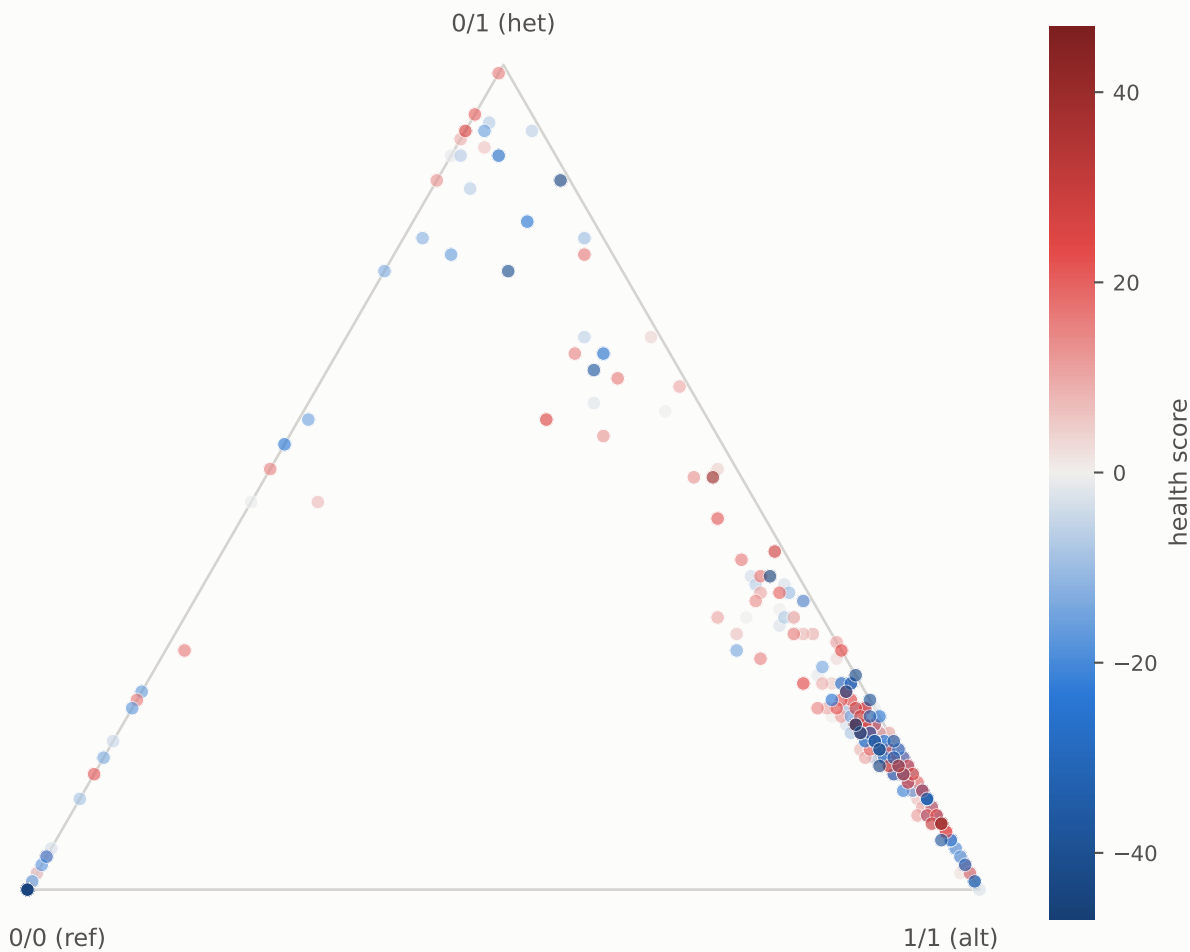
#91 by genotype uncertainty CHR_02:35,667,037 C>T
AF=0.5 DR2=0.81 $r=-0.004$ $\bar{H}=0.398$ F=0.0



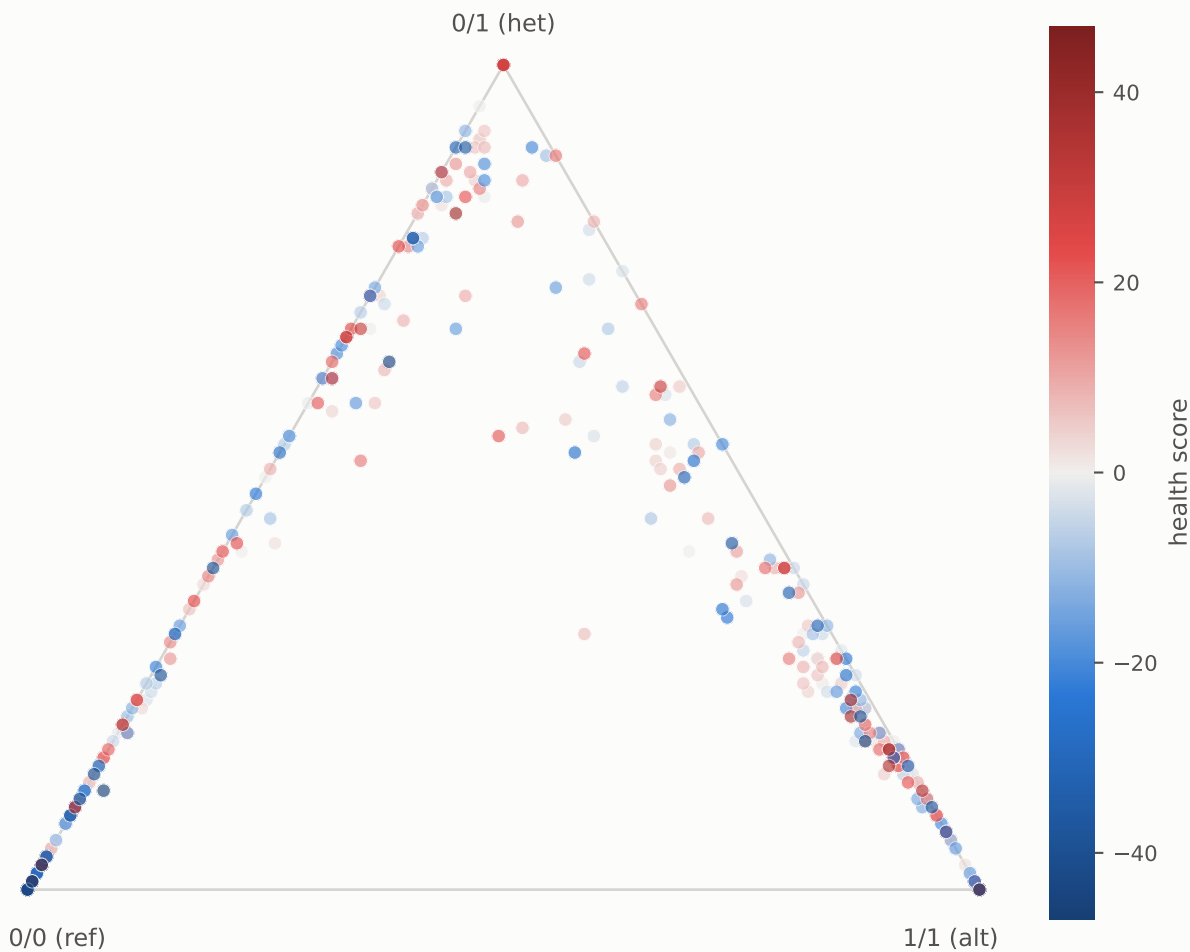
#92 by genotype uncertainty CHR_13:22,744,913 G>C
AF=0.64 DR2=0.81 $r=-0.037$ $\bar{H}=0.398$ $F=1.2$



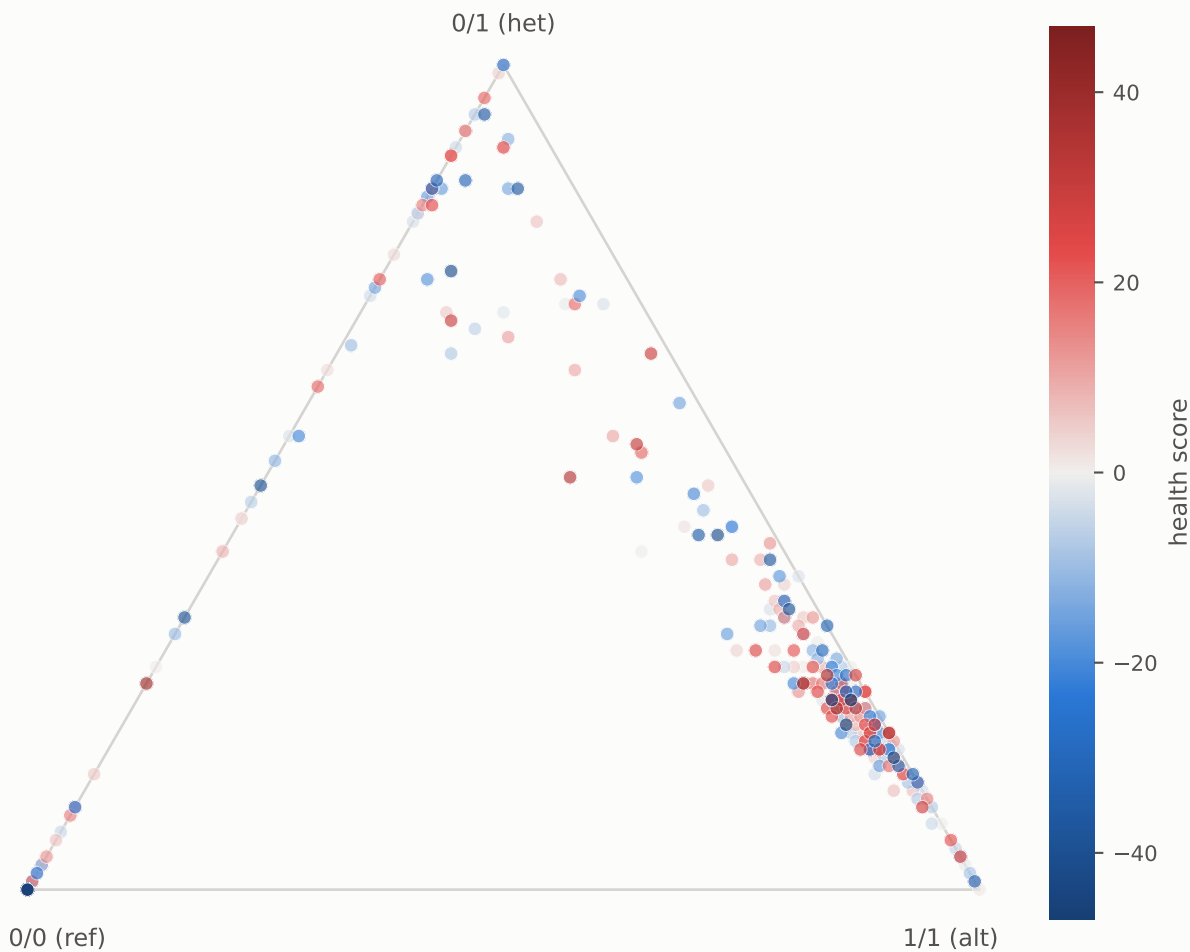
#93 by genotype uncertainty CHR_13:16,417,056 A>G
AF=0.62 DR2=0.81 $r=-0.028$ $\bar{H}=0.398$ F=0.4



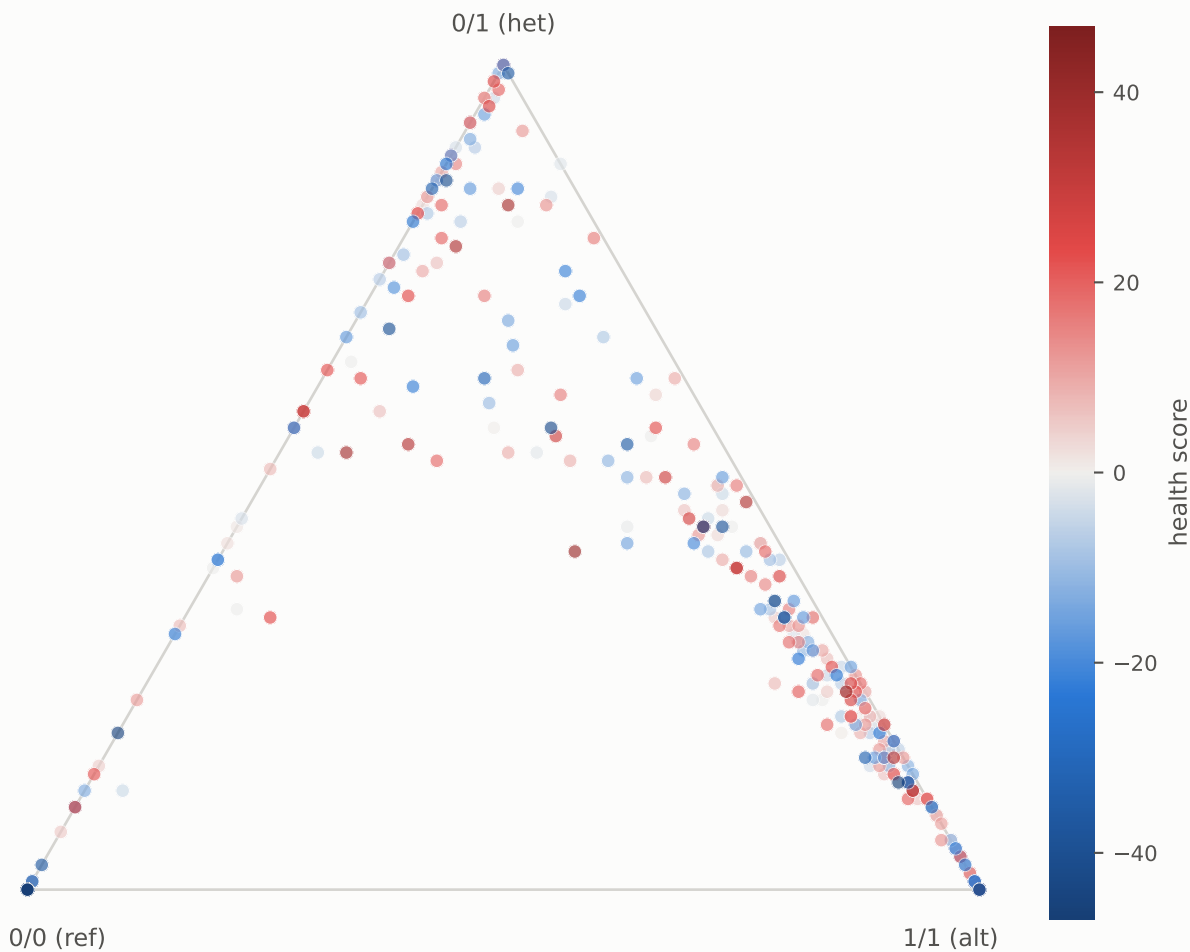
#94 by genotype uncertainty CHR_19:19,897,043 C>A
AF=0.39 DR2=0.81 $r=+0.063$ $H=0.398$ $F=1.1$



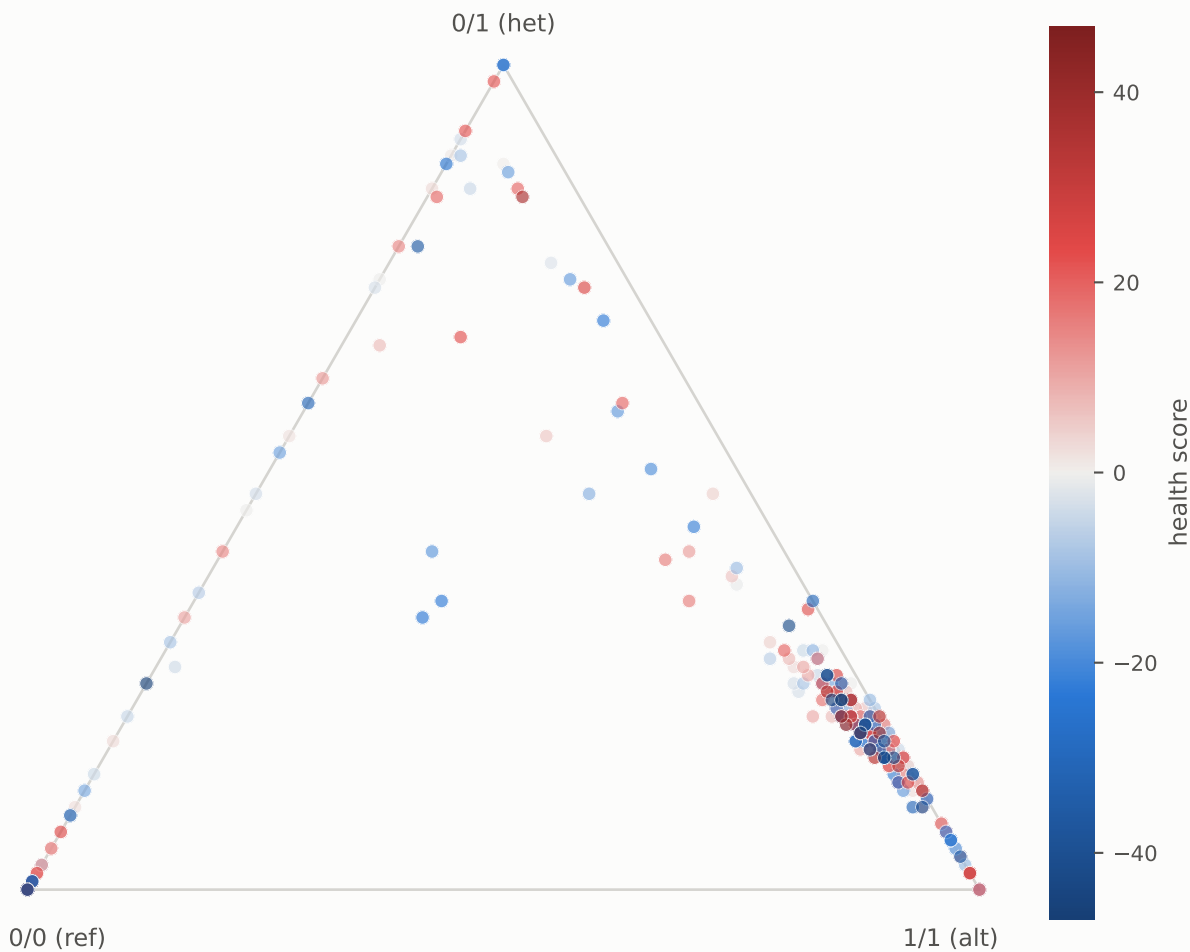
#95 by genotype uncertainty CHR_13:23,868,929 C>T
AF=0.47 DR2=0.81 $r=+0.067$ $H=0.398$ $F=0.9$



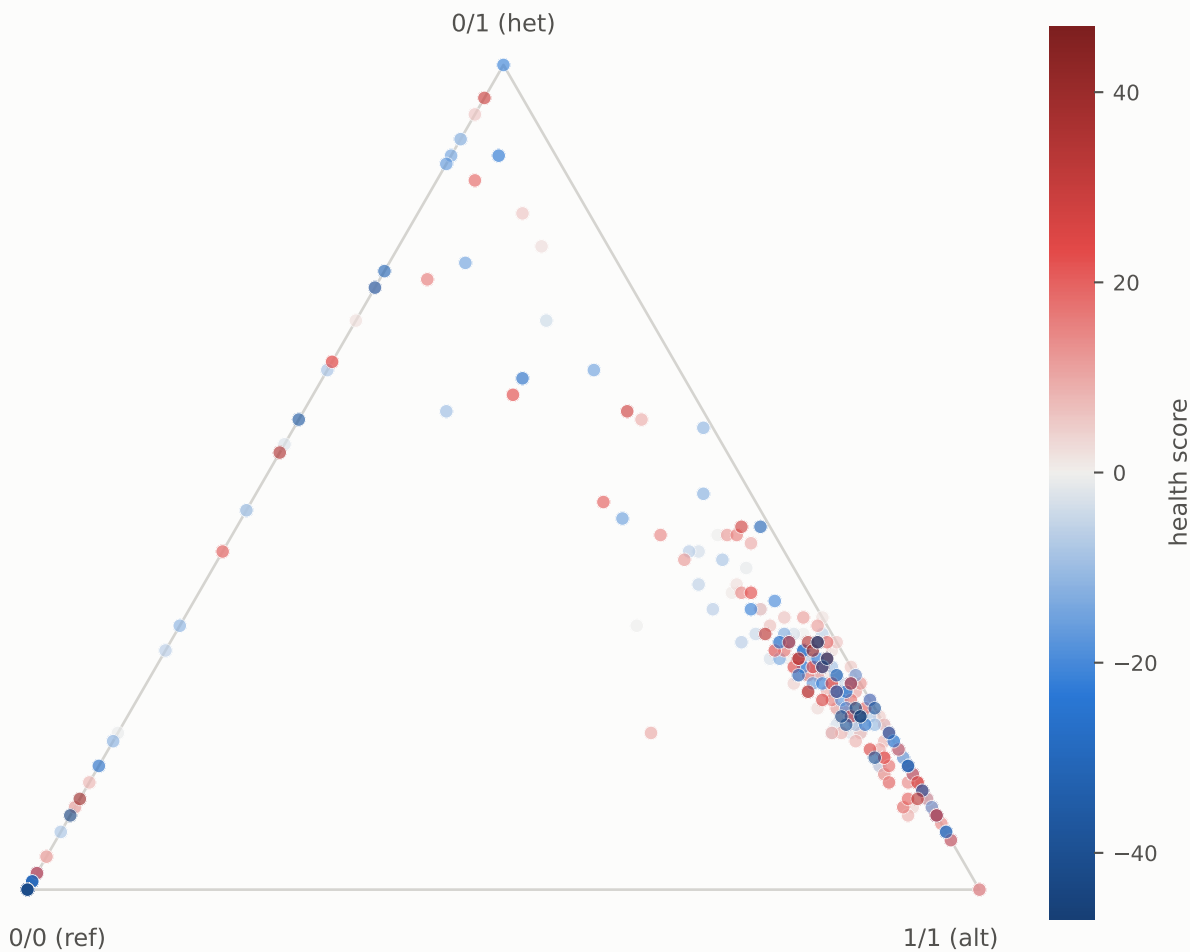
#96 by genotype uncertainty CHR_05:1,826,484 G>A
AF=0.45 DR2=0.81 $r=+0.080$ $\bar{H}=0.398$ F=2.2



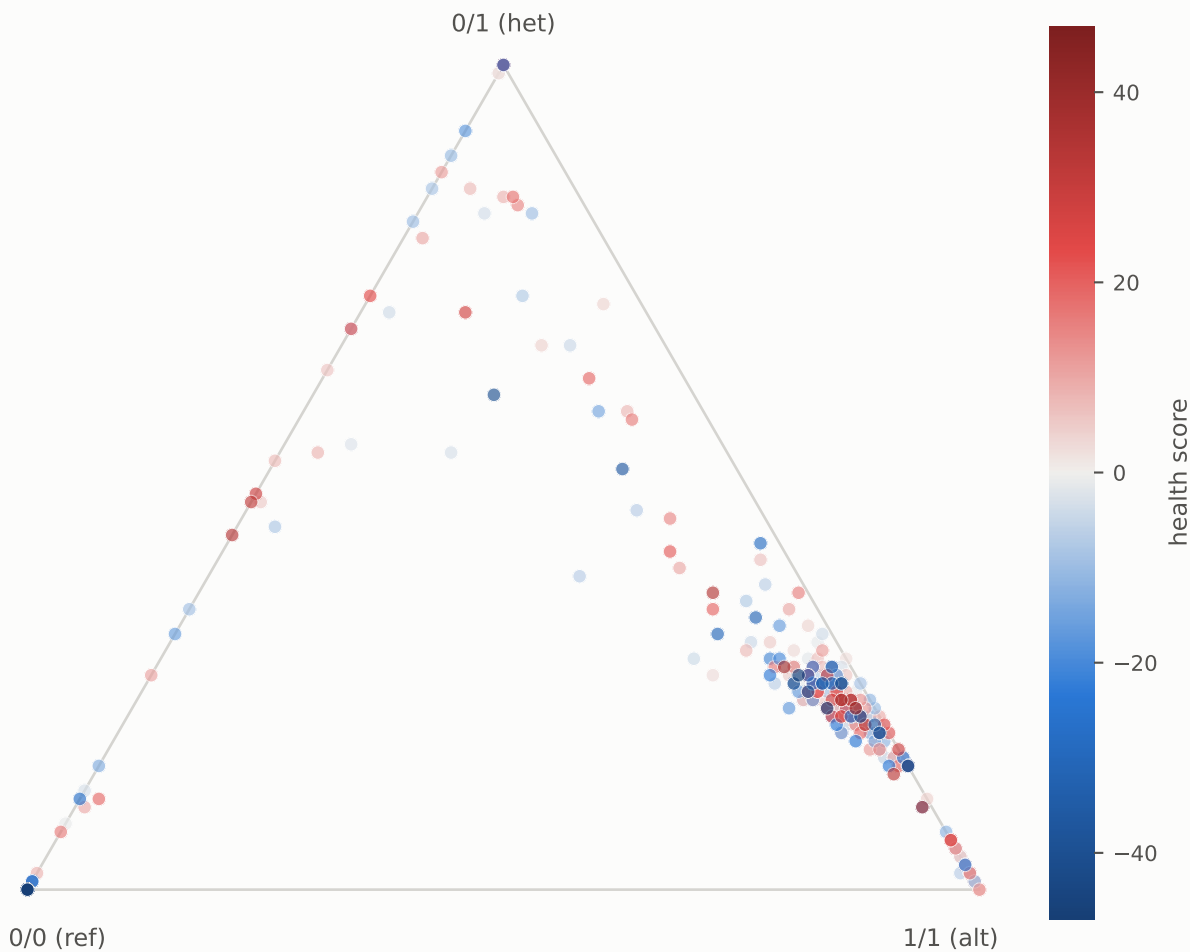
#97 by genotype uncertainty CHR_12:29,750,760 T>G
AF=0.55 DR2=0.81 $r=-0.036$ $\bar{H}=0.398$ F=0.4



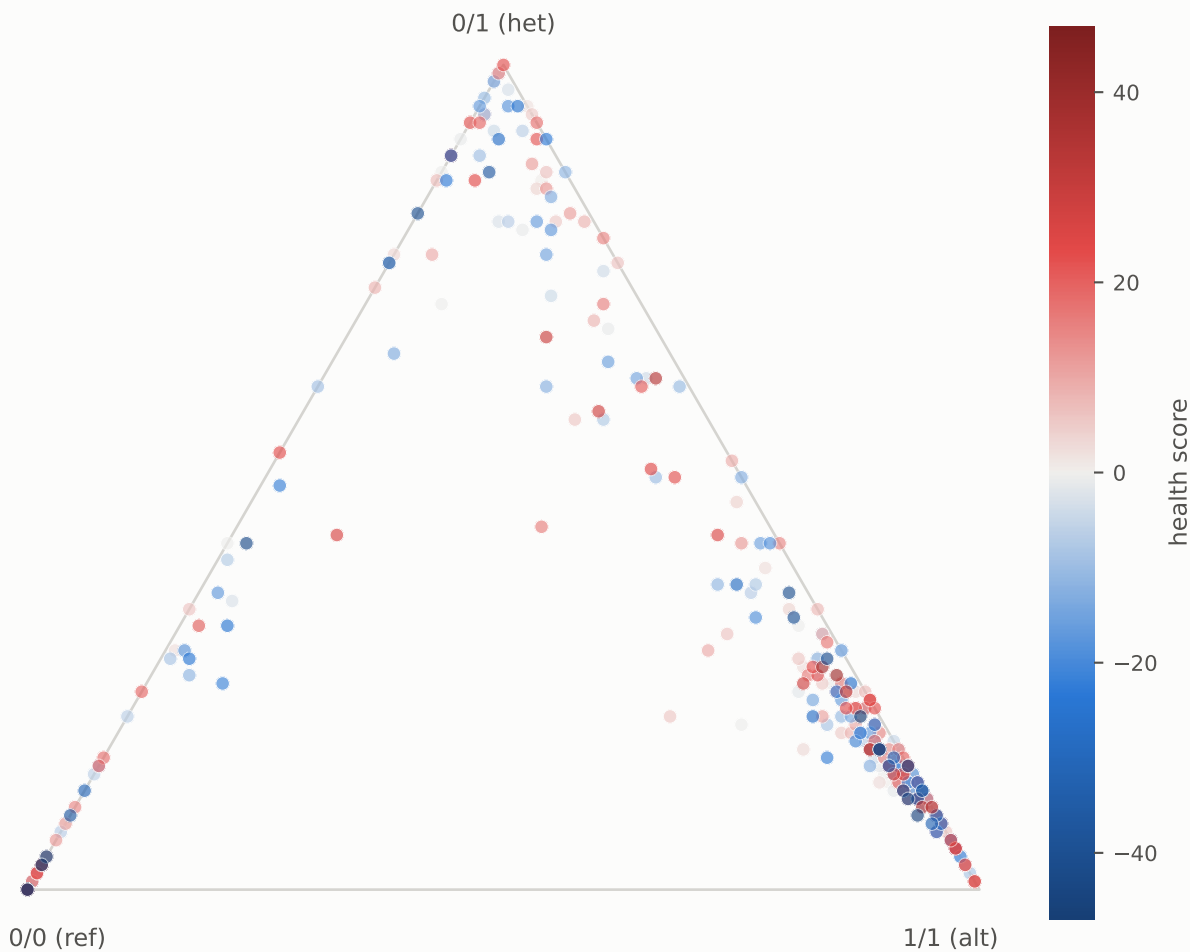
#98 by genotype uncertainty CHR_03:37,248,219 A>T
AF=0.46 DR2=0.81 $r=+0.019$ $\bar{H}=0.398$ F=0.4



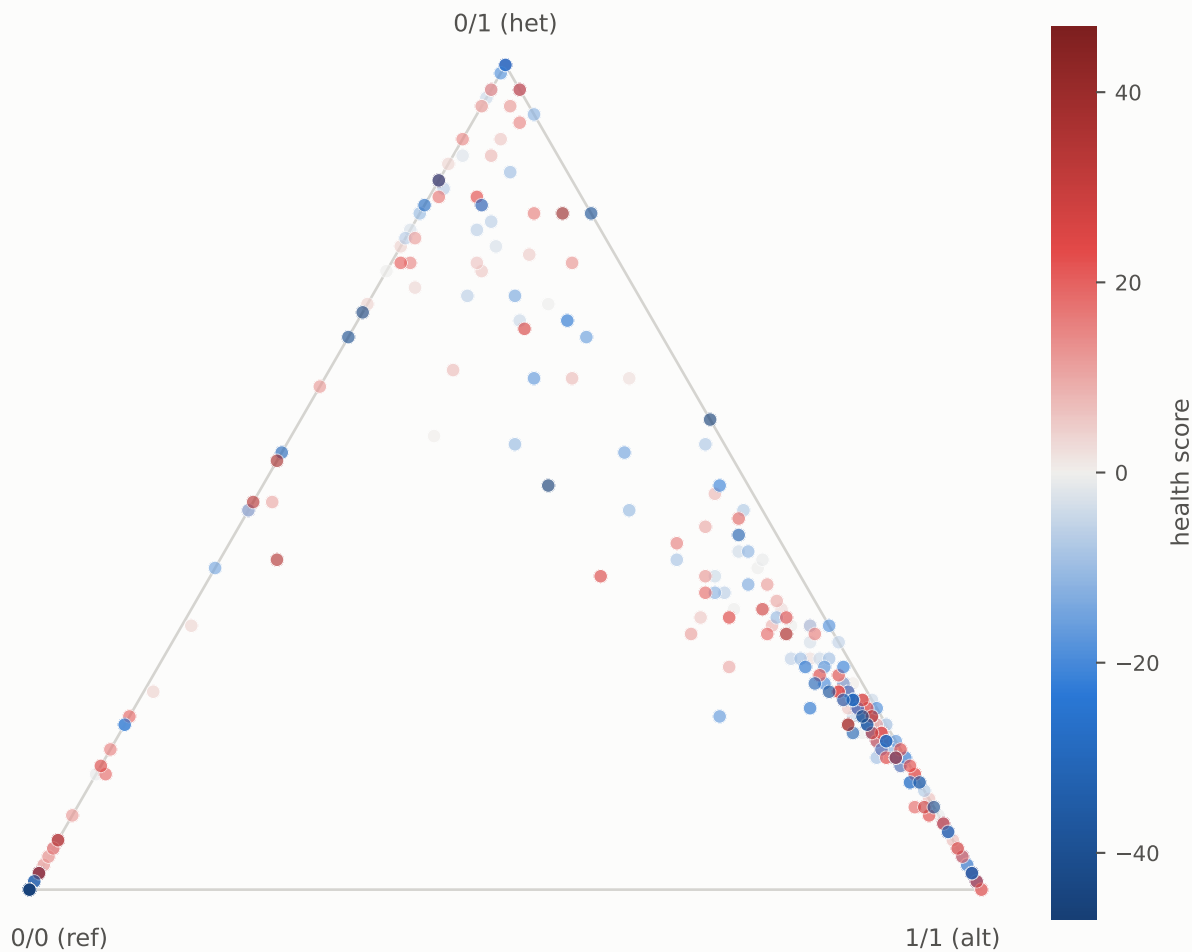
#99 by genotype uncertainty CHR_02:35,654,799 T>A
AF=0.48 DR2=0.81 $r=-0.001$ $\bar{H}=0.398$ $F=0.2$



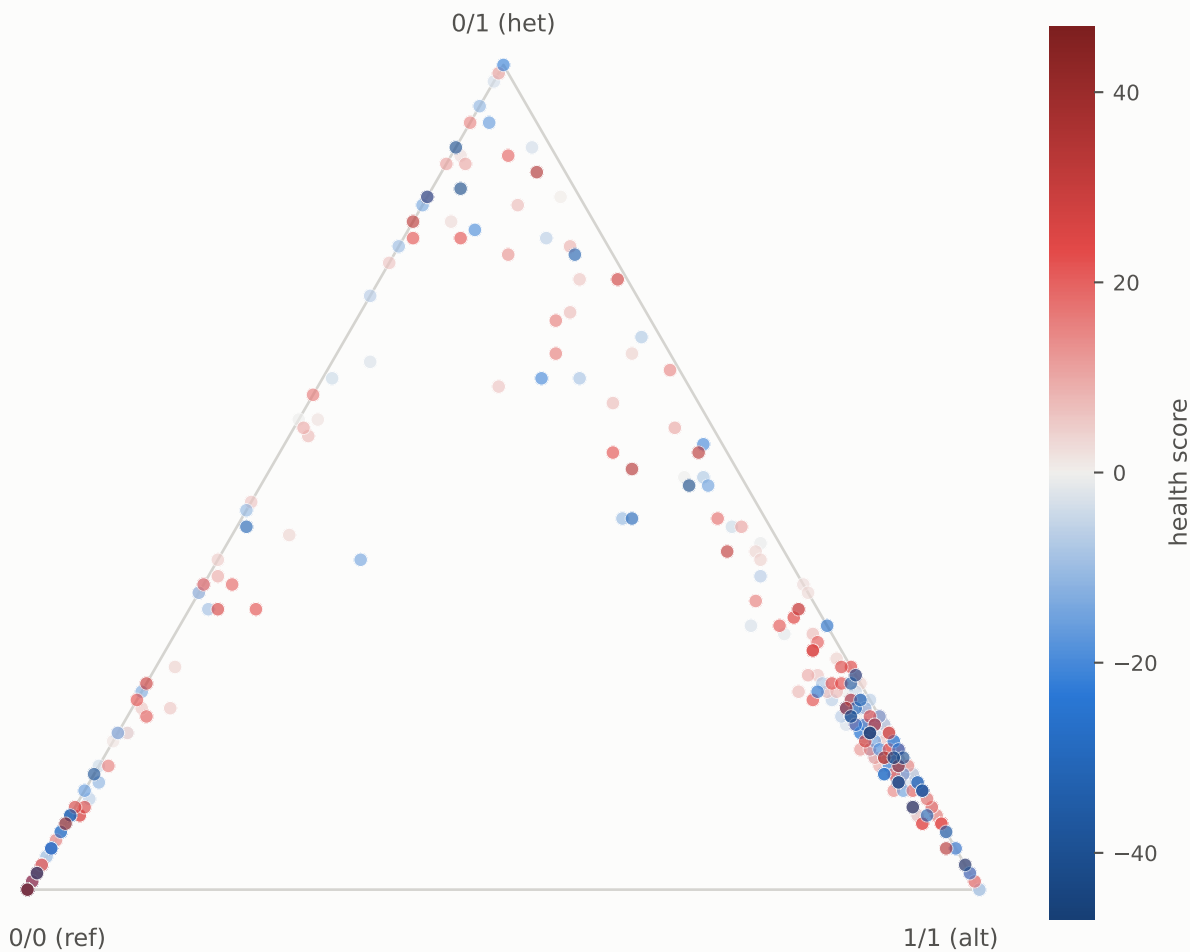
#100 by genotype uncertainty CHR_20:5,460,885 C>T
AF=0.54 DR2=0.81 $r=+0.009$ $\bar{H}=0.398$ $F=0.0$



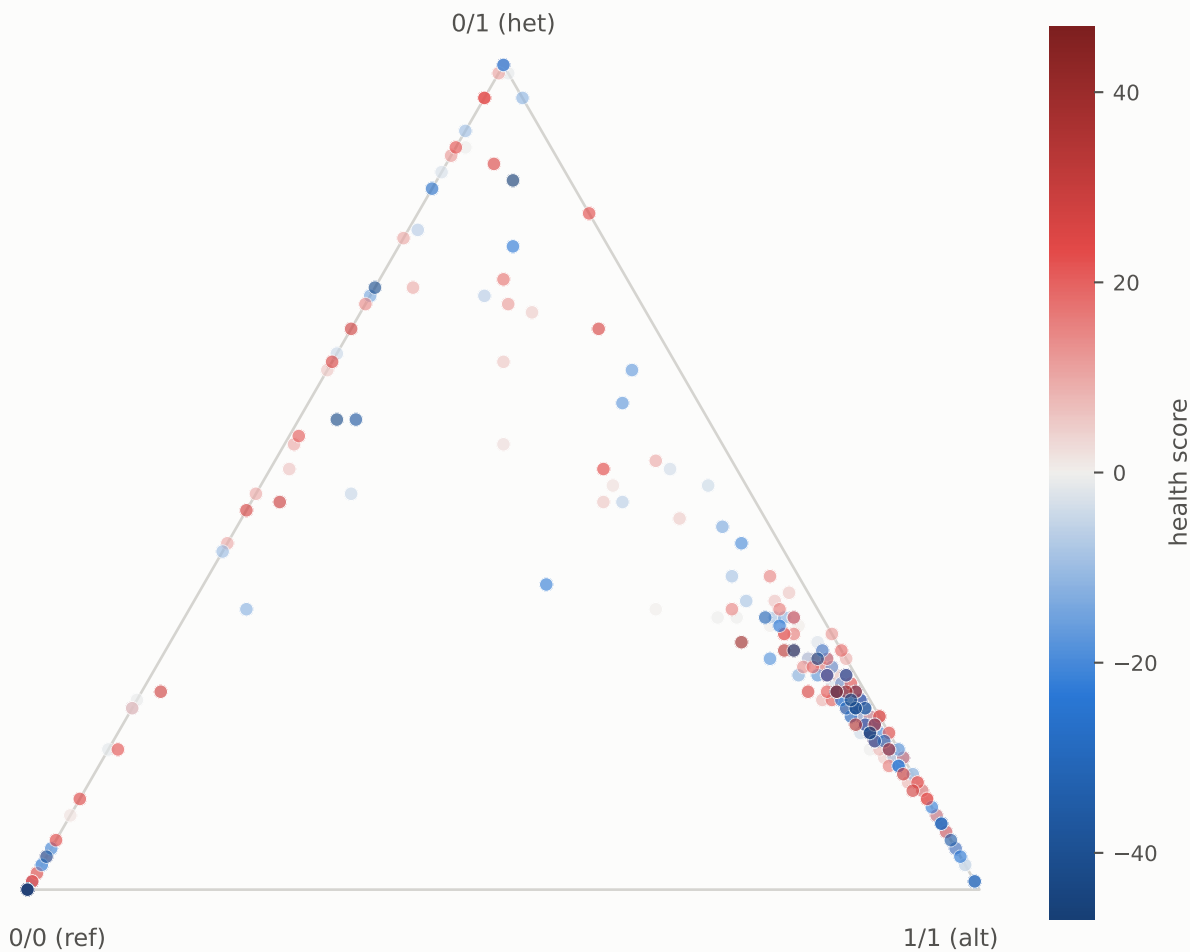
#101 by genotype uncertainty CHR_06:9,389,098 G>A
AF=0.5 DR2=0.81 r=-0.040 H=0.398 F=1.1



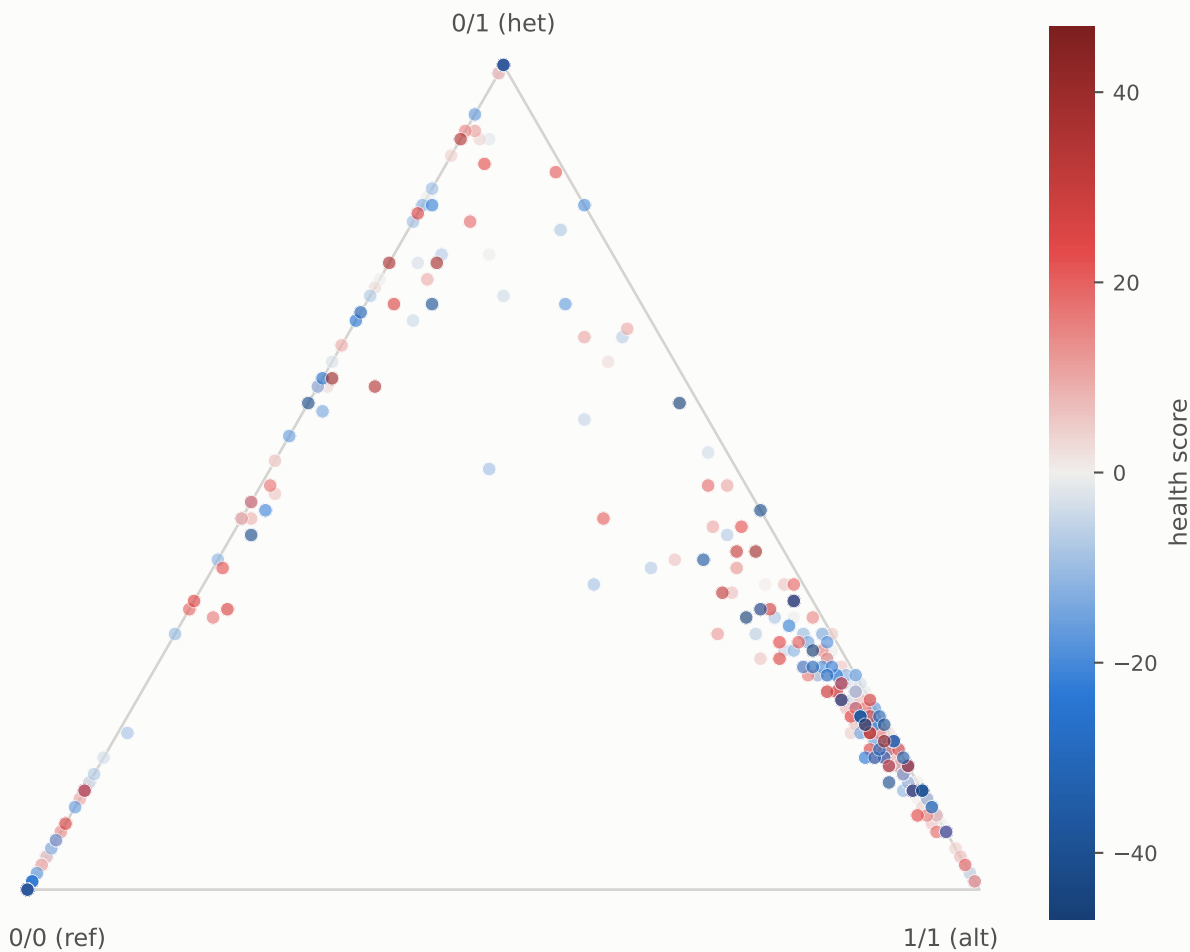
#102 by genotype uncertainty CHR_09:27,660,971 C>T
AF=0.5 DR2=0.82 r=+0.012 $\bar{H}$ =0.398 F=0.1



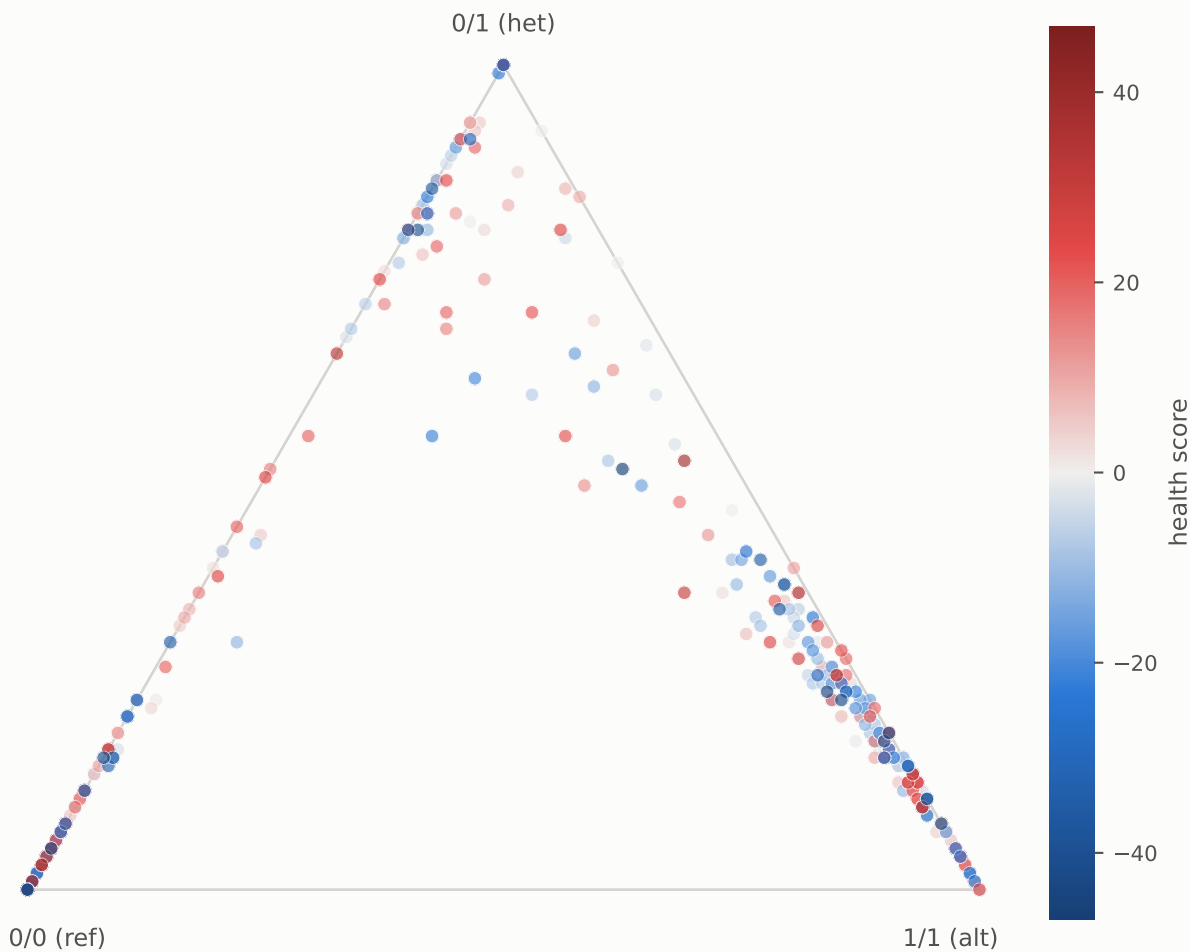
#103 by genotype uncertainty CHR_21:20,595,867 A>G
AF=0.48 DR2=0.81 $r=-0.066$ $\bar{H}=0.398$ F=1.0



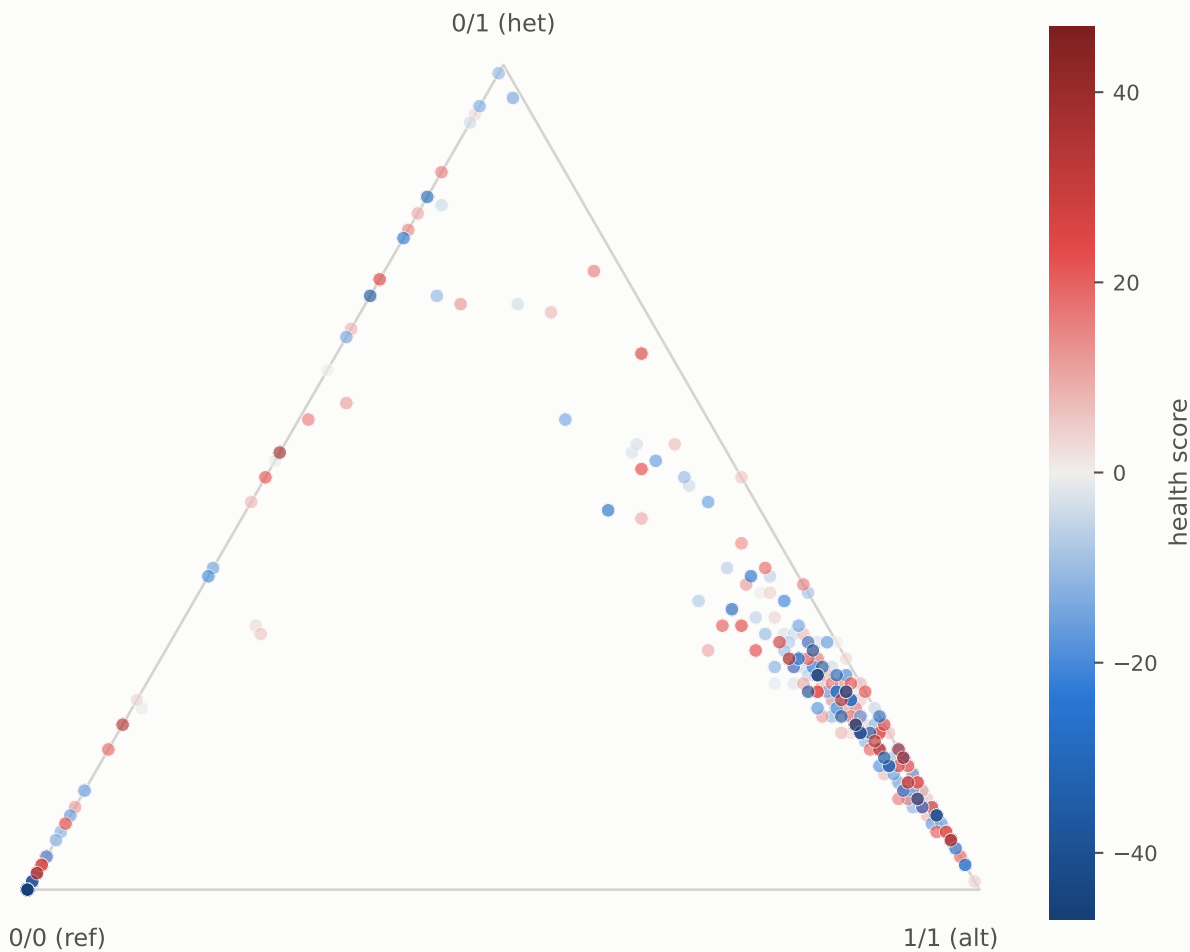
#104 by genotype uncertainty CHR_02:11,191,568 C>T
AF=0.5 DR2=0.81 r=-0.053 H=0.398 F=0.8



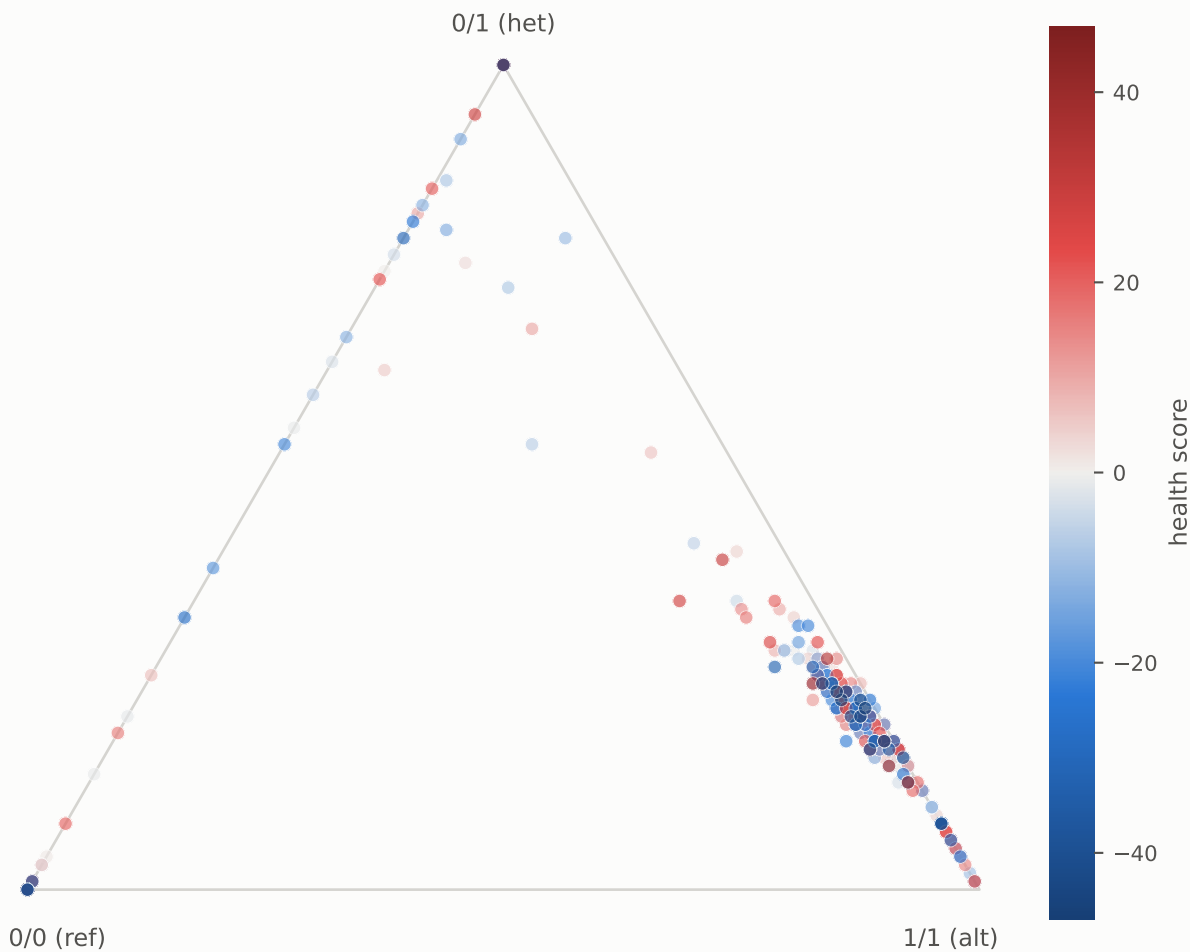
#105 by genotype uncertainty CHR_09:19,984,546 C>T
AF=0.46 DR2=0.81 $r=-0.078$ $\bar{H}=0.398$ $F=1.6$



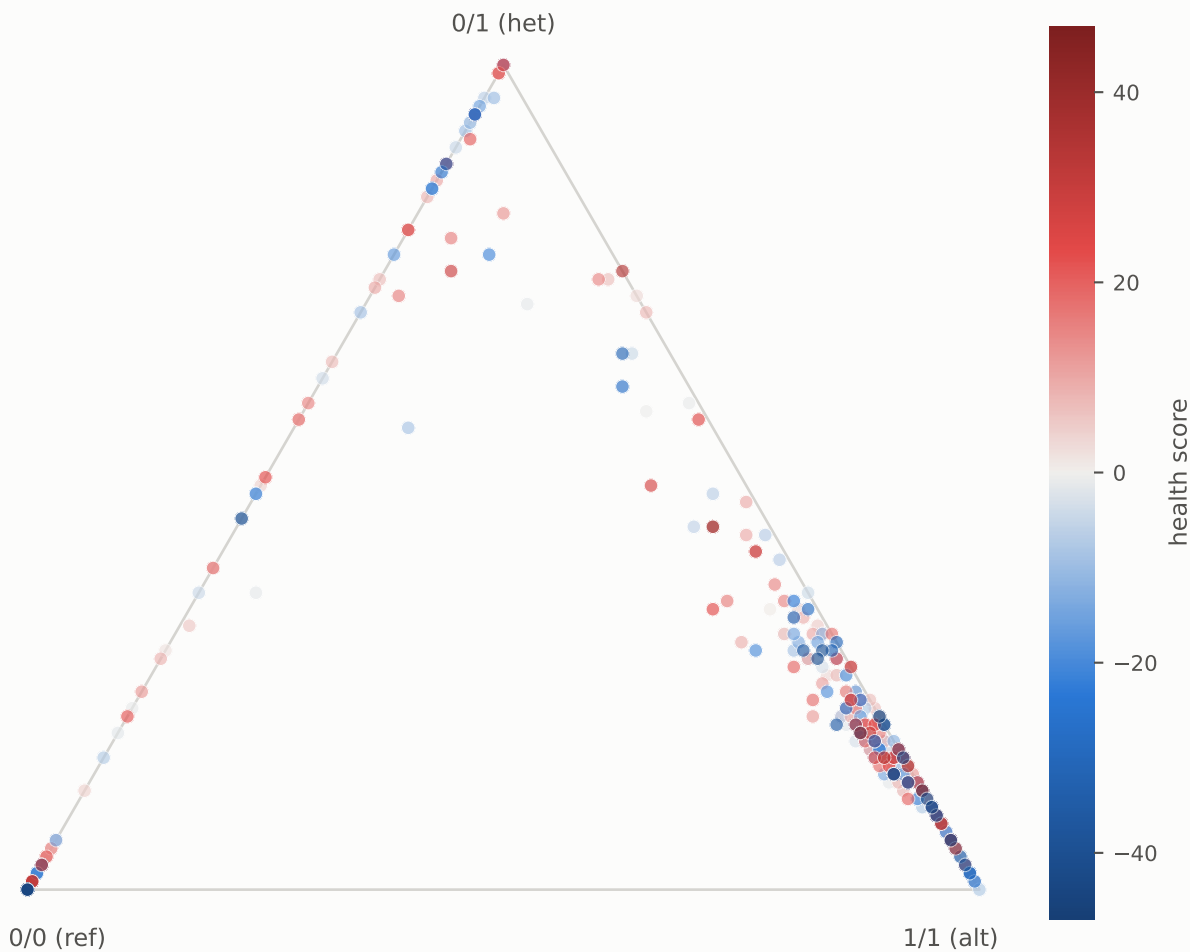
#106 by genotype uncertainty CHR_18:26,525,774 A>T
AF=0.51 DR2=0.82 $r=-0.047$ $\bar{H}=0.398$ F=0.6



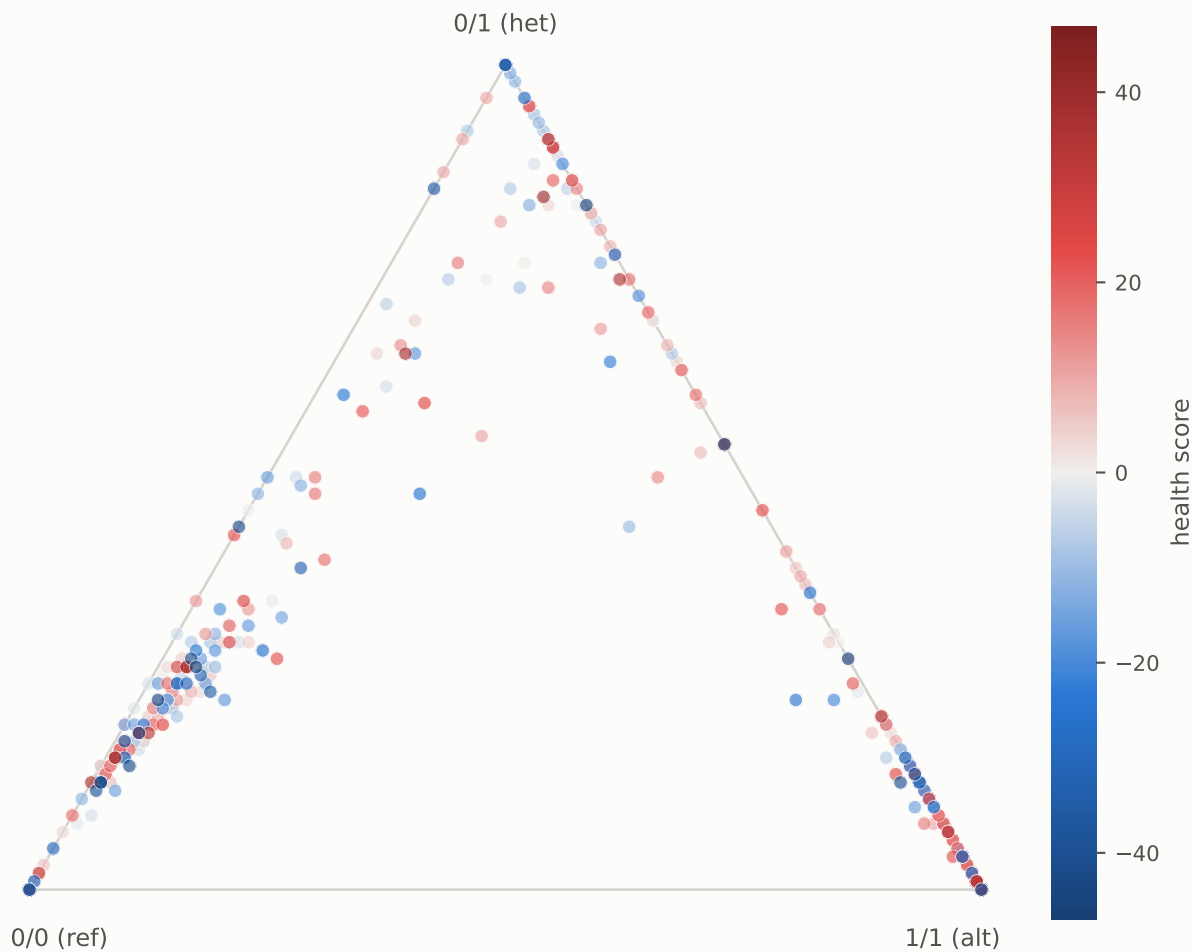
#107 by genotype uncertainty CHR_21:17,081,620 A>G
AF=0.53 DR2=0.83 $r=-0.153$ $\bar{H}=0.397$ F=5.5



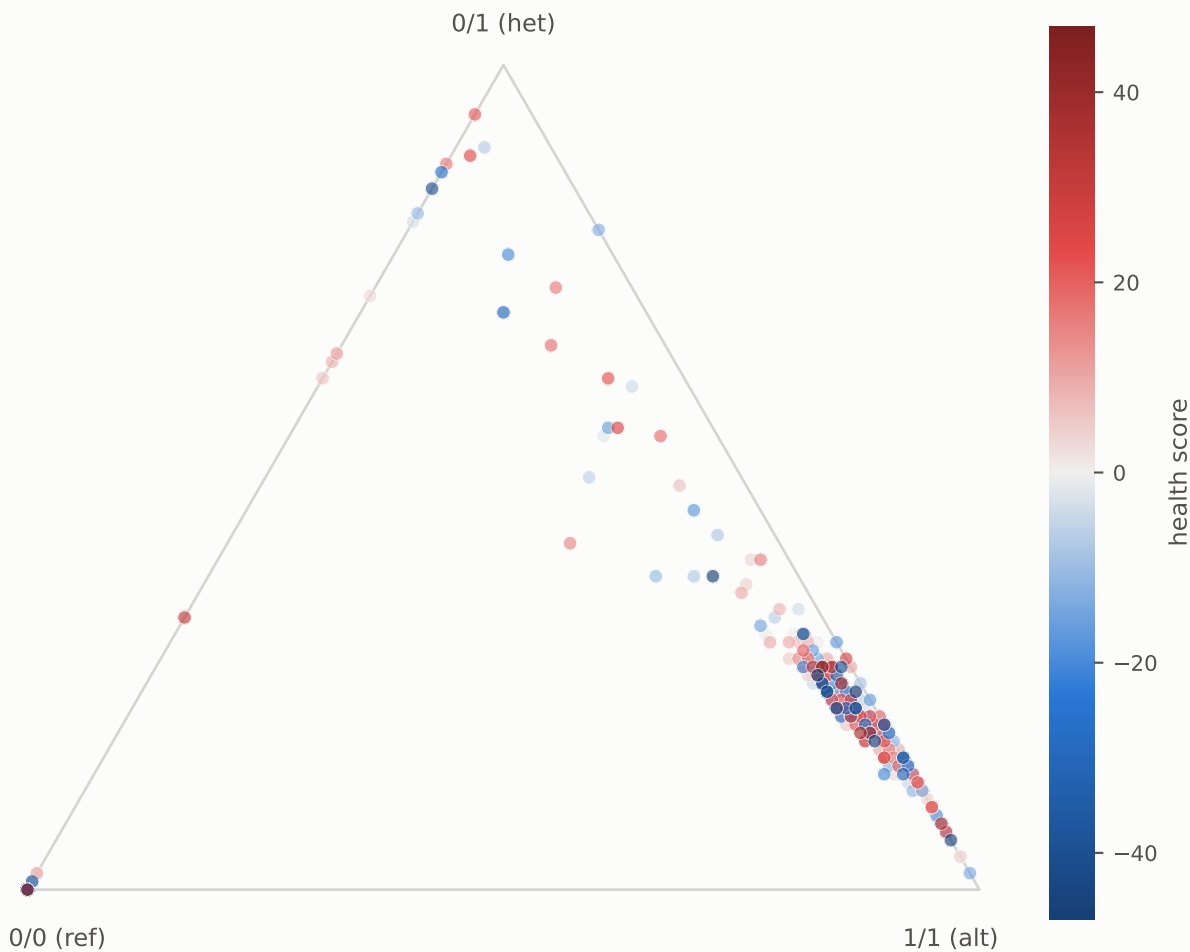
#108 by genotype uncertainty CHR_06:11,327,564 G>T
AF=0.56 DR2=0.81 $r=-0.041$ $\bar{H}=0.397$ F=0.7



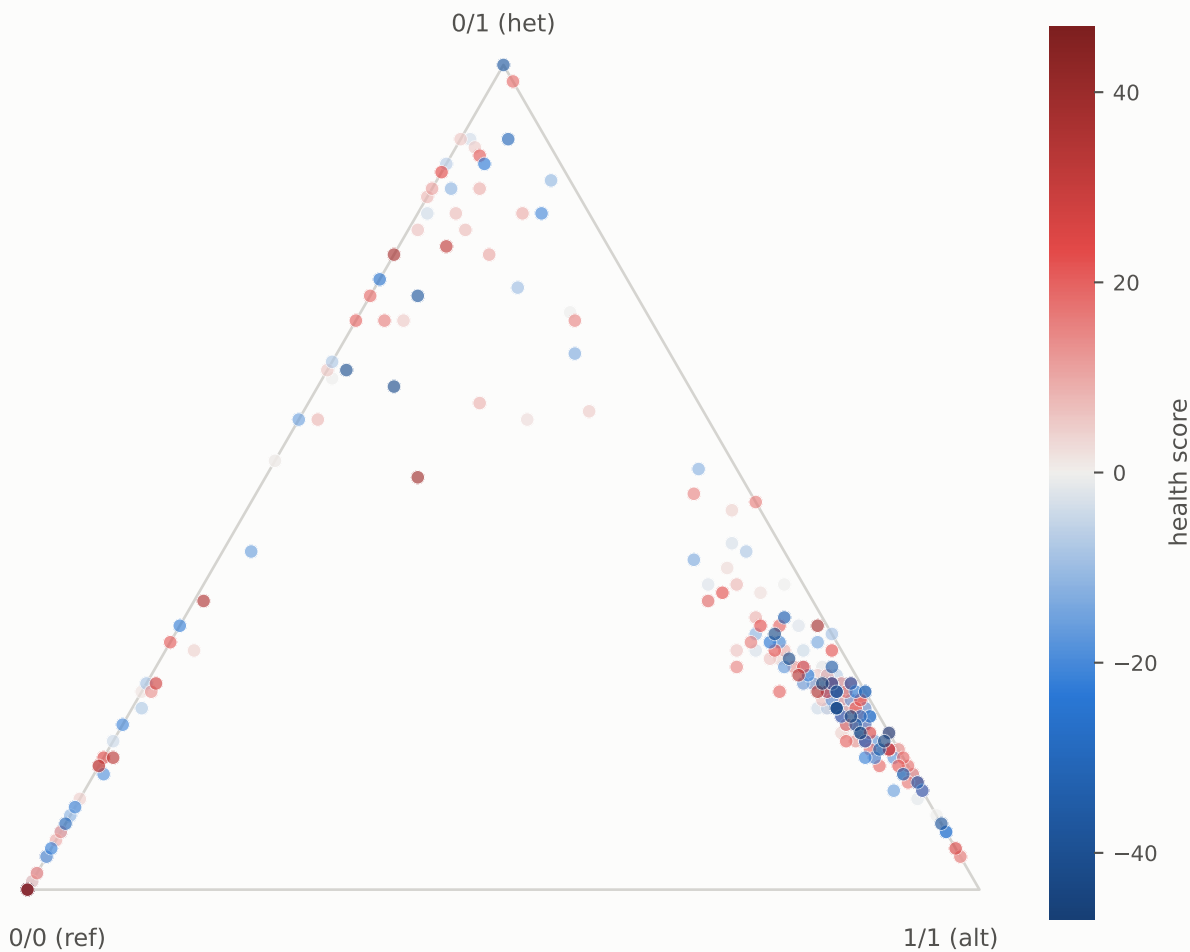
#109 by genotype uncertainty CHR_14:1,059,419 A>G
AF=0.53 DR2=0.81 $r=+0.053$ $\bar{H}=0.397$ F=1.1



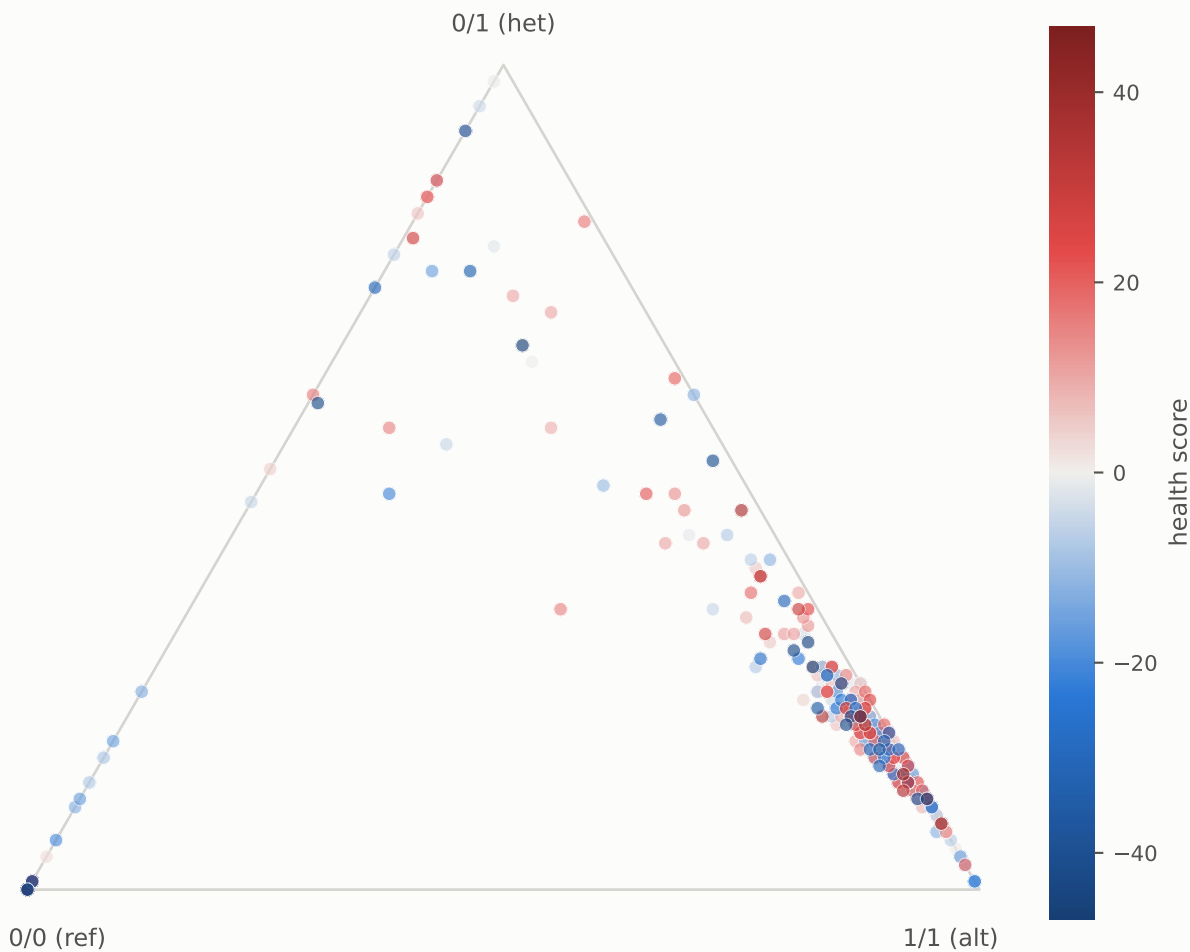
#110 by genotype uncertainty CHR_21:18,191,039 G>A
AF=0.51 DR2=0.82 r=-0.006 $\bar{H}$ =0.397 F=0.1



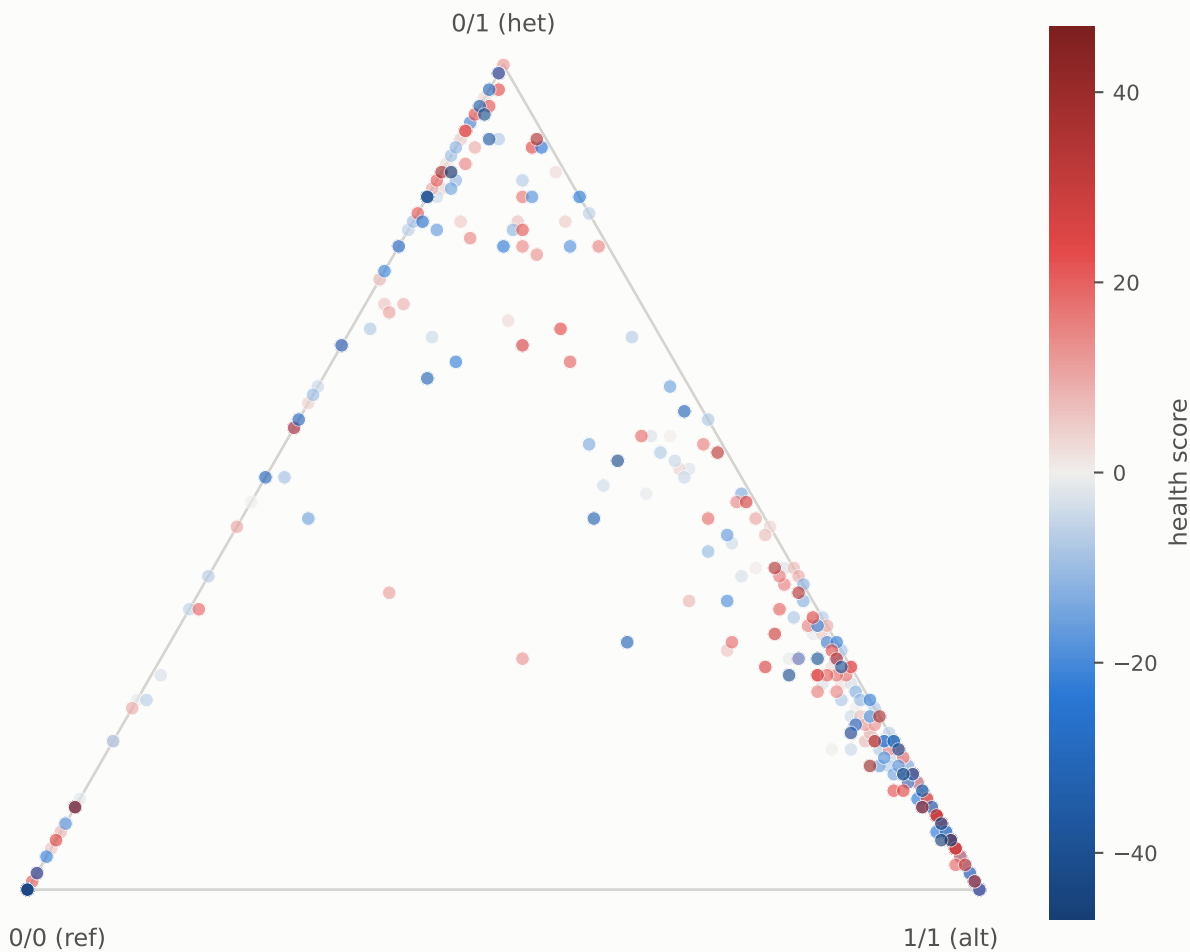
#111 by genotype uncertainty CHR_01:45,042,153 G>A
AF=0.44 DR2=0.81 $r=-0.092$ $\bar{H}=0.397$ F=1.8



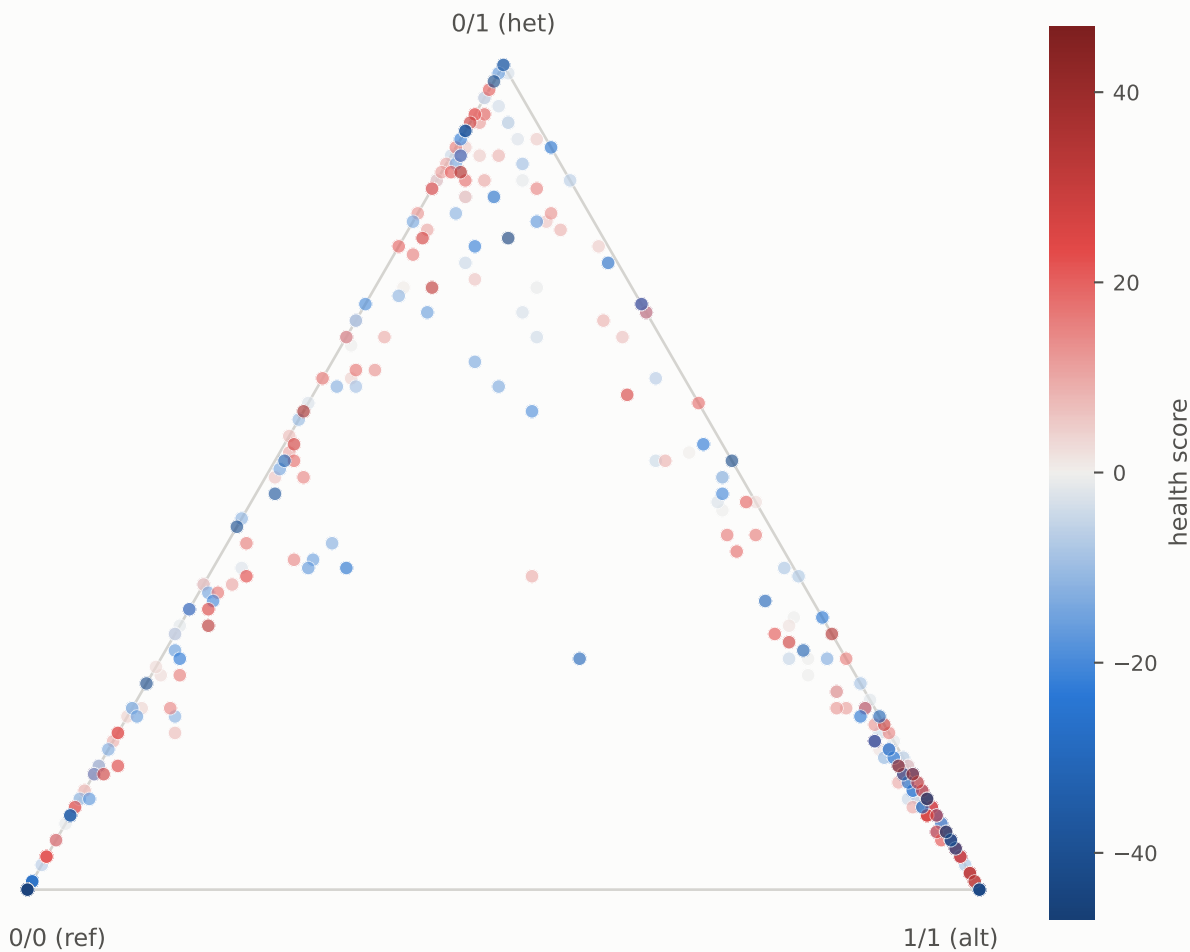
#112 by genotype uncertainty CHR_18:916,576 T>A
AF=0.56 DR2=0.81 r=+0.047 H=0.397 F=1.1



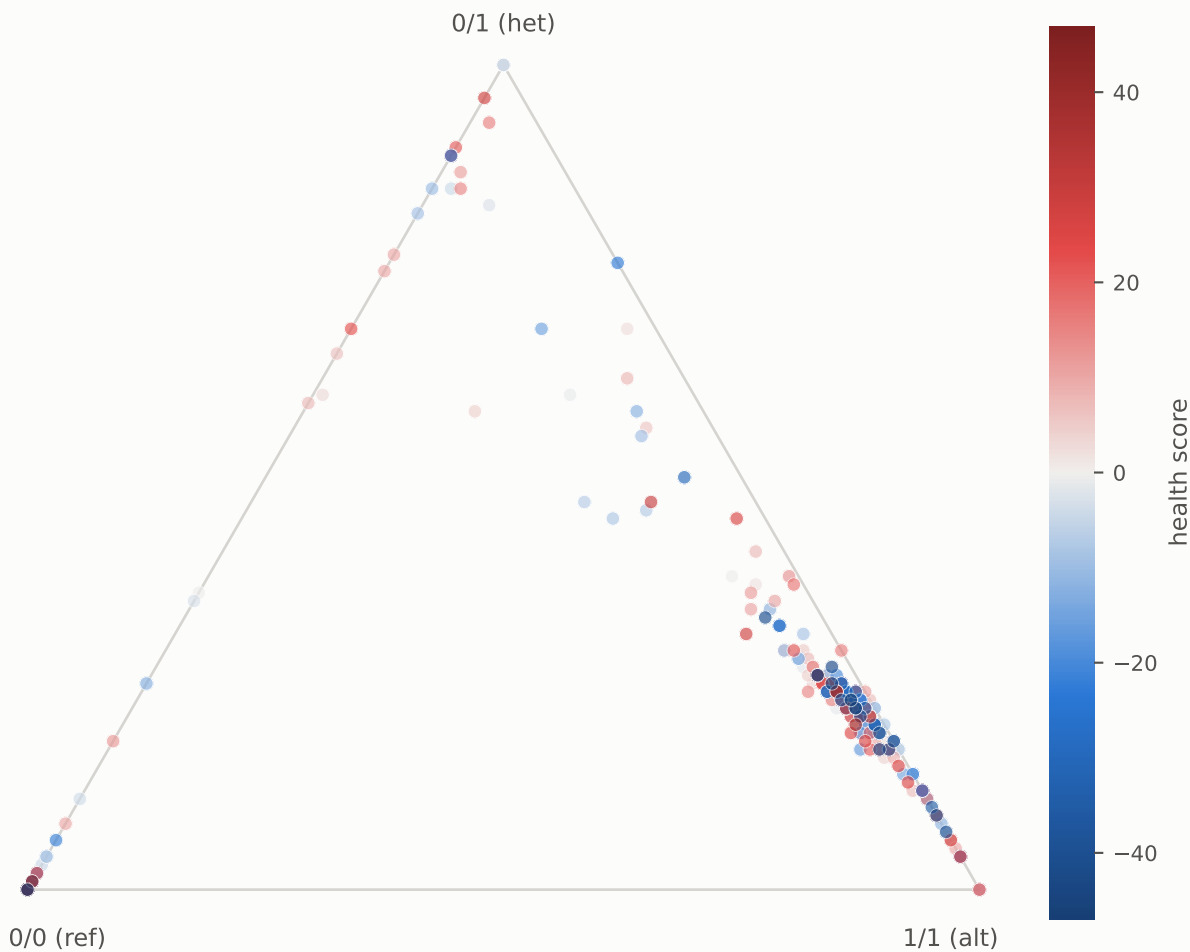
#113 by genotype uncertainty CHR_09:35,479,078 A>G
AF=0.54 DR2=0.81 r=+0.029 H=0.397 F=1.3



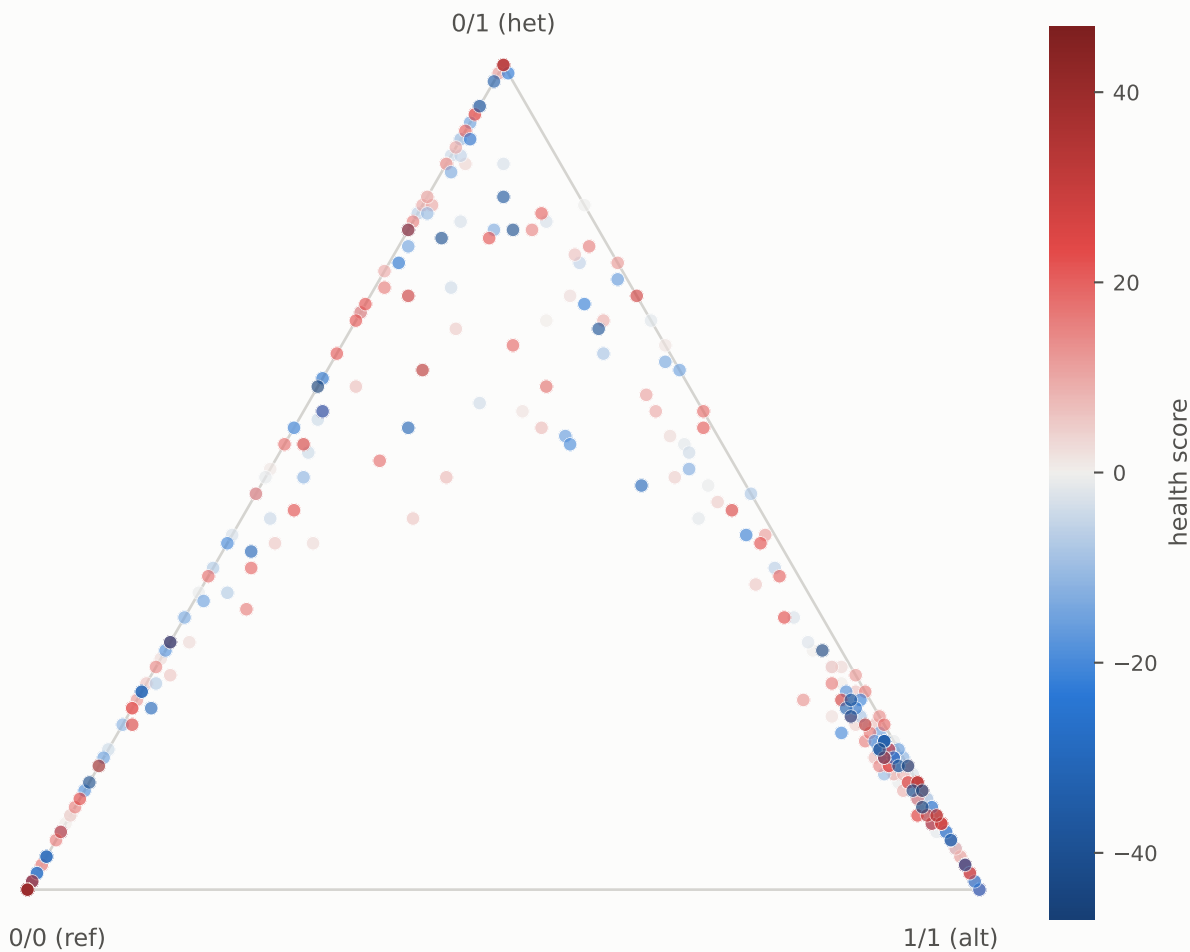
#114 by genotype uncertainty CHR_10:4,636,407 T>G
AF=0.53 DR2=0.81 $r=+0.051$ $\bar{H}=0.397$ F=0.9



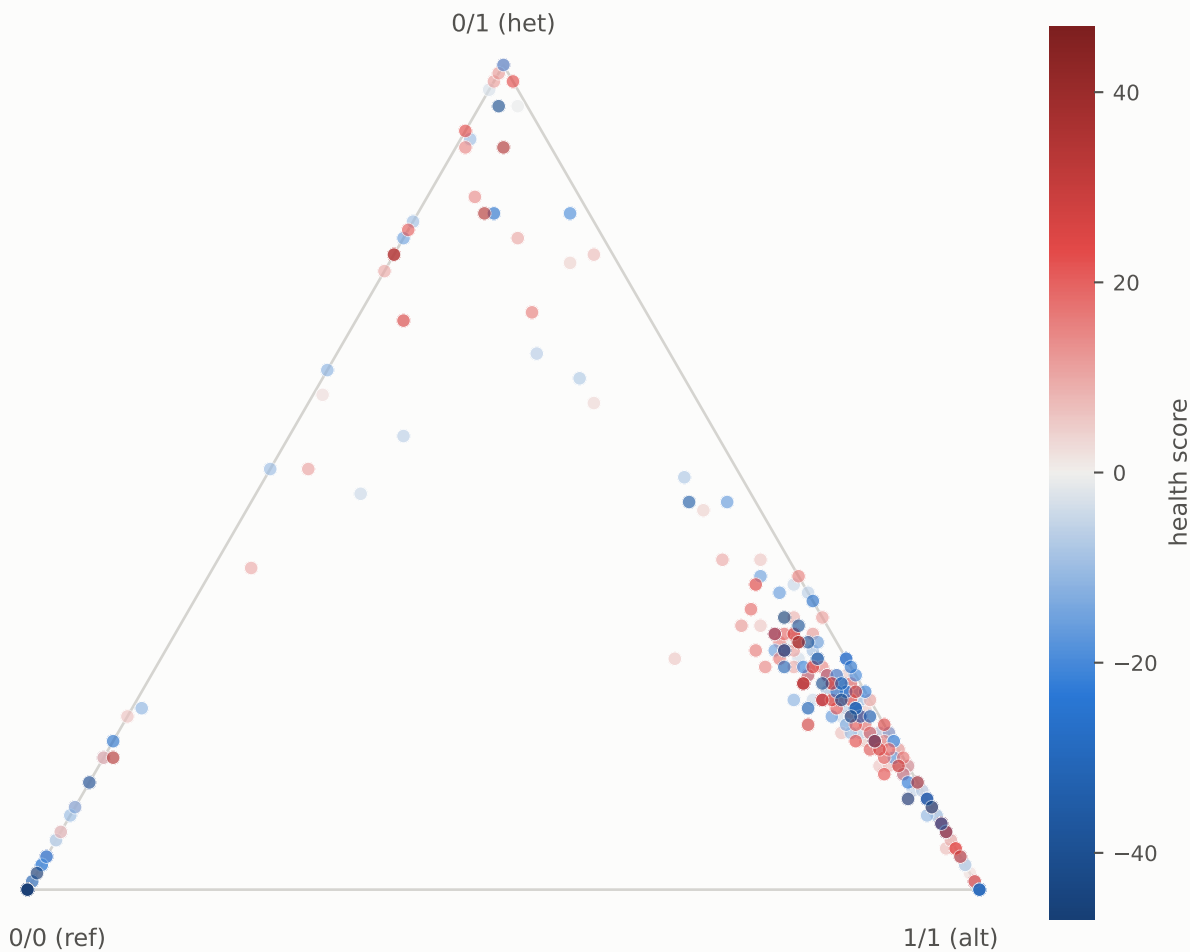
#115 by genotype uncertainty CHR_20:1,328,625 C>A
AF=0.53 DR2=0.81 $r=-0.079$ $H=0.397$ $F=1.2$



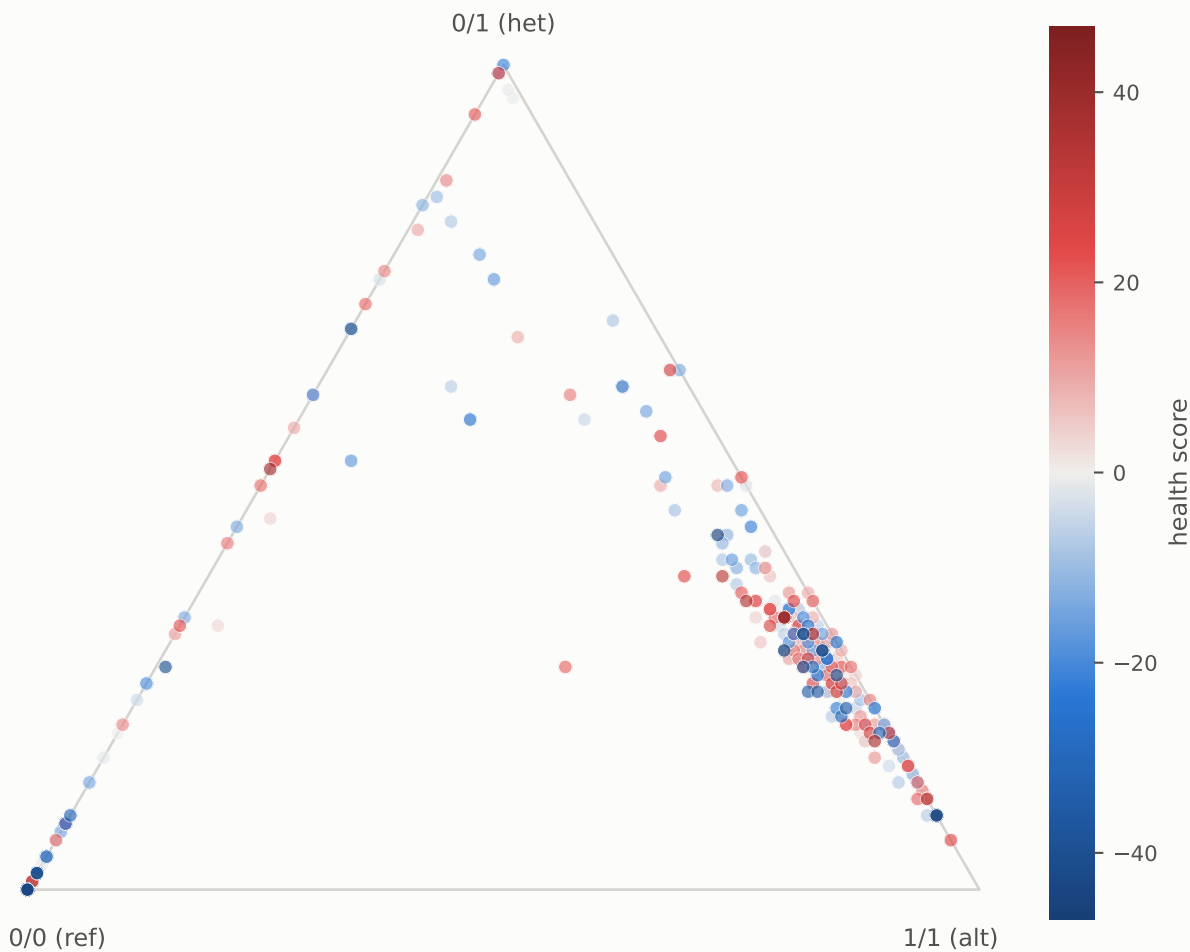
#116 by genotype uncertainty CHR_19:5,010,699 G>C
AF=0.49 DR2=0.81 $r=-0.041$ $\bar{H}=0.397$ $F=0.3$



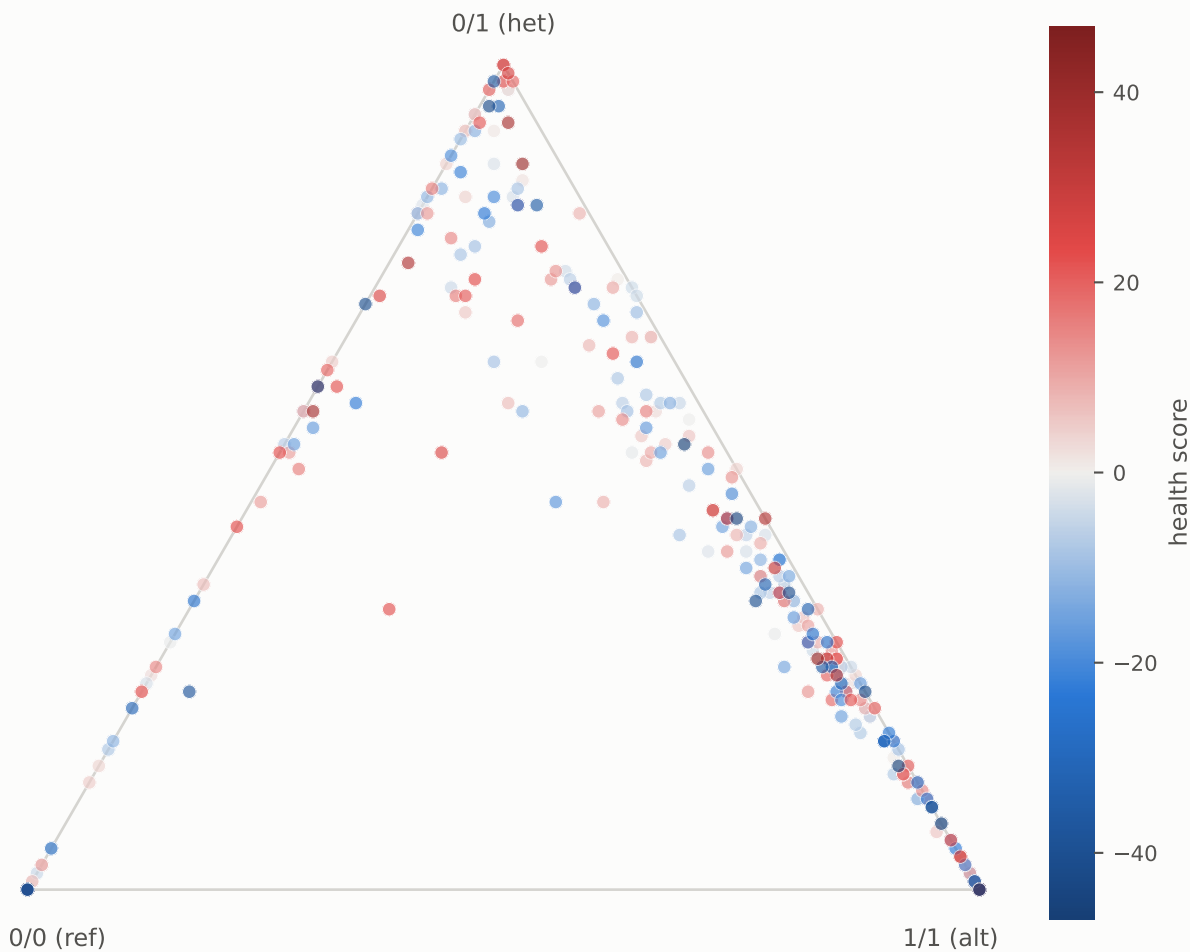
#117 by genotype uncertainty CHR_04:11,605,558 T>G
AF=0.55 DR2=0.82 $r=+0.036$ $\bar{H}=0.396$ F=1.2



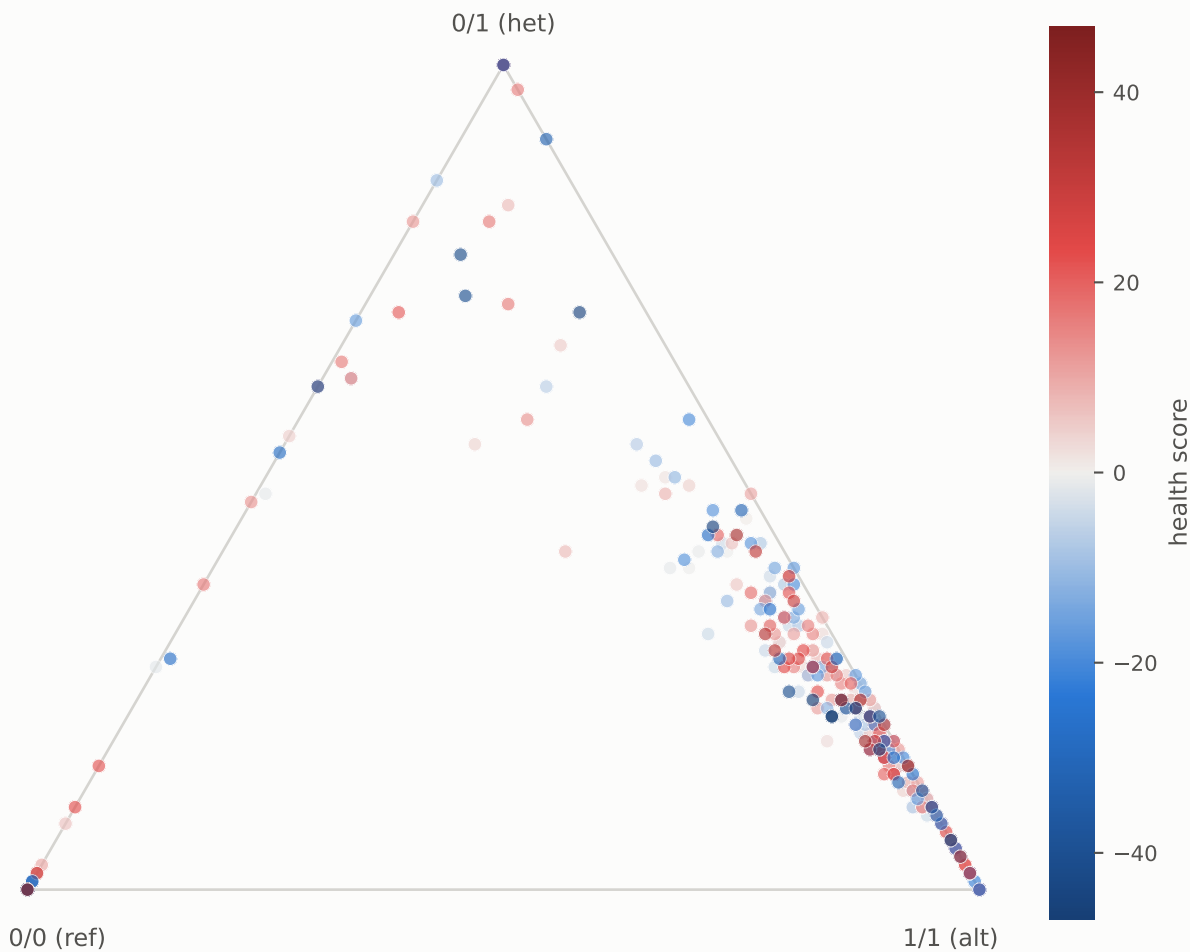
#118 by genotype uncertainty CHR_10:13,663,740 C>A
AF=0.43 DR2=0.81 $r=+0.040$ $\bar{H}=0.396$ F=0.5



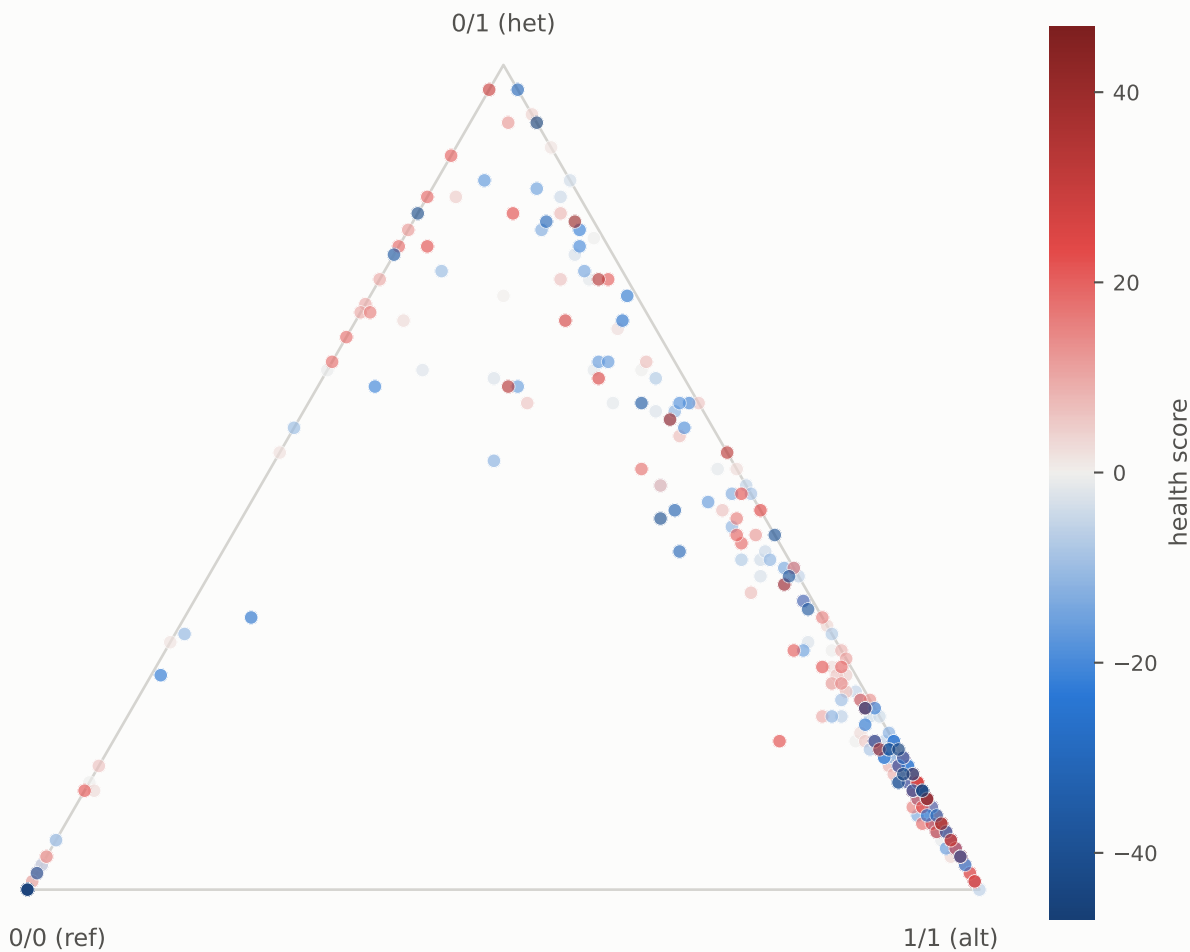
#119 by genotype uncertainty CHR_21:17,065,034 T>C
AF=0.5 DR2=0.81 r=-0.086 H=0.396 F=1.9



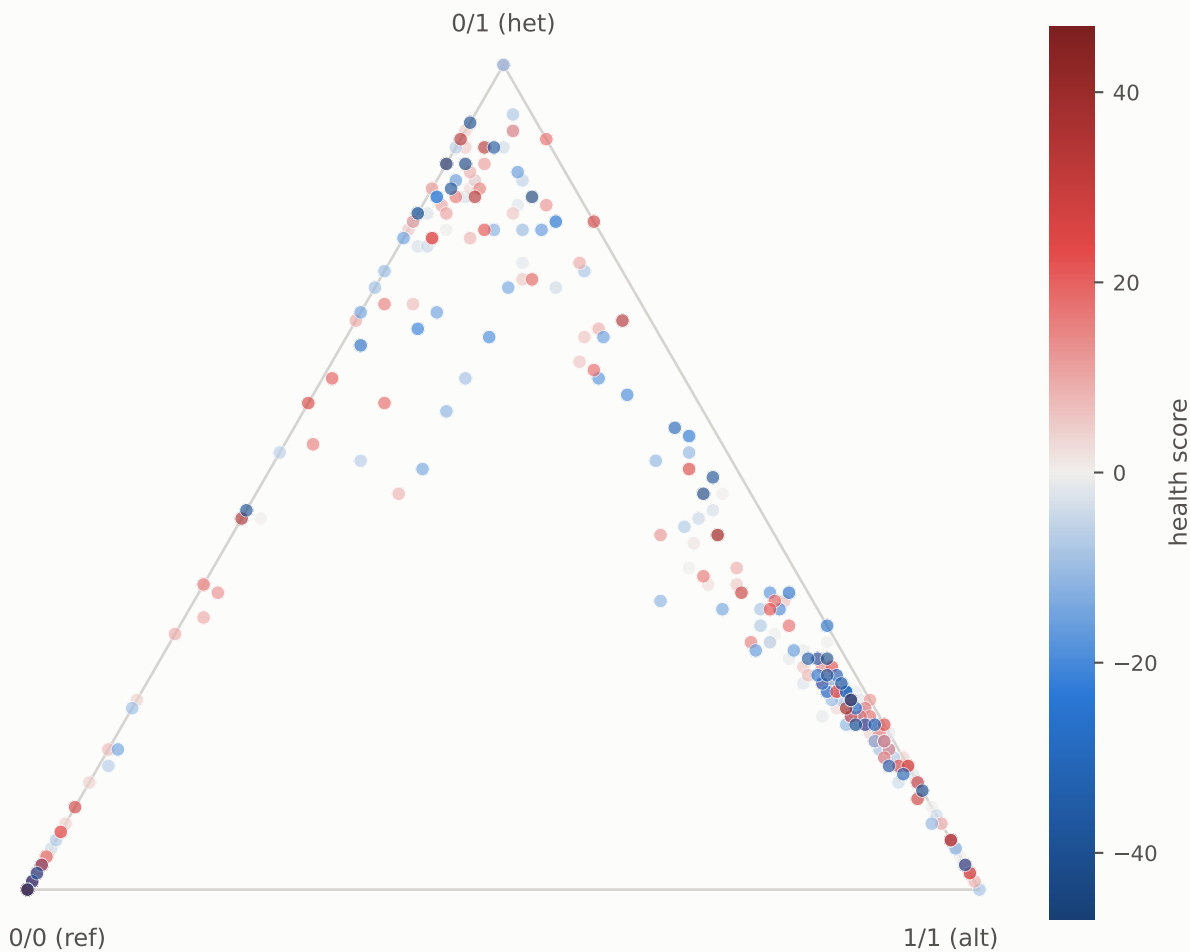
#120 by genotype uncertainty CHR_03:17,359,228 T>C
AF=0.57 DR2=0.81 $r=+0.036$ $\bar{H}=0.396$ F=1.1



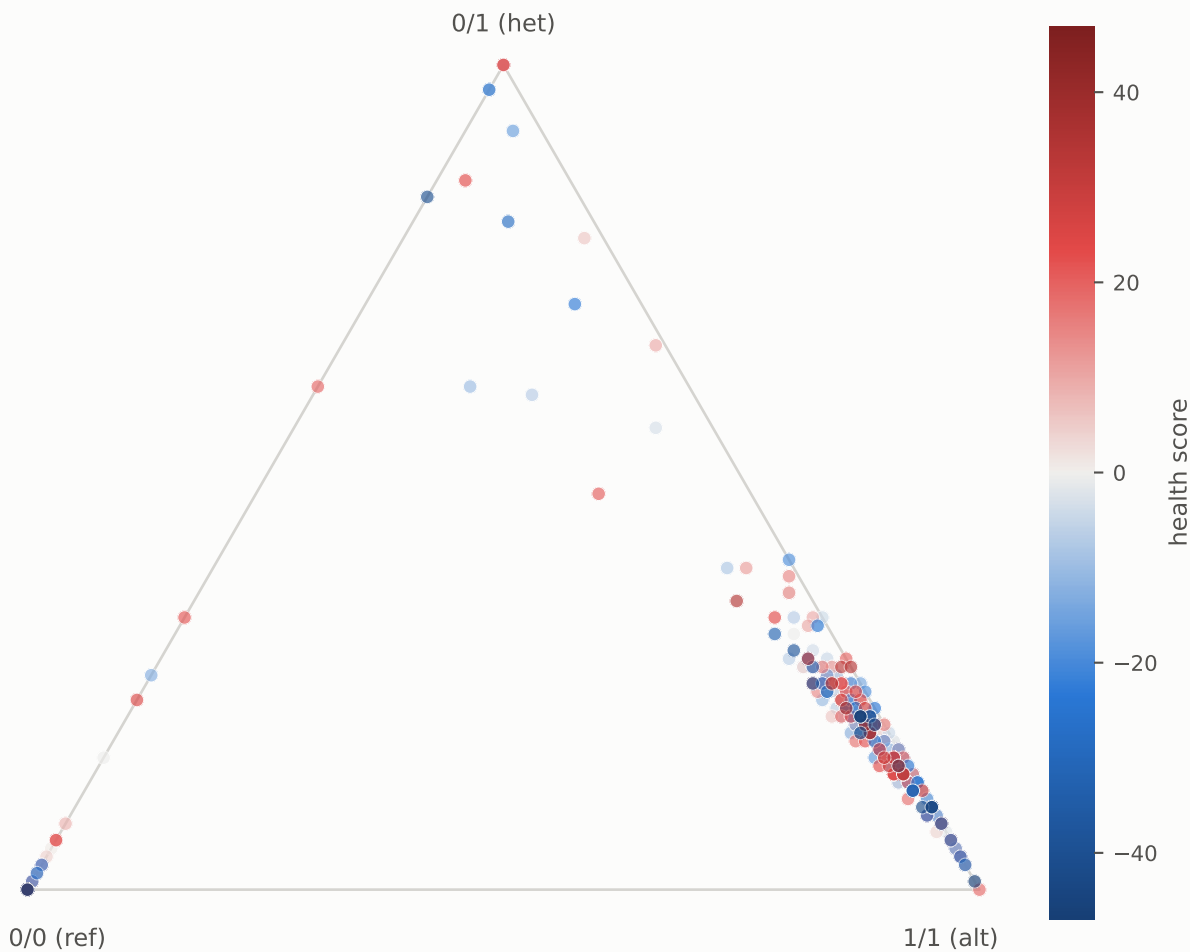
#121 by genotype uncertainty CHR_10:15,342,503 C>T
AF=0.63 DR2=0.82 $r=+0.005$ $\bar{H}=0.396$ F=0.2



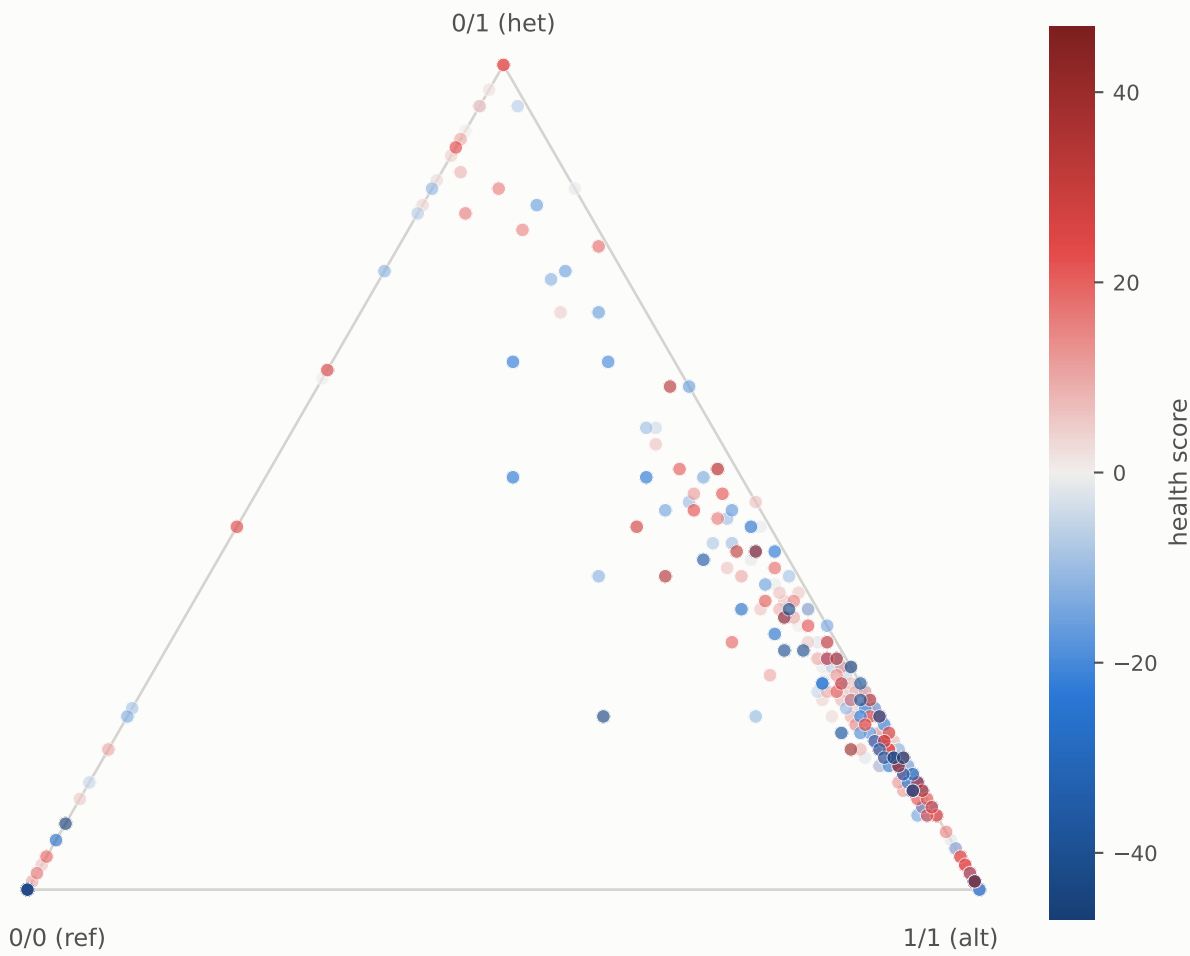
#122 by genotype uncertainty CHR_08:34,878,428 C>G
AF=0.39 DR2=0.81 $r=-0.084$ $\bar{H}=0.396$ F=2.8



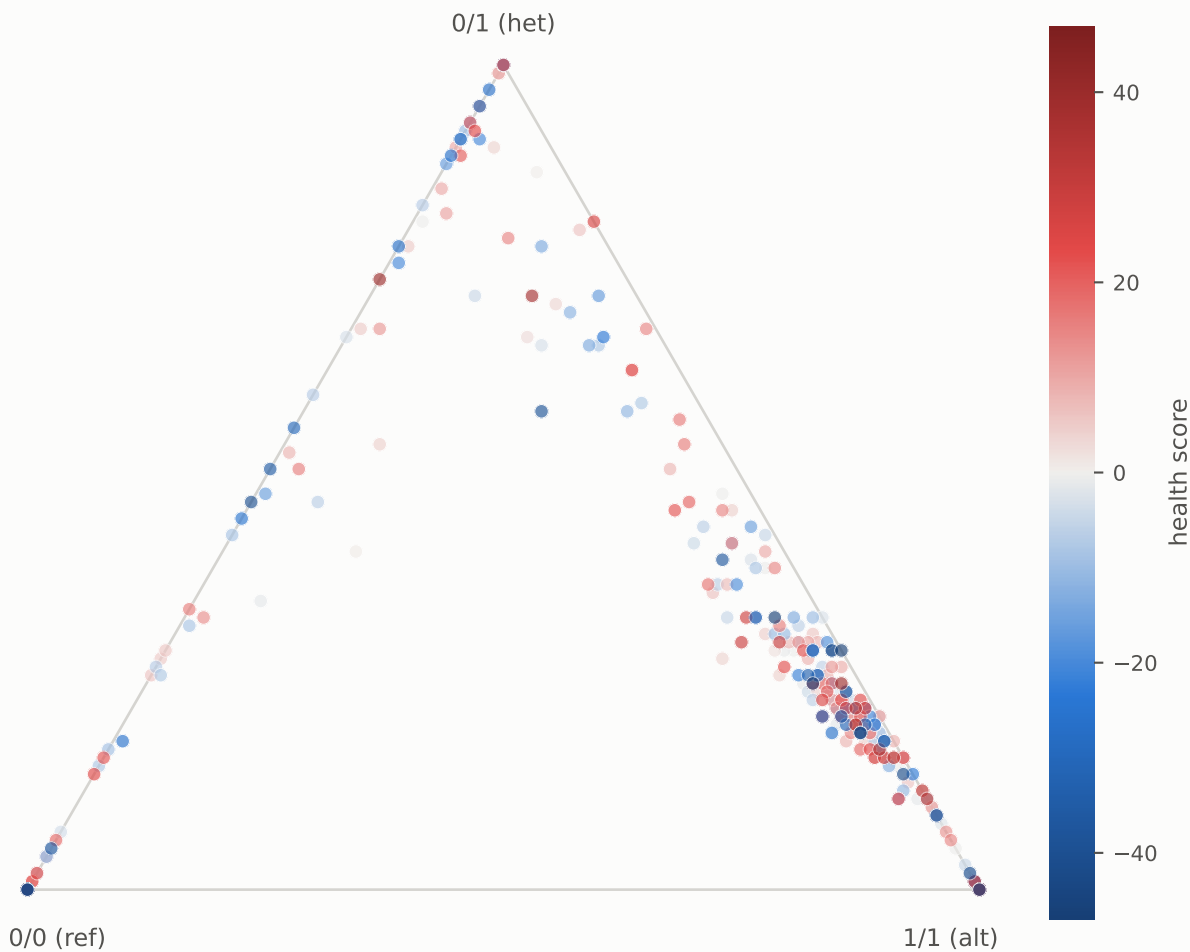
#123 by genotype uncertainty CHR_06:7,937,108 A>G
AF=0.61 DR2=0.81 r=-0.062 H=0.396 F=1.0



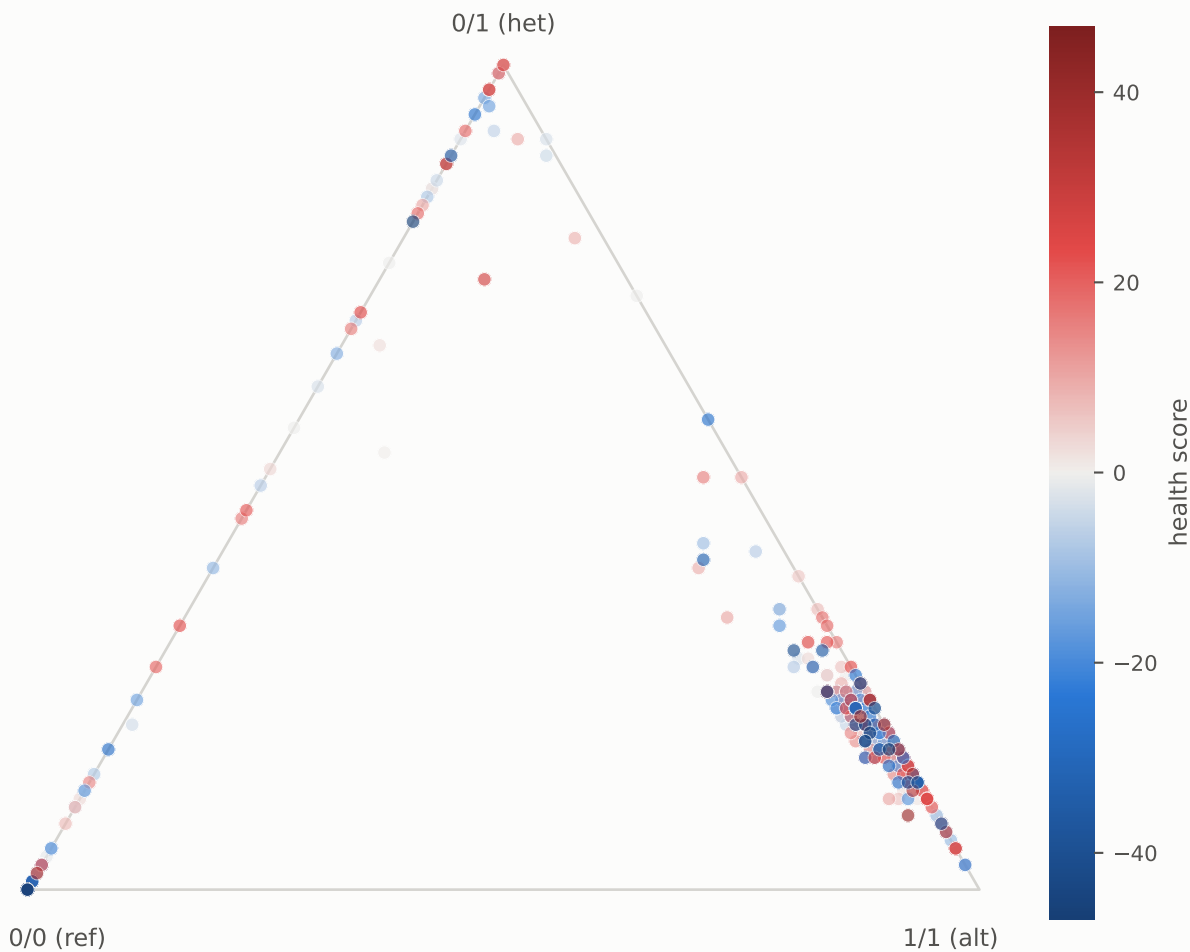
#124 by genotype uncertainty CHR_13:14,758,284 A>G
AF=0.58 DR2=0.81 $r=+0.008$ $\bar{H}=0.396$ F=0.3



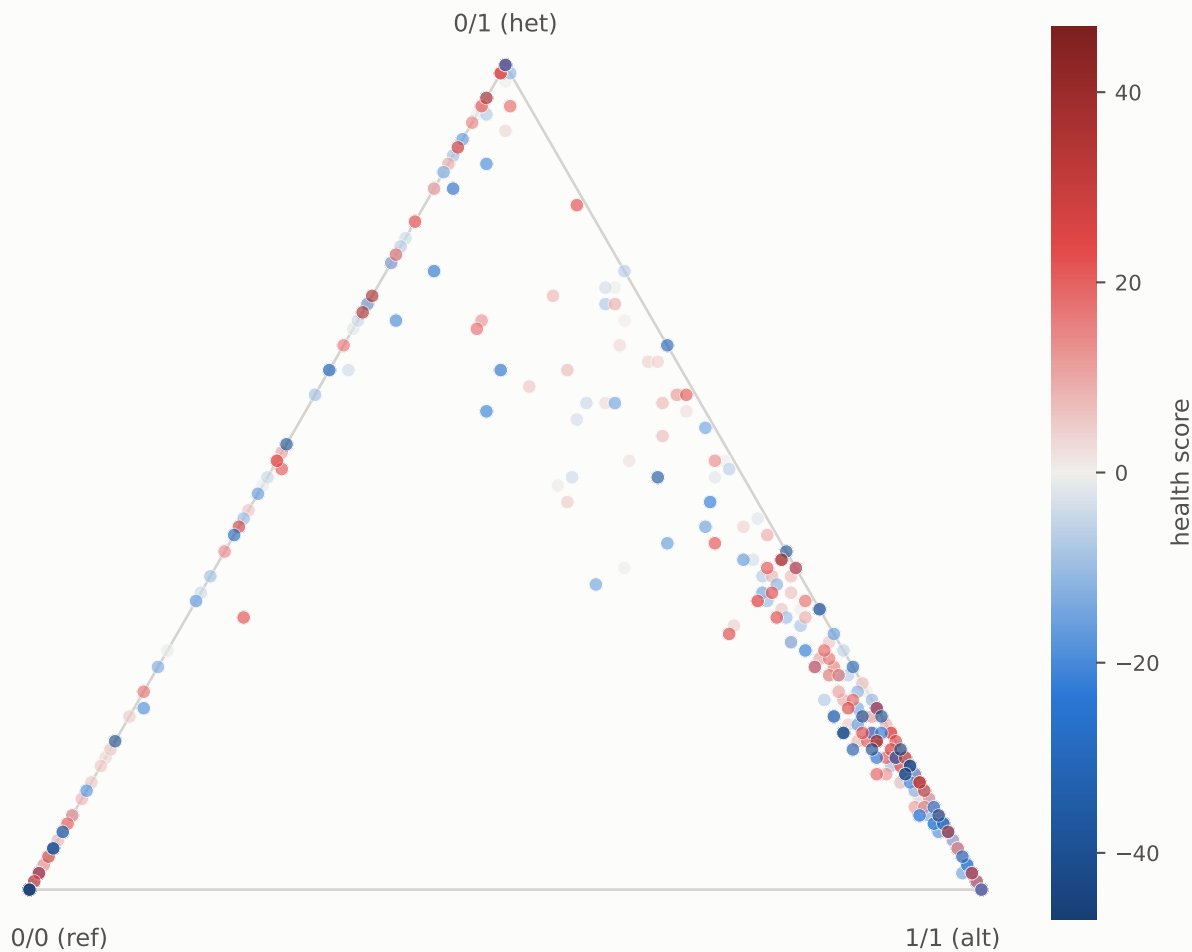
#125 by genotype uncertainty CHR_09:24,820,257 A>T
AF=0.54 DR2=0.81 $r=-0.015$ $\bar{H}=0.396$ F=0.1



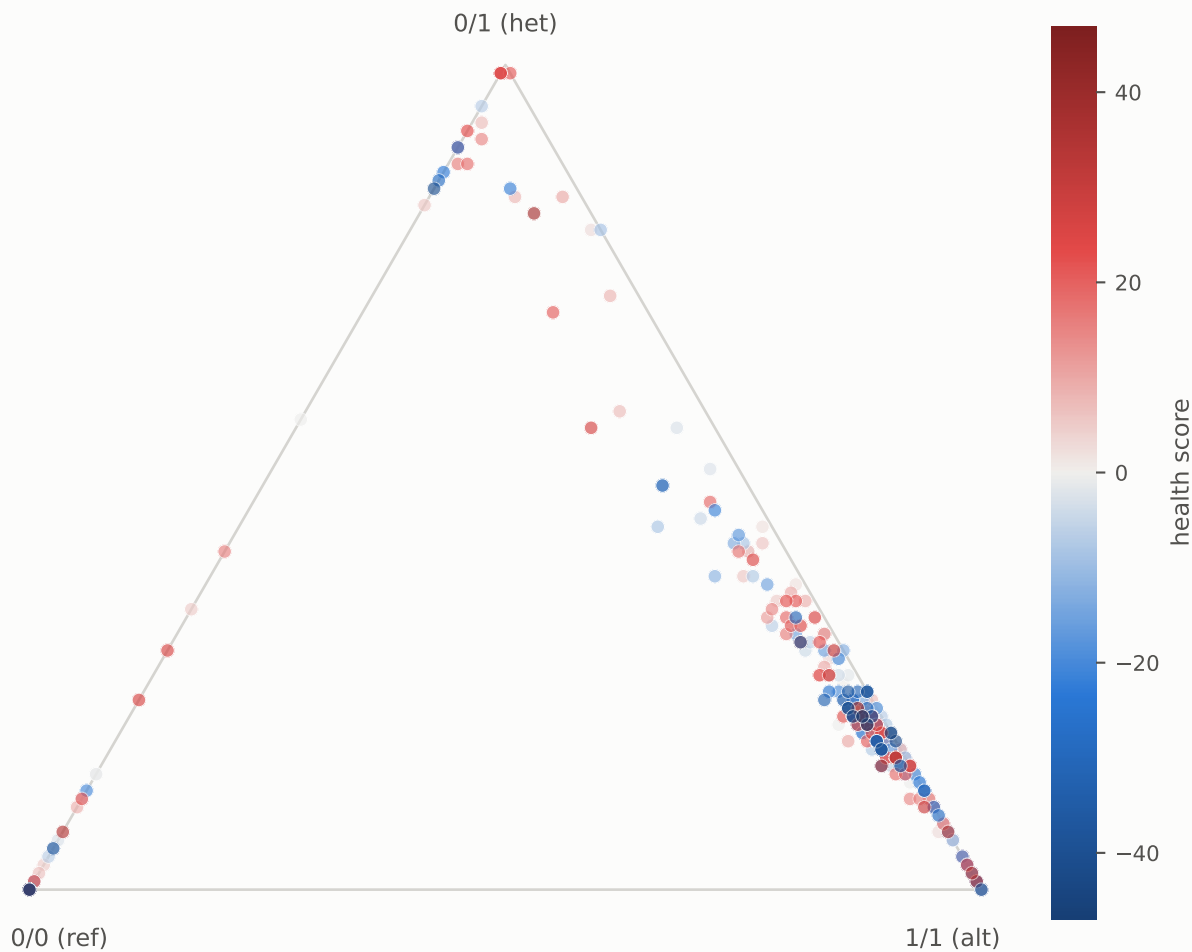
#126 by genotype uncertainty CHR_01:12,525,006 C>A
AF=0.58 DR2=0.81 $r=-0.002$ $\bar{H}=0.396$ $F=0.4$



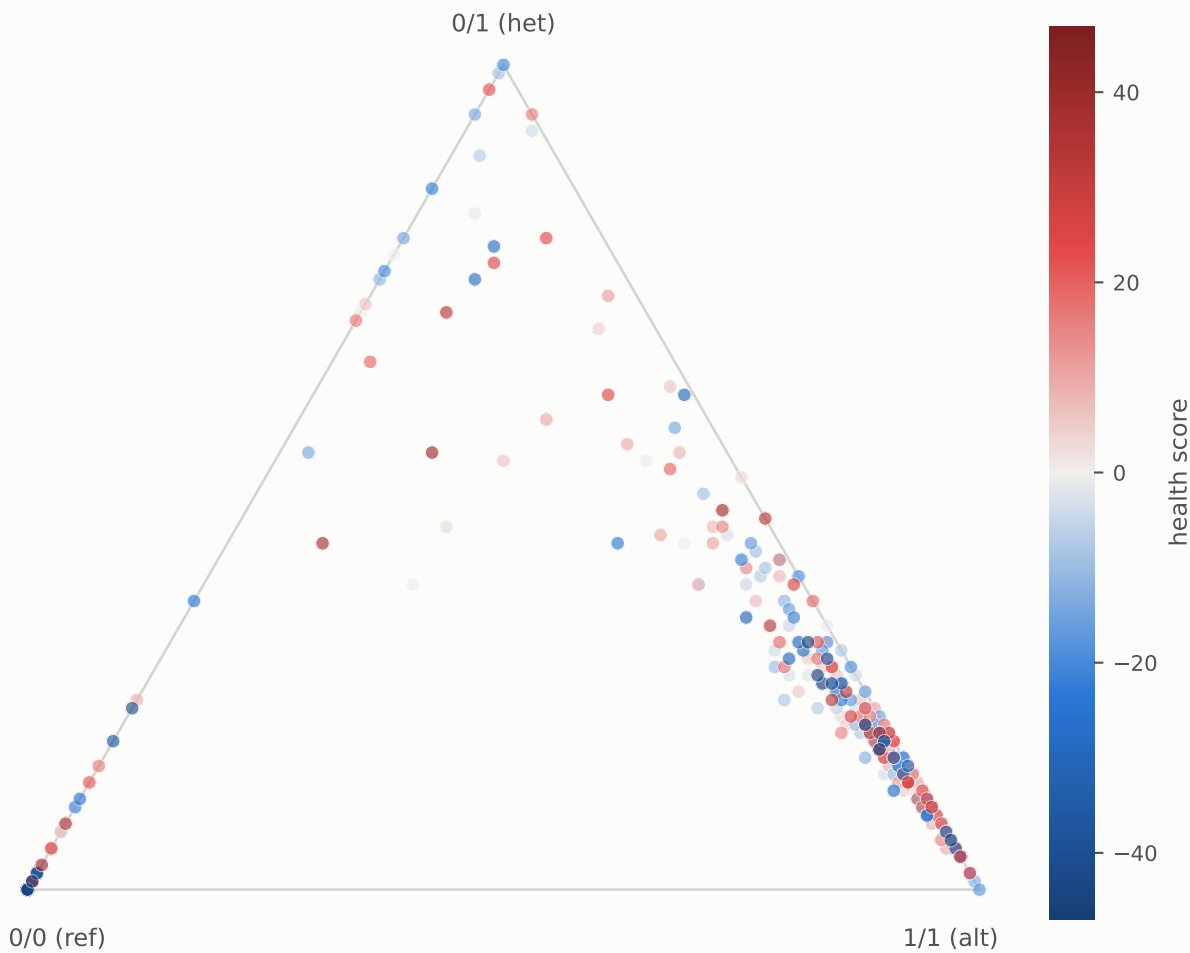
#127 by genotype uncertainty CHR_21:8,793,788 A>G
AF=0.54 DR2=0.81 $r=-0.052$ $\bar{H}=0.396$ $F=0.8$



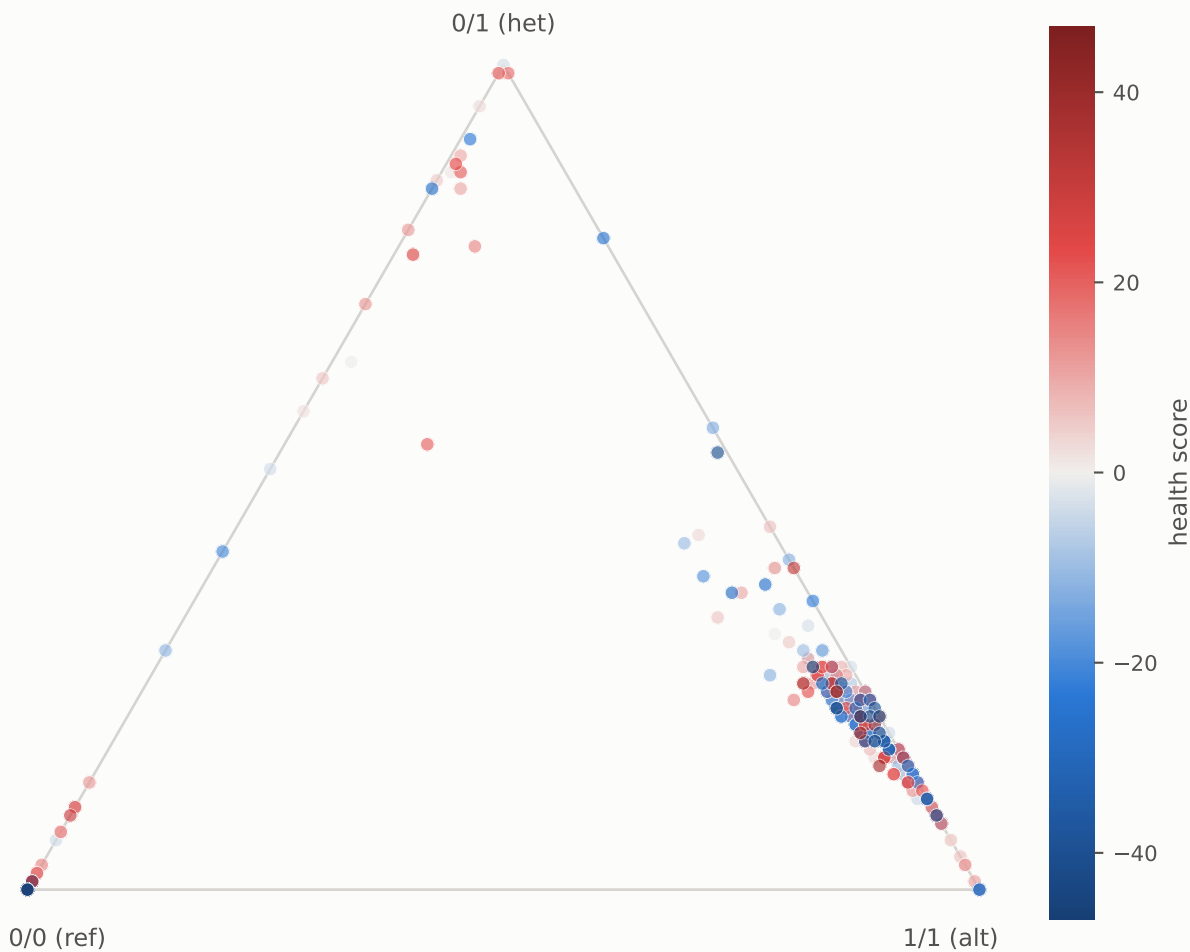
#128 by genotype uncertainty CHR_06:7,938,686 G>A
AF=0.58 DR2=0.81 $r=-0.086$ $\bar{H}=0.396$ $F=2.0$



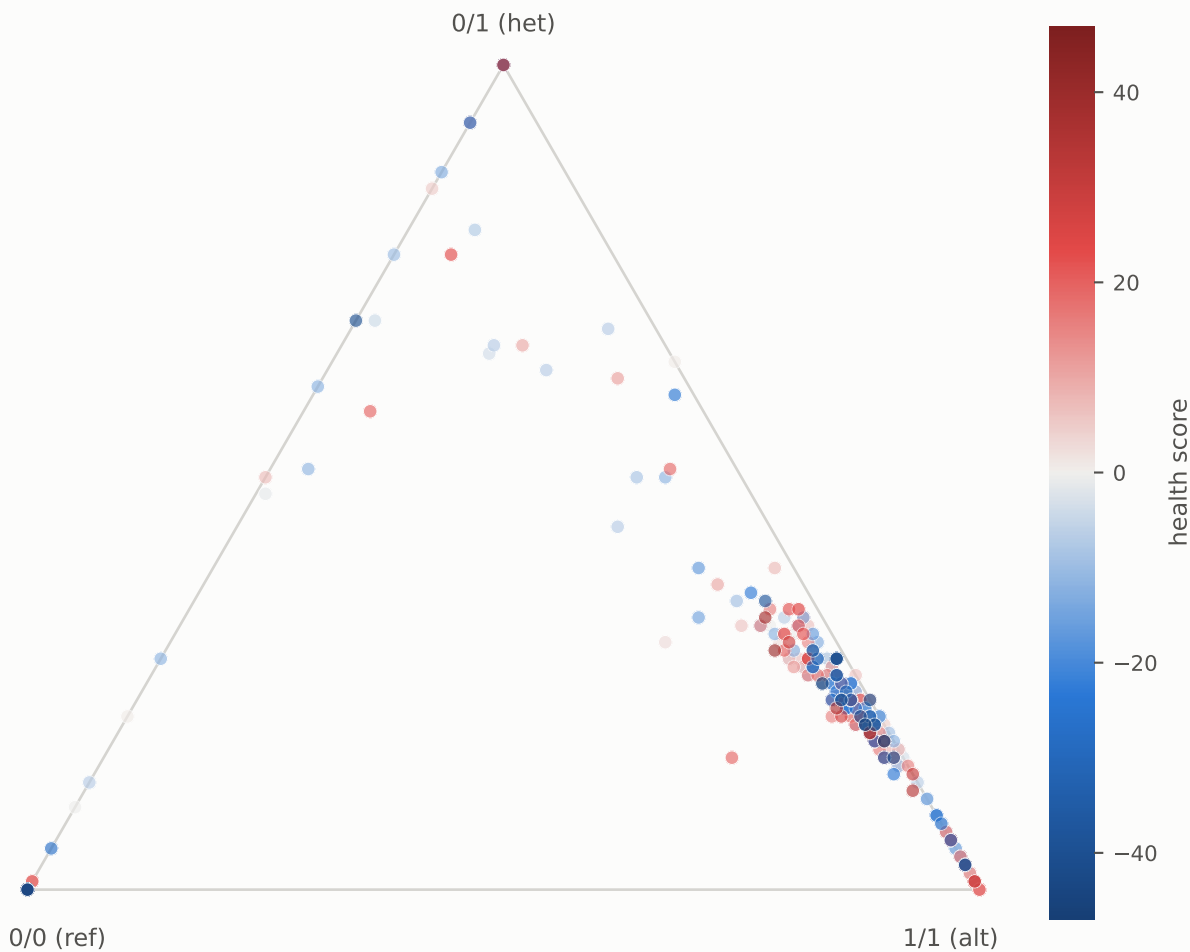
#129 by genotype uncertainty CHR_14:16,463,931 C>T
AF=0.58 DR2=0.81 $r=+0.038$ $\bar{H}=0.396$ F=0.3



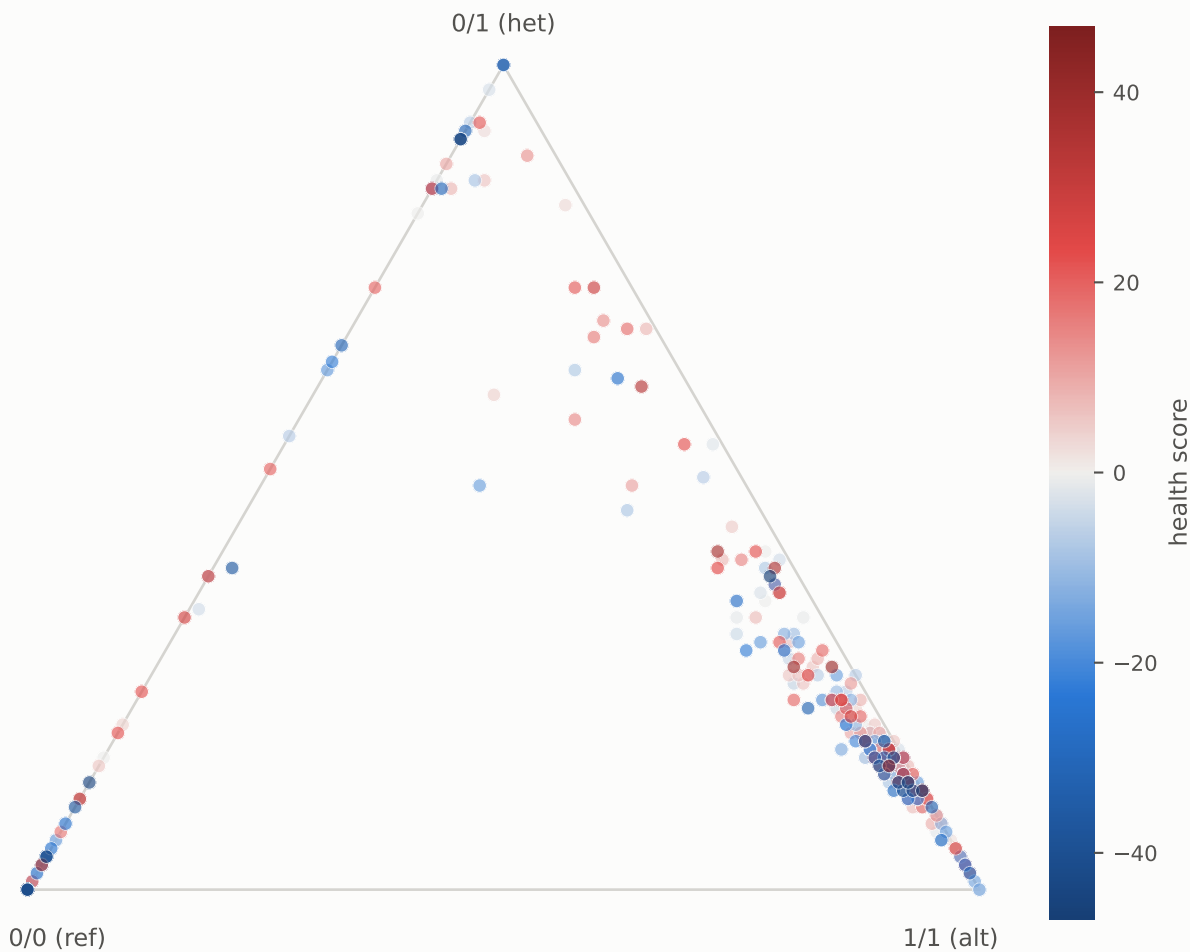
#130 by genotype uncertainty CHR_19:637,186 T>C
AF=0.53 DR2=0.83 r=-0.092 H=0.396 F=1.8



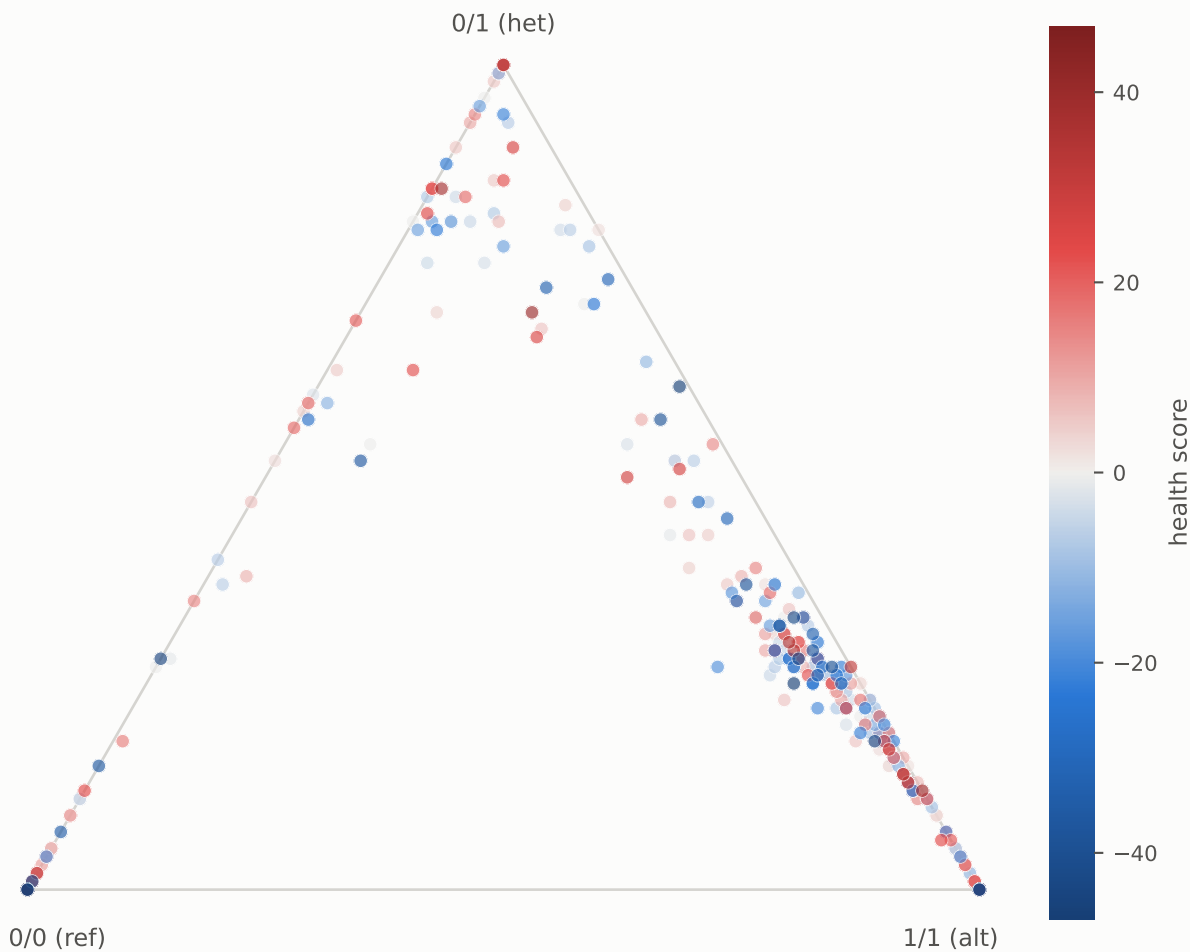
#131 by genotype uncertainty CHR_21:17,092,498 A>C
AF=0.52 DR2=0.82 $r=-0.124$ $\bar{H}=0.396$ F=4.4



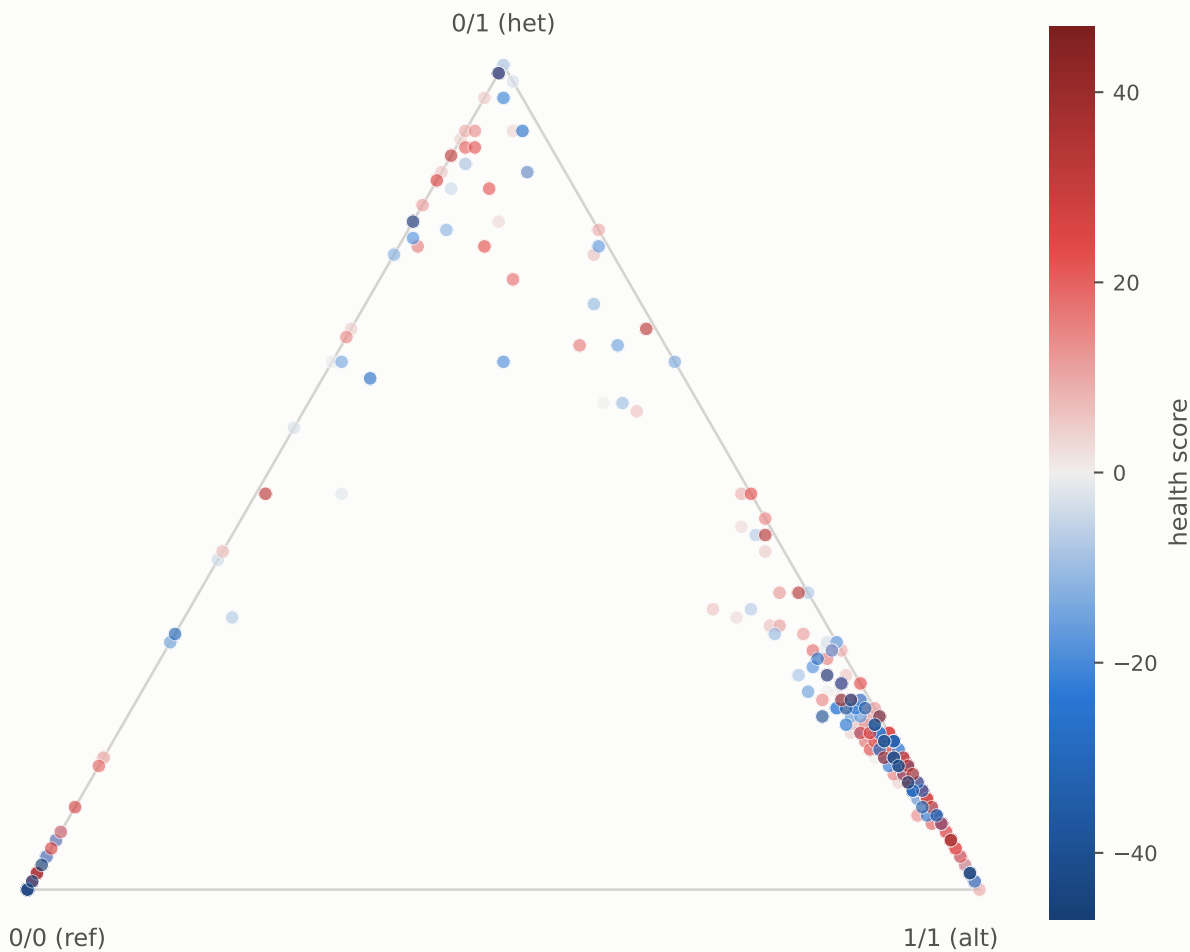
#132 by genotype uncertainty CHR_11:23,428,565 C>G
AF=0.58 DR2=0.81 $r=+0.012$ $\bar{H}=0.396$ F=0.1



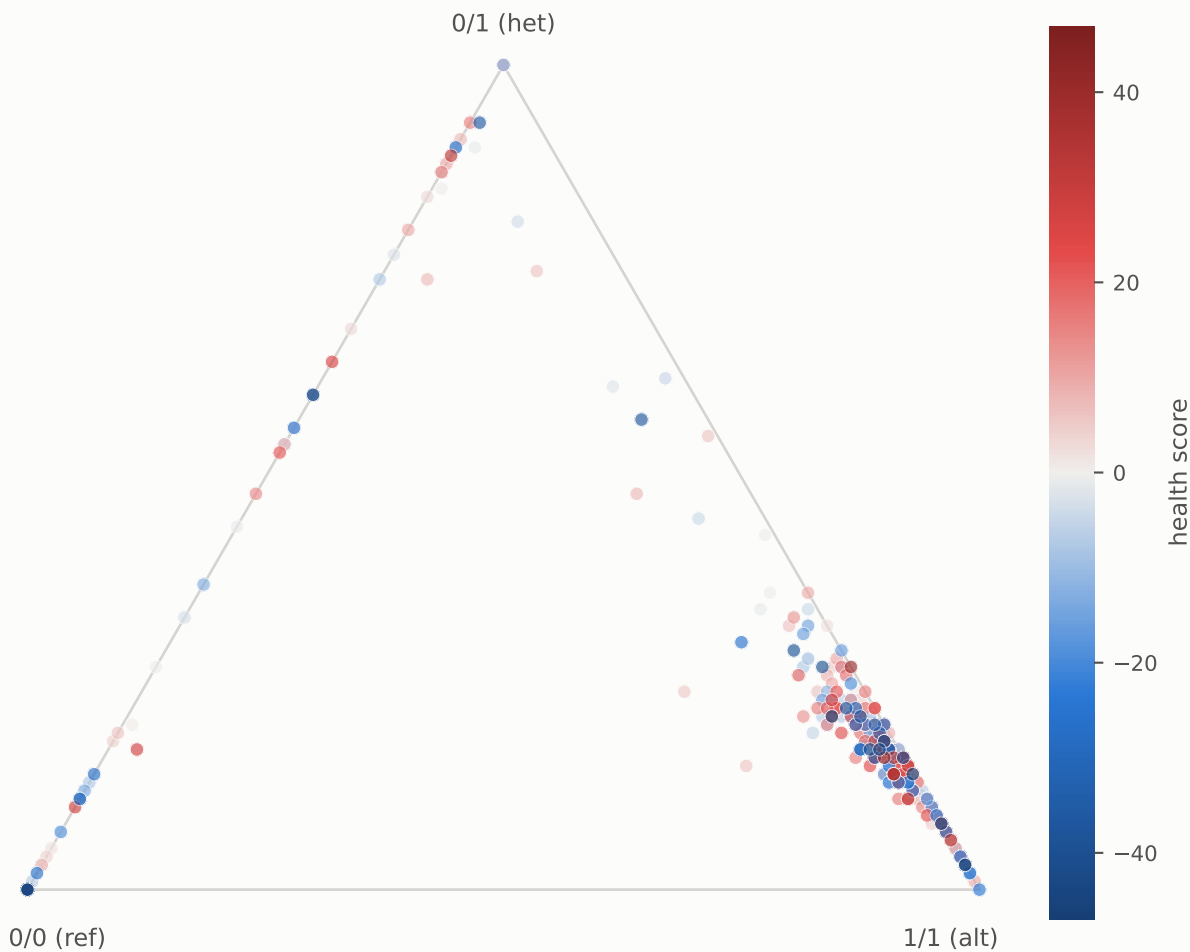
#133 by genotype uncertainty CHR_22:16,865,485 T>C
AF=0.48 DR2=0.82 $r=-0.085$ $\bar{H}=0.396$ F=2.0



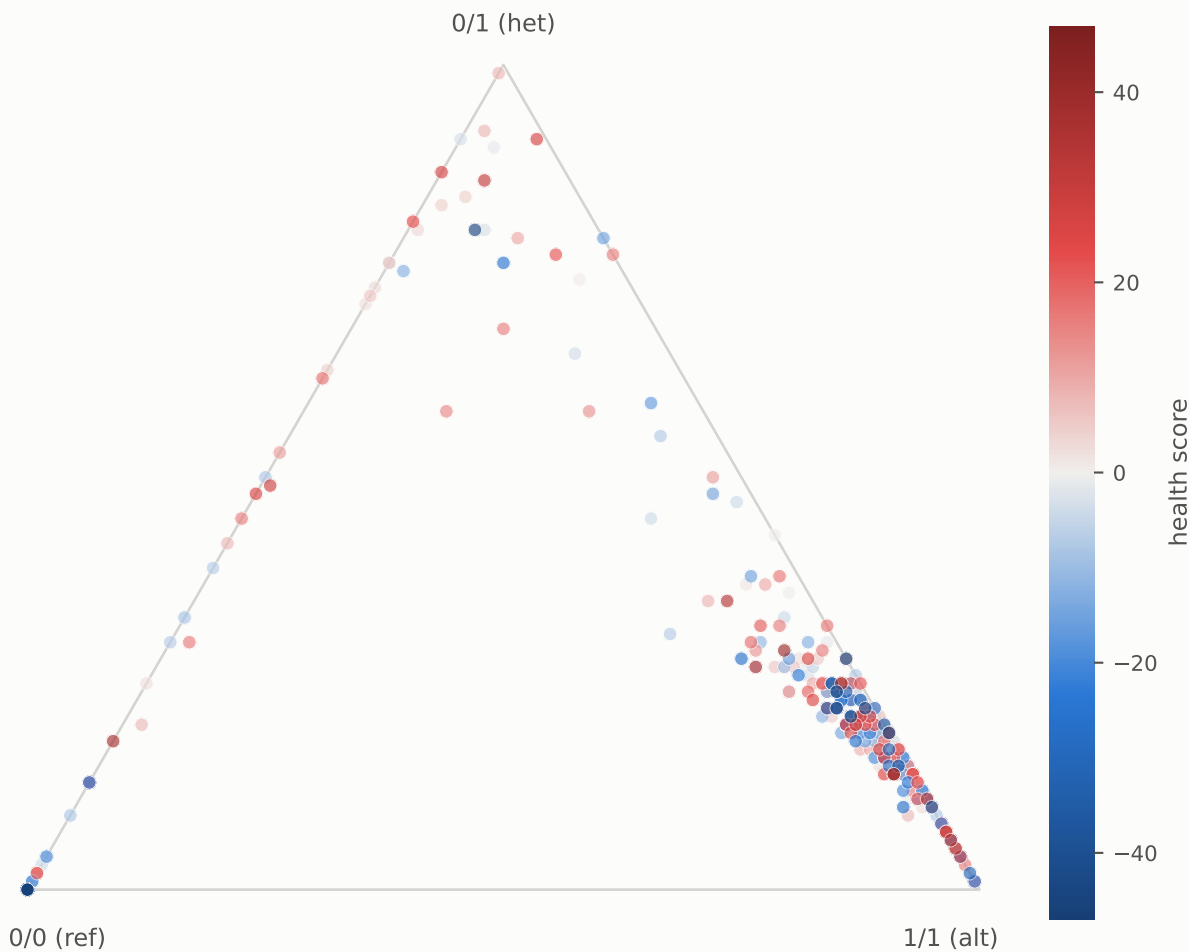
#134 by genotype uncertainty CHR_09:35,475,751 T>C
AF=0.63 DR2=0.81 r=-0.040 $\bar{H}$ =0.396 F=0.4



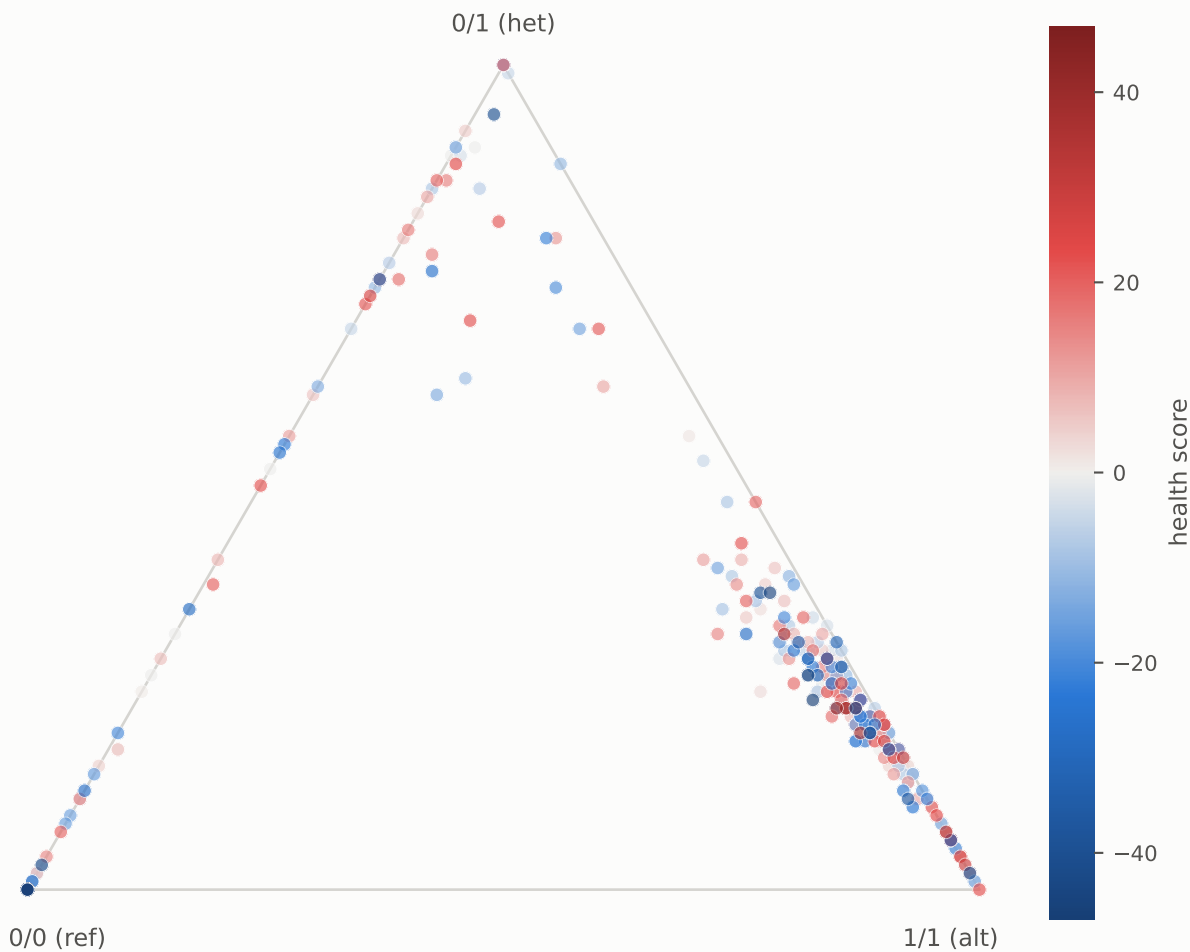
#135 by genotype uncertainty CHR_15:20,831,432 G>T
AF=0.62 DR2=0.81 $r=+0.052$ $\bar{H}=0.396$ F=0.7



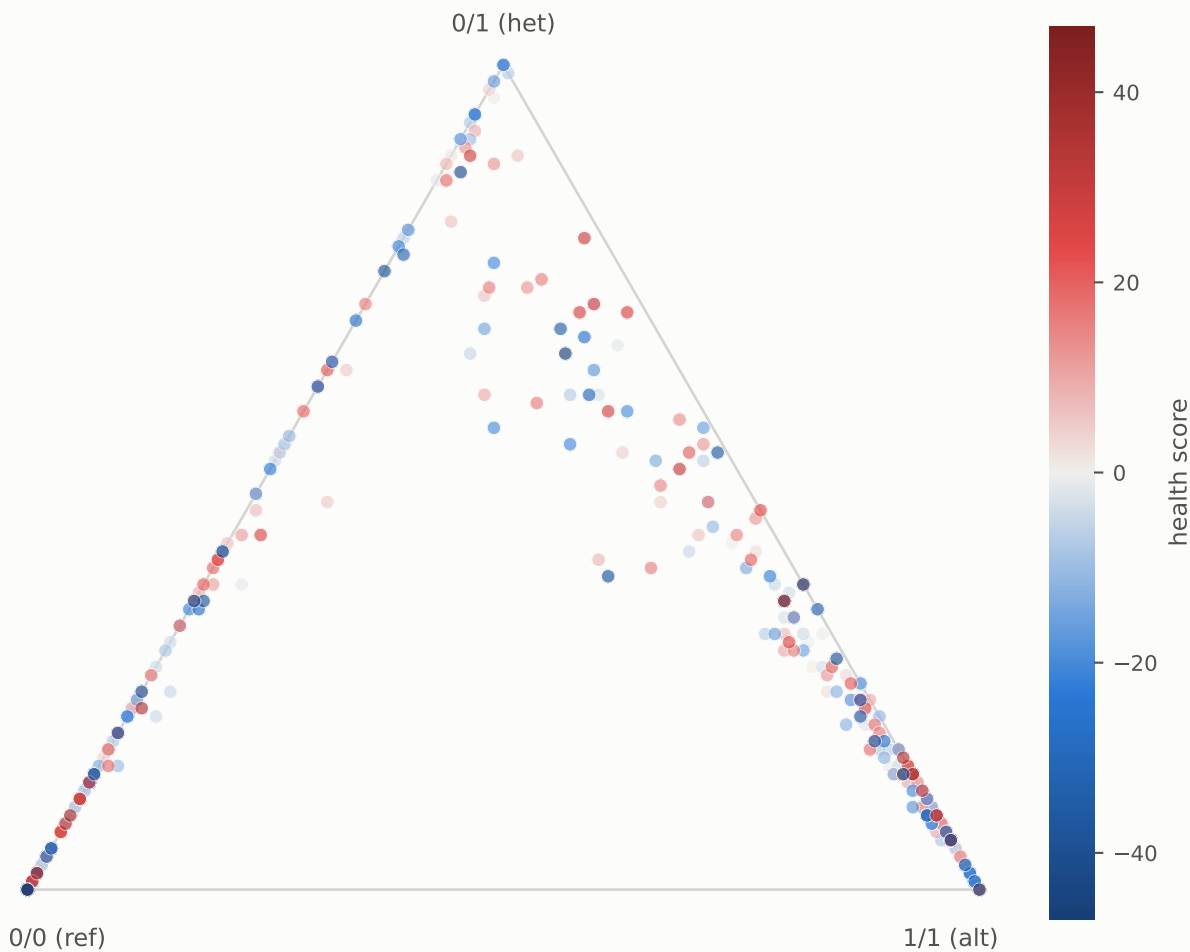
#136 by genotype uncertainty CHR_11:30,680,916 T>C
AF=0.57 DR2=0.81 $r=+0.065$ $\bar{H}=0.395$ F=1.8



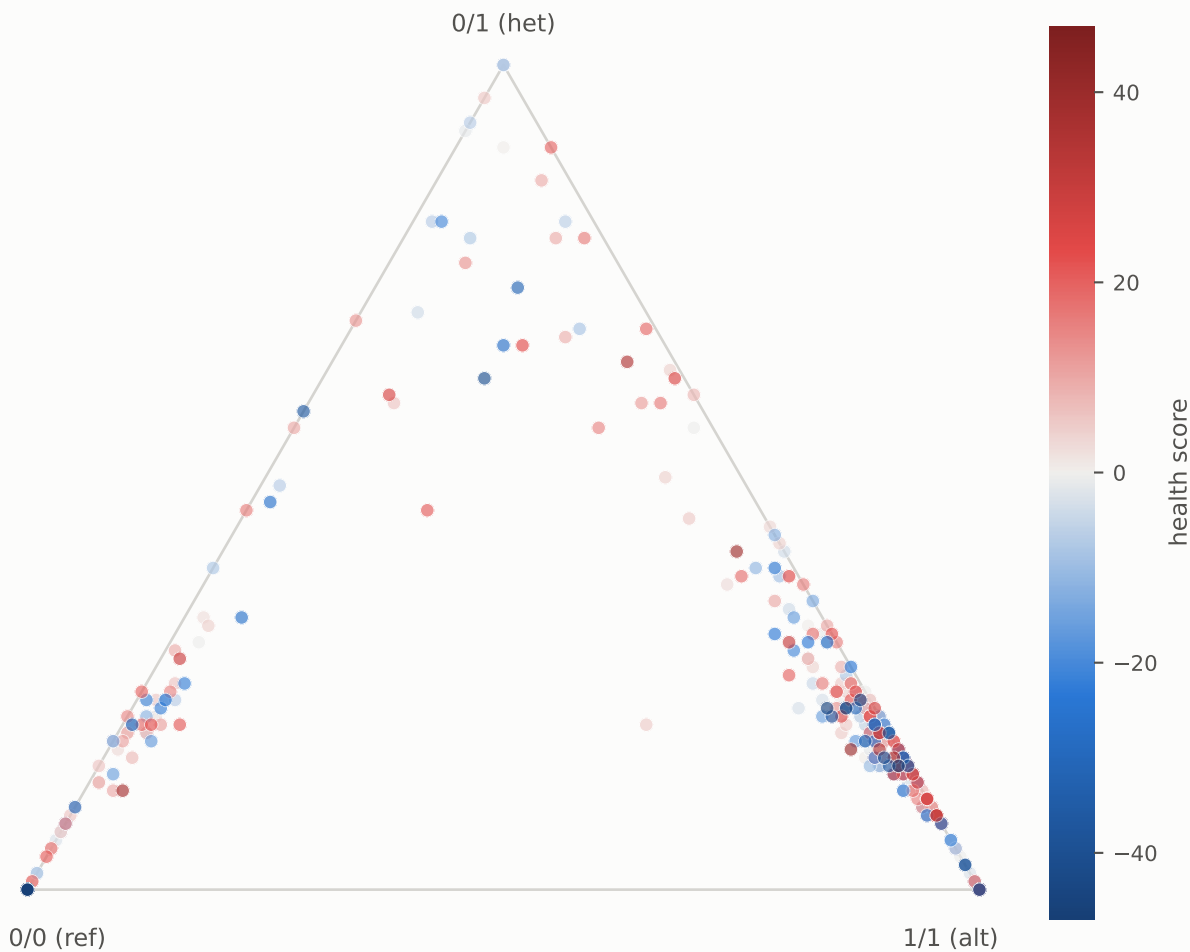
#137 by genotype uncertainty CHR_14:27,801,628 C>T
AF=0.51 DR2=0.81 r=-0.016 $\bar{H}$ =0.395 F=0.2



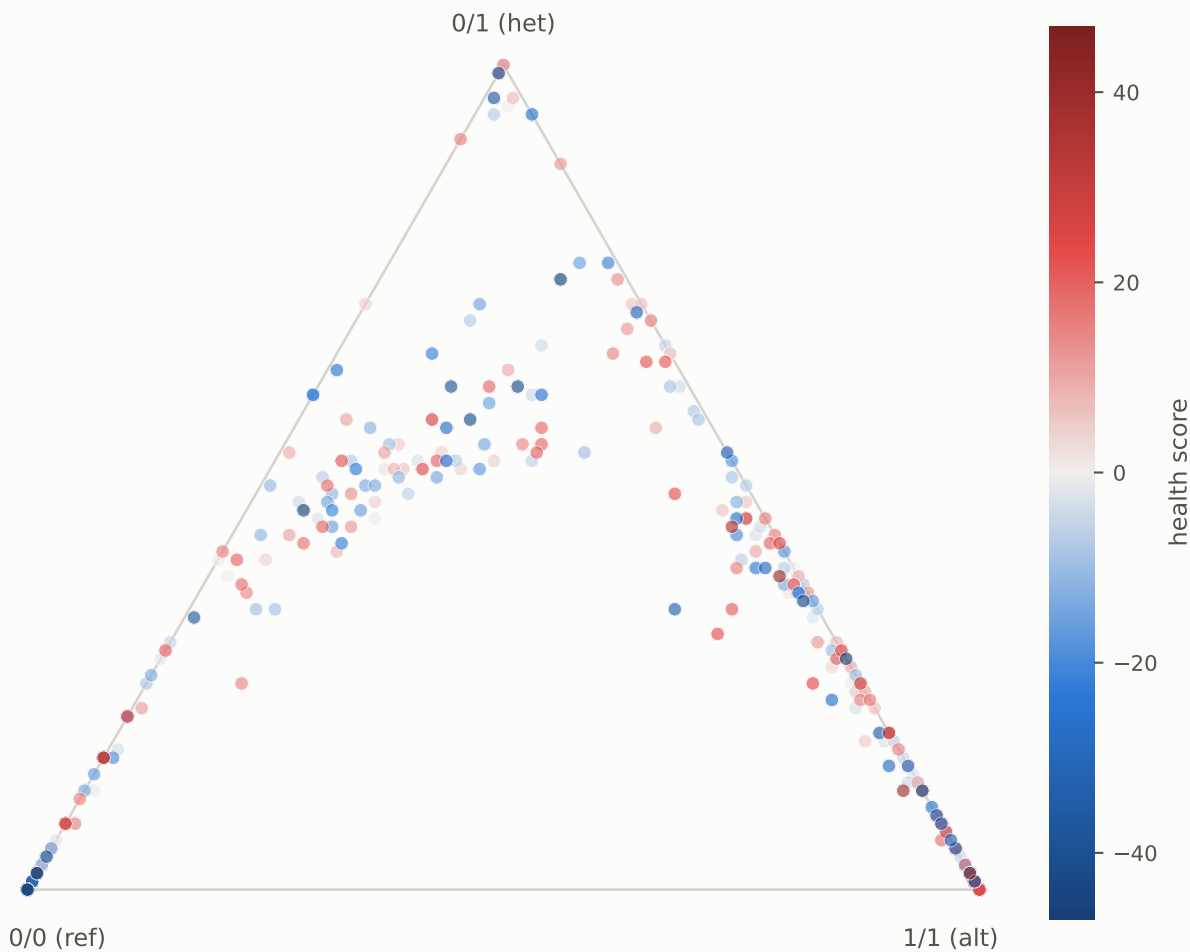
#138 by genotype uncertainty CHR_06:11,676,679 A>C
AF=0.45 DR2=0.81 $r=-0.076$ $\bar{H}=0.395$ F=2.4



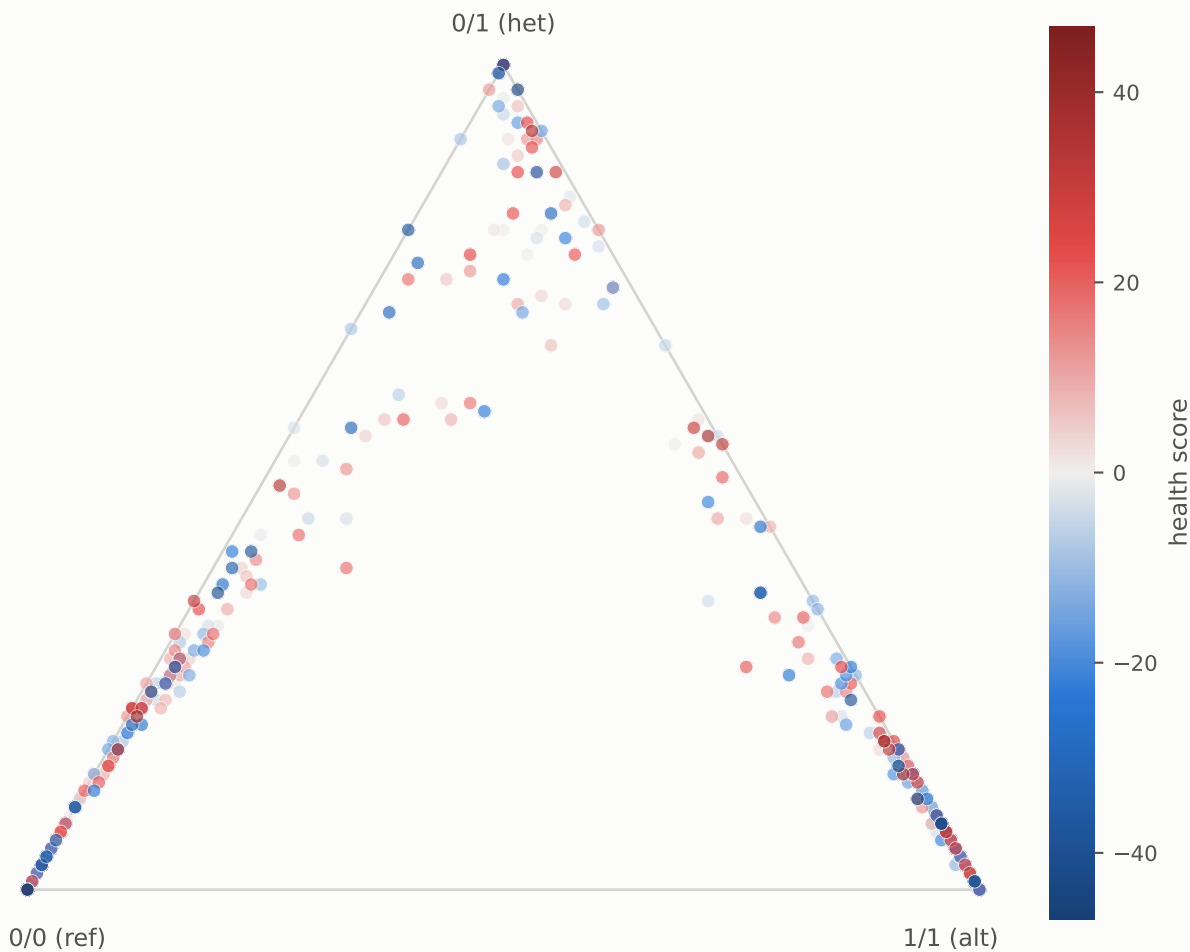
#139 by genotype uncertainty CHR_22:5,002,877 T>C
AF=0.55 DR2=0.81 $r=+0.030$ $H=0.395$ $F=0.8$



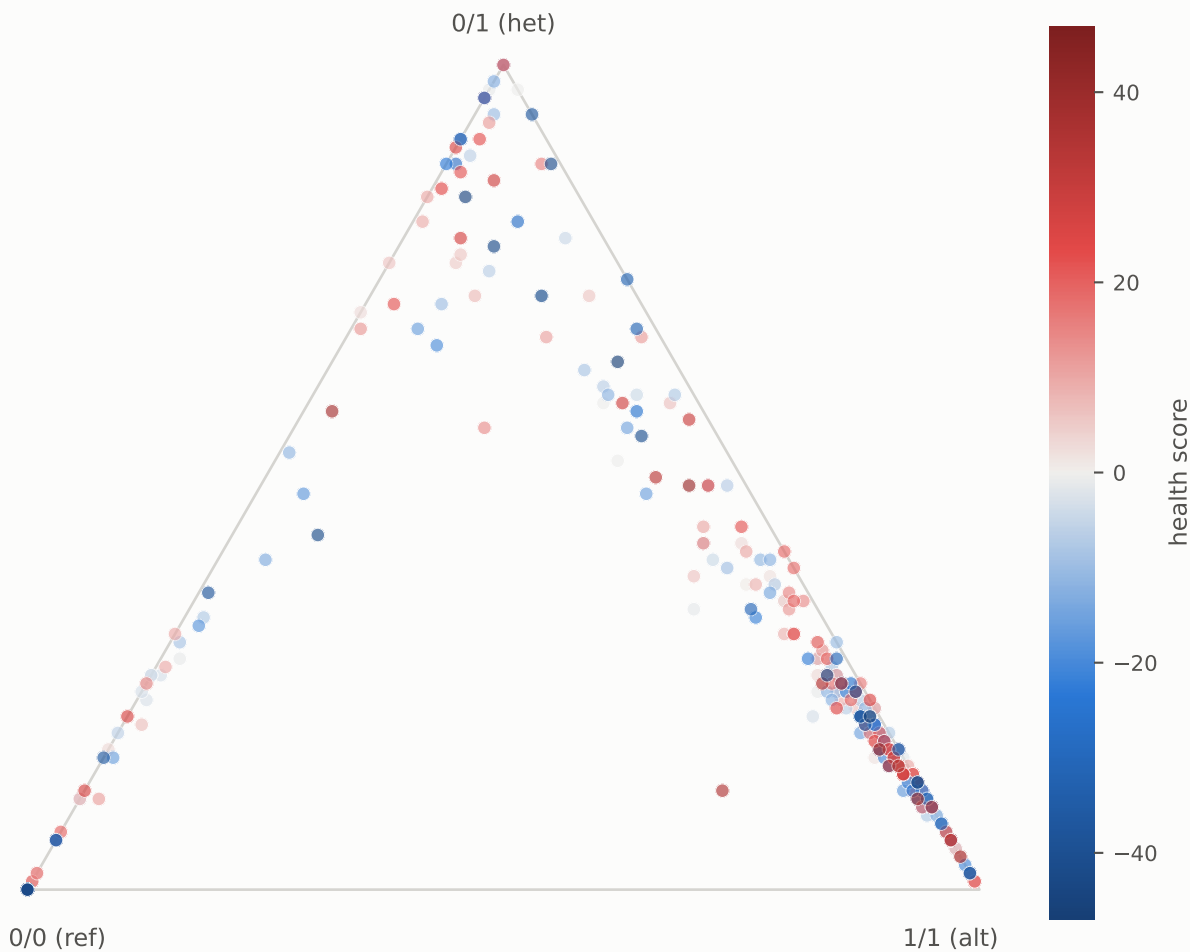
#140 by genotype uncertainty CHR_22:2,643,928 T>C
AF=0.46 DR2=0.81 $r=+0.008$ $\bar{H}=0.395$ $F=2.3$



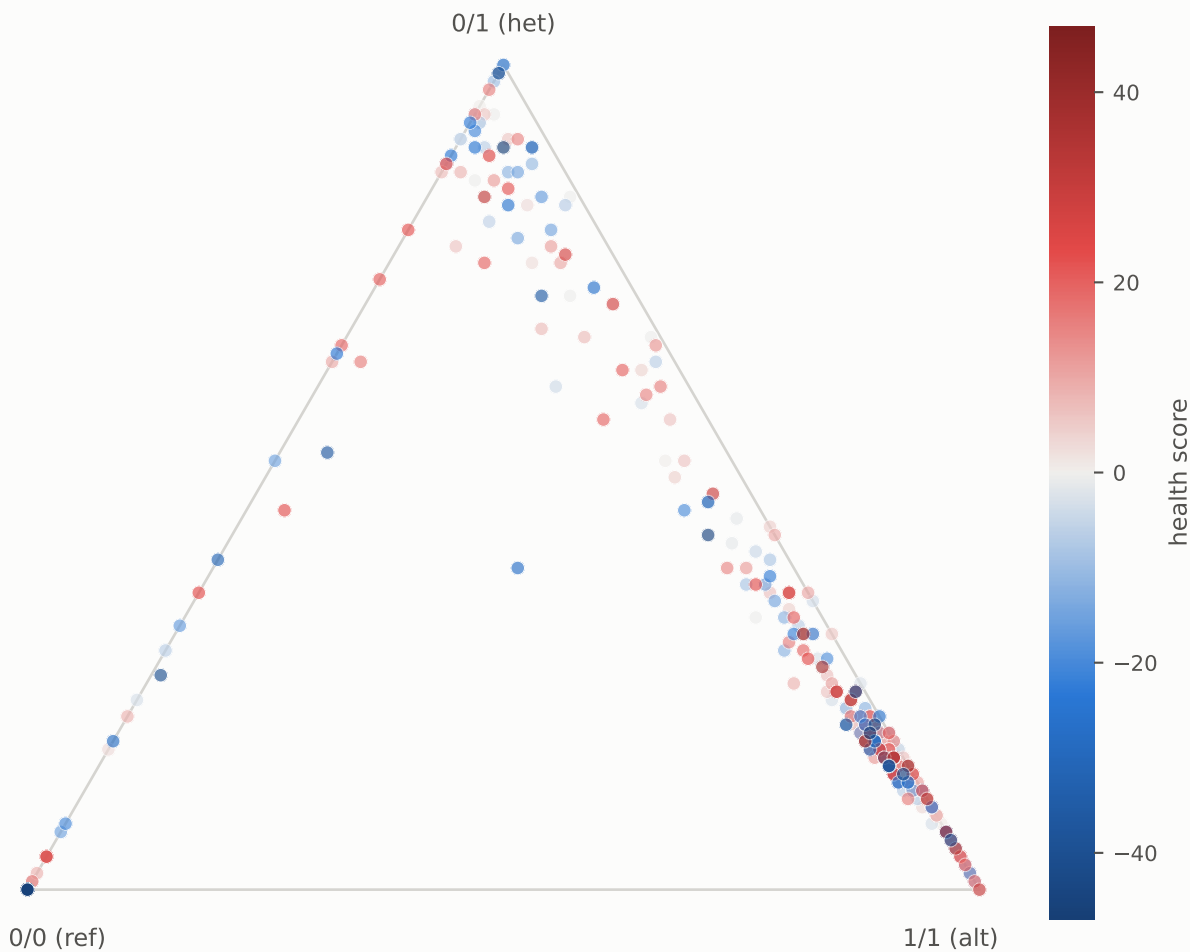
#141 by genotype uncertainty CHR_21:20,530,751 G>A
AF=0.51 DR2=0.81 $r=-0.035$ $\bar{H}=0.395$ F=0.8



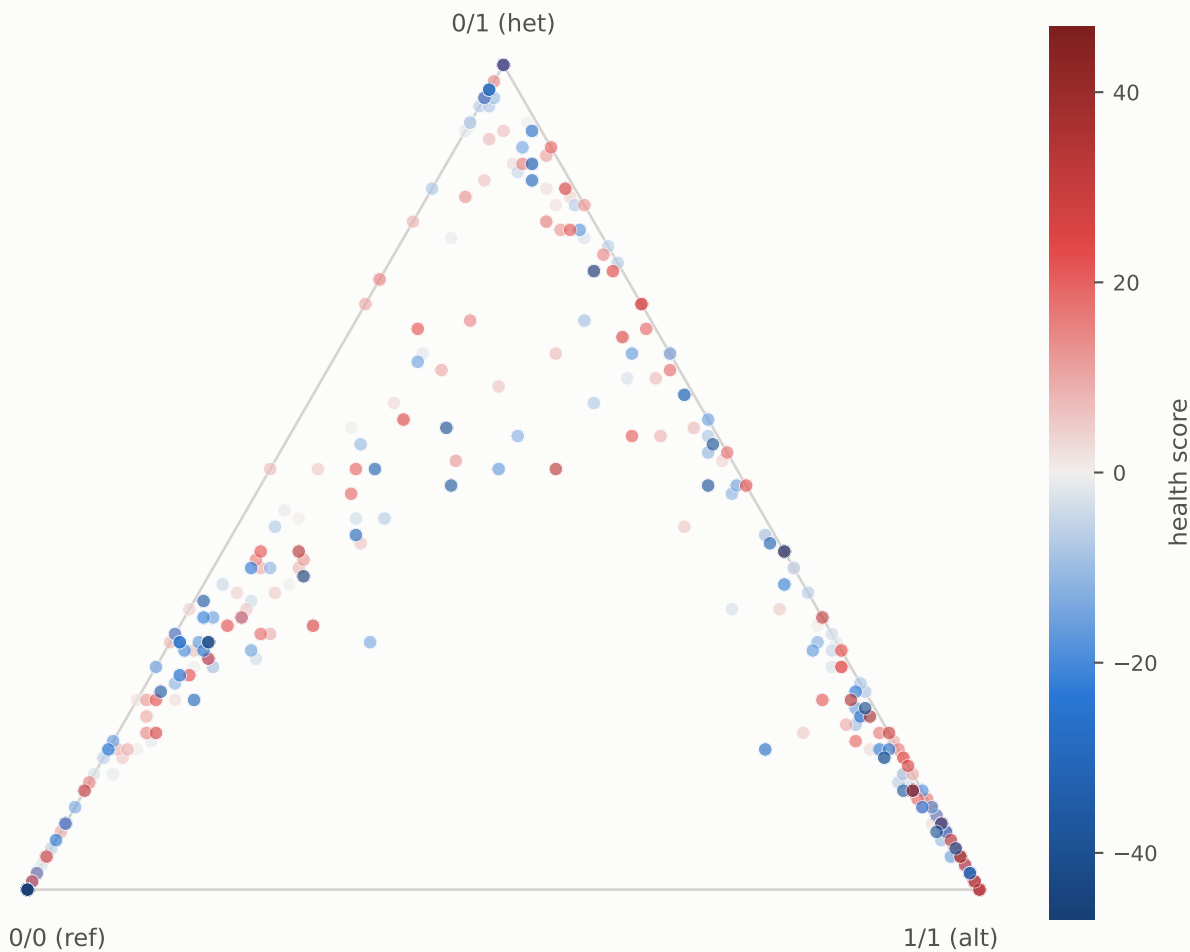
#142 by genotype uncertainty CHR_18:2,046,824 T>G
AF=0.51 DR2=0.81 $r=+0.007$ $\bar{H}=0.395$ F=1.0



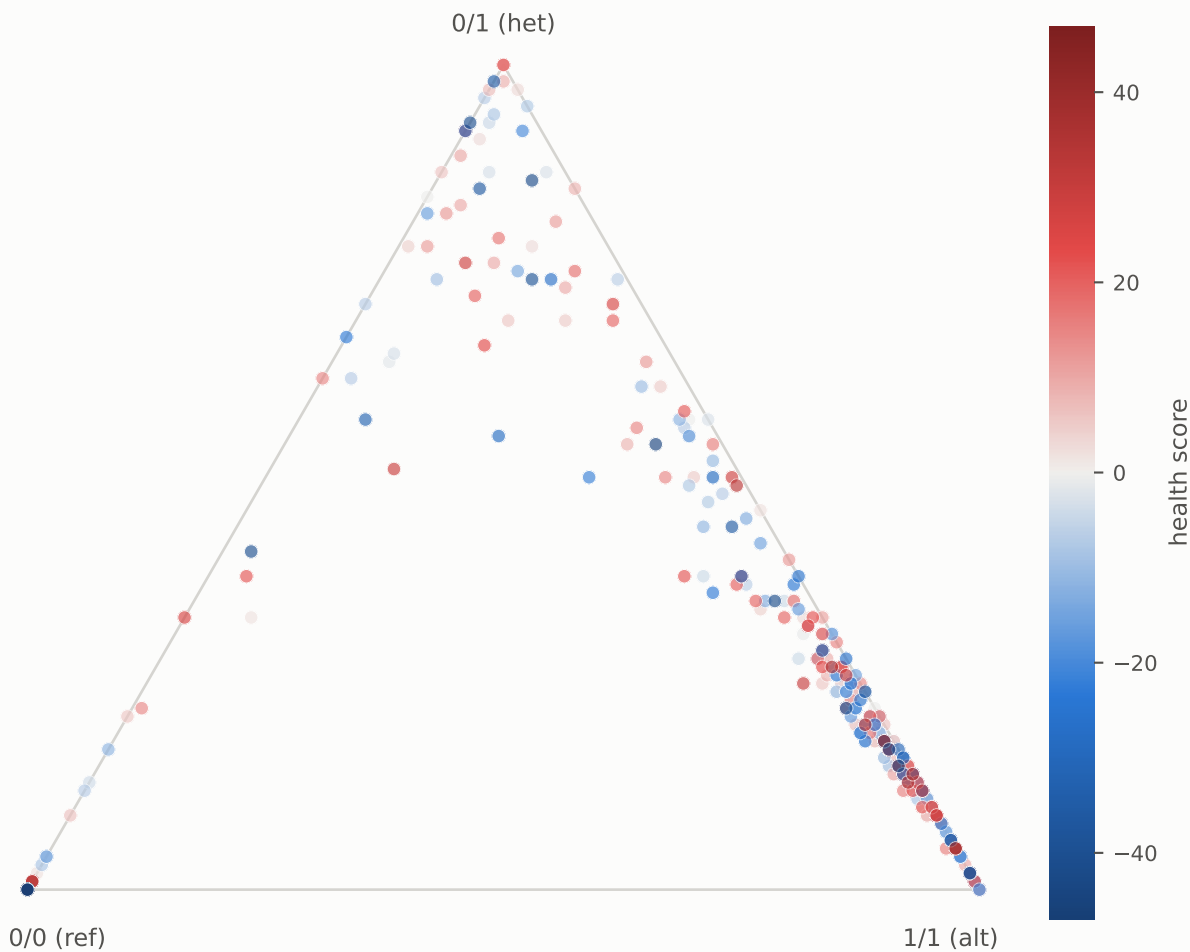
#143 by genotype uncertainty CHR_05:23,236,576 G>T
AF=0.57 DR2=0.81 $r=+0.084$ $\bar{H}=0.395$ F=1.3



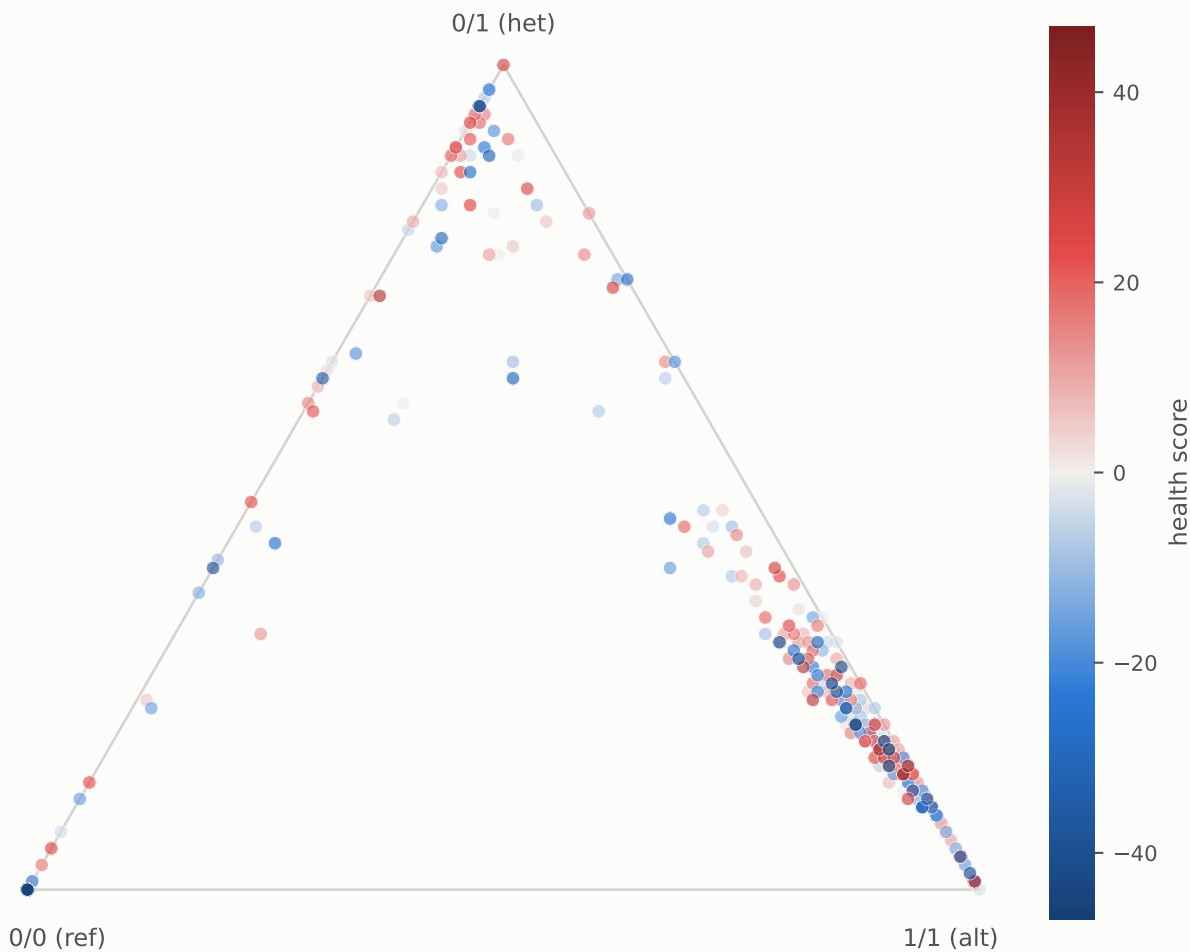
#144 by genotype uncertainty CHR_16:7,234,438 A>G
AF=0.44 DR2=0.81 $r=-0.031$ $\bar{H}=0.395$ $F=0.1$



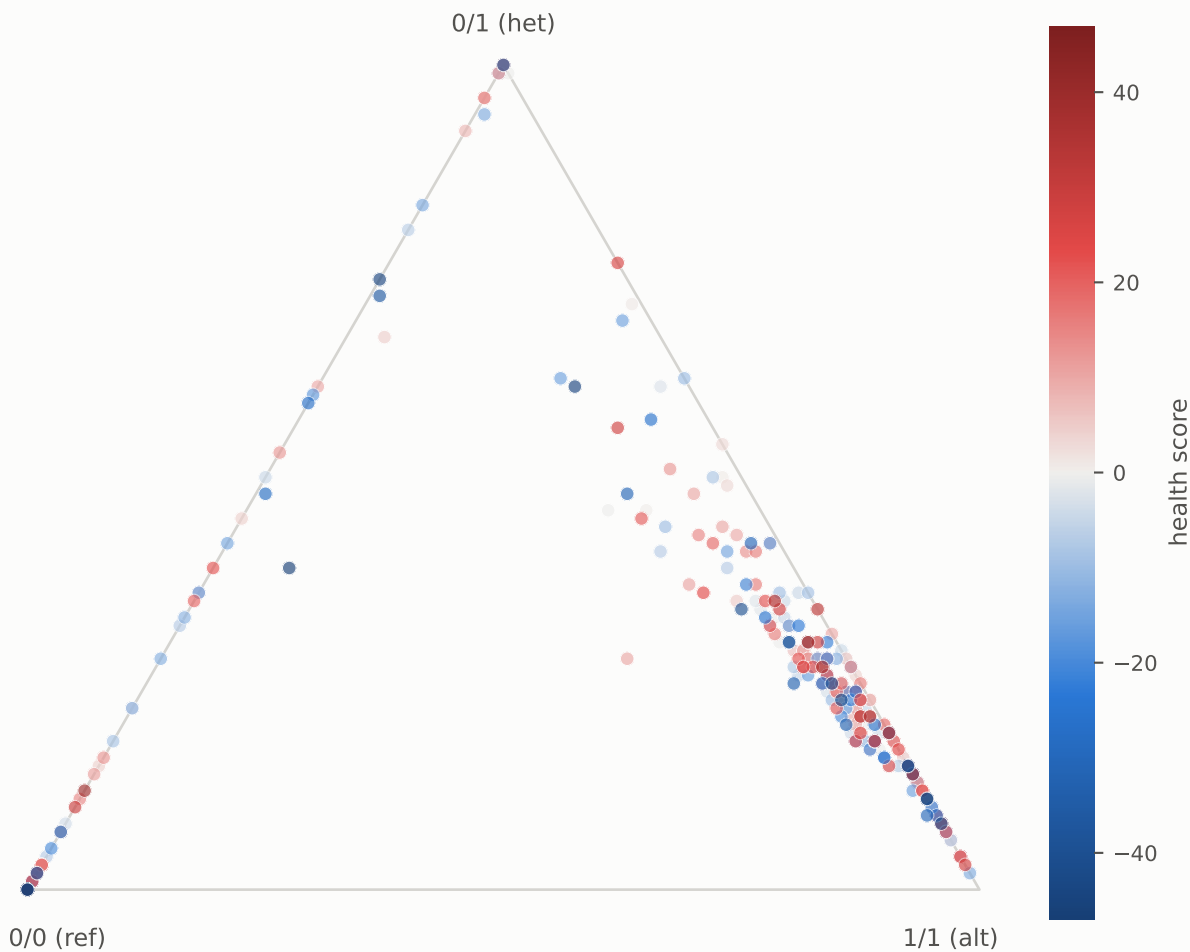
#145 by genotype uncertainty CHR_13:22,761,917 T>G
AF=0.57 DR2=0.82 $r=-0.014$ $\bar{H}=0.395$ F=0.3



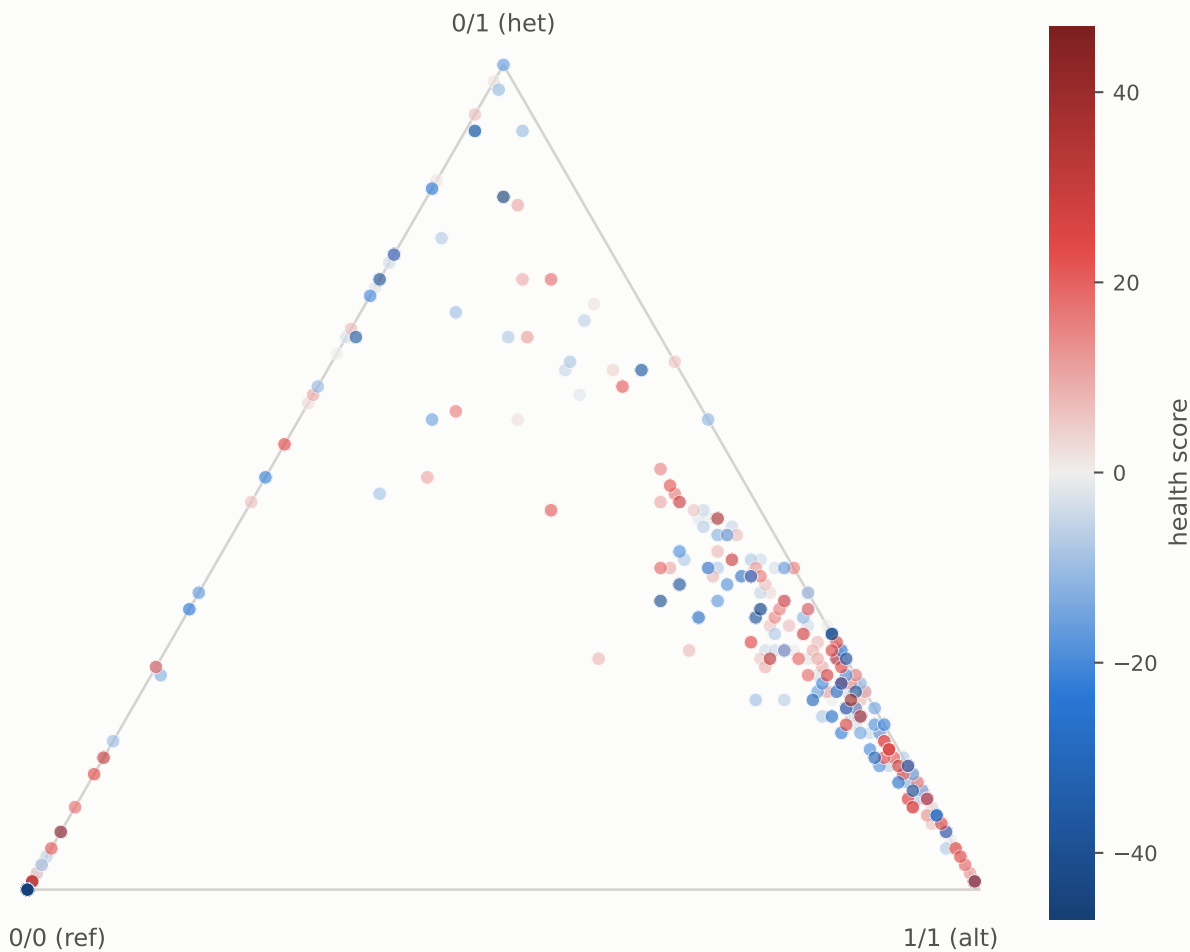
#146 by genotype uncertainty CHR_09:11,981,686 G>T
AF=0.52 DR2=0.81 r=-0.005 $\bar{H}$ =0.395 F=0.0



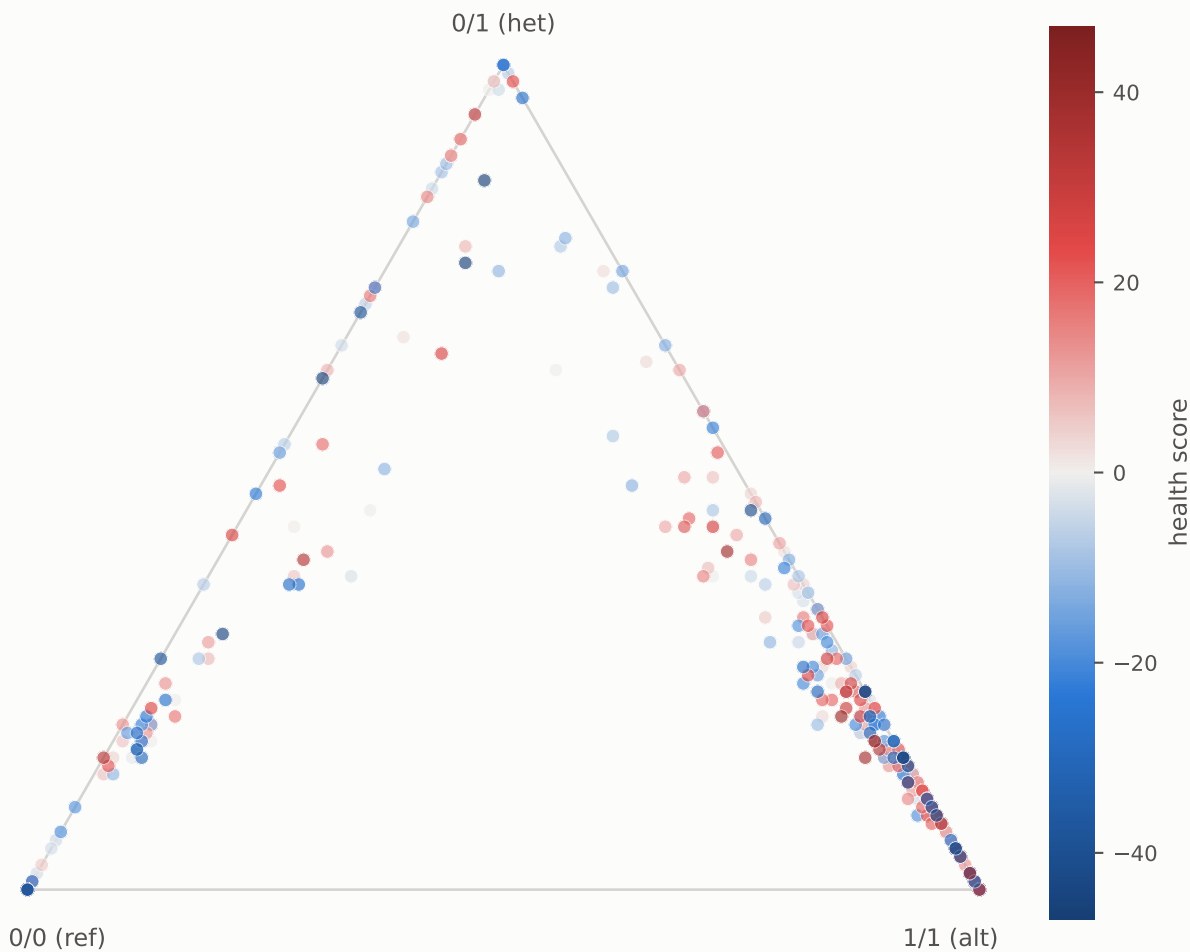
#147 by genotype uncertainty CHR_19:21,146,444 C>T
AF=0.49 DR2=0.81 $r=+0.045$ $\bar{H}=0.395$ F=1.6



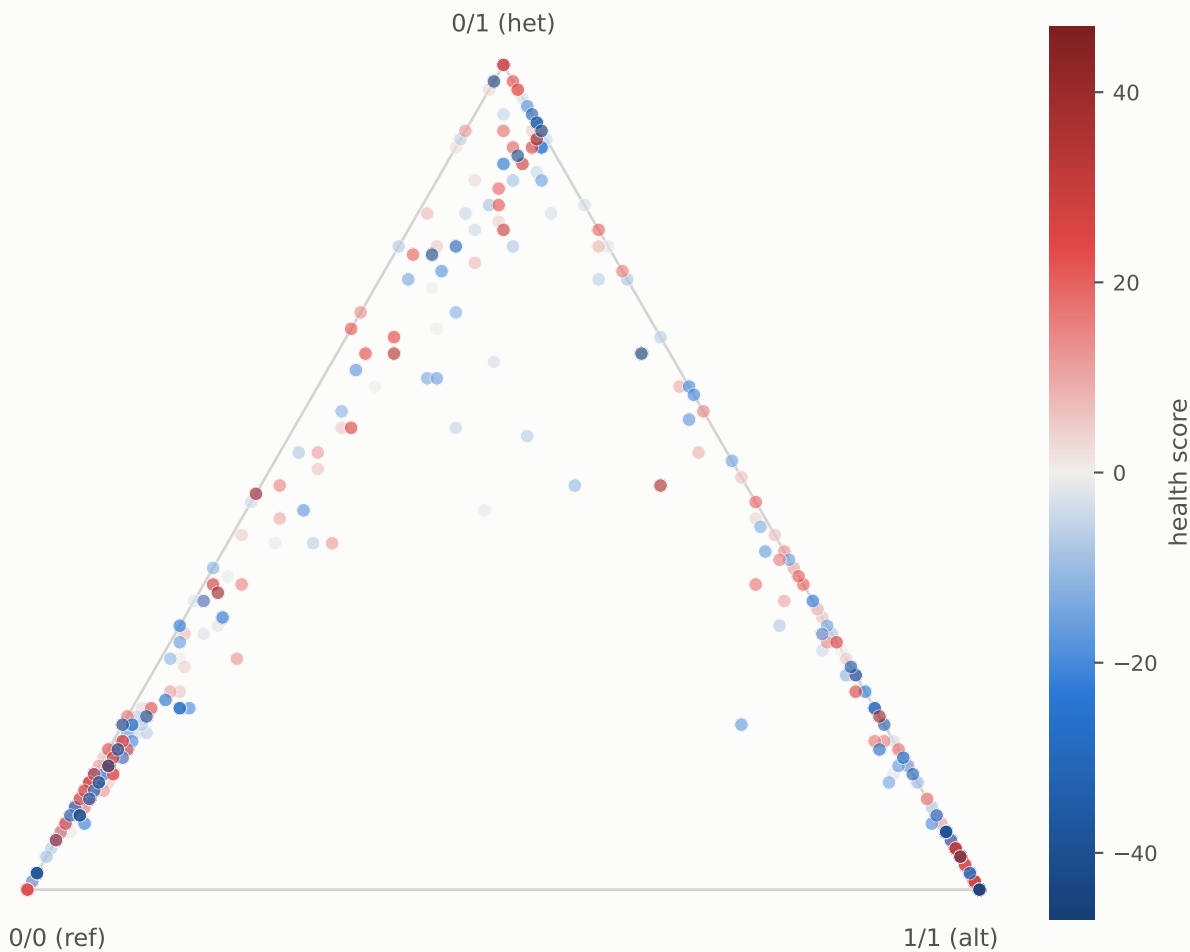
#148 by genotype uncertainty CHR_05:16,905,760 T>C
AF=0.46 DR2=0.81 $r=+0.007$ $\bar{H}=0.395$ F=0.4



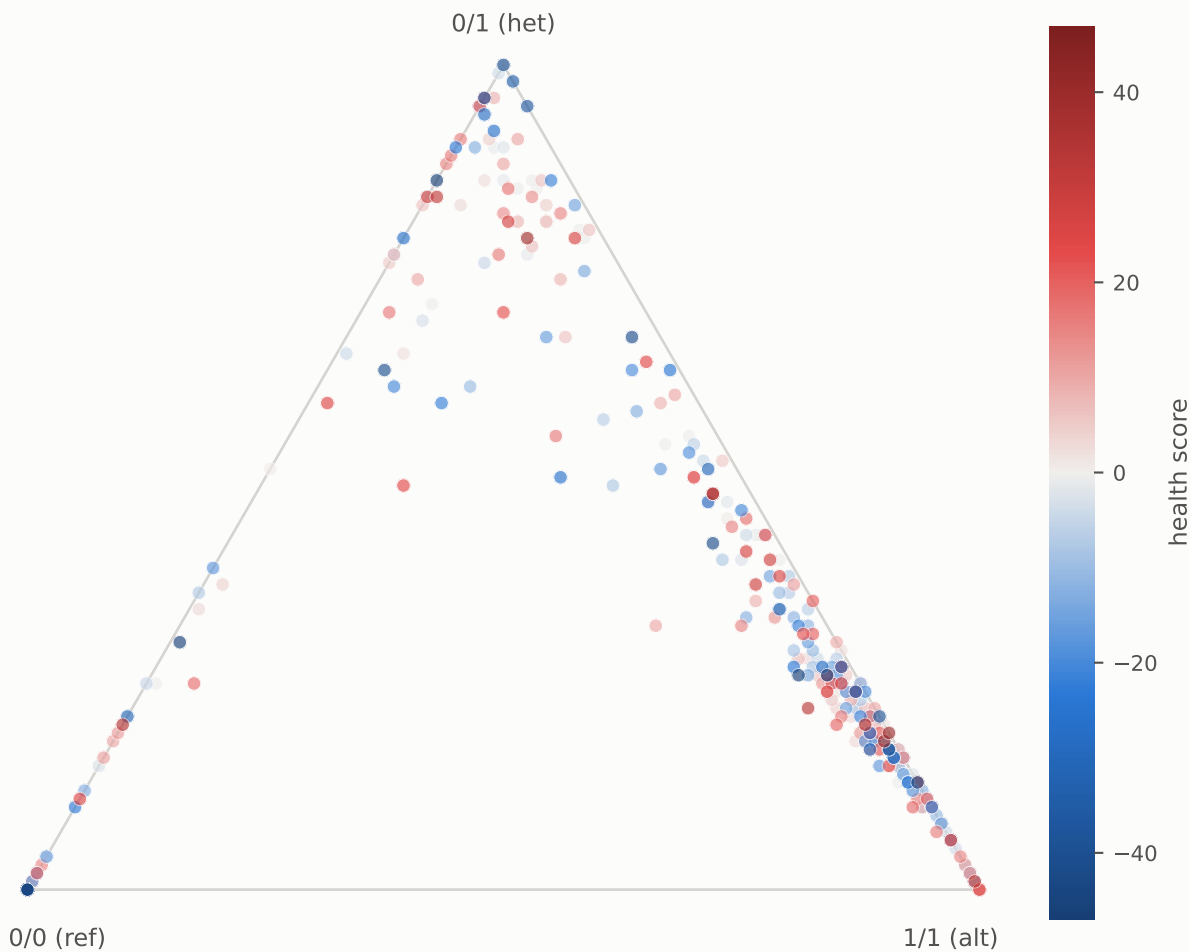
#149 by genotype uncertainty CHR_10:465,288 T>A
AF=0.58 DR2=0.81 $r=+0.065$ $H=0.394$ $F=1.9$



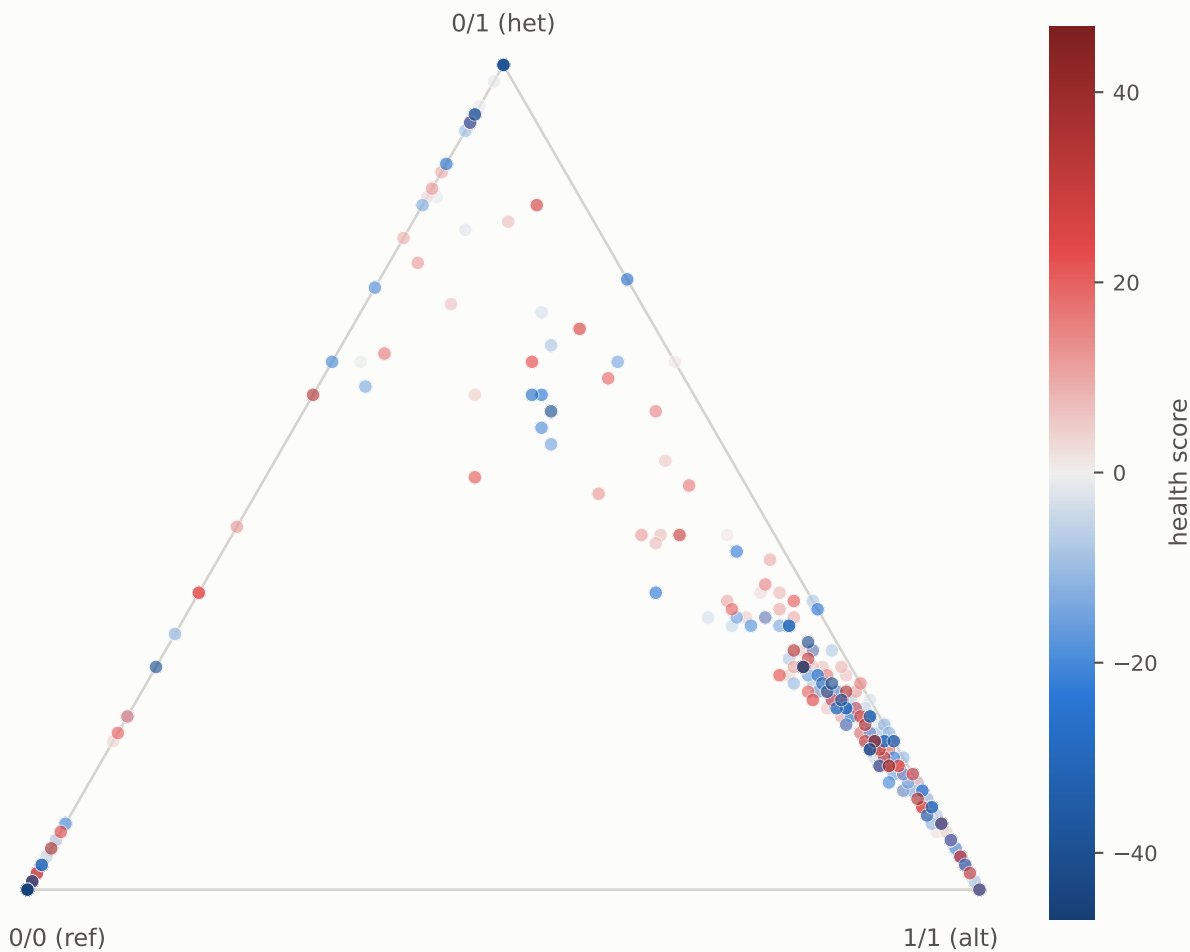
#150 by genotype uncertainty unpl-scaff_001:42,958 C>T
AF=0.55 DR2=0.81 $r=+0.007$ H=0.394 F=0.1



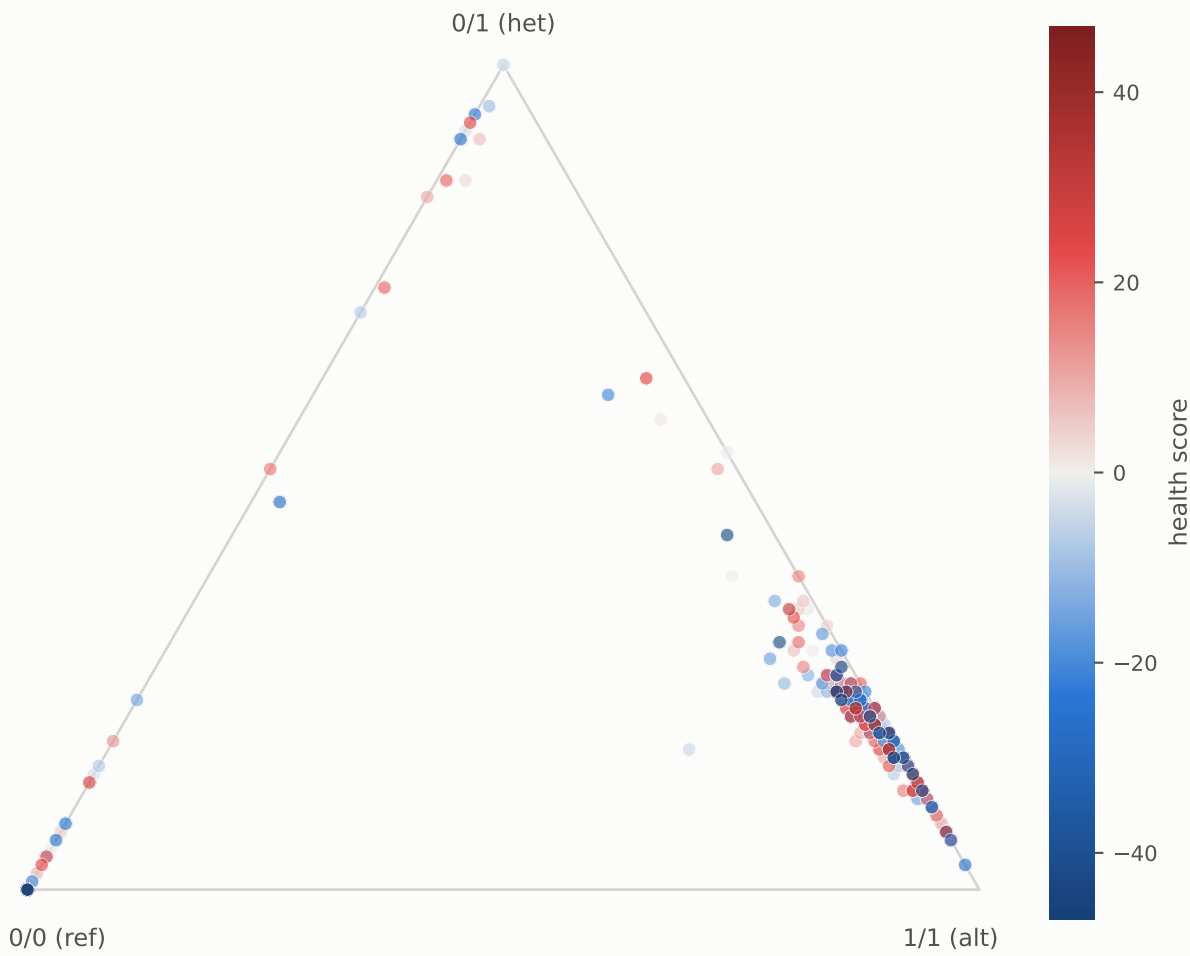
#151 by genotype uncertainty CHR_05:34,337,221 T>G
AF=0.5 DR2=0.81 $r=+0.001$ $\bar{H}=0.394$ F=0.0



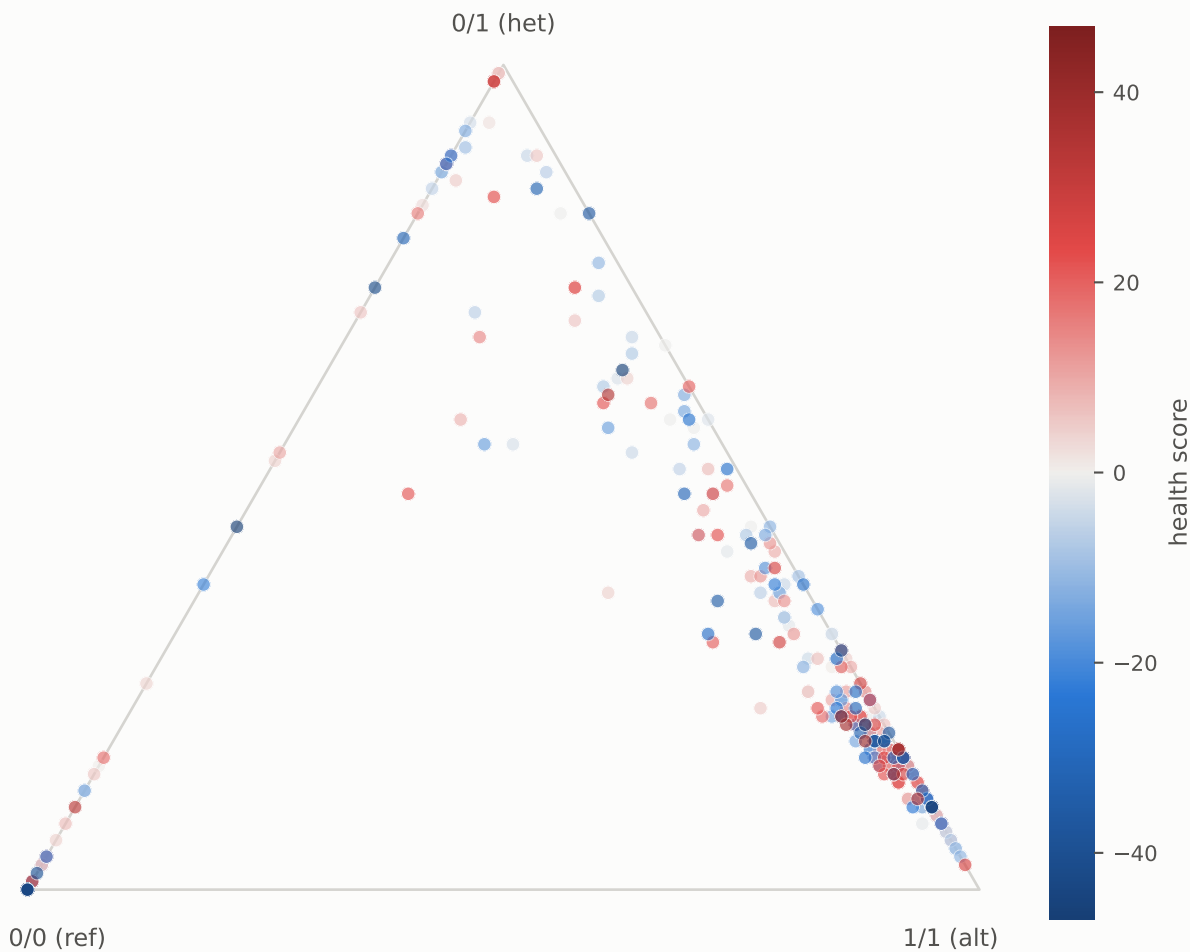
#152 by genotype uncertainty CHR_17:24,612,962 G>T
AF=0.56 DR2=0.81 $r=-0.071$ $\bar{H}=0.394$ F=2.0



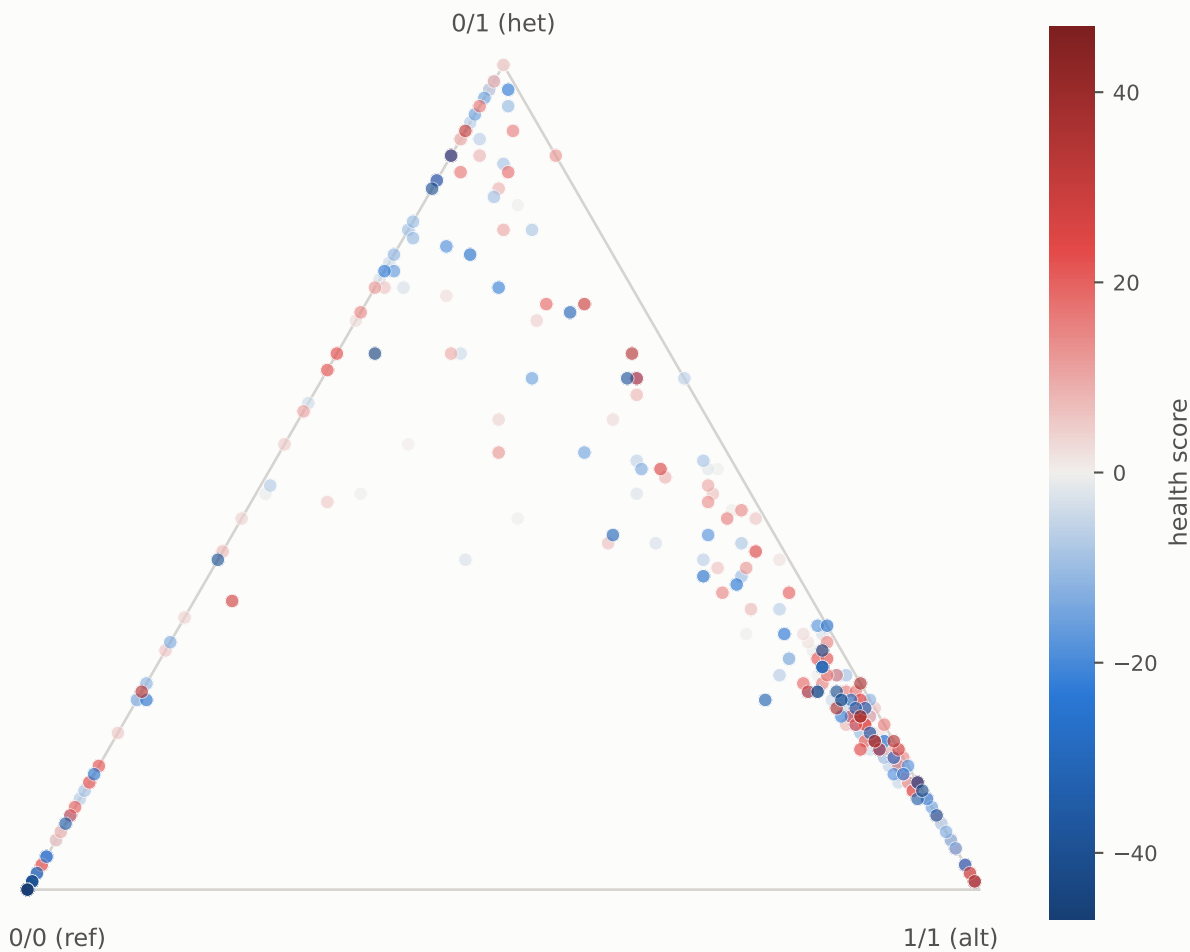
#153 by genotype uncertainty CHR_19:892,260 C>T
AF=0.62 DR2=0.81 $r=-0.011$ H=0.394 F=0.1



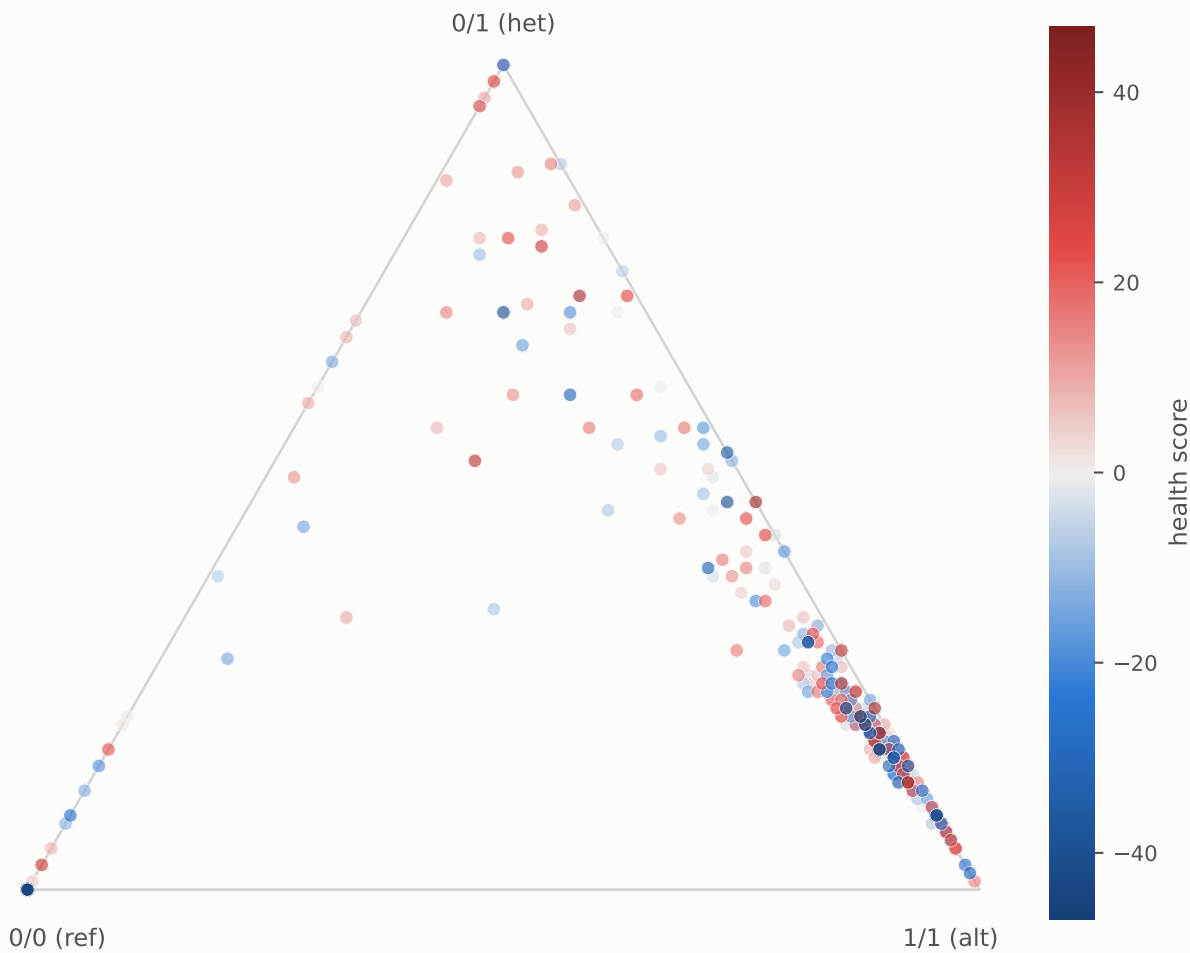
#154 by genotype uncertainty CHR_20:12,168,643 A>C
AF=0.54 DR2=0.81 $r=-0.022$ $\bar{H}=0.394$ F=0.4



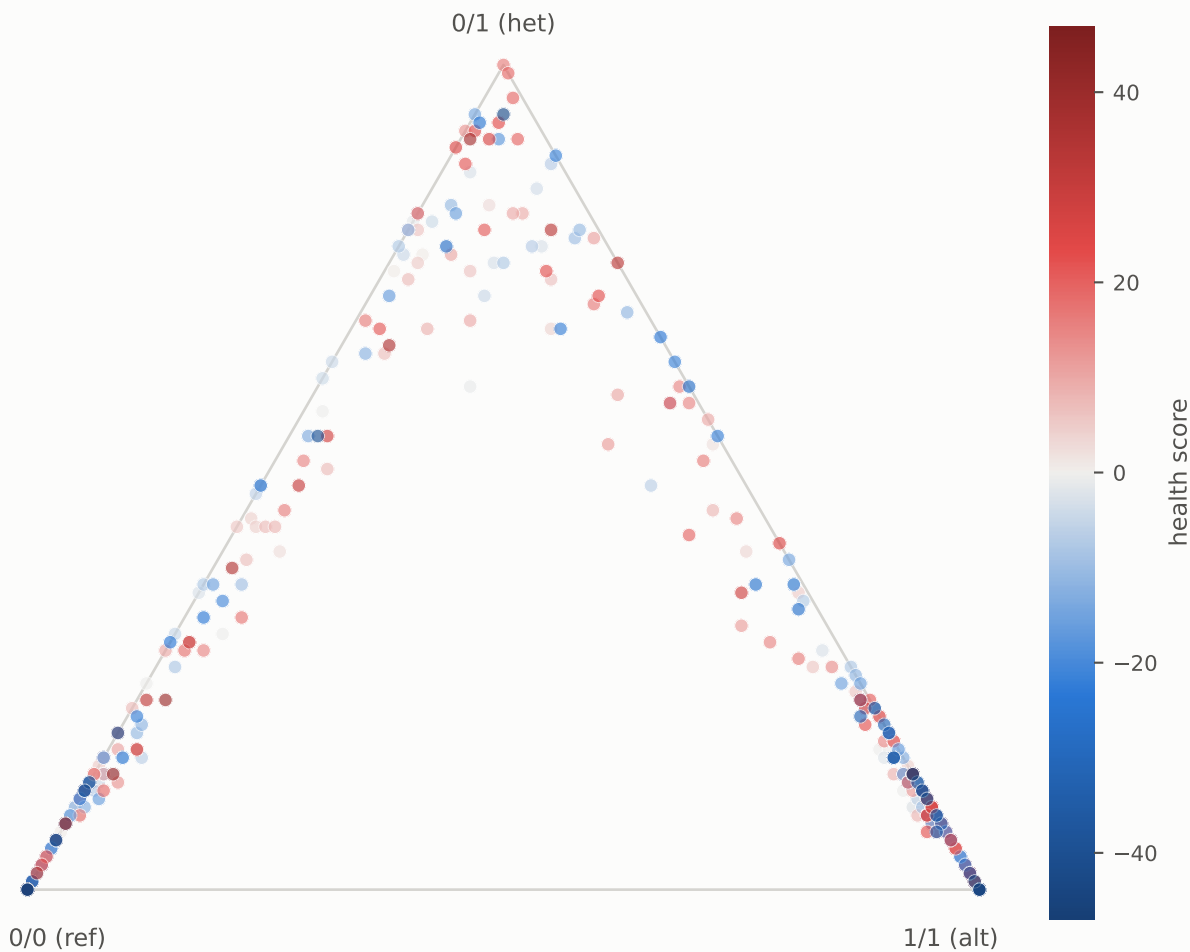
#155 by genotype uncertainty CHR_07:22,455,072 G>C
AF=0.45 DR2=0.81 $r=-0.005$ $\bar{H}=0.394$ F=0.2



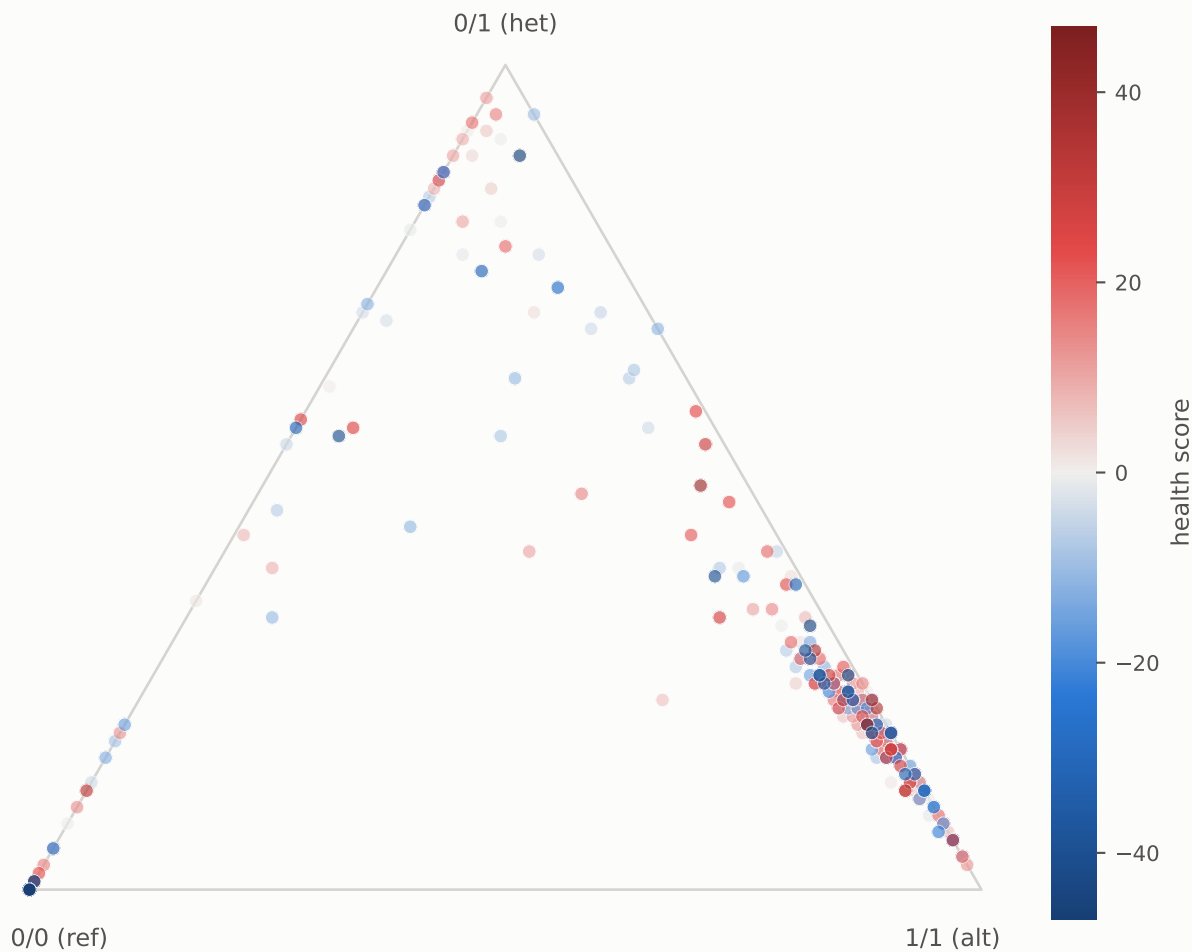
#156 by genotype uncertainty CHR_20:19,862,781 G>T
AF=0.55 DR2=0.81 $r=-0.021$ $\bar{H}=0.394$ F=0.8



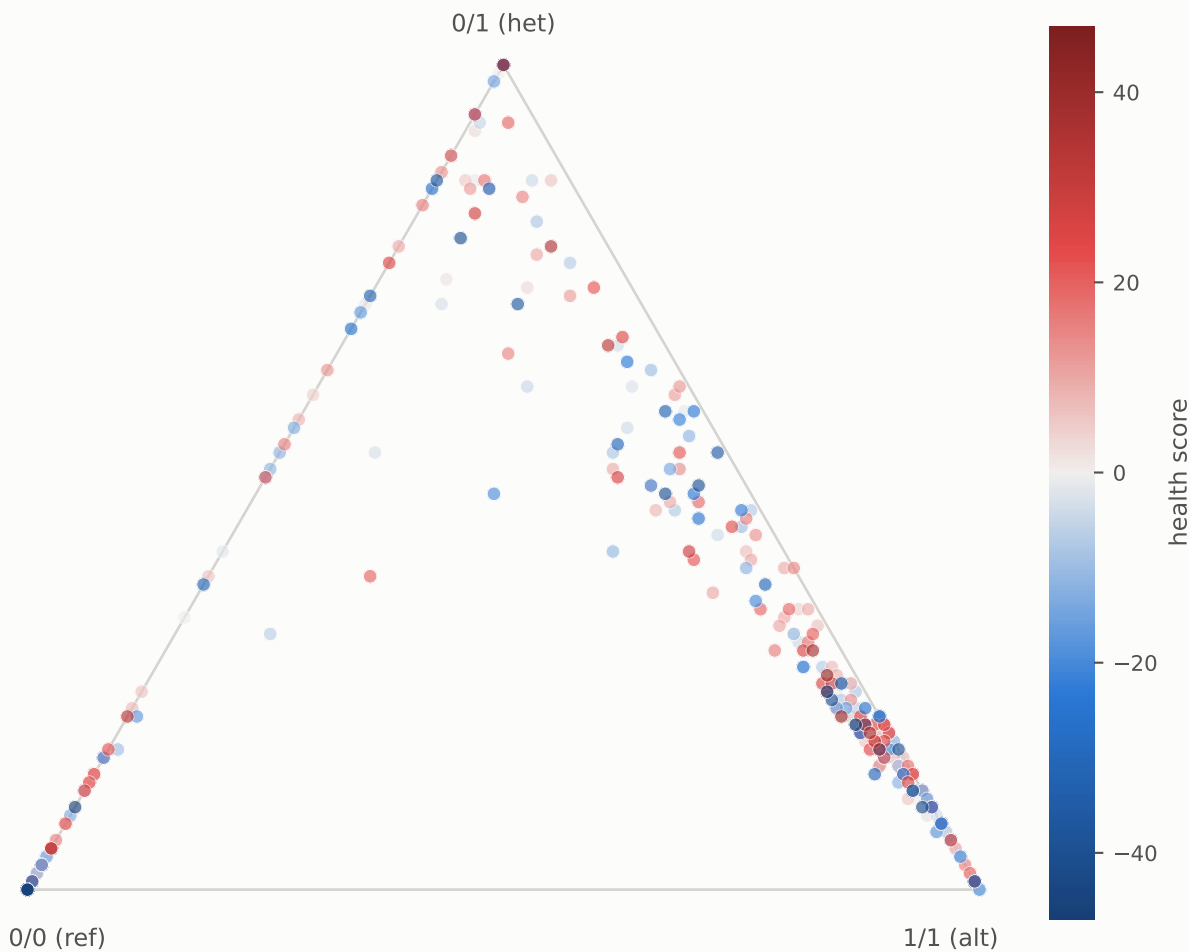
#157 by genotype uncertainty CHR_05:2,087,337 G>T
AF=0.56 DR2=0.82 r=-0.004 H=0.394 F=1.8



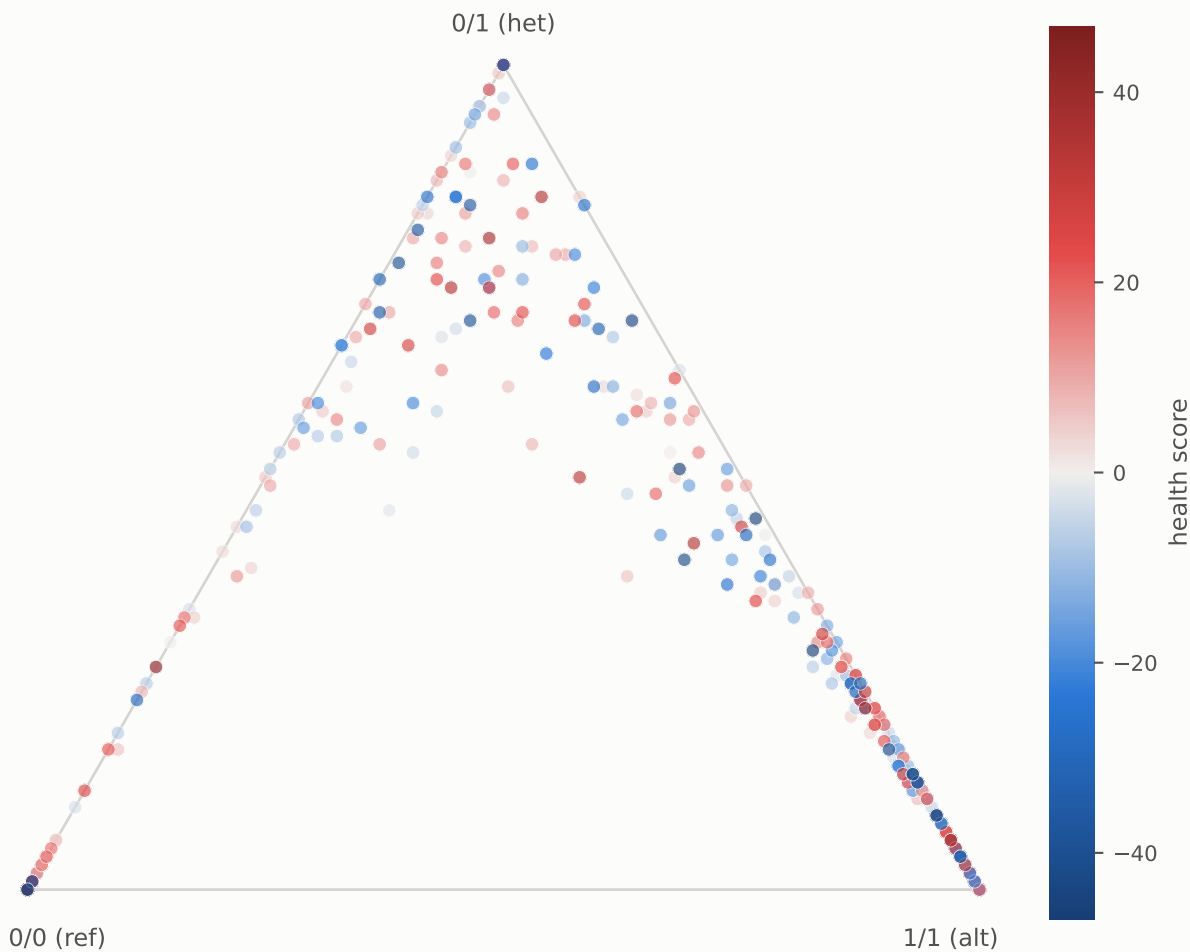
#158 by genotype uncertainty CHR_11:23,419,617 A>T
AF=0.51 DR2=0.82 $r=+0.048$ $\bar{H}=0.394$ F=0.4



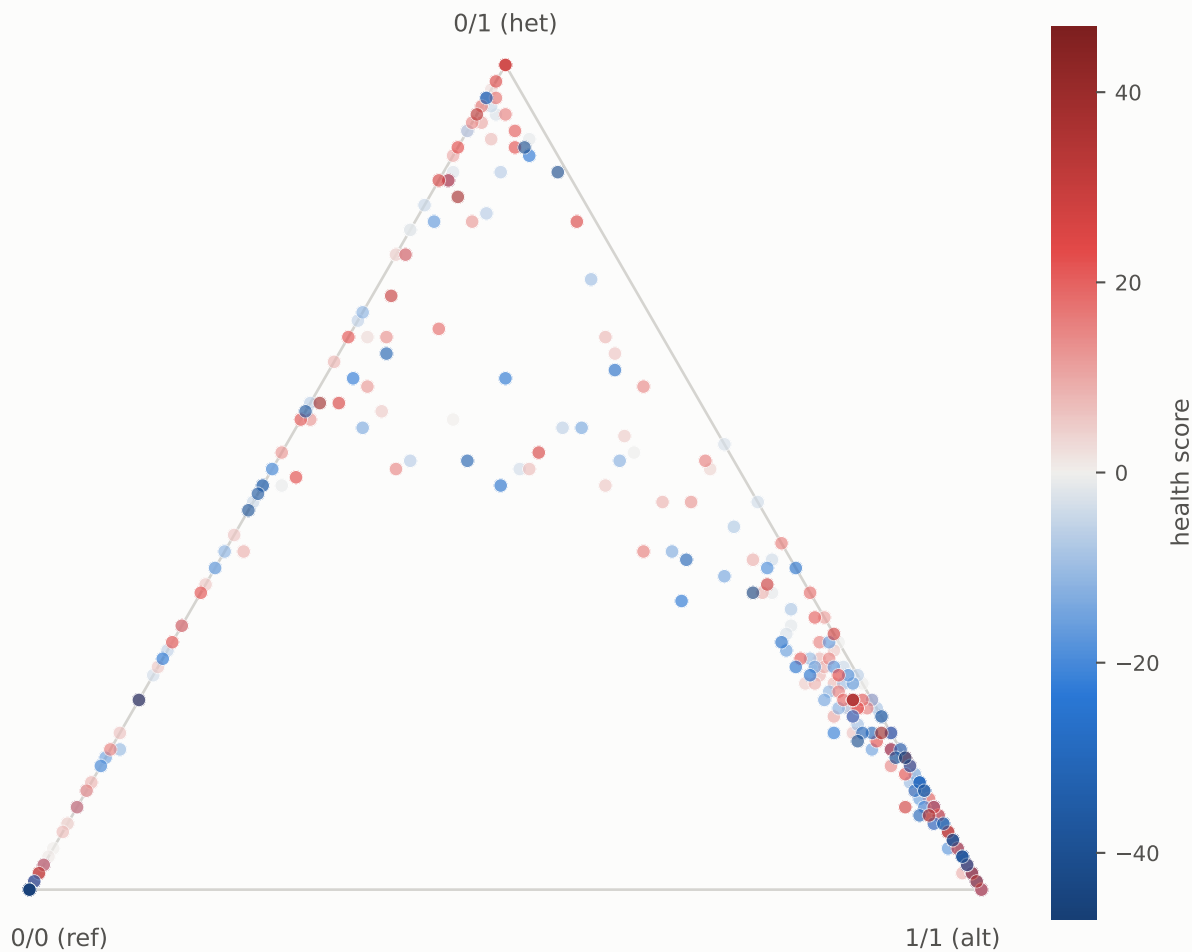
#159 by genotype uncertainty CHR_06:34,789,741 C>T
AF=0.5 DR2=0.81 $r=+0.026$ $\bar{H}=0.394$ F=0.7



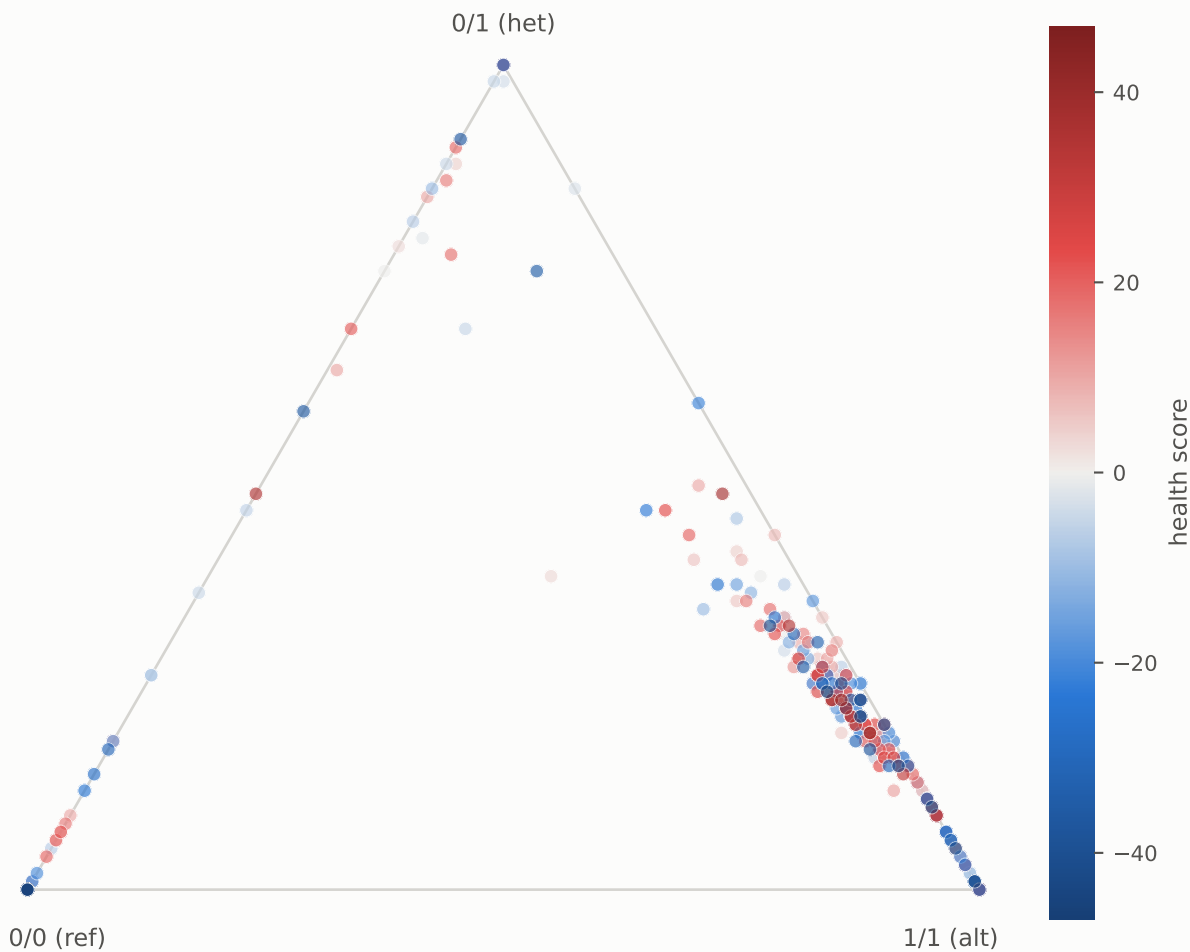
#160 by genotype uncertainty CHR_09:24,825,202 C>G
AF=0.51 DR2=0.82 $r=-0.096$ $\bar{H}=0.394$ F=3.2



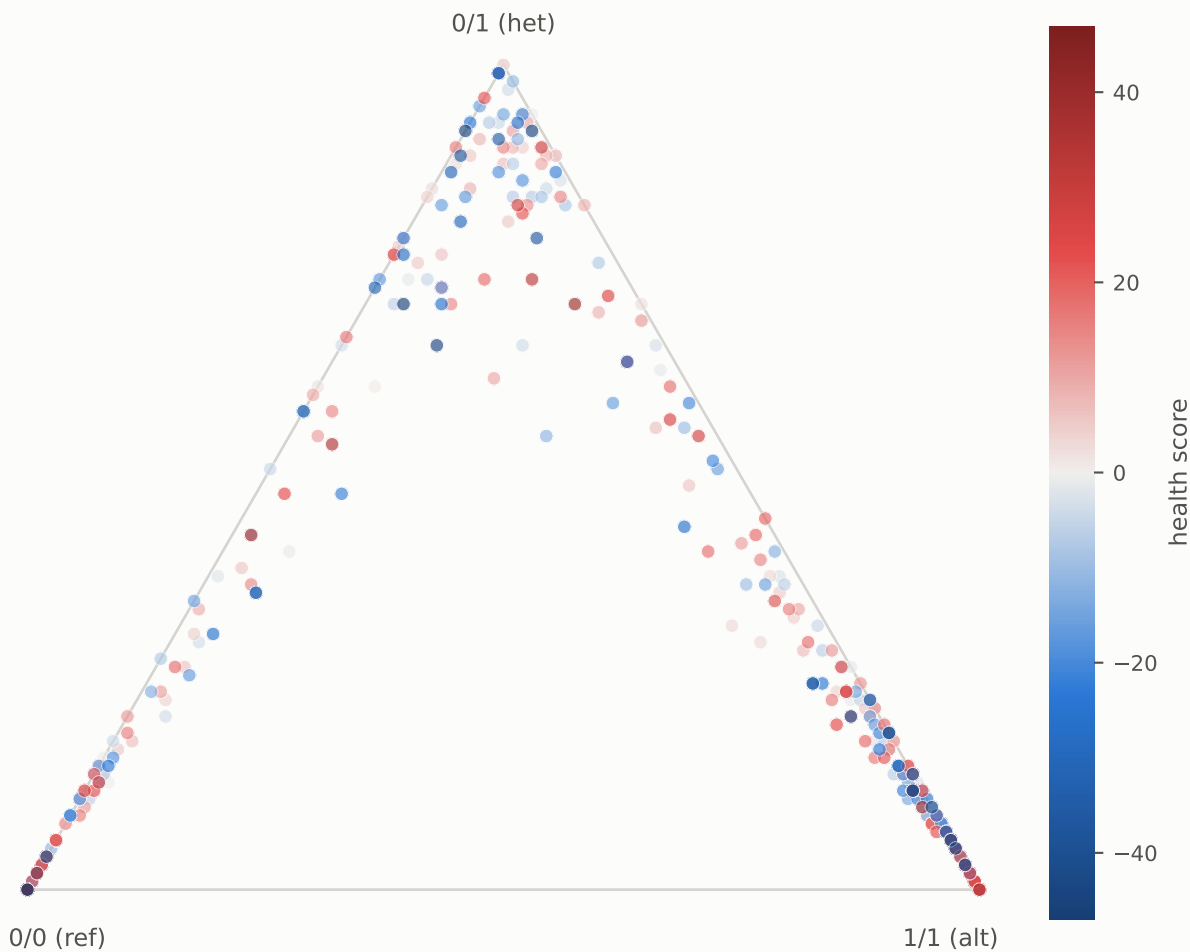
#161 by genotype uncertainty CHR_10:5,697,747 G>A
AF=0.56 DR2=0.81 $r=-0.071$ $\bar{H}=0.394$ $F=2.5$



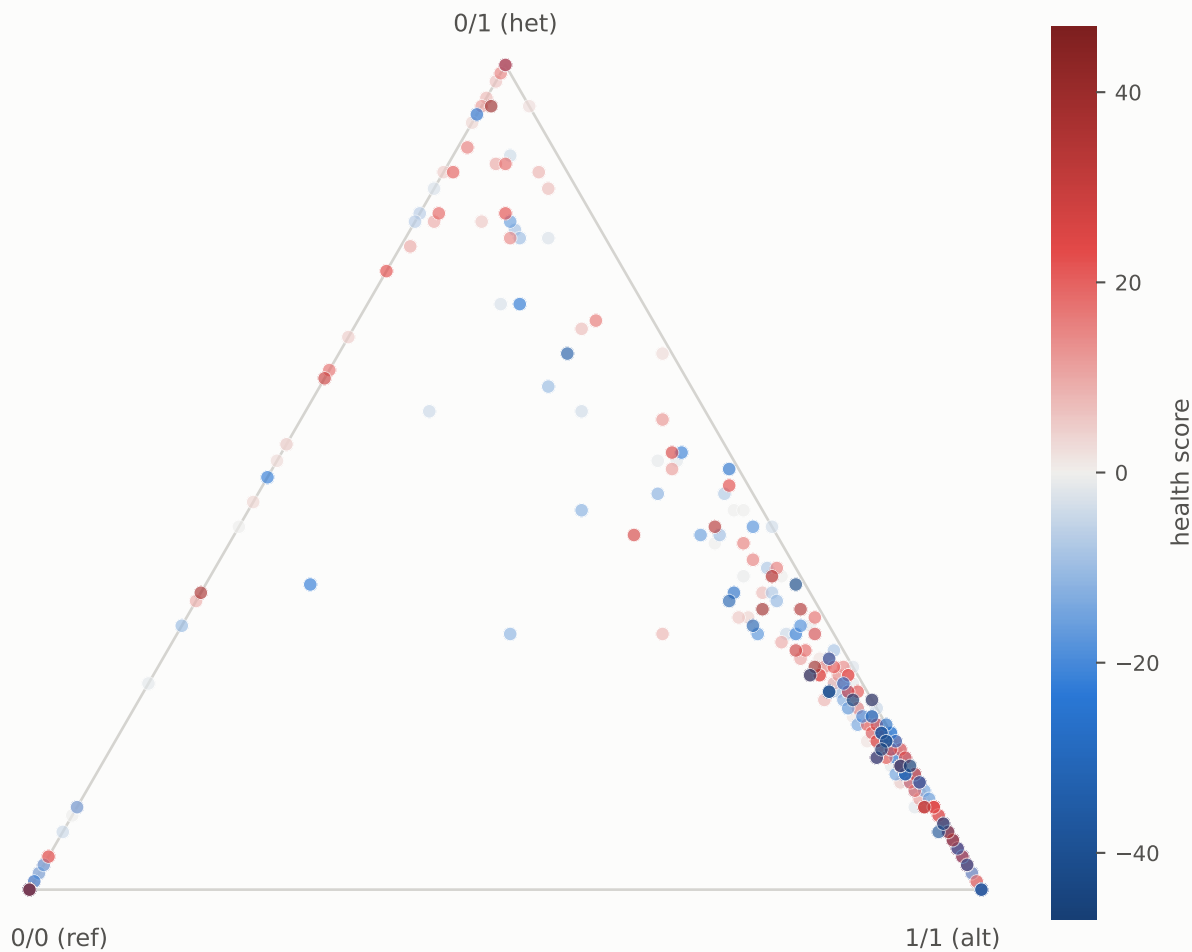
#162 by genotype uncertainty CHR_09:20,058,659 T>C
AF=0.56 DR2=0.82 $r=-0.019$ $\bar{H}=0.394$ $F=0.3$



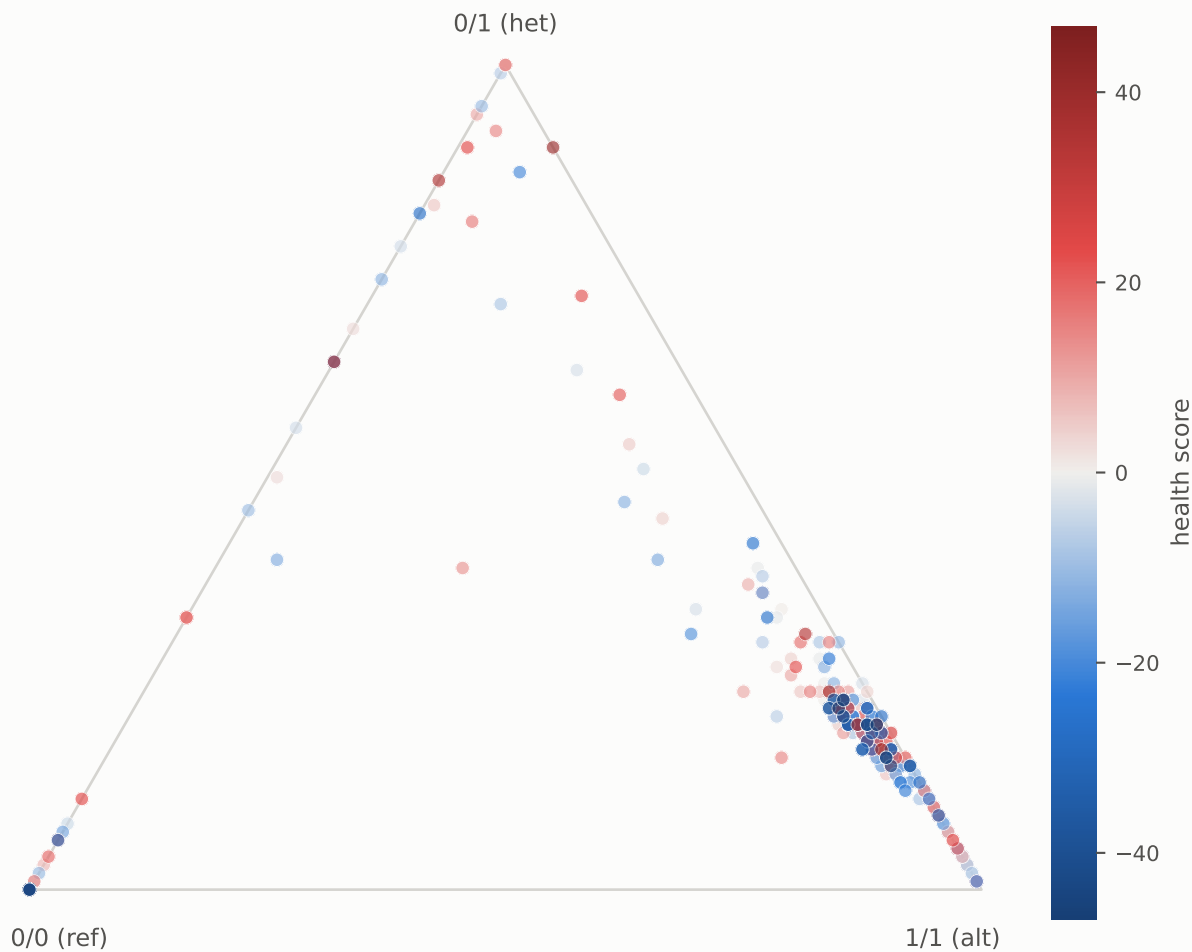
#163 by genotype uncertainty CHR_07:11,977,784 T>A
AF=0.53 DR2=0.81 $r=-0.039$ $\bar{H}=0.394$ F=2.0



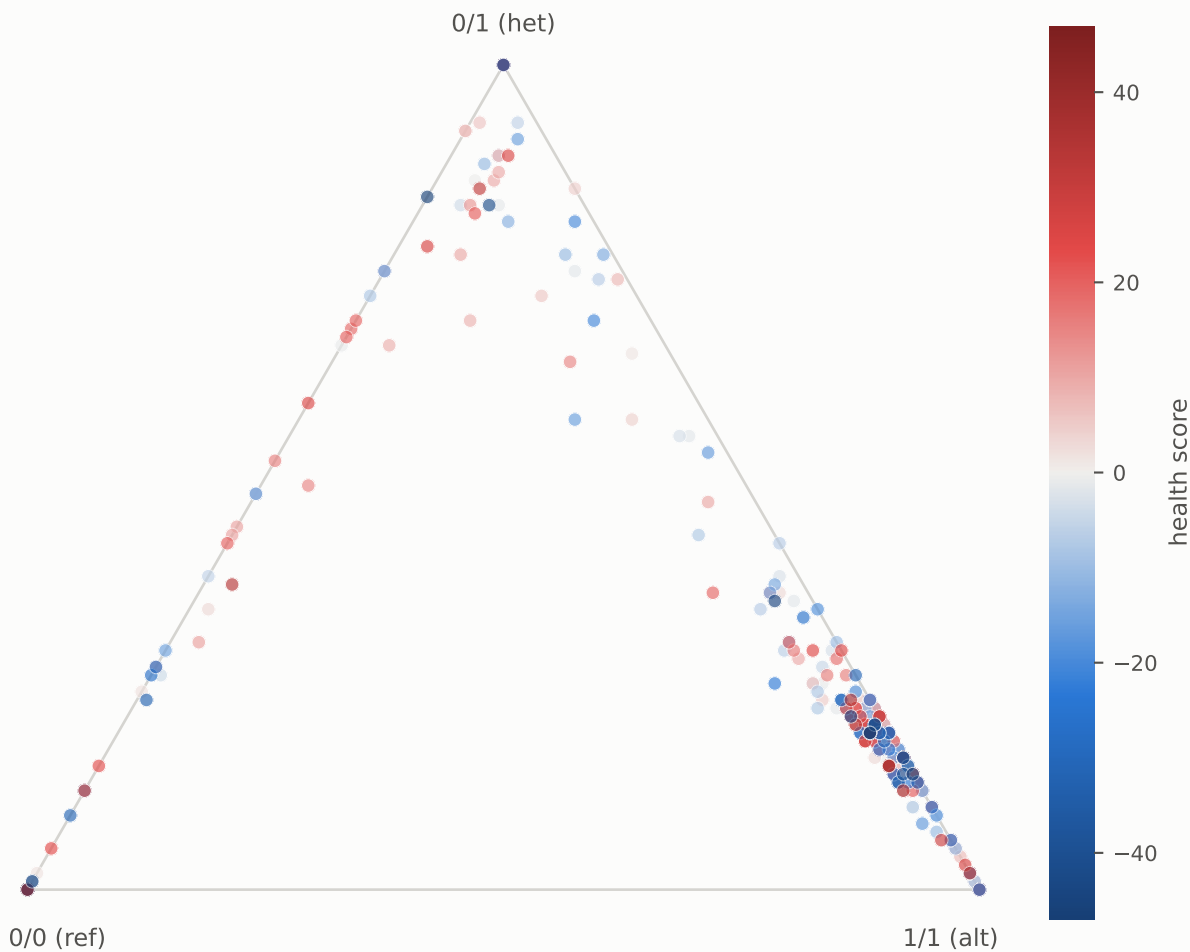
#164 by genotype uncertainty CHR_13:21,765,533 C>G
AF=0.6 DR2=0.81 $r=+0.001$ $\bar{H}=0.394$ F=2.2



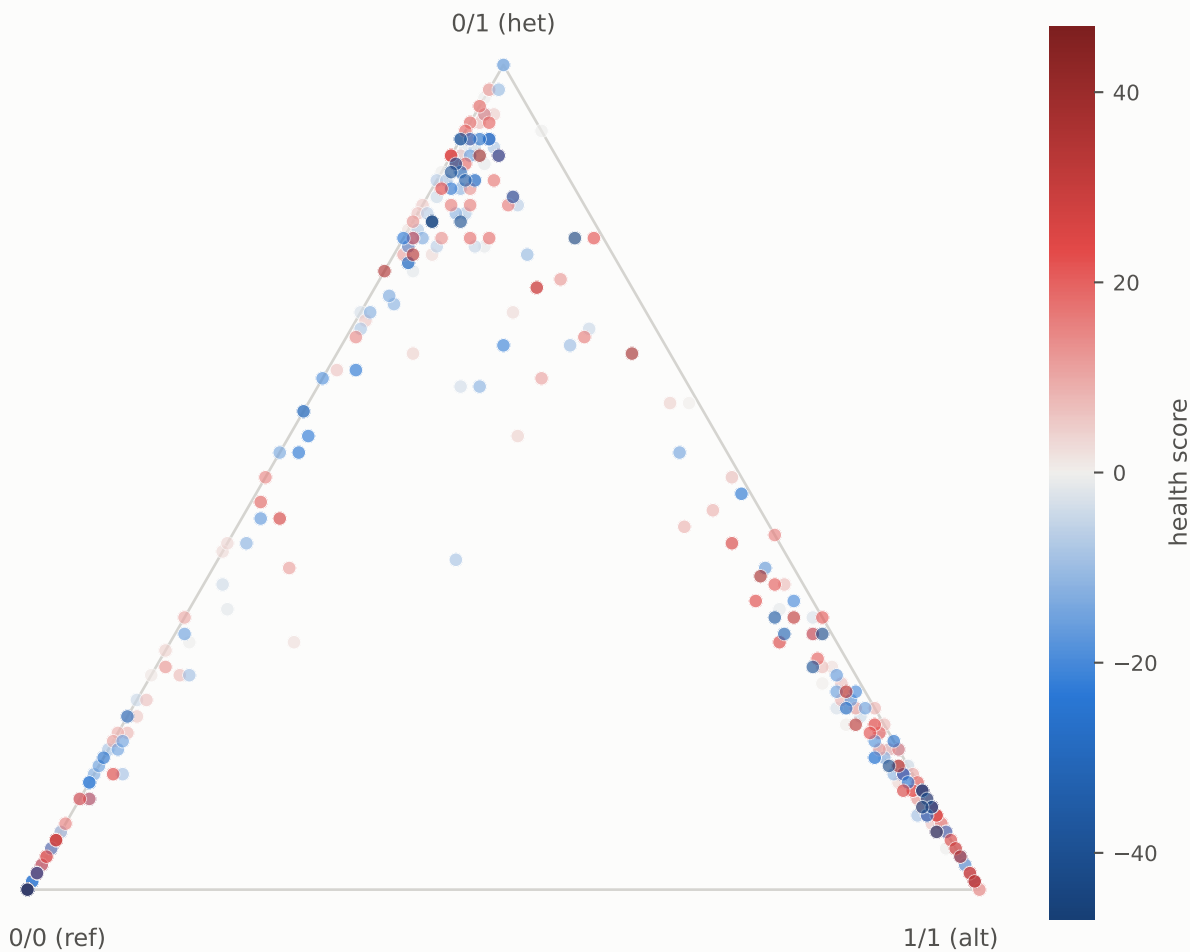
#165 by genotype uncertainty CHR_21:17,075,323 C>T
AF=0.52 DR2=0.82 $r=-0.141$ $\bar{H}=0.394$ F=5.6



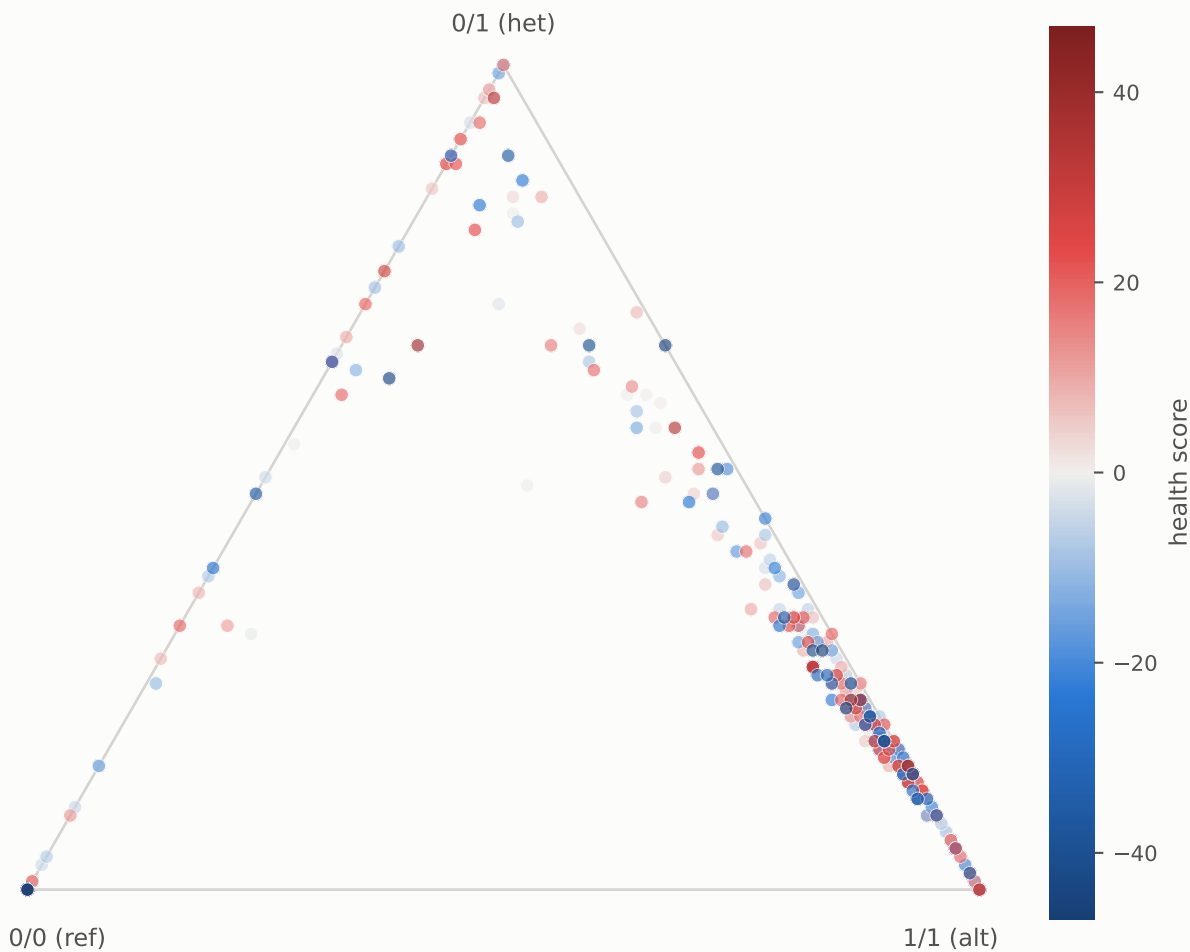
#166 by genotype uncertainty CHR_15:21,468,022 A>C
AF=0.6 DR2=0.81 $r=+0.037$ $\bar{H}=0.394$ F=0.6



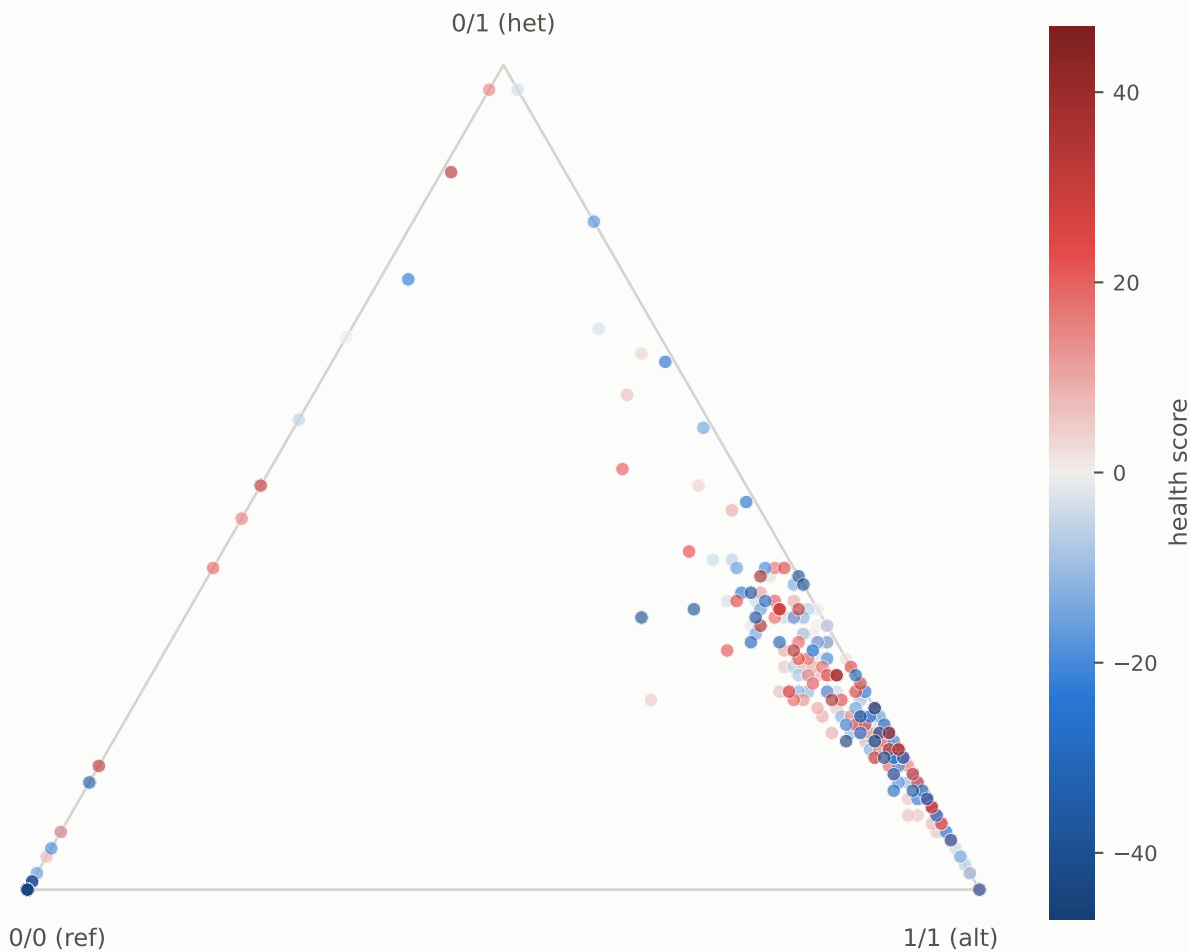
#167 by genotype uncertainty CHR_19:5,909,649 T>G
AF=0.48 DR2=0.81 $r=+0.032$ $\bar{H}=0.394$ F=1.2



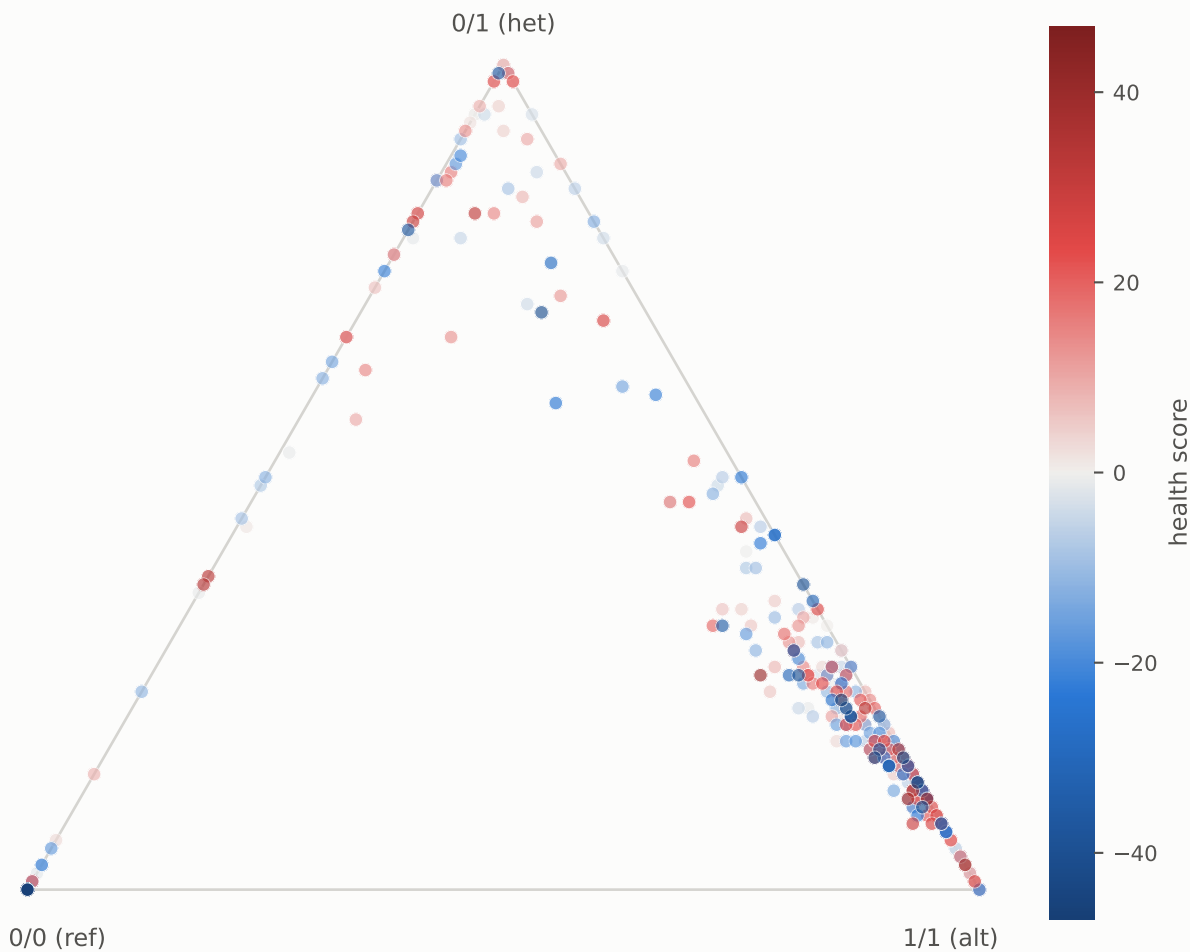
#168 by genotype uncertainty CHR_13:23,709,495 A>T
AF=0.57 DR2=0.81 $r=+0.007$ $\bar{H}=0.394$ F=0.3



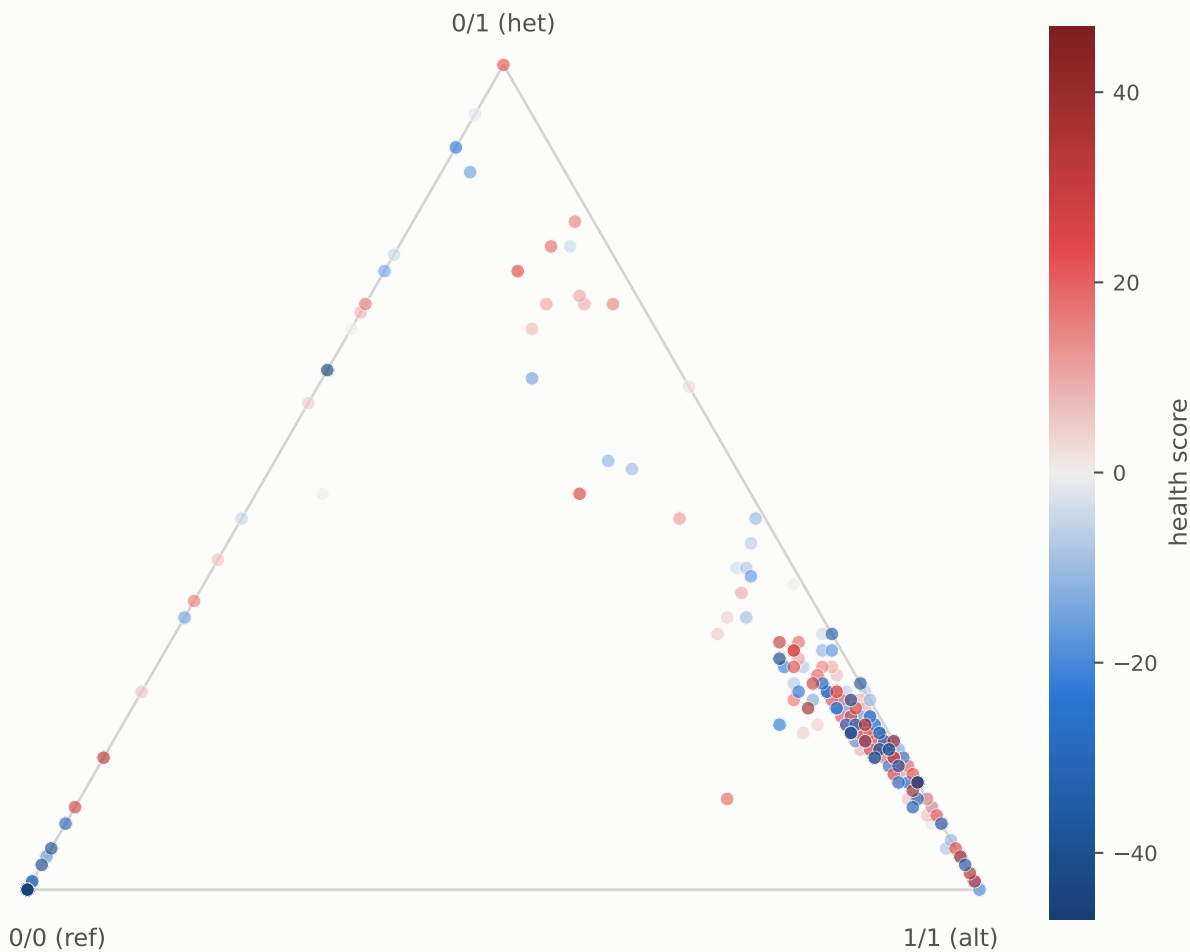
#169 by genotype uncertainty CHR_11:23,584,448 A>C
AF=0.56 DR2=0.81 $r=-0.033$ $\bar{H}=0.393$ F=0.2



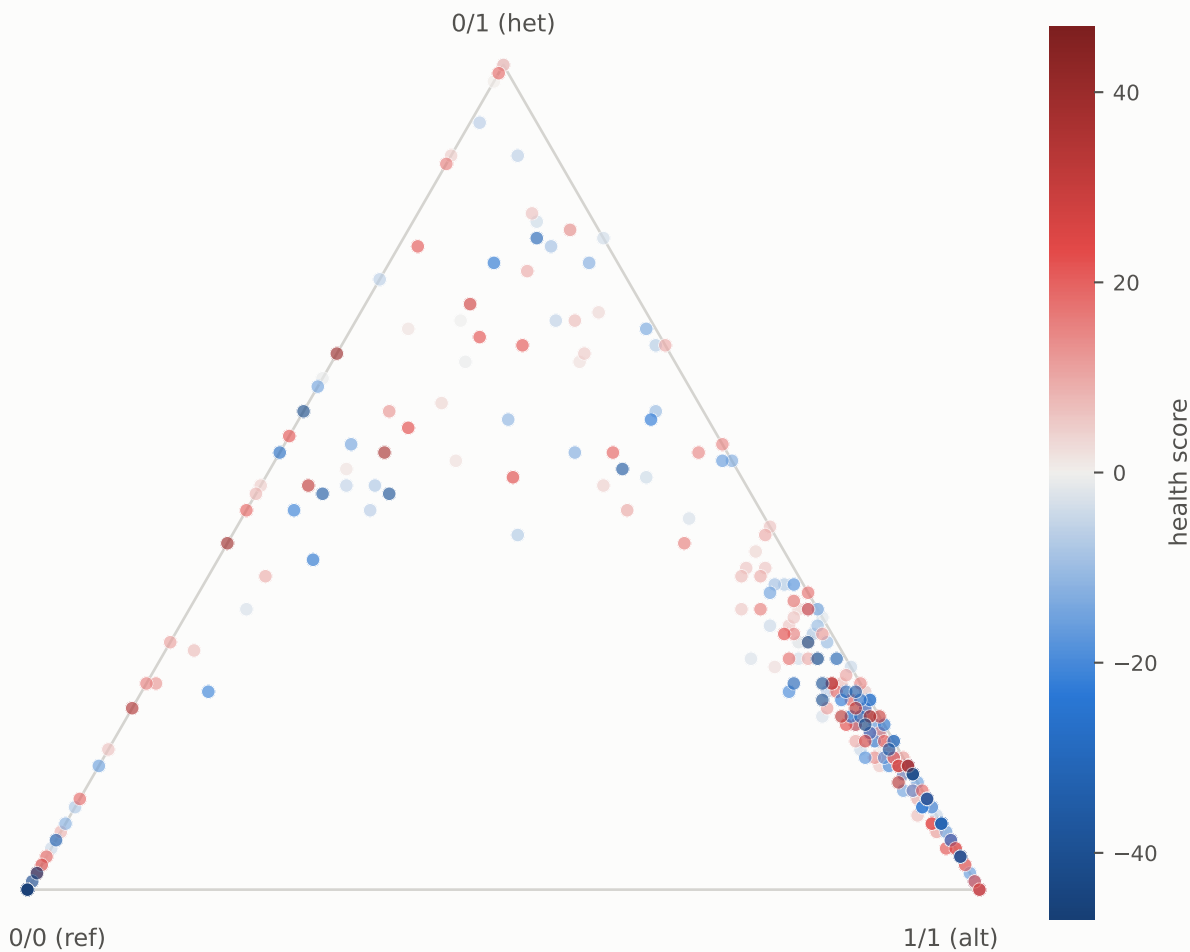
#170 by genotype uncertainty CHR_20:8,526,060 A>G
AF=0.58 DR2=0.81 $r=-0.013$ $\bar{H}=0.393$ $F=0.1$



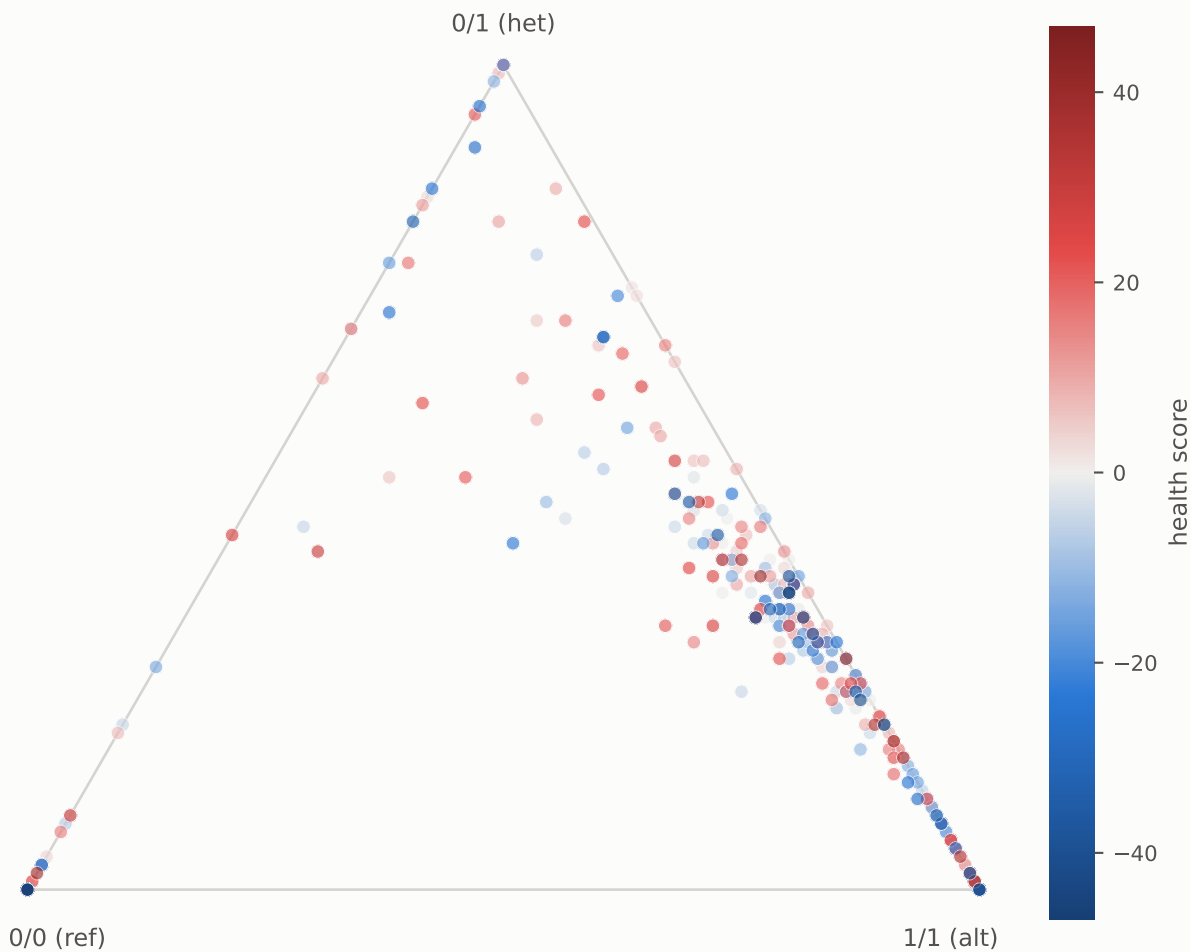
#171 by genotype uncertainty CHR_14:15,234,425 C>T
AF=0.57 DR2=0.81 $r=+0.024$ $\bar{H}=0.393$ F=0.3



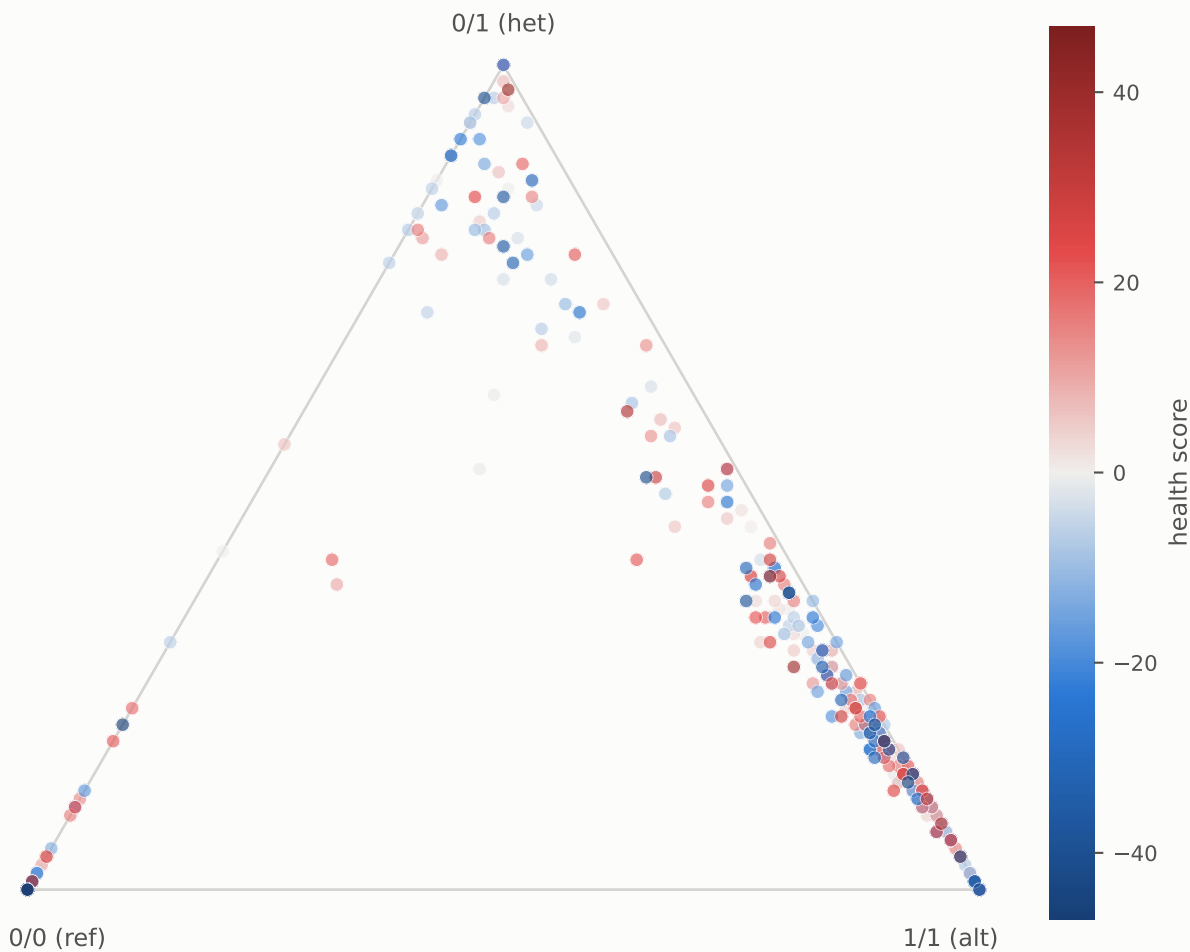
#172 by genotype uncertainty CHR_04:21,766,643 A>G
AF=0.55 DR2=0.81 $r=-0.047$ $\bar{H}=0.393$ F=0.5



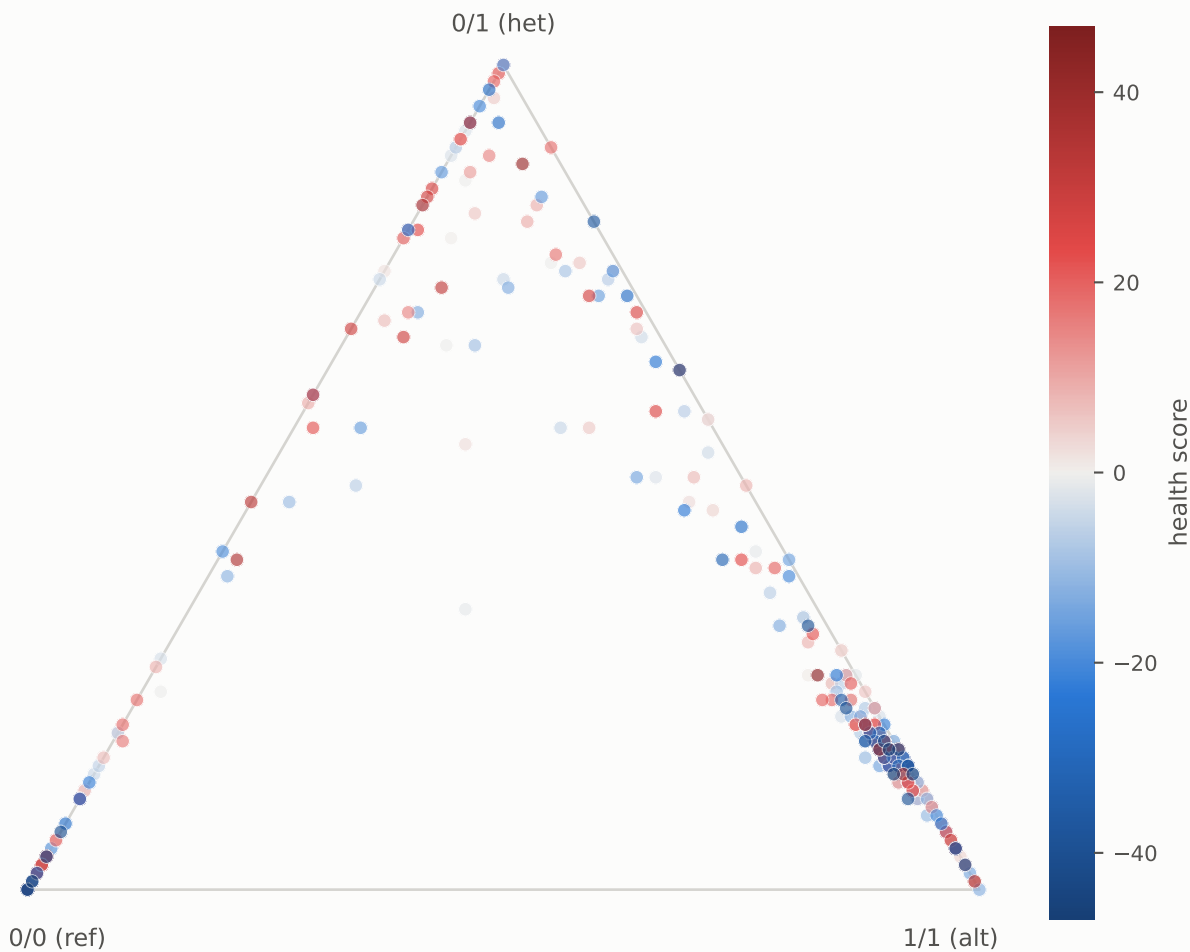
#173 by genotype uncertainty CHR_10:29,031,566 G>C
AF=0.52 DR2=0.81 $r=-0.034$ $\bar{H}=0.393$ F=0.5



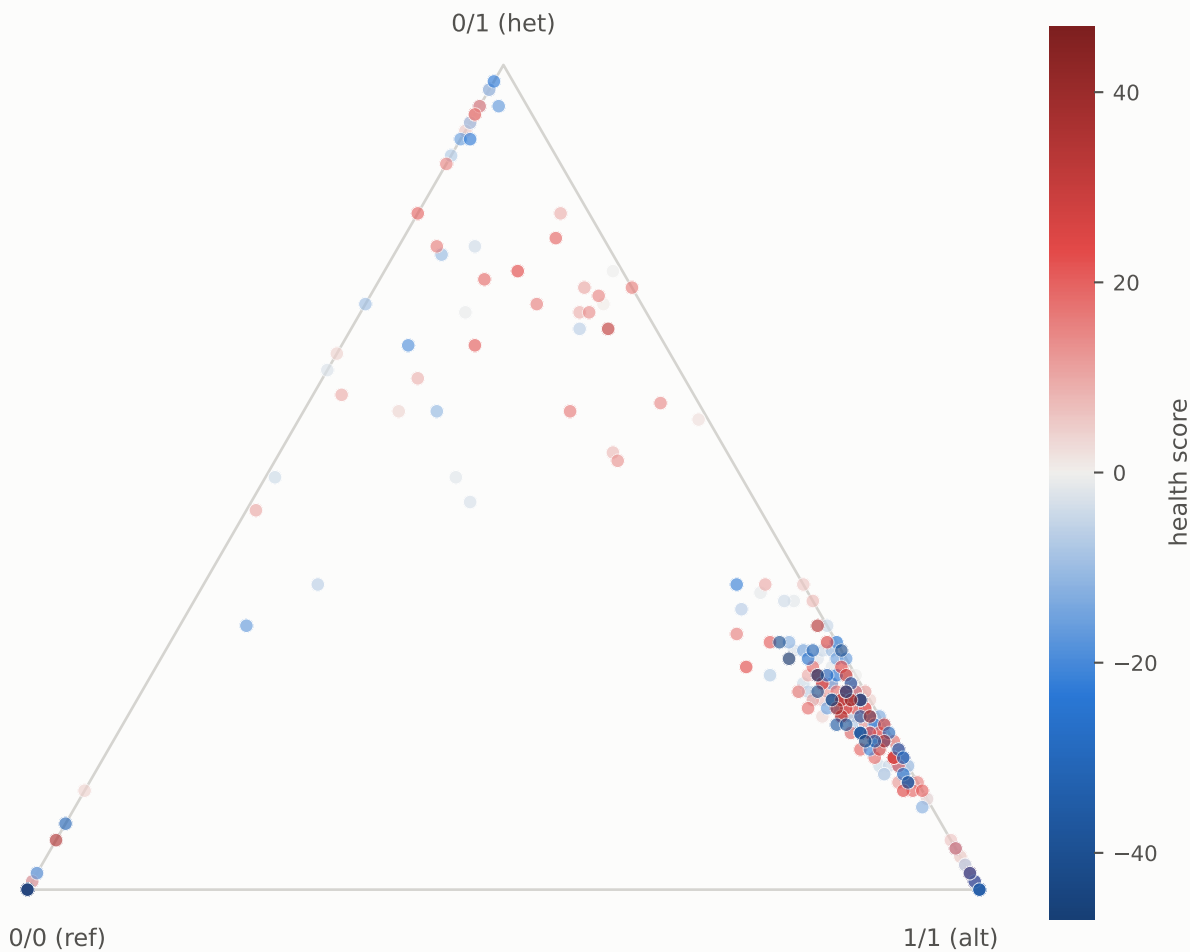
#174 by genotype uncertainty CHR_07:7,876,901 G>T
AF=0.56 DR2=0.81 $r=-0.031$ $H=0.393$ $F=1.0$



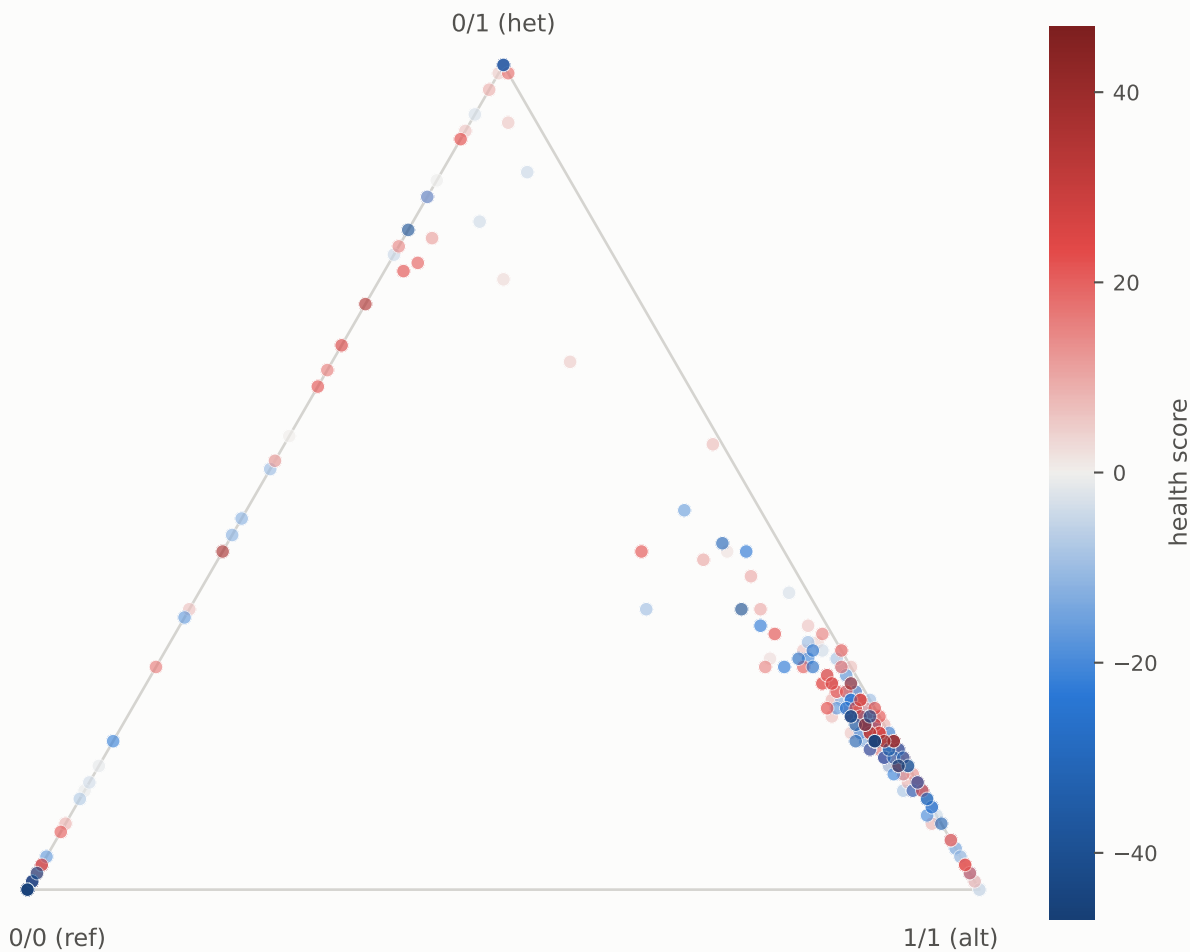
#175 by genotype uncertainty unpl-scaff_013:65,911 C>T
AF=0.54 DR2=0.81 $r=-0.062$ H=0.393 F=1.6



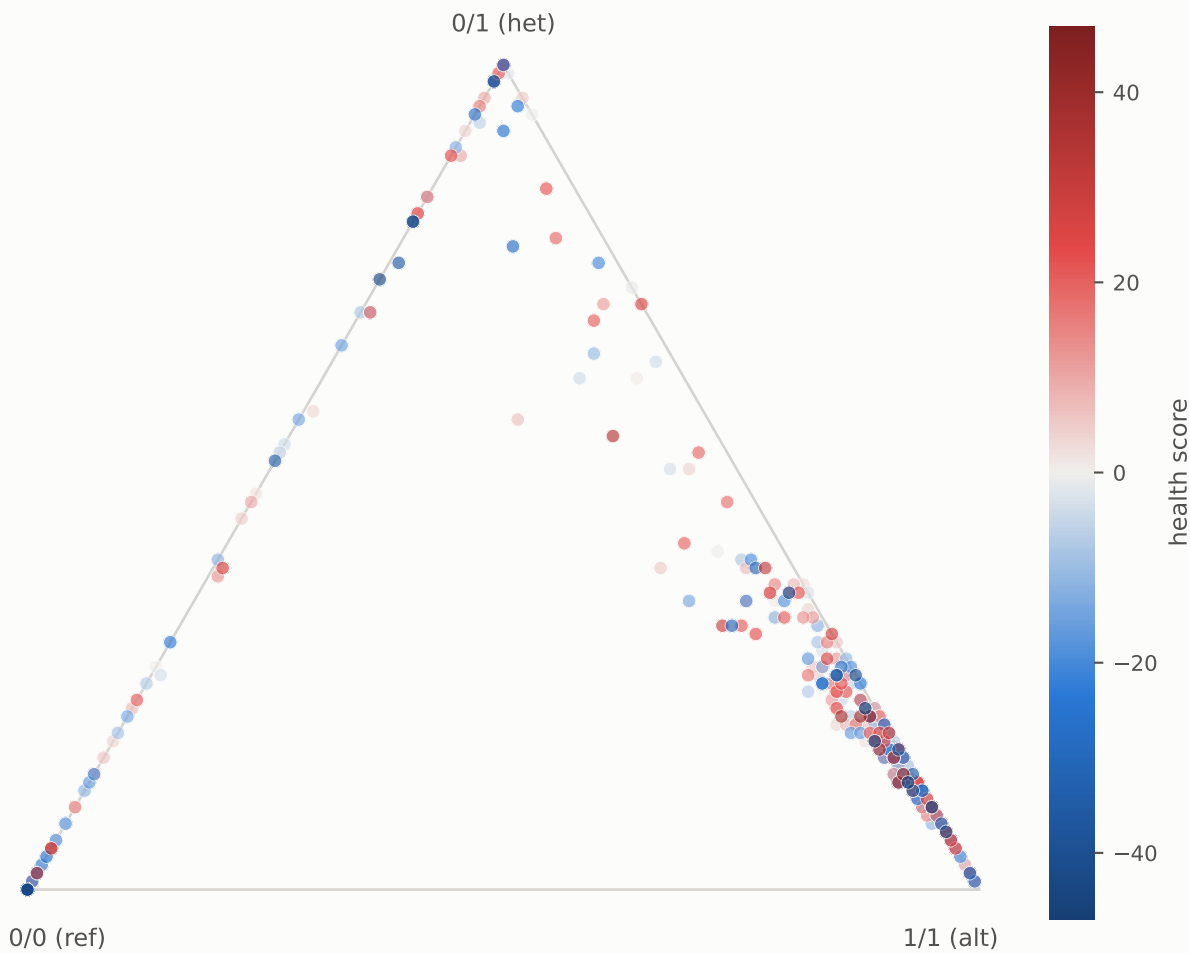
#176 by genotype uncertainty CHR_11:30,926,140 C>T
AF=0.54 DR2=0.81 $r=+0.016$ $\bar{H}=0.393$ F=1.7



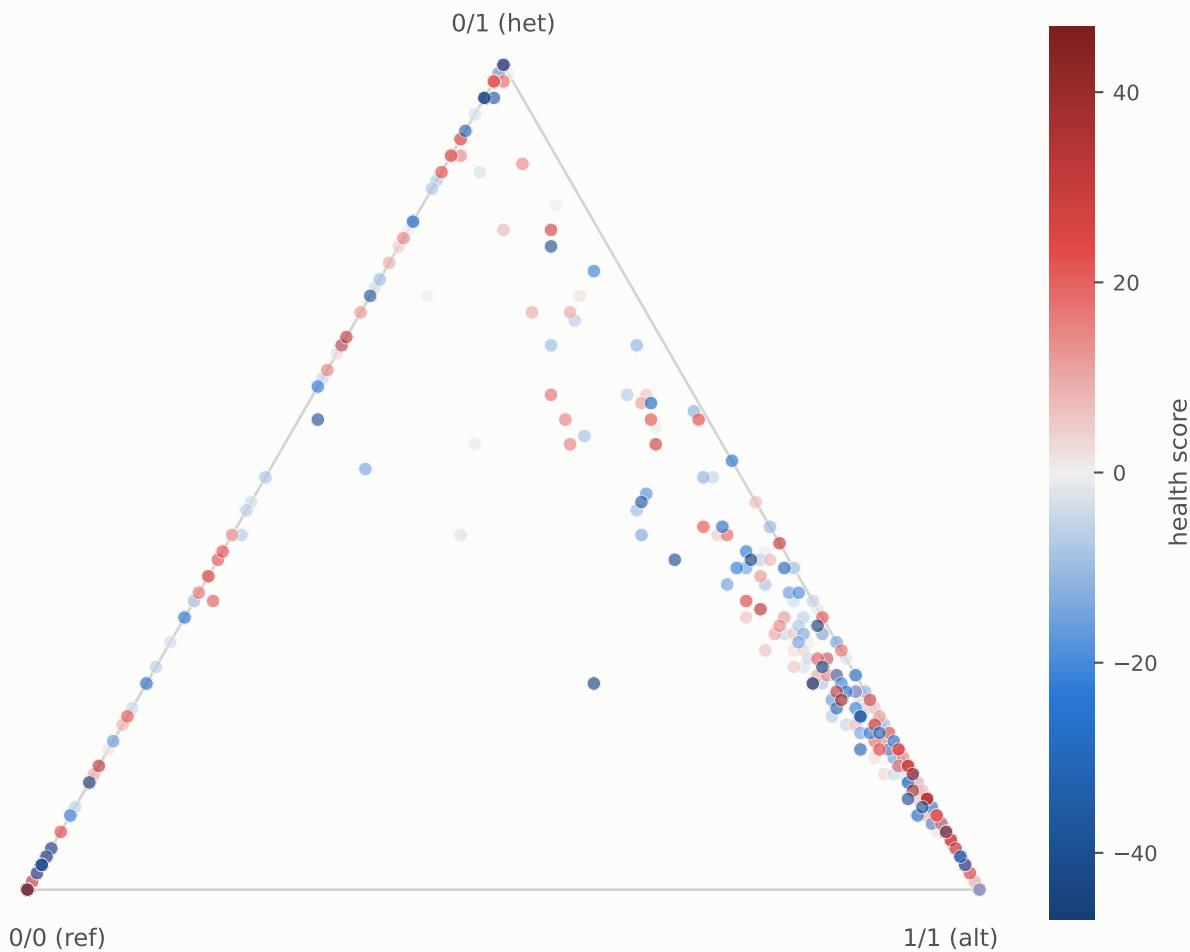
#177 by genotype uncertainty CHR_09:9,022,910 G>A
AF=0.6 DR2=0.81 r=-0.013 H=0.393 F=0.9



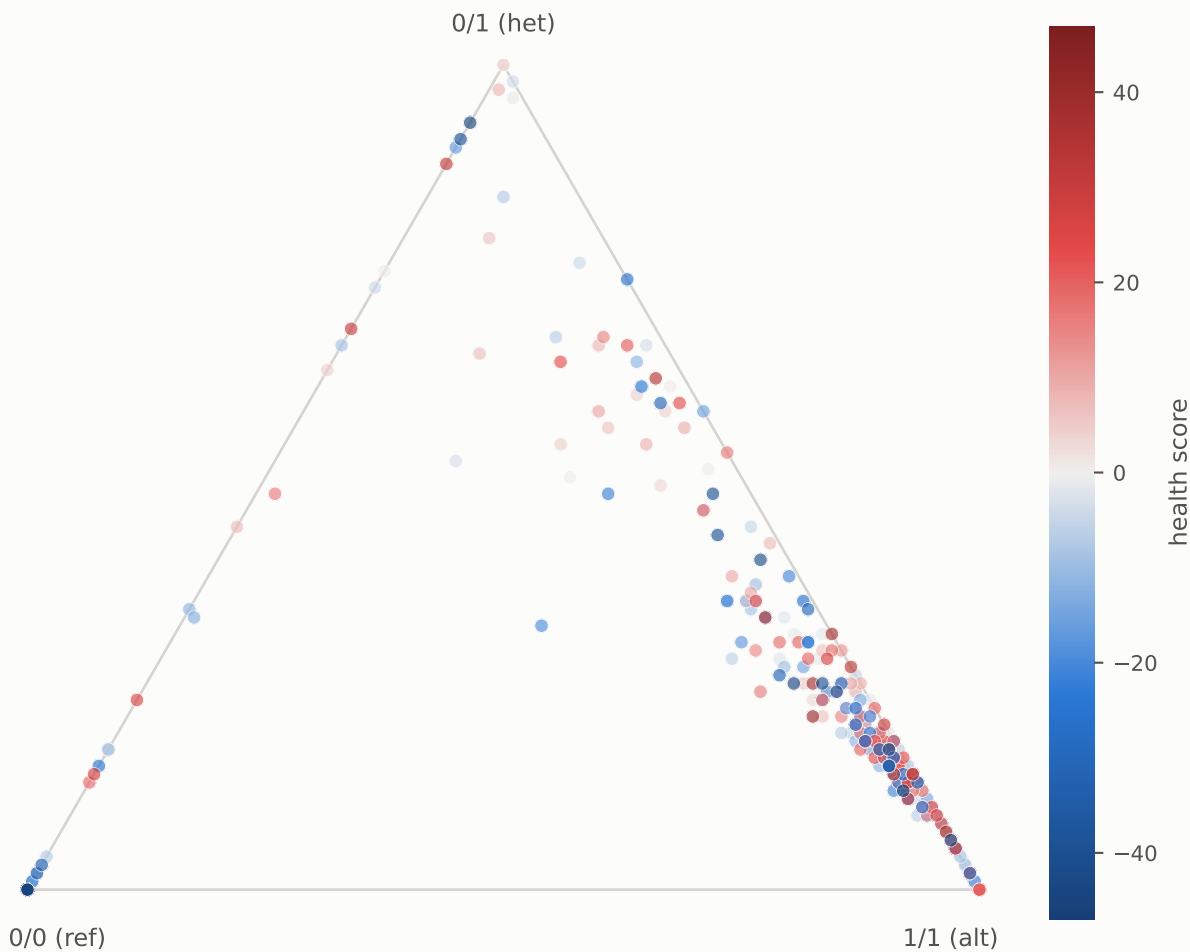
#178 by genotype uncertainty CHR_04:28,822,626 G>A
AF=0.59 DR2=0.82 $r=+0.011$ $\bar{H}=0.393$ F=0.3



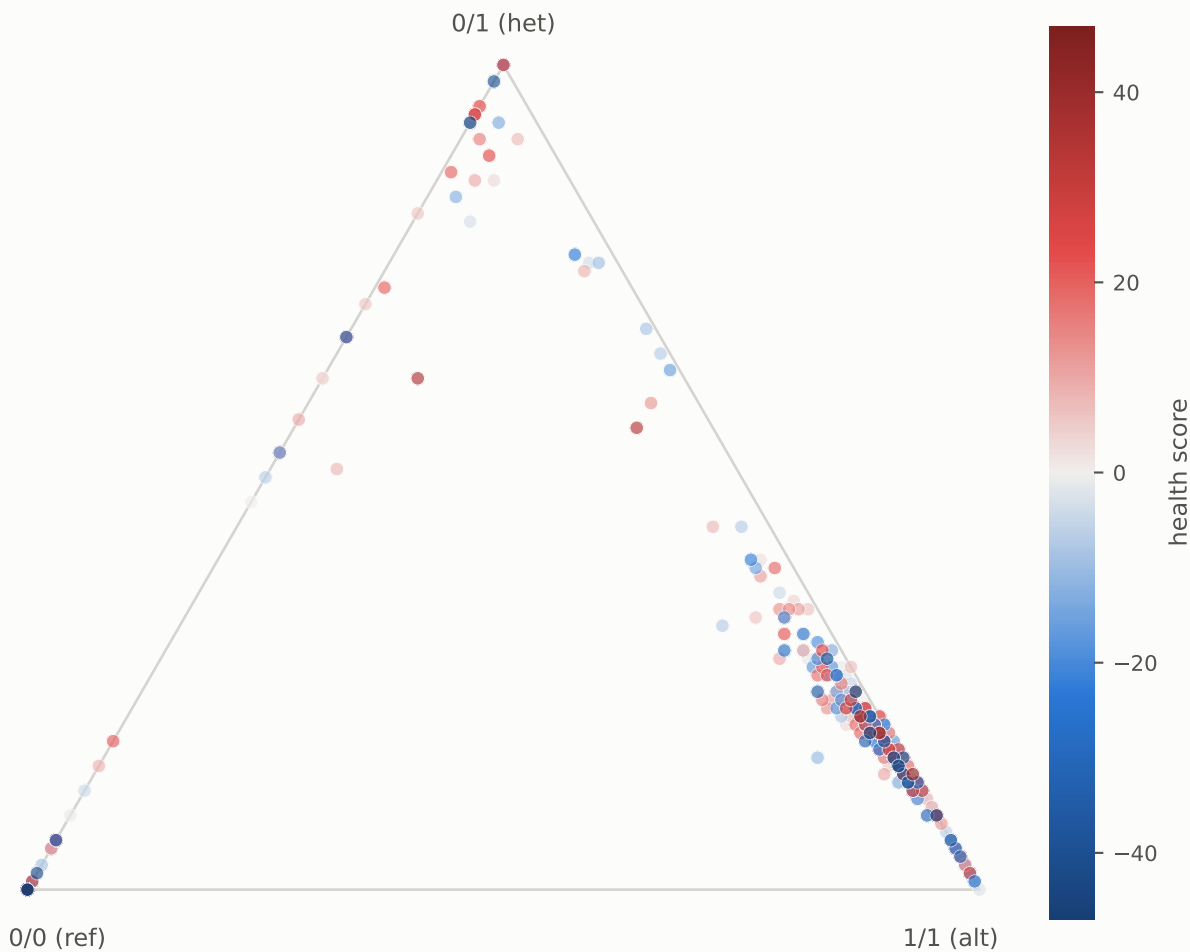
#179 by genotype uncertainty CHR_19:1,669,754 A>G
AF=0.51 DR2=0.81 $r=-0.005$ $\bar{H}=0.393$ $F=0.4$



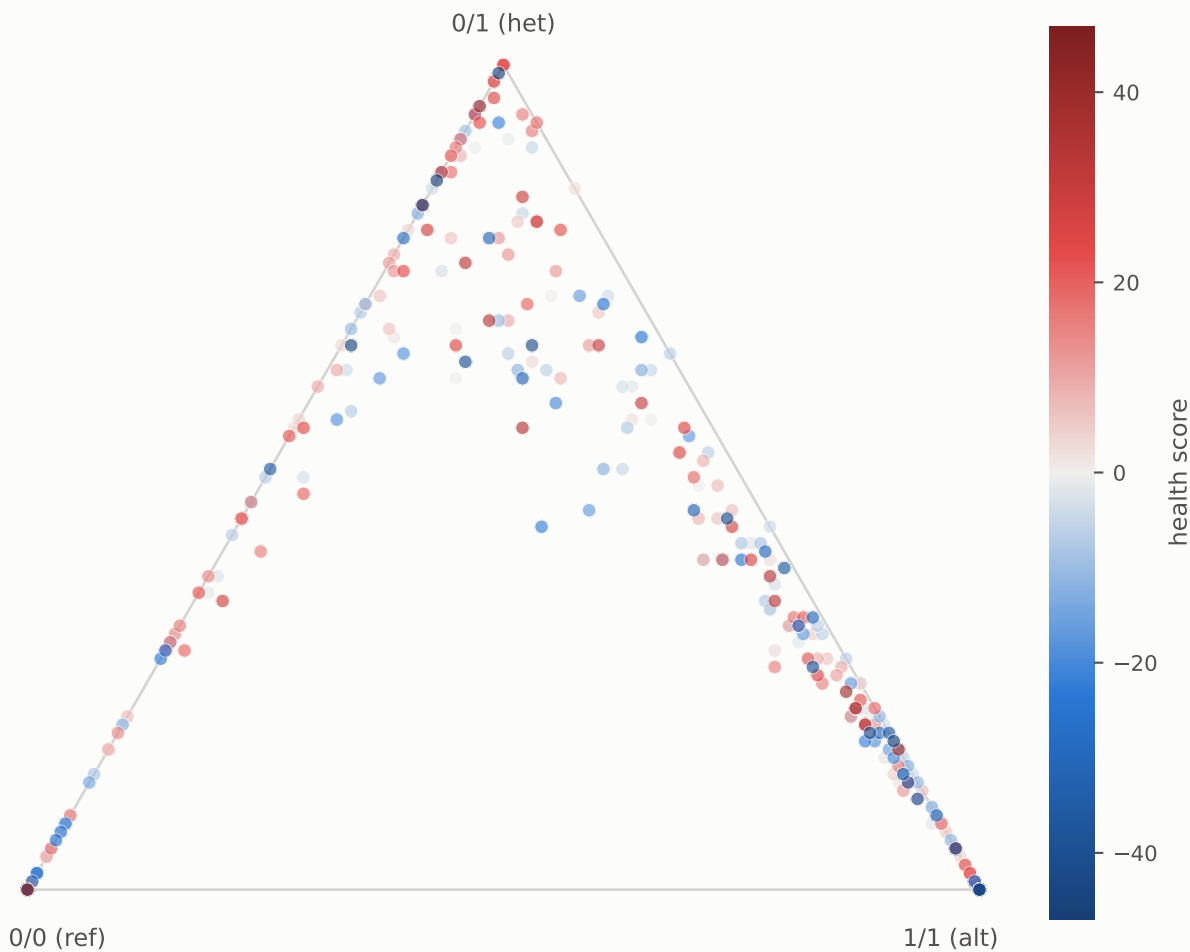
#180 by genotype uncertainty CHR_05:8,851,602 G>T
AF=0.59 DR2=0.81 $r=+0.031$ $\bar{H}=0.393$ F=0.1



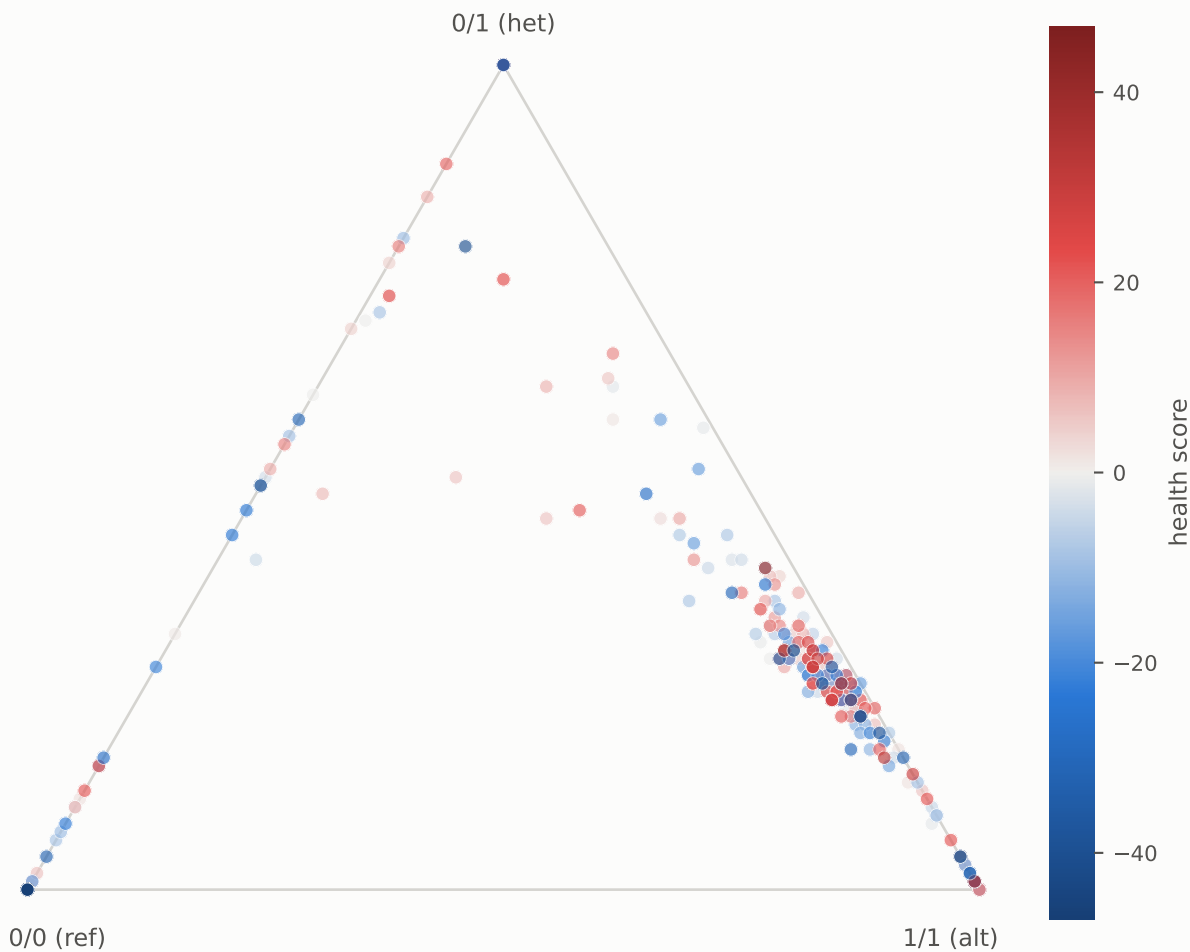
#181 by genotype uncertainty CHR_12:17,784,934 A>T
AF=0.6 DR2=0.81 $r=-0.003$ $\bar{H}=0.393$ $F=0.5$



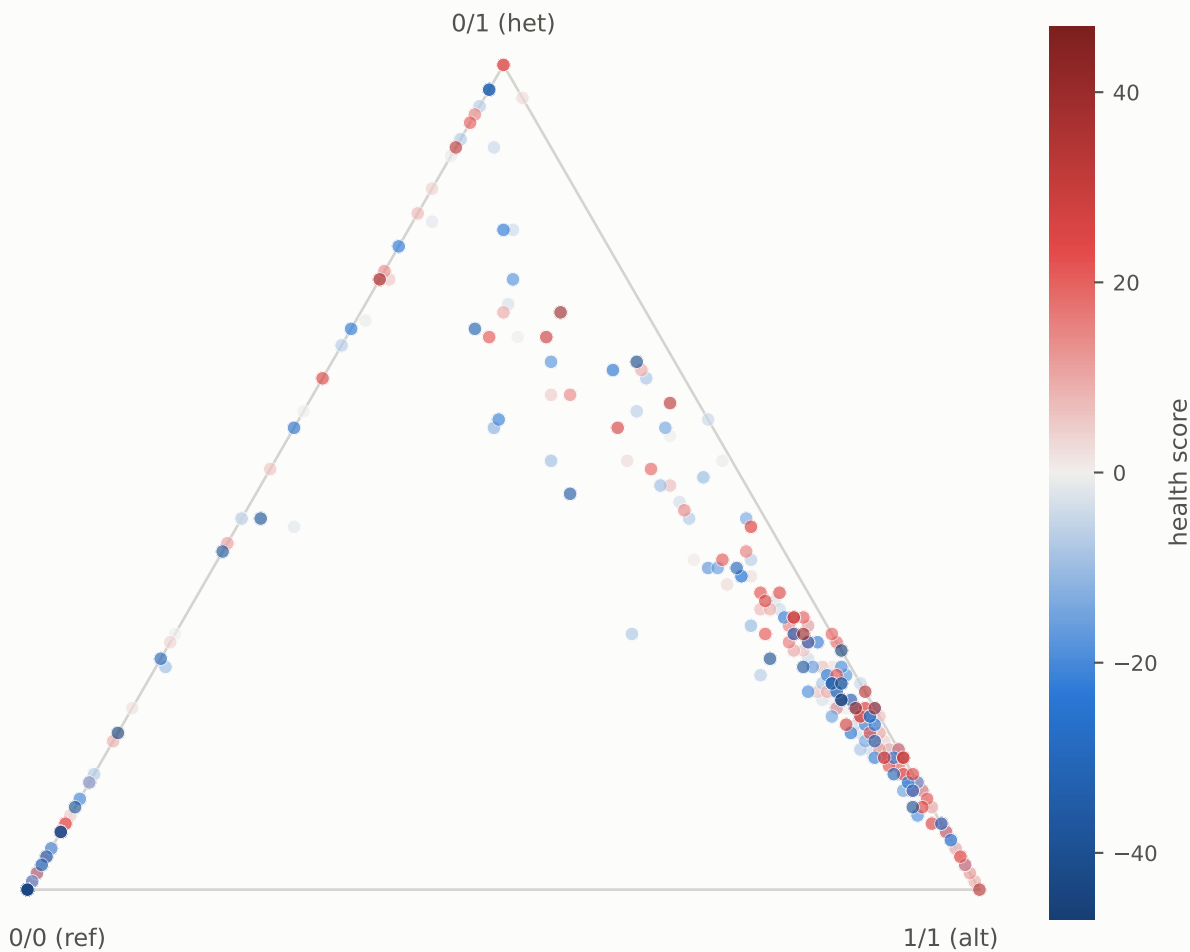
#182 by genotype uncertainty CHR_08:28,050,344 G>A
AF=0.5 DR2=0.81 $r=-0.016$ $\bar{H}=0.393$ F=1.3



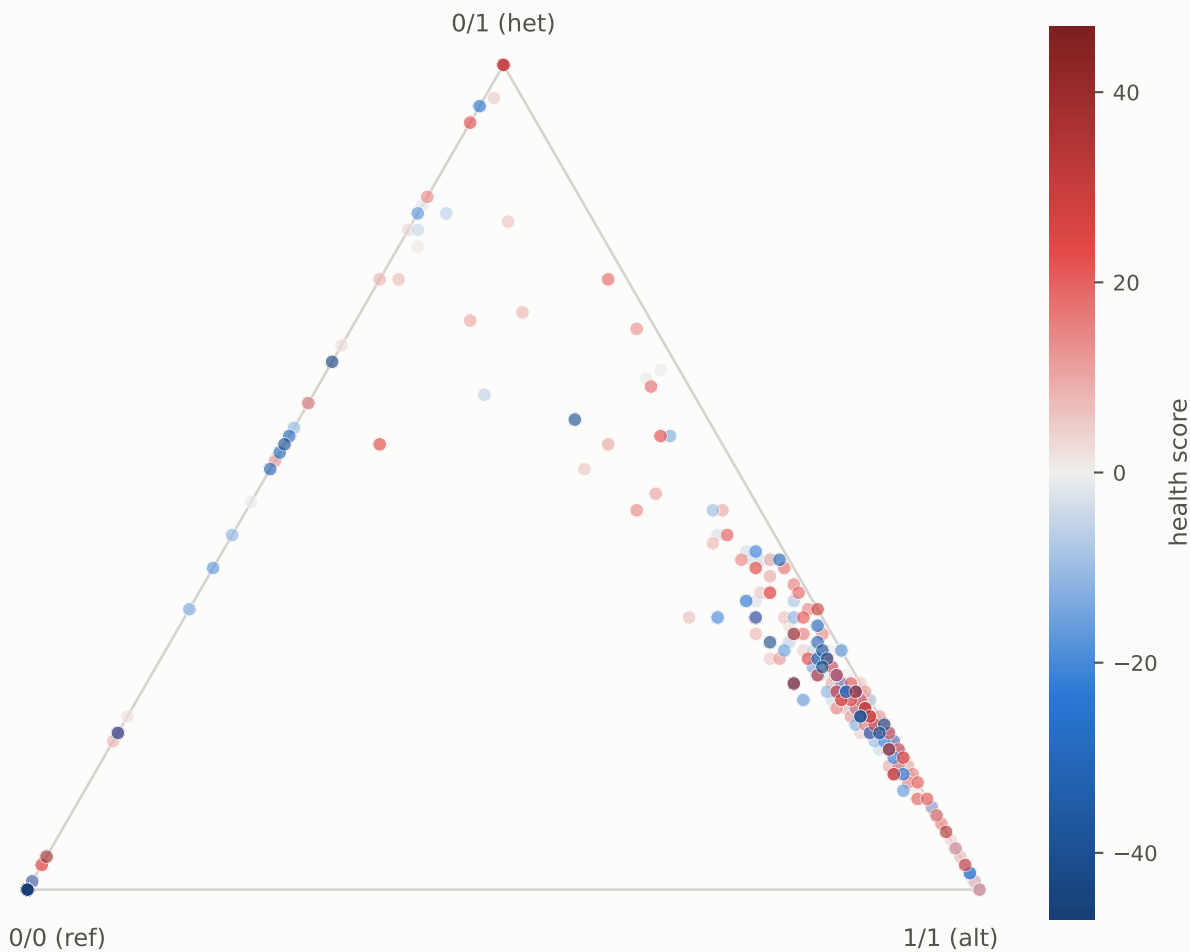
#183 by genotype uncertainty CHR_05:16,912,766 A>T
AF=0.48 DR2=0.81 $r=+0.020$ $\bar{H}=0.393$ F=0.3



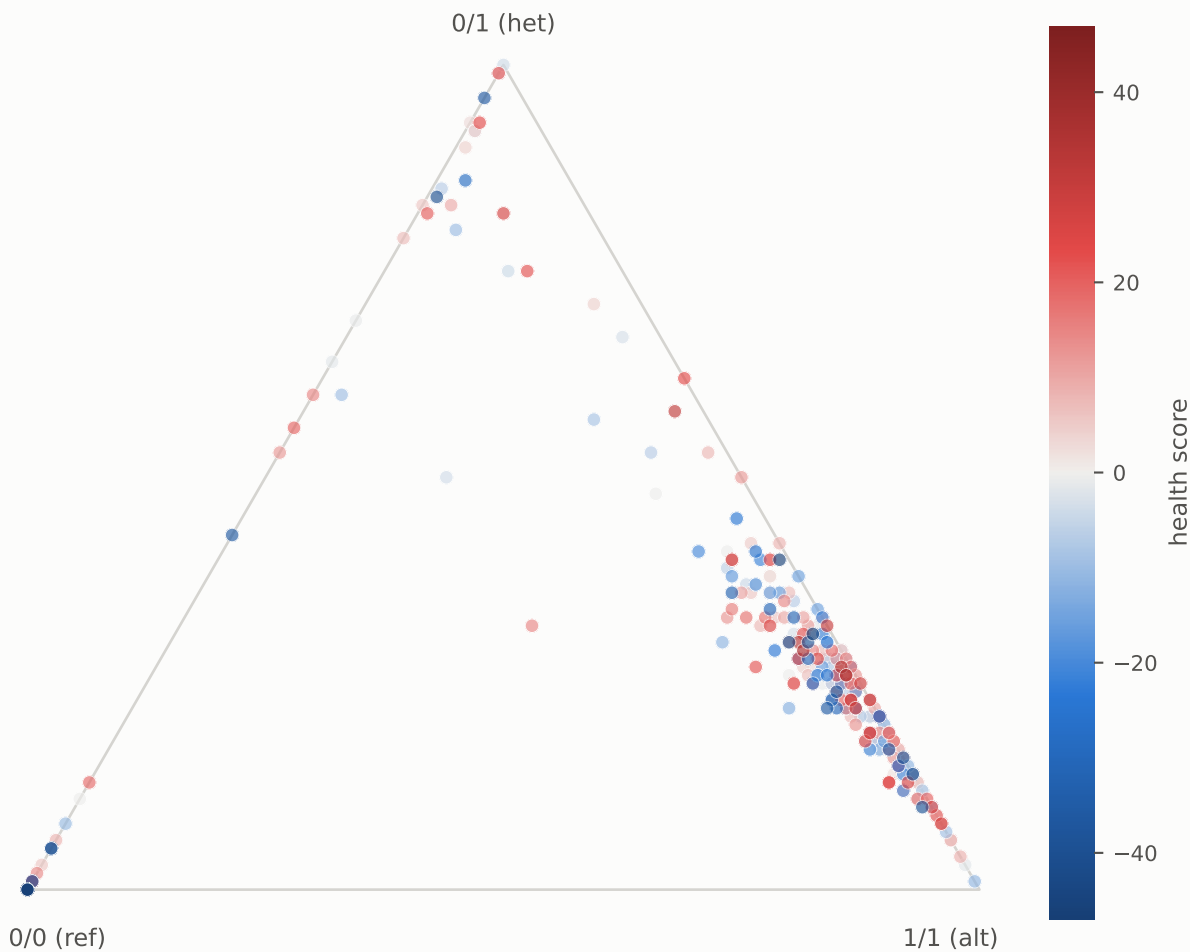
#184 by genotype uncertainty CHR_06:22,516,177 T>A
AF=0.47 DR2=0.81 $r=-0.008$ $\bar{H}=0.393$ $F=0.0$



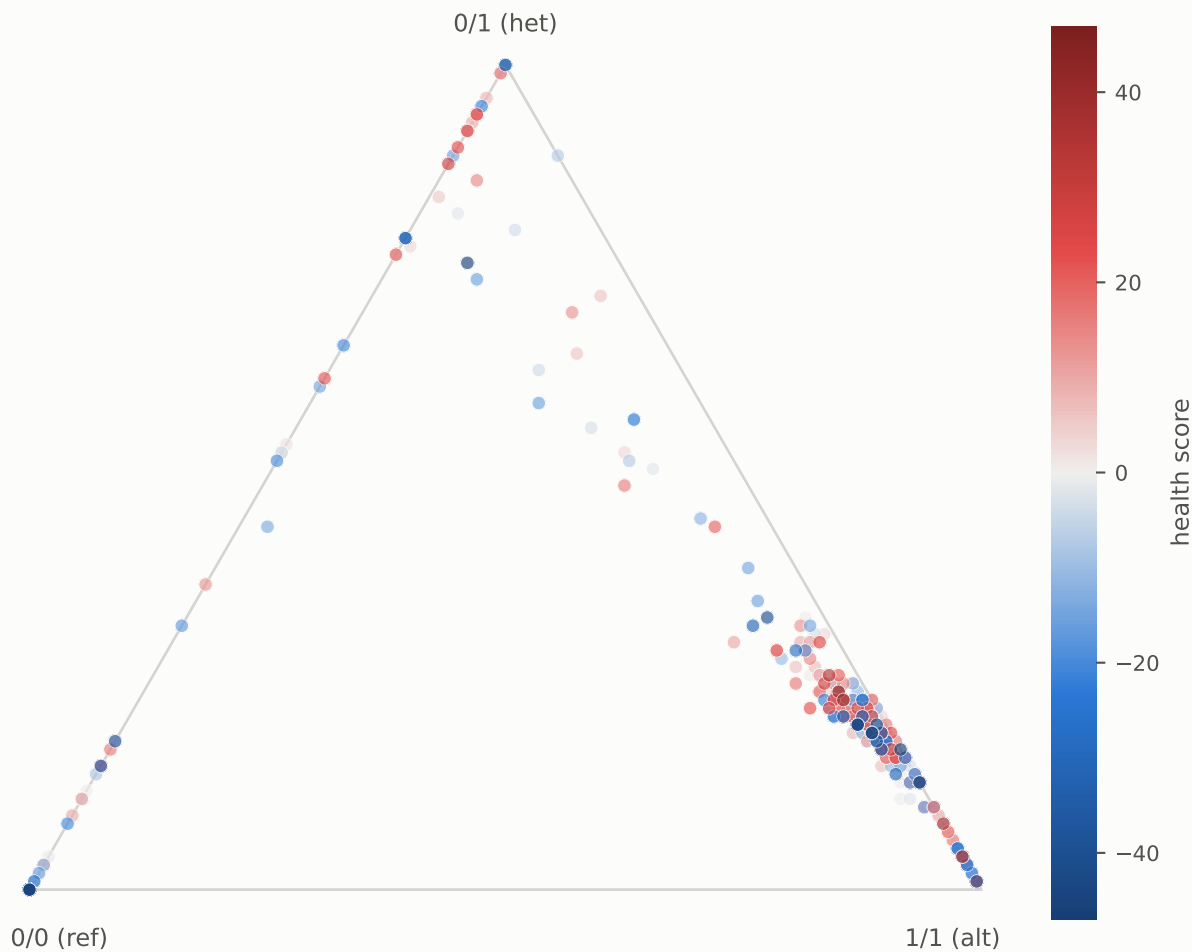
#185 by genotype uncertainty CHR_19:11,162,544 C>T
AF=0.54 DR2=0.81 $r=+0.091$ $\bar{H}=0.393$ F=1.4



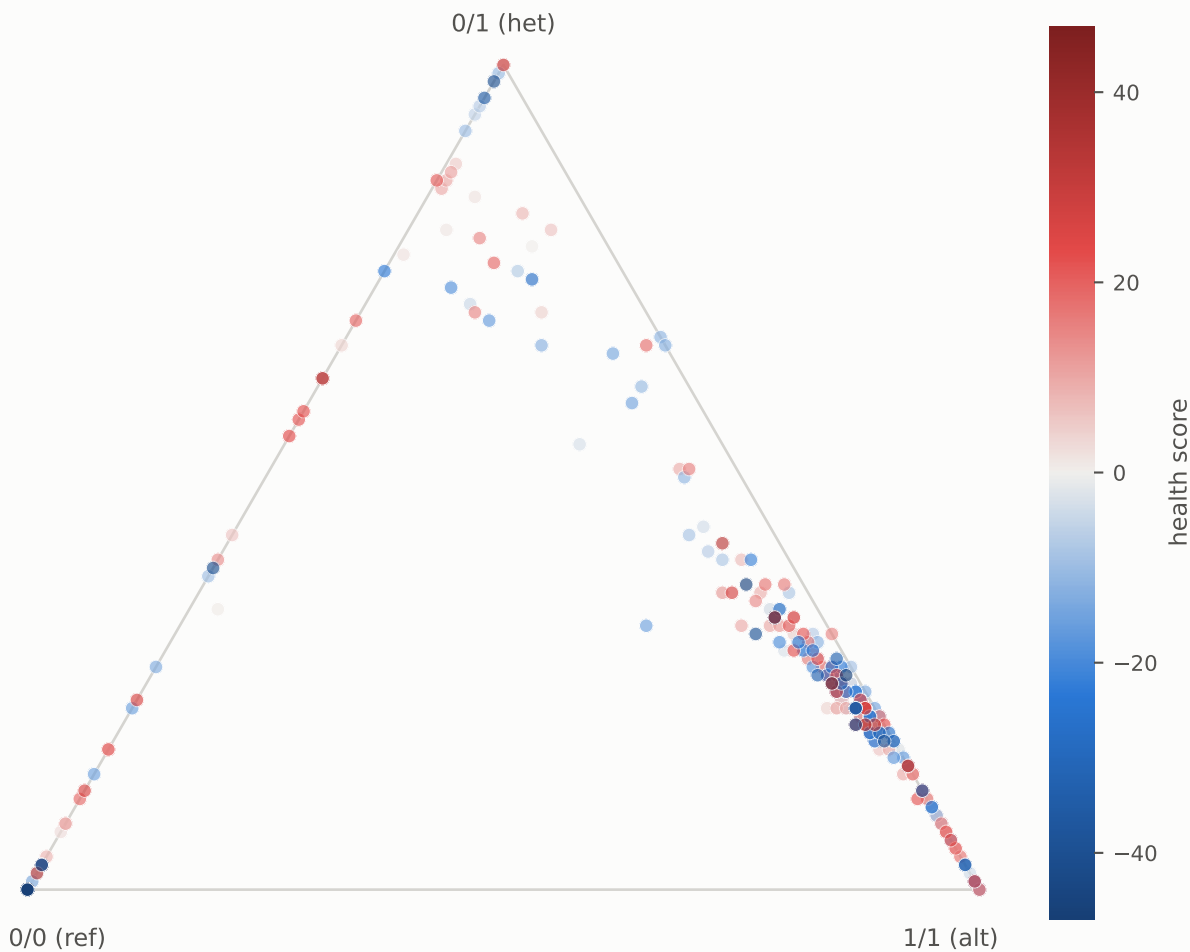
#186 by genotype uncertainty CHR_17:3,114,448 T>C
AF=0.51 DR2=0.81 $r=+0.059$ $\bar{H}=0.393$ F=1.3



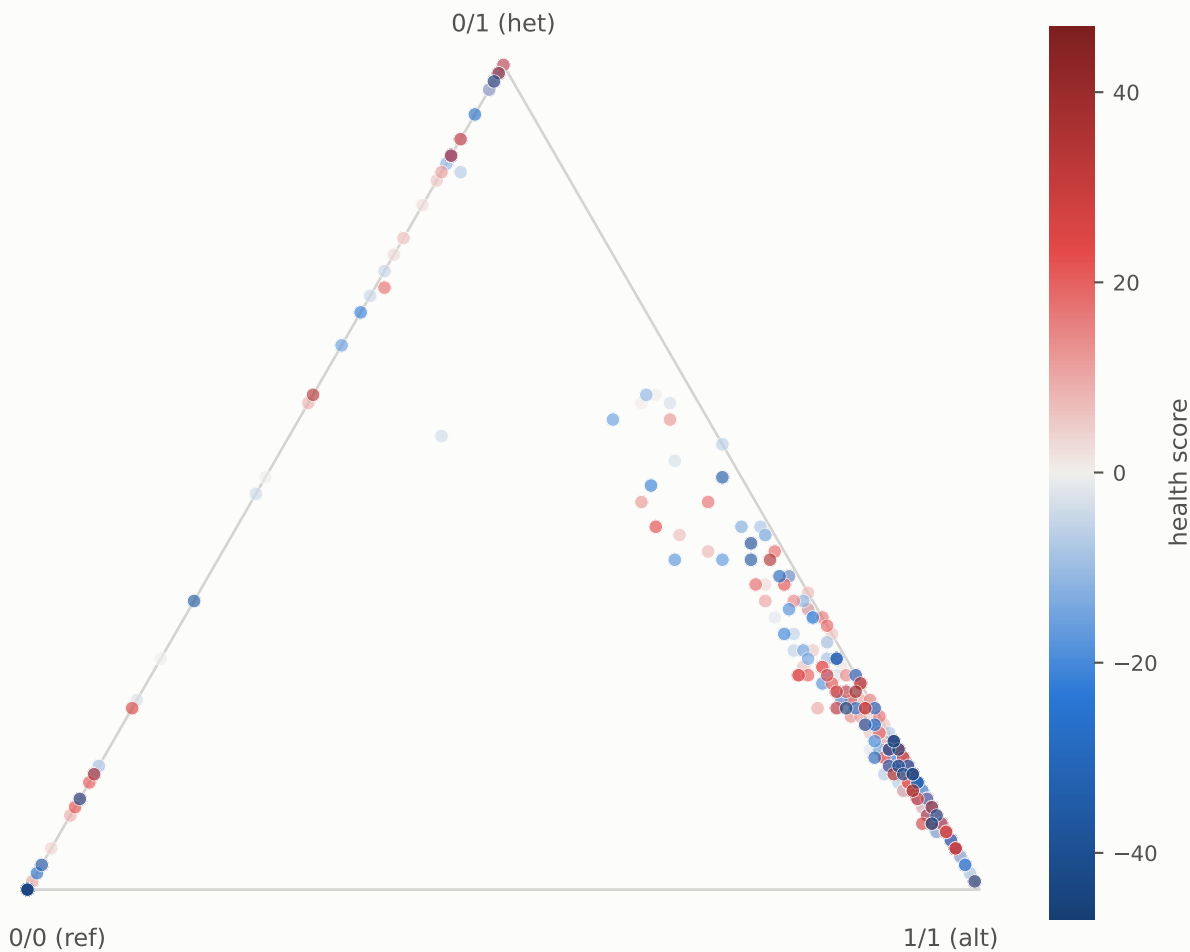
#187 by genotype uncertainty CHR_10:8,136,708 A>G
AF=0.56 DR2=0.82 $r=+0.009$ $\bar{H}=0.393$ F=0.2



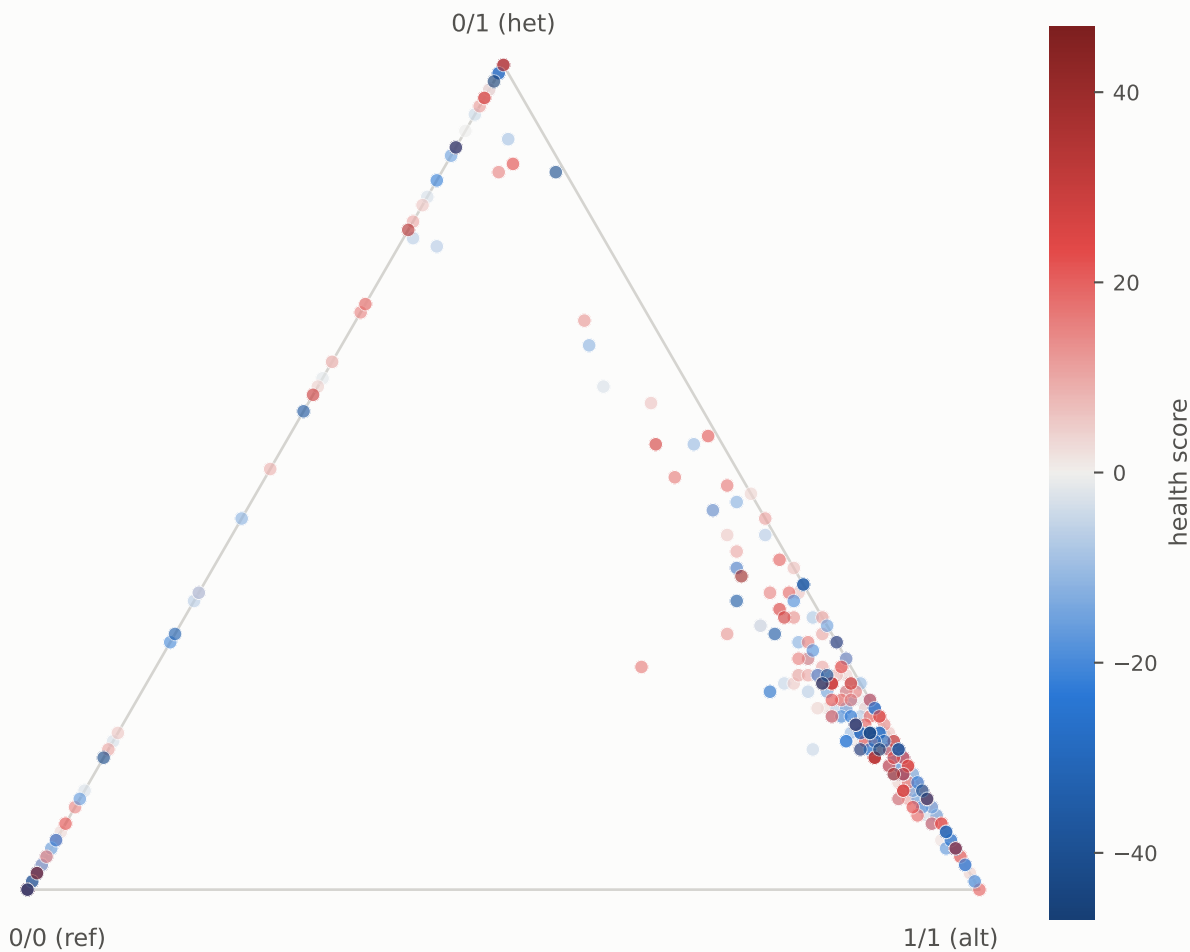
#188 by genotype uncertainty CHR_02:17,537,256 T>C
AF=0.52 DR2=0.81 $r=-0.055$ $\bar{H}=0.393$ F=0.6



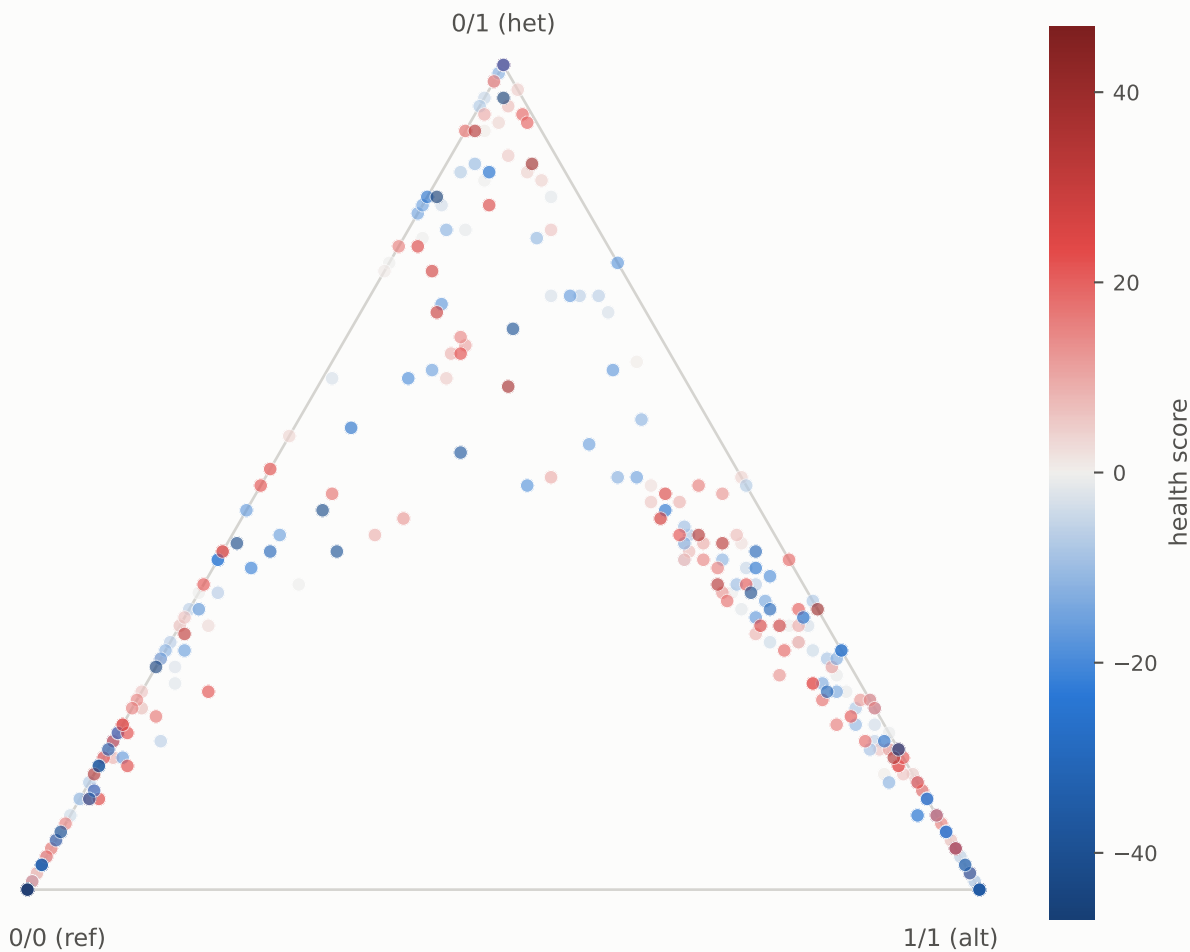
#189 by genotype uncertainty CHR_04:23,282,557 A>G
AF=0.63 DR2=0.81 $r=+0.029$ $\bar{H}=0.393$ F=0.3



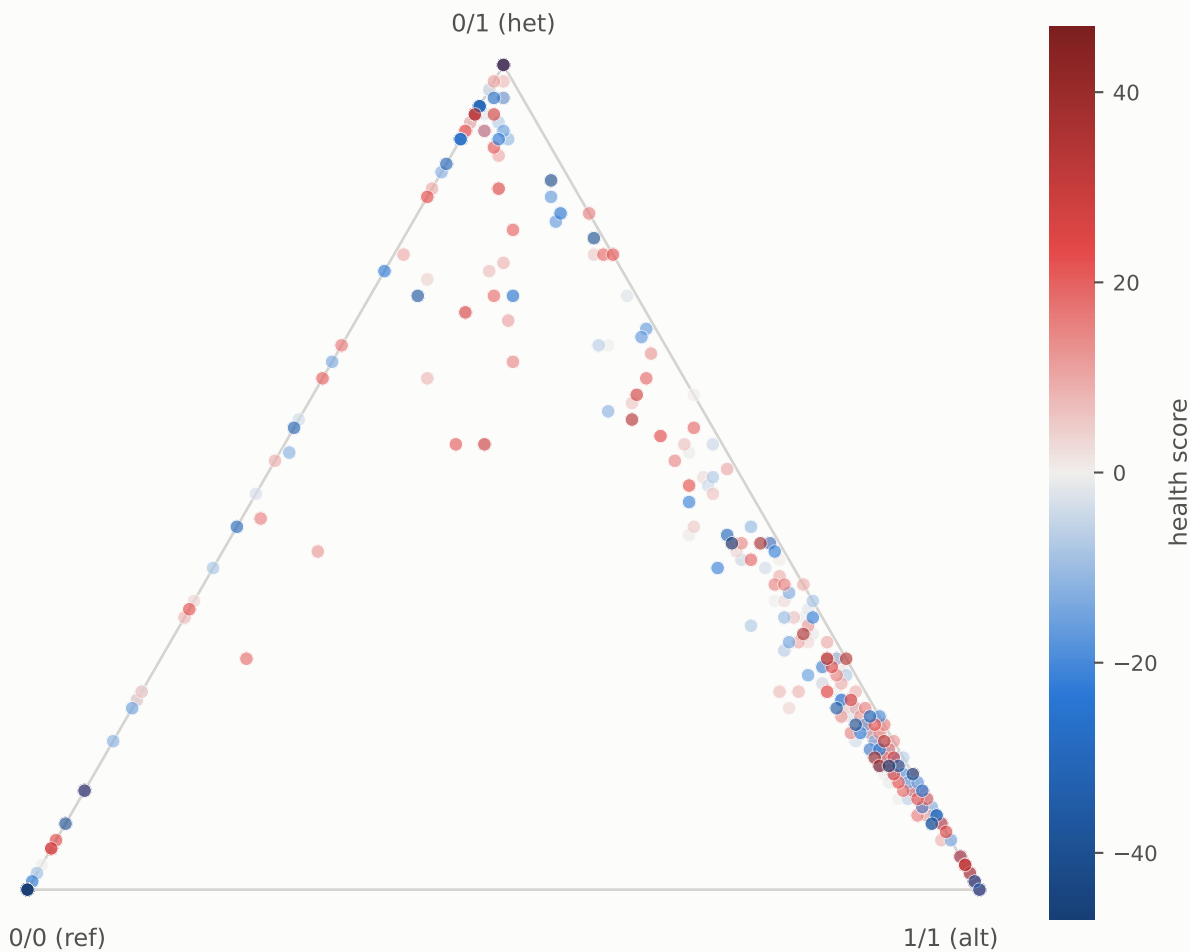
#190 by genotype uncertainty CHR_07:34,900,224 A>G
AF=0.58 DR2=0.81 $r=-0.016$ $\bar{H}=0.393$ $F=0.3$



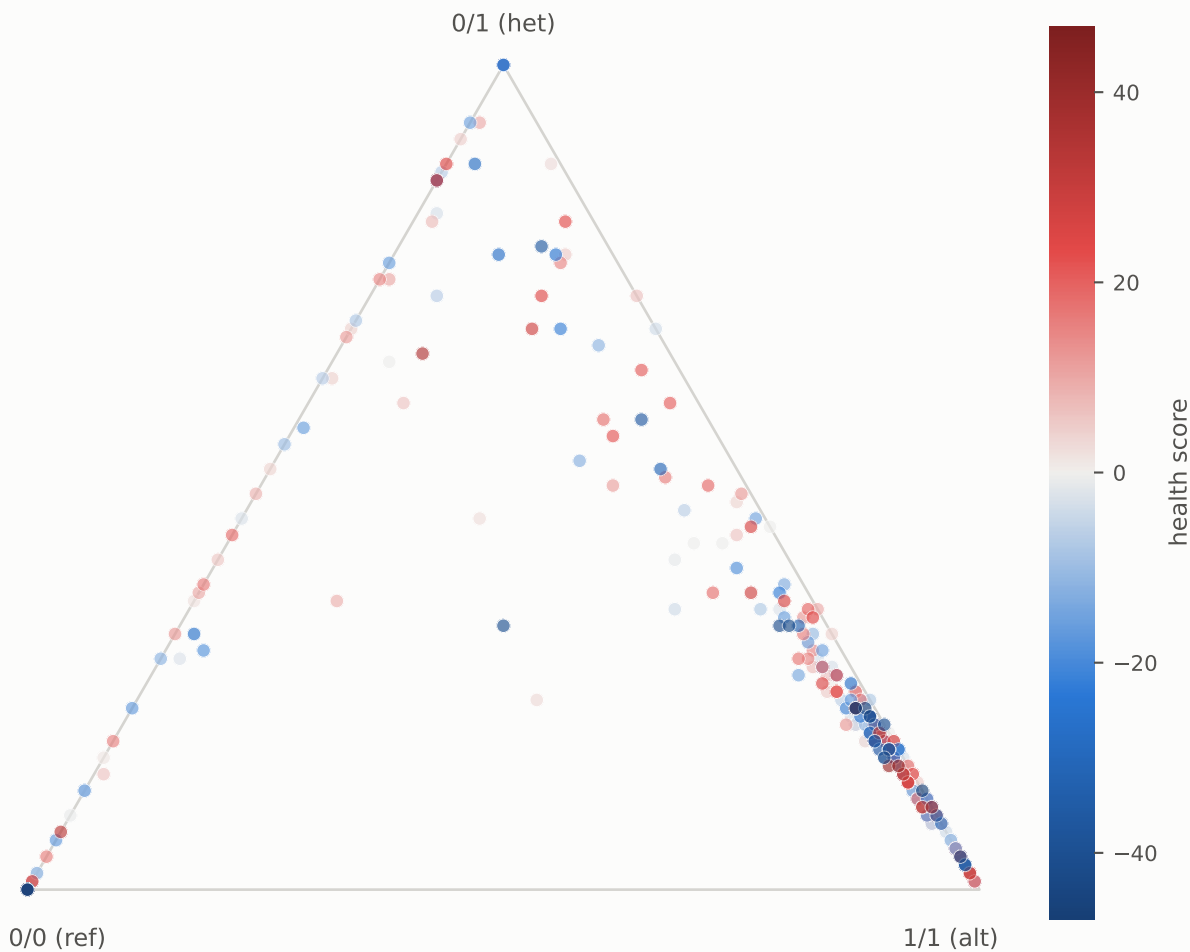
#191 by genotype uncertainty CHR_16:30,142,532 A>G
AF=0.44 DR2=0.81 $r=+0.011$ $\bar{H}=0.393$ F=0.3



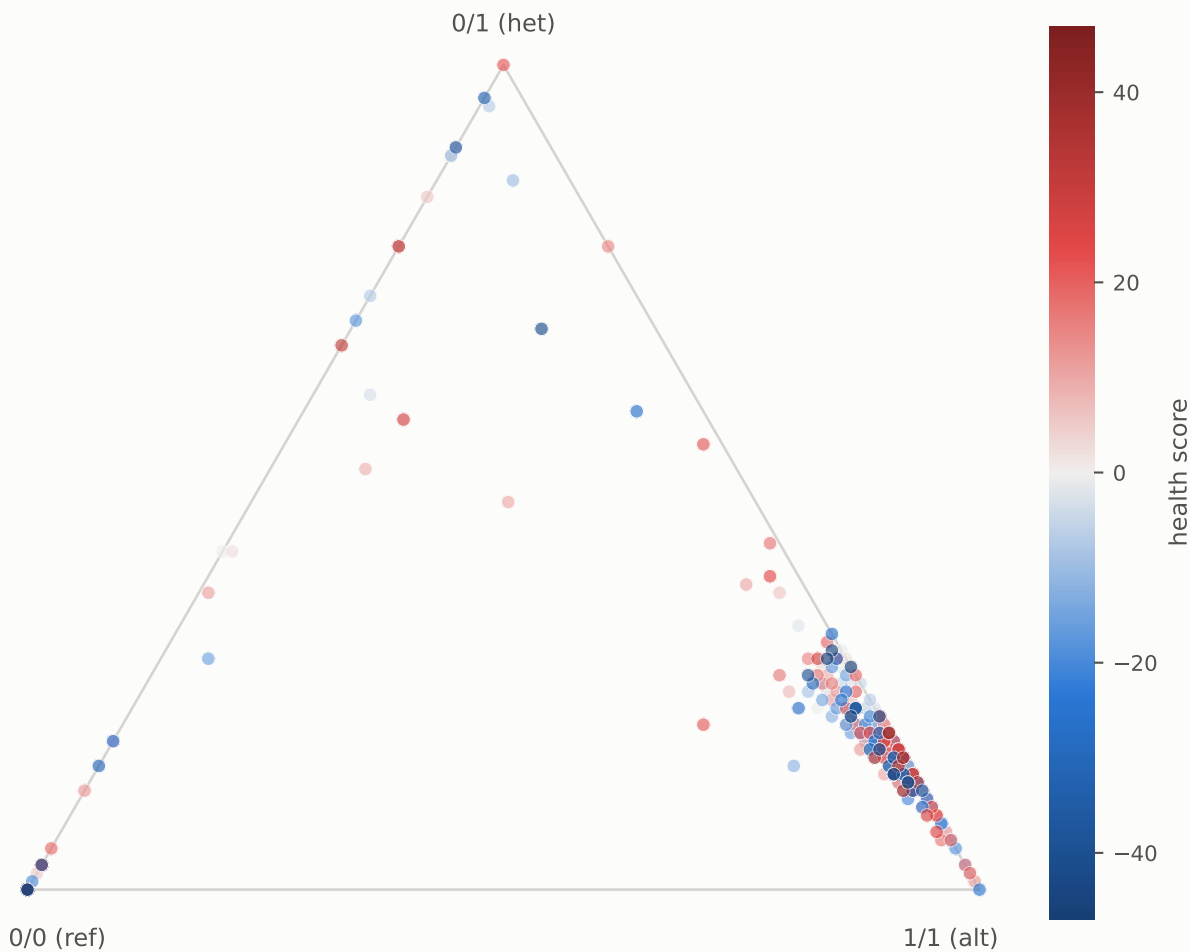
#192 by genotype uncertainty CHR_05:1,844,004 A>C
AF=0.52 DR2=0.81 $r=+0.070$ $\bar{H}=0.393$ F=0.9



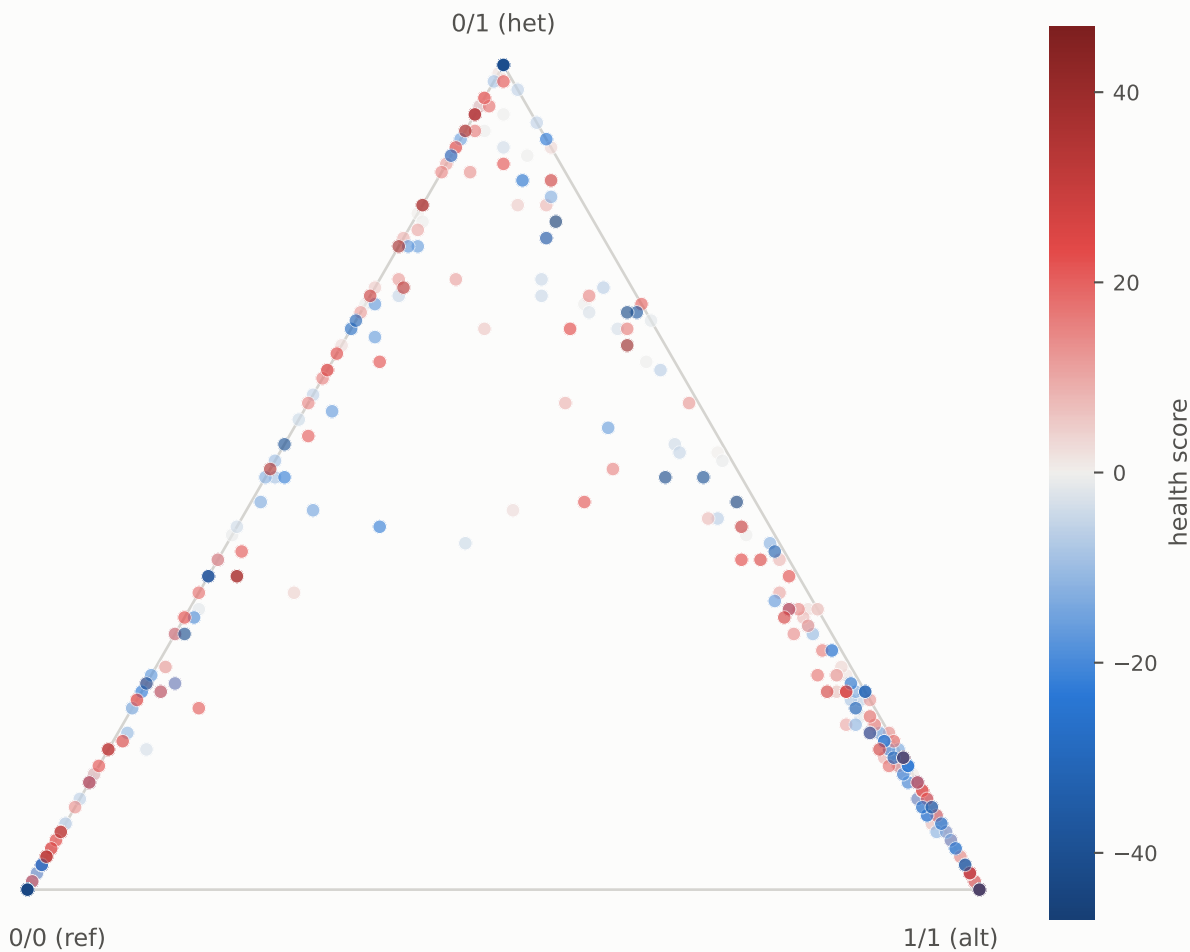
#193 by genotype uncertainty CHR_14:19,104,595 T>A
AF=0.57 DR2=0.81 $r=-0.044$ $\bar{H}=0.393$ $F=0.6$



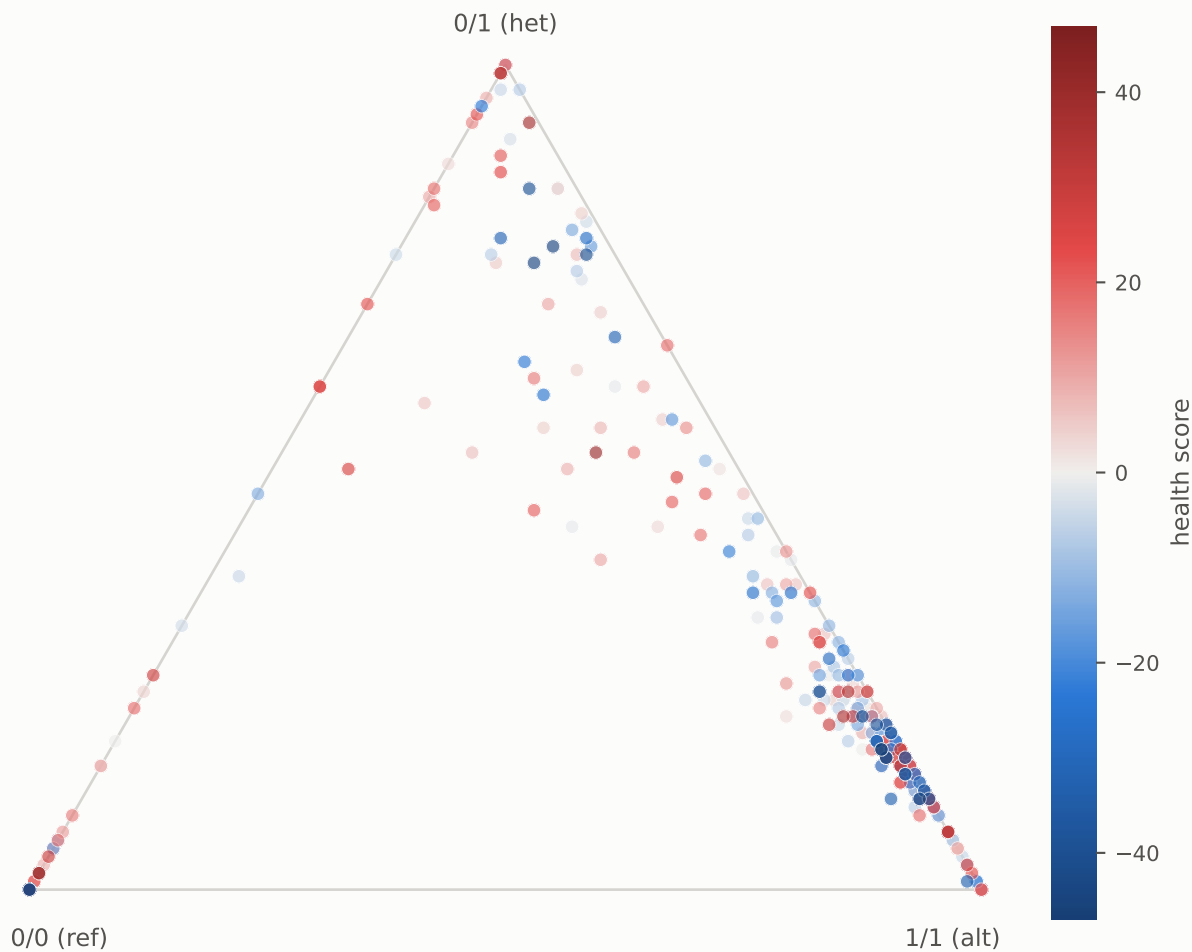
#194 by genotype uncertainty CHR_08:34,824,923 A>G
AF=0.58 DR2=0.83 $r=-0.073$ $\bar{H}=0.393$ F=1.2



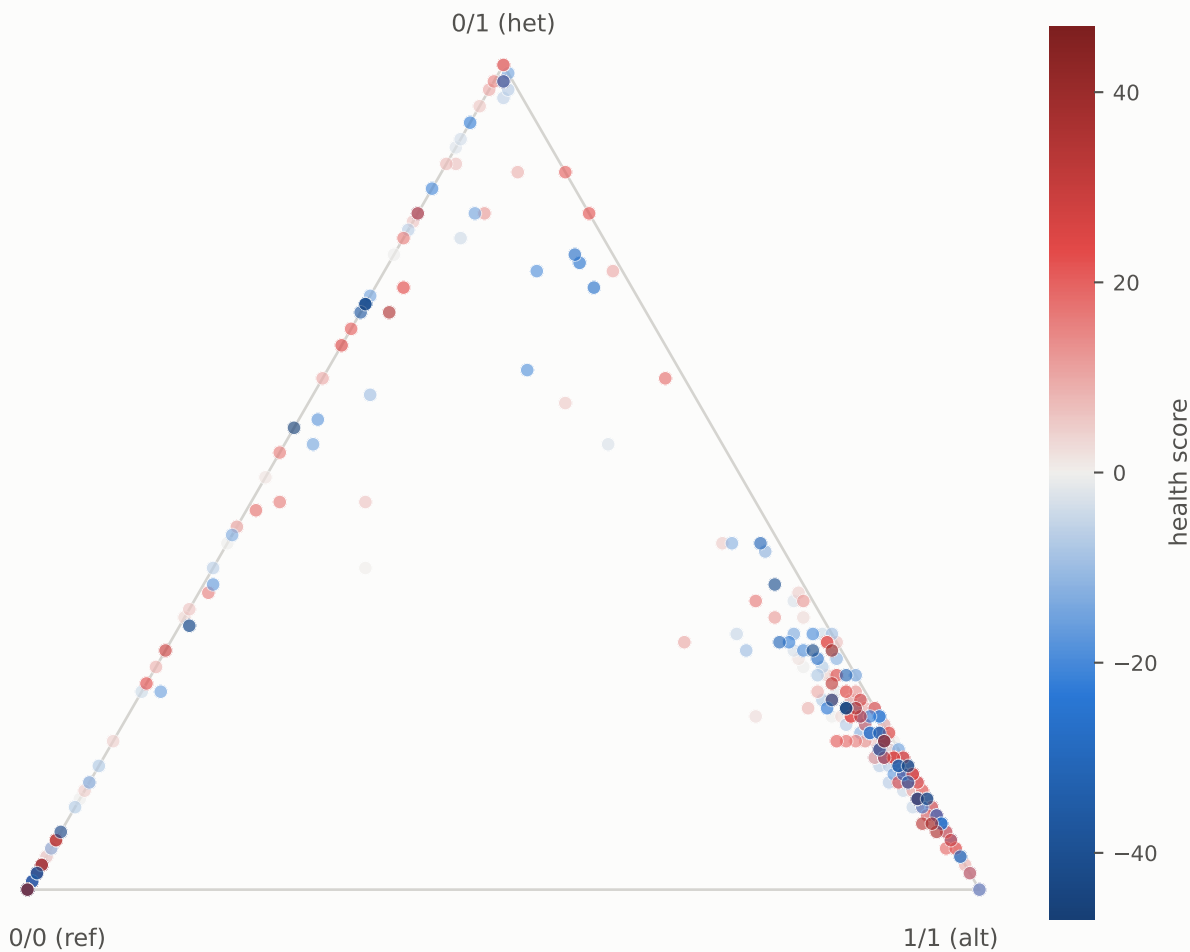
#195 by genotype uncertainty CHR_11:10,210,342 G>C
AF=0.48 DR2=0.81 $r=+0.005$ $\bar{H}=0.393$ F=0.2



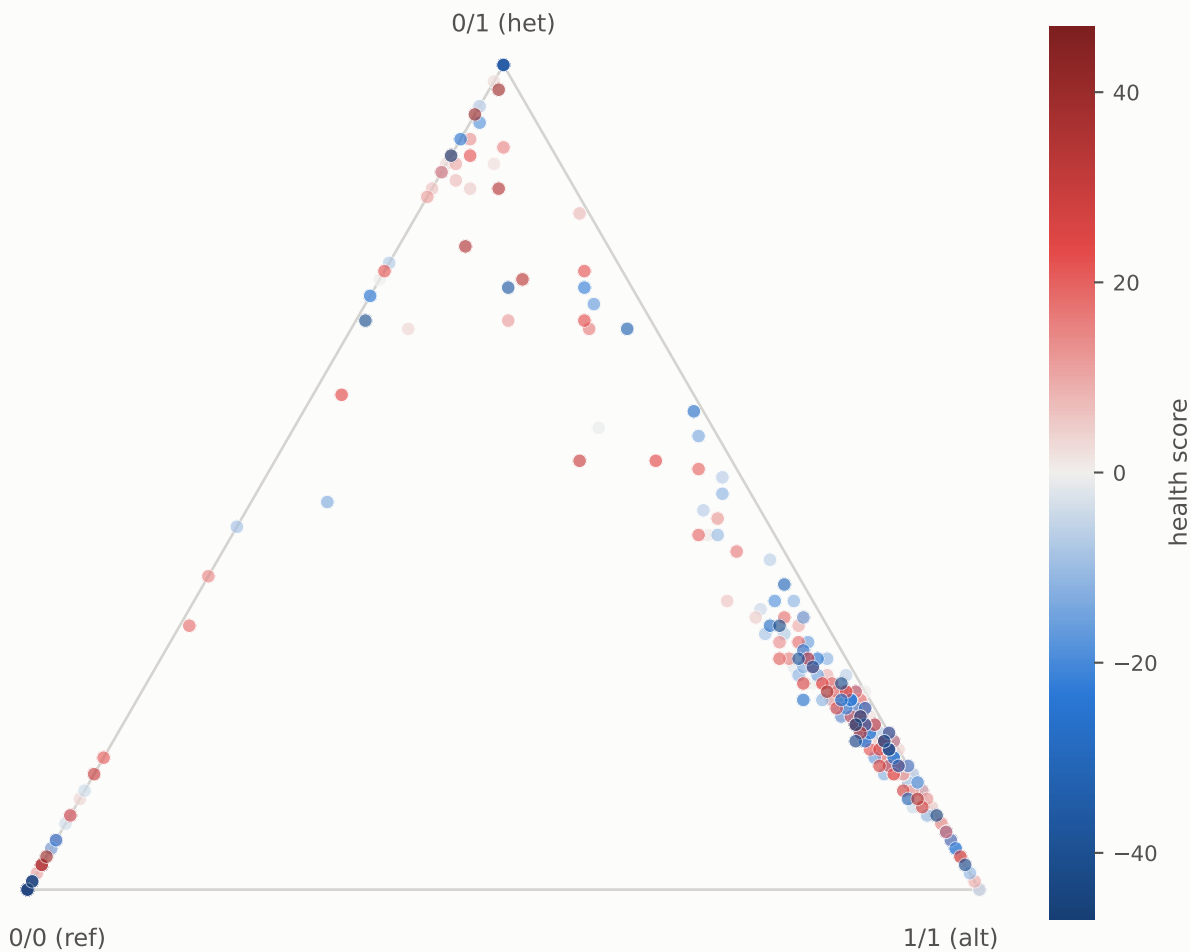
#196 by genotype uncertainty CHR_11:4,858,930 G>A
AF=0.58 DR2=0.81 $r=-0.093$ $\bar{H}=0.392$ $F=3.0$



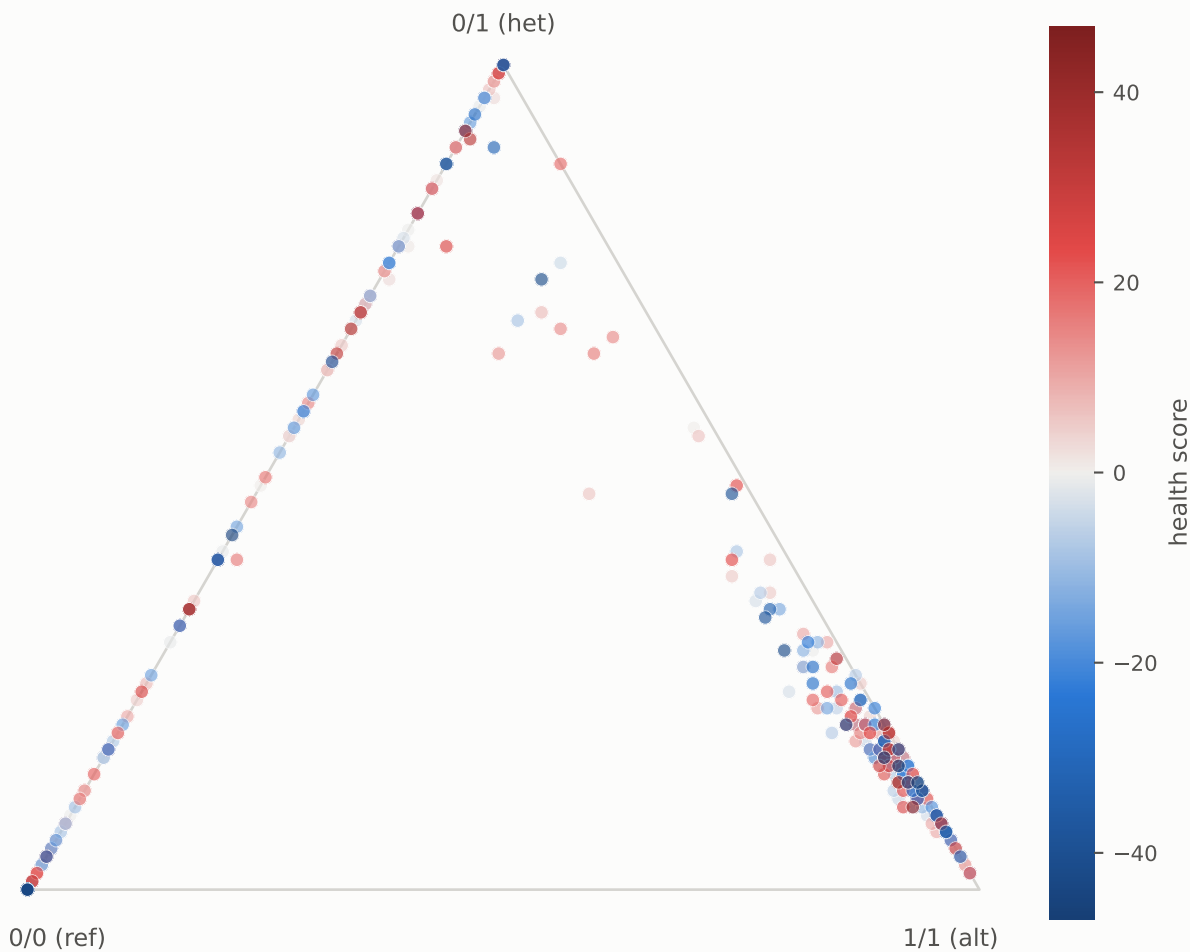
#197 by genotype uncertainty CHR_19:15,469,932 T>C
AF=0.59 DR2=0.81 $r=-0.001$ $\bar{H}=0.392$ $F=0.5$



#198 by genotype uncertainty CHR_20:5,568,559 T>C
AF=0.55 DR2=0.81 r=-0.057 H=0.392 F=1.1



#199 by genotype uncertainty CHR_01:37,873,444 T>C
AF=0.54 DR2=0.81 $r=-0.049$ $\bar{H}=0.392$ F=0.7



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

