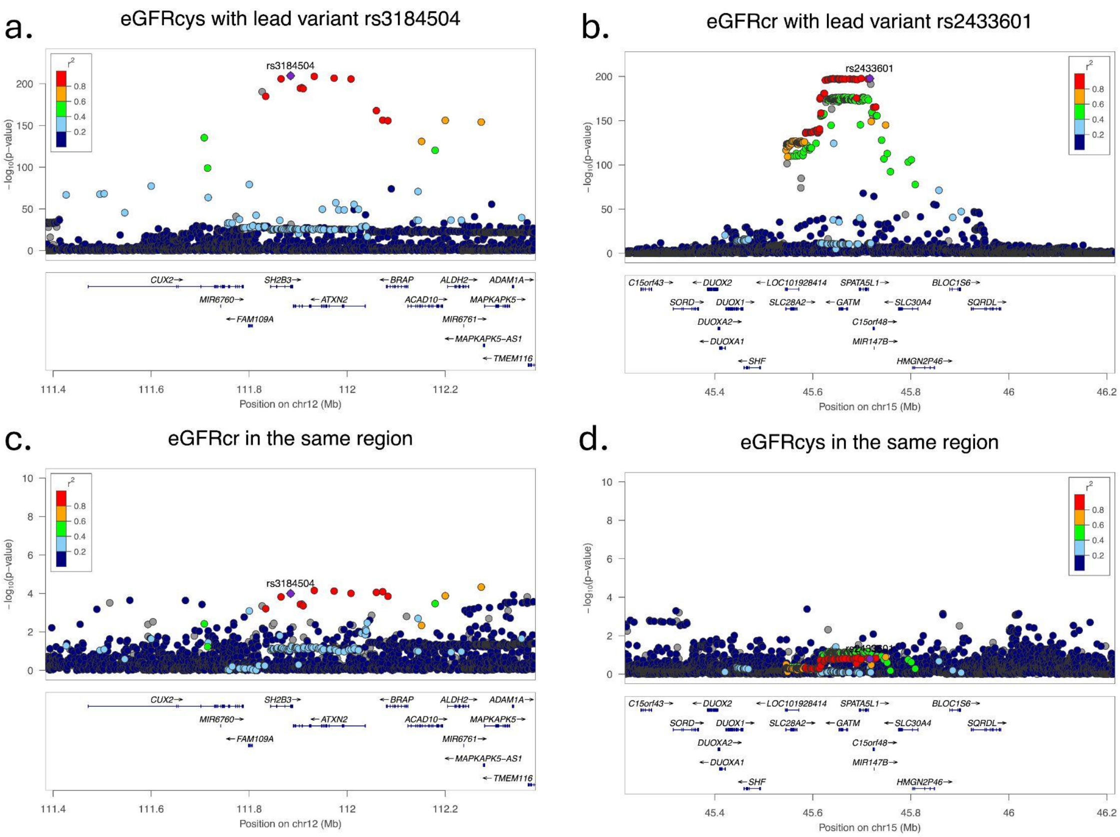
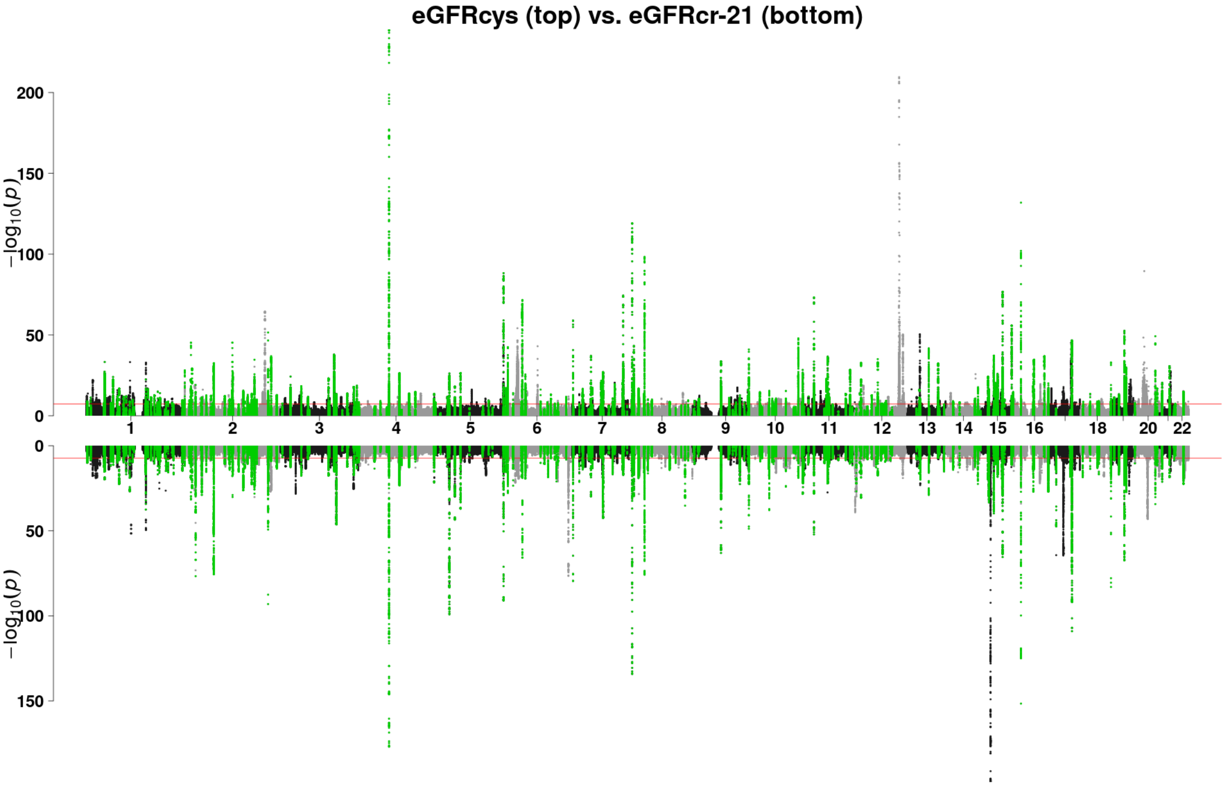
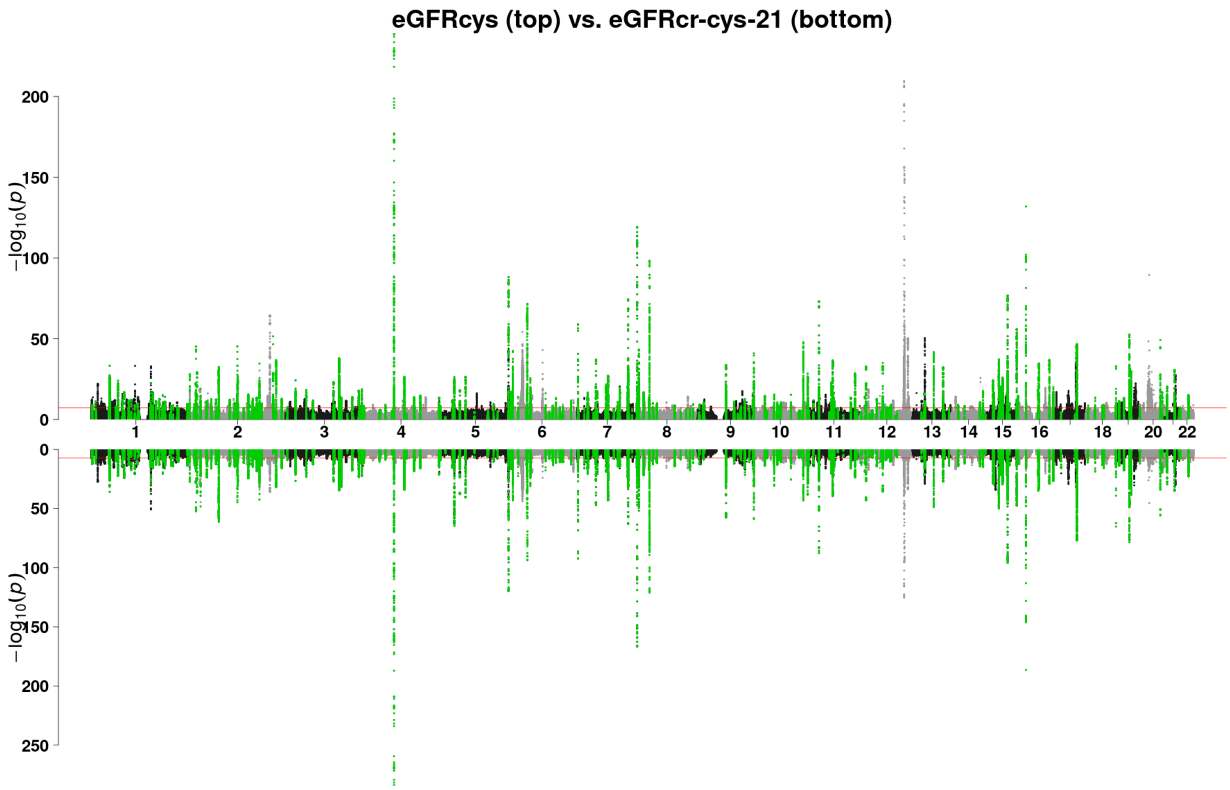


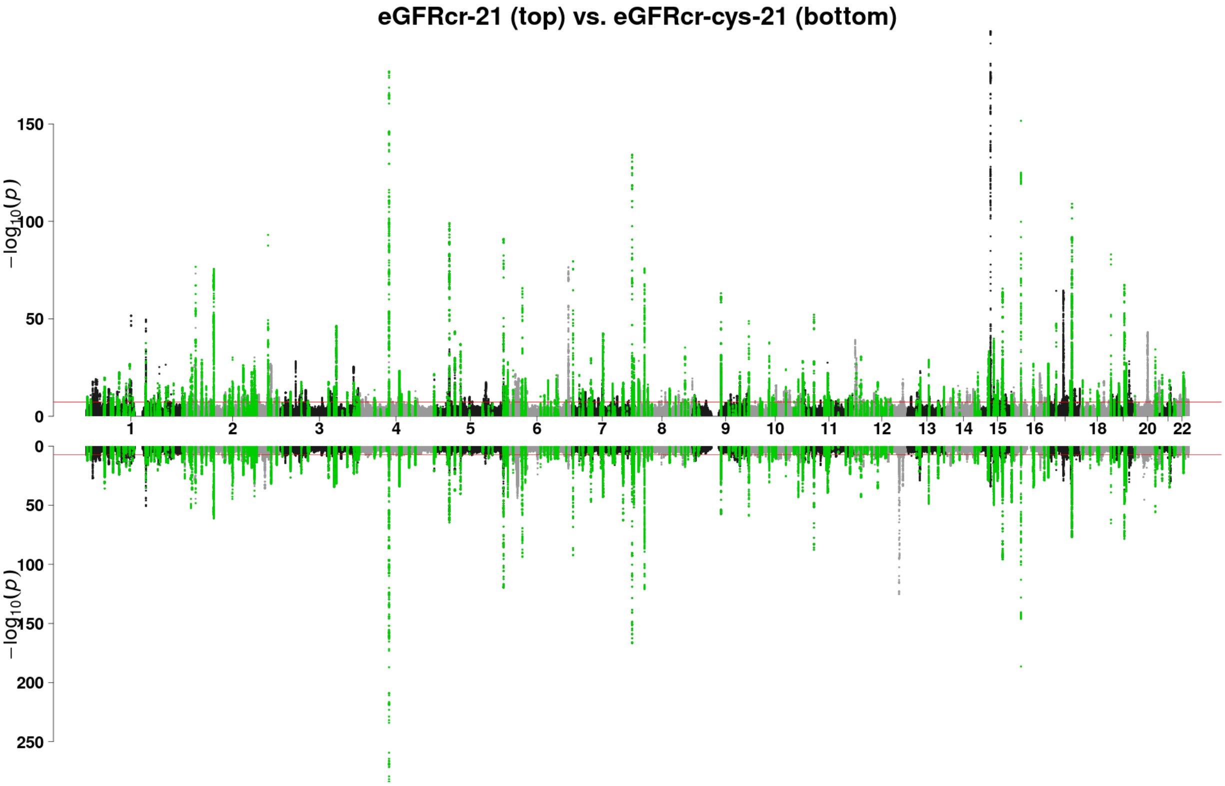
Extended Data Fig 1. Locuszoom plot showing inconsistencies between eGFRcys and eGFRcr. **a,c.** On chromosome 12, eGFRcys has a significant signal with leading variant rs3184504 (a, p-value = 4.5e-210), while this region doesn't show any significant signal in eGFRcr (c, p-value = 1e-4). **b,d.** On chromosome 15, eGFRcr has a significant signal with leading variant rs2433601 (b, p-value = 1.9e-198), while this region also doesn't show any significant signal in eGFRcys (d, p-value = 0.159).



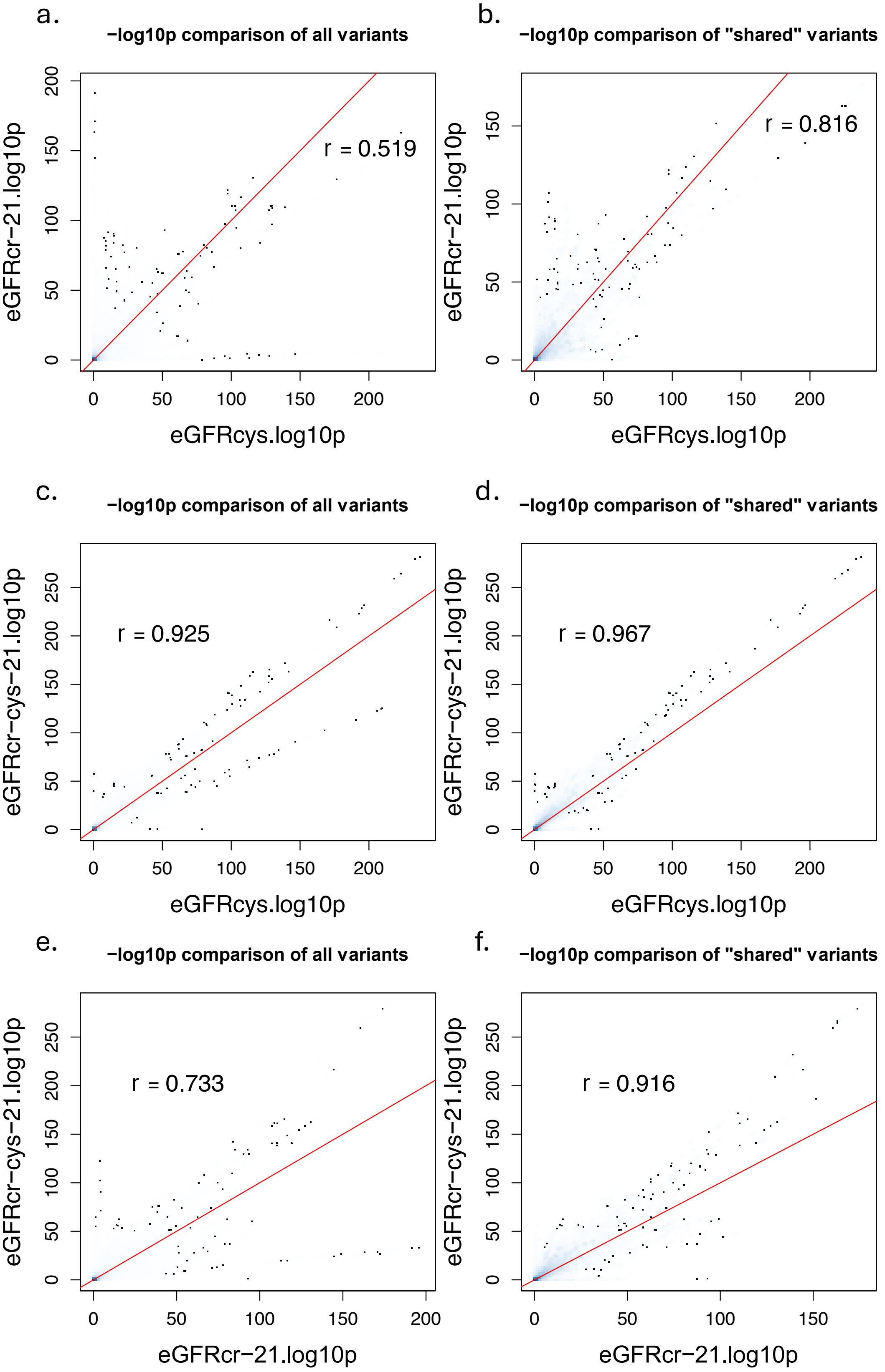
Extended Data Fig 2. Mirror Manhattan plot comparing the GWAS between eGFRcys (top panel) and eGFRcr^{2021} (bottom panel). The variants inside the shared regions are highlighted as green.



Extended Data Fig 3. Mirror Manhattan plot comparing the GWAS between eGFRcys (top panel) and eGFRcys-cr^{2021} (bottom panel). The variants inside the shared regions are highlighted as green.



Extended Data Fig 4. Mirror Manhattan plot comparing the GWAS between eGFRcr^{2021} (top panel) and eGFRcys-cr^{2021} (bottom panel). The variants inside the shared regions are highlighted as green.



a.
−log10p comparison of all variants
eGFRcr−21.log10p
eGFRcys.log10p
0
50
100
150
200
r = 0.519
b.
−log10p comparison of "shared" variants
eGFRcr−21.log10p
eGFRcys.log10p
0
50
100
150
200
r = 0.816
c.
−log10p comparison of all variants
eGFRcr−cys−21.log10p
eGFRcys.log10p
0
50
100
150
200
250
r = 0.925
d.
−log10p comparison of "shared" variants
eGFRcr−cys−21.log10p
eGFRcys.log10p
0
50
100
150
200
250
r = 0.967
e.
−log10p comparison of all variants
eGFRcr−cys−21.log10p
eGFRcr−21.log10p
0
50
100
150
200
250
r = 0.733
f.
−log10p comparison of "shared" variants
eGFRcr−cys−21.log10p
eGFRcr−21.log10p
0
50
100
150
200
250
r = 0.916

Extended Data Fig 5. Scatterplot comparing the -log10p values for all GWAS variants and “shared” variants. **a,b.** Comparing the GWAS -log10p between eGFRcys and eGFRcr^{2021}. The correlation for all GWAS variants and variants only inside the shared regions are 0.519 and 0.816, respectively; **c,d.** Comparing the GWAS -log10p between eGFRcys and eGFRcys-cr^{2021}. The correlation for all GWAS variants and variants only inside the shared regions are 0.925 and 0.967, respectively; **e.f.** Comparing the GWAS -log10p between eGFRcr^{2021} and eGFRcys-cr^{2021}. The correlation for all GWAS variants and variants only inside the shared regions are 0.733 and 0.916, respectively;