Supporting Information

Epoxidation Activities of Human Cytochromes P450c17 and P450c21

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<u>16,17-epoxyprogesterone (2):</u>





Figure S1. Extracted ion chromatograms, MS and MS^2 spectra for 21-hydroxy-16,17-dehydroprogesterone (**3**, 11.05 min), 16,17-epoxyprogesterone (**2**, 18.21 min) and 16,17-dehydroprogesterone (**1**, 20.98 min) standards. The $[M+H]^+$ ions of products **3** and **2** or of substrate **1** are m/z 329, 329 and 313 respectively. Proposed fragmentation pathways are shown in Figure S9.







Metabolite B:



Figure S2. Extracted ion chromatograms, MS and MS^2 spectra of Metabolite A = 21-hydroxy-16,17dehydroprogesterone (**3**) and Metabolite B = 16,17-epoxyprogesterone (**2**) obtained by LC-MS/MS analysis of products derived from incubations of wild-type CYP17A1 in yeast microsomes with compound **1** (16,17-dehydroprogesterone) in the presence of NADPH.







Metabolite B:



Figure S2. Extracted ion chromatograms, MS and MS^2 spectra of Metabolite A = 21-hydroxy-16,17dehydroprogesterone (**3**) and Metabolite B = 16,17-epoxyprogesterone (**2**) obtained by LC-MS/MS analysis of products derived from incubations of CYP17A1 mutation A105L in yeast microsomes with compound **1** (16,17-dehydroprogesterone) in the presence of NADPH.











Figure S4. Extracted ion chromatograms, MS and MS^2 spectra of Metabolite A = 21-hydroxy-16,17dehydroprogesterone (**3**) and Metabolite B = 16,17-epoxyprogesterone (**2**) obtained by LC-MS/MS analysis of products derived from incubations of wild-type CYP21A2 in yeast microsomes with compound **1** (16,17-dehydroprogesterone) in the presence of NADPH.







Metabolite B:



Figure S5. Extracted ion chromatograms, MS and MS^2 spectra of Metabolite A = 21-hydroxy-16,17dehydroprogesterone (**3**) and Metabolite B = 16,17-epoxyprogesterone (**2**) obtained by LC-MS/MS analysis of products derived from incubations of CYP21A2 mutation V359A in yeast microsomes with compound **1** (16,17-dehydroprogesterone) in the presence of NADPH.



Figure S6. HPLC chromatograms of products from incubations of CYP17A1 with compound 1 (16,17dehydroprogesterone) in the absence and presence of ketoconazole or abiraterone. (A) CYP17A1 incubation with compound 1. (B) CYP17A1 A105L incubation with compound 1. (C) CYP17A1 incubation with compound 1 and ketoconazole (50 μ M). (D) CYP17A1 incubation with compound 1 and abiraterone (20 μ M). Ketoconazole and abiraterone inhibit formation of both products.



Figure S7. Inhibition of CYP21A2-catalyzed product formation by 3-keto- Δ^4 -abiraterone. A, Total products formed (primarily compound **3**) from incubations of CYP21A2 (30 pmol) and POR with compound **1** (16,17-dehydroprogesterone, 20 µM) are progressively reduced by increasing amounts of added 3-keto- Δ^4 -abiraterone. B, Type 2 spectral changes from titration of purified CYP21A2 (200 pmol) with 3-keto- Δ^4 -abiraterone and curve fitting (ref 23), yielding $K_s = 1.1 \pm 0.5$ nM, $\varepsilon = 15 \pm 1$ mM⁻¹cm⁻¹.



Figure S8. Lack of time-dependent CYP17A1 inhibition by compound **1** or epoxide **2**. Purified CYP17A1 and POR were pre-incubated with progesterone, compound **1**, or epoxide **2** for specified times, then the reaction was diluted and assayed for 17-hydroxylase activity with pregnenolone substrate.



Figure S9. Proposed fragmentation pathways of parent ions in LC-MS/MS experiments.





FYVII-044B.delta5.delta16.prog





Standard Carbon



























