

## Supplementary Information

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**Figure S11.**  $^{13}\text{C-NMR}$  (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide secondary alcohol **1a**.

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**Figure S13.**  $^{13}\text{C-NMR}$  (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide tertiary alcohol **2**.

**Figure S14.**  $^{13}\text{C-NMR}$  (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide ketone **3**.

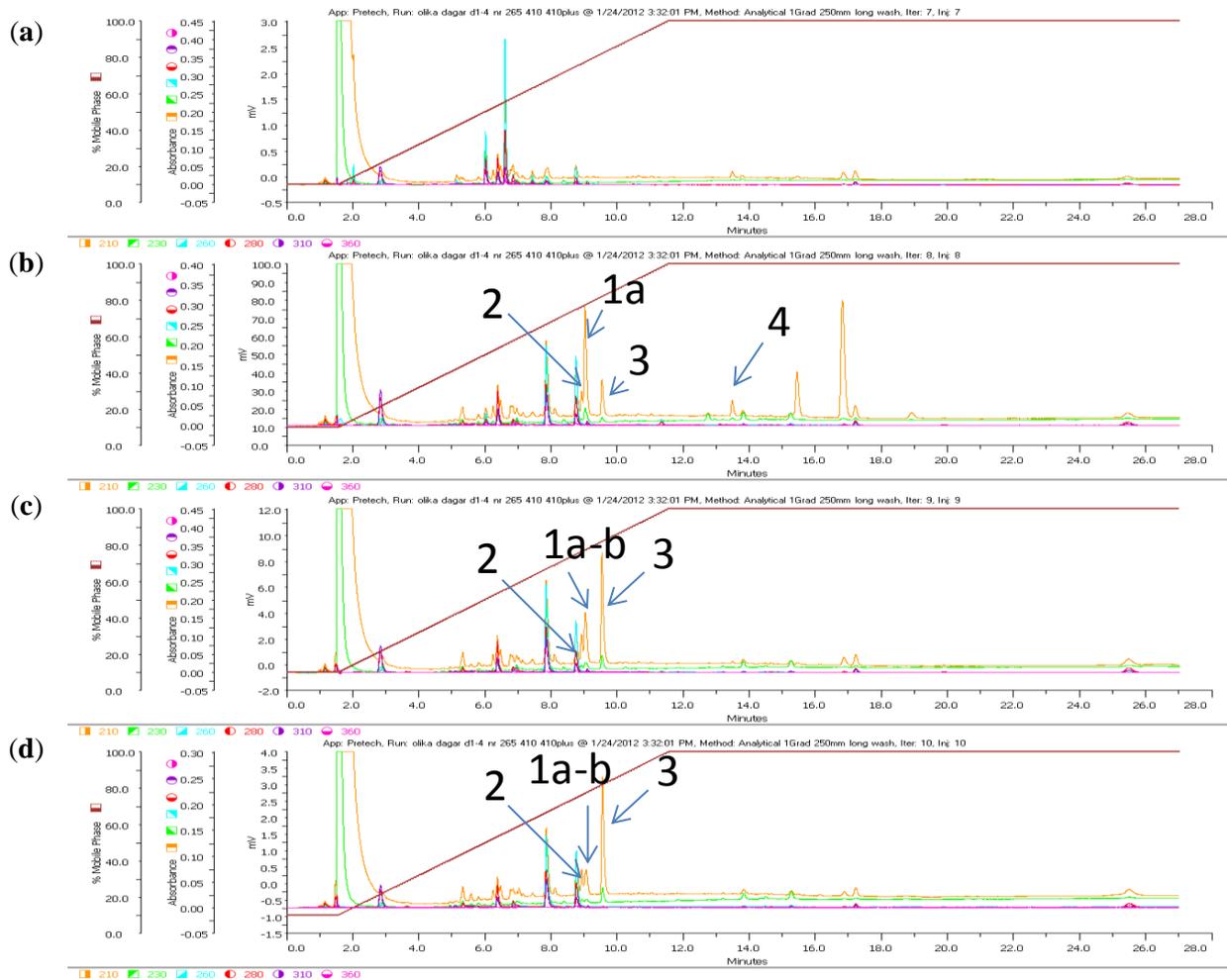
**Figure S15.**  $^{13}\text{C-NMR}$  (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide with non functional side chain **4**.

**Figure S16.**  $^{13}\text{C-NMR}$  (100 MHz,  $\text{CDCl}_3$ ) spectrum of saturated butenolide ketone **5**.

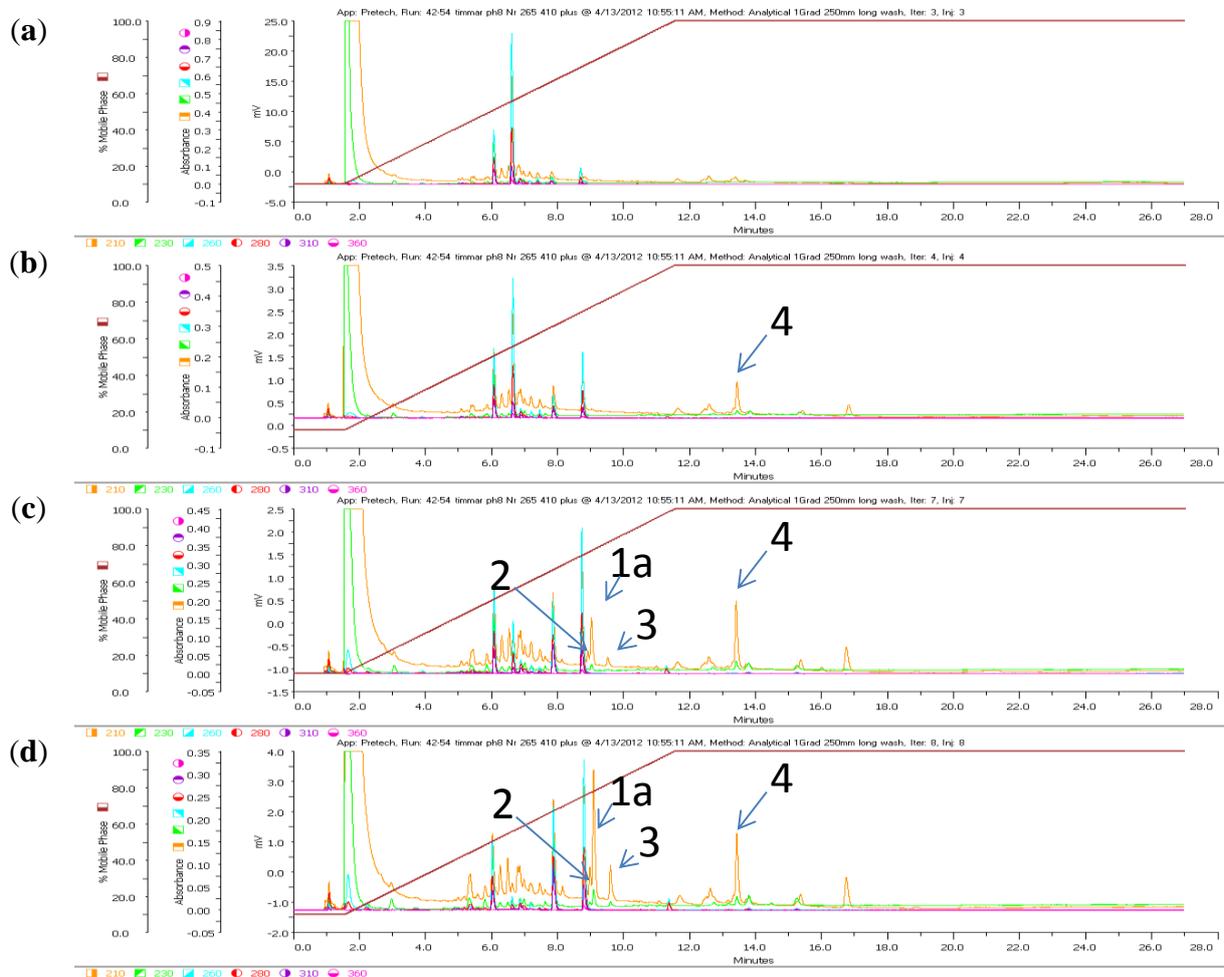
**Figure S17.**  $^{13}\text{C-NMR}$  (100 MHz  $\text{CDCl}_3$ ) spectrum of saturated butenolide **6**.

**Figure S18.** Phylogenetic analysis of *Streptomyces* sp. AW28M48.

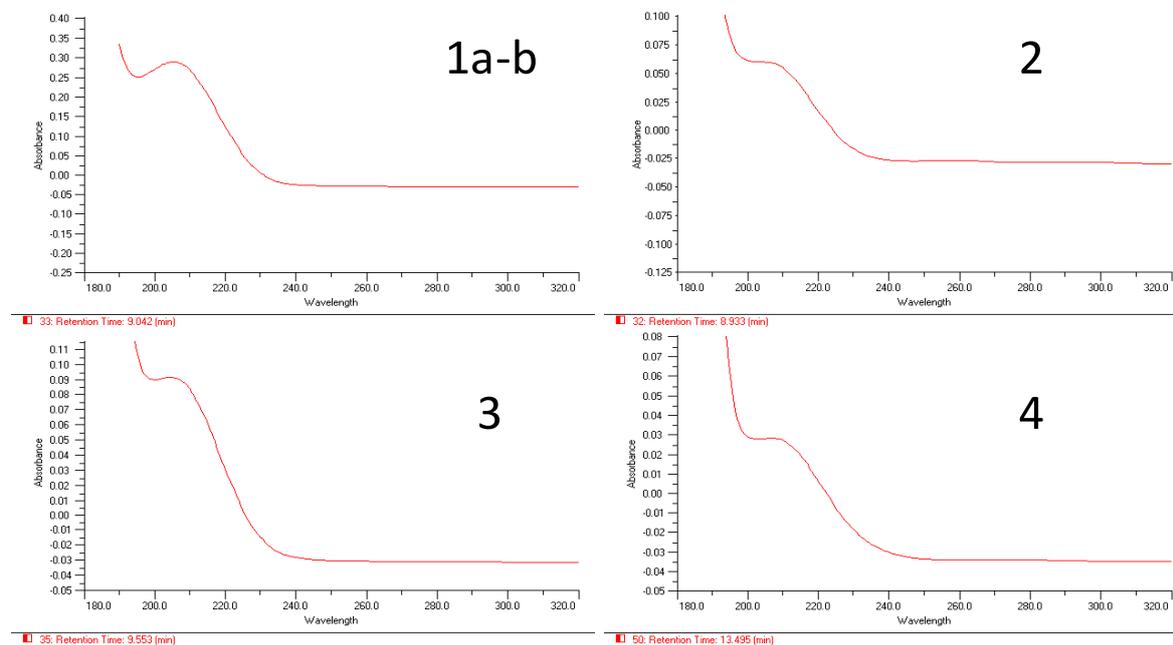
**Figure S1.** Ethyl acetate extract of media supernatant after different time of cultivation: (a) 1 day; (b) 2 days; (c) 3 days; (d) 4 days. Retention times for butenolides **1–4**: **1a** and **1b** = 9.04 min; **2** = 8.93 min; **3** = 9.55 min; **4** = 13.50 min.

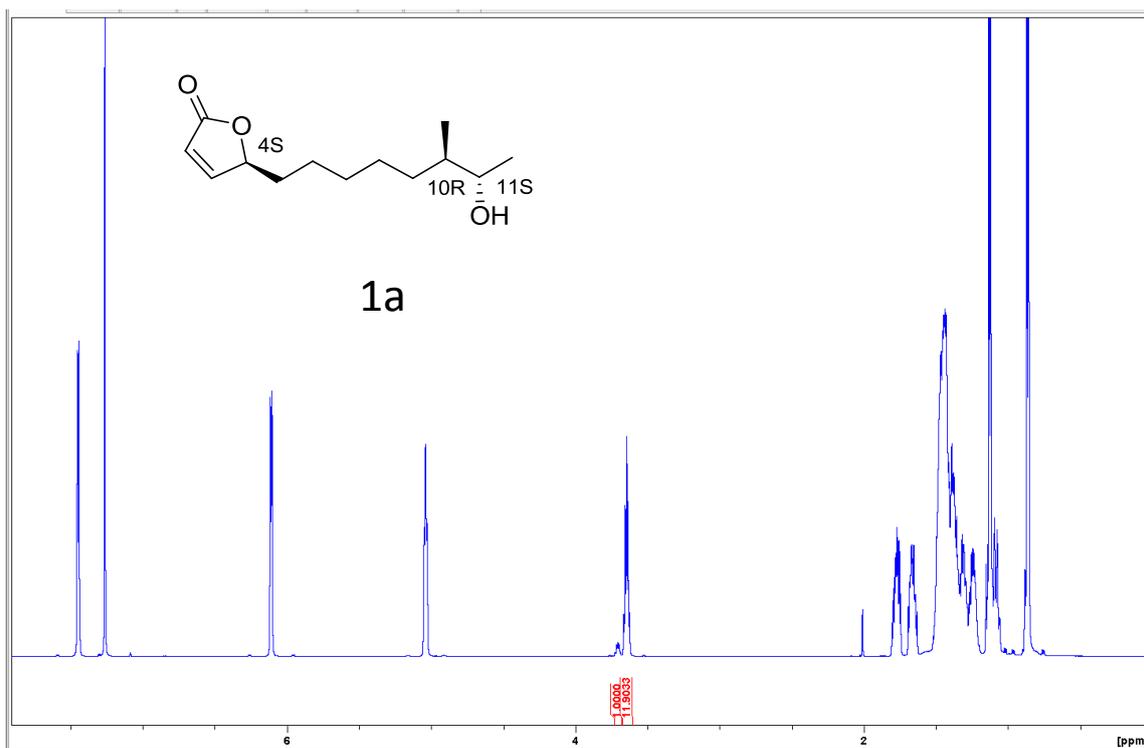
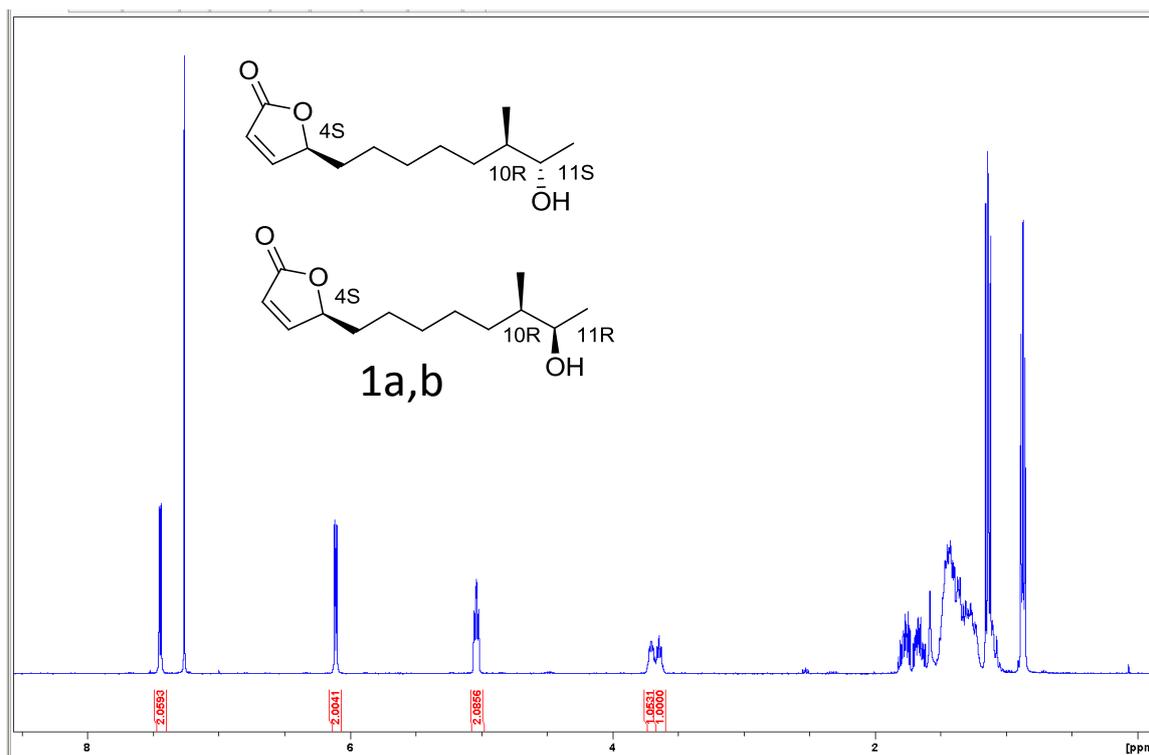


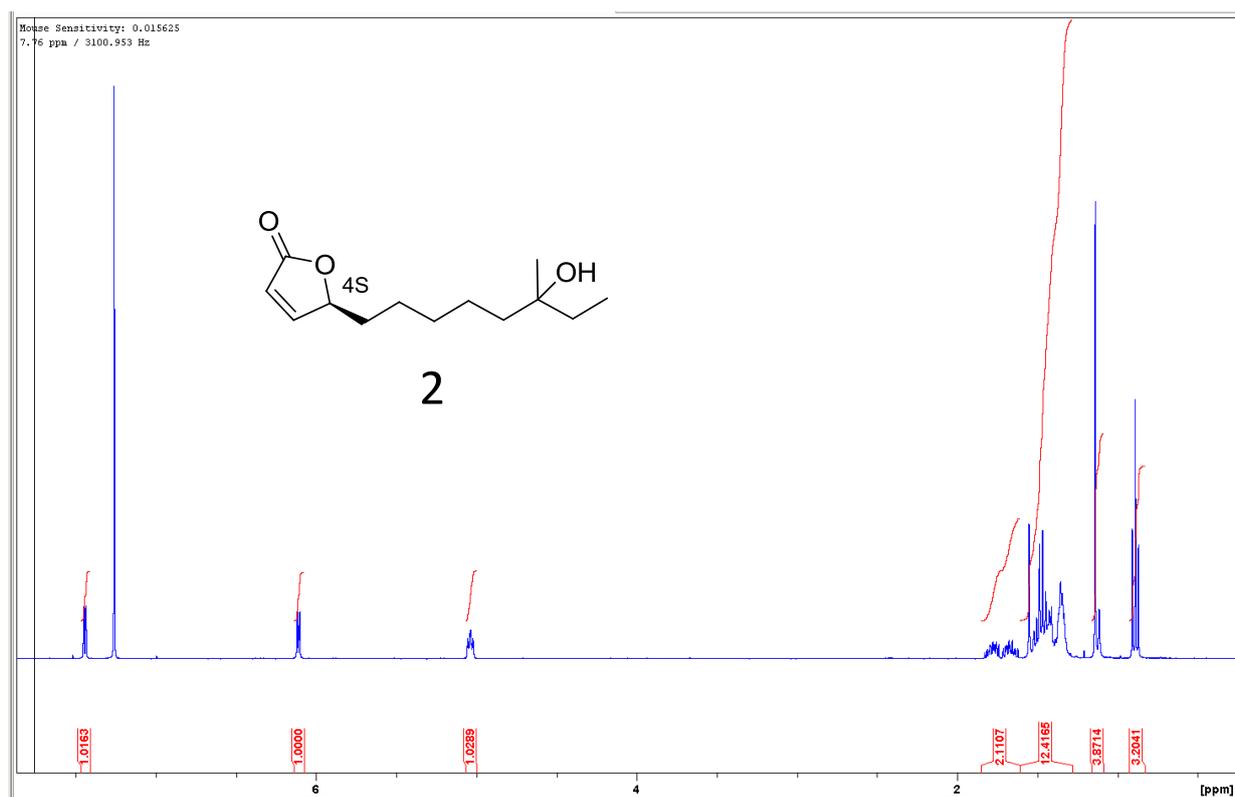
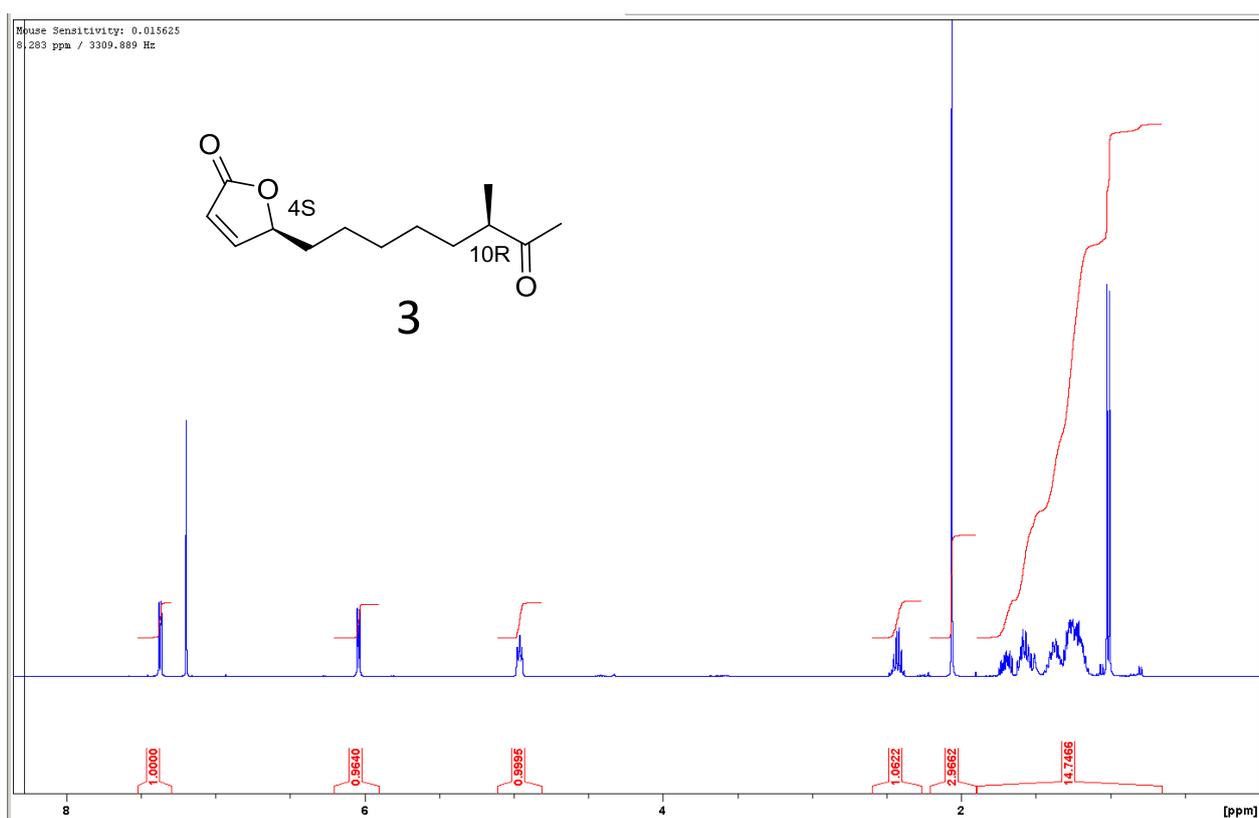
**Figure S2.** Ethyl acetate extract of bacterial pellet after different time of cultivation: (a) 44 h; (b) 46 h; (c) 52 h; (d) 54 h. Retention times for butenolide 1–4: 1a and 1b = 9.04 min; 2 = 8.93 min; 3 = 9.55 min; 4 = 13.5 min.

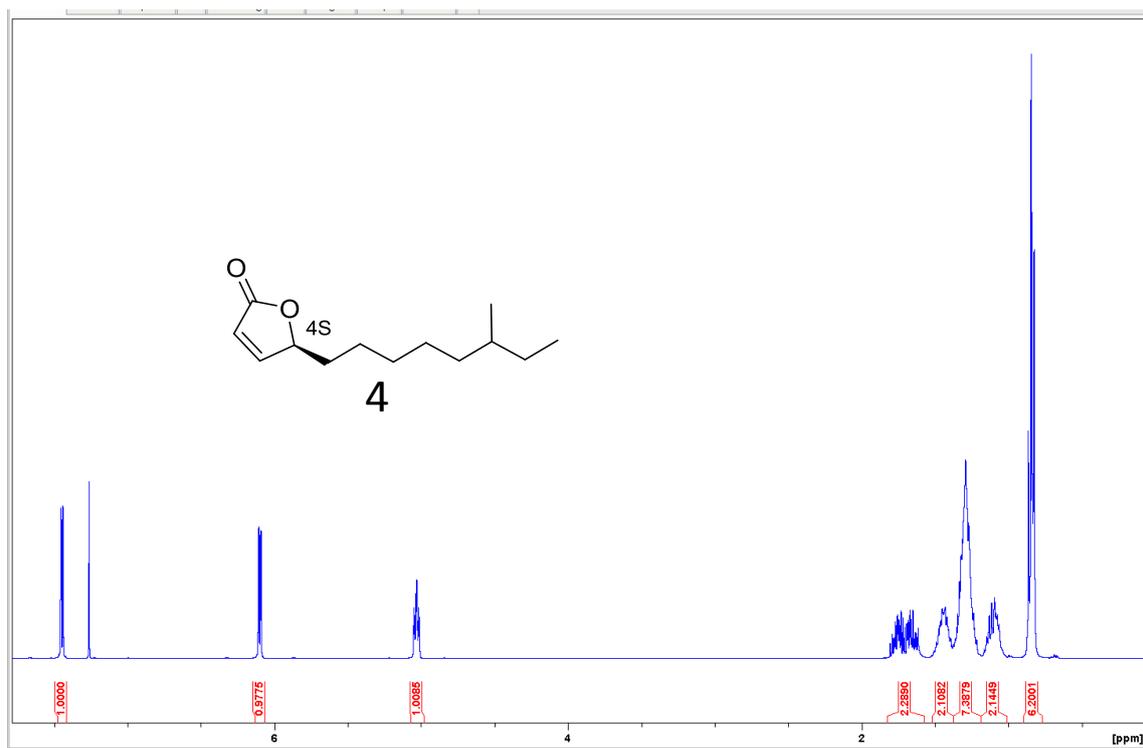
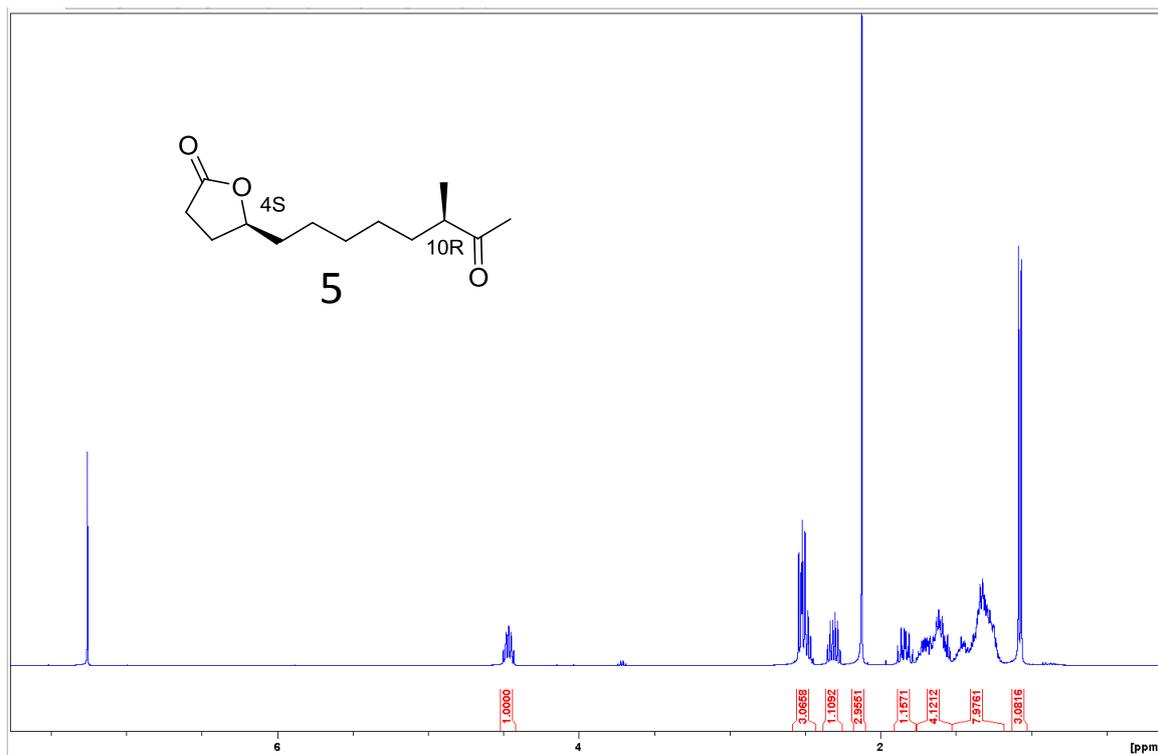


**Figure S3.** UV-vis spectra of butenolides 1–4.

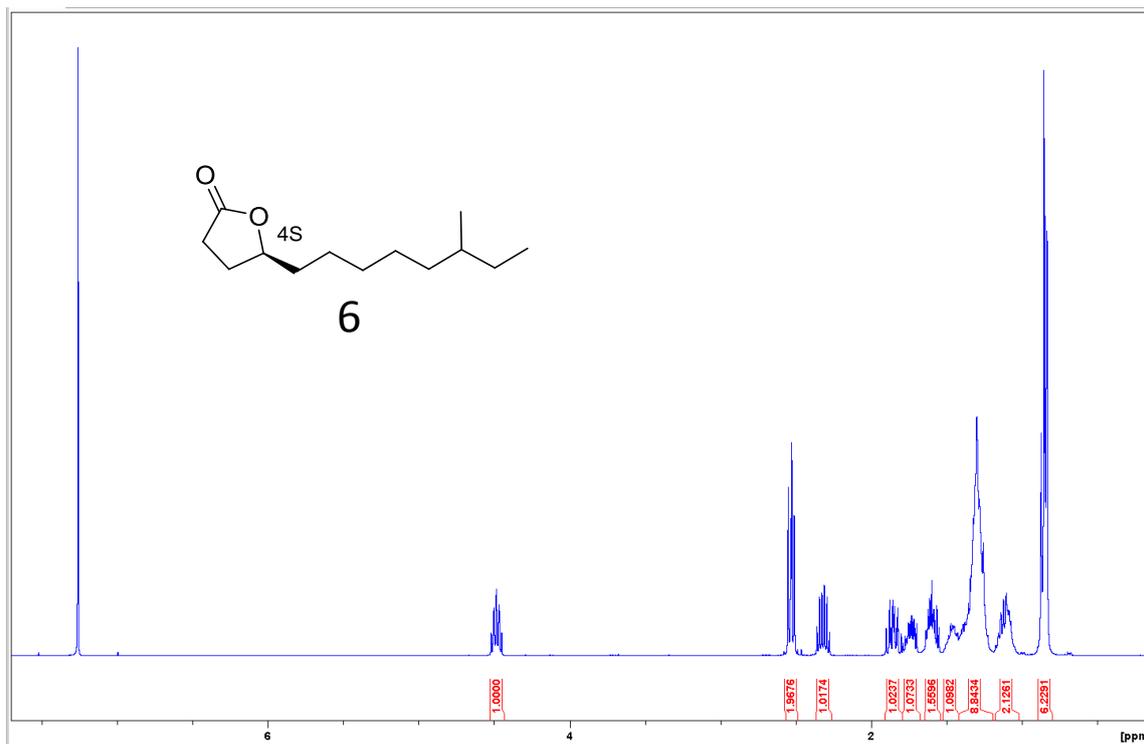


**Figure S4.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide secondary alcohol **1a**.**Figure S5.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide secondary alcohols **1a** and **1b** (1:1).

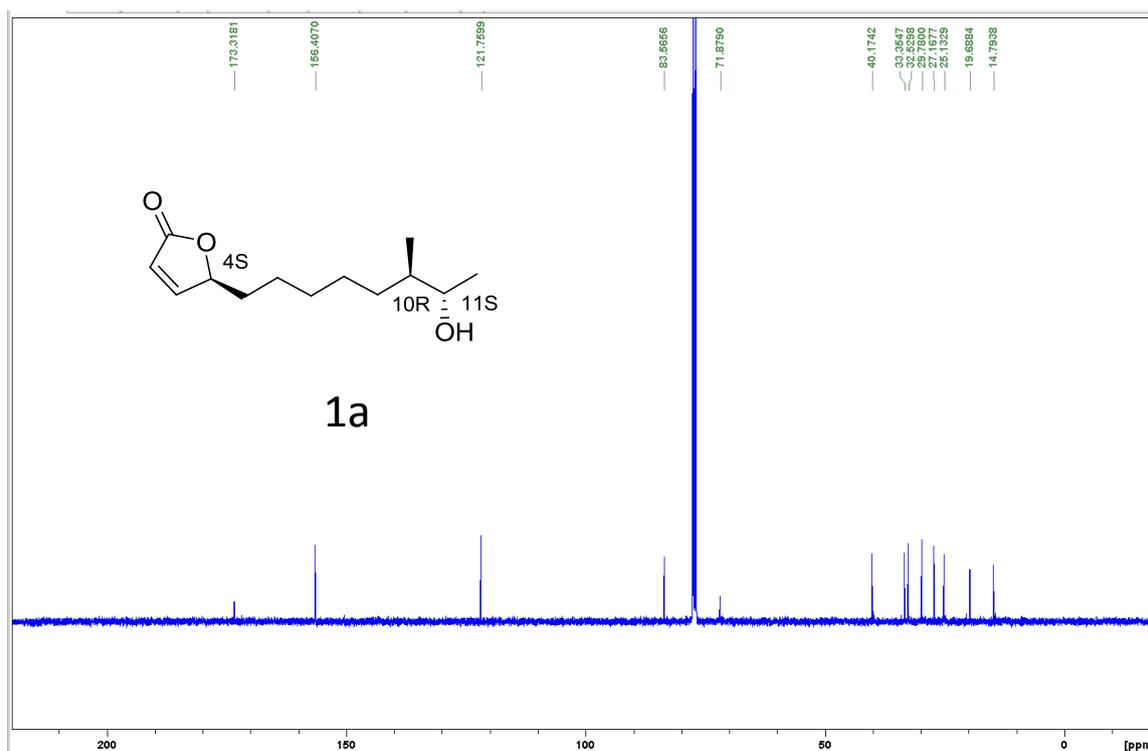
**Figure S6.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) of spectrum of butenolide tertiary alcohol **2**.**Figure S7.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide ketone **3**.

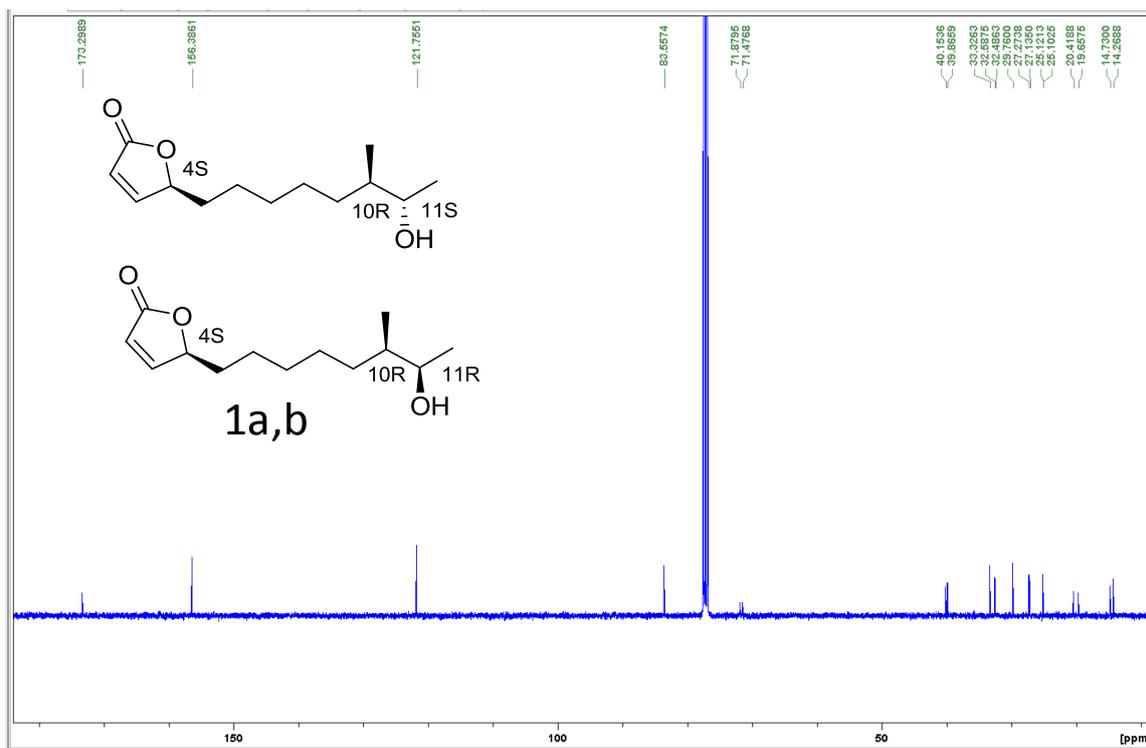
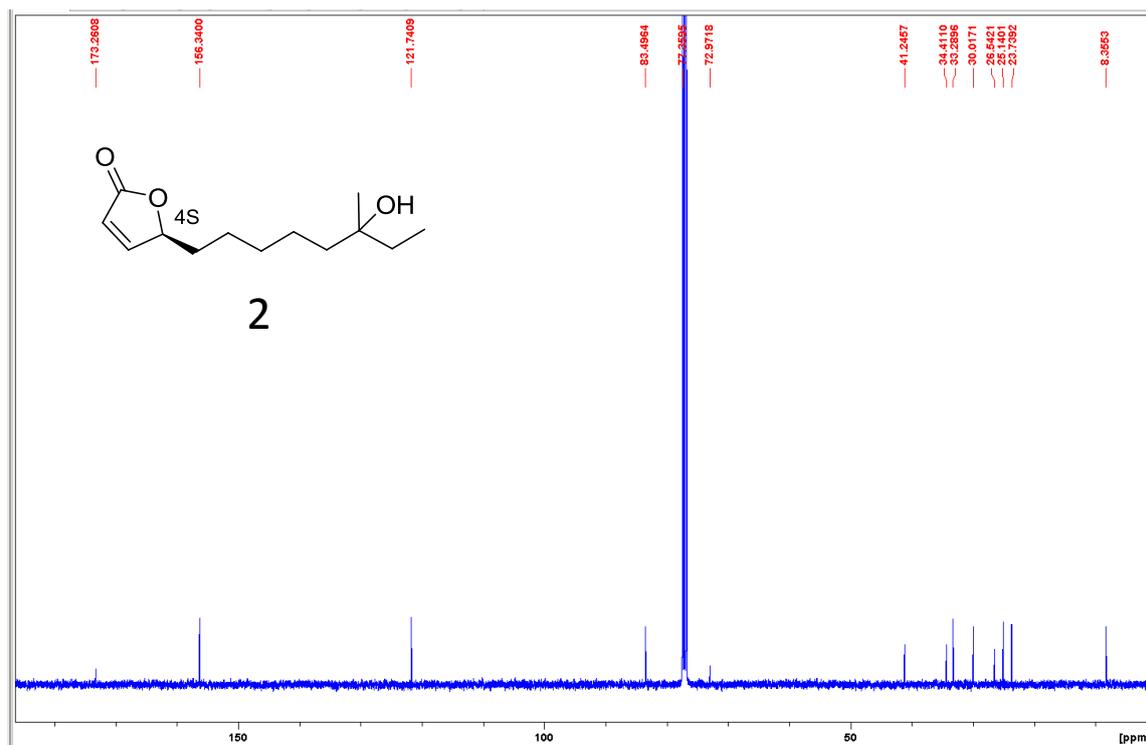
**Figure S8.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide non functional side chain **4**.**Figure S9.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) spectrum of saturated butenolide ketone **5**.

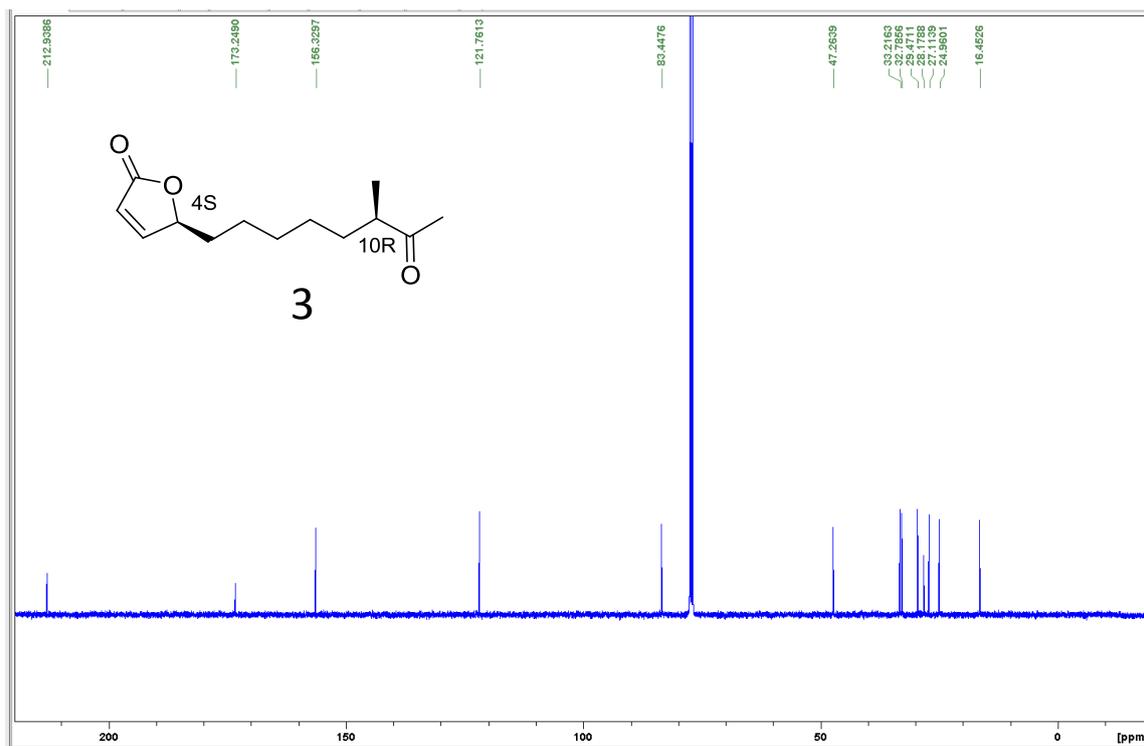
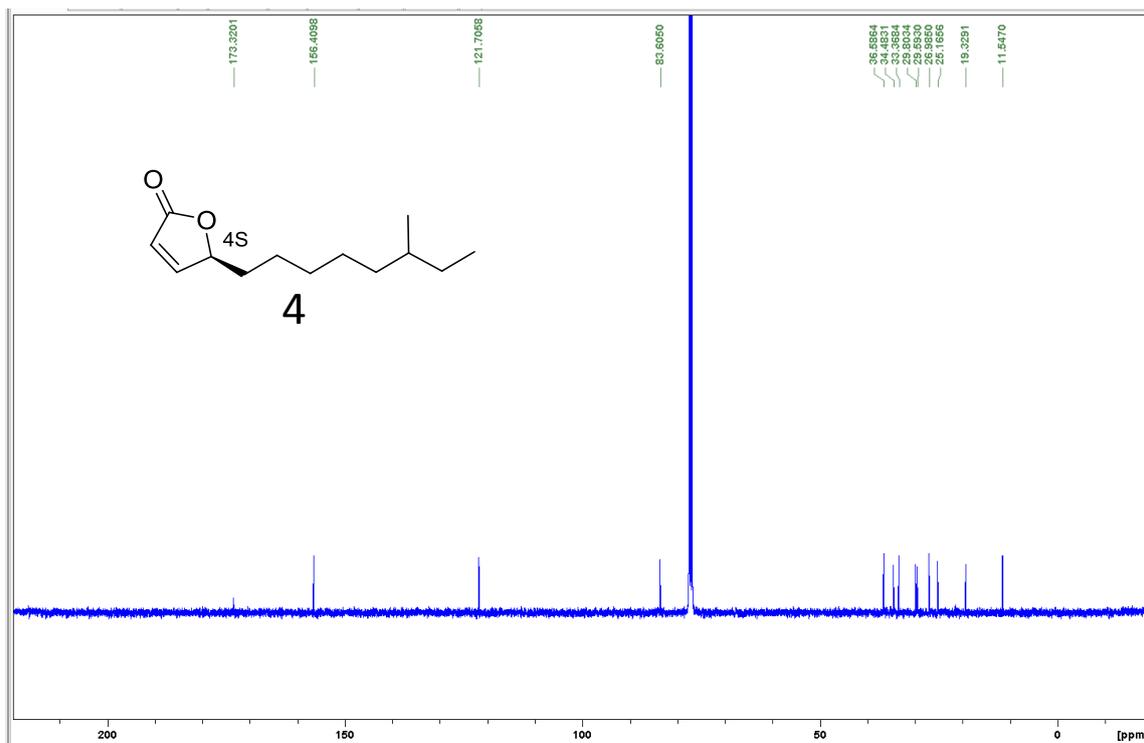
**Figure S10.**  $^1\text{H-NMR}$  (400 MHz,  $\text{CDCl}_3$ ) spectrum of saturated butenolide non functional side chain **6**.

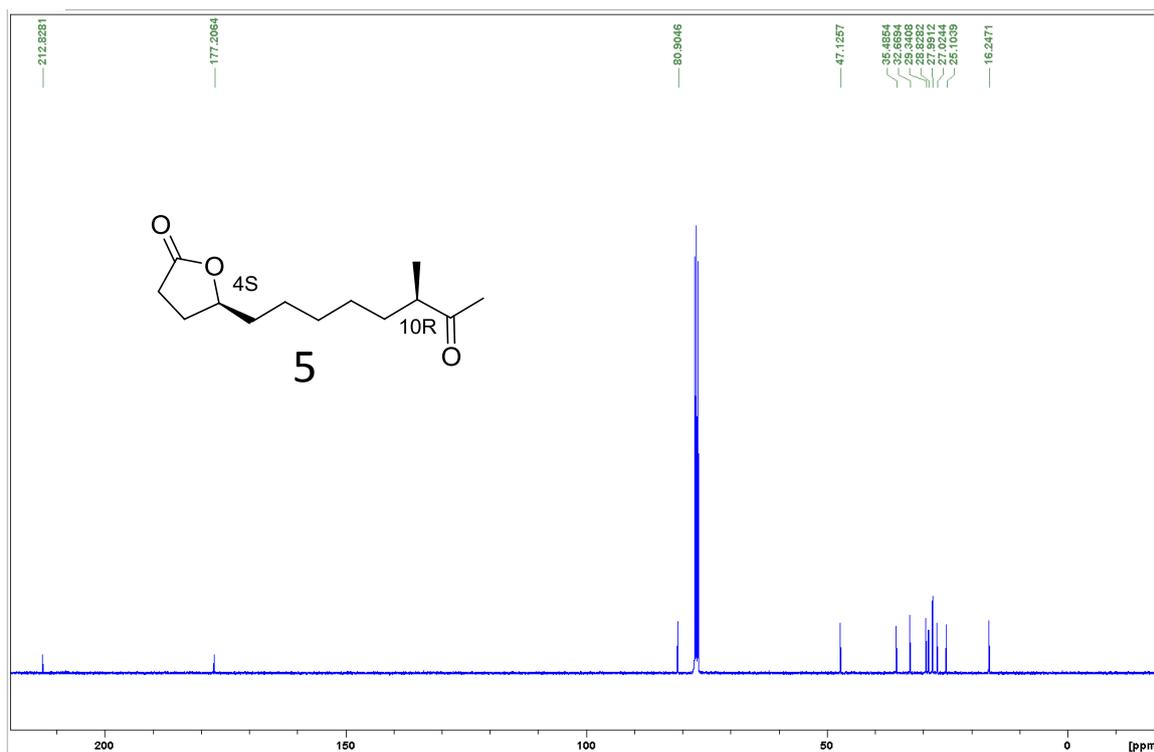
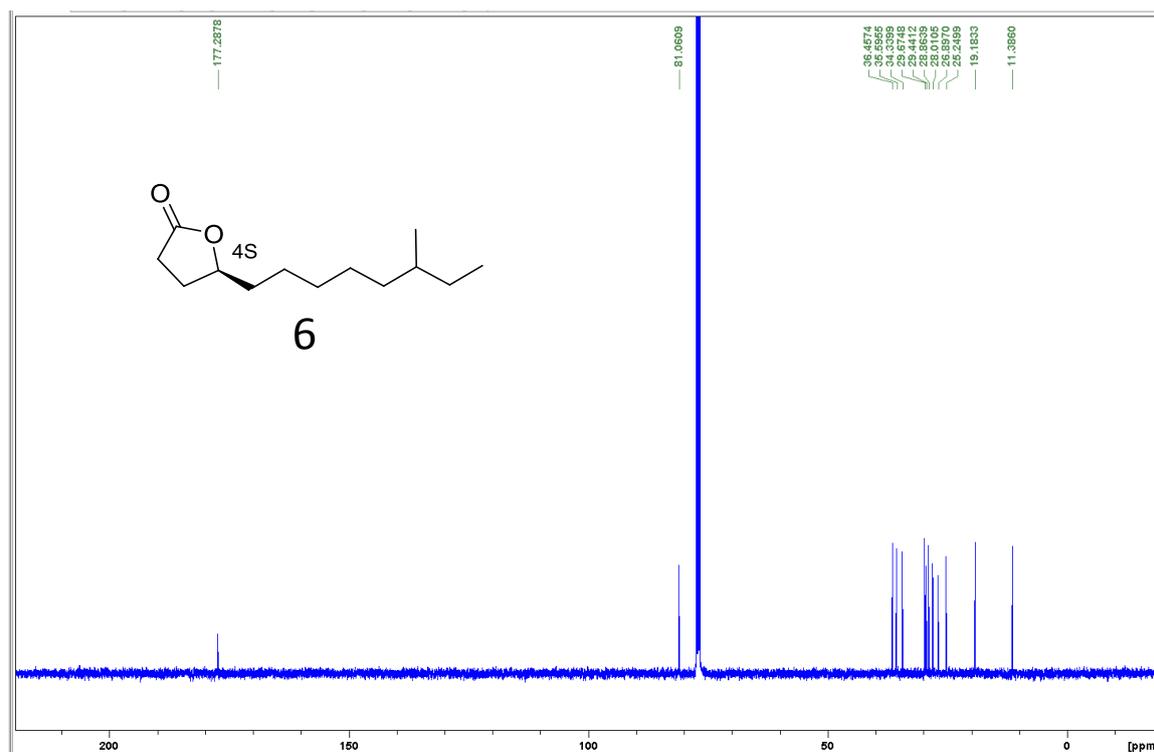


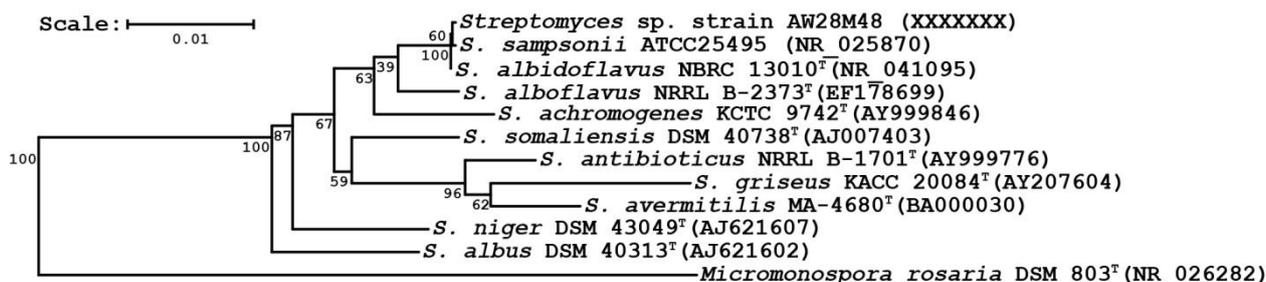
**Figure S11.**  $^{13}\text{C-NMR}$  (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide secondary alcohol **1a**.



**Figure S12.**  $^{13}\text{C}$ -NMR (100 MHz,  $\text{CDCl}_3$ ) of spectrum of butenolide secondary alcohols **1a–b**.**Figure S13.**  $^{13}\text{C}$ -NMR (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide tertiary alcohol **2**.

**Figure S14.**  $^{13}\text{C}$ -NMR (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide ketone **3**.**Figure S15.**  $^{13}\text{C}$ -NMR (100 MHz,  $\text{CDCl}_3$ ) spectrum of butenolide with non functional side chain **4**.

**Figure S16.**  $^{13}\text{C}$ -NMR (100 MHz,  $\text{CDCl}_3$ ) spectrum of saturated butenolide ketone **5**.**Figure S17.**  $^{13}\text{C}$ -NMR (100 MHz  $\text{CDCl}_3$ ) spectrum of saturated butenolide **6**.

**Figure S18.** Phylogenetic analysis of *Streptomyces* sp. AW28M48.

Phylogenetic relationships between *Streptomyces* sp. strain AW28M48 and selected *Streptomyces* type strains based on almost complete 16S rRNA sequences. The tree was constructed using online web-tools at the Ribosomal Database Project [1,2]. Percentages at nodes represent levels of bootstrap support from 100 resampled datasets. The bar indicates 1% estimated sequence divergence. *Micromonospora rosaria* DSM 803 was used as an outgroup. The phylogenetic tree shows that *Streptomyces* sp. strain AW28M48 is very much related to *S. albidoflavus*. The taxonomy of *Streptomyces* belonging to this clade has been reevaluated [3] and based on different analysis it is proposed that many species (like *S. sampsonii*) are strains of *S. albidoflavus*.

## References

1. Cole, J.R.; Wang, Q.; Cardenas, E.; Fish, J.; Chai, B.; Farris, R.J.; Kulam-Syed-Mohideen, A.S.; McGarrell, D.M.; Marsh, T.; Garrity, G.M.; *et al.* The Ribosomal Database Project: Improved alignments and new tools for rRNA analysis. *Nucleic Acids Res.* **2009**, *37*, D141–D145.
2. Ribosomal Database Project. Available online: <http://rdp.cme.msu.edu/> (accessed on 21 January 2014).
3. Rong, X.; Guo, Y.; Huang, Y. Proposal to reclassify the *Streptomyces albidoflavus* clade on the basis of multilocus sequence analysis and DNA-DNA hybridization, and taxonomic elucidation of *Streptomyces griseus* subsp. *solvifaciens*. *Syst. Appl. Microbiol.* **2009**, *32*, 314–322.

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