Figure S1

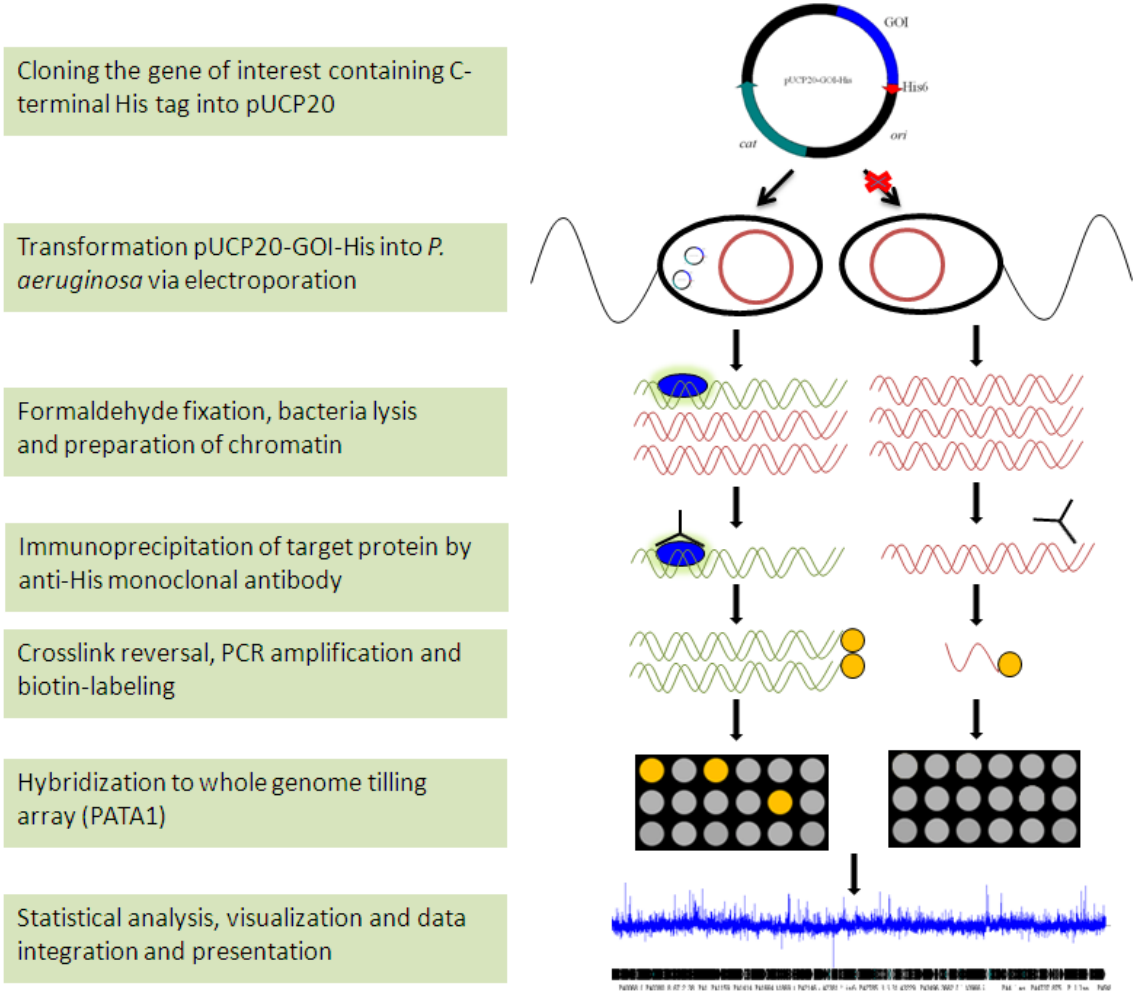


**Figure S1. Establishment of ChIP -chip approach for OxyR binding analysis in *P. aeruginosa*.** See in the figure for more details of the method.

Figure S2

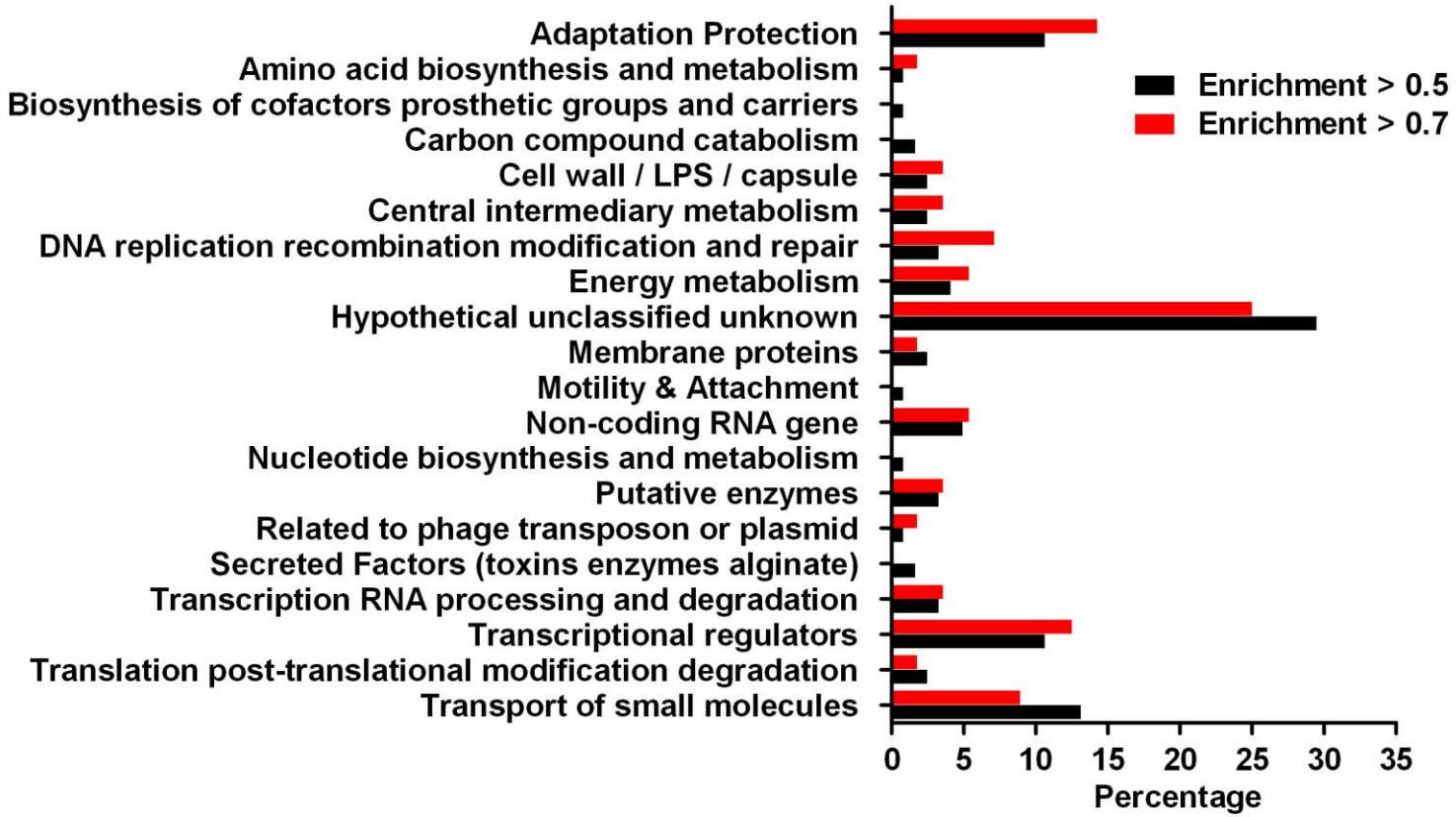


**Figure S2. Functional classification of genes directly targeted by OxyR.**
Functional classes were obtained from www.pseudomonas.com.
Two groups of cutoff values (Log2 ratio = 0.5 or 0.7) were chosen and compared.
Values indicate the percentage of OxyR-enriched regions within the respective classes.
The two groups exhibit the same trend for classification of enriched regions.

Figure S3

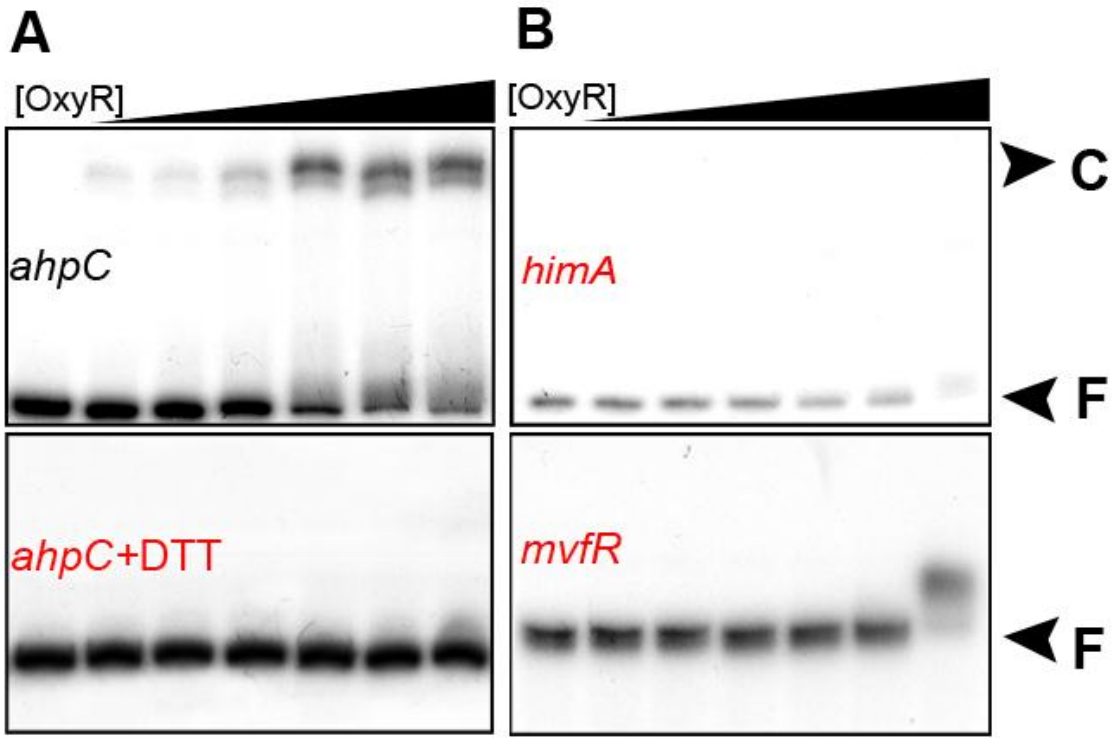


**Figure S3. Binding of OxyR to its target regions *in vitro* by EMSA analysis.** Promoter regions of *aphC* (positive control) (A) and *himA* as well as *mvfR* (B) were amplified and used for EMSA analyses as described in Materials and Methods. OxyR was purified as described above and applied in the following concentration (from left to right) (nM): 0, 84, 168, 336, 504, 840 and 1680. Protein-DNA complex (C) and free DNA (F) are labeled on the right. The lower panel of (A) demonstrated the effect of reducing agent dithiothreitol (DTT) on OxyR binding, which lead to the complete loss of binding to its target. Promoter regions with positive binding results are shown in black while regions with negative results are highlighted in red.

Figure S4

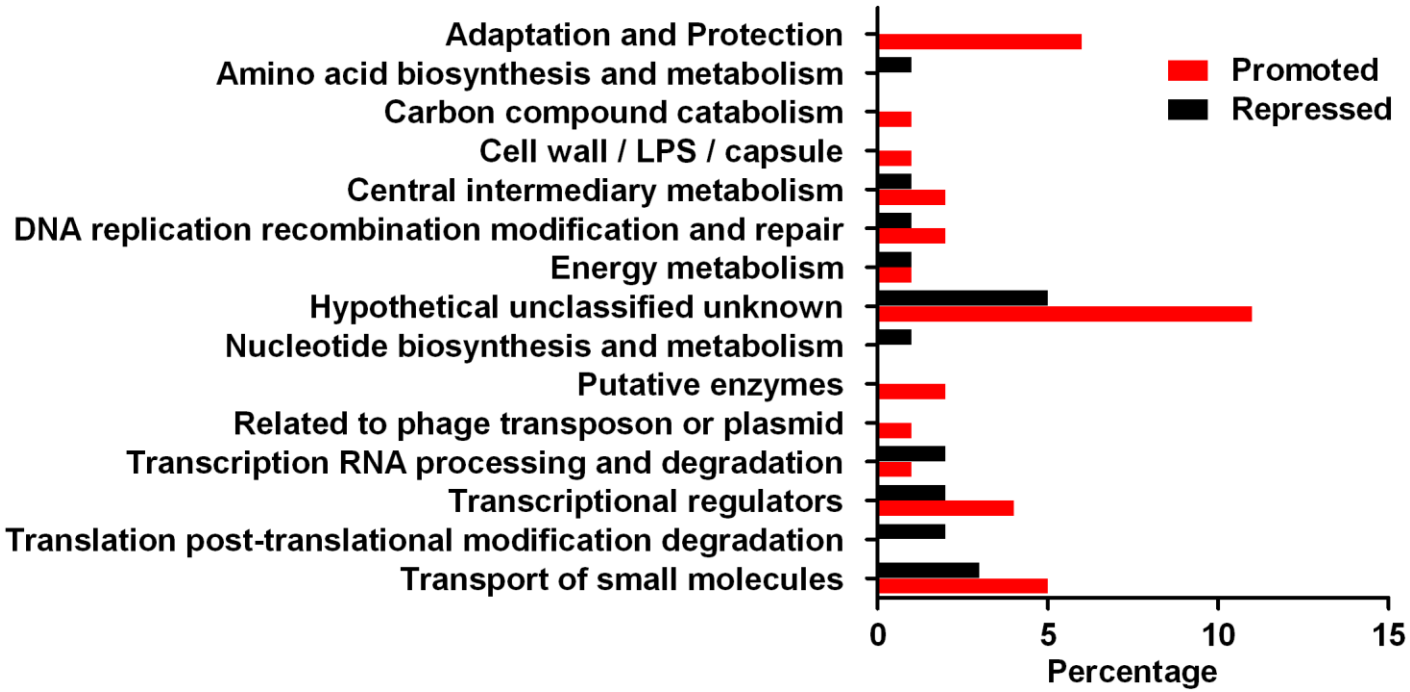


**Figure S4. Functional classification of genes directly targeted by OxyR confirmed by transcriptomic analyses.** Functional classes were obtained from www.pseudomonas.com. 56 out of 122 targets were confirmed in previous t ranscriptomic studies of the response to $H_2O_2$ (23,24) and classified according to their individual functional classes. Values indicate the percentage of OxyR-enriched regions within the respective classes.

Figure S5

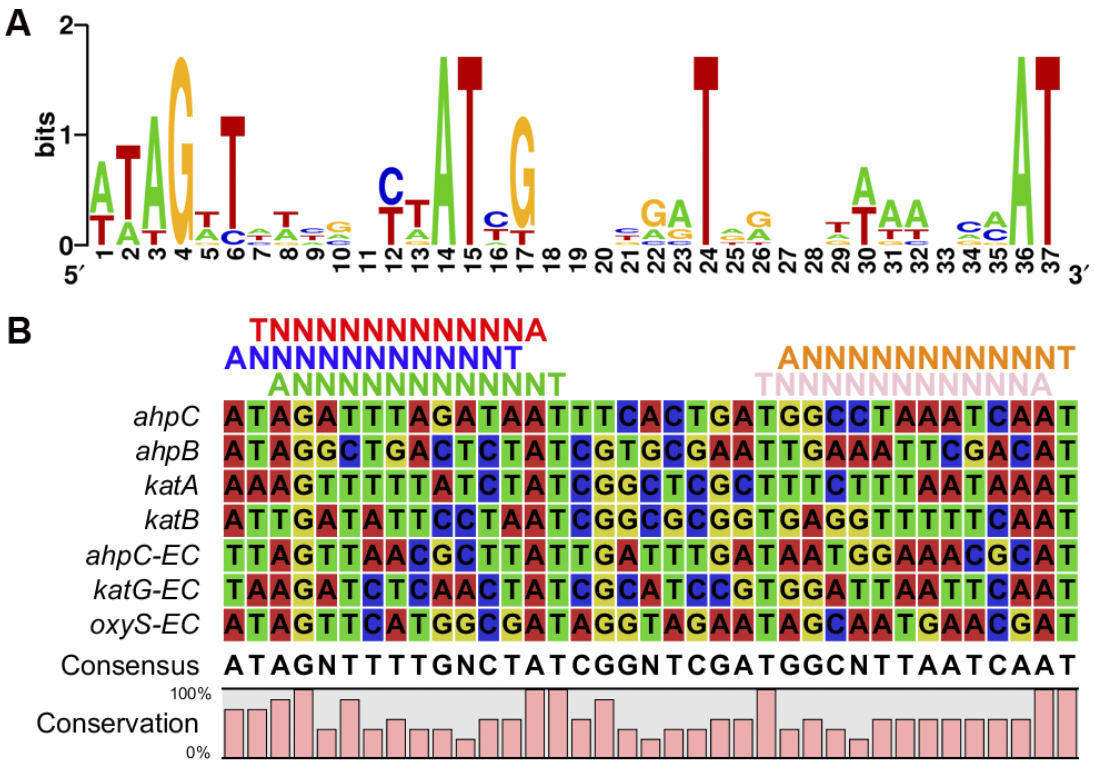


**Figure S5. Features OxyR binding.** (A) Putative OxyR consensus sequences determined according to previous findings (8,9). (B) The alignment of previously identified OxyR -regulated genes using CLC main workbench 5.0 to show the existence of the T -$N_{11}$-A motif within the OxyR consensus sequence. Promoter regions used here are as follows: *ahpB*, *ahpC*, *katA* and *katB* (*P. aeruginosa*), *ahpC-EC*, *katG-EC* and *oxyS-EC* (*Escherichia coli*).