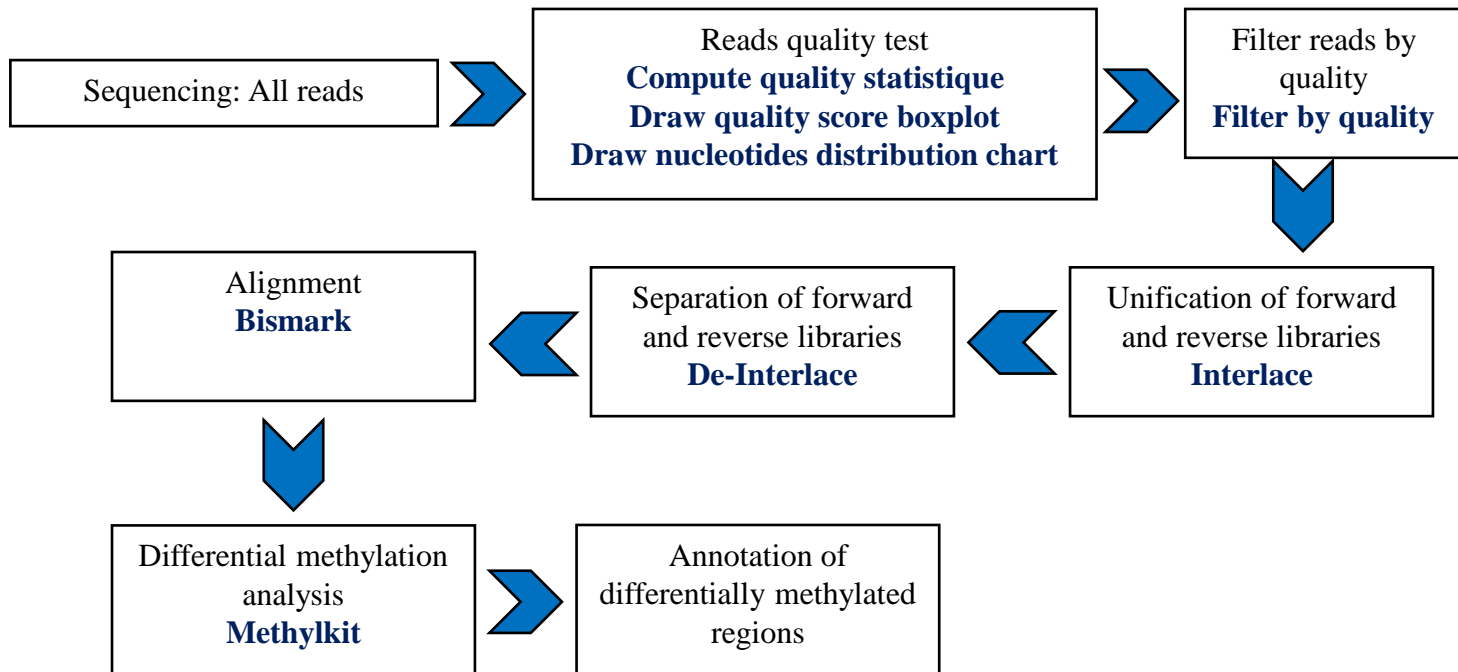


Figure S1: Workflow of bioinformatics procedure of BS-seq data.



Number of reads by step per each library.

	Sea water controls			Diuron exposed samples			Total	Average
Sample names	TE1-11	TE1-14	TE3-19	D3-17	D1-19	D3-12		
Raw reads forward	76947787	99450823	135093644	78957937	100256574	129459645	620166410	103361068
Raw reads reverse	76947787	99450823	135093644	78957937	100256574	129459645	620166410	103361068
Filter by quality forward	63893441	80059937	107827971	34306993	82902496	106249848	475240686	79206781
Filter by quality reverse	61610394	79060596	102015384	59809977	80811534	97446437	480754322	80125720,3
Reads pairs interlace	56813297	71877493	93170937	29052121	74333200	89366412	414613460	69102243,3
Aligned reads ^{*(1)}	30603790	39276420	56044244	15822868	39697570	40349780	221794672	36965778,7
500 bp windows with $\geq 10\times$ cov.	201,672	287,928	398,091	57,819	281,736	279,167		251,069
Large highMeth regions	9,339	10,344	11,332	4,956	7,529	10,242		8,957

**(1) Final line represent reads number obtained after alignment with Bismark and used for differential of methylation.*