

Table S2. Statistical table of sequence alignment results between sample data and reference genome.

Sample	Raw Reads No	Raw Bases(bp)	Q30(bp)	GC(%)	Q30(%)
Control 1	40140818	6061263518	5659379407	49.49	93.37
Control 2	42337536	6392967936	5965329198	49.88	93.31
Control 3	41229438	6225645138	5825337783	51.32	93.57
CuCl ₂ 1	44532344	6724383944	6350362538	52.17	94.44
CuCl ₂ 2	44730162	6754254462	6379867702	49.43	94.46
CuCl ₂ 3	44860616	6773953016	6367629469	51.2	94
HA-PEG@CuO ₂ 1	45392844	6854319444	6466883339	53.54	94.35
HA-PEG@CuO ₂ 2	45301456	6840519856	6437387547	53.22	94.11
HA-PEG@CuO ₂ 3	44501126	6719670026	6323682941	53	94.11
X-ray 1	43913292	6630907092	6251162276	50.3	94.27
X-ray 2	39914156	6027037556	5613084223	50.66	93.13
X-ray 3	44955992	6788354792	6380786351	49.69	94
CuCl ₂ +X-ray 1	36825474	5560646574	5205254395	49.18	93.61
CuCl ₂ +X-ray 2	38650428	5836214628	5436274918	50.23	93.15
CuCl ₂ +X-ray 3	39666968	5989712168	5573055710	49.56	93.04
HA-PEG@CuO ₂ +X-ray 1	46119970	6964115470	6559919697	52.16	94.2
HA-PEG@CuO ₂ +X-ray 2	46334860	6996563860	6630967421	51.6	94.77
HA-PEG@CuO ₂ +X-ray 3	38477098	5810041798	5425563518	52.19	93.38

Clean_Reads: Total number of sequences used for comparison; Total_Mapped: total number of

sequences in the reference genome on the comparison, in percent $\text{Total Mapped} / \text{Clean Reads}$;
Multiple_Mapped: Total number of sequences aligned to multiple positions, percentage $\text{Multiple Mapped} / \text{Total Mapped}$; Uniquely_Mapped: Total number of sequences aligned to only one position, in percent $\text{Uniquely Mapped} / \text{Total Mapped}$.