

Library	Medium (Iron-free 7H9 agar, Tyloxapol, Kan)	Mapped reads	Template counts	NZmean	#TA sites hit	Density (%)	NCBI BioSample accession no.
Fe-cMBT_rep1*	500 ng/ml Fe-cMBT	9,652,517	697,522	12.3	56,724	76.2	SAMN12913093
Fe-cMBT_rep2	500 ng/ml Fe-cMBT	2,305,805	283,558	5.7	49,620	66.7	SAMN12913094
High Fe-MBT_rep1*	250 ng/ml Fe-MBT	8,993,212	764,055	13.8	55,351	74.4	SAMN12913095
High Fe-MBT_rep2	250 ng/ml Fe-MBT	2,231,988	393,946	7.9	50,169	67.4	SAMN12913096
High Fe-MBT_rep3	250 ng/ml Fe-MBT	4,173,269	538,618	10.0	53,894	72.4	SAMN12913097
Low Fe-MBT_rep1*	50 ng/ml Fe-MBT	13,288,416	873,980	15.8	55,381	74.4	SAMN12913098
Low Fe-MBT_rep2	50 ng/ml Fe-MBT	9,345,606	839,566	15.0	56,018	75.3	SAMN12913099
Hemin_rep1*	20 μ M hemin	11,218,510	587,959	10.8	54,654	73.4	SAMN12913100
Hemin_rep2	20 μ M hemin	7,952,349	676,152	12.3	55,001	73.9	SAMN12913101
Hemin_rep3	20 μ M hemin	6,281,407	608,542	11.1	55,065	74.0	SAMN12913102
Hemoglobin_rep1*	5 μ M hemoglobin	10,724,437	597,622	10.6	56,181	75.5	SAMN12913103
Hemoglobin_rep2	5 μ M hemoglobin	8,626,564	963,195	17.0	56,640	76.1	SAMN12913104
Hemin-MBT_rep1*	20 μ M hemin, 250 ng/ml Fe-MBT	13,721,967	788,621	14.0	56,230	75.6	SAMN12913105
Hemin-MBT_rep2	20 μ M hemin, 250 ng/ml Fe-MBT	10,408,244	921,888	16.2	56,995	76.6	SAMN12913106
Average		8,494,592	681,087	12.3	54,851	73.7	

S5 Table. Statistical analysis of the *M. tuberculosis* transposon libraries used in this work.

The *Mtb* $\Delta mbtD::hyg^r$ (ML1600) genome contains 74,410 TA sites. NZmean denotes the average template count at non-zero TA sites. Density denotes the fraction of TA sites with at least one insertion.

* The data sets were used for HMM analysis.