

S4 Table. Number of NRF1 peaks called with and without duplicate removal

Accession	Sample	Rep	Dup	Dup in rate (%)	Dup peak (%)	With Duplicate removal		No duplicate removal	
						Shared	Unique	Shared	Unique
GSM2574780	HepG2	1	35.81	48.34	7680	147	7676	1528	(23.89;22.25;25.72)
GSM2574769	K562	1	23.57	81.38	15078	1272	15153	115	(12.89;57.55;71.23)
GSM2574770	K562	2	8.77	30.06	7144	80	7138	355	(na;68.75;80)
GSM2574771	K562	3	21.21	79.49	13177	999	13234	185	(51.55;60.85;71.27)
GSM2574812	MCF7	1	17.86	91.61	8321	589	8338	32	(36.84;62.26;76.68)
GSM2574813	MCF7	2	2.94	29.08	3907	18	3906	127	(20.03;64.69;60.1)
									(na;72.22;72.22)
									(58.27;77.95;77.95)

Number in the parenthesis refers to the percentage of unique peaks with the NRF1 DNA binding motif, overlapping the 4-kb windows centered on the transcriptional start sites and the H3K4me3 peaks from the reference epigenome in HepG2, K562 and HMEC (PMID: 25693563). Rep, replicate; Dup, duplicate; na, not available due to small peak number (<100).