

Table S6 Summary of whole genome sequencing (WGS) analysis

Sample	Library index	Raw reads (M)	Raw bases (G)	Clean reads (M)	Clean bases (G)	Clean Rate (%)	Mapped reads (M)	Mapped bases (G)	Mapped ratio (%)	Unique mapped reads (M)	Unique mapped bases (G)	Unique mapped ratio (%)
<i>Crygc</i> ^{-/-} -4W-SSCs	10	647.5	65.40	616.0	62.18	95.08	594.9	59.07	95.00	512.7	51.18	82.30
Line-HDR1-SC-8	3	707.2	71.43	684.4	69.13	96.78	667.5	66.29	95.90	573.0	57.18	82.72