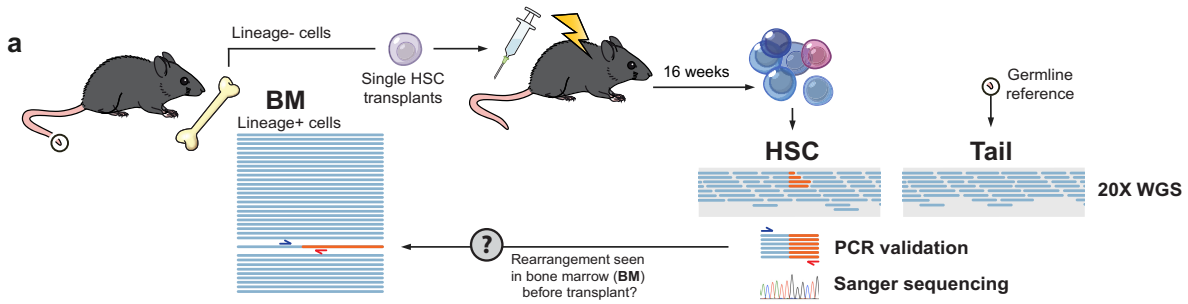


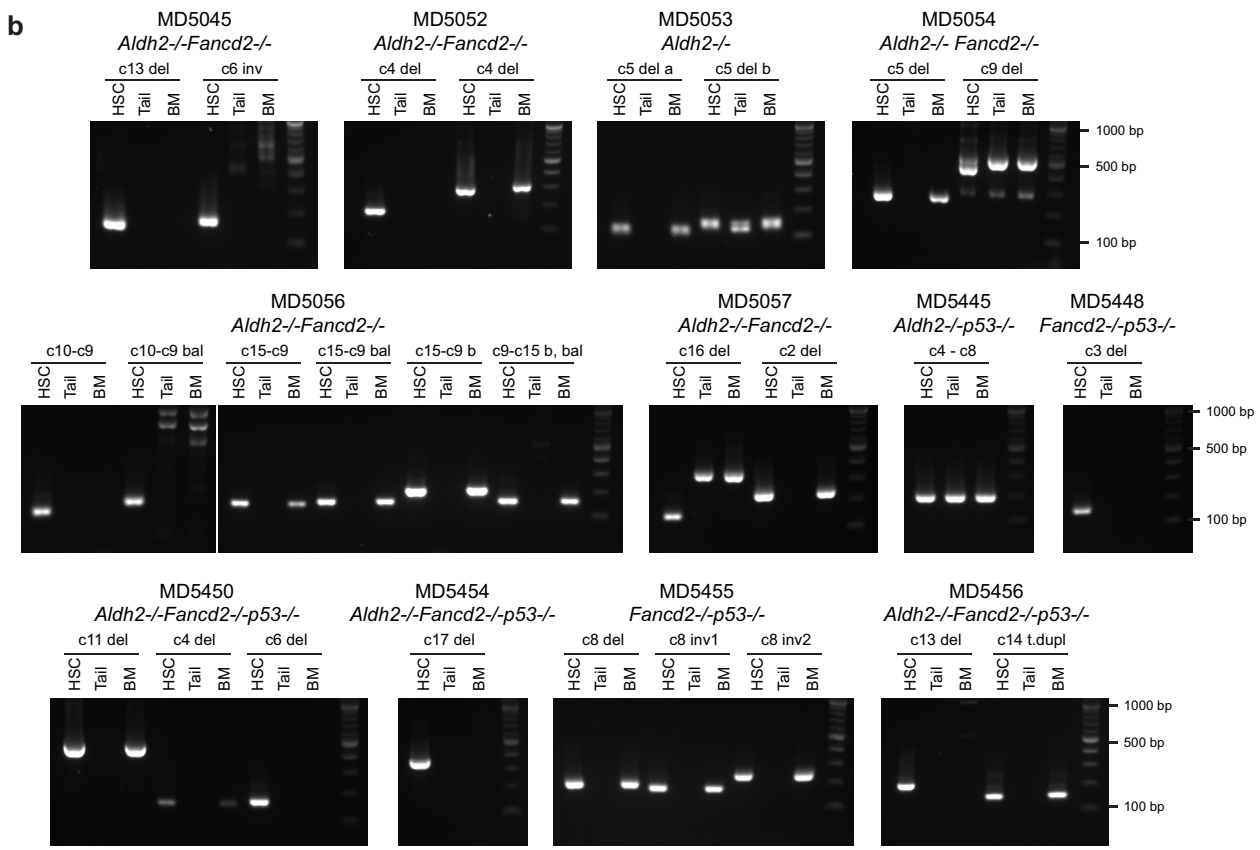


c

| Sample | Type | Start location | Size (bp) | PCR | HSC | Tail | BM |
|---|---|---|---|---|---|---|---|
| MD5045a | deletion | c13:112244133 | 2999 | 161 | ● | | |
| *Aldh2-/- Fancd2-/-* | inversion | c6:69207252 | 36822 | 135 | ● | | |
| MD5052a | deletion | c4:29837258 | 9957 | 173 | ● | | |
| *Aldh2-/- Fancd2-/-* | deletion | c5:145424065 | 24239 | 336 | ● | | ● |
| MD5053a | deletion | c13:19185501 | 24841 | 103 | ● | | ● |
| *Aldh2-/-* | deletion | c13:19311304 | 25273 | 132 | ● | | ● |
| MD5054a | deletion | c5:59377956 | 1148 | 268 | ● | | ● |
| *Aldh2-/- Fancd2-/-* | deletion/duplication | c9:117677119 | 342 | 198 | ● | | |
| MD5056a | translocation | c10:82901864-c9:49792783 | - | 169 | ● | | |
| *Aldh2-/- Fancd2-/-* | translocation (bal) | c10:82901948-c9:49793011 | - | 161 | ● | | |
| | translocation | c15:80199437-c9:77318662 | - | 152 | ● | | ● |
| | translocation (bal) | c15:80199443-c9:77318664 | - | 163 | ● | | ● |
| | translocation | c15:80200657-c9:77317682 | - | 226 | ● | | ● |
| | translocation (bal) | c15:80200668-c9:77317689 | - | 176 | ● | | ● |
| MD5057a | deletion | c16:56319262 | 10056 | 131 | ● | | |
| *Aldh2-/- Fancd2-/-* | deletion | c2:177355146 | 3657 | 229 | ● | | ● |

| Sample | Type | Start location | Size (bp) | PCR | HSC | Tail | BM |
|---|---|---|---|---|---|---|---|
| MD5445a | translocation | c4:128611975-c8:106880788 | - | 199 | ● | ● | ● |
| *Aldh2-/- p53-/-* | | | | | | | |
| MD5448a | deletion | c3:81290371 | 10604 | 167 | ● | | |
| *Fancd2-/- p53-/-* | | | | | | | |
| MD5450a | deletion | c11:37239409 | 6950 | 477 | ● | | ● |
| *Aldh2-/- Fancd2-/- p53-/-* | deletion | c4:124986607 | 24307 | 164 | ● | | ● |
| | deletion | c6:86545624 | 47656 | 177 | ● | | |
| MD5454a | deletion | c17:46760471 | 88447 | 321 | ● | | |
| *Aldh2-/- Fancd2-/- p53-/-* | | | | | | | |
| MD5455a | deletion | c8:44991181 | 7530 | 191 | ● | | ● |
| *Fancd2-/- p53-/-* | inversion | c8:45073529 | 72375 | 180 | ● | | ● |
| | inversion | c8:45070602 | 69445 | 244 | ● | | ● |
| MD5456a | deletion | c13:84517083 | 54157 | 212 | ● | | |
| *Aldh2-/- Fancd2-/- p53-/-* | duplication | c14:64748311 | 1651 | 153 | ● | | ● |

**Extended Data Figure 10 | Validation of rearrangements by PCR.** **a**, Scheme depicting the generation of HSC clones by transplantation of single stem cells, subsequent whole-genome sequencing and validation of rearrangement calls by PCR. We designed primers for nested PCRs flanking the breakpoints calculated by the BRASS algorithm, and the identity of the products was confirmed by Sanger sequencing. In addition, we attempted to detect the rearrangements in DNA samples of bone-marrow cells from the mice that provided the transplanted HSCs, demonstrating that these changes did not arise during clonal expansion and were present in the stem cell at the time of transplantation. **b**, Agarose gels (one experiment) showing presence of specific PCR amplification from DNA of HSC clones, absence in matched germline samples from the tail of the same mouse and, in some cases, detection in bone-marrow tissue that predates the transplants. PCR amplification in these samples is dependent on the contribution of the transplanted HSC to blood production, and the sensitivity of each PCR. Gel source data is shown in Supplementary Fig. 1. **c**, List summarizing the rearrangements found in 28 HSC clones and the results from **b**. All 27 rearrangements could be detected by PCR and confirmed by Sanger sequencing. 16/27 (59%) rearrangements could be detected before transplantation.