Supplementary Data
Supplementary Tables

**Supplementary Table 1.** Percentages of reconstituted animals for 16 experiments at 12 weeks post injection.

| Experiment# | #injected animals | #reconstituted animals | % of reconstituted animals | #injected animals | #reconstituted animals | % of reconstituted animals |
|-------------|-------------------|------------------------|---------------------------|-------------------|------------------------|---------------------------|
| 1           | 29                | 2                      | 7                         | 4                 | 4                      | 100                       |
| 2           | 28                | 1                      | 4                         | 2                 | 0                      | 0                         |
| 3           | 26                | 4                      | 15                        | 2                 | 2                      | 100                       |
| 4           | 21                | 2                      | 10                        | 2                 | 2                      | 100                       |
| 5           | 54                | 3                      | 6                         | 3                 | 2                      | 66                        |
| 6           | 58                | 11                     | 19                        | 4                 | 4                      | 100                       |
| 7           | 21                | 1                      | 5                         | 4                 | 4                      | 100                       |
| 8           | 18                | 1                      | 6                         | 2                 | 1                      | 50                        |
| 9           | 26                | 1                      | 4                         | 2                 | 1                      | 50                        |
| 10          | 15                | 0                      | 0                         | 2                 | 2                      | 100                       |
| 11          | 15                | 0                      | 0                         | 2                 | 0                      | 0                         |
| 12          | 16                | 0                      | 0                         | 2                 | 0                      | 0                         |
| 13          | 34                | 2                      | 6                         | 2                 | 2                      | 100                       |
| 14          | 36                | 0                      | 0                         | 2                 | 2                      | 100                       |
| 15          | 26                | 4                      | 15                        | 2                 | 2                      | 100                       |
| 16          | 30                | 3                      | 10                        | 2                 | 2                      | 100                       |
| mean        |                   |                        |                           |                   |                        | 7.7                       |

|              |                   |                        |                           |                   |                        | 76.9                      |
**Supplementary Table 2.** List of genes with nonrandom allelic imbalance (AI) in the B and T cell samples of this study (TMM-normalized counts > 10) or reported in the literature to display parental imprinting.

| Gene       | Chr | Biased? | Imprinted | Control | E13.1 | E13.2 | E15.2 | E13.24 | E15.29 | E15.10 | E6.1 | E6.2 | E6.42 | E6.43 | Mean(AI) | Std(AI) | Mean | Std |
|------------|-----|---------|-----------|---------|-------|-------|-------|-------|-------|-------|------|------|-------|-------|----------|--------|------|-----|
| Dyrk3      | chr1| yes     |           | 0.10    | 0.12  | 0.11  | 0.11  | 0.07  | 0.08  | 0.08  | 0.10 | 0.13 | 0.12  | 0.08  | 0.10     | 0.02   | 29.45| 6.98 |
| Cyp27a1    | chr1| yes     |           | 1.00    | 0.99  | 1.00  | 1.00  | 0.99  | 0.99  | 0.99  | 0.99  | 0.99 | 0.99  | 0.99  | 0.99     | 0.00   | 26.62| 8.49 |
| Kcnk2      | chr1| yes     |           | 0.00    | 0.00  | 0.00  | 0.00  | 0.01  | 0.01  | 0.00  | 0.01 | 0.01 | 0.00  | 0.02  | 0.01     | 0.01   | 20.76| 5.10 |
| Gm10075    | chr1| yes     |           | -       | -     | 0.90  | 0.93  | 0.91  | 0.90  | 0.93  | 0.90 | 0.91  | 0.86  | 0.90  | 0.90     | 0.02   | 14.89| 4.55 |
| A530040E14Rk| chr1| yes     |           | 0.06    | 0.09  | 0.08  | 0.03  | 0.12  | 0.02  | 0.01  | 0.03 | 0.03  | 0.03  | 0.07  | 0.05     | 0.04   | 34.66| 9.75 |
| Nek6       | chr2| yes     |           | 0.05    | 0.11  | 0.07  | 0.07  | 0.08  | 0.08  | 0.14  | 0.10 | 0.09  | 0.11  | 0.11  | 0.09     | 0.02   | 26.97| 6.01 |
| Fmn1       | chr2| yes     |           | 0.01    | 0.05  | 0.03  | 0.01  | 0.07  | 0.05  | 0.02  | 0.05 | 0.07  | 0.07  | 0.10  | 0.05     | 0.03   | 28.41| 7.02 |
| Bmyc       | chr2| yes     |           | 0.98    | 0.99  | 1.00  | 0.97  | 1.00  | 1.00  | 0.99  | 1.00 | 0.99  | 1.00  | -      | 0.99     | 0.01   | 18.70| 4.62 |
| Gm13699    | chr2| yes     |           | 1.00    | 1.00  | 0.99  | 1.00  | 0.99  | 0.99  | 1.00  | 0.99 | 0.97  | 1.00  | 0.98  | 0.99     | 0.01   | 52.72| 22.39 |
| Gm13654    | chr2| yes     |           | 0.95    | 0.97  | 0.96  | 0.99  | 0.99  | 0.99  | 1.00  | 0.98 | 0.99  | 0.98  | 0.96  | 0.98     | 0.02   | 30.81| 8.13 |
| Gm13456    | chr2| yes     |           | 0.00    | 0.10  | 0.07  | 0.00  | -     | 0.15  | 0.12  | -   | -    | -     | -      | 0.07     | 0.06   | 25.22| 6.60 |
| Mir15115   | chr2| yes     |           | 0.00    | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00  | 0.00 | 0.00  | 0.00  | 0.00  | 0.00     | 0.00   | 202.32| 118.67 |
| Adamsms44  | chr3| yes     |           | 0.03    | 0.04  | 0.08  | 0.02  | 0.02  | 0.02  | 0.03  | 0.03 | 0.03  | 0.01  | 0.03  | 0.03     | 0.02   | 24.18| 13.28 |
| Gnb4       | chr3| yes     |           | 0.02    | 0.04  | 0.03  | 0.02  | 0.12  | 0.05  | 0.03  | 0.01 | 0.04  | 0.08  | 0.08  | 0.05     | 0.03   | 69.14| 11.29 |
| Alpkl      | chr3| yes     |           | 0.00    | 0.02  | 0.01  | -     | 0.01  | 0.02  | 0.01  | 0.02 | 0.03  | 0.03  | 0.01  | 0.01     | 0.01   | 19.44| 6.26 |
| Sec24d     | chr3| yes     |           | 0.11    | 0.08  | 0.13  | 0.07  | 0.09  | 0.13  | 0.12  | 0.04 | 0.09  | 0.06  | 0.05  | 0.09     | 0.03   | 33.45| 12.01 |
| Rpsa-ps10   | chr3| yes     |           | 0.04    | 0.05  | 0.07  | 0.04  | 0.02  | -    | 0.05  | -   | -    | -      | -      | 0.05     | 0.02   | 11.94| 0.98 |
| Synpo2     | chr3| yes     |           | 0.00    | 0.01  | 0.01  | -    | -     | -    | 0.02  | 0.08  | 0.02  | -    | 0.03  | 0.03     | 0.03   | 15.36| 3.89 |
| Cgn        | chr3| yes     |           | 0.01    | 0.01  | 0.02  | 0.00  | 0.04  | 0.05  | 0.00  | 0.01 | 0.04  | 0.07  | 0.11  | 0.03     | 0.04   | 14.70| 3.38 |
| Coro2a     | chr4| yes     |           | 0.96    | 0.98  | 0.95  | 0.98  | 0.96  | 0.94  | 0.92  | 0.98 | 0.95  | 0.98  | 0.93  | 0.96     | 0.02   | 55.64| 8.31 |

**Mean(AI)** represents the average mean of the TMM-normalized counts across all samples. **Abundance** represents the sum of the TMM-normalized counts across all samples.
| Gene     | Chr  | Status | BP1 | BP2 | BP3 | BP4 | BP5 | BP6 | BP7 | BP8 | BP9 | BP10 | BP11 | BP12 | BP13 | BP14 | BP15 | BP16 | BP17 | BP18 | BP19 | BP20 | Value1 | Value2 |
|----------|------|--------|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|-------|-------|
| ApoE    | chr7 | yes    | 0.97| 0.98| 0.97| 0.98| 0.97| 0.97| 0.98| 0.96| 0.97| 0.97 | 0.97 | 0.97 | 0.97 | 0.97 | 0.97 | 0.97 | 0.97 | 0.97 | 0.97 | 107.02| 46.32 |
| Gipre5b | chr7 | yes    | 0.01| 0.03| 0.03| 0.02| 0.01| 0.01| 0.02 | -    | -    | -    | 0.02 | 0.01 | 0.01 | 0.01 | 0.02 | 0.02 | 0.02 | 0.01 | 0.01 | 0.01 | 17.15 | 5.23  |
| Pglyrp1 | chr7 | yes    | 0.93| 0.97| 0.97| 0.98| 0.92| 0.98| 0.91 | 0.99 | 0.96| 0.96 | 0.96 | 0.96 | 0.96 | 0.96 | 0.96 | 0.96 | 0.96 | 0.96 | 0.96 | 23.61 | 6.66  |
| Lilra6  | chr7 | yes    | -   | 0.93| 0.93| 0.90| 0.87| 0.92| 0.94| 0.95 | 0.87| 0.94 | 0.89 | 0.91 | 0.91 | 0.91 | 0.91 | 0.91 | 0.91 | 0.91 | 19.78 | 4.45  |
| Gene   | Chr  | Yes | 0.95 | 0.96 | 0.97 | 0.98 | 0.99 | 1.00 |
|--------|------|-----|-------|-------|-------|-------|-------|-------|
| Gm9855 | chr7 | yes | -0.05 | -0.04 | -0.02 | -0.03 | -0.02 | -0.02 | -0.03 | -0.01 | -0.01 | -0.02 | -0.03 | -0.01 | 0.03 | 0.03 | 14.69 | 4.79 |
| Gstt3  | chr10| yes | -0.05 | -0.10 | -0.05 | -0.02 | -0.01 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | 0.03 | 0.03 | 14.69 | 4.79 |
| Rho49b | chr10| yes | -0.02 | -0.05 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | -0.02 | 0.03 | 0.03 | 14.69 | 4.79 |
| Mtap7  | chr10| yes | -0.94 | -0.97 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | -1.00 | 0.03 | 0.03 | 14.69 | 4.79 |
| Tspan8 | chr10| yes | -0.00 | -0.00 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | -0.01 | 0.03 | 0.03 | 14.69 | 4.79 |
| Gene       | Chromosome | Case | Control | p1  | p2  | p3  | p4  | p5  | p6  | p7  | p8  | p9  | p10 | p11 | p12 | p13 | p14 | p15 | p16 | p17 | p18 | p19 | p20 | p21 | p22 | p23 | p24 | p25 | p26 | p27 | p28 | p29 | p30 | p31 | p32 | Average |
|------------|------------|------|---------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-------|
| Arhgap27   | chr11      | yes  | -       | 0.06| 0.04| 0.03| 0.03| 0.04| 0.04| 0.04| 0.03| 0.03| 0.02| 0.03| 0.01| 25.44| 5.30|
| Haver1     | chr11      | yes  | -       | 0.93| 0.95| 0.94| 0.95| 0.90| 0.94| 0.93| 0.94| 0.95| 0.96| 0.95| 0.94| 0.01| 86.25| 18.85|
| Gm12185    | chr11      | yes  | -       | 0.09| 0.11| 0.06| 0.06| 0.07| 0.07| 0.05| 0.10| 0.03| 0.06| 0.05| 0.07| 0.02| 17.52| 2.98 |
| Gm3435     | chr11      | yes  | -       | 0.08| 0.09| 0.13| 0.08| 0.08| 0.11| 0.10| 0.08| 0.14| 0.10| 0.15| 0.10| 0.03| 29.21| 5.81 |
| Gm11428    | chr11      | yes  | -       | -   | 0.03| 0.03| 0.12| -   | -   | 0.03| 0.06| 0.12| 0.05| -   | 0.06| 0.04| 14.29| 2.66 |
| 9930111321Rk1 | chr11      | yes  | -       | 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 91.04| 23.50|
| Gm12355    | chr11      | yes  | -       | 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.01| 0.00| 0.00| 16.00| 4.57 |
| Hmga1-rs1  | chr11      | yes  | -       | 0.01| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.01| 0.00| 0.00| 24.46| 12.21|
| Faau-pn2   | chr11      | yes  | -       | -   | 0.11| 0.06| -   | 0.04| 0.07| -   | 0.02| 0.05| 0.02| 0.05| 0.03| 34.60| 17.87|
| 2610035D17Rik | chr11      | yes  | -       | 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 1.00| 0.99| -   | 0.99| 1.00| 0.00| 35.28| 11.03|
| Itpk1      | chr12      | yes  | -       | 0.92| 0.95| 0.95| 0.92| 0.90| 0.94| 0.95| 0.96| -   | 0.94| 0.94| 0.94| 0.02| 15.62| 3.64 |
| AC073565.1 | chr12      | yes  | -       | -   | 0.07| 0.05| 0.04| 0.12| 0.07| 0.06| 0.04| 0.04| 0.06| 0.05| 0.06| 0.02| 27.18| 8.57 |
| AC160990.6 | chr12      | yes  | -       | -   | 0.06| 0.06| 0.04| 0.07| -   | 0.05| 0.03| -   | 0.04| 0.06| 0.05| 0.01| 13.17| 2.35 |
| Scamp1     | chr13      | yes  | -       | 0.13| 0.06| 0.04| 0.03| -   | 0.08| 0.04| 0.10| 0.15| 0.05| 0.05| 0.07| 0.04| 14.81| 2.33 |
| mmu-mir-2134-4 | chr13   | yes  | -       | 0.00| 0.00| 0.00| -   | 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 128.09| 100.87|
| Gm9800     | chr14      | yes  | -       | 0.08| 0.05| 0.05| 0.05| 0.07| 0.05| 0.05| 0.04| 0.03| 0.04| 0.07| 0.05| 0.02| 52.77| 14.85|
| Lgals3     | chr14      | yes  | -       | -   | 0.95| -   | 0.95| 0.99| 0.95| 0.97| 0.93| -   | -   | 0.96| 0.02| 15.45| 4.66 |
| Gm10076    | chr14      | yes  | -       | 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 0.00| 78.84| 21.72|
| AC242409.1 | chr14      | yes  | -       | -   | 0.01| 0.02| -   | 0.01| 0.01| 0.01| 0.01| 0.01| 0.01| 0.01| 0.01| 0.01| 1802.84| 1412.14 |
| Ly6c       | chr15      | yes  | -       | 0.94| 0.95| 0.97| 0.96| 0.97| 0.98| 0.97| 0.96| 0.96| 0.95| 0.98| 0.96| 0.01| 1998.51| 544.30|
| Ly6a       | chr15      | yes  | -       | 0.97| 0.99| 0.99| 0.99| 0.99| 1.00| 1.00| 0.99| 0.99| 0.98| 1.00| 0.99| 0.01| 264.51| 97.88 |
| Sdf2l1     | chr16      | yes  | -       | 0.98| 0.96| 0.96| 0.99| 0.91| 0.96| 0.97| 0.96| 0.95| 0.98| 0.99| 0.96| 0.02| 31.13| 15.07 |
| Mx2        | chr16      | yes  | -       | 0.04| 0.06| 0.05| 0.03| 0.10| 0.04| 0.07| 0.04| 0.03| 0.05| 0.06| 0.05| 0.02| 46.56| 21.27 |
| Pcp4       | chr16      | yes  | -       | 0.09| 0.12| 0.12| 0.13| 0.14| 0.15| 0.12| 0.02| 16.33| 6.40 |

**Note:** The table provides a summary of gene expression data across different conditions, with columns indicating gene names, chromosome locations, and various expression ratios or values.
| Gene       | chr    | Status | - | 0.02 | 0.04 | 0.04 | 0.01 | 0.03 | 0.04 | 0.04 | 0.01 | 0.03 | 0.02 | 0.02 | 0.03 | 0.01 | 213.75 | 48.73 |
|------------|--------|--------|---|------|------|------|------|------|------|------|------|------|------|------|------|------|--------|------|
| H2-Q4      | chr17  | yes    | - | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 1529.94 | 258.23 |
| H2-Ea-ps   | chr17  | yes    | - | 0.97 | 0.89 | -    | 1.00 | 0.92 | -    | -    | 0.94 | -    | 0.96 | -    | 0.95 | 0.04 | 11.70 | 1.09  |
| Decr2      | chr17  | yes    | - | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 50.80  | 9.51   |
| Gm11127    | chr17  | yes    | - | -    | 0.94 | 0.91 | 0.92 | 0.97 | 0.92 | 0.91 | 0.89 | 0.92 | 0.90 | 0.93 | 0.92 | 0.02 | 25.66 | 5.65  |
| H2-Q2      | chr17  | yes    | - | -    | 0.05 | 0.00 | 0.00 | -    | 0.00 | 0.05 | 0.00 | -    | 0.10 | -    | 0.03 | 0.04 | 28.56 | 8.50  |
| D17H6S56E-5| chr17  | yes    | - | 0.99 | 0.99 | 0.98 | 0.99 | 0.99 | 0.99 | 0.98 | 0.99 | 0.98 | 0.99 | 0.99 | 0.99 | 0.00 | 614.17 | 129.62 |
| Rnase2a    | chr17  | yes    | - | 1.00 | 0.99 | 1.00 | 0.99 | 1.00 | 1.00 | 1.00 | 0.98 | 1.00 | 1.00 | 1.00 | 1.00 | 0.01 | 23.76 | 5.11  |
| Rnf125     | chr18  | yes    | - | 0.06 | 0.02 | 0.10 | 0.05 | 0.06 | 0.06 | 0.07 | 0.04 | 0.05 | 0.03 | 0.06 | 0.06 | 0.02 | 22.10 | 5.89  |
| Osbpl11a   | chr18  | yes    | - | 0.01 | 0.04 | 0.04 | 0.02 | 0.06 | 0.04 | 0.03 | 0.06 | 0.10 | 0.04 | 0.09 | 0.05 | 0.03 | 22.08 | 5.77  |
| Gm5506     | chr18  | yes    | - | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 0.99 | 0.99 | 0.98 | 1.00 | 0.00 | 68.35 | 28.15 |
| 4930481A15Rik| chr19  | yes    | - | -    | -    | -    | -    | 0.97 | 0.98 | 1.00 | 1.00 | -    | 1.00 | 0.99 | 0.99 | 0.01 | 13.24 | 1.95  |
| Zrsr1*     | chr11  | yes    | yes| 0.00 | 0.02 | 0.00 | 0.00 | 0.00 | 0.01 | 0.00 | 0.00 | 0.01 | 0.01 | 0.01 | 0.01 | 0.00 | 49.36 | 14.26 |
| Iqf2a*     | chr17  | yes    | yes| -    | 0.97 | 1.00 | -    | 1.00 | 0.97 | 0.94 | 0.97 | 0.92 | 0.97 | 0.87 | 0.96 | 0.04 | 18.65 | 5.97  |
| Eoflhb2    | chr1   | no     | yes| 0.45 | 0.40 | 0.46 | 0.49 | 0.47 | 0.43 | 0.46 | 0.50 | 0.46 | 0.48 | 0.48 | 0.46 | 0.03 | 11.83 | 26.24 |
| Stx6       | chr1   | no     | yes| 0.49 | 0.49 | 0.52 | 0.46 | 0.46 | 0.52 | 0.50 | 0.44 | 0.49 | 0.47 | 0.41 | 0.48 | 0.03 | 74.91 | 14.47 |
| Mr1        | chr1   | no     | yes| 0.60 | 0.51 | 0.51 | 0.49 | 0.54 | 0.51 | 0.52 | 0.50 | 0.56 | 0.46 | 0.40 | 0.51 | 0.05 | 15.15 | 3.74  |
| Bcl211     | chr2   | no     | yes| -    | 0.36 | -    | -    | -    | -    | -    | 0.60 | -    | 0.48 | 0.17 | 10.77 | 0.49  |
| H13        | chr2   | no     | yes| 0.50 | 0.50 | 0.45 | 0.45 | 0.46 | 0.43 | 0.44 | 0.44 | 0.47 | 0.44 | 0.48 | 0.46 | 0.03 | 153.46| 38.25 |
| Rbms1      | chr2   | no     | yes| 0.48 | 0.55 | 0.52 | 0.56 | 0.56 | 0.54 | 0.52 | 0.51 | 0.59 | 0.54 | 0.55 | 0.54 | 0.03 | 112.54| 25.06 |
| Stx16      | chr2   | no     | yes| 0.37 | 0.54 | 0.55 | 0.46 | 0.53 | 0.49 | 0.48 | 0.53 | 0.53 | 0.56 | 0.52 | 0.51 | 0.05 | 37.78 | 8.41  |
| Gnas       | chr2   | no     | yes| 0.24 | 0.37 | 0.44 | -    | 0.30 | 0.32 | 0.38 | -    | -    | -    | 0.30 | 0.34 | 0.06 | 32.03 | 45.22 |
| Zlp64      | chr2   | no     | yes| 0.47 | 0.56 | 0.54 | 0.49 | 0.58 | 0.52 | 0.53 | 0.56 | 0.54 | 0.55 | 0.28 | 0.51 | 0.08 | 23.72 | 5.30  |
| Npepl1     | chr2   | no     | yes| 0.48 | 0.52 | 0.52 | 0.52 | 0.50 | 0.50 | 0.50 | 0.51 | 0.49 | 0.54 | 0.48 | 0.51 | 0.02 | 155.37| 28.31 |
| Bicup      | chr2   | no     | yes| 0.68 | 0.54 | 0.47 | 0.55 | 0.63 | 0.52 | 0.61 | 0.51 | 0.28 | 0.54 | 0.55 | 0.53 | 0.10 | 27.23 | 6.29  |
| Genes | Chromosome | TREATMENT | SHH | IRF1 | INH | RUNX2 | NOTCH | WNT | PI3K | MEK | MAPK | E2F3 | OCT4 | ETS | SOX | BRG1 | SMARCA4 | KSHV | HSP27 | HSP22 | HSP90 | HSP70 | 90KDa | 70KDa | 50KDa | 30KDa | 10KDa | 0.29 | 0.53 | 0.57 | 0.53 | 0.49 | 0.50 | 0.47 | 0.50 | 0.48 | 0.52 | 0.57 | 0.52 | 0.03 | 70.24 | 13.51 |
|-------|------------|-----------|-----|------|-----|------|-------|-----|------|-----|------|------|------|-----|-----|-----|------|----------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|
| Gene   | Chr | Biased | Imprinted | Control | E13.1 | E13.2 | E13.24 | E13.29 | Mean(AI) | Std(AI) | Mean  | Std   |
|--------|-----|--------|-----------|---------|-------|-------|--------|-------|----------|--------|-------|-------|
| Slc41a1| chr1| yes    | -         | 0.13    | 0.13  | 0.13  | 0.12   | 0.12  | 0.13     | 0.01   | 159.17| 27.98 |
| Ica1l  | chr1| yes    | -         | 0.04    | 0.07  | 0.05  | 0.05   | 0.05  | 0.05     | 0.01   | 93.14 | 13.99 |
| Chst10 | chr1| yes    | -         | 0.89    | 0.91  | 0.89  | 0.92   | 0.91  | 0.90     | 0.01   | 58.83 | 10.24 |
| Gene      | Chromosome | Presence | Strand | Mean | SD | MOE | Median | Proportion | Mean | SD | MOE | Median | Proportion |
|-----------|------------|----------|--------|------|----|-----|--------|-----------|------|----|-----|--------|-----------|
| A630001G21Rik | chr1       | yes      | -      | 0.95 | 0.91 | 0.92 | 0.94 | 0.92 | 0.93 | 0.01 | 16.10 | 2.25 |
| Gm10075   | chr1       | yes      | -      | 0.88 | 0.90 | 0.89 | 0.90 | 0.88 | 0.89 | 0.01 | 56.92 | 25.13 |
| Slc30a4   | chr2       | yes      | -      | 0.97 | 0.98 | 0.94 | 0.96 | 0.98 | 0.97 | 0.02 | 27.91 | 11.33 |
| Sgrd1     | chr2       | yes      | -      | 1.00 | 1.00 | 0.99 | 0.98 | 0.99 | 0.99 | 0.01 | 28.84 | 7.37  |
| Serinc3   | chr2       | yes      | -      | 0.11 | 0.13 | 0.10 | 0.10 | 0.09 | 0.10 | 0.01 | 2287.71 | 472.72 |
| Eya2      | chr2       | yes      | -      | 0.95 | 0.97 | 0.93 | 0.90 | 0.98 | 0.95 | 0.03 | 15.14 | 2.20 |
| Lypd6b    | chr2       | yes      | -      | 1.00 | 1.00 | 0.99 | 1.00 | 1.00 | 1.00 | 0.00 | 26.13 | 2.72  |
| Ltk       | chr2       | yes      | -      | -    | 0.00 | 0.06 | 0.02 | 0.02 | 0.03 | 0.03 | 12.02 | 0.88 |
| Pkg       | chr2       | yes      | -      | 0.04 | 0.04 | 0.05 | 0.04 | 0.04 | 0.04 | 0.00 | 200.04 | 112.50 |
| Ldrlad3   | chr2       | yes      | -      | 0.92 | 0.95 | 0.96 | 0.95 | 0.95 | 0.95 | 0.01 | 75.77 | 17.22 |
| Rapgef4   | chr2       | yes      | -      | 0.02 | 0.01 | 0.03 | 0.02 | 0.01 | 0.02 | 0.01 | 38.93 | 9.36  |
| Gm13699   | chr2       | yes      | -      | 1.00 | 1.00 | 0.99 | 0.99 | 0.99 | 0.99 | 0.00 | 41.56 | 22.89 |
| D430041D05Rik | chr2       | yes      | -      | 0.02 | 0.01 | 0.02 | 0.02 | 0.03 | 0.02 | 0.01 | 98.80 | 30.47 |
| Gm13654   | chr2       | yes      | -      | 0.98 | 0.99 | 0.99 | 0.98 | 0.97 | 0.98 | 0.01 | 19.98 | 8.29  |
| Gm13736   | chr2       | yes      | -      | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 196.70 | 80.98 |
| MIR5115   | chr2       | yes      | -      | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 74.54 | 21.42 |
| Serpini1  | chr3       | yes      | -      | 0.04 | 0.08 | 0.05 | 0.11 | 0.07 | 0.07 | 0.03 | 22.81 | 4.81  |
| Ugt8a     | chr3       | yes      | -      | 0.00 | 0.00 | 0.07 | 0.05 | 0.02 | 0.04 | 0.03 | 22.81 | 4.81  |
| Cnn3      | chr3       | yes      | -      | 0.92 | 0.94 | 0.94 | 0.94 | 0.96 | 0.94 | 0.01 | 199.41 | 36.28 |
| Ptger1    | chr4       | yes      | -      | 0.12 | 0.13 | 0.13 | 0.10 | 0.12 | 0.12 | 0.01 | 51.67 | 9.07  |
| S1c5a9    | chr4       | yes      | -      | 0.96 | 0.98 | 0.95 | 0.97 | 0.95 | 0.96 | 0.01 | 16.36 | 3.16  |
| Spata6    | chr4       | yes      | -      | 0.93 | 0.90 | 0.90 | 0.86 | 0.89 | 0.89 | 0.02 | 65.59 | 7.33  |
| 2010015L04Rik | chr4       | yes      | -      | 0.91 | 0.92 | 0.85 | 0.86 | 0.87 | 0.88 | 0.03 | 66.96 | 8.51  |
| Tnfrsf14  | chr4       | yes      | -      | 0.07 | 0.14 | 0.15 | 0.11 | 0.10 | 0.11 | 0.03 | 13.73 | 2.69  |
| Ubxn10    | chr4       | yes      | -      | 0.02 | 0.02 | 0.02 | 0.06 | 0.03 | 0.03 | 0.02 | 22.41 | 2.61  |
| Gene       | Chromosome | Stranded | Fold Change 1 | Fold Change 2 | Fold Change 3 | Fold Change 4 | Fold Change 5 | Fold Change 6 | Fold Change 7 | Fold Change 8 | Average 1 | Average 2 |
|------------|------------|----------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|---------------|-----------|-----------|
| Gm11223    | chr4       | yes      | 0.03          | 0.03          | 0.02          | 0.02          | 0.02          | 0.01          | 274.90        | 59.44         |
| Tmem245    | chr4       | yes      | 0.89          | 0.85          | 0.88          | 0.87          | 0.88          | 0.88          | 0.02          | 59.50         | 20.27     |
| Gm12715    | chr4       | yes      | 0.98          | 0.98          | 0.99          | 0.99          | 0.97          | 0.98          | 43.82         | 8.38          |
| Impad1     | chr4       | yes      | 0.95          | 0.89          | 0.90          | 0.88          | 0.87          | 0.90          | 0.03          | 37.78         | 10.39     |
| Gm12372    | chr4       | yes      | 0.00          | -             | 0.01          | 0.04          | 0.00          | 0.01          | 18.85         | 2.02          |
| Crmp1      | chr5       | yes      | 0.06          | 0.04          | 0.04          | 0.03          | 0.03          | 0.04          | 132.65        | 23.10        |
| Acad12     | chr5       | yes      | 0.01          | 0.02          | 0.04          | 0.08          | 0.02          | 0.04          | 22.37         | 2.27          |
| Cltn4      | chr5       | yes      | 0.13          | 0.15          | 0.10          | 0.08          | 0.09          | 0.11          | 72.85         | 27.50        |
| Zip498     | chr5       | yes      | 0.05          | 0.08          | 0.07          | 0.11          | 0.10          | 0.08          | 11.94         | 2.29          |
| Ccld164    | chr5       | yes      | 0.10          | 0.08          | 0.12          | 0.07          | 0.08          | 0.09          | 135.51        | 26.84        |
| Mtr5105    | chr5       | yes      | 0.00          | 0.00          | 0.00          | 0.00          | 0.00          | 0.00          | 356.07        | 161.94       |
| Plekha8    | chr6       | yes      | 0.00          | 0.01          | 0.05          | 0.02          | 0.04          | 0.02          | 21.32         | 5.88          |
| Ctsm3      | chr6       | yes      | 0.00          | 0.01          | 0.03          | 0.02          | 0.01          | 0.01          | 21.45         | 4.25          |
| Gimap8     | chr6       | yes      | 0.95          | 0.87          | 0.94          | 0.93          | 0.91          | 0.92          | 39.72         | 6.51          |
| Lpar5      | chr6       | yes      | 0.05          | 0.06          | 0.07          | 0.05          | 0.06          | 0.06          | 13.87         | 2.77          |
| Trb21      | chr6       | yes      | 0.01          | 0.01          | 0.01          | 0.01          | 0.01          | 0.00          | 37.43         | 6.57          |
| Dynl1-ps1  | chr6       | yes      | 0.00          | -             | 0.00          | 0.00          | 0.00          | 0.00          | 29.11         | 9.16          |
| Apoe       | chr7       | yes      | 0.95          | 0.98          | 0.90          | 0.94          | 0.97          | 0.95          | 24.59         | 8.53          |
| Capn5      | chr7       | yes      | 0.05          | 0.07          | 0.09          | 0.07          | 0.09          | 0.07          | 169.72        | 44.46        |
| Capn12     | chr7       | yes      | -             | -             | 0.01          | 0.01          | 0.03          | 0.00          | 14.92         | 3.14          |
| Trim12a    | chr7       | yes      | 0.92          | 0.95          | 0.98          | 0.96          | 0.97          | 0.96          | 49.85         | 7.66          |
| Plekhf1    | chr7       | yes      | 0.11          | 0.10          | 0.10          | 0.11          | 0.12          | 0.11          | 107.04        | 36.15        |
| Mtr5102    | chr7       | yes      | 0.00          | 0.00          | 0.00          | 0.00          | 0.00          | 0.00          | 155.10        | 16.95        |
| Lass4      | chr8       | yes      | 0.06          | 0.07          | 0.12          | 0.07          | 0.05          | 0.07          | 20.44         | 1.84          |
| Rab11fip1  | chr8       | yes      | 0.93          | -             | 0.88          | 0.89          | 0.91          | 0.90          | 14.06         | 1.79          |
| Gene  | Chromosome | Strata | p-value 1 | p-value 2 | p-value 3 | p-value 4 | p-value 5 | p-value 6 | p-value 7 | p-value 8 | p-value 9 | p-value 10 |
|-------|------------|--------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|------------|
| Nwd1  | chr8       | yes    | -         | 0.99      | 0.96      | 0.97      | 0.98      | 0.98      | 0.01      | 32.60     | 14.59     |            |
| Lig4  | chr8       | yes    | -         | 0.93      | 0.92      | 0.93      | 0.93      | 0.93      | 0.01      | 78.18     | 18.31     |            |
| Gm10282 | chr8     | yes    | -         | 0.09      | 0.04      | 0.06      | 0.08      | 0.08      | 0.07      | 0.02      | 54.31     | 13.17      |
| Slc37a2 | chr9     | yes    | -         | 0.90      | 0.92      | 0.94      | 0.91      | 0.94      | 0.92      | 0.02      | 46.03     | 5.23       |
| Arpp21 | chr9      | yes    | -         | 0.91      | 0.89      | 0.91      | 0.89      | 0.89      | 0.90      | 0.01      | 590.87    | 66.46      |
| Ip6k2  | chr9       | yes    | -         | 0.04      | 0.08      | 0.08      | 0.06      | 0.06      | 0.07      | 0.02      | 98.49     | 28.55      |
| Lars2  | chr9       | yes    | -         | 0.07      | 0.15      | 0.10      | 0.09      | 0.11      | 0.10      | 0.03      | 5596.21   | 486.73     |
| Ncam1  | chr9       | yes    | -         | 0.04      | 0.03      | 0.03      | 0.03      | 0.03      | 0.00      | 27.51     | 20.57     |            |
| Slc35f2 | chr9      | yes    | -         | 0.06      | 0.07      | 0.06      | 0.11      | 0.10      | 0.08      | 0.02      | 52.46     | 3.76       |
| Rpl29  | chr9       | yes    | -         | 0.87      | 0.93      | 0.96      | 0.86      | 0.88      | 0.90      | 0.04      | 92.68     | 25.55      |
| Mmp13  | chr9       | yes    | -         | 0.01      | -         | 0.00      | 0.03      | 0.00      | 0.01      | 0.01      | 15.18     | 3.71       |
| Pchp3  | chr10      | yes    | -         | 0.08      | 0.06      | 0.06      | 0.06      | 0.04      | 0.06      | 0.01      | 200.81    | 60.52      |
| Perp   | chr10      | yes    | -         | 0.01      | 0.01      | 0.00      | 0.00      | 0.00      | 0.00      | 0.00      | 20.42     | 4.97       |
| Slc17a8 | chr10     | yes    | -         | 0.00      | -         | 0.00      | 0.02      | 0.00      | 0.01      | 0.01      | 16.07     | 4.89       |
| Arkap12 | chr10     | yes    | -         | 0.97      | 0.97      | 0.97      | 0.98      | 0.98      | 0.97      | 0.00      | 45.49     | 9.65       |
| Lyz2   | chr10      | yes    | -         | 0.09      | 0.03      | 0.03      | 0.03      | 0.09      | 0.05      | 0.03      | 38.75     | 11.67      |
| P4ha2  | chr11      | yes    | -         | 0.00      | 0.03      | 0.02      | 0.03      | 0.01      | 0.02      | 0.01      | 15.45     | 3.41       |
| Il9r   | chr11      | yes    | -         | 0.13      | 0.10      | 0.08      | 0.08      | 0.06      | 0.09      | 0.02      | 20.33     | 6.78       |
| Cacng4 | chr11      | yes    | -         | 0.09      | 0.06      | 0.00      | 0.08      | 0.05      | 0.06      | 0.03      | 39.10     | 9.33       |
| Nnt1   | chr11      | yes    | -         | 0.91      | 0.96      | 0.89      | 0.91      | 0.88      | 0.91      | 0.03      | 19.86     | 5.28       |
| Arhgap27 | chr11    | yes    | -         | 0.89      | 0.89      | 0.91      | 0.94      | 0.92      | 0.91      | 0.02      | 45.40     | 9.11       |
| Stit3  | chr11      | yes    | -         | 0.08      | 0.04      | 0.03      | 0.10      | 0.02      | 0.05      | 0.03      | 30.59     | 14.82      |
| Gm12355 | chr11     | yes    | -         | 0.00      | 0.00      | 0.00      | 0.00      | 0.00      | 0.00      | 0.00      | 30.80     | 8.11       |
| Hmgal1-rs1 | chr11  | yes    | -         | 0.00      | 0.00      | 0.00      | 0.00      | 0.00      | 0.00      | 35.95     | 14.22      |
| 2610035D17Rik | chr11  | yes    | -         | 1.00      | 1.00      | 0.99      | 1.00      | 1.00      | 1.00      | 0.00      | 28.46     | 6.97       |
| Gene  | Chromosome | Status | Gene IDs | Gene IDs | Gene IDs | Gene IDs | Gene IDs | Gene IDs |
|-------|------------|--------|----------|----------|----------|----------|----------|----------|
| Srp54a| chr12      | yes    | -        | 0.85     | -        | 1.00     | 0.93     | 0.98     | 0.94     | 0.07     | 11.61    | 1.75     |
| Map4k5| chr12      | yes    | -        | 0.92     | 0.90     | 0.87     | 0.89     | 0.91     | 0.90     | 0.02     | 51.42    | 12.59    |
| Greb1 | chr12      | yes    | -        | 0.08     | 0.11     | 0.08     | 0.10     | 0.08     | 0.09     | 0.02     | 35.51    | 13.28    |
| Fam177a| chr12     | yes    | -        | 0.02     | 0.07     | 0.12     | 0.08     | 0.07     | 0.07     | 0.03     | 11.91    | 0.86     |
| Cap2  | chr13      | yes    | -        | 0.09     | 0.08     | 0.08     | 0.09     | 0.13     | 0.10     | 0.02     | 13.90    | 3.52     |
| Ctsl  | chr13      | yes    | -        | 0.08     | 0.08     | 0.08     | 0.09     | 0.09     | 0.09     | 0.00     | 1196.91  | 252.12   |
| Gzma  | chr13      | yes    | -        | 0.04     | 0.06     | 0.05     | 0.04     | 0.05     | 0.05     | 0.01     | 258.18   | 35.25    |
| Cdc14b| chr13      | yes    | -        | 0.06     | 0.09     | 0.09     | 0.09     | 0.07     | 0.08     | 0.01     | 64.69    | 11.97    |
| Tubb2b| chr13      | yes    | -        | 0.95     | 0.99     | 0.98     | 0.97     | 0.97     | 0.97     | 0.01     | 56.25    | 9.22     |
| Actn2 | chr13      | yes    | -        | 0.09     | 0.09     | 0.06     | 0.05     | 0.04     | 0.07     | 0.02     | 11.98    | 1.41     |
| Tubb2a| chr13      | yes    | -        | 0.97     | 0.96     | 0.96     | 0.96     | 0.96     | 0.96     | 0.01     | 158.10   | 45.86    |
| mmu-mir-2134-4| chr13 | yes | - | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 121.93 | 50.67 |
| Chth  | chr14      | yes    | -        | 0.96     | 0.95     | 0.96     | 0.94     | 0.95     | 0.95     | 0.01     | 33.60    | 12.49    |
| Epsti1| chr14      | yes    | -        | 0.96     | 0.96     | 0.97     | 0.93     | 0.95     | 0.95     | 0.02     | 29.50    | 3.79     |
| Dzip1 | chr14      | yes    | -        | 0.85     | 0.88     | 0.89     | 0.87     | 0.89     | 0.88     | 0.01     | 59.19    | 6.58     |
| Gm9800| chr14      | yes    | -        | 0.06     | 0.06     | 0.05     | 0.05     | 0.05     | 0.05     | 0.01     | 117.84   | 41.71    |
| Gm10076| chr14    | yes    | -        | 0.01     | 0.00     | 0.00     | 0.00     | 0.00     | 0.00     | 0.00     | 41.03    | 8.26     |
| Trav1 | chr14      | yes    | -        | 0.08     | 0.13     | 0.13     | 0.09     | 0.14     | 0.11     | 0.03     | 21.39    | 10.01    |
| Itga5 | chr15      | yes    | -        | 0.91     | 0.97     | 0.89     | 0.89     | 0.89     | 0.91     | 0.04     | 12.58    | 1.50     |
| Endou | chr15      | yes    | -        | 0.92     | 0.91     | 0.90     | 0.89     | 0.89     | 0.90     | 0.01     | 387.52   | 123.13   |
| Ly6e  | chr15      | yes    | -        | 0.98     | 0.98     | 0.97     | 0.98     | 0.97     | 0.98     | 0.00     | 1177.22  | 420.62   |
| Prickle1| chr15   | yes    | -        | 0.98     | 0.99     | 0.96     | 0.98     | 0.98     | 0.98     | 0.01     | 28.64    | 7.53     |
| Apol11b | chr15  | yes    | -        | 0.00     | 0.00     | 0.00     | 0.01     | 0.00     | 0.00     | 0.00     | 13.82    | 2.38     |
| Cd96  | chr16      | yes    | -        | 0.98     | 0.98     | 0.98     | 0.97     | 0.98     | 0.98     | 0.00     | 128.58   | 9.45     |
| Cd200 | chr16      | yes    | -        | 0.07     | 0.03     | 0.05     | 0.03     | 0.02     | 0.04     | 0.02     | 68.90    | 11.12    |
| Gene    | Chromosome | Imprint | Zygosity | Score1 | Score2 | Score3 | Score4 | Score5 | Score6 | Score7 | Max Score | Min Score |
|---------|------------|----------|----------|--------|--------|--------|--------|--------|--------|--------|-----------|-----------|
| Sdf2l1  | chr16      | yes      | -        | 0.99   | 0.94   | 0.93   | 0.95   | 0.95   | 0.03   | 20.04  | 11.85     |           |
| Bach1   | chr16      | yes      | -        | 0.11   | 0.09   | 0.11   | 0.10   | 0.10   | 0.01   | 484.93 | 142.50    |           |
| A930003A15Rik | chr16  | yes      | -        | 1.00   | 1.00   | 1.00   | 0.99   | 1.00   | 0.00   | 29.01  | 5.67      |           |
| Plcxd2  | chr16      | yes      | -        | 0.96   | 0.93   | 0.97   | 0.98   | 0.99   | 0.97   | 0.02   | 53.11     | 9.34      |
| Crim1   | chr17      | yes      | -        | 0.10   | 0.13   | 0.07   | 0.11   | 0.09   | 0.03   | 17.41  | 3.50      |           |
| H2-T3   | chr17      | yes      | -        | 0.01   | 0.01   | 0.01   | 0.01   | 0.01   | 0.00   | 1.00   | 473.51    | 111.29    |
| H2-Q5   | chr17      | yes      | -        | 0.01   | 0.00   | 0.01   | 0.01   | 0.00   | 0.01   | 0.00   | 31.66     | 13.08     |
| H2-Q10  | chr17      | yes      | -        | 0.00   | 0.00   | 0.00   | 0.06   | 0.02   | 0.03   | 48.31  | 13.36     |           |
| H2-B1I  | chr17      | yes      | -        | 0.01   | 0.04   | 0.02   | 0.03   | 0.02   | 0.01   | 19.40  | 2.97      |           |
| H2-T10  | chr17      | yes      | -        | 0.07   | 0.08   | 0.08   | 0.11   | 0.10   | 0.09   | 0.01   | 434.18    | 74.75     |
| H2-Q3   | chr17      | yes      | -        | 0.01   | 0.01   | 0.01   | 0.01   | 0.01   | 0.00   | 106.11 | 45.78     |           |
| Rnase2a | chr17      | yes      | -        | 0.97   | 1.00   | 1.00   | 0.99   | 0.99   | 0.01   | 22.32  | 6.32      |           |
| Cyb5    | chr18      | yes      | -        | 0.87   | 0.89   | 0.86   | 0.90   | 0.90   | 0.88   | 0.02   | 323.56    | 77.01     |
| Osbpl1a | chr18      | yes      | -        | 0.06   | 0.11   | 0.15   | 0.13   | 0.12   | 0.11   | 0.03   | 32.58     | 0.87      |
| Gm5506  | chr18      | yes      | -        | 1.00   | 1.00   | 1.00   | 0.99   | 1.00   | 0.00   | 53.87  | 29.92     |           |
| Ptpnm1  | chr19      | yes      | -        | 0.86   | 0.92   | 0.89   | 0.90   | 0.95   | 0.90   | 0.03   | 29.55     | 3.78      |
| Paps2   | chr19      | yes      | -        | 1.00   | 0.99   | 0.99   | 0.99   | 0.99   | 0.99   | 0.00   | 24.48     | 3.40      |
| Nmrk1   | chr19      | yes      | -        | 0.13   | 0.09   | 0.09   | 0.08   | 0.08   | 0.09   | 0.02   | 44.58     | 13.36     |
| Pcan-ps2| chr19      | yes      | -        | 0.00   | 0.00   | 0.01   | 0.01   | 0.01   | 0.01   | 0.00   | 19.69     | 13.79     |
| Hnuph2  | chrX       | yes      | -        | 0.86   | -      | 0.96   | 0.92   | 1.00   | 0.93   | 0.06   | 167.43    | 30.16     |
| Zrsr1*  | chr11      | yes      | Imprinted| 0.00   | 0.00   | 0.01   | 0.01   | 0.03   | 0.01   | 12.96  | 2.26      |           |
| Ifg2r*  | chr17      | yes      | Imprinted| 0.96   | 1.00   | 0.99   | 0.98   | 1.00   | 0.98   | 0.02   | 72.77     | 36.72     |
| Airn*   | chr17      | yes      | Imprinted| -      | 0.00   | 0.01   | 0.05   | 0.00   | 0.01   | 0.02   | 14.28     | 1.59      |
| Cdkn1c  | chr7       | maybe    | Imprinted| 0.98   | 1.00   | -      | -      | -      | 0.99   | 0.02   | 13.12     | 1.15      |
| Gm16299 | chr19      | maybe    | Imprinted| -      | -      | -      | 0.01   | -      | 0.01   | -      | 11.85     | -         |
| Gene    | Chromosome | Imprinted | log2FoldChange1 | log2FoldChange2 | log2FoldChange3 | log2FoldChange4 | log2FoldChange5 | log2FoldChange6 | log2FoldChange7 | log2FoldChange8 | log2FoldChange9 |
|---------|------------|-----------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| Eef1b2  | chr1       | no        | 0.49           | 0.51           | 0.48           | 0.51           | 0.50           | 0.50           | 0.01           | 79.40          | 15.84          |
| Stx6    | chr1       | no        | 0.48           | 0.48           | 0.49           | 0.49           | 0.49           | 0.49           | 0.00           | 431.38         | 99.20          |
| Mr1     | chr1       | no        | 0.33           | 0.32           | 0.34           | 0.33           | 0.32           | 0.33           | 0.01           | 291.43         | 43.75          |
| Bcl2l1  | chr2       | no        | 0.48           | 0.48           | 0.49           | 0.48           | 0.48           | 0.48           | 0.01           | 599.45         | 98.84          |
| Bmp7    | chr2       | no        | 0.39           | 0.45           | 0.38           | 0.41           | 0.44           | 0.41           | 0.03           | 25.43          | 4.63           |
| H13     | chr2       | no        | 0.48           | 0.49           | 0.51           | 0.46           | 0.47           | 0.48           | 0.02           | 300.74         | 56.81          |
| Rhmsl1  | chr2       | no        | 0.48           | 0.55           | 0.51           | 0.47           | 0.52           | 0.51           | 0.03           | 91.87          | 24.27          |
| Tpx2    | chr2       | no        | 0.47           | 0.50           | 0.50           | 0.47           | 0.49           | 0.49           | 0.02           | 135.57         | 32.64          |
| Stx16   | chr2       | no        | 0.59           | 0.55           | 0.54           | 0.52           | 0.51           | 0.54           | 0.03           | 74.25          | 8.49           |
| Zlp64   | chr2       | no        | 0.54           | 0.51           | 0.48           | 0.48           | 0.48           | 0.50           | 0.03           | 52.93          | 9.22           |
| Npepl1  | chr2       | no        | 0.60           | 0.57           | 0.55           | 0.54           | 0.56           | 0.56           | 0.02           | 73.55          | 13.99          |
| Sfmbt2  | chr2       | no        | 0.72           | -              | 0.77           | 0.64           | 0.53           | 0.67           | 0.10           | 11.43          | 0.53           |
| Bicup   | chr2       | no        | 0.67           | 0.45           | 0.71           | 0.42           | 0.62           | 0.57           | 0.13           | 17.58          | 2.21           |
| Mafb    | chr2       | no        | 0.55           | 0.54           | 0.52           | 0.62           | 0.49           | 0.54           | 0.05           | 21.42          | 12.51          |
| Casd1   | chr6       | no        | 0.49           | 0.45           | 0.53           | 0.52           | 0.50           | 0.50           | 0.03           | 57.56          | 8.67           |
| Copg2   | chr6       | no        | 0.47           | 0.45           | 0.44           | 0.44           | 0.45           | 0.45           | 0.01           | 77.31          | 21.66          |
| Kldlc100| chr6       | no        | 0.44           | 0.36           | 0.48           | 0.44           | 0.44           | 0.44           | 0.05           | 60.90          | 13.34          |
| Herc3   | chr6       | no        | 0.35           | 0.41           | 0.37           | 0.36           | 0.39           | 0.38           | 0.02           | 71.32          | 22.53          |
| Etv6    | chr6       | no        | 0.46           | 0.46           | 0.56           | 0.60           | 0.54           | 0.52           | 0.06           | 30.21          | 4.28           |
| Lsp1    | chr7       | no        | 0.44           | 0.47           | 0.44           | 0.44           | 0.44           | 0.45           | 0.01           | 650.93         | 178.81         |
| Ube3a   | chr7       | no        | 0.53           | 0.42           | 0.52           | 0.51           | 0.51           | 0.50           | 0.04           | 155.62         | 27.91          |
| Cdh1    | chr7       | no        | 0.42           | 0.42           | 0.43           | 0.44           | 0.44           | 0.43           | 0.01           | 224.34         | 50.12          |
| Inpp5f6 | chr7       | no        | 0.36           | 0.35           | 0.36           | 0.43           | 0.35           | 0.37           | 0.04           | 21.92          | 3.71           |
| Tnfrsf26| chr7       | no        | 0.73           | 0.71           | 0.72           | 0.70           | 0.72           | 0.71           | 0.01           | 26.71          | 3.42           |
| Tssc4   | chr7       | no        | 0.57           | 0.61           | 0.56           | 0.57           | 0.54           | 0.57           | 0.02           | 55.94          | 23.75          |
| Genes     | Chromosome | Imprint | 0.59 | 0.60 | 0.49 | 0.49 | 0.49 | 0.53 | 0.06 | 101.61 | 15.29 |
|-----------|------------|---------|------|------|------|------|------|------|------|--------|-------|
| Dhcr7     | chr7       | no      | 0.59 | 0.60 | 0.49 | 0.49 | 0.49 | 0.53 | 0.06 | 101.61 | 15.29 |
| Nap1l4    | chr7       | no      | 0.48 | 0.47 | 0.46 | 0.48 | 0.45 | 0.47 | 0.01 | 266.64 | 64.05 |
| R74862    | chr7       | no      | 0.46 | 0.39 | -    | 0.38 | -    | 0.41 | 0.04 | 12.06  | 2.29  |
| Arrdc2    | chr8       | no      | 0.55 | 0.49 | 0.50 | 0.45 | 0.44 | 0.49 | 0.04 | 29.27  | 10.18 |
| Tle3      | chr9       | no      | 0.71 | 0.71 | 0.73 | 0.73 | 0.77 | 0.73 | 0.02 | 84.37  | 8.03  |
| Snx14     | chr9       | no      | 0.35 | 0.36 | 0.42 | 0.29 | 0.42 | 0.37 | 0.06 | 20.79  | 2.88  |
| Gramd1b   | chr9       | no      | 0.25 | 0.24 | 0.27 | 0.26 | 0.30 | 0.26 | 0.02 | 18.93  | 3.81  |
| Phactr2   | chr10      | no      | 0.45 | 0.52 | 0.61 | 0.43 | 0.59 | 0.52 | 0.08 | 55.94  | 18.73 |
| Commd1*   | chr11      | no      | 0.71 | 0.64 | 0.68 | 0.66 | 0.66 | 0.67 | 0.03 | 87.50  | 15.63 |
| Actn1     | chr12      | no      | 0.58 | 0.58 | 0.59 | 0.57 | 0.57 | 0.58 | 0.01 | 318.86 | 13.55 |
| Ppp2r5c   | chr12      | no      | 0.53 | 0.47 | 0.49 | 0.49 | 0.50 | 0.50 | 0.02 | 81.05  | 16.74 |
| Dyncl1    | chr12      | no      | 0.67 | 0.67 | 0.69 | 0.53 | 0.64 | 0.64 | 0.07 | 73.06  | 19.38 |
| Smoc1     | chr12      | no      | 0.45 | 0.45 | 0.50 | 0.49 | 0.45 | 0.47 | 0.02 | 73.17  | 7.26  |
| Wars      | chr12      | no      | 0.63 | 0.63 | 0.61 | 0.63 | 0.64 | 0.62 | 0.01 | 142.15 | 18.08 |
| E2f3      | chr13      | no      | 0.58 | 0.58 | 0.59 | 0.57 | 0.57 | 0.58 | 0.01 | 318.86 | 13.55 |
| Pde4d     | chr13      | no      | 0.68 | 0.64 | 0.69 | 0.69 | 0.69 | 0.68 | 0.02 | 366.56 | 76.16 |
| Mbnl2     | chr14      | no      | 0.54 | 0.56 | 0.47 | 0.49 | 0.50 | 0.51 | 0.04 | 177.38 | 18.60 |
| Slic38a2  | chr15      | no      | 0.58 | 0.45 | 0.51 | 0.53 | 0.52 | 0.52 | 0.05 | 98.36  | 12.03 |
| Slic38a3  | chr15      | no      | 0.63 | 0.65 | 0.69 | 0.54 | 0.63 | 0.63 | 0.05 | 25.34  | 5.74  |
| Eif2c2    | chr15      | no      | 0.56 | 0.53 | 0.49 | 0.50 | 0.48 | 0.51 | 0.03 | 63.74  | 7.71  |
| Gahrt6    | chr15      | no      | 0.45 | 0.56 | 0.52 | 0.52 | 0.55 | 0.52 | 0.04 | 64.57  | 26.40 |
| Chrac1    | chr15      | no      | 0.44 | 0.45 | 0.42 | 0.41 | 0.44 | 0.43 | 0.02 | 88.84  | 15.54 |
| Bbx       | chr16      | no      | 0.42 | 0.41 | 0.43 | 0.41 | 0.44 | 0.42 | 0.01 | 136.01 | 9.63  |
| Runx1     | chr16      | no      | 0.42 | 0.41 | 0.43 | 0.41 | 0.44 | 0.42 | 0.01 | 136.01 | 9.63  |
| Gene   | Chromosome | Imprinted | Affymetrix Expression Mean 1 | Affymetrix Expression Mean 2 | Affymetrix Expression Mean 3 | Affymetrix Expression Mean 4 | Affymetrix Expression Mean 5 | Affymetrix Expression Mean 6 | Affymetrix Expression Mean 7 | Affymetrix Expression Mean 8 | Affymetrix Expression Mean 9 | Affymetrix Expression Mean 10 | Affymetrix Expression Mean 11 | Affymetrix Expression Mean 12 | Affymetrix Expression Mean 13 | Affymetrix Expression Mean 14 | Affymetrix Expression Mean 15 | Affymetrix Expression Mean 16 | Mean  |
|--------|------------|-----------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-----------------------------|-------|
| Qk     | chr17      | no        | Imprinted                  | 0.51                        | 0.51                        | 0.54                        | 0.51                        | 0.51                        | 0.52                        | 0.01                        | 175.28                     | 25.65                       |                             |                             |                             |                             |                             |                             |       |
| Arid1b | chr17      | no        | Imprinted                  | 0.58                        | 0.55                        | 0.56                        | 0.54                        | 0.56                        | 0.56                        | 0.02                        | 131.69                     | 36.87                       |                             |                             |                             |                             |                             |                             |       |
| Impact*| chr18      | no        | Imprinted                  | 0.28                        | 0.35                        | 0.41                        | 0.53                        | 0.00                        | 0.31                        | 0.20                        | 13.81                      | 3.72                        |                             |                             |                             |                             |                             |                             |       |
| Xlr4c  | chrX       | no        | Imprinted                  | 0.71                        | -                           | 0.99                        | 0.96                        | 1.00                        | 0.91                        | 0.14                        | 17.94                      | 7.80                        |                             |                             |                             |                             |                             |                             |       |
| Xlr4b  | chrX       | no        | Imprinted                  | 0.49                        | 0.56                        | 0.89                        | 0.96                        | 0.99                        | 0.78                        | 0.23                        | 42.19                      | 3.33                        |                             |                             |                             |                             |                             |                             |       |
| Xist   | chrX       | no        | Imprinted                  | 0.54                        | 0.45                        | 0.15                        | 0.01                        | 0.01                        | 0.23                        | 0.25                        | 197.56                     | 24.32                       |                             |                             |                             |                             |                             |                             | 143.98|

The list of imprinted genes was retrieved from [https://www.geneimprint.com](https://www.geneimprint.com) and Tucci et al., 2019. A total of 167 genes were discoverable in the annotation file used in this study ([ftp://ftp.ensembl.org/pub/release-68/gtf/Mus_musculus.GRCm38.68.gtf](ftp://ftp.ensembl.org/pub/release-68/gtf/Mus_musculus.GRCm38.68.gtf)). The “Bias” threshold was set at 15% expression for the silenced allele and inclusion criteria was “all samples with a measurement”. Additionally, an exclusion criteria due to missing datapoints was applied: for B cells (total = 11 samples), a minimum number of non-missing values was N=6, and if less than 6, the gene was classified as “maybe”; for T cell (total = 5 samples), one failed sample was enough for the gene to be classified as “maybe”. Of the reported imprinted genes, 55 were expressed in our B cell samples, and 62 in T cell samples. To our knowledge, there are no accounts of imprinted genes in B or T cells in the literature. Of the 55 imprinted genes expressed in B cells, only 4 have been confirmed as imprinted in a related lymphoid tissue, the spleen (asterisks [*]; Andergassen et al, 2017), while only 5 genes were imprinted in the thymus among the 62 “imprinted” genes that were also expressed in T cells (Andergassen et al, 2017). The rows in the table are ordered: first biased (yes>maybe=no), then imprinted. Blue highlights the genes described in the literature as imprinted and expressed biallelically in both B and T cells in our study. Purple highlights genes with nonrandom bias in both B and T cells. Red highlights genes with nonrandom bias in both B and T cells and described in the literature as imprinted. There are imprinted genes in the literature that in our samples do not reach the AI nonrandom bias threshold criteria (<15% expression for the silenced allele), but are biased (e.g., Impact, see also Supplementary Figure 6). The only confirmed lymphoid imprinted gene (in spleen or thymus) we studied that is not biased in our B or T cell samples is Commd1. The abundance mean of all analyzed genes is 115.03 ± 477.90 in B cells and 101.65 ± 218.74 in T cells (not significantly different from the abundance mean from this table by t-test). Genes with low expression levels (<10 TMM-normalized counts) and genes suspected of LOH (detected by WES) were removed from the study and this table.
**Supplementary Table 3.** XCI escapees identified by other studies and our study showing values of AI and expression in HSC-derived lymphocytes *in vivo* from our NGS data. Genes in bold are escapees identified in our study. Genes in red are X escapees reported in the literature that were not expressed in our samples. Genes in blue were not included in our study due to lack of SNPs to estimate allelic imbalance. The abundance mean is represented in TMM-normalized counts.

| gene          | T cells | B cells | Abundance mean | Xi expression |
|---------------|---------|---------|----------------|---------------|
|               | E13.2   | E13.29  | E13.24         | E13.29        | E15.10 | E6.42 | E6.43 |                  |
| I810630007Rik | 1.00    | 1.00    | 0.98           | 0.96          | 0.98   | 0.01  | 0.03  | 62.94            |
| 5550601H04Rik | 0.73    | 0.74    | 0.73           | 0.74          | 0.78   | 0.16  | 0.17  | 29.65  yes       |
| 5730416F02Rik | -       | -       | -              | -             | -      | -     | -     | 0.23              |
| Abcb7         | 0.99    | 1.00    | 0.99           | 0.97          | 0.99   | 0.00  | 0.01  | 36.13            |
| Alg13         | 0.95    | 0.97    | 0.81           | 0.93          | 0.99   | 0.09  | 0.10  | 14.65            |
| Amot          | 0.42    | -       | -              | -             | -      | 0.32  | 0.28  | 1.93              |
| Apis2         | 0.97    | 1.00    | 0.93           | 0.90          | 0.96   | 0.01  | 0.01  | 30.45            |
| Atp7a         | 0.95    | 0.99    | 0.82           | 0.93          | 0.99   | 0.04  | 0.10  | 47.07            |
| AU0155836     | -       | -       | -              | -             | -      | -     | -     | 0.49              |
| AU022751      | -       | -       | 0.00           | -             | -      | -     | -     | 0.21              |
| BC0229660     | 0.98    | 0.94    | 1.00           | 0.89          | 0.96   | -     | -     | 0.86              |
| Bcor          | 1.00    | 1.00    | 0.93           | 0.95          | 0.97   | 0.01  | 0.01  | 71.23            |
| Bgn           | -       | -       | -              | -             | -      | -     | -     | 0.19              |
| Bhlhb9        | 0.99    | 1.00    | 0.97           | 0.92          | 0.97   | 0.02  | 0.01  | 53.61            |
| Bmp15         | -       | -       | -              | -             | -      | -     | -     | 0.22              |
| Cur5b         | 0.48    | 0.77    | 0.28           | 0.45          | 0.59   | 0.44  | 0.35  | 1.18              |
| Cfp           | 0.89    | NA      | 0.96           | 0.96          | 0.99   | 0.12  | 0.01  | 28.36            |
| Cols4a5       | -       | -       | -              | -             | -      | -     | -     | 1.81              |
| Cstf2         | 0.99    | 1.00    | 0.94           | 0.95          | 0.97   | 0.00  | 0.01  | 118.51           |
| Ctns2         | 0.99    | 1.00    | 0.96           | 0.95          | 0.98   | 0.01  | 0.01  | 113.44           |
| Cybb          | 0.30    | 0.54    | 0.93           | 0.84          | 0.93   | 0.00  | 0.01  | 291.67           |
| Ddx3x         | 0.79    | 0.99    | 0.73           | 0.91          | 0.72   | 0.02  | 0.02  | 299.47           |
| Dlg3          | 0.97    | 0.99    | 0.94           | 0.91          | 0.98   | 0.01  | 0.08  | 16.77            |
| Dynl3         | -       | -       | -              | -             | -      | -     | -     | 54.06            |
| Ebp           | 1.00    | 1.00    | 0.91           | 0.90          | 0.97   | 0.01  | 0.01  | 44.00            |
| Efg2x3x       | 0.49    | 0.52    | 0.53           | 0.56          | 0.56   | 0.25  | 0.19  | 46.76  yes       |
| Exc61         | 1.00    | 1.00    | 0.90           | 0.89          | 0.98   | 0.01  | 0.10  | 21.35            |
| F8            | 0.88    | 1.00    | -              | 0.76          | 1.00   | 0.33  | 3.55  | 8.42             |
| Fam199x       | 0.99    | 1.00    | 0.98           | 0.97          | 0.94   | 0.06  | 0.05  | 21.38            |
| Fam3a         | 0.99    | 1.00    | 0.94           | 0.96          | 0.97   | 0.01  | 0.01  | 27.94            |
| Fam50a        | 0.98    | 0.99    | 0.97           | 0.90          | 0.96   | 0.00  | 0.00  | 48.07            |
| Farc          | 0.93    | 0.93    | -              | -             | -      | 0.00  | -     | 8.42             |
| Flna          | 1.00    | 0.99    | 0.96           | 0.94          | 0.96   | 0.01  | 0.01  | 811.48           |
| Fmr1          | 0.99    | 1.00    | 0.93           | 0.94          | 0.98   | 0.10  | 0.03  | 93.35            |
| Ftx           | 0.91    | 0.91    | 0.96           | 0.92          | 0.95   | 0.35  | 0.21  | 25.17            |
| Gene   | 1.00 | 1.00 | 0.97 | 0.92 | 0.98 | 0.01 | 0.00 |      |      | 29.13 |
|--------|------|------|------|------|------|------|------|------|------|-------|
| G530011006Rik | 0.20 | 0.13 | 0.57 | 0.71 | 0.48 | 0.61 | 0.44 |      |      | 1.66  |
| G6pd6c | 0.99 | 1.00 | 0.96 | 0.95 | 0.97 | 0.01 | 0.01 |      |      | 73.63 |
| Gald1  | 0.99 | 0.98 | 0.93 | 0.94 | 0.95 | 0.01 | 0.01 |      |      | 463.40|
| Gla    | 0.97 | 1.00 | -    | 0.84 | 1.00 | -    |      |      |      | 5.44  |
| Gn33l  | 0.99 | 0.99 | 0.95 | 0.92 | 0.94 | 0.03 | 0.03 |      |      | 64.96 |
| Gpm6b  | 0.58 | -    | 0.93 | 0.79 | 0.95 | 0.23 | 0.24 |      |      | 3.03  |
| Gprasp1| 0.98 | 0.99 | 0.93 | 0.90 | 0.94 | 0.01 | 0.01 |      |      | 51.27 |
| Griasp1| 0.99 | 0.99 | 0.96 | 0.95 | 0.97 | 0.01 | 0.02 |      |      | 104.11|
| Gk     | 0.95 | 0.99 | 0.97 | 0.89 | 0.99 | 0.01 | 0.10 |      |      | 15.92 |
| Hdac6  | 0.94 | 0.98 | 0.95 | 0.92 | 0.95 | 0.05 | 0.12 |      |      | 23.25 |
| Hesat2 |        |      |      |      |      |      |      |       |      |       |
| Huatsf1| 0.99 | 1.00 | 0.95 | 0.96 | 0.96 | 0.01 | 0.00 |      |      | 75.27 |
| Howe1  | 0.98 | 0.99 | 0.92 | 0.93 | 0.95 | 0.02 | 0.03 |      |      | 100.25|
| Idh3g  | 1.00 | 1.00 | 0.95 | 0.94 | 0.97 | 0.01 | 0.00 |      |      | 221.82|
| Ids    | 1.00 | 0.99 | 0.97 | 0.92 | 0.96 | 0.01 | 0.02 |      |      | 47.79 |
| Ihkg   | 0.99 | 1.00 | 0.96 | 0.95 | 0.97 | 0.01 | 0.01 |      |      | 85.87 |
| Il13ral1| 0.68 | 0.68 | 0.58 | 0.58 | 0.58 | 0.58 | 0.58 |      |      | 175.94|
| Isx    | 0.96 | 1.00 | 0.98 | 0.95 | 0.96 | 0.01 | 0.00 |      |      | 4.83  |
| Magt1  | 0.99 | 0.99 | 0.94 | 0.94 | 0.97 | 0.01 | 0.01 |      |      | 70.50 |
| Mecp2  | 0.99 | 0.99 | 0.95 | 0.95 | 0.95 | 0.01 | 0.04 |      |      | 44.26 |
| Mid1   | 0.45 | 0.40 | 0.62 | 0.68 | 0.65 | 0.08 | 0.06 |      |      | 6.87  |
| Mid2   | 0.99 | 1.00 | 0.93 | 0.91 | 0.98 | 0.04 | 0.05 |      |      | 43.28 |
| Mngt1  | 0.96 | 0.99 | 0.91 | 0.91 | 0.90 | 0.00 | 0.06 |      |      | 134.74|
| Nkd1   | 0.90 | 0.99 | 0.94 | 0.94 | 0.97 | 0.01 | 0.02 |      |      | 38.00 |
| Nudat1 | 0.97 | 0.99 | 0.94 | 0.94 | 0.96 | 0.02 | 0.06 |      |      | 5.44  |
| Og1    | 1.00 | 1.00 | 0.96 | 0.94 | 0.96 | 0.01 | 0.01 |      |      | 556.30|
| Ond15  | 0.99 | 1.00 | 0.93 | 0.94 | 0.96 | 0.03 | 0.04 |      |      | 227.57|
| Phd6c1 | 0.65 | 0.77 | 0.75 | 0.71 | 0.80 | 0.30 | 0.23 |      |      | 53.17 |
| Pdha1  | 1.00 | 1.00 | 0.93 | 0.96 | 0.96 | 0.01 | 0.02 |      |      | 107.61|
| Pim2   | 0.99 | 0.99 | 0.83 | 0.88 | 0.95 | 0.01 | 0.01 |      |      | 55.97 |
| Plp1   | 1.00 | 0.97 | 0.89 | 0.92 | 0.99 | 0.23 | 0.12 |      |      | 2.59  |
| Ptx3   | 0.99 | 0.99 | 0.94 | 0.94 | 0.97 | 0.01 | 0.02 |      |      | 2.18  |
| Gene  | V | V | V | V | V | V | V | V | V |   |
|-------|---|---|---|---|---|---|---|---|---|---|
| Pqbp1 | 0.99 | 0.99 | 0.95 | 0.90 | 0.96 | 0.01 | 0.01 |   |   | 104.39 |
| Rbbp7 | - | - | - | - | - | - | - | - | - | 192.46 |
| Rilm | 0.98 | 1.00 | 0.93 | 0.96 | 0.96 | 0.01 | 0.01 |   |   | 84.62 |
| Rsp128 | - | - | - | - | - | - | - | - | - | 0.53 |
| Rps4x | 0.99 | 1.00 | 0.95 | 0.94 | 0.96 | 0.01 | 0.01 |   |   | 196.71 |
| Sh3bg1 | 0.99 | 0.99 | 0.93 | 0.94 | 0.96 | 0.01 | 0.04 |   |   | 134.77 |
| Shroom4 | - | - | - | - | - | - | - | - | 0.65 | 1.07 |
| Stah1b | 0.89 | 0.98 | 0.95 | 0.90 | 0.97 | 0.02 | 0.00 |   |   | 7.53 |
| Slec16a2 | - | - | - | - | - | - | - | - | - | 0.50 |
| Slec35a2 | 0.99 | 1.00 | 0.96 | 0.96 | 0.97 | 0.02 | 0.02 |   |   | 36.33 |
| Slec8 | - | - | - | - | - | - | - | - | - | 0.66 |
| Smul12 | 0.99 | 0.99 | 0.98 | 0.95 | 0.97 | 0.23 | 0.19 |   |   | 42.85 |
| Sxcb3 | - | - | - | - | - | - | - | - | - | 0.15 |
| Sx3901 | 0.99 | 1.00 | 0.88 | 0.93 | 0.97 | 0.05 | 0.14 |   |   | 62.48 |
| Syap1 | 0.99 | 1.00 | 0.99 | 0.96 | 0.97 | 0.01 | 0.00 |   |   | 35.80 |
| Syt | - | - | - | - | - | - | - | - | - | 1.33 |
| Tab3 | 0.98 | 0.99 | 0.95 | 0.90 | 0.97 | 0.02 | 0.07 |   |   | 20.34 |
| Tal1 | 0.98 | 1.00 | 0.86 | 0.90 | 0.94 | 0.05 | 0.03 |   |   | 64.98 |
| S40427O19Rik | 0.63 | 0.93 | 0.96 | 0.92 | 0.98 | 0.02 | 0.03 |   |   | 40.30 |
| Smem164 | 0.99 | 1.00 | 0.88 | 0.90 | 0.96 | 0.01 | 0.02 |   |   | 88.06 |
| Smem29 | 0.83 | 0.83 | 0.86 | 0.89 | 0.83 | 0.25 | 0.29 |   |   | 3.81 |
| Smem47 | - | - | - | - | - | 0.20 | - | - | - | 0.74 |
| Smem131 | - | 1.00 | 1.00 | 0.74 | 1.00 | - | - | - | - | 0.28 |
| Smem54x | 1.00 | 1.00 | 0.96 | 0.96 | 0.97 | 0.00 | 0.00 |   |   | 2015.50 |
| Uba1 | 1.00 | 0.99 | 0.95 | 0.93 | 0.96 | 0.00 | 0.00 |   |   | 326.39 |
| Ub4a | 1.00 | 0.99 | 0.95 | 0.90 | 0.95 | 0.01 | 0.00 |   |   | 69.97 |
| Usp9x | 0.94 | 0.99 | 0.95 | 0.92 | 0.95 | 0.05 | 0.04 |   |   | 80.36 |
| Utp14a | 0.99 | 0.62 | 0.94 | 0.77 | 0.77 | 0.03 | 0.03 | 26.22 | yes |
| Vbp1 | 1.00 | 1.00 | 0.95 | 0.96 | 0.98 | 0.01 | 0.01 |   |   | 121.16 |
| Vsig4 | - | - | - | - | - | - | - | - | - | 0.27 |
| Wdr13 | 0.99 | 1.00 | 0.95 | 0.95 | 0.96 | 0.03 | 0.00 |   |   | 43.80 |
| Xist | 0.01 | 0.01 | 0.10 | 0.09 | 0.07 | 0.96 | 0.99 |   |   | 162.43 | yes |
| Yif6 | 0.99 | 0.99 | 0.96 | 0.97 | 0.97 | 0.05 | 0.08 |   |   | 43.46 |
| Zbms33 | 1.00 | - | - | - | - | - | - | - | 5.64 |
| Zfp280a | 0.96 | 0.99 | 0.90 | 0.92 | 0.94 | 0.03 | 0.06 |   |   | 26.07 |
| Zmys3 | 0.99 | 1.00 | 0.93 | 0.93 | 0.96 | 0.02 | 0.04 |   |   | 37.85 |
| Zrs2 | 0.98 | 1.00 | 0.92 | 0.93 | 0.95 | 0.01 | 0.11 |   |   | 33.89 |
| Gm8822 | 0.38 | 0.35 | 0.44 | 0.35 | 0.38 | 0.39 | 0.30 |   | yes |
| Gm8822 | 0.38 | 0.35 | 0.44 | 0.35 | 0.38 | 0.39 | 0.30 |   | yes |
**Supplementary Table 4.** List of all statistically significant AI differences between samples for the 14 genes identified as putatively RME in B cells (related with Figure 4A). P-value associated with each comparison after applying the QCC correction to the binomial test (Mendelevich et al., 2021). The dAI is the difference between AI values. Clonality indicates whether the sample was originated upon expansion of 1, 50 or 200 transplanted cells. Shaded rows highlight comparisons between only monoclonal (shaded) or only polyclonal samples (unshaded).

| Gene   | chr  | sample1   | sample2   | AI (1) | AI (2) | p-val (BT, CC) | dAI   | Abundance (1) | Abundance (2) | clonality (1) | clonality (2) |
|--------|------|-----------|-----------|--------|--------|----------------|-------|---------------|---------------|---------------|---------------|
| Dpp7   | chr2 | E6.42_B   | E6.43_B   | 0.70   | 0.21   | 9.10E-13       | 0.49  | 28.88         | 26.50         | 1 HSC         | 1 HSC         |
| Dpp7   | chr2 | E13.29_B  | E6.43_B   | 0.51   | 0.21   | 1.76E-06       | 0.30  | 39.69         | 26.50         | 1 HSC         | 1 HSC         |
| Dpp7   | chr2 | E15.10_B  | E6.42_B   | 0.46   | 0.70   | 1.45E-06       | 0.24  | 48.56         | 28.88         | 1 HSC         | 1 HSC         |
| Dpp7   | chr2 | E13.2_B   | E6.42_B   | 0.42   | 0.70   | 1.63E-07       | 0.28  | 55.67         | 28.88         | 200 HSCs      | 1 HSC         |
| Dpp7   | chr2 | E13.2_B   | E6.42_B   | 0.45   | 0.70   | 4.26E-07       | 0.25  | 42.23         | 28.88         | 200 HSCs      | 1 HSC         |
| Dpp7   | chr2 | E13.2_B   | E6.42_B   | 0.45   | 0.70   | 2.87E-07       | 0.25  | 56.67         | 28.88         | 50 HSCs       | 1 HSC         |
| Aldh4a1| chr4 | E15.10_B  | E6.42_B   | 0.94   | 0.44   | 3.54E-31       | 0.50  | 10.42         | 40.17         | 1 HSC         | 1 HSC         |
| Aldh4a1| chr4 | E15.10_B  | E6.43_B   | 0.94   | 0.48   | 1.02E-20       | 0.46  | 10.42         | 18.46         | 1 HSC         | 1 HSC         |
| Aldh4a1| chr4 | E13.24_B  | E15.10_B  | 0.49   | 0.94   | 3.10E-18       | 0.45  | 13.12         | 10.42         | 1 HSC         | 1 HSC         |
| Aldh4a1| chr4 | E13.29_B  | E15.10_B  | 0.58   | 0.94   | 8.23E-17       | 0.36  | 18.59         | 10.42         | 1 HSC         | 1 HSC         |
| Aldh4a1| chr4 | E15.10_B  | E6.42_B   | 0.94   | 0.48   | 2.50E-27       | 0.49  | 35.58         | 10.42         | 200 HSCs      | 1 HSC         |
| Aldh4a1| chr4 | E15.10_B  | E15.10_B  | 0.45   | 0.94   | 6.44E-27       | 0.46  | 10.42         | 34.19         | 1 HSC         | 50 HSCs       |
| Aldh4a1| chr4 | E15.10_B  | E6.2_B    | 0.94   | 0.48   | 1.47E-19       | 0.46  | 10.42         | 13.83         | 1 HSC         | 50 HSCs       |
| Aldh4a1| chr4 | E13.1_B   | E15.10_B  | 0.50   | 0.94   | 5.69E-24       | 0.45  | 22.65         | 10.42         | 200 HSCs      | 1 HSC         |
| Aldh4a1| chr4 | E13.2_B   | E15.10_B  | 0.50   | 0.94   | 3.58E-24       | 0.44  | 21.88         | 10.42         | 200 HSCs      | 1 HSC         |
| Gnpda2 | chr5 | E15.10_B  | E6.42_B   | 0.71   | 0.31   | 2.85E-07       | 0.41  | 37.79         | 28.76         | 1 HSC         | 1 HSC         |
| Gnpda2 | chr5 | E13.29_B  | E6.42_B   | 0.69   | 0.31   | 5.44E-07       | 0.38  | 29.53         | 28.76         | 1 HSC         | 1 HSC         |
| Gnpda2 | chr5 | E13.2_B   | E6.42_B   | 0.68   | 0.31   | 7.53E-08       | 0.38  | 34.71         | 28.76         | 200 HSCs      | 1 HSC         |
| Igkv6-25| chr6 | E13.24_B  | E15.10_B  | 0.72   | 0.34   | 5.66E-58       | 0.39  | 50.26         | 30.99         | 1 HSC         | 1 HSC         |
| Igkv6-25| chr6 | E13.24_B  | E13.29_B  | 0.72   | 0.37   | 1.08E-44       | 0.35  | 50.26         | 26.51         | 1 HSC         | 1 HSC         |
| Igkv6-25| chr6 | E13.24_B  | E6.42_B   | 0.72   | 0.37   | 1.41E-49       | 0.35  | 50.26         | 38.39         | 1 HSC         | 1 HSC         |
| Igkv6-25| chr6 | E13.24_B  | E6.43_B   | 0.72   | 0.45   | 2.38E-20       | 0.27  | 50.26         | 26.38         | 1 HSC         | 1 HSC         |
| Gene       | Chr  | E15.10_B | E6.43_B | 0.34 | 0.45 | 5.44E-07 | 0.12 | 30.99 | 26.38 | 1 HSC | 1 HSC |
|------------|------|----------|---------|------|------|----------|------|------|------|-------|-------|
| Igk6v-25   | chr6 | E13.24_B | E6.1_B  | 0.72 | 0.29 | 3.78E-74 | 0.43 | 50.26 | 25.65 | 1 HSC | 50 HSCs |
| Igk6v-25   | chr6 | E13.24_B | E6.1_B  | 0.30 | 0.72 | 4.08E-65 | 0.42 | 39.43 | 50.26 | 200 HSCs | 1 HSC |
| Igk6v-25   | chr6 | E13.24_B | E6.1_B  | 0.33 | 0.72 | 2.44E-60 | 0.39 | 24.48 | 50.26 | 200 HSCs | 1 HSC |
| Igk6v-25   | chr6 | E13.24_B | E6.2_B  | 0.72 | 0.36 | 3.95E-36 | 0.36 | 50.26 | 18.01 | 1 HSC | 50 HSCs |
| Igk6v-25   | chr6 | E6.1_B   | E6.43_B | 0.29 | 0.45 | 1.33E-12 | 0.16 | 25.65 | 26.38 | 50 HSCs | 1 HSC |
| Igk6v-25   | chr6 | E13.24_B | E6.43_B | 0.30 | 0.45 | 1.98E-10 | 0.15 | 39.43 | 26.38 | 200 HSCs | 1 HSC |
| Igk6v-25   | chr6 | E13.24_B | E6.43_B | 0.33 | 0.45 | 1.18E-07 | 0.12 | 24.48 | 26.38 | 200 HSCs | 1 HSC |
| Igk6v-25   | chr6 | E13.29_B | E6.1_B  | 0.37 | 0.29 | 4.19E-06 | 0.08 | 26.51 | 25.65 | 1 HSC | 50 HSCs |
| Igk6v-25   | chr6 | E6.1_B   | E6.42_B | 0.29 | 0.37 | 7.85E-07 | 0.08 | 25.65 | 38.39 | 50 HSCs | 1 HSC |
| Plekha8    | chr6 | E15.10_B | E6.42_B | 0.09 | 0.45 | 4.63E-11 | 0.37 | 13.41 | 13.31 | 1 HSC | 1 HSC |
| Plekha8    | chr6 | E13.29_B | E6.42_B | 0.15 | 0.45 | 1.83E-07 | 0.31 | 14.34 | 13.31 | 1 HSC | 1 HSC |
| Plekha8    | chr6 | E13.10_B | E6.42_B | 0.09 | 0.37 | 6.23E-07 | 0.29 | 13.41 | 16.40 | 1 HSC | 1 HSC |
| Plekha8    | chr6 | E13.2_B  | E4.42_B | 0.20 | 0.45 | 1.72E-06 | 0.26 | 17.30 | 13.31 | 200 HSCs | 1 HSC |
| Kdm8       | chr7 | E15.10_B | E6.43_B | 0.03 | 0.55 | 3.53E-24 | 0.53 | 12.81 | 16.94 | 1 HSC | 1 HSC |
| Kdm8       | chr7 | E13.29_B | E15.10_B| 0.48 | 0.03 | 3.26E-24 | 0.45 | 24.54 | 12.81 | 1 HSC | 1 HSC |
| Kdm8       | chr7 | E13.24_B | E15.10_B| 0.44 | 0.03 | 1.41E-17 | 0.42 | 17.24 | 12.81 | 1 HSC | 1 HSC |
| Kdm8       | chr7 | E15.10_B | E6.42_B | 0.03 | 0.43 | 1.82E-20 | 0.40 | 12.81 | 25.94 | 1 HSC | 1 HSC |
| Kdm8       | chr7 | E15.2_B  | E15.10_B| 0.56 | 0.03 | 8.42E-28 | 0.53 | 27.69 | 12.81 | 200 HSCs | 1 HSC |
| Kdm8       | chr7 | E15.10_B | E6.2_B  | 0.03 | 0.53 | 1.35E-23 | 0.50 | 12.81 | 14.96 | 1 HSC | 50 HSCs |
| Kdm8       | chr7 | E13.2_B  | E15.10_B| 0.41 | 0.03 | 1.01E-19 | 0.39 | 19.70 | 12.81 | 200 HSCs | 1 HSC |
| Kdm8       | chr7 | E13.1_B  | E15.10_B| 0.41 | 0.03 | 8.32E-19 | 0.38 | 20.61 | 12.81 | 200 HSCs | 1 HSC |
| Kdm8       | chr7 | E15.10_B | E6.1_B  | 0.03 | 0.39 | 3.98E-18 | 0.36 | 12.81 | 27.73 | 1 HSC | 50 HSCs |
| Pkg3       | chr7 | E13.29_B | E6.42_B | 0.94 | 0.12 | 8.75E-159| 0.82 | 47.17 | 96.81 | 1 HSC | 1 HSC |
| Pkg3       | chr7 | E13.29_B | E15.10_B| 0.94 | 0.18 | 1.51E-132| 0.76 | 47.17 | 79.42 | 1 HSC | 1 HSC |
| Pkg3       | chr7 | E6.42_B  | E6.43_B | 0.12 | 0.84 | 5.12E-120| 0.72 | 96.81 | 71.84 | 1 HSC | 1 HSC |
| Pkg3       | chr7 | E15.10_B | E6.43_B | 0.18 | 0.84 | 2.55E-96 | 0.66 | 79.42 | 71.84 | 1 HSC | 1 HSC |
| Pkp3 | chr7 | E13.24_B | E13.29_B | 0.43 | 0.94 | 4.60E-61 | 0.51 | 139.94 | 47.17 | 1 HSC | 1 HSC |
|------|------|----------|----------|------|------|----------|------|--------|-----|-----|------|
| Pkp3 | chr7 | E13.24_B | E6.42_B  | 0.43 | 0.12 | 1.29E-36 | 0.30 | 139.94 | 96.81 | 1 HSC | 1 HSC |
| Pkp3 | chr7 | E13.24_B | E15.10_B | 0.43 | 0.18 | 9.35E-23 | 0.25 | 139.94 | 79.42 | 1 HSC | 1 HSC |
| Pkp3 | chr7 | E13.29_B | E6.1_B   | 0.94 | 0.32 | 1.01E-97 | 0.62 | 47.17  | 110.71| 50 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.2_B  | E13.29_B | 0.39 | 0.94 | 1.91E-74 | 0.55 | 79.17  | 47.17 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E6.1_B   | E6.43_B  | 0.32 | 0.84 | 1.66E-64 | 0.52 | 110.71| 71.84 | 50 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.1_B  | E13.29_B | 0.44 | 0.94 | 1.19E-60 | 0.50 | 75.25  | 47.17 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.29_B | E6.2_B   | 0.94 | 0.47 | 3.69E-45 | 0.48 | 47.17  | 55.39 | 1 HSC | 50 HSCs |
| Pkp3 | chr7 | E13.2_B  | E15.10_B | 0.56 | 0.18 | 1.96E-46 | 0.38 | 119.50| 79.42 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E6.2_B   | E6.43_B  | 0.47 | 0.84 | 4.44E-24 | 0.37 | 55.39 | 71.84 | 50 HSCs | 1 HSC |
| Pkp3 | chr7 | E6.2_B   | E6.42_B  | 0.47 | 0.12 | 2.65E-33 | 0.34 | 55.39 | 96.81 | 50 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.1_B  | E6.42_B  | 0.44 | 0.12 | 1.08E-40 | 0.32 | 75.25  | 96.81 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E15.10_B | E6.2_B   | 0.18 | 0.47 | 5.09E-21 | 0.29 | 79.42  | 55.39 | 1 HSC | 50 HSCs |
| Pkp3 | chr7 | E15.2_B  | E6.43_B  | 0.56 | 0.84 | 1.67E-19 | 0.28 | 119.50| 71.84 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.2_B  | E6.42_B  | 0.39 | 0.12 | 3.05E-34 | 0.27 | 79.17  | 96.81 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.1_B  | E15.10_B | 0.44 | 0.18 | 7.47E-26 | 0.26 | 75.25  | 79.42 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E13.2_B  | E15.10_B | 0.39 | 0.18 | 2.00E-20 | 0.21 | 79.17  | 79.42 | 200 HSCs | 1 HSC |
| Pkp3 | chr7 | E6.1_B   | E6.42_B  | 0.32 | 0.12 | 4.60E-21 | 0.19 | 110.71| 96.81 | 50 HSCs | 1 HSC |
| Pkp3 | chr7 | E15.10_B | E6.1_B   | 0.18 | 0.32 | 1.84E-10 | 0.14 | 79.42  | 110.71| 50 HSCs | 1 HSC |
| Pkp3 | chr7 | E15.2_B  | E6.1_B   | 0.56 | 0.32 | 5.36E-21 | 0.24 | 119.50| 110.71| 200 HSCs | 50 HSCs |
| Pkp3 | chr7 | E13.2_B  | E15.2_B  | 0.39 | 0.56 | 7.22E-10 | 0.16 | 79.17  | 119.50| 200 HSCs | 200 HSCs |
| Pkp3 | chr7 | E6.1_B   | E6.2_B   | 0.32 | 0.47 | 2.62E-06 | 0.15 | 110.71| 55.39 | 50 HSCs | 50 HSCs |
| Pkp3 | chr7 | E13.1_B  | E6.1_B   | 0.44 | 0.32 | 4.24E-07 | 0.12 | 75.25  | 110.71| 200 HSCs | 50 HSCs |
| Trim5 | chr7  | E13.24_B | E6.43_B | 0.63 | 0.29 | 6.30E-13 | 0.34 | 64.65 | 38.39 | 1 HSC | 1 HSC |
|-------|------|----------|---------|------|------|----------|------|-------|------|------|------|
| Trim5 | chr7  | E15.10_B | E6.43_B | 0.64 | 0.29 | 4.36E-14 | 0.34 | 39.52 | 38.39 | 1 HSC | 1 HSC |
| Trim5 | chr7  | E13.29_B | E6.43_B | 0.62 | 0.29 | 7.95E-16 | 0.33 | 88.81 | 38.39 | 1 HSC | 1 HSC |
| Trim5 | chr7  | E13.24_B | E6.42_B | 0.63 | 0.36 | 3.39E-11 | 0.27 | 64.65 | 42.07 | 1 HSC | 1 HSC |
| Trim5 | chr7  | E15.10_B | E6.42_B | 0.64 | 0.36 | 1.56E-12 | 0.27 | 39.52 | 42.07 | 1 HSC | 1 HSC |
| Trim5 | chr7  | E13.29_B | E6.42_B | 0.62 | 0.36 | 7.46E-15 | 0.26 | 88.81 | 42.07 | 1 HSC | 1 HSC |
| Trim5 | chr7  | E6.2_B | E6.43_B | 0.63 | 0.29 | 4.23E-14 | 0.33 | 78.92 | 38.39 | 50 HSCs | 1 HSC |
| Trim5 | chr7  | E13.1_B | E6.43_B | 0.59 | 0.29 | 8.62E-13 | 0.30 | 70.32 | 38.39 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E6.1_B | E6.43_B | 0.56 | 0.29 | 6.88E-11 | 0.27 | 88.97 | 38.39 | 50 HSCs | 1 HSC |
| Trim5 | chr7  | E6.2_B | E6.42_B | 0.63 | 0.36 | 1.30E-12 | 0.26 | 78.92 | 42.07 | 50 HSCs | 1 HSC |
| Trim5 | chr7  | E13.1_B | E6.42_B | 0.59 | 0.36 | 2.40E-11 | 0.23 | 70.32 | 42.07 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E13.2_B | E6.43_B | 0.51 | 0.29 | 5.15E-08 | 0.22 | 73.83 | 38.39 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E15.2_B | E13.24_B | 0.43 | 0.63 | 3.62E-07 | 0.20 | 71.47 | 64.65 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E15.2_B | E15.10_B | 0.43 | 0.64 | 4.56E-08 | 0.20 | 71.47 | 39.52 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E6.1_B | E6.42_B | 0.56 | 0.36 | 2.97E-09 | 0.20 | 88.97 | 42.07 | 50 HSCs | 1 HSC |
| Trim5 | chr7  | E15.2_B | E13.29_B | 0.43 | 0.62 | 1.85E-09 | 0.19 | 71.47 | 88.81 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E13.2_B | E6.42_B | 0.51 | 0.36 | 3.93E-06 | 0.15 | 73.83 | 42.07 | 200 HSCs | 1 HSC |
| Trim5 | chr7  | E15.2_B | E6.2_B | 0.43 | 0.63 | 5.15E-08 | 0.19 | 71.47 | 78.92 | 200 HSCs | 50 HSCs |
| Trim5 | chr7  | E13.1_B | E15.2_B | 0.59 | 0.43 | 1.13E-06 | 0.16 | 70.32 | 71.47 | 200 HSCs | 200 HSCs |
| Fam32a | chr8  | E13.29_B | E6.43_B | 0.50 | 0.02 | 4.72E-119 | 0.48 | 203.22 | 102.07 | 1 HSC | 1 HSC |
| Fam32a | chr8  | E15.10_B | E6.43_B | 0.47 | 0.02 | 9.48E-113 | 0.46 | 255.71 | 102.07 | 1 HSC | 1 HSC |
| Fam32a | chr8  | E6.42_B | E6.43_B | 0.45 | 0.02 | 4.55E-103 | 0.44 | 239.69 | 102.07 | 1 HSC | 1 HSC |
| Fam32a | chr8  | E13.24_B | E6.43_B | 0.42 | 0.02 | 6.73E-82 | 0.40 | 238.14 | 102.07 | 1 HSC | 1 HSC |
| Fam32a | chr8  | E13.24_B | E13.29_B | 0.42 | 0.50 | 1.95E-06 | 0.08 | 238.14 | 203.22 | 1 HSC | 1 HSC |
| Fam32a | chr8  | E15.2_B | E6.43_B | 0.44 | 0.02 | 8.56E-98 | 0.43 | 317.59 | 102.07 | 200 HSCs | 1 HSC |
| Fam32a | chr8  | E13.2_B | E6.43_B | 0.44 | 0.02 | 8.11E-99 | 0.42 | 197.30 | 102.07 | 200 HSCs | 1 HSC |
| Fam32a | chr8  | E13.1_B | E6.43_B | 0.41 | 0.02 | 8.05E-86 | 0.39 | 189.71 | 102.07 | 200 HSCs | 1 HSC |
| Fam32a | chr8  | E6.1_B | E6.43_B | 0.39 | 0.02 | 6.52E-82 | 0.37 | 261.42 | 102.07 | 50 HSCs | 1 HSC |
|     | chr8 |  E6.2_B  |  E6.43_B  |      |      |      |      |      |      |      |      |
|-----|------|----------|----------|------|------|------|------|------|------|------|------|
| Fam32a | chr8 |  E13.29_B |  E6.2_B  |  0.50 |  0.36 |  2.93E-15 |  0.13 |  203.22 |  163.06 |  102.07 |  50 HSCs |
| Fam32a | chr8 |  E13.29_B |  E6.1_B  |  0.50 |  0.39 |  6.50E-18 |  0.11 |  203.22 |  261.42 |  1 HSC  |  50 HSCs |
| Fam32a | chr8 |  E15.10_B |  E6.2_B  |  0.47 |  0.36 |  1.82E-11 |  0.11 |  255.71 |  163.06 |  1 HSC  |  50 HSCs |
| Fam32a | chr8 |  E13.1_B  |  E13.29_B |  0.41 |  0.50 |  3.18E-11 |  0.09 |  189.71 |  203.22 |  200 HSCs |  1 HSC |
| Fam32a | chr8 |  E15.10_B |  E6.1_B  |  0.47 |  0.39 |  6.07E-13 |  0.09 |  255.71 |  261.42 |  1 HSC  |  50 HSCs |
| Fam32a | chr8 |  E6.2_B   |  E6.42_B |  0.36 |  0.45 |  9.54E-08 |  0.09 |  163.06 |  239.69 |  50 HSCs |  1 HSC |
| Fam32a | chr8 |  E13.1_B  |  E15.10_B |  0.41 |  0.47 |  2.22E-07 |  0.07 |  189.71 |  255.71 |  200 HSCs |  1 HSC |
| Fam32a | chr8 |  E13.2_B  |  E13.29_B |  0.44 |  0.50 |  3.15E-06 |  0.06 |  197.30 |  203.22 |  200 HSCs |  1 HSC |
| Fam32a | chr8 |  E6.1_B   |  E6.42_B |  0.39 |  0.45 |  1.30E-07 |  0.06 |  261.42 |  239.69 |  50 HSCs |  1 HSC |
| Fam32a | chr8 |  E15.2_B  |  E6.2_B  |  0.44 |  0.36 |  2.79E-06 |  0.08 |  317.59 |  163.06 |  200 HSCs |  50 HSCs |
| SLC38a7 | chr8 |  E13.24_B |  E13.29_B |  0.60 |  0.13 |  2.25E-18 |  0.47 |  21.53 |  11.72 |  1 HSC  |  1 HSC |
| SLC38a7 | chr8 |  E13.29_B |  E6.43_B |  0.13 |  0.53 |  6.39E-14 |  0.40 |  11.72 |  20.15 |  1 HSC  |  1 HSC |
| SLC38a7 | chr8 |  E13.29_B |  E6.42_B |  0.13 |  0.51 |  7.50E-17 |  0.38 |  11.72 |  30.82 |  1 HSC  |  1 HSC |
| SLC38a7 | chr8 |  E13.29_B |  E15.10_B |  0.13 |  0.44 |  2.39E-11 |  0.31 |  11.72 |  20.46 |  1 HSC  |  1 HSC |
| SLC38a7 | chr8 |  E13.29_B |  E6.1_B  |  0.13 |  0.59 |  1.33E-23 |  0.46 |  11.72 |  32.01 |  1 HSC  |  50 HSCs |
| SLC38a7 | chr8 |  E15.2_B  |  E13.29_B |  0.57 |  0.13 |  3.51E-19 |  0.44 |  33.63 |  11.72 |  200 HSCs |  1 HSC |
| SLC38a7 | chr8 |  E13.2_B  |  E13.29_B |  0.56 |  0.13 |  3.06E-20 |  0.43 |  22.21 |  11.72 |  200 HSCs |  1 HSC |
| SLC38a7 | chr8 |  E13.1_B  |  E13.29_B |  0.49 |  0.13 |  1.60E-14 |  0.36 |  25.01 |  11.72 |  200 HSCs |  1 HSC |
| SLC38a7 | chr8 |  E13.29_B |  E6.2_B  |  0.13 |  0.45 |  9.03E-10 |  0.32 |  11.72 |  16.73 |  1 HSC  |  50 HSCs |
| Apba3 | chr10 |  E13.29_B |  E6.43_B |  0.52 |  0.02 |  9.71E-20 |  0.50 |  31.56 |  18.60 |  1 HSC  |  1 HSC |
| Apba3 | chr10 |  E13.29_B |  E15.10_B |  0.52 |  0.05 |  2.04E-29 |  0.47 |  31.56 |  20.35 |  1 HSC  |  1 HSC |
| Apba3 | chr10 |  E6.42_B  |  E6.43_B |  0.48 |  0.02 |  1.26E-18 |  0.46 |  59.59 |  18.60 |  1 HSC  |  1 HSC |
| Apba3 | chr10 |  E13.24_B |  E6.43_B |  0.46 |  0.02 |  9.78E-15 |  0.44 |  31.16 |  18.60 |  1 HSC  |  1 HSC |
| Apba3 | chr10 |  E15.10_B |  E6.42_B |  0.05 |  0.48 |  7.11E-29 |  0.42 |  20.35 |  59.59 |  1 HSC  |  1 HSC |
| Apba3 | chr10 |  E13.24_B |  E15.10_B |  0.46 |  0.05 |  1.55E-20 |  0.40 |  31.16 |  20.35 |  1 HSC  |  1 HSC |
| Apba3 | chr10 |  E15.2_B  |  E6.43_B |  0.60 |  0.02 |  1.84E-26 |  0.58 |  67.69 |  18.60 |  200 HSCs |  1 HSC |
| Apba3 | chr10 |  E13.2_B  |  E6.43_B |  0.57 |  0.02 |  4.05E-24 |  0.55 |  34.72 |  18.60 |  200 HSCs |  1 HSC |

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| Gene    | Chr  | E15.2_B  | E15.10_B   | 0.60 | 0.05 | 2.34E-40 | 0.55 | 67.69 | 20.35 | 200 HSCs | 1 HSC |
|---------|------|-----------|------------|------|------|----------|------|-------|-------|----------|-------|
| Apba3   | chr10| E15.2_B   | E15.10_B   | 0.54 | 0.02 | 4.77E-21 | 0.52 | 33.81 | 18.60 | 200 HSCs | 1 HSC |
| Apba3   | chr10| E6.2_B    | E6.43_B    | 0.54 | 0.02 | 2.04E-18 | 0.52 | 25.21 | 18.60 | 50 HSCs  | 1 HSC |
| Apba3   | chr10| E13.2_B   | E15.10_B   | 0.57 | 0.05 | 4.62E-37 | 0.51 | 34.72 | 20.35 | 200 HSCs | 1 HSC |
| Apba3   | chr10| E6.1_B    | E6.43_B    | 0.53 | 0.02 | 3.08E-22 | 0.51 | 53.93 | 18.60 | 50 HSCs  | 1 HSC |
| Apba3   | chr10| E13.1_B   | E15.10_B   | 0.54 | 0.05 | 1.21E-31 | 0.48 | 33.81 | 20.35 | 200 HSCs | 1 HSC |
| Apba3   | chr10| E15.10_B  | E6.1_B     | 0.05 | 0.53 | 9.84E-35 | 0.48 | 20.35 | 53.93 | 1 HSC    | 50 HSCs|
| Apba3   | chr10| E15.10_B  | E6.2_B     | 0.05 | 0.54 | 2.67E-26 | 0.48 | 20.35 | 25.21 | 1 HSC    | 50 HSCs|
| Zfp873  | chr10| E13.1_B   | E6.43_B    | 0.54 | 0.06 | 1.60E-07 | 0.48 | 26.78 | 17.10 | 200 HSCs | 1 HSC |
| Zfp873  | chr10| E6.1_B    | E6.43_B    | 0.52 | 0.06 | 1.39E-07 | 0.46 | 46.67 | 17.10 | 50 HSCs  | 1 HSC |
| Zfp873  | chr10| E15.2_B   | E6.43_B    | 0.52 | 0.06 | 1.52E-06 | 0.45 | 33.69 | 17.10 | 200 HSCs | 1 HSC |
| Zfp873  | chr10| E6.2_B    | E6.43_B    | 0.48 | 0.06 | 4.06E-06 | 0.42 | 45.50 | 17.10 | 50 HSCs  | 1 HSC |
| Flnb    | chr14| E15.10_B  | E6.43_B    | 0.47 | 0.11 | 3.74E-08 | 0.36 | 32.79 | 15.31 | 1 HSC    | 1 HSC |
| Flnb    | chr14| E13.24_B  | E6.43_B    | 0.45 | 0.11 | 1.39E-06 | 0.34 | 26.12 | 15.31 | 1 HSC    | 1 HSC |
| Flnb    | chr14| E6.42_B   | E6.43_B    | 0.40 | 0.11 | 4.40E-06 | 0.29 | 34.86 | 15.31 | 1 HSC    | 1 HSC |
| Flnb    | chr14| E13.29_B  | E15.10_B   | 0.20 | 0.47 | 2.12E-10 | 0.27 | 25.82 | 32.79 | 1 HSC    | 1 HSC |
| Flnb    | chr14| E13.24_B  | E13.29_B   | 0.45 | 0.20 | 9.07E-07 | 0.24 | 26.12 | 25.82 | 1 HSC    | 1 HSC |
| Flnb    | chr14| E13.29_B  | E6.42_B    | 0.20 | 0.40 | 1.40E-06 | 0.20 | 25.82 | 34.86 | 1 HSC    | 1 HSC |
| Flnb    | chr14| E15.2_B   | E6.43_B    | 0.62 | 0.11 | 3.08E-12 | 0.51 | 23.97 | 15.31 | 200 HSCs | 1 HSC |
| Flnb    | chr14| E15.2_B   | E13.29_B   | 0.62 | 0.20 | 7.49E-16 | 0.42 | 23.97 | 25.82 | 200 HSCs | 1 HSC |
| Flnb    | chr14| E13.1_B   | E6.43_B    | 0.52 | 0.11 | 2.38E-10 | 0.41 | 39.50 | 15.31 | 200 HSCs | 1 HSC |
| Flnb    | chr14| E13.2_B   | E6.43_B    | 0.45 | 0.11 | 6.92E-08 | 0.34 | 44.62 | 15.31 | 200 HSCs | 1 HSC |
| Flnb    | chr14| E13.1_B   | E13.29_B   | 0.52 | 0.20 | 6.39E-15 | 0.32 | 39.50 | 25.82 | 200 HSCs | 1 HSC |
| Flnb    | chr14| E6.1_B    | E6.43_B    | 0.41 | 0.11 | 2.80E-06 | 0.30 | 27.33 | 15.31 | 50 HSCs  | 1 HSC |
| Flnb    | chr14| E13.2_B   | E13.29_B   | 0.45 | 0.20 | 1.41E-10 | 0.25 | 44.62 | 25.82 | 200 HSCs | 1 HSC |
| Flnb    | chr14| E13.29_B  | E6.1_B     | 0.20 | 0.41 | 7.56E-07 | 0.21 | 25.82 | 27.33 | 1 HSC    | 50 HSCs|
| Pacsin1 | chr17| E13.24_B  | E6.42_B    | 0.29 | 0.70 | 3.27E-10 | 0.40 | 24.21 | 29.09 | 1 HSC    | 1 HSC |
| Pacsin1 | chr17| E6.42_B   | E6.43_B    | 0.70 | 0.31 | 1.69E-06 | 0.38 | 29.09 | 10.74 | 1 HSC    | 1 HSC |
| Pacsin1 | chr17 | E13.29_B | E6.42_B |  0.32 |  0.70 |  5.11E-11 |  0.37 |  17.04 |  29.09 | 1 HSC | 1 HSC |
|---------|-------|----------|---------|-------|-------|-----------|-------|-------|-------|-------|-------|
| Pacsin1 | chr17 | E13.24_B | E15.10_B |  0.29 |  0.63 |  6.09E-07 |  0.33 |  24.21 |  25.47 | 1 HSC | 1 HSC |
| Pacsin1 | chr17 | E13.29_B | E15.10_B |  0.32 |  0.63 |  3.14E-07 |  0.30 |  17.04 |  25.47 | 1 HSC | 1 HSC |
| Pacsin1 | chr17 | E13.1_B  | E13.24_B |  0.62 |  0.29 |  6.78E-07 |  0.33 |  26.21 |  24.21 | 200 HSCs | 1 HSC |
| Pacsin1 | chr17 | E13.1_B  | E13.29_B |  0.62 |  0.32 |  3.53E-07 |  0.30 |  26.21 |  17.04 | 200 HSCs | 1 HSC |
| Pacsin1 | chr17 | E15.2_B  | E6.42_B  |  0.42 |  0.70 |  1.89E-06 |  0.28 |  26.33 |  29.09 | 200 HSCs | 1 HSC |
**Supplementary Table 5.** Probability of finding AI for any given gene in the monoclonal animals due to somatic indels and single nucleotide variants (null hypothesis). The parameter values based on the literature that are overestimations (as explained in the comments) are shown in bold. We privileged studies of murine cells (references in bold) and used studies on human cells as the second-best option (references in italics). Most parameter values based on assumptions (in italics) are also overestimations. This estimation suggests that not all AI patterns of the 14 genes we identify can be explained by somatic mutations. The most notable example is *Pkp3*, for which we show the probability (which led us to reject the null hypothesis of a genetic mutation explanation for the AI pattern).

| Parameter Description | Value for estimation | Comment | Ref. |
|-----------------------|----------------------|---------|------|
| SNV per HSC (n_s)     | 195                  | Overestimation. We used the HSC with the highest number of mutations (195). The average number is around 105. The animals used for WGS were 8-month old, and ours were <5 months (mutations accumulate over time). | (Druce, 2021) |
| Indels per HSC (n_i)  | 42                   | Overestimation. The HSC with the highest number of mutations (42) was used. The average number is around 26. | |
| Total number of genes expressed by a cell (n_g) | 24,000 | Overestimation. The average number of expressed genes in a given cell is 10,700, but all genes were assumed to be expressed. | (Ramsköld, Wang, Burge, & Sandber, 2009) |
| Intergenic mutations (P_intergenic) | | These mutations were assumed to have no impact on AI. | |
| **Mutations in cis** | | | |
| Impact of indels in exons (P_{iie}) | 1.000 | Overestimation. All indels are assumed to lead to non-sense mediated mRNA decay, which is unlikely. | |
| Impact of indels in introns (P_{iii}) | 0.200 | Overestimation. 20% of indels in introns are assumed to lead to AI, which is unlikely. | |
| Impact of indels in regulatory regions (P_{iir}) | 0.200 | Overestimation. 20% of indels in regulatory regions are assumed to lead to AI, which is unlikely. | |
| Frequency of indels in exons (P_{fie}) | 0.015 | The values were assumed to be identical to the frequencies of SNVs. | |
| Frequency of indels in introns (P_{fii}) | 0.261 | | |
| Frequency of indels in regulatory regions (P_{fir}) | 0.020 | | |
| **Probability of impactful cis indel in a given gene (P_{cis})** | \(1 - (1 - P_{fie} P_{fii} n_g) (1 - P_{iie} P_{iii} n_g) (1 - P_{iir} P_{fir} n_g))^{m} \) | \(1.25 \times 10^{-4} \) | (Druce, 2021) |
| Impact on transcription of SNVs in exons (P_{iex}) | 0.061 | Empirical frequency of premature stop codons. | (Druce, 2021) |
| Impact on transcription SNVs in introns (P_{iin}) | 0.200 | 20% of SNVs in introns are assumed to lead to AI, which is unlikely. | |
**Impact on transcription SNVs in regulatory regions (P_{isr})**

| Impact on transcription SNVs in regulatory regions (P_{isr}) | 0.200 |
|-------------------------------------------------------------|-------|
| 20% of SNVs in regulatory regions are assumed to lead to AI, which is unlikely. |

**Frequency of SNVS in exons (P_{fse})**

| Frequency of SNVS in exons (P_{fse}) | 0.015 |
|--------------------------------------|-------|
| Empirical estimations. (Druce, 2021) |

**Frequency of SNVs in introns (P_{fsi})**

| Frequency of SNVs in introns (P_{fsi}) | 0.261 |
|----------------------------------------|-------|
| |

**Frequency of SNVs in regulatory regions (P_{fsr})**

| Frequency of SNVs in regulatory regions (P_{fsr}) | 0.020 |
|--------------------------------------------------|-------|
| |

**Probability of impactful cis SNV in a given gene (P_{scis})**

| Probability of impactful cis SNV in a given gene (P_{scis}) | 1-(1-P_{fsi}^{1-n/2}) = (1-P_{fsi}^{1-n/2})^{1-n/2} |
|-------------------------------------------------------------|------------------------------------------------------|
| 4.64*10^{-4}                                                |                                                      |

**Mutations in trans**

**Transcription factors**

| Number of transcription factors | 1,500 |
|---------------------------------|-------|
| (Zhou, Liu, Xia, Gong, Feng, Liu et al., 2017) |

**Probability of affecting transcription in trans. Only mutations changing the protein (exonic non-synonymous) were assumed to impact the transcription of a gene in trans (if they affect a region of the protein that interacts with the alleles) (P_{TFtrans})**

| Probability of affecting transcription in trans. Only mutations changing the protein (exonic non-synonymous) were assumed to impact the transcription of a gene in trans (if they affect a region of the protein that interacts with the alleles) (P_{TFtrans}) | 0.2 |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|
| Overestimation. Gene-specific transcription factors are relatively small (~50 kDa/1.35 kb). Promoters typically recognize binding sites of 10 bp (5-31 bp). The homeobox sequence encodes the homeodomain, a globular domain of about 60 amino acids that normally functions as a DNA-binding domain. That's roughly 13% of the TF. |

**Probability of interfering with AI (if the mutation and SNP are close) (P_{TFtransAI})**

| Probability of interfering with AI (if the mutation and SNP are close) (P_{TFtransAI}) | 0.5 |
|--------------------------------------------------------------------------------------------|-------|
| Overestimation.                                                                          |

**Number of transcription factors regulating a gene (n_{tfg})**

| Number of transcription factors regulating a gene (n_{tfg}) | 58 |
|-------------------------------------------------------------|---|
| Overestimation. 90% of genes have between 0 and 26 transcription factor binding sites. The maximum number is 58. (Hurst, Sachenkova, Daub, Forrest, Huminecki, 2014) |

**Probability of impactful mutation from a transcription factor gene (P_{TFtrans})**

| Probability of impactful mutation from a transcription factor gene (P_{TFtrans}) | 1-(1-P_{fsi} * P_{TFtrans}^{1-n/2}) |
|-------------------------------------------------------------------------------|-----------------------------------|
| 1.95*10^{-4}                                                                | 0.2 |

**RNA binding proteins**

| Number of RNA binding proteins | 1,870 |
|--------------------------------|-------|
| The database contains 292 mouse RNA-seq datasets for a comprehensive list of 187 RNA-binding proteins (RBPs). These RBPs account for only 10% of all known RBPs annotated in Gene Ontology, indicating that most are still unexplored using high-throughput sequencing. (Li, Deng, Vieira, Thomas, Costa, Tseng et al., 2018) |

**Assume only mutations changing the protein (exonic non-synonymous) can impact the transcription of a gene in cis if they affect a region of the protein that interacts with the SNP distinguishing the two alleles. (P_{RNAptrans})**

| Assume only mutations changing the protein (exonic non-synonymous) can impact the transcription of a gene in cis if they affect a region of the protein that interacts with the SNP distinguishing the two alleles. (P_{RNAptrans}) | 0.2 |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------|
| |

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| Probability of interfering with AI (if the mutation and SNP are close) \((P_{RNA\text{ptrans}AI})\) | 0.1 |
|---|---|
| Number of RNA binding proteins regulating a gene \(\left(n_{\text{rnap}}\right)\) | 197 |
| On average, a human mRNA transcript has 197 RBP binding sites (median 85 binding sites). | |
| **Probability of impactful mutation from an RNA protein gene** \((P_{RNA\text{ptrans}})\) \(= 1 - (1 - P_{icis}^* P_{scis}^* P_{Tf\text{trans}}^* P_{RNA\text{ptrans}AI}) \left(1 - P_{ise}^* P_{RNA\text{ptrans}}^* P_{RNA\text{ptrans}AI}^* n_{\text{rnap}} / n_{\text{g}} \right)^n \) | \(1.38 \times 10^{-4}\) |
| **REGULATORY RNAs** (miRNA, snRNA, miscellaneous small noncoding, and lncRNA) | |
| The number of RNA regulatory RNAs \(\left(n_{\text{rnareg}}\right)\) | 3,918 |
| (Isakova, Fehlmann, Keller, & Quake, 2020; Zhou, Wan, Jiang, Liu, Qiang, & Sun, 2020) |
| Assume only mutations changing the RNA (exonic) can impact the transcription of a gene in cis if they affect a region of the RNA that interacts with the two alleles \((P_{RNA\text{regtrans}})\) | 0.15 |
| Informed assumption. |
| Probability of interfering with AI (if the mutation and SNP are close) \((P_{RNA\text{regtrans}AI})\) | 0.5 |
| Overestimation. |
| The average number of regulatory RNAs regulating a gene \(\left(n_{\text{rnareg}}\right)\) | 195 |
| (Genmarino, D'Angelo, Dharmalingam, Fernandez, Russolillo, Sanges et al., 2012) |
| **Probability of impactful mutation from a regulatory RNA gene** \((P_{RNA\text{regtrans}})\) \(= 1 - (1 - P_{icis}^* P_{scis}^* P_{Tf\text{trans}}^* P_{RNA\text{regtrans}AI}) \left(1 - P_{ise}^* P_{RNA\text{regtrans}}^* P_{RNA\text{regtrans}AI}^* n_{\text{rnareg}} / n_{\text{g}} \right)^n \) | \(4.92 \times 10^{-4}\) |
| **PROBABILITY OF AT LEAST ONE MUTATION IMPACTING AI IN A GIVEN GENE** \((P_{AI})\) \(= 1 - (1 - P_{icis}^*)(1 - P_{scis}^*)(1 - P_{Tf\text{trans}}^*)(1 - P_{RNA\text{ptrans}}^*)(1 - P_{RNA\text{regtrans}}^*)\) | \(1.41 \times 10^{-3}\) |
| Considering \(P_{AI}\) and the binomial distribution, the probability of finding 4 animals in 5 with an AI deviating from 0.5 (in any direction) for a given gene (as observed for \(Pkp3\)) is: | |
| 0.001 alpha value with Bonferroni correction for the total number of analyzed genes (7,088) is \(1.4 \times 10^{-6}\) | 1.97 \times 10^{-11}\) |
Supplementary Table 6. Pkp3 AI data from the 28 libraries. We emphasize the concordance of the AI data between replicas of the same samples (3rd and 4th columns; $r^2=0.987$, $P= 1.577\times10^{-14}$) and between B and T cells (AI average, in red; $r^2=0.976$, $P= 0.0123$) from the same animal (E13, in bold). The dispersion (standard deviation) of the monoclonal and polyclonal AI values for B cells is distinct (asterisks, F test, P-value = 0.0155).

| Clonality     | Sample  | AI 1     | AI 2     | Average | Mean  | STD  |
|---------------|---------|----------|----------|---------|-------|------|
| **B cells**   |         |          |          |         |       |      |
| nonclonal     | Control | 0.426    | 0.472    | 0.449   | -     | -    |
| monoclonal    | E13.1   | 0.451    | 0.431    | 0.441   |       |      |
|               | E13.2   | 0.397    | 0.392    | 0.394   |       |      |
|               | E6.1    | 0.313    | 0.323    | 0.318   |       |      |
|               | E6.2    | 0.467    | 0.432    | 0.450   |       |      |
|               | E15.2   | 0.560    | 0.554    | 0.557   |       |      |
| polyclonal    | E13.24  | 0.417    | 0.435    | 0.426   | 0.380 | 0.373* |
|               | E13.29  | 0.946    | 0.939    | 0.943   |       |      |
|               | E6.42   | 0.148    | 0.101    | 0.124   |       |      |
|               | E6.43   | 0.842    | 0.830    | 0.836   |       |      |
|               | E15.10  | 0.176    | 0.185    | 0.181   |       |      |
| **T cells**   |         |          |          |         |       |      |
| nonclonal     | Control | 0.432    | 0.478    | 0.455   | -     | -    |
| polyclonal    | E13.1   | 0.531    | 0.535    | 0.533   | 0.464 | 0.097 |
|               | E13.2   | 0.370    | 0.421    | 0.395   |       |      |
| monoclonal    | E13.24  | 0.433    | 0.411    | 0.422   | 0.708 | 0.404 |
|               | E13.29  | 0.987    | 1.000    | 0.994   |       |      |
Supplementary Figures

**Supplementary Figure 1.** Ly5.1 and Ly5.2 pan-leukocytic markers were used to distinguish recipient and donor cells in reconstituted animals, respectively. Ly5.1 and Ly5.2 do not label the CAST progenitor line, and when CAST is crossed with B6\textsuperscript{Ly5.1/Ly5.1} or B6\textsuperscript{Ly5.2/Ly5.2} to produce the recipient and donor F1 animals, respectively, the recipient and donor cells are distinguishable by these two markers. Blood samples of progenitor and descendants (F1) were lysed for red cells, stained with FITC-conjugated anti-Ly5.2 and PE-conjugated anti-Ly5.1, and analyzed using FACSCanto.
**Supplementary Figure 2.** Percentages of chimerism identified in the blood of reconstituted animals for 16 experiments at 12 weeks post-injection (orange dots, monoclonal animals; blue dots, polyclonal animals). An animal was considered reconstituted if the chimerism percentage was above 1%. The sequenced samples in this study belong to experiments 6, 13, and 15 (marked with asterisk (*)).
Supplementary Figure 3. Representative plots of pre-sorted and post-sorted B/T-cell populations of an animal reconstituted with a single HSC. Cells from the spleen and thymus of recipient animals were isolated, stained for B-cell markers with PE anti-Ly5.2, FITC anti-Ly5.1, and PE-Cy7 anti-CD19 and APC anti-IgM (spleocytes), or T-cell markers with PE-Cy7 anti-CD4 and BV605 anti-CD8 (thymocytes), and sorted on a FACS Aria. The cells were gated for PI⁻ to exclude dead cells and on Ly5.2⁺/Ly5.1⁻ to obtain pure donor cells, and then for CD19⁺/IgM⁺ to select B-cells or for CD4⁺/CD8⁺ to select for T-cells. The purity of sorted cells was assessed by analyzing 150–250 of the sorted cells.
Supplementary Figure 4. Monoclonality screening was used to confirm if the recipient system was reconstituted with a single HSC. The cDNA Sanger sequencing chromatograms cover a region with two SNPs in the Xist locus that allow us to assign the Xist transcript to the CAST or B6 X chromosome. Due to XCI, when a single cell is used for the reconstitution, a single peak is expected in the position of the SNP; when multiple cells were used for reconstitutions, two peaks should be observed in each of the SNP positions. Samples E6.1, E6.2, E13.1, E13.2 and E13.5 are cells expanded after the injection of multiple HSCs (polyclonal samples), samples E6.42, E6.43, E13.24, E13.29 and E15.10 are cells expanded after the injection of a single HSC (monoclonal samples).
Supplementary Figure 5. Estimation of donor population contamination with recipient cells. (A) Identification and cDNA Sanger sequencing focusing on three different SNPs for the *Ly5* gene that distinguish two pan-leukocytic markers, *Ly5.1* and *Ly5.2*, present in the recipient and donor animals, respectively. CAST and B6 *Ly5.2* loci are indistinguishable, but B6 *Ly5.1* has different variation, allowing the estimation of the level of recipient cell contamination in the sorted donor cell populations. (B) Percentages of recipient cells (Ly5.1+ cells) estimated in the sorted donor cell populations based on next-generation sequencing results. Nucleotide bases for *Ly5.1* and *Ly5.2* were counted for each SNP position. The bar corresponds to the average of two replicates. The dashed line (0.5%) represents the percentage of artifactual SNPs due to errors introduced by sequencing, which was estimated by sequencing of an unmanipulated donor mouse.
Supplementary Figure 6. Imprinted genes expressed in B cells or T cells in this study. The list of imprinted genes was retrieved from [https://www.geneimprint.com](https://www.geneimprint.com) and from Tucci et al., 2019. A total of 66 imprinted genes were expressed (55 in B cells and 62 in T cells), out of 167 imprinted genes discoverable in the annotation file used in this study (ftp://ftp.ensembl.org/pub/release-68/gtf/Mus_musculus.GRCm38.68.gtf). Genes highlighted in purple are randomly biased in B cells and T cells. Genes highlighted in light blue or light red could have tissue-specific interest, although not necessarily reaching our criteria for “randomly biased”. Genes in bold were classified as randomly biased. Genes with low expression levels (<10 TMM-normalized counts) and genes suspected of LOH (detected by WES) were not included. This figure is related to Supplementary Table 2.
Supplementary Figure 7. Identification of XCI escapees. (A), (B) AI of X-linked genes for B and T cells. As a convention, an AI=1 means that the gene is 100% expressed from the allele of the inactive chromosome X (Xi); Xi allelic imbalance=1 means that the gene is 100% expressed from the inactive X-linked allele; Xi allelic imbalance=0 means that only the active X-linked allele was detected. Dots represent genes with expression higher than 10 TMM-normalized counts and only genes that were statistically different from the threshold at least once are shown. Yellow dots represent monoclonal samples; dotted violet stroke surrounding yellow dots denote statistical significance for that sample. Red dots represent the median of the AI observed for polyclonal and control samples (which are otherwise excluded from this top panel). Statistical significance was calculated by comparison of the AI with the sample-corrected threshold using binomial test and QCC correction. The threshold was calculated per sample, as 0.1 (which is the value usually found in the literature) + the value of the median of AI of all X-linked genes in the sample. (C), (D) Abundance (TMM-normalized counts) of the same genes and same samples represented in (A), (B). In addition, individual polyclonal and control samples are shown, as well as samples with abundance <10. Violet dots represent the monoclonal samples in which the AI significantly deviates from the sample-corrected threshold. Yellow dots represent the other monoclonal samples, blue dots, the polyclonal samples, and black dots are the control samples. Genes in violet (x-axis) were identified as escapees using three criteria: 1) only samples with abundance higher than 10 were considered; 2) the median of AI in the control samples (polyclonal and control samples) was balanced (0.5±0.2); and 3) the AI of the gene is statistically different from the threshold in at least two samples, irrespective of the tissue.
Supplementary Figure 8. Pairwise comparisons of AI between animals for B and T cells, with values of Pearson’s coefficient correlation and the number of genes with a significant differential AI after applying QCC correction on the binomial tests. Abundance values are TMM-normalized counts.
Supplementary Figure 9. Dot plot showing the AI standard deviation (SD) of five B-cell monoclonal samples (x-axis) against the AI SD of five polyclonal samples (y-axis). Dashed vertical and horizontal lines - arbitrarily set at an AI SD of 0.15 - represent the threshold above which genes were considered as potentially intrinsically imbalanced. Dots represent genes, black-circled dots highlight genes with the highest AI variance among monoclonal samples in the autosomes (from Figure 4A), while pink-circled dots denote the X-linked genes (control). In contrast to Figure 4A, here are shown all genes, and not only those statistically significant after QCC correction in at least one pairwise comparison (see Figure 3 and Supplementary Figure 8 - grey genes are included, not only the ones with at least one red dot). As in Figure 4A, only genes expressed in all the 10 B-cell samples were kept, and genes with evidence of nonrandom (genetic or imprinted) AI were excluded.
Supplementary Figure 10. Pairwise comparisons of AI between Abelson-immortalized B-cell clones, with values of Pearson’s coefficient correlation and the number of genes with a significant differential AI after applying QCC correction on the binomial tests. Abundance values are TMM-normalized counts.
Supplementary Figure 11. Location of 14 genes with persistent clone- and allele-specific autosomal transcriptional states across distributions of locus size, open reading frame (ORF) size, and expression in long-term hematopoietic stem cells (LT-HSCs), including all protein-coding genes. Gene sizes were obtained from the latest release of the gencode mouse genome annotations downloaded GTF file (http://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_mouse/release_M27/gencode.vM27.annotation.gtf.gz) with custom scripts. ORFs were generated from the downloaded gencode transcript
sequences fasta file (https://ftp.ebi.ac.uk/pub/databases/gencode/Gencode_mouse/release_M27/gencode.vM27.transcripts.fa.gz) using the orfipy tool (Singh & Wurtele, 2021) with the standard codon table and default parameters. The longest ORF for each gene was plotted for distribution. Expression in LT-HSC was obtained from the Immunological Genome Project (https://www.immgen.org/), GEO:GSE109125. *Locus* and expression plots were zoomed-in for more fitting representation. The blue lines correspond to genes with stable allele-specific transcription through HSC differentiation and the red line corresponds to the gene *Pkp3*. 
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