

## SKEWED X-INACTIVATION: CAUSES AND ITS IMPACT ON DISEASE

Skewed X inactivation can lead to the manifestation of X-linked disorders in heterozygous females. But what actually drives this skewing? A review in *Nature Reviews Genetics* (1) proposes that heterozygous variants can give cells a competitive advantage or disadvantage, that creates clonal competition between cells expressing one or the other X chromosome. The paper explores how these selective forces shape development and influence disease expression.

### Reported examples

- **STAG2 variants:** In mouse models, STAG2-variant clones contribute normally to many tissues but are excluded from the lymphoid lineage when competing with wild-type clones. Notably, these same variants can produce full lymphocyte lineages when no wild-type competitors are present, showing that the disadvantage is relative, not intrinsic [2].
- **HDAC8 and STAG2 in humans:** Female carriers of heterozygous mutations frequently show strong skewing in blood in favor of the X chromosome with the wild-type allele, consistent with selection against clones expressing the mutant variant [2].
- **Immunodeficiency genes (IL2RG, BTK, WAS, NEMO):** These X-linked mutations impair the survival or maturation of specific immune cell types. In heterozygous females, only clones expressing the wild-type allele can complete lymphocyte development, producing dramatic skewing driven by cell-intrinsic fitness differences [2] [2].
- **ABCD1 (X-linked adrenoleukodystrophy):** Interestingly, in this case blood cells skew toward the mutant allele, even though the disease manifests in the brain. This shows that competition and skewing are tissue-specific, and that selection in one compartment (blood) does not predict disease risk in another (brain microglia) [2].

Overall, the article argues that skewed X inactivation often reflects underlying competitive interactions between clones with different X-linked alleles. Rare variants, tissue-specific fitness effects, and developmental bottlenecks collectively determine which clones dominate. These processes may modulate the severity of X-linked diseases in females and shape X-linked genetic diversity in human populations.

1. <https://www.nature.com/articles/s41576-025-00840-3>