a,

b,

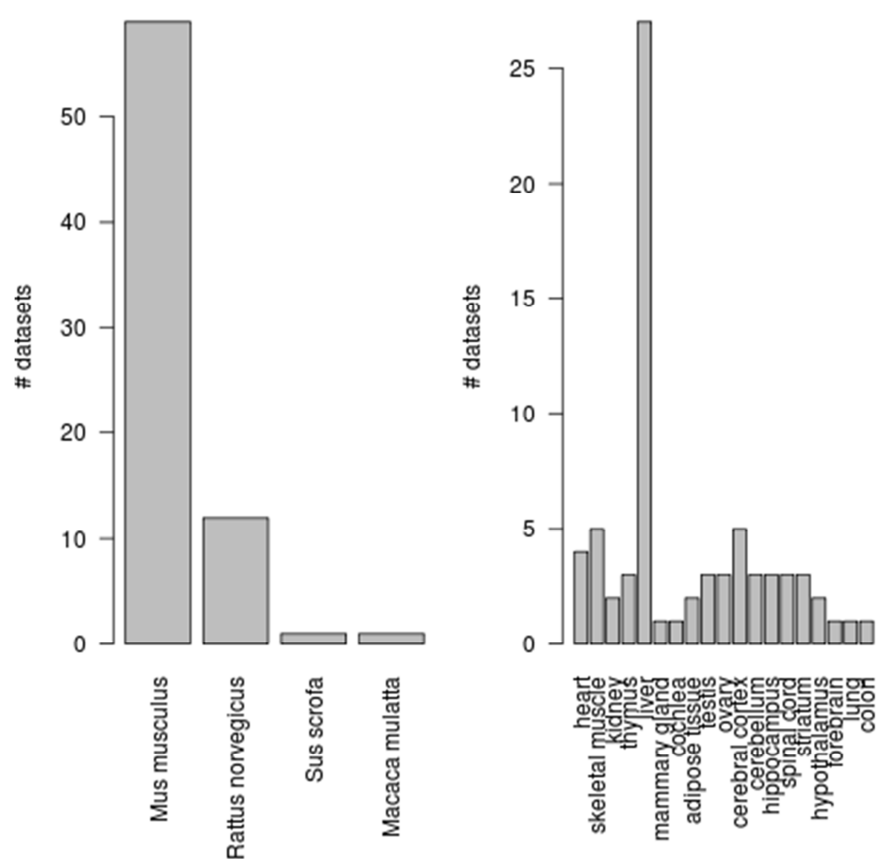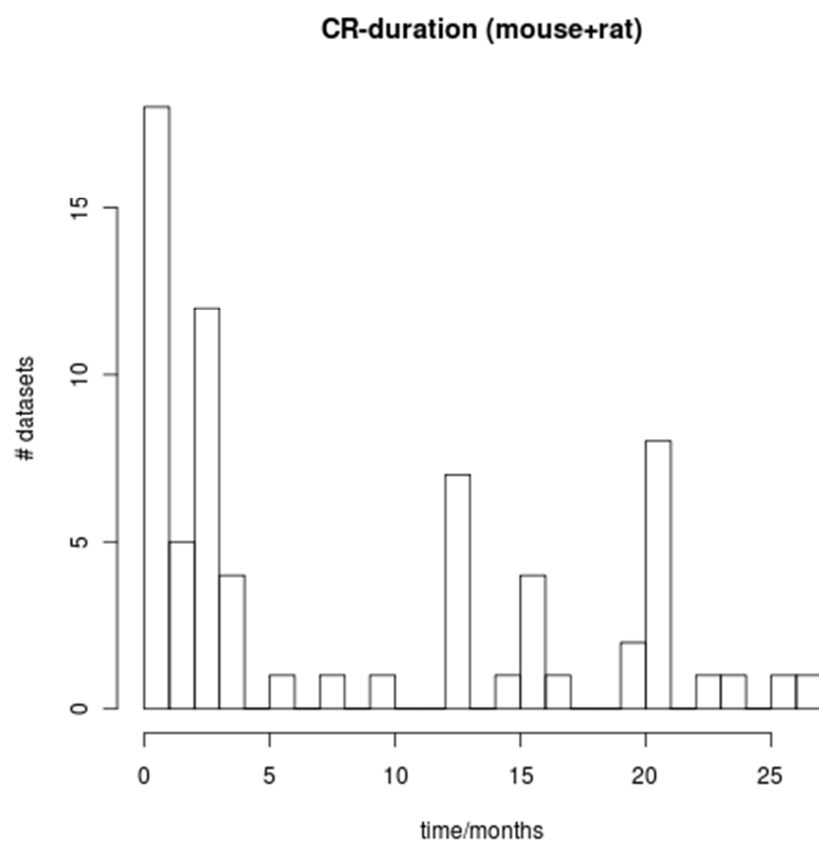**CR-duration (mouse+rat)**
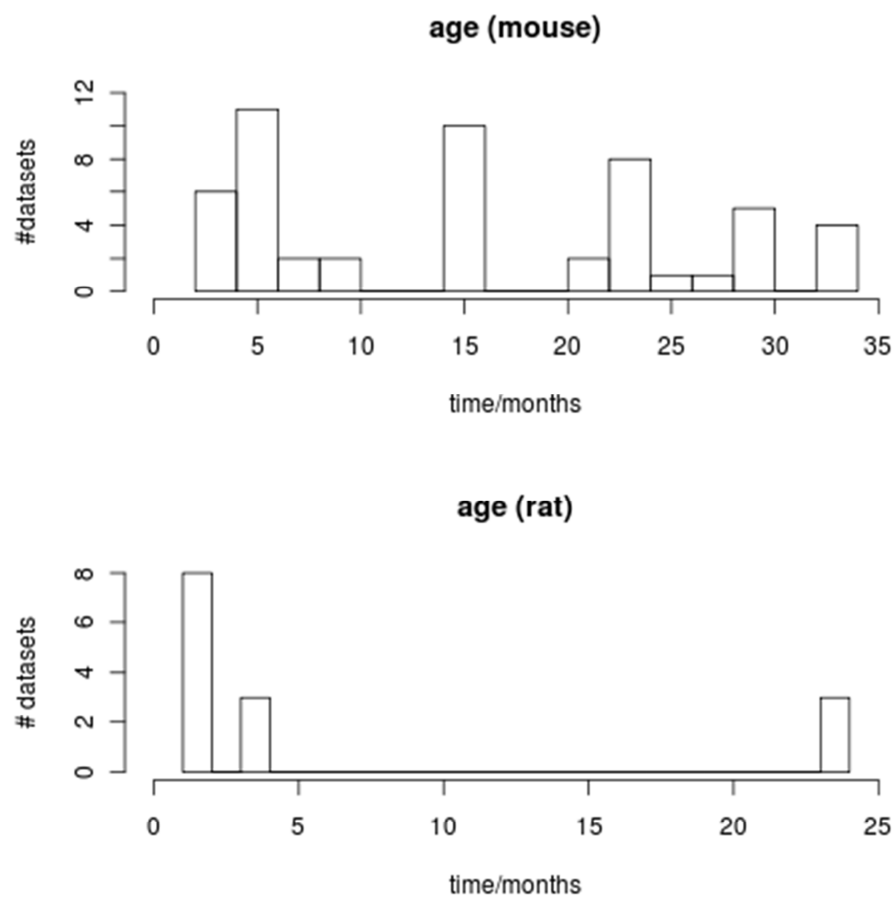
c,

age (mouse)

age (rat)

Fig. S1: Distribution of datasets used in the meta-analysis over (a,) organism and tissue, (b,) duration of CR (only for mouse and rat data) and (c,) age (separately for mouse and rat).
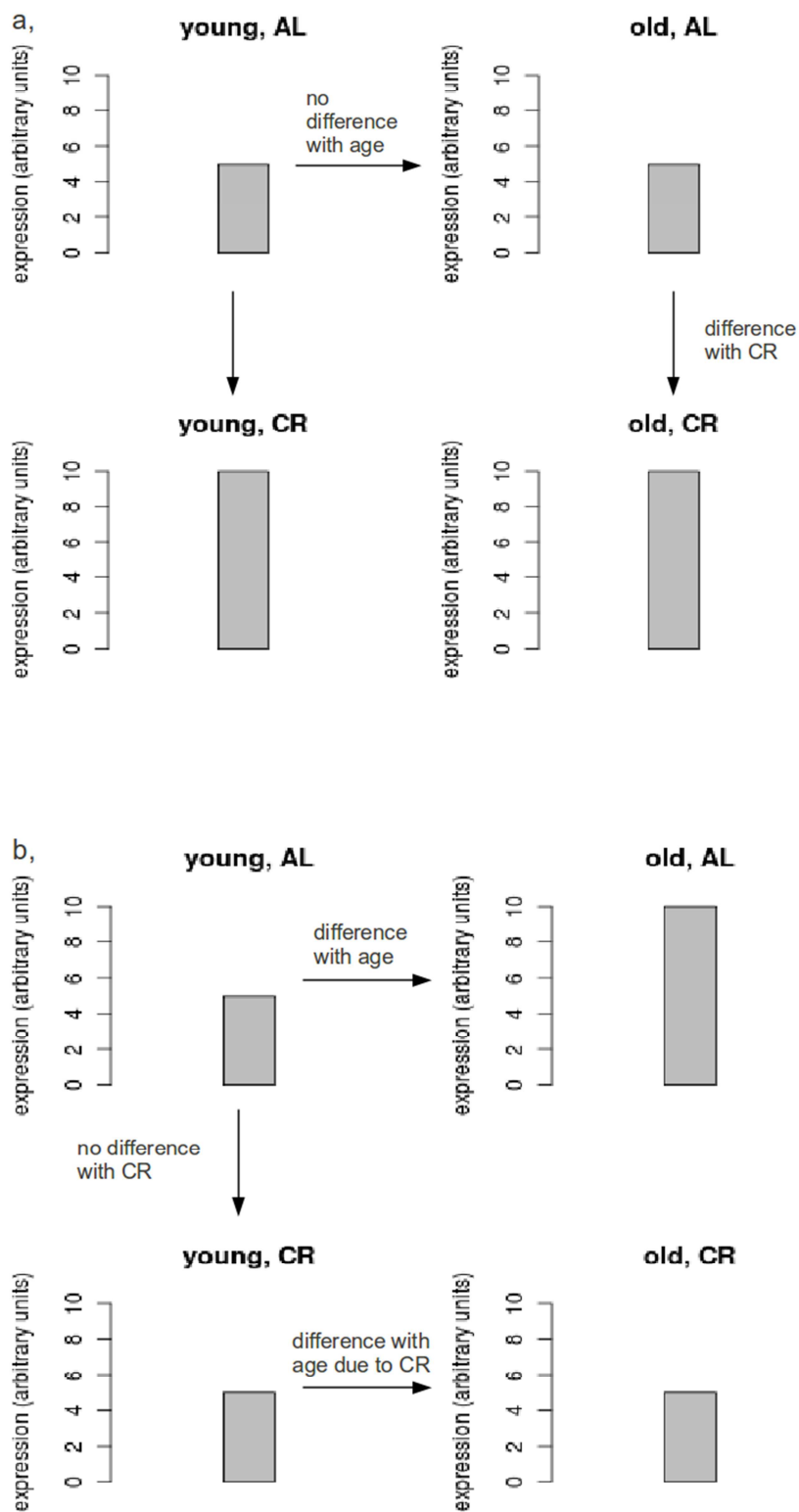
Fig. S2: Example demonstrating the reasoning, why genes differentially expressed with age were excluded. a, No differential expression with age, but with CR; this gene is expected to contribute as mechanistic reason to the effect of CR; b, Difference between old AL and old CR, because the gene is differentially expressed with age under AL, but not CR conditions; this gene is expected to be differentially expressed only as an effect of CR

a,																																							
EntrezID

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22390
26358
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56794
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64209
66277
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66350
66968
67460
68241
68396
69083
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70273
70807
71760
73095
74147
74156
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77027
80290
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93671
171282
209039
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384783
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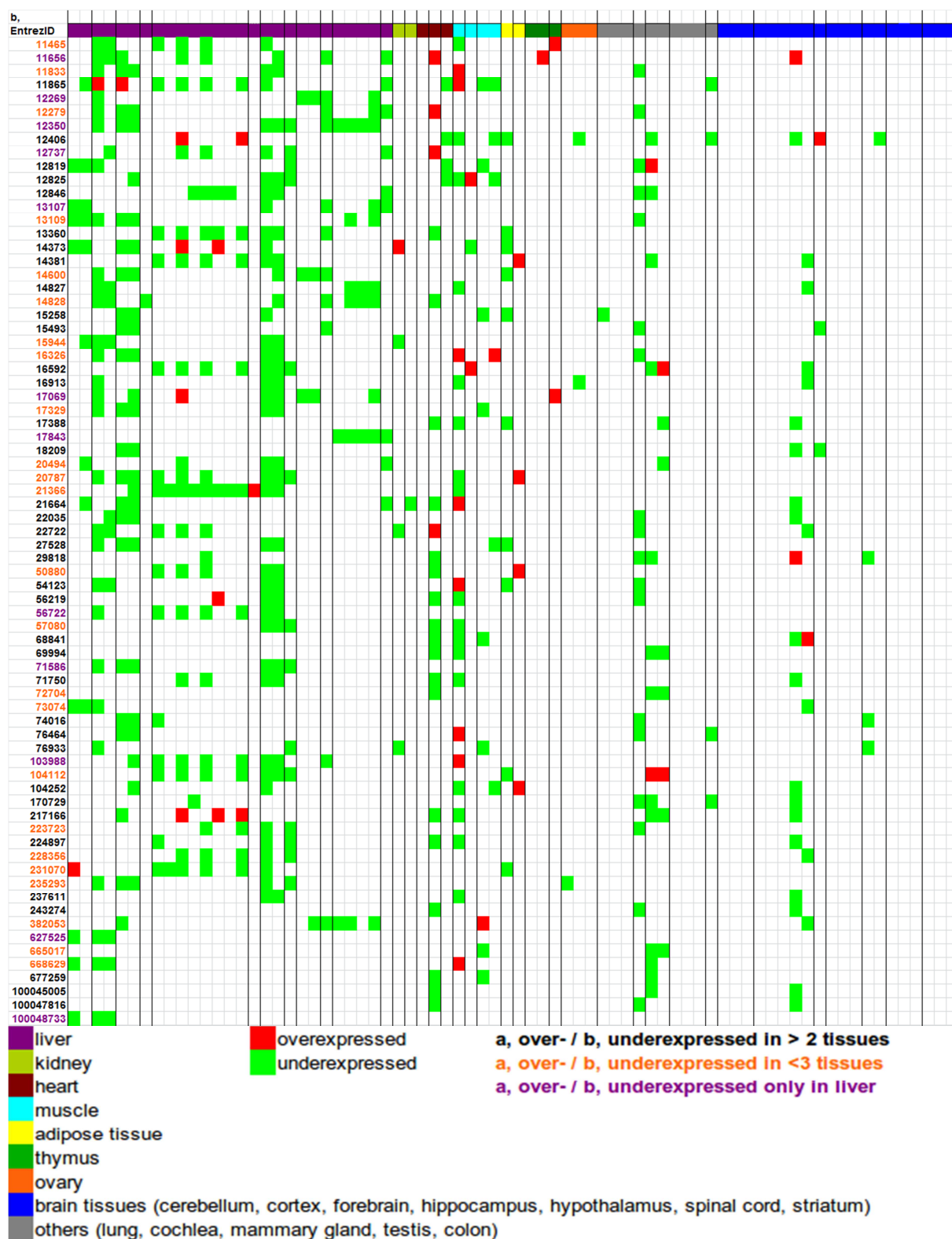100042570
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Fig S.3: Matrix view of genes (rows) vs. datasets (columns) for genes enriched for a, overexpression and b, underexpression. Red fields indicate over-, green underexpression (p<0.05, effect size >1.5-fold). See legend for color coding of different tissues in the top row. For brain tissues and "others" black vertical lines seperate datasets from different tissues, for all other tissues datasets from different studies. Font colors in the first column: black: the gene is (a,) over- / (b,) underexpressed in at least 3 different tissues; orange: the gene is (a,) over- / (b,) underexpressed in less than 3 different tissues; purple: the gene is only differentially expressed in tissues liver.
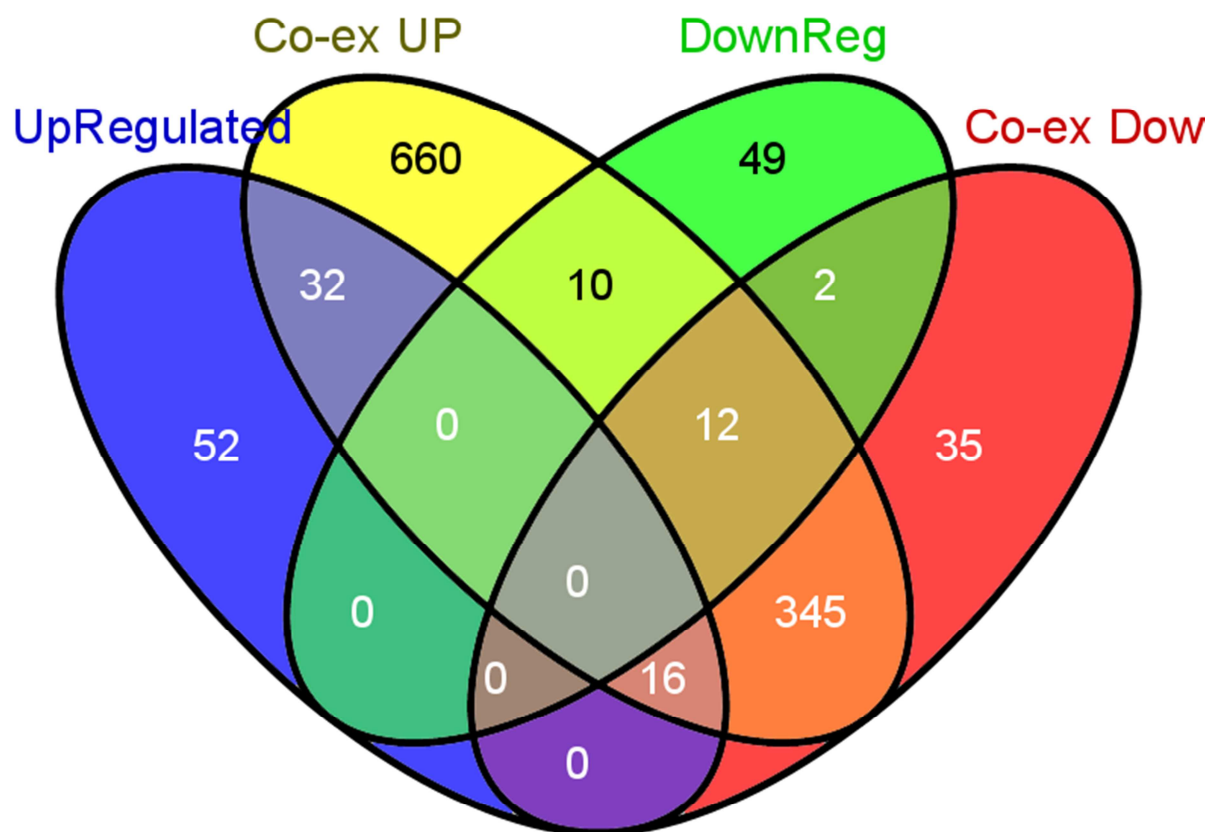
Fig. S4: Overlaps between overexpressed, underexepressed genes and their co-expressed genes with respect to each other.