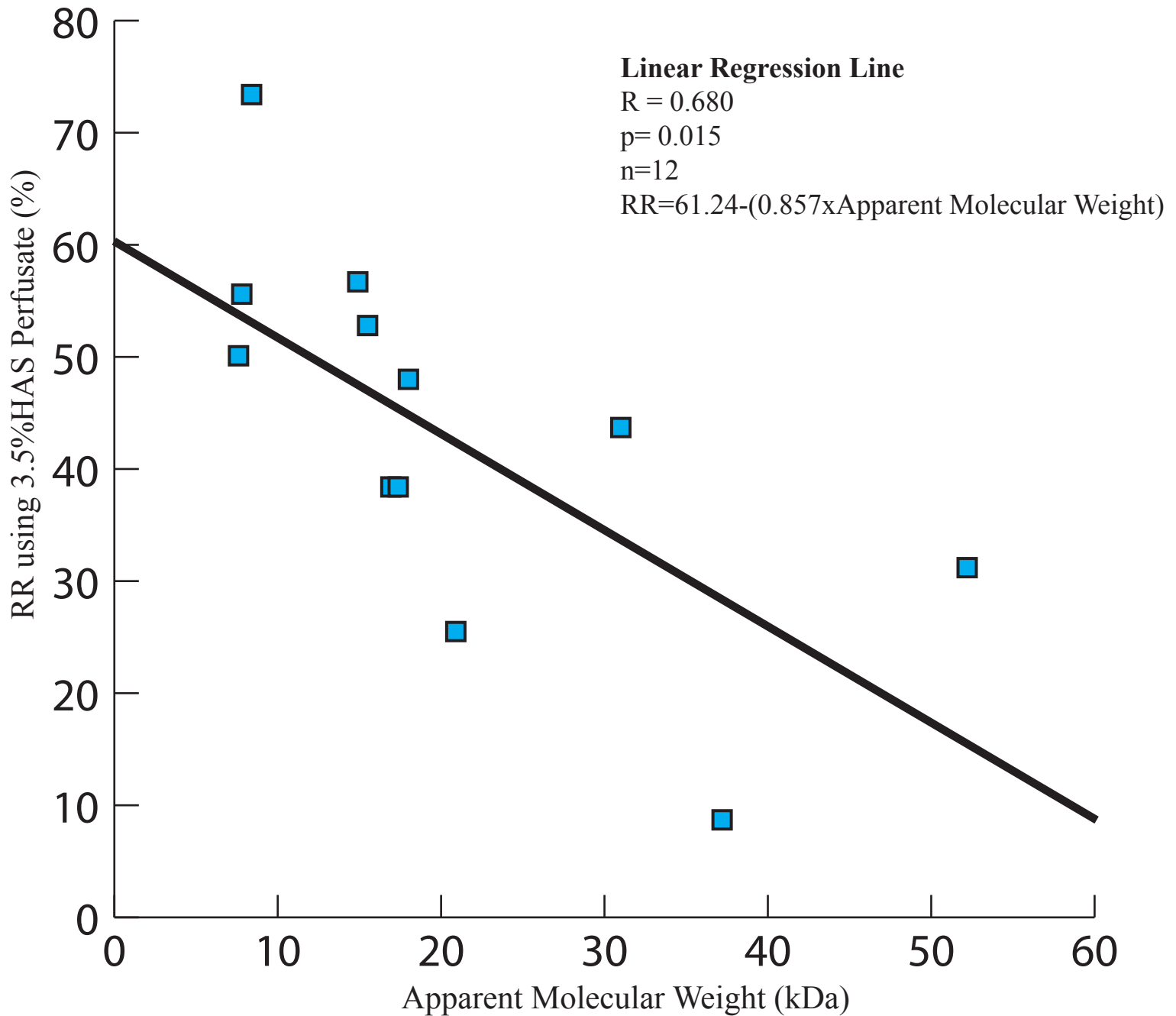


Estimation of 3.5% HAS perfusate RR based on previous *in vitro* data



Supplementary Figure 4: Estimation of RR based on previous *in vitro* data

The scatter plot is derived from empirical *in vitro* data from Figure 6, Helmy et al, 2009. RR was determined for a panel of 12 cytokines (IL1a, IL1b, IL1ra, IL2, IL4, IL6, IL8, IL10, IL17, TNF, MIPa1, MIP1b). Apparent molecular weight is the molecular weight of each cytokine taking into account any dimerisation/trimerisation. The linear regression line has been used to estimate RR for those cytokines where no *in vitro* data exists. The p-value derives from an ANOVA. The apparent molecular weights (kDa) for the additional cytokines, where no *in vitro* recovery data are available, are reproduced below. The estimated RR values are shown in table 4 in the manuscript.

Cytokine	Cytokine	Cytokine	Cytokine	Cytokine	
EGF	6.2	IL3	15.0	MCP3	9.0
Eotaxin	8.3	IL5	26.0	MDC	8.0
FGF2	17.2	IL7	17.4	PDGFAA	28.5
Flt3lig	17.6	IL9	14.0	PDGFAB/BB	24.9
Fractalkine	8.5	IL12p40	40.0	RANTES	7.8
GCSF	18.7	IL12p70	70.0	sCD40L	18.0
GMCSF	14.6	IL13	12.5	sIL2R	31.0
GRO	7.8	IL15	14.0	TGFa	5.5
IFNa2	19.2	IP10	8.5	TNFb	55.8 (trimer)
IFNg	16.7	MCP1	8.6	VEGF	66.6