Silencing *KRIT1* Partially Reverses the Effects of Disturbed Flow on the Endothelial Cell Transcriptome

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Running title: Silencing endothelial cell *KRIT1* under disturbed flow.

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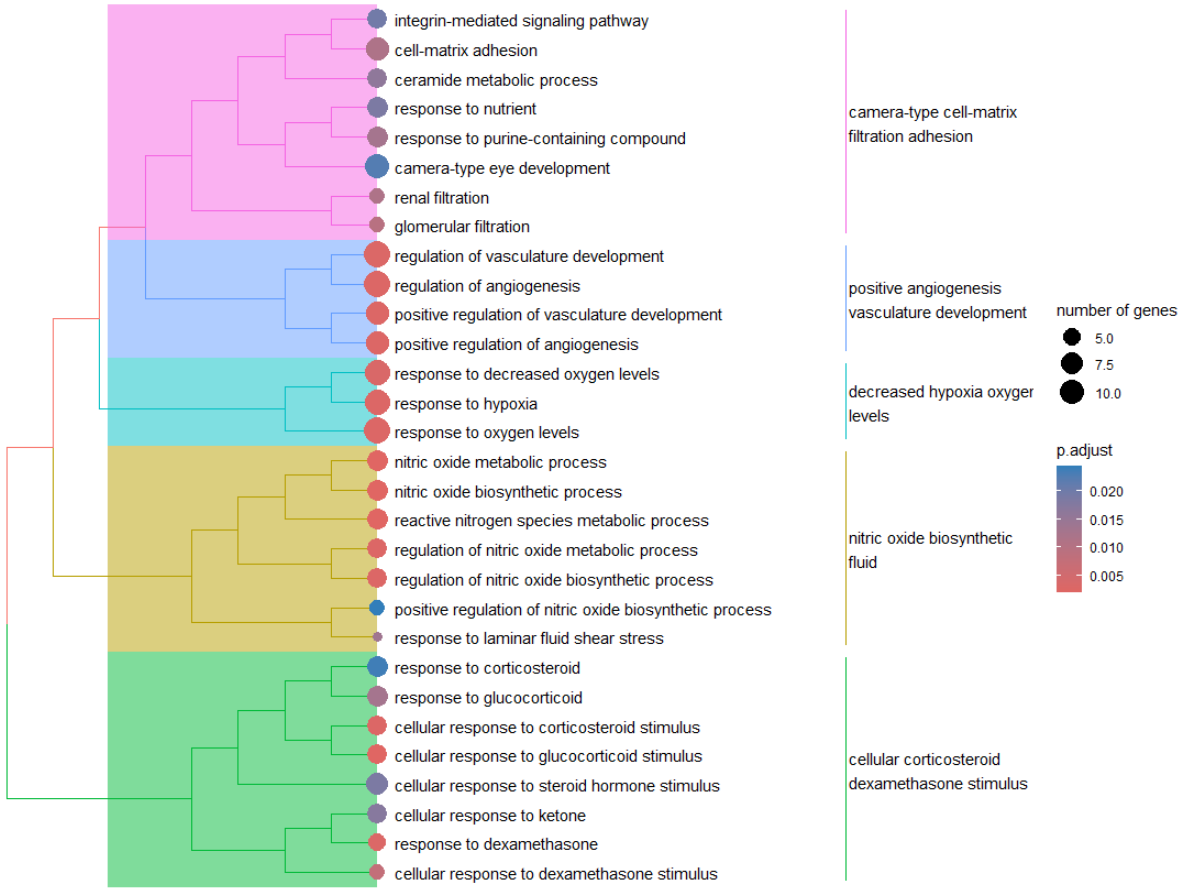
The authors declare no conflict of interest.

Supplemental



Supplemental Figure 1. Integration of significantly enriched pathways. Visualisation of pathway enrichment analysis. Tree plot clustering significantly enriched pathways using 'clusterprofiler'. Genes overlapping in different pathways are adjusted for revealing 5 distinct branches used as the basis for heatmaps in Figure 2B.

Supplemental Table 1. Primer Sequences

Primer	Sequence
huKrit1 Fwd	CCA TCG TAC CTG TTA CCA AAC T
huKrit1 Rev	ACT GAC ACC TTC ACT TGT ACT G
hu KLF2 Fwd	AGA CCA CGA TCC TCC TTG A
hu KLF2 Rev	TCA CAA GCC TCG ATC CTC TA
hu KLF4 Fwd	GGT CTG TGA CTG GAT CTT CTA TC
hu KLF4 Rev	ACC CTG ATA TCC ACA ACT TCC
hu eNOS Fwd	CAT CAC CAG GAA GAA GAC CTT TA
hu eNOS Rev	TAC AGG ATT GTC GCC TTC AC

Supplemental Table 2. Differential expression analysis of key genes, those associated with inflammation and endothelial cell activation.

	Scr Os vs PS		Krit1 OS vs PS		Scr OS vs Krit1 OS		Scr PS vs Krit1 PS		Scr Stat vs Krit1 Stat	
	P VALUE	LOG2FOLD CHANGE	P VALUE	LOG2FOLDC HANGE	P VALUE	LOG2FOLDC HANGE	P VALUE	LOG2FOLD CHANGE	P VALUE	LOG2FOLD CHANGE
KRIT1	0.891	0.084	0.002	-1.545	<0.001	-1.534	<0.001	-1.461	<0.001	-1.781
NOS3	<0.001	1.247	0.405	-0.399	<0.001	1.551	<0.001	0.848	<0.001	1.240
KLF2	<0.001	4.768	<0.001	-3.761	<0.001	4.403	0.030	1.007	<0.001	4.756
KLF4	<0.001	3.612	0.011	-1.924	<0.001	3.871	<0.001	1.688	<0.001	5.140
MCP1	0.485	-0.733	0.959	-0.213	0.407	-0.751	0.260	-0.946	<0.001	-3.529
VCAM1	<0.001	0.847	0.434	-0.278	<0.001	1.081	<0.001	0.569	<0.001	0.803
ICAM1	0.163	1.079	0.564	-1.098	0.006	1.742	0.993	-0.018	0.006	-1.725
SELE	0.400	-0.876	0.794	-0.715	0.050	-1.539	0.041	-1.591	<0.001	-5.659
SELP	0.897	0.196	0.100	-2.417	0.238	-0.912	0.001	-2.221	0.187	0.981
CXCL8	0.323	-1.482	0.973	0.265	0.185	-1.694	0.384	-1.218	<0.001	-4.747
IL6	0.707	-0.460	0.920	-0.341	0.438	-0.706	0.356	-0.802	0.002	-2.085