Supplementary Tables

Supplementary materials for *Boer C.G., et al., Stratified hand phenotypes identifies WNT9A as novel gene associated with thumb osteoarthritis.*

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Supplementary Tables

Supplementary table 1: human cartilage eQTL summary statistics meta-analysis reults.

	Meta-Analysis				Heterogeneity analysis				
Gene	**Weight (n)**	**Zscore**	**P-value**	**Direction**	**HetISq**	**ChiSq**	**Df**	**P-value**	**Weight (n)**
ARF1	116	-1.81	0.0703	--	0	0.042	1	0.8373	116
C1orf35	116	1.818	0.06901	++	0	0.223	1	0.6369	116
CDC42BPA	116	-0.285	0.776	--	0	0	1	0.9968	116
GJC2	29	1.192	0.2334	?+	0	0	0	1	29
GUK1	116	0.229	0.8192	+-	0	0.215	1	0.6428	116
IBA57	116	2.01	0.04439	++	0	0.81	1	0.3682	116
JMJD4	29	-0.686	0.4928	?-	0	0	0	1	29
LINC01641	.	.	.	.	.	.	.	.	.
MIR3629	.	.	.	.	.	.	.	.	.
MIR5008	29	0.021	0.9832	?+	0	0	0	1	29
MRPL55	116	0.105	0.9165	++	0	0.001	1	0.9727	116
OBSCN	116	0.412	0.6802	++	0	0.015	1	0.9021	116
OBSCN-AS1	.	.	.	.	.	.	.	.	.
PRSS38	29	0.135	0.8925	?+	0	0	0	1	29
SNAP47	29	-1.569	0.1166	?-	0	0	0	1	29
WNT3A	29	-0.123	0.9024	?-	0	0	0	1	29
WNT9A	116	1.273	0.2029	+-	81.8	5.489	1	0.01914	116
ZNF678	116	1.605	0.1085	++	0	0.177	1	0.6738	116

OA: osteoarthritis, SE: standard Error, METAL implements Cochran's Q-test for heterogeneity: Df: degrees of Freedom, ChiSq: Chi-Squared test result of heterogeneity, HetISq: heterogeneity I^2 statistic.

Supplementary table 2: Differential expression in OA cartilage

Differential expression OA preserved vs. OA lesioned cartilage (n=21)

GeneNames	**baseMean**	**FoldChange**	**log2FoldChange**	**SE**	**P-value**	**P-value adjusted (FDR)**
ARF1	1413.89	1.00	$5.7*10^{-03}$	$3.7*10^{-02}$	0.88	0.95
C1orf35	57.34	0.95	$-6.7*10^{-02}$	0.13	0.62	0.82
CDC42BPA	579.25	1.06	$8.9*10^{-02}$	$9.8*10^{-02}$	0.36	0.63
GJC2	6.57	0.67	-0.58	0.23	$1.0*10^{-02}$	$7.4*10^{-02}$
GJC2	16.45	0.78	-0.37	0.23	$8.6*10^{-02}$	0.53
GUK1	697.69	1.02	$2.6*10^{-02}$	0.10	0.80	0.92
IBA57	58.63	0.84	-0.25	0.13	$4.7*10^{-02}$	0.20
JMJD4	129.36	0.97	$-4.7*10^{-02}$	0.11	0.67	0.84
LINC01641	0	1	1.65	2.93	1	1
MIR5008	0.10	1.51	0.60	2.46	0.34	0.87
MRPL55	113.24	1.04	0.057	0.13	0.65	0.84
OBSCN	376.52	0.60	-0.74	0.18	$2,7*10^{-05}$	$7.8*10^{-04}$
OBSCN-AS1	8.94	0.55	-0.86	0.23	$1.8*10^{-04}$	$3.6*10^{-03}$
PRSS38	0.33	0.79	-0,34	2.92	0.64	1
SNAP47	257.91	1.11	0.16	$8.6*10^{-02}$	$7.0*10^{-02}$	0.26
WNT9A	**98.48**	**2.42**	**1.27**	**0.20**	$\mathbf{4.9*10^{-10}}$	$\mathbf{9.4*10^{-08}}$
ZNF678	38.41	1.08	0.11	0.18	0.54	0.77

OA: osteoarthritis, SE: standard Error, BaseMean: mean expression gene (lesioned/preserved cartilage).

Supplementary Table 3: Transcription Factor binding motifs affected by rs11588850

SNV	Chr	Ref	Alt
rs11588850	1	A	G

Transcription Factor	Motif Altered	Ref	Alt	Strand	*WNT9A*	*WNT3A*	*SNAP47*	*JMJD4*
RAD21	Rad21_disc8	9.8	11.2	-	A549 ECC-1 GM12878 H1-hESC HCT116 HCT116 HeLa-S3 HepG2 IMR-90 K562 MCF-7 SK-N-SH	H1-hESC	.	.
AhR/ARNT1 complex	AhR::Arnt_1	10.4	15	-	.	.	.	.
ARNT1	Arnt_1	-14.7	-10.1	+	.	.	.	.